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(54) **Title:** THERAPEUTIC USES OF A C-RAF INHIBITOR

(57) **Abstract:** The present invention relates to the use of a c-Raf inhibitor for use in the treatment of a proliferative disease, particularly a solid tumor that harbors Mitogen-activated protein kinase (MAPK). The present invention also relates to a pharmaceutical combination which comprises (a) at least one antibody molecule (e.g., humanized antibody molecules) that binds to Programmed Death 1 (PD-1), and (b) a c-Raf inhibitor or pharmaceutically acceptable salt thereof. The present invention also relates to such a combination for simultaneous, separate or sequential administration for the treatment of a proliferative disease, particularly a solid tumor that harbors Mitogen-activated protein kinase (MAPK) alteration and a commercial package comprising such a combination.

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THERAPEUTIC USES OF A C-RAF INHIBITOR

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on June 7, 2017, is named PAT057346_SL.TXT and is 190,381 bytes in size.

FIELD OF THE INVENTION

The present invention relates to the use of a c-Raf (C-RAF or CRAF) inhibitor for the treatment of a cancer which is a solid tumor that harbors mitogen-activated protein kinase (MAPK) alterations, such as *KRAS*-mutant tumors, *NRAS*-mutant tumors, and certain *BRAF*-mutant tumors. The c-Raf inhibitor is particularly provided for use in the treatment of a cancer which is selected from *KRAS*-mutant NSCLC (non-small cell lung cancer), *BRAF*-mutant NSCLC (non-small cell lung cancer), *KRAS*-mutant and *BRAF*-mutant NSCLC (non-small cell lung cancer), *KRAS*-mutant ovarian cancer, *BRAF*-mutant ovarian cancer, *KRAS*-mutant and *BRAF*-mutant ovarian cancer, and *NRAS*-mutant melanoma. The present invention also provides the c-Raf inhibitor for use in the treatment of relapsed or refractory *BRAF* V600-mutant melanoma.

The present invention also relates to a pharmaceutical combination which comprises (a) at least one antibody molecule *(e.g.*, humanized antibody molecules) that bind to Programmed Death 1 (PD-1), and (b) a c-Raf (C-RAF or CRAF) inhibitor, said combination for simultaneous, separate or sequential administration for use in the treatment of a proliferative disease, a pharmaceutical composition comprising such combination; a method of treating a subject having a proliferative disease comprising administration of said combination to a subject in need thereof; use of such combination for the treatment of proliferative disease; and a commercial package comprising such combination; said proliferative disease being a solid tumor that harbors Mitogen-activated protein kinase (MAPK) alterations, such as *KRAS*-mutant tumors and *NRAS*-mutant tumors , and in particular, *KRAS*-mutant NSCLC (non-small cell lung cancer) and *NRAS*-mutant tumors, and in particular, *NRAS*-mutant melanoma.

BACKGROUND

The RAS/RAF/MEK/ERK or MAPK pathway is a key signaling cascade that drives cell proliferation, differentiation, and survival. Dysregulation of this pathway underlies many instances of tumorigenesis. Aberrant signaling or inappropriate activation of the MAPK pathway has been shown in multiple tumor types, including melanoma, lung and pancreatic cancer, and can occur through several distinct mechanisms, including activating mutations in RAS and *BRAF*. RAS is a superfamily of GTPases, and includes *KRAS* (v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog), which is a regulated signaling protein that can be turned on (activated) by various single-point mutations, which are known as gain of function mutations. The MAPK pathway is frequently mutated in human cancer with *KRAS* and *BRAF* mutations being among the most frequent (approximately 30%).

RAS mutations, particularly gain of function mutations, have been detected in 9–30% of all cancers, with *KRAS* mutations having the highest prevalence (86%), followed by *NRAS* (11%), and, infrequently, *HRAS* (3%) (Cox AD, Fesik SW, Kimmelman AC, et al (2014), Nat Rev Drug Discov. Nov; 13(11):828-51). Although selective *BRAF* inhibitors (BRAFi), and to a lesser extent, MEK inhibitors (MEKi) have demonstrated good activity in *BRAF*-mutant tumors, currently no effective therapies exist for *KRAS*-mutant tumors (Cantwell-Dorris ER, O'Leary JJ, Sheils OM (2011) Mol Cancer Ther. Mar;10(3):385-94.). For example, BRAFi such as vemurafenib and encorafenib, which are efficacious in melanomas with the *BRAF* V600E mutation, were found to be ineffective in RAS-mutant cancers. Allosteric MEK inhibitors (MEKi) have not demonstrated robust clinical efficacy in patients with tumors harboring RAS mutations, likely due to the narrow therapeutic index and feedback-mediated pathway reactivation. Thus, (K)RAS-mutant tumors remain a high unmet medical need for which no effective treatment exists.

Emerging evidence on the role of c-Raf in mediating *KRAS* signaling and in the development of *KRAS*-mutant non-small cell lung cancer (NSCLC) makes it a suitable target for therapeutic intervention (Blasco RB, Francoz S, Santamaría D, et al (2011) *c-Raf, but not B-Raf, is essential for development of K-Ras oncogene-driven non-small cell lung carcinoma.* Cancer Cell. 2011 May 17;19(5):652-63.). c-Raf was shown to promote feedback-mediated pathway reactivation following MEKi treatment in *KRAS*-mutant cancers (Lito P, Saborowski A, Yue J, et al (2014) *Disruption of c-Raf-Mediated MEK Activation Is Required for Effective MEK Inhibition in KRAS Mutant Tumors*. Cancer Cell 25, 697–710., Lamba et al 2014). In addition, c-Raf plays an essential role in mediating paradoxical activation following BRAFi

treatment (Poulikakos PI, Zhang C, Bollag G, et al. (2010), Nature. Mar 18;464(7287):427-30., Hatzivassiliou et al 2010, Heidorn et al 2010). Thus, selective pan-RAF inhibitors that potently inhibit the activity of c-Raf and *BRAF* could be effective in blocking *BRAF*-mutant tumors and RAS-mutant driven tumorigenesis and may also alleviate feedback activation.

The ability of T cells to mediate an immune response against an antigen requires two distinct signaling interactions (Viglietta, V. *et al.* (2007) *Neurotherapeutics* 4:666-675; Korman, A. J. *et al.* (2007) *Adv. Immunol.* 90:297-339). First, an antigen that has been arrayed on the surface of antigen-presenting cells (APC) is presented to an antigen-specific naive $CD4^+$ T cell. Such presentation delivers a signal via the T cell receptor (TCR) that directs the T cell to initiate an immune response specific to the presented antigen. Second, various co-stimulatory and inhibitory signals mediated through interactions between the APC and distinct T cell surface molecules trigger the activation and proliferation of the T cells and ultimately their inhibition.

The Programmed Death 1 (PD-1) protein is an inhibitory member of the extended CD28/CTLA-4 family of T cell regulators (Okazaki *et al.* (2002) *Curr Opin Immunol* 14: 391779-82; Bennett *et al.* (2003) *J. Immunol.* 170:711-8). Other members of the CD28 family include CD28, CTLA-4, ICOS and BTLA. It is one of the target sites in the immune checkpoint pathways that many tumors use to evade attack by the immune system. PD-1 is suggested to exist as a monomer, lacking the unpaired cysteine residue characteristic of other CD28 family members. PD-1 is expressed on activated B cells, T cells, and monocytes.

Given the importance of immune checkpoint pathways in regulating an immune response to tumors, the need exists for developing novel combination therapies that modulate the activity of immunoinhibitory proteins, such as PD-1, thus leading to activation of the immune system. Such agents can be used, *e.g.*, for cancer immunotherapy and treatment of other conditions, and can be used in combination with other therapeutic agents including kinase inhibitors.

Lung cancer is a common type of cancer that affects men and women around the globe. NSCLC is the most common type (roughly 85%) of lung cancer with approximately 70% of these patients presenting with advanced disease (Stage IIIB or Stage IV) at the time of diagnosis. About 30% of NSCLC contain activating *KRAS* mutations, and these mutations

are associated with resistance to EGFR TKIs (Pao W, Wang TY, Riely GJ, et al (2005) PLoS Med; 2(1): e17).

Immunotherapies currently in development have started to offer significant benefit to lung cancer patients, including those for whom conventional treatments are ineffective. Recently, pembrolizumab and nivolumab, two inhibitors of the PD-1/PD-L1 interaction have been approved for use in NSCLC under the trade names Keytruda ® and Opdivo ®, respectively. However, results indicate that many patients treated with single agent PD-1 inhibitors do not benefit adequately from treatment.

Melanoma is a common type of cancer that affects men and women around the globe. About 15-20% of melanoma contain activating *NRAS* mutations, and these mutations were identified as an independent predictor of shorter survival after a diagnosis of stage IV melanoma (Jakob JA et al (2012), Cancer, Volume 118, Issue 16, Pages 4014–4023).

Immunotherapies currently in development have started to offer significant benefit to melanoma cancer patients, including those for whom conventional treatments are ineffective. Recently, pembrolizumab and nivolumab, two inhibitors of the PD-1/PD-L1 interaction have been approved for use in melanoma under the trade names Keytruda ® and Opdivo ®, respectively. However, results indicate that many patients treated with single agent PD-1 inhibitors do not benefit adequately from treatment.

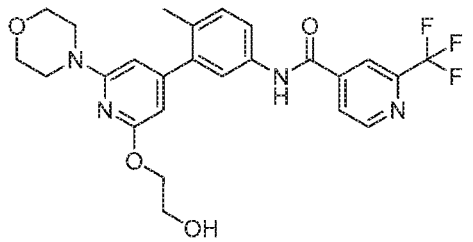
Direct inhibition of *KRAS* and *NRAS* has proven challenging. For example, to date, no approved targeted therapies are available for patients with *KRAS*-mutant NSCLC or patients with *NRAS*-mutant melanoma. There is thus the need for targeted therapy which is safe and/or well tolerated. A therapy which results in durable and sustained responses in such a clinical setting is also needed.

SUMMARY

The present invention provides COMPOUND A, or a pharmaceutically acceptable salt thereof, for use in the treatment of a cancer which is a solid tumor that harbors mitogen-activated protein kinase (MAPK) alterations, such as *KRAS*-mutant tumors and *NRAS*-mutant tumors. These include *NRAS*-mutant melanoma, *KRAS*-mutant NSCLC (non-small cell lung cancer), *BRAF*-mutant NSCLC, *KRAS*- and *BRAF*-mutant NSCLC, *KRAS*-mutant ovarian cncer, *BRAF*-mutant ovarian cancer, and *KRAS*- and *BRAF*- mutant ovarian cancer, and relapsed or refractory *BRAF* V600-mutant melanoma (e.g. said melanoma being relapsed

after failure of BRAFi/MEKi combination therapy or refractory to BRAFi/MEKi combination therapy).

COMPOUND A is the compound with the following structure:



The present invention also provides a pharmaceutical combination which comprises (a) at least one antibody molecule *(e.g.*, humanized antibody molecules) that binds to Programmed Death 1 (PD-1), especially the exemplary antibody molecule as described below, and (b) a c-Raf inhibitor which is Compound A, or pharmaceutically acceptable salt thereof. The pharmaceutical combination may be used for the simultaneous, separate or sequential administration for the treatment of a proliferative disease, particularly a solid tumor that harbors Mitogen-activated protein kinase (MAPK) alterations, such as *KRAS*-mutant tumors and *NRAS*-mutant tumors. These tumors include *KRAS*-mutant NSCLC (non-small cell lung cancer), *NRAS*-mutant melanoma, *KRAS*- and/or *BRAF*-mutated NSCLC, or *KRAS*- and/or *BRAF*-mutated ovarian cancer and *BRAF*-mutated melanoma resistant to BRAFi/MEKi combination treatment.

The present invention also relates to a pharmaceutical combination comprising
(A) a c-Raf inhibitor which is COMPOUND A, or pharmaceutically acceptable salt thereof; and
(B) an isolated antibody molecule capable of binding to a human Programmed Death-1 (PD-1) comprising a heavy chain variable region (VH) comprising a HCDR1, a HCDR2 and a HCDR3 amino acid sequence of BAP049-Clone-B or BAP049-Clone-E as described in Table 1 and a light chain variable region (VL) comprising a LCDR1, a LCDR2 and a LCDR3 amino acid sequence of BAP049-Clone-B or BAP049-Clone-E as described in Table 1 below.

There is also provided a pharmaceutical composition comprising such a combination; a method of treating a subject having a proliferative disease comprising administration of said combination to a subject in need thereof; use of such combination for the treatment of proliferative disease; and a commercial package comprising such combination.

The PD-1 inhibitor is an anti-PD-1 antibody molecule as described in USSN 14/604,415, entitled "Antibody Molecules to PD-1 and Uses Thereof," and WO/2015/112900, both incorporated by reference in its entirety. In one embodiment, the anti-PD-1 antibody molecule comprises at least one antigen-binding region, *e.g.*, a variable region or an antigen-binding fragment thereof, from an antibody described herein, including the three complementarity determining regions (CDRs) from the heavy and the three CDRs from the light chain, *e.g.*, an antibody chosen from any of BAP049-hum01, BAP049-hum02, BAP049-hum03, BAP049-hum04, BAP049-hum05, BAP049-hum06, BAP049-hum07, BAP049-hum08, BAP049-hum09, BAP049-hum10, BAP049-hum11, BAP049-hum12, BAP049-hum13, BAP049-hum14, BAP049-hum15, BAP049-hum16, BAP049-Clone-A, BAP049-Clone-B, BAP049-Clone-C, BAP049-Clone-D, or BAP049-Clone-E; or as described in Table 1, or encoded by the nucleotide sequence in Table 1; or a sequence substantially identical (*e.g.*, at least 80%, 85%, 90%, 92%, 95%, 97%, 98%, 99% or higher identical) to any of the aforesaid sequences.

For example, the anti-PD-1 antibody molecule can include VH CDR1 according to Kabat *et al.* or VH hypervariable loop 1 according to Chothia *et al.*, or a combination thereof, *e.g.*, as shown in Table 1. In one embodiment, the combination of Kabat and Chothia CDR of VH CDR1 comprises the amino acid sequence GYTFTTYWMH (SEQ ID NO: 224), or an amino acid sequence substantially identical thereto (*e.g.*, having at least one amino acid alteration, but not more than two, three or four alterations (*e.g.,* substitutions, deletions, or insertions, *e.g.,* conservative substitutions)). The anti-PD-1 antibody molecule can further include, *e.g.,* VH CDRs 2-3 according to Kabat *et al.* and VL CDRs 1-3 according to Kabat *et al., e.g.*, as shown in Table 1. Accordingly, in some embodiments, framework regions are defined based on a combination of CDRs defined according to Kabat *et al.* and hypervariable loops defined according to Chothia *et al.* For example, the anti-PD-1 antibody molecule can include VH FR1 defined based on VH hypervariable loop 1 according to Chothia *et al.* and VH FR2 defined based on VH CDRs 1-2 according to Kabat *et al.*, *e.g.*, as shown in Table 1. The anti-PD-1 antibody molecule can further include, *e.g.,* VH FRs 3-4 defined based on VH

CDRs 2-3 according to Kabat *et al.* and VL FRs 1-4 defined based on VL CDRs 1-3 according to Kabat *et al.*

A preferred antibody molecule *(e.g.*, humanized antibody molecules) that binds to Programmed Death 1 (PD-1) in the combination of the present invention is the exemplary antibody molecule which is BAP049-Clone-E and the preferred amino acid sequences are described in Table 1 herein (VH: SEQ ID NO: 38; VL: SEQ ID NO: 70). The preferred antibody molecule is also referred herein as Antibody B.

The present invention further provides a pharmaceutical combination comprising a c-Raf kinase inhibitor, which is COMPOUND A, or a pharmaceutically acceptable salt thereof, and an anti-PD-1 antibody molecule, as described herein, for simultaneous, separate or sequential administration, for use in the treatment of a proliferative disease.

The present invention is particularly related to the combination of the invention for use in the treatment of a proliferative disease characterized by activating mutations in the MAPK pathway, and in particular by one or more mutations in *KRAS* or *NRAS*.

The present invention also provides the use of the combination of the invention for the treatment of a proliferative disease, particularly a cancer. In particular, the combination of the invention may be useful for the treatment of a cancer which is selected from *KRAS*-mutant NSCLC (non-small cell lung cancer), *NRAS*-mutant melanoma, *KRAS*- and/or *BRAF*-mutant NSCLC, *KRAS*- and/or *BRAF*-mutant ovarian cancer and *BRAF*-mutant melanoma resistant to BRAFi/MEKi combination treatment.

The present invention also provides the use of the combination of the invention for the preparation of a medicament for the treatment of a proliferative disease, particularly a cancer, particularly a solid tumor that harbors Mitogen-activated protein kinase (MAPK) alterations, e.g. *KRAS*-mutant NSCLC (non-small cell lung cancer), *NRAS*-mutant melanoma, *KRAS*- and/or *BRAF*-mutant NSCLC, *KRAS*- and/or *BRAF*-mutant ovarian cancer and *BRAF*-mutant melanoma resistant to BRAFi/MEKi combination treatment.

The present invention also provides a method of treating a proliferative disease comprising simultaneously, separately or sequentially administering to a subject in need

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thereof a combination of the invention in a quantity which is jointly therapeutically effective against said proliferative disease.

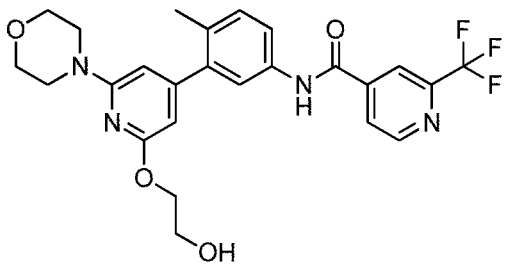
The present invention also provides a pharmaceutical composition or combined preparation comprising a quantity of the combination of the invention, which is jointly therapeutically effective against a proliferative disease, and optionally at least one pharmaceutically acceptable carrier.

The present invention also provides a combined preparation comprising (a) one or more dosage units of a c-Raf inhibitor, which is COMPOUND A, or a pharmaceutically acceptable salt thereof, and (b) an anti-PD-1 antibody molecule, for use in the treatment of a proliferative disease.

The present invention also provides a commercial package comprising as active ingredients a combination of the invention and instructions for simultaneous, separate or sequential administration of a combination of the invention to a patient in need thereof for use in the treatment of a proliferative disease, particularly a solid tumor that harbors Mitogen activated protein kinase (MAPK) alterations, e.g. *KRAS*-mutant NSCLC (non-small cell lung cancer), *NRAS*-mutant melanoma, *KRAS*- and/or *BRAF*-mutant NSCLC, *KRAS*- and/or *BRAF*-mutant ovarian cancer and *BRAF*-mutant melanoma resistant to BRAFi/MEKi combination treatment.

In one aspect, the present invention provides a method for treating a proliferative disease in a subject comprising the separate, simultaneous or sequential administration of a pharmaceutical combination comprising

(A) a c-Raf inhibitor which is COMPOUND A,



,

or a pharmaceutically acceptable salt thereof;

and

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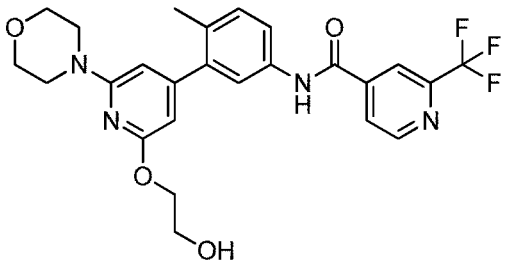
(B) an isolated antibody molecule capable of binding to a human Programmed Death-1 (PD-1) comprising a heavy chain variable region (VH) comprising a HCDR1 amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 4, a HCDR2 amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 5, and a HCDR3 amino acid sequence of SEQ ID NO: 3, and a light chain variable region (VL) comprising a LCDR1 amino acid sequence of SEQ ID NO: 10 or SEQ ID NO: 13, a LCDR2 amino acid sequence of SEQ ID NO: 11 or SEQ ID NO: 14, and a LCDR3 amino acid sequence of SEQ ID NO: 32 or SEQ ID NO: 33,
to a subject in need thereof, wherein the anti-PD-1 antibody molecule is administered in a dose of about 300 mg to 400 mg once every three weeks or once every four weeks.

In another aspect, the present invention provides a method for treating a solid tumor that harbors at least one Mitogen-activated protein kinase (MAPK) alteration in a subject comprising the separate, simultaneous or sequential administration of a pharmaceutical combination comprising
(A) a c-Raf inhibitor which is COMPOUND A,



,
or a pharmaceutically acceptable salt thereof;
and
(B) an isolated antibody molecule capable of binding to a human Programmed Death-1 (PD-1) comprising a heavy chain variable region (VH) comprising a HCDR1 amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 4, a HCDR2 amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 5, and a HCDR3 amino acid sequence of SEQ ID NO: 3, and a light chain variable region (VL) comprising a LCDR1 amino acid sequence of SEQ ID NO: 10 or SEQ ID NO: 13, a LCDR2 amino acid sequence of SEQ ID NO: 11 or SEQ ID NO: 14, and a LCDR3 amino acid sequence of SEQ ID NO: 32 or SEQ ID NO: 33,
to a subject in need thereof, wherein the anti-PD-1 antibody molecule is administered in a dose of about 300 mg to 400 mg once every three weeks or once every four weeks.

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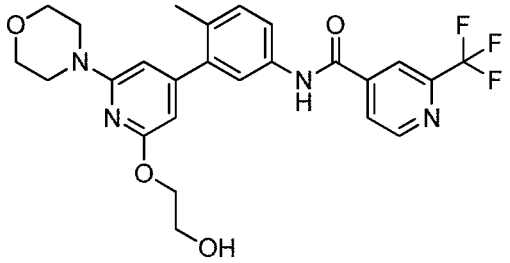
In another aspect, the present invention provides a method for treating a cancer which is selected from *NRAS*-mutant melanoma, *KRAS*-mutant NSCLC (non-small cell lung cancer), *BRAF*-mutant NSCLC, *KRAS*- and *BRAF*-mutant NSCLC, *KRAS*-mutant ovarian cncer, *BRAF*-mutant ovarian cancer, and *KRAS*- and *BRAF*- mutant ovarian cancer, and relapsed or refractory *BRAF* V600-mutant melanoma in a subject comprising the separate, simultaneous or sequential administration of a pharmaceutical combination comprising

(A) a c-Raf inhibitor which is COMPOUND A,



,

or a pharmaceutically acceptable salt thereof;

and

(B) an isolated antibody molecule capable of binding to a human Programmed Death-1 (PD-1) comprising a heavy chain variable region (VH) comprising a HCDR1 amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 4, a HCDR2 amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 5, and a HCDR3 amino acid sequence of SEQ ID NO: 3, and a light chain variable region (VL) comprising a LCDR1 amino acid sequence of SEQ ID NO: 10 or SEQ ID NO: 13, a LCDR2 amino acid sequence of SEQ ID NO: 11 or SEQ ID NO: 14, and a LCDR3 amino acid sequence of SEQ ID NO: 32 or SEQ ID NO: 33,

to a subject in need thereof, wherein the anti-PD-1 antibody molecule is administered in a dose of about 300 mg to 400 mg once every three weeks or once every four weeks.

In another aspect, the present invention provides use of (A) a c-Raf inhibitor which is COMPOUND A,

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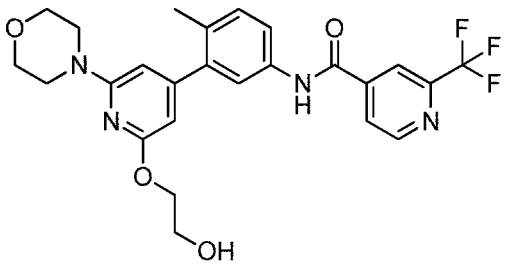


,

or a pharmaceutically acceptable salt thereof;

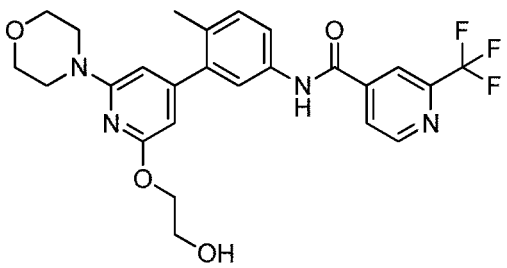
and

(B) an isolated antibody molecule capable of binding to a human Programmed Death-1 (PD-1) comprising a heavy chain variable region (VH) comprising a HCDR1 amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 4, a HCDR2 amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 5, and a HCDR3 amino acid sequence of SEQ ID NO: 3, and a light chain variable region (VL) comprising a LCDR1 amino acid sequence of SEQ ID NO: 10 or SEQ ID NO: 13, a LCDR2 amino acid sequence of SEQ ID NO: 11 or SEQ ID NO: 14, and a LCDR3 amino acid sequence of SEQ ID NO: 32 or SEQ ID NO: 33,

for the preparation of a medicament for the treatment of a proliferative disease,

wherein the medicament is formulated for separate, simultaneous or sequential administration of the c-Raf inhibitor, or a pharmaceutically acceptable salt thereof, and the anti-PD-1 antibody molecule to a subject, and wherein treatment comprises administration of the anti-PD-1 antibody molecule to the subject in a dose of about 300 mg to 400 mg once every three weeks or once every four weeks.

In another aspect, the present invention provides use of (A) a c-Raf inhibitor which is COMPOUND A,



,

or a pharmaceutically acceptable salt thereof;

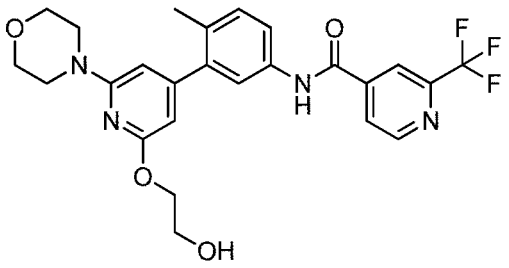
and

(B) an isolated antibody molecule capable of binding to a human Programmed Death-1 (PD-1) comprising a heavy chain variable region (VH) comprising a HCDR1 amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 4, a HCDR2 amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 5, and a HCDR3 amino acid sequence of SEQ ID NO: 3, and a light chain variable region (VL) comprising a LCDR1 amino acid sequence of SEQ ID NO: 10 or SEQ ID NO: 13, a LCDR2 amino acid sequence of SEQ ID NO: 11 or SEQ ID NO: 14, and a LCDR3 amino acid sequence of SEQ ID NO: 32 or SEQ ID NO: 33,

for the preparation of a medicament for the treatment of a solid tumor that harbors at least one Mitogen-activated protein kinase (MAPK) alteration,

wherein the medicament is formulated for separate, simultaneous or sequential administration of the c-Raf inhibitor, or a pharmaceutically acceptable salt thereof, and the anti-PD-1 antibody molecule to a subject, and wherein treatment comprises administration of the anti-PD-1 antibody molecule to the subject in a dose of about 300 mg to 400 mg once every three weeks or once every four weeks.

In another aspect, the present invention provides use of (A) a c-Raf inhibitor which is COMPOUND A,



,

or a pharmaceutically acceptable salt thereof;

and

(B) an isolated antibody molecule capable of binding to a human Programmed Death-1 (PD-1) comprising a heavy chain variable region (VH) comprising a HCDR1 amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 4, a HCDR2 amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 5, and a HCDR3 amino acid sequence of SEQ ID NO: 3, and a light chain variable region (VL) comprising a LCDR1 amino acid sequence of SEQ ID NO: 10 or SEQ ID NO: 13, a LCDR2 amino acid sequence of SEQ ID NO: 11 or SEQ ID NO: 14, and a LCDR3 amino acid sequence of SEQ ID NO: 32 or SEQ ID NO: 33,

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for the preparation of a medicament for the treatment of a cancer which is selected from *NRAS*-mutant melanoma, *KRAS*-mutant NSCLC (non-small cell lung cancer), *BRAF*-mutant NSCLC, *KRAS*- and *BRAF*-mutant NSCLC, *KRAS*-mutant ovarian cncer, *BRAF*-mutant ovarian cancer, and *KRAS*- and *BRAF*- mutant ovarian cancer, and relapsed or refractory *BRAF* V600-mutant melanoma,

wherein the medicament is formulated for separate, simultaneous or sequential administration of the c-Raf inhibitor, or a pharmaceutically acceptable salt thereof, and the anti-PD-1 antibody molecule to a subject, and wherein treatment comprises administration of the anti-PD-1 antibody molecule to the subject in a dose of about 300 mg to 400 mg once every three weeks or once every four weeks.

The present invention also provides a commercial package comprising a c-Raf inhibitor, which is COMPOUND A, or a pharmaceutically acceptable salt thereof, and an anti-PD-1 antibody molecule, and instructions for the simultaneous, separate or sequential use in the treatment of a proliferative disease.

In another aspect, the invention features diagnostic or therapeutic kits that include the antibody molecules described herein and instructions for use.

All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety.

Other features and advantages of the invention will be apparent from the description and drawings, and from the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 depicts the amino acid sequences of the light and heavy chain variable regions of murine anti-PD-1 mAb BAPO49. The upper and lower sequences were from two

independent analyses. The light and heavy chain CDR sequences based on Kabat numbering are underlined. The light heavy chain CDR sequences based on Chothia numbering are shown in bold italics. The unpaired Cys residue at position 102 of the light chain sequence is boxed. Sequences are disclosed as SEQ ID NOs: 8, 228, 16 and 229, respectively, in order of appearance.

Figure 2A depicts the amino acid sequences of the light and heavy chain variable regions of murine anti-PD-1 mAb BAP049 aligned with the germline sequences. The upper and lower sequences are the germline (GL) and BAP049 (Mu mAb) sequences, respectively. The light and heavy chain CDR sequences based on Kabat numbering are underlined. The light heavy chain CDR sequences based on Chothia numbering are shown in bold italics. "-" means identical amino acid residue. Sequences disclosed as SEQ ID NOs: 230, 8, 231 and 16, respectively, in order of appearance.

Figure 2B depicts the sequence of murine κ J2 gene and the corresponding mutation in murine anti-PD-1 mAb BAP049. "-" means identical nucleotide residue. Sequences disclosed as SEQ ID NOs: 233, 232, 234 and 235, respectively, in order of appearance.

Figures 3A-3B depict the competition binding between fluorescently labeled murine anti-PD-1 mAb BAP049 (Mu mAb) and three chimeric versions of BAP049 (Chi mAb). Experiment was performed twice, and the results are shown in Figures 3A and 3B, respectively. The three chimeric BAP049 antibodies (Chi mAb (Cys), Chi mAb (Tyr) and Chi mAb (Ser)) have Cys, Tyr and Ser residue at position 102 of the light chain variable region, respectively. Chi mAb (Cys), Chi mAb (Tyr) and Chi mAb (Ser) are also known as BAP049-chi, BAP049-chi-Y, and BAP049-chi-S, respectively.

Figure 4 is a bar graph showing the results of FACS binding analysis for the sixteen humanized BAP049 clones (BAP049-hum01 to BAP049-hum16). The antibody concentrations are 200, 100, 50, 25 and 12.5 ng/ml from the leftmost bar to the rightmost bar for each tested mAb.

Figure 5 depicts the structural analysis of the humanized BAP049 clones (a, b, c, d and e represent various types of framework region sequences). The concentrations of the mAbs in the samples are also shown.

Figure 6A-6B depicts the binding affinity and specificity of humanized BAP049 mAbs measured in a competition binding assay using a constant concentration of Alexa 488-labeled murine mAb BAP049, serial dilutions of the test antibodies, and PD-1-expressing 300.19 cells. Experiment was performed twice, and the results are shown in Figures 6A and 6B, respectively.

Figure 7 depicts the ranking of humanized BAP049 clones based on FACS data, competition binding and structural analysis. The concentrations of the mAbs in the samples are also shown.

Figures 8A-8B depict blocking of ligand binding to PD-1 by selected humanized BAP049 clones. Blocking of PD-L1-Ig and PD-L2-Ig binding to PD-1 is shown in Figire 8A. Blocking of PD-L2-Ig binding to PD-1 is shown in Figire 8B. BAP049-hum01, BAP049-hum05, BAP049-hum08, BAP049-hum09, BAP049-hum10, and BAP049-hum11 were evaluated. Murine mAb BAP049 and chimeric mAb having Tyr at position 102 of the light chain variable region were also included in the analyses.

Figures 9A-9B depict the alignment of heavy chain variable domain sequences for the sixteen humanized BAP049 clones and BAP049 chimera (BAP049-chi). In Figure 9A, all of the sequences are shown (SEQ ID NOs: 22, 38, 38, 38, 38, 38, 38, 38, 38, 38, 50, 50, 50, 50, 82, 82 and 86, respectively, in order of appearance). In Figure 9B, only amino acid sequences that are different from mouse sequence are shown (SEQ ID NOs: 22, 38, 38, 38, 38, 38, 38, 38, 38, 38, 50, 50, 50, 50, 82, 82 and 86, respectively, in order of appearance).

Figures 10A-10B depict the alignment of light chain variable domain sequences for the sixteen humanized BAP049 clones and BAP049 chimera (BAP049-chi). In Figure 10A, all of the sequences are shown (SEQ ID NOs: 24, 66, 66, 66, 66, 70, 70, 70, 58, 62, 78, 74, 46, 46, 42, 54 and 54, respectively, in order of appearance). In Figure 10B, only amino acid sequences that are different from mouse sequence are shown (SEQ ID NOs: 24, 66, 66, 66, 66, 70, 70, 70, 58, 62, 78, 74, 46, 46, 42, 54 and 54, respectively, in order of appearance).

Figure 11 is a schematic diagram that outlines the antigen processing and presentation, effector cell responses and immunosuppression pathways targeted by the combination therapies disclosed herein.

Figure 12 depicts the predicted Ctrough (Cmin) concentrations across the different weights for patients while receiving the same dose of an exemplary anti-PD-1 antibody molecule.

Figure 13 depicts observed versus model predicted (population or individual based) Cmin concentrations.

Figure 14 depicts the accumulation, time course and within subject variability of the model used to analyze pharmacokinetics.

Figures 15A, 15B and 15C depict the single agent activity of Compound A in various *KRASmt* NSCLC models.

Figure 16 depicts the single agent activity of Compound A in an *NRASmt* melanoma model.

BRIEF DESCRIPTION OF THE TABLES

Table 1 is a summary of the amino acid and nucleotide sequences for the murine, chimeric and humanized anti-PD-1 antibody molecules. The antibody molecules include murine mAb BAP049, chimeric mAbs BAP049-chi and BAP049-chi-Y, and humanized mAbs BAP049-hum01 to BAP049-hum16 and BAP049-Clone-A to BAP049-Clone-E. The amino acid and nucleotide sequences of the heavy and light chain CDRs, the amino acid and nucleotide sequences of the heavy and light chain variable regions, and the amino acid and nucleotide sequences of the heavy and light chains are shown in this Table.

Table 2 depicts the amino acid and nucleotide sequences of the heavy and light chain framework regions for humanized mAbs BAP049-hum01 to BAP049-hum16 and BAP049-Clone-A to BAP049-Clone-E.

Table 3 depicts the constant region amino acid sequences of human IgG heavy chains and human kappa light chain.

Table 4 shows the amino acid sequences of the heavy and light chain leader sequences for humanized mAbs BAP049-Clone-A to BAP049-Clone-E.

Table 5 depicts exemplary PK parameters based on flat dosing schedules.

DETAILED DESCRIPTION

c-Raf Kinase Inhibitor

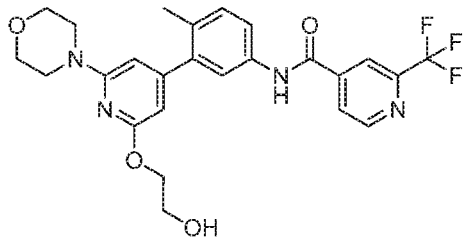
CRAF has been demonstrated to be the critical mediator of mutant *KRAS*-driven development in many cancers including NSCLC and plays an essential role in mediating paradoxical activation following BRAFi treatment. Compound A, a c-RAF inhibitor, may therefore be useful in treating (*e.g.*, one or more of reducing, inhibiting, or delaying progression) a proliferative disease, particularly a solid tumor that harbors Mitogen-activated protein kinase (MAPK) alterations, *e.g. NRAS*-mutant melanoma, *KRAS*-mutant NSCLC (non-small cell lung cancer), *BRAF*-mutant NSCLC, *KRAS*- and *BRAF*-mutant NSCLC, *KRAS*-mutant ovarian cncer, *BRAF*-mutant ovarian cancer, and *KRAS*- and *BRAF*- mutant ovarian cancer, and relapsed or refractory *BRAF* V600-mutant melanoma (e.g. said

melanoma being relapsed after failure of BRAFi/MEKi combination therapy or refractory to BRAFi/MEKi combination therapy).

As used herein, the term "Raf inhibitor" refers to an adenosine triphosphate (ATP)-competitive inhibitor of B-Raf protein kinase (also referred to herein as b-RAF, *BRAF* or b-Raf) and C-Raf protein kinase (also referred to herein as c-RAF, c-Raf or CRAF) that selectively targets, decreases, or inhibits at least one activity of serine/threonine-protein kinase B-Raf or C-Raf. The Raf inhibitor may inhibit both Raf monomers and Raf dimers.

In a preferred embodiment of the methods, treatments, combination and compositions described herein, the c-Raf inhibitor is COMPOUND A, or pharmaceutically acceptable salt thereof.

COMPOUND A has the following structure:



The c-Raf kinase inhibitor of the present invention, i.e. COMPOUND A, is disclosed, in WO2014/151616, which is incorporated herein by reference in its entirety, as example 1156.

COMPOUND A (Compound A) is also known by the name of N-(3-(2-(2-hydroxyethoxy)-6-morpholinopyridin-4-yl)-4-methylphenyl)-2-(trifluoromethyl)isonicotinamide.

COMPOUND A (also referred to herein as "Compound A") is an adenosine triphosphate (ATP)-competitive inhibitor of *BRAF* (also referred to herein as b-RAF or b-Raf) and c-Raf (also referred to herein as c-RAF or CRAF) protein kinases. Throughout the present disclosure, COMPOUND A is also referred to as a c-RAF (or CRAF) inhibitor or a C-RAF/c-Raf kinase inhibitor.

In cell-based assays, COMPOUND A demonstrated anti-proliferative activity in cell lines that contain a variety of mutations that activate MAPK signaling. For instance,

COMPOUND A inhibited the proliferation of melanoma models, including A-375 (*BRAF* V600E) and A-375 engineered to express BRAFi/MEKi resistance alleles, MEL-JUSO (*NRAS* Q61L), and IPC-298 (*NRAS* Q61L), as well as the non-small cell lung cancer cell line Calu-6 (*KRAS* Q61K) with IC_{50} values ranging from 0.2 – 1.2μM.

In vivo, treatment with COMPOUND A generated tumor regression in several *KRAS*-mutant models including the NSCLC-derived Calu-6 (*KRAS* Q61K) and NCI-H358 (*KRAS* G12C) as well as the ovarian Hey-A8 (*KRAS* G12D, *BRAF* G464E) xenografts and in *NRAS*-mutant models including the SK-MEL-30 melanoma model. In all cases, anti-tumor effects were dose-dependent and well tolerated as judged by lack of significant body weight loss.

Collectively, the in vitro and *in vivo* MAPK-pathway suppression and anti-proliferative activity observed for COMPOUND A at well-tolerated doses suggests that COMPOUND A may have anti-tumor activity in patients with tumors harboring activating lesions in the MAPK pathway.

Based on the mechanism of action of COMPOUND A, preclinical data and published literature on the importance of c-Raf in MAPK pathway regulation, COMPOUND A, as a single agent or in combination with an antibody molecule *(e.g.*, a humanized antibody molecule) that binds to Programmed Death 1 (PD-1), especially the exemplary antibody molecule as described below, can be useful in the treatment of adult patients with advanced solid tumors harboring MAPK pathway alterations, and in particular, *KRAS*-mutant NSCLC (non-small cell lung cancer) and *NRAS*-mutant melanoma.

COMPOUND A, or a pharmaceutically acceptable salt thereof, may be administered orally. In one embodiment, COMPOUND A, or a pharmaceutically acceptable salt thereof, is administered at a dose of about 50-1200 mg (*e.g.*, per day). COMPOUND A, or a pharmaceutically acceptable salt thereof, can be administered at a unit dosage of about 50 mg, about 100 mg, about 150 mg, about 200 mg, about 250 mg, about 300 mg, about 350 mg, about 400 mg, about 450 mg, about 500 mg about 550 mg, about 600 mg, about 650 mg, about 700 mg, about 750 mg, about 800 mg, about 850 mg, about 900 mg, about 950 mg, about 1000 mg, about 1050 mg, about 1100 mg, about 1150 mg or about 1200 mg. The unit dosage of COMPOUND A, or a pharmaceutically acceptable salt thereof, may be administered once daily, or twice daily, or three times daily, or four times daily, with the

actual dosage and timing of administration determined by criteria such as the patient's age, weight, and gender; the extent and severity of the cancer to be treated; and the judgment of a treating physician. Preferably, the unit dosage of COMPOUND A is administered once daily. In another preferred embodiment, the unit dosage of COMPOUND A is administered twice daily.

COMPOUND A may in particular be administered at a dose of 100 mg once daily (QD), 200 mg once daily, 300 mg once daily , 400 mg once daily, 800 mg once daily or 1200 mg once daily (QD). COMPOUND A may also be administered at a dose of 200 mg twice daily or 400 mg twice daily. The dosages quoted herein may apply to the administration of COMPOUND A as monotherapy (single agent) or as part of a combination therapy, e.g as part of the combination of the present invention, as described herein.

When describing a dosage herein as 'about' a specified amount, the actual dosage can vary by up to 5-7% from the stated amount: this usage of 'about' recognizes that the precise amount in a given dosage form may differ slightly from an intended amount for various reasons without materially affecting the *in vivo* effect of the administered compound. The unit dosage of the c-Raf inhibitor may be administered once daily, or twice daily, or three times daily, or four times daily, with the actual dosage and timing of administration determined by criteria such as the patient's age, weight, and gender; the extent and severity of the cancer to be treated; and the judgment of a treating physician.

Since the MAPK signaling cascade has an important role in immune defense, it is expected that RAF targeted therapies with COMPOUND A may modulate an immune response to tumors. The present invention therefore also provides a medicament comprising COMPOUND A and an antibody (a) at least one antibody molecule *(e.g.*, humanized antibody molecules) that binds to Programmed Death 1 (PD-1), especially the exemplary antibody molecule as described below, for simultaneous, sequentially, or separate administration. The combination may be useful for the treatment of a proliferative disease, particularly a solid tumor that harbors Mitogen-activated protein kinase (MAPK) alterations, *e.g. KRAS*-mutant NSCLC (non-small cell lung cancer), *NRAS*-mutant melanoma, *KRAS*- and/or *BRAF*-mutant NSCLC, *KRAS*- and/or *BRAF*-mutant ovarian cancer and *BRAF*-mutant melanoma resistant to BRAFi/MEKi combination treatment.

For example, it is expected that the combination of targeted therapy and immunotherapy in *KRAS*-mutated NSCLC may lead to early and robust antitumor responses from targeted therapy associated with long-term benefit of immunotherapy. It is also expected that the combination of the present invention may be beneficial (with potential synergistic activity) in *NRAS* mutant melanoma which is an aggressive disease which is highly susceptible to immunotherapy.

Antibody Molecules to PD-1

In one embodiment, the PD-1 inhibitor is an anti-PD-1 antibody molecule as described in USSN 14/604,415, entitled "Antibody Molecules to PD-1 and Uses Thereof," and WO/2015/112900, both incorporated by reference in its entirety. In one embodiment, the anti-PD-1 antibody molecule comprises at least one antigen-binding region, *e.g.*, a variable region or an antigen-binding fragment thereof, from an antibody described herein, including the three complementarity determining regions (CDRs) from the heavy and the three CDRs from the light chain , *e.g.*, an antibody chosen from any of BAP049-hum01, BAP049-hum02, BAP049-hum03, BAP049-hum04, BAP049-hum05, BAP049-hum06, BAP049-hum07, BAP049-hum08, BAP049-hum09, BAP049-hum10, BAP049-hum11, BAP049-hum12, BAP049-hum13, BAP049-hum14, BAP049-hum15, BAP049-hum16, BAP049-Clone-A, BAP049-Clone-B, BAP049-Clone-C, BAP049-Clone-D, or BAP049-Clone-E; or as described in Table 1, or encoded by the nucleotide sequence in Table 1; or a sequence substantially identical (*e.g.*, at least 80%, 85%, 90%, 92%, 95%, 97%, 98%, 99% or higher identical) to any of the aforesaid sequences.

For example, the anti-PD-1 antibody molecule can include VH CDR1 according to Kabat *et al.* or VH hypervariable loop 1 according to Chothia *et al.*, or a combination thereof, *e.g.*, as shown in Table 1. In one embodiment, the combination of Kabat and Chothia CDR of VH CDR1 comprises the amino acid sequence GYTFTTYWMH (SEQ ID NO: 224), or an amino acid sequence substantially identical thereto (*e.g.*, having at least one amino acid alteration, but not more than two, three or four alterations (*e.g.,* substitutions, deletions, or insertions, *e.g.,* conservative substitutions)). The anti-PD-1 antibody molecule can further include, *e.g.,* VH CDRs 2-3 according to Kabat *et al.* and VL CDRs 1-3 according to Kabat *et al., e.g.*, as shown in Table 1. Accordingly, in some embodiments, framework regions are

defined based on a combination of CDRs defined according to Kabat *et al.* and hypervariable loops defined according to Chothia *et al.* For example, the anti-PD-1 antibody molecule can include VH FR1 defined based on VH hypervariable loop 1 according to Chothia *et al.* and VH FR2 defined based on VH CDRs 1-2 according to Kabat *et al.*, *e.g.*, as shown in Table 1. The anti-PD-1 antibody molecule can further include, *e.g.,* VH FRs 3-4 defined based on VH CDRs 2-3 according to Kabat *et al.* and VL FRs 1-4 defined based on VL CDRs 1-3 according to Kabat *et al.*

A preferred antibody molecule *(e.g.*, humanized antibody molecule) that binds to Programmed Death 1 (PD-1) in the combination of the present invention is the exemplary antibody molecule which is BAP049-Clone-E and the preferred amino acid sequences are described in Table 1 herein (VH: SEQ ID NO: 38; VL: SEQ ID NO: 70).

The present invention further relates to a pharmaceutical combination comprising (a) at least one antibody molecule *(e.g.*, humanized antibody molecules) that binds to Programmed Death 1 (PD-1), especially the exemplary antibody molecule as described herein, and (b) a c-Raf inhibitor, such as Compound A, or pharmaceutically acceptable salt thereof, for simultaneous, separate or sequential administration for the treatment of a proliferative disease, particularly a solid tumor that harbors Mitogen-activated protein kinase (MAPK) alterations, such as a *KRAS*-mutant tumor, and in particular *KRAS*-mutant NSCLC (non-small cell lung cancer) and *NRAS*-mutant tumor, and in particular *NRAS*-mutant melanoma.

In one embodiment, the invention features a method of treating (*e.g.*, inhibiting, reducing, or ameliorating) a disorder, *e.g.*, a hyperproliferative condition or disorder (*e.g.*, a cancer) in a subject. The method includes administering, in combination with a c-Raf inhibitor, to the subject an anti-PD-1 antibody molecule, *e.g.,* the preferred anti-PD-1 antibody molecule described herein, at a dose of about 300 mg to 400 mg once every three weeks or once every four weeks. In certain embodiments, the *e.g.,* the preferred anti-PD-1 antibody molecule is administered at a dose of about 300 mg once every three weeks. In other embodiments, the *e.g.,* the preferred anti-PD-1 antibody molecule is administered at a dose of about 400 mg once every four weeks. In some embodiments, the proliferative disorder is a *KRAS*-mutant tumor with a gain-of-function *KRAS* mutation as described herein, and in particular, *KRAS*-mutant NSCLC (non-small cell lung cancer). In some embodiments, the proliferative disorder is a *NRAS*-mutant tumor with a gain-of-function *NRAS* mutation as described herein, and in particular, *NRAS*-mutant melanoma.

In some embodiments, the proliferative disorder is a *KRAS*-mutant tumor with a gain-of-function *KRAS* mutation as described herein, and in particular, *KRAS*-mutant melanoma. In some embodiments, the proliferative disorder is a *NRAS*-mutant tumor with a gain-of-function *NRAS* mutation as described herein, and in particular, *NRAS*-mutant ovarian cancer.

In some embodiments, the proliferative disorder is a *KRAS*-mutant tumor with a gain-of-function *KRAS* mutation as described herein, and in particular, and *KRAS*-mutant ovarian cancer.

In some embodiments, the anti-PD-1 antibody molecule is administered by injection (*e.g.*, subcutaneously or intravenously) at a dose (*e.g.,* a flat dose) of about 200 mg to 500 mg, *e.g.,* about 250 mg to 450 mg, about 300 mg to 400 mg, about 250 mg to 350 mg, about 350 mg to 450 mg, or about 300 mg or about 400 mg. The dosing schedule (*e.g.,* flat dosing schedule) can vary from *e.g.*, once a week to once every 2, 3, 4, 5, or 6 weeks. In one embodiment, the anti-PD-1 antibody molecule, *e.g.*, the exemplary antibody molecule, is administered at a dose from about 300 mg to 400 mg once every three weeks or once every four weeks. In one embodiment, the anti-PD-1 antibody molecule is administered at a dose of about 300 mg once every three weeks. In one embodiment, the anti-PD-1 antibody molecule is administered at a dose of about 400 mg once every four weeks. In one embodiment, the anti-PD-1 antibody molecule, *e.g.*, the exemplary antibody molecule, is administered at a dose from about 300 mg once every four weeks. In one embodiment, the the anti-PD-1 antibody molecule, *e.g.*, the exemplary antibody molecule, is administered at a dose from about 400 mg once every three weeks.

In another aspect, the invention features a method of reducing an activity (*e.g.*, growth, survival, or viability, or all), of a hyperproliferative (*e.g.*, a cancer) cell. The method includes contacting the cell with an anti-PD-1 antibody molecule, *e.g.*, an anti-PD-1 antibody molecule described herein. The method can be performed in a subject, *e.g.*, as part of a therapeutic protocol in combination with a c-Raf receptor tyrosine kinase inhibitor, *e.g.,* at a dose of about 300 mg to 400 mg of an anti-PD-1 antibody molecule once every three weeks or once every four weeks. In certain embodiments, the dose is about 300 mg of an anti-PD-1 antibody molecule once every three weeks. In other embodiments, the dose is about 400 mg of an anti-PD-1 antibody molecule once every four weeks.

In another aspect, the invention features a composition (*e.g.*, one or more compositions or dosage forms), that includes an anti-PD-1 antibody molecule *(e.g.*, an anti-PD-1 antibody molecule as described herein). Formulations, *e.g.*, dosage formulations, and

kits, *e.g.*, therapeutic kits, that include an anti-PD-1 antibody molecule *(e.g.*, an anti-PD-1 antibody molecule as described herein), are also described herein. In certain embodiments, the composition or formulation comprises 300 mg or 400 mg of an anti-PD-1 antibody molecule (*e.g.*, an anti-PD-1 antibody molecule as described herein). In some embodiments, the composition or formulation is administered or used once every three weeks or once every four weeks. Such composition is used in combination with a c-Raf inhibitor or pharmaceutically acceptable salt thereof, for simultaneous, separate or sequential administration, often for treatment of NSCLC, and particularly for treating a patient having NSCLC that exhibits at least one *KRAS* mutation, especially a gain of function mutation such as those described herein. Such composition is used in combination with a c-Raf inhibitor, or a pharmaceutically acceptable salt thereof, for simultaneous, separate or sequential administration, often for treatment of melanoma, and particularly for treating a patient having melanoma that exhibits at least one *NRAS* mutation, especially a mutation such as those described herein.

In another aspect, the invention provides an anti-PD-1 antibody for use in treating NSCLC, wherein the anti-PD-1 antibody is administered, or prepared for administration, separately, simultaneously, or sequentially with a c-Raf inhibitor. It also provides a c-Raf inhibitor for use in treating NSCLC, wherein the c-Raf inhibitor is administered, or prepared for administration, separately, simultaneously, or sequentially with an anti-PD-1 antibody.

In another aspect, the invention provides an anti-PD-1 antibody for use in treating melanoma, wherein the anti-PD-1 antibody is administered, or prepared for administration, separately, simultaneously, or sequentially with a c-Raf inhibitor. It also provides a c-Raf inhibitor for use in treating melanoma, wherein the c-Raf inhibitor is administered, or prepared for administration, separately, simultaneously, or sequentially with an anti-PD-1 antibody. Typically, the anti-PD-1 antibody is administered intravenously, and is thus administered separately or sequentially with the c-Raf inhibitor, which is preferably administered orally. Suitable methods, routes, dosages and frequency of administration of the c-Raf inhibitor and the anti-PD-1 antibody are described herein.

The combinations disclosed herein can be administered together in a single composition or administered separately in two or more different compositions, *e.g.*, compositions or dosage forms as described herein. The administration of the therapeutic agents can be in any order. The first agent and the additional agents (*e.g.,* second, third agents) can be administered via the same administration route or via different administration routes.

The pharmaceutical combinations described herein, in particular the pharmaceutical combination of the invention, may be a free combination product, i.e. a combination of two or more active ingredients, e.g. COMPOUND A and the exemplary antibody molecule described herein (Antibody B), which is administered simultaneously, separately or sequentially as two or more distinct dosage forms.

A free combination product can be: (a) two or more separate drug products packaged together in a single package or kit, or (b) a drug product packaged separately that according to its labelling is for use only with other individually specified drugs where each drug is required to achieve the intended use, indication, or effect.

The present invention also provides a combined preparation comprising (a) one or more dosage units of the c-Raf inhibitor Compound A, or a pharmaceutically acceptable salt thereof, and (b) one or more dosage units of an anti-PD-1 antibody as described herein, and at least one pharmaceutically acceptable carrier.

In a further embodiment, the present invention is particularly related to a method of treating a cancer harboring one or more Mitogen-activated protein kinase (MAPK) pathway alterations. In one embodiment, the present invention relates to the use of the combination of the invention for the preparation of a medicament for the treatment of a proliferative disease, particularly a cancer. In one embodiment, the combination of the invention is for use in the preparation of a medicament for the treatment of cancer.

In a further embodiment, the present invention relates to the use of COMPOUND A as a single agent and the use of the combination of the invention for the preparation of a medicament for the treatment of a cancer characterized by gain-of-function mutation in the MAPK pathway.

In a further embodiment, the present invention relates to the use of COMPOUND A as a single agent and the use of the combination of the invention for the preparation of a medicament for the treatment of a cancer characterized by gain-of-function mutation in the MAPK pathway. These tumors are further described below.

In a further embodiment, the present invention relates to COMPOUND A, as a single agent, for use in the treatment of a solid tumor that harbors mitogen-activated protein kinase (MAPK) alterations, such as *KRAS*-mutant tumors, *NRAS*-mutant tumors and certain *BRAF*-

mutant tumors. In a further embodiment, the present invention relates to the pharmaceutical combination of the present invention for use in the treatment of a solid tumor that harbors mitogen-activated protein kinase (MAPK) alterations, such as *KRAS*-mutant tumors and *NRAS*-mutant tumors. These tumors are further described below.

Solid tumor that harbors mitogen-activated protein kinase (MAPK) alterations

MAPK alterations are generally regarded as strong driver mutations that might be acquired in the early stages of carcinogenesis and do not change over time.

The present invention provides useful treatment options with patients with solid tumors harboring MAPK alteration(s). Examples of such alterations are listed in the Table below. The mutational status of tumors of such patients may be determined by using commercial kits and methods readily available in the art.

Table: Genes of MAPK pathway.

Genes	Alteration(s)
NRAS	Mutation, Amplification
KRAS	Mutation, Amplification
NF1	Mutation, Deletion
BRAF V600	Mutation
Other *BRAF* (other than *BRAF* V600)	Mutation, Amplification
CRAF	Mutation, Amplification
MEK1	Mutation, Amplification
MEK2	Mutation, Amplification
GNAQ	Mutation, Amplification
GNA11	Mutation, Amplification

The present invention therefore provides treatment options for patients suffering from a solid tumor which harbors one of more MAPK alteration as described in the Table above.

KRAS-mutant tumors

The term "*KRAS*- mutant" tumor or cancer includes any tumor that exhibits a mutated *KRAS* protein, in particular gain-of-function *KRAS*- mutation; especially any G12X, G13X, Q61X or A146X *KRAS*- mutant, where X is any amino acid other than the one naturally occurring at that position. *E.g.*, a G12V mutation means that a glycine is substituted with valine at codon 12. Examples of *KRAS* mutations in tumors include Q61K, G12V, G12C and

A146T. Thus *KRAS*-mutant NSCLC include Q61K, G12V, G12C and A146T NSCLC. The cancer may be at an early, intermediate or late stage.

Non-small cell lung cancer (NSCLC)

NSCLC is the most common type (roughly 85%) of lung cancer with approximately 70% of these patients presenting with advanced disease (Stage IIIB or Stage IV) at the time of diagnosis. Recently, two inhibitors of the PD-1/PD-L1 interaction have been approved for use in NSCLC (pembrolizumab and nivolumab). However, results available so far indicate that many patients treated with single agent PD-1 inhibitors do not benefit adequately from treatment. *KRAS*-mutant NSCLC remains an elusive target for cancer therapy. About 30% of NSCLC contain activating *KRAS* mutations, and these mutations are associated with resistance to EGFR TKIs (Pao W, Wang TY, Riely GJ, et al (2005) *KRAS* mutations and primary resistance of lung adenocarcinomas to gefitinib or erlotinib. PLoS Med; 2(1): e17). Direct inhibition of *KRAS* has proven challenging.

BRAF mutations have been observed in up to 3 % of NSCLC and have also been described as a resistance mechanism in *EGFR* mutation positive NSCLC (Paik PK, Arcila ME, Fara M, et al (2011). Clinical characteristics of patients with lung adenocarcinomas harboring *BRAF* mutations. J Clin Oncol. May 20;29(15):2046-51).

The present invention therefore provides COMPOUND A, or a pharmaceutically acceptable salt thereof, for use in the treatment of *KRAS*-mutant NSCLC, and/or the treatment of *BRAF*-mutant NSCLC.

The present invention also provides COMPOUND A, or a pharmaceutically acceptable salt thereof, for use in the treatment of *KRAS*- and *BRAF*-mutant NSCLC, i.e. NSCLC which is both *KRAS*- and *BRAF*-mutant.

The present invention also provides a pharmaceutical combination described herein, -e.g. the pharmaceutical combination comprising (a) COMPOUND A, or a pharmaceutically acceptable salt thereof, and (b) an isolated antibody molecule capable of binding to a human Programmed Death-1 (PD-1) comprising a heavy chain variable region (VH) comprising a HCDR1, a HCDR2 and a HCDR3 amino acid sequence of BAP049-Clone-B or BAP049-

Clone-E as described in Table 1 and a light chain variable region (VL) comprising a LCDR1, a LCDR2 and a LCDR3 amino acid sequence of BAP049-Clone-B or BAP049-Clone-E as described in Table 1 below-for use in the treatment of *KRAS*-mutant NSCLC.

Ovarian cancer

Ovarian cancer is the most lethal gynecologic cancer and is a heterogeneous disease comprised of a collection of different histologic and molecular subtypes with variable prognosis. The epithelial subtype comprises 90% of ovarian cancers.

The most common histologic subtype of epithelial ovarian cancer is serous carcinoma accounting for 60 to 70% of epithelial ovarian cancers. A two tiered grading system separates serous carcinoma into low-grade serous (LGS) and high-grade serous (HGS) that have different molecular characteristics, immunohistochemical profile, epidemiologic features, and clinical behavior. LGS carcinoma accounts for up to 10% of the serous epithelial ovarian cancers and ovarian carcinomas with *KRAS* (up to 40%) or *BRAF* mutations (2-6%) are predominantly LGS carcinomas. LGS carcinoma is chemoresistant, not only to first-line agents, but also in the setting of recurrent disease.

It is expected that COMPOUND A may be useful in the treatment of patients with *KRAS- and/ or BRAF*-mutant ovarian cancer.

The present invention therefore provides COMPOUND A, or a pharmaceutically acceptable salt thereof, for use in the treatment of *KRAS*-mutant ovarian cancer, and/or the treatment of *BRAF*-mutant ovarian cancer.

The present invention also provides COMPOUND A, or a pharmaceutically acceptable salt thereof, for use in the treatment of *KRAS*- and *BRAF*-mutant ovarian cancer, i.e. ovarian cancer which is both *KRAS*- mutant and *BRAF*-mutant.

NRAS-mutant tumors

The term "*NRAS*- mutant" tumor or cancer includes any tumor that exhibits a mutated *NRAS* protein, in particular gain-of-function *NRAS*-mutation; especially any G12X, G13X, or Q61X *NRAS*- mutant, where X is any amino acid other than the one naturally occurring at that position. *E.g.,* a G12V mutation means that a glycine is substituted with valine at codon

12. Examples of *NRAS* mutations in tumors include G12C, G12R, G12S, G12A, G12D, G12V, G13R, G13C, G13A, G13D, G13V,Q61E, Q61K, Q61L, Q61P, Q61R, Q61H . Thus, *NRAS*-mutant melanoma comprise G12C, G12R, G12S, G12A, G12D, G12V, G13R, G13C, G13A, G13D, G13V,Q61E, Q61K, Q61L, Q61P, Q61R, Q61H melanoma. The cancer may be at an early, intermediate or late stage.

Melanoma

The MAPK pathway plays a major role in the development and progression of melanoma). *BRAF* mutations occur in 40-60% and *NRAS* mutations in 15-20% of melanoma patients *BRAF* V600E and *BRAF* V600K-mutant patients reportedly account for 93-98% of all *BRAF* V600-mutant metastatic melanoma patients. These mutations constitutively activate *BRAF* and downstream signal transduction in the MAPK pathway, which signals for cancer cell proliferation and survival. Currently, the existing targeted therapeutic options for patients with *BRAF* V600-mutant melanoma comprise therapies including BRAFi (e.g. dabrafenib) and MEKi (trametinib) as a single agent or in combination. Blockade of MAPK signaling through targeted inhibition of *BRAF* or its downstream effector MEK has been associated with improved PFS (progression free survival) and OS (overall survival); however, patients commonly experience disease progression after a few months of treatment. Although there are multiple paths to resistance, the main mechanisms result in reactivation of the MAPK signaling pathway in the presence of an inhibitor.

It is thus important to identify appropriate targeted therapy for melanoma patients after relapse on BRAFi and/or MEKi treatment. BRAFi include vemurafenib, dabrafenib and encorafenib, which are efficacious in melanomas with the *BRAF* V600E mutation, are found to be ineffective in RAS-mutant cancers.

NRAS missense mutations in codons 12, 13, and 61 arise in 13-25 % of all melanomas and are usually mutually exclusive to *BRAF* and other driver mutations. These tumors show aggressive behavior, with a high rate of liver and brain metastases at initial diagnosis, and, therefore, poor prognosis. Response to standard of care chemotherapy is very limited, and so far, there are no targeted therapies approved specifically for patients with *NRAS*-mutated melanoma, although a Phase 3 study demonstrated some benefit of the MEK inhibitor binimetinib as compared to standard of care chemotherapy with dacarbazine, e.g. improved overall response rate of 15 vs. 7% (Dummer R, Schadendorf D, Ascierto PA et al (2017)

Binimetinib versus dacarbazine in patients with advanced NRAS-mutant melanoma (NEMO): a multicentre, open-label, randomised, phase 3 trial. Lancet Oncol 2017; 18: 435–45). 402 patients were randomly assigned in a 2:1 fashion. A median PFS of 2.8 (95% CI: 2.8-3.6) vs. 1.5 (1.5-1.7), HR 0.62 (0.47-0.80) in favor of binimetinib has been observed. However, discontinuation rate as a result of adverse events suspected to be related to study drug was high (20% vs. 5%), and the benefit in PFS did not transfer into improvements in overall survival (11.0 (95% CI: 8.9-13.6) vs. 10.1 (7.0-16.5) months. Treatment options for patients suffering from *NRAS*-mutated melanoma are therefore still needed.

The present invention therefore provides COMPOUND A, or a pharmaceutically acceptable salt thereof, for use in the treatment of relapsed and/or refractory *BRAF* V600-mutated melanoma after failure of BRAFi/MEKi, (e.g. dabrafenib and trametinib as single agents or in combination; e.g. binimetinib) therapy.

The present invention also provides COMPOUND A, or a pharmaceutically acceptable salt thereof, for use in the treatment of *NRAS*-mutated melanoma.

The present invention also provides a pharmaceutical combination described herein, -e.g. the pharmaceutical combination comprising (a) COMPOUND A, or a pharmaceutically acceptable salt thereof, and (b) an isolated antibody molecule capable of binding to a human Programmed Death-1 (PD-1) comprising a heavy chain variable region (VH) comprising a HCDR1, a HCDR2 and a HCDR3 amino acid sequence of BAP049-Clone-B or BAP049-Clone-E as described in Table 1 and a light chain variable region (VL) comprising a LCDR1, a LCDR2 and a LCDR3 amino acid sequence of BAP049-Clone-B or BAP049-Clone-E as described in Table 1 below-for use in the treatment of *NRAS*-mutated melanoma. The pharmaceutical combinations described herein may be useful in patients suffering from *NRAS*-mutated melanoma who may have received prior immunotherapies or may be immunotherapy naïve.

Uses of the Combination Therapies

The combinations disclosed herein can result in one or more of: an increase in antigen presentation, an increase in effector cell function (*e.g.*, one or more of T cell proliferation,

IFN-γ secretion or cytolytic function), inhibition of regulatory T cell function, an effect on the activity of multiple cell types, such as regulatory T cell, effector T cells and NK cells), an increase in tumor infiltrating lymphocytes, an increase in T-cell receptor mediated proliferation, and a decrease in immune evasion by cancerous cells. In one embodiment, the use of a PD-1 inhibitor in the combination inhibits, reduces or neutralizes one or more activities of PD-1, resulting in blockade or reduction of an immune checkpoint. Thus, such combinations can be used to treat or prevent disorders where enhancing an immune response in a subject is desired.

Accordingly, in another aspect, a method of modulating an immune response in a subject is provided. The method comprises administering to the subject a combination disclosed herein (*e.g.,* a combination comprising a therapeutically effective amount of an anti-PD-1 antibody molecule and a therapeutically effective amount of COMPOUND A, or a pharmaceutically acceptable salt thereof), such that the immune response in the subject is modulated. In one embodiment, the antibody molecule enhances, stimulates or increases the immune response in the subject. The subject can be a mammal, *e.g.*, a primate, preferably a higher primate, *e.g.*, a human (*e.g.*, a patient having, or at risk of having, a disorder described herein). In one embodiment, the subject is in need of enhancing an immune response. In one embodiment, the subject has, or is at risk of, having a disorder described herein, *e.g.*, a cancer or an infectious disorder as described herein. In certain embodiments, the subject is, or is at risk of being, immunocompromised. For example, the subject is undergoing or has undergone a chemotherapeutic treatment and/or radiation therapy. Alternatively, or in combination, the subject is, or is at risk of being, immunocompromised as a result of an infection.

In one aspect, a method of treating (*e.g.*, one or more of reducing, inhibiting, or delaying progression) proliferative disease which is a solid tumor that harbors Mitogen-activated protein kinase (MAPK) alterations, such as *KRAS*-mutant tumors, and in particular, *KRAS*-mutant NSCLC (non-small cell lung cancer) in a subject is provided. In another aspect, a method of treating (*e.g.*, one or more of reducing, inhibiting, or delaying progression) proliferative disease which is a solid tumor that harbors Mitogen-activated protein kinase (MAPK) alterations, such as *NRAS*-mutant tumors, and in particular, *NRAS*-mutant melanoma in a subject is provided. The method comprises administering to the subject a combination disclosed herein (*e.g.,* a combination comprising a therapeutically effective amount of an anti-PD-1 antibody molecule and a therapeutically effective amount of Compound A, or a pharmaceutically acceptable salt thereof).

The combinations as described herein can be administered to the subject systemically (*e.g.*, orally, parenterally, subcutaneously, intravenously, rectally, intramuscularly, intraperitoneally, intranasally, transdermally, or by inhalation or intracavitary installation), topically, or by application to mucous membranes, such as the nose, throat and bronchial tubes.

Dosages and therapeutic regimens of the therapeutic agents disclosed herein can be determined by a skilled artisan. In certain embodiments, the anti-PD-1 antibody molecule is administered by injection (*e.g.*, subcutaneously or intravenously) at a dose of about 1 to 30 mg/kg, *e.g.*, about 5 to 25 mg/kg, about 10 to 20 mg/kg, about 1 to 5 mg/kg, or about 3 mg/kg. The dosing schedule can vary from *e.g.*, once a week to once every 2, 3, or 4 weeks. In one embodiment, the anti-PD-1 antibody molecule is administered at a dose from about 10 to 20 mg/kg every other week.

In some embodiments, the anti-PD-1 antibody molecule is administered by injection (*e.g.*, subcutaneously or intravenously) at a dose (*e.g.,* a flat dose) of about 200 mg to 500 mg, *e.g.,* about 250 mg to 450 mg, about 300 mg to 400 mg, about 250 mg to 350 mg, about 350 mg to 450 mg, or about 300 mg or about 400 mg. The dosing schedule (*e.g.,* flat dosing schedule) can vary from e.g., once a week to once every 2, 3, 4, 5, or 6 weeks. In one embodiment, the anti-PD-1 antibody molecule is administered at a dose from about 300 mg to 400 mg once every three weeks or once every four weeks. In one embodiment, the anti-PD-1 antibody molecule is administered at a dose from about 300 mg once every three weeks. In one embodiment, the anti-PD-1 antibody molecule is administered at a dose from about 400 mg once every four weeks. In one embodiment, the anti-PD-1 antibody molecule is administered at a dose from about 300 mg once every four weeks. In one embodiment, the anti-PD-1 antibody molecule is administered at a dose from about 400 mg once every three weeks.

The total daily dose of COMPOUND A may be administered in a single dose (i.e. once daily) or twice daily. For example, COMPOUND A may be administered at a dose of 1200 mg once daily, or 400 mg twice daily.

The c-Raf inhibitor which is COMPOUND A may be administered at a dose of about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200 mg once a day and the preferred anti-PD-1 antibody molecule is administered at a dose of about 400 mg once every three weeks.

The c-Raf inhibitor which is COMPOUND A may be the c-Raf inhibitor is administered at a dose of about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650,

700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200 mg once a day and the anti-PD-1 antibody molecule is administered at a dose of about 400 mg once every four weeks.

COMPOUND A may in particular be administered at a once daily (QD) dose of 100, 200, 400, 800 or 1200 mg; or 200 mg twice daily; or 400 mg twice daily. The dosages quoted herein may apply to the administration of COMPOUND A as monotherapy or as part of a combination therapy, e.g., as part of the combination of the present invention, as described herein.

In a preferred embodiment, the exemplary anti-PD-1 molecule may be administered at a dose of 400 mg once every four weeks and COMPOUND A may be administered at a total dose of at a once daily (QD) dose of 100, 200, 400, 800 or 1200 mg; or 200 mg twice daily; or 400 mg twice daily.

Further Combination Therapies

The methods and combinations described herein can be used in combination with other agents or therapeutic modalities. In one embodiment, the methods described herein include administering to the subject a combination comprising an anti-PD-1 antibody molecule as described herein, in combination with an agent or therapeutic procedure or modality, in an amount effective to treat or prevent a disorder. The anti-PD-1 antibody molecule and the agent or therapeutic procedure or modality can be administered simultaneously or sequentially in any order. Any combination and sequence of the anti-PD-1 antibody molecules and other therapeutic agents, procedures or modalities (*e.g.,* as described herein) can be used. The antibody molecule and/or other therapeutic agents, procedures or modalities can be administered during periods of active disorder, or during a period of remission or less active disease. The antibody molecule can be administered before the other treatment, concurrently with the treatment, post-treatment, or during remission of the disorder.

In certain embodiments, the methods and compositions described herein are administered in combination with one or more of other antibody molecules, chemotherapy, other anti-cancer therapy (*e.g.*, targeted anti-cancer therapies, gene therapy, viral therapy, RNA therapy bone marrow transplantation, nanotherapy, or oncolytic drugs), cytotoxic agents, immune-based therapies (*e.g.*, cytokines or cell-based immune therapies), surgical procedures (*e.g.*, lumpectomy or mastectomy) or radiation procedures, or a combination of any of the foregoing. The additional therapy may be in the form of adjuvant or neoadjuvant therapy. In some embodiments, the additional therapy is an enzymatic inhibitor (*e.g.*, a small

molecule enzymatic inhibitor) or a metastatic inhibitor. Exemplary cytotoxic agents that can be administered in combination with include antimicrotubule agents, topoisomerase inhibitors, anti-metabolites, mitotic inhibitors, alkylating agents, anthracyclines, vinca alkaloids, intercalating agents, agents capable of interfering with a signal transduction pathway, agents that promote apoptosis, proteosome inhibitors, and radiation (*e.g.*, local or whole body irradiation (*e.g.*, gamma irradiation). In other embodiments, the additional therapy is surgery or radiation, or a combination thereof. In other embodiments, the additional therapy is a therapy targeting one or more of PI3K/AKT/mTOR pathway, an HSP90 inhibitor, or a tubulin inhibitor.

Alternatively, or in combination with the aforesaid combinations, the methods and compositions described herein can be administered in combination with one or more of: an immunomodulator (*e.g.*, an activator of a costimulatory molecule or an inhibitor of an inhibitory molecule, *e.g.,* an immune checkpoint molecule); a vaccine, *e.g.*, a therapeutic cancer vaccine; or other forms of cellular immunotherapy.

In one embodiment, the combination disclosed herein, *e.g.*, a combination comprising an anti-PD-1 antibody molecule, is used in combination with chemotherapy to treat a lung cancer, *e.g.*, non-small cell lung cancer. In one embodiment, the anti-PD-1 antibody molecule is used with standard lung, *e.g.*, NSCLC, chemotherapy, *e.g.*, platinum doublet therapy, to treat lung cancer. The cancer may be at an early, intermediate or late stage.

In one embodiment, the combination disclosed herein, *e.g.*, a combination comprising an anti-PD-1 antibody molecule, is used in combination with chemotherapy to treat skin cancer, *e.g.*, melanoma. In one embodiment, the anti-PD-1 antibody molecule is used with standard skin, *e.g.*, melanoma, chemotherapy, *e.g.*, platinum doublet therapy, to treat skin cancer. The cancer may be at an early, intermediate or late stage.

Any combination and sequence of the anti-PD-1 antibody molecules and other therapeutic agents, procedures or modalities (*e.g.*, as described herein) can be used. The antibody molecule and/or other therapeutic agents, procedures or modalities can be administered during periods of active disorder, or during a period of remission or less active disease. The antibody molecule can be administered before the other treatment, concurrently with the treatment, post-treatment, or during remission of the disorder.

Disclosed herein, at least in part, are antibody molecules *(e.g.*, humanized antibody molecules) that bind to Programmed Death 1 (PD-1) with high affinity and specificity. Nucleic acid molecules encoding the antibody molecules, expression vectors, host cells and

methods for making the antibody molecules are also provided. Pharmaceutical compositions and dose formulations comprising the antibody molecules are also provided. The anti-PD-1 antibody molecules disclosed herein can be used (alone or in combination with other agents or therapeutic modalities) to treat, prevent and/or diagnose disorders, such as cancerous disorders (*e.g.*, solid and soft-tissue tumors). Thus, compositions and methods for detecting PD-1, as well as methods for treating various disorders including cancer using the anti-PD-1 antibody molecules are disclosed herein. In certain embodiments, the anti-PD-1 antibody molecule is administered or used at a flat or fixed dose.

Additional terms are defined below and throughout the application.

As used herein, the articles "a" and "an" refer to one or to more than one (*e.g.*, to at least one) of the grammatical object of the article.

The term "or" is used herein to mean, and is used interchangeably with, the term "and/or", unless context clearly indicates otherwise.

"About" and "approximately" shall generally mean an acceptable degree of error for the quantity measured given the nature or precision of the measurements. Exemplary degrees of error are within 20 percent (%), typically, within 10%, and more typically, within 5% of a given value or range of values.

By “a combination” or “in combination with,” it is not intended to imply that the therapy or the therapeutic agents must be administered at the same time and/or formulated for delivery together, although these methods of delivery are within the scope described herein. The therapeutic agents in the combination can be administered concurrently with, prior to, or subsequent to, one or more other additional therapies or therapeutic agents. The therapeutic agents or therapeutic protocol can be administered in any order. In general, each agent will be administered at a dose and/or on a time schedule determined for that agent. In will further be appreciated that the additional therapeutic agent utilized in this combination may be administered together in a single composition or administered separately in different compositions. In general, it is expected that additional therapeutic agents utilized in combination be utilized at levels that do not exceed the levels at which they are utilized individually. In some embodiments, the levels utilized in combination will be lower than those utilized individually.

In embodiments, the additional therapeutic agent is administered at a therapeutic or lower-than therapeutic dose. In certain embodiments, the concentration of the second therapeutic agent that is required to achieve inhibition, *e.g.*, growth inhibition is lower when the second therapeutic agent is administered in combination with the first therapeutic agent,

e.g., the anti-PD-1 antibody molecule, than when the second therapeutic agent is administered individually. In certain embodiments, the concentration of the first therapeutic agent that is required to achieve inhibition, *e.g.*, growth inhibition is lower when the first therapeutic agent is administered in combination with the second therapeutic agent than when the first therapeutic agent is administered individually. In certain embodiments, in a combination therapy, the concentration of the second therapeutic agent that is required to achieve inhibition, *e.g.*, growth inhibition is lower than the therapeutic dose of the second therapeutic agent as a monotherapy, *e.g.*, 10-20%, 20-30%, 30-40%, 40-50%, 50-60%, 60-70%, 70-80%, or 80-90% lower. In certain embodiments, in a combination therapy, the concentration of the first therapeutic agent that is required to achieve inhibition, *e.g.* growth inhibition, is lower than the therapeutic dose of the first therapeutic agent as a monotherapy, *e.g.*, 10-20%, 20-30%, 30-40%, 40-50%, 50-60%, 60-70%, 70-80%, or 80-90% lower.

The term "inhibition," "inhibitor," or "antagonist" includes a reduction in a certain parameter, *e.g.*, an activity, of a given molecule, *e.g.*, an immune checkpoint inhibitor. For example, inhibition of an activity, *e.g.*, a PD-1 or PD-L1 activity, of at least 5%, 10%, 20%, 30%, 40% or more is included by this term. Thus, inhibition need not be 100%.

The term "activation," "activator," or "agonist" includes an increase in a certain parameter, *e.g.*, an activity, of a given molecule, *e.g.*, a costimulatory molecule. For example, increase of an activity, *e.g.*, a costimulatory activity, of at least 5%, 10%, 25%, 50%, 75% or more is included by this term.

The term "cancer" refers to a disease characterized by the rapid and uncontrolled growth of aberrant cells. Cancer cells can spread locally or through the bloodstream and lymphatic system to other parts of the body. As used herein, the term "cancer" or "tumor" includes premalignant, as well as malignant cancers and tumors.

As used herein, the terms "treat", "treatment" and "treating" refer to the reduction or amelioration of the progression, severity and/or duration of a disorder, *e.g.,* a proliferative disorder, or the amelioration of one or more symptoms (preferably, one or more discernible symptoms) of the disorder resulting from the administration of one or more therapies. In specific embodiments, the terms "treat," "treatment" and "treating" refer to the amelioration of at least one measurable physical parameter of a proliferative disorder, such as growth of a tumor, not necessarily discernible by the patient. In other embodiments the terms "treat", "treatment" and "treating" refer to the inhibition of the progression of a proliferative disorder, either physically by, *e.g.,* stabilization of a discernible symptom, physiologically by, *e.g.,* stabilization of a physical parameter, or both. In other embodiments the terms "treat",

"treatment" and "treating" refer to the reduction or stabilization of tumor size or cancerous cell count.

The term "isolated," as used herein, refers to material that is removed from its original or native environment (*e.g.*, the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated by human intervention from some or all of the co-existing materials in the natural system, is isolated. Such polynucleotides could be part of a vector and/or such polynucleotides or polypeptides could be part of a composition, and still be isolated in that such vector or composition is not part of the environment in which it is found in nature.

Various aspects of the invention are described in further detail below. Additional definitions are set out throughout the specification.

Antibody Molecules

In one embodiment, the antibody molecule binds to a mammalian, *e.g.*, human, PD-1. For example, the antibody molecule binds specifically to an epitope, *e.g.*, linear or conformational epitope, (*e.g.*, an epitope as described herein) on PD-1.

As used herein, the term "antibody molecule" refers to a protein, *e.g.*, an immunoglobulin chain or fragment thereof, comprising at least one immunoglobulin variable domain sequence. The term "antibody molecule" includes, for example, a monoclonal antibody (including a full length antibody which has an immunoglobulin Fc region). In an embodiment, an antibody molecule comprises a full length antibody, or a full length immunoglobulin chain. In an embodiment, an antibody molecule comprises an antigen binding or functional fragment of a full length antibody, or a full length immunoglobulin chain. In an embodiment, an antibody molecule is a multispecific antibody molecule, *e.g.,* it comprises a plurality of immunoglobulin variable domain sequences, wherein a first immunoglobulin variable domain sequence of the plurality has binding specificity for a first epitope and a second immunoglobulin variable domain sequence of the plurality has binding specificity for a second epitope. In an embodiment, a multispecific antibody molecule is a bispecific antibody molecule. A bispecific antibody has specificity for no more than two antigens. A bispecific antibody molecule is characterized by a first immunoglobulin variable domain sequence which has binding specificity for a first epitope and a second immunoglobulin variable domain sequence that has binding specificity for a second epitope.

In an embodiment, an antibody molecule is a monospecific antibody molecule and binds a single epitope. *E.g.*, a monospecific antibody molecule having a plurality of immunoglobulin variable domain sequences, each of which binds the same epitope.

In an embodiment an antibody molecule is a multispecific antibody molecule, *e.g.*, it comprises a plurality of immunoglobulin variable domains sequences, wherein a first immunoglobulin variable domain sequence of the plurality has binding specificity for a first epitope and a second immunoglobulin variable domain sequence of the plurality has binding specificity for a second epitope. In an embodiment the first and second epitopes are on the same antigen, *e.g.*, the same protein (or subunit of a multimeric protein). In an embodiment the first and second epitopes overlap. In an embodiment the first and second epitopes do not overlap. In an embodiment the first and second epitopes are on different antigens, *e.g.*, the different proteins (or different subunits of a multimeric protein). In an embodiment a multispecific antibody molecule comprises a third, fourth or fifth immunoglobulin variable domain. In an embodiment, a multispecific antibody molecule is a bispecific antibody molecule, a trispecific antibody molecule, or tetraspecific antibody molecule,

In an embodiment a multispecific antibody molecule is a bispecific antibody molecule. A bispecific antibody has specificity for no more than two antigens. A bispecific antibody molecule is characterized by a first immunoglobulin variable domain sequence which has binding specificity for a first epitope and a second immunoglobulin variable domain sequence that has binding specificity for a second epitope. In an embodiment the first and second epitopes are on the same antigen, *e.g.*, the same protein (or subunit of a multimeric protein). In an embodiment the first and second epitopes overlap. In an embodiment the first and second epitopes do not overlap. In an embodiment the first and second epitopes are on different antigens, *e.g.*, the different proteins (or different subunits of a multimeric protein). In an embodiment a bispecific antibody molecule comprises a heavy chain variable domain sequence and a light chain variable domain sequence which have binding specificity for a first epitope and a heavy chain variable domain sequence and a light chain variable domain sequence which have binding specificity for a second epitope. In an embodiment a bispecific antibody molecule comprises a half antibody having binding specificity for a first epitope and a half antibody having binding specificity for a second epitope. In an embodiment a bispecific antibody molecule comprises a half antibody, or fragment thereof, having binding specificity for a first epitope and a half antibody, or fragment thereof, having binding specificity for a second epitope. In an embodiment a bispecific antibody molecule comprises a scFv, or fragment thereof, have binding specificity

for a first epitope and a scFv, or fragment thereof, have binding specificity for a second epitope. In an embodiment the first epitope is located on PD-1 and the second epitope is located on a TIM-3, LAG-3, CEACAM (*e.g.*, CEACAM-1 and/or CEACAM-5), PD-L1, or PD-L2.

In an embodiment, an antibody molecule comprises a diabody, and a single-chain molecule, as well as an antigen-binding fragment of an antibody (*e.g.*, Fab, F(ab')$_2$, and Fv). For example, an antibody molecule can include a heavy (H) chain variable domain sequence (abbreviated herein as VH), and a light (L) chain variable domain sequence (abbreviated herein as VL). In an embodiment an antibody molecule comprises or consists of a heavy chain and a light chain (referred to herein as a half antibody). In another example, an antibody molecule includes two heavy (H) chain variable domain sequences and two light (L) chain variable domain sequence, thereby forming two antigen binding sites, such as Fab, Fab', F(ab')$_2$, Fc, Fd, Fd', Fv, single chain antibodies (scFv for example), single variable domain antibodies, diabodies (Dab) (bivalent and bispecific), and chimeric (*e.g.*, humanized) antibodies, which may be produced by the modification of whole antibodies or those synthesized de novo using recombinant DNA technologies. These functional antibody fragments retain the ability to selectively bind with their respective antigen or receptor. Antibodies and antibody fragments can be from any class of antibodies including, but not limited to, IgG, IgA, IgM, IgD, and IgE, and from any subclass (*e.g.*, IgG1, IgG2, IgG3, and IgG4) of antibodies. The preparation of antibody molecules can be monoclonal or polyclonal. An antibody molecule can also be a human, humanized, CDR-grafted, or in vitro generated antibody. The antibody can have a heavy chain constant region chosen from, *e.g.*, IgG1, IgG2, IgG3, or IgG4. The antibody can also have a light chain chosen from, *e.g.*, kappa or lambda. The term "immunoglobulin" (Ig) is used interchangeably with the term "antibody" herein.

Examples of antigen-binding fragments of an antibody molecule include: (i) a Fab fragment, a monovalent fragment consisting of the VL, VH, CL and CH1 domains; (ii) a F(ab')2 fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the VH and CH1 domains; (iv) a Fv fragment consisting of the VL and VH domains of a single arm of an antibody, (v) a diabody (dAb) fragment, which consists of a VH domain; (vi) a camelid or camelized variable domain; (vii) a single chain Fv (scFv), *see e.g.*, Bird *et al.* (1988) *Science* 242:423-426; and Huston *et al.* (1988) *Proc. Natl. Acad. Sci. USA* 85:5879-5883); (viii) a single domain antibody. These antibody fragments are obtained using conventional techniques

known to those with skill in the art, and the fragments are screened for utility in the same manner as are intact antibodies.

The term "antibody" includes intact molecules as well as functional fragments thereof. Constant regions of the antibodies can be altered, *e.g.*, mutated, to modify the properties of the antibody (*e.g.*, to increase or decrease one or more of: Fc receptor binding, antibody glycosylation, the number of cysteine residues, effector cell function, or complement function).

The VH and VL regions can be subdivided into regions of hypervariability, termed "complementarity determining regions" (CDR), interspersed with regions that are more conserved, termed "framework regions" (FR or FW).

The extent of the framework region and CDRs has been precisely defined by a number of methods (*see*, Kabat, E. A., *et al.* (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242; Chothia, C. *et al.* (1987) *J. Mol. Biol.* 196:901-917; and the AbM definition used by Oxford Molecular's AbM antibody modeling software. See, generally, *e.g.*, *Protein Sequence and Structure Analysis of Antibody Variable Domains.* In: Antibody Engineering Lab Manual (Ed.: Duebel, S. and Kontermann, R., Springer-Verlag, Heidelberg).

The terms "complementarity determining region," and "CDR," as used herein refer to the sequences of amino acids within antibody variable regions which confer antigen specificity and binding affinity. In general, there are three CDRs in each heavy chain variable region (HCDR1, HCDR2, HCDR3) and three CDRs in each light chain variable region (LCDR1, LCDR2, LCDR3).

The precise amino acid sequence boundaries of a given CDR can be determined using any of a number of well-known schemes, including those described by Kabat *et al.* (1991), "Sequences of Proteins of Immunological Interest," 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD ("Kabat" numbering scheme), Al-Lazikani *et al.*, (1997) *JMB* 273,927-948 ("Chothia" numbering scheme). As used herein, the CDRs defined according the "Chothia" number scheme are also sometimes referred to as "hypervariable loops."

For example, under Kabat, the CDR amino acid residues in the heavy chain variable domain (VH) are numbered 31-35 (HCDR1), 50-65 (HCDR2), and 95-102 (HCDR3); and the CDR amino acid residues in the light chain variable domain (VL) are numbered 24-34 (LCDR1), 50-56 (LCDR2), and 89-97 (LCDR3). Under Chothia the CDR amino acids in the VH are numbered 26-32 (HCDR1), 52-56 (HCDR2), and 95-102 (HCDR3); and the amino

acid residues in VL are numbered 26-32 (LCDR1), 50-52 (LCDR2), and 91-96 (LCDR3). By combining the CDR definitions of both Kabat and Chothia, the CDRs consist of amino acid residues 26-35 (HCDR1), 50-65 (HCDR2), and 95-102 (HCDR3) in human VH and amino acid residues 24-34 (LCDR1), 50-56 (LCDR2), and 89-97 (LCDR3) in human VL.

Generally, unless specifically indicated, the anti-PD-1 antibody molecules can include any combination of one or more Kabat CDRs and/or Chothia hypervariable loops, *e.g.*, described in Table 1. In one embodiment, the following definitions are used for the anti-PD-1 antibody molecules described in Table 1: HCDR1 according to the combined CDR definitions of both Kabat and Chothia, and HCCDRs 2-3 and LCCDRs 1-3 according the CDR definition of Kabat. Under all definitions, each VH and VL typically includes three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4.

As used herein, an "immunoglobulin variable domain sequence" refers to an amino acid sequence which can form the structure of an immunoglobulin variable domain. For example, the sequence may include all or part of the amino acid sequence of a naturally-occurring variable domain. For example, the sequence may or may not include one, two, or more N- or C-terminal amino acids, or may include other alterations that are compatible with formation of the protein structure.

The term "antigen-binding site" refers to the part of an antibody molecule that comprises determinants that form an interface that binds to the PD-1 polypeptide, or an epitope thereof. With respect to proteins (or protein mimetics), the antigen-binding site typically includes one or more loops (of at least four amino acids or amino acid mimics) that form an interface that binds to the PD-1 polypeptide. Typically, the antigen-binding site of an antibody molecule includes at least one or two CDRs and/or hypervariable loops, or more typically at least three, four, five or six CDRs and/or hypervariable loops.

The terms "monoclonal antibody" or "monoclonal antibody composition" as used herein refer to a preparation of antibody molecules of single molecular composition. A monoclonal antibody composition displays a single binding specificity and affinity for a particular epitope. A monoclonal antibody can be made by hybridoma technology or by methods that do not use hybridoma technology (*e.g.*, recombinant methods).

A humanized or CDR-grafted antibody will have at least one or two but generally all three recipient CDRs (of heavy and or light immuoglobulin chains) replaced with a donor CDR. The antibody may be replaced with at least a portion of a non-human CDR or only some of the CDRs may be replaced with non-human CDRs. It is only necessary to replace the

number of CDRs required for binding of the humanized antibody to PD-1. Preferably, the donor will be a rodent antibody, *e.g.,* a rat or mouse antibody, and the recipient will be a human framework or a human consensus framework. Typically, the immunoglobulin providing the CDRs is called the "donor" and the immunoglobulin providing the framework is called the "acceptor". In one embodiment, the donor immunoglobulin is a non-human (*e.g.,* rodent). The acceptor framework is a naturally-occurring (*e.g.,* a human) framework or a consensus framework, or a sequence about 85% or higher, preferably 90%, 95%, 99% or higher identical thereto.

Exemplary PD-1 Inhibitors

PD-1 is a CD28/CTLA-4 family member expressed, *e.g.,* on activated $CD4^+$ and $CD8^+$ T cells, T_{regs}, and B cells. It negatively regulates effector T cell signaling and function. PD-1 is induced on tumor-infiltrating T cells, and can result in functional exhaustion or dysfunction (Keir *et al.* (2008) *Annu. Rev. Immunol.* 26:677-704; Pardoll *et al.* (2012) *Nat Rev Cancer* 12(4):252-64). PD-1 delivers a coinhibitory signal upon binding to either of its two ligands, Programmed Death-Ligand 1 (PD-L1) or Programmed Death-Ligand 2 (PD-L2). PD-L1 is expressed on a number of cell types, including T cells, natural killer (NK) cells, macrophages, dendritic cells (DCs), B cells, epithelial cells, vascular endothelial cells, as well as many types of tumors. High expression of PD-L1 on murine and human tumors has been linked to poor clinical outcomes in a variety of cancers (Keir *et al.* (2008) *Annu. Rev. Immunol.* 26:677-704; Pardoll *et al.* (2012) *Nat Rev Cancer* 12(4):252-64). PD-L2 is expressed on dendritic cells, macrophages, and some tumors. Blockade of the PD-1 pathway has been pre-clinically and clinically validated for cancer immunotherapy. Both preclinical and clinical studies have demonstrated that anti-PD-1 blockade can restore activity of effector T cells and results in robust anti-tumor response. For example, blockade of PD-1 pathway can restore exhausted/dysfunctional effector T cell function (*e.g.,* proliferation, IFN-γ secretion, or cytolytic function) and/or inhibit T_{reg} cell function (Keir *et al.* (2008) *Annu. Rev. Immunol.* 26:677-704; Pardoll *et al.* (2012) *Nat Rev Cancer* 12(4):252-64). Blockade of the PD-1 pathway can be effected with an antibody, an antigen binding fragment thereof, an immunoadhesin, a fusion protein, or oligopeptide of PD-1, PD-L1 and/or PD-L2.

As used herein, the term “Programmed Death 1” or “PD-1” include isoforms, mammalian, *e.g.*, human PD-1, species homologs of human PD-1, and analogs comprising at least one common epitope with PD-1. The amino acid sequence of PD-1, *e.g.*, human PD-1,

is known in the art, *e.g.*, Shinohara T *et al.* (1994) *Genomics* 23(3):704-6; Finger LR, *et al.* *Gene* (1997) 197(1-2):177-87.

The anti-PD-1 antibody molecules described herein can be used alone or in combination with one or more additional agents described herein in accordance with a method described herein. In certain embodiments, the combinations described herein include a PD-1 inhibitor, *e.g.*, an anti-PD-1 antibody molecule *(e.g.*, humanized antibody molecules) as described herein.

In one embodiment, the anti-PD-1 antibody molecule includes:

(a) a heavy chain variable region (VH) comprising a HCDR1 amino acid sequence of SEQ ID NO: 4, a HCDR2 amino acid sequence of SEQ ID NO: 5, and a HCDR3 amino acid sequence of SEQ ID NO: 3; and a light chain variable region (VL) comprising a LCDR1 amino acid sequence of SEQ ID NO: 13, a LCDR2 amino acid sequence of SEQ ID NO: 14, and a LCDR3 amino acid sequence of SEQ ID NO: 33;

(b) a VH comprising a HCDR1 amino acid sequence chosen from SEQ ID NO: 1; a HCDR2 amino acid sequence of SEQ ID NO: 2; and a HCDR3 amino acid sequence of SEQ ID NO: 3; and a VL comprising a LCDR1 amino acid sequence of SEQ ID NO: 10, a LCDR2 amino acid sequence of SEQ ID NO: 11, and a LCDR3 amino acid sequence of SEQ ID NO: 32;

(c) a VH comprising a HCDR1 amino acid sequence of SEQ ID NO: 4, a HCDR2 amino acid sequence of SEQ ID NO: 5, and a HCDR3 amino acid sequence of SEQ ID NO: 3; and a VL comprising a LCDR1 amino acid sequence of SEQ ID NO: 13, a LCDR2 amino acid sequence of SEQ ID NO: 14, and a LCDR3 amino acid sequence of SEQ ID NO: 33; or

(d) a VH comprising a HCDR1 amino acid sequence of SEQ ID NO: 1; a HCDR2 amino acid sequence of SEQ ID NO: 2; and a HCDR3 amino acid sequence of SEQ ID NO: 3; and a VL comprising a LCDR1 amino acid sequence of SEQ ID NO: 10, a LCDR2 amino acid sequence of SEQ ID NO: 11, and a LCDR3 amino acid sequence of SEQ ID NO: 32.

2. The pharmaceutical combination of claim 1, wherein the anti-PD-1 antibody molecule comprises:

(a) a heavy chain variable region (VH) comprising a HCDR1 amino acid sequence of SEQ ID NO: 4, a HCDR2 amino acid sequence of SEQ ID NO: 5, and a HCDR3 amino acid sequence of SEQ ID NO: 3; and a light chain variable region (VL) comprising a LCDR1 amino acid sequence of SEQ ID NO: 13, a LCDR2 amino acid sequence of SEQ ID NO: 14, and a LCDR3 amino acid sequence of SEQ ID NO: 33;

(b) a VH comprising a HCDR1 amino acid sequence of SEQ ID NO: 1; a HCDR2 amino acid sequence of SEQ ID NO: 2; and a HCDR3 amino acid sequence of SEQ ID NO: 3; and a VL comprising a LCDR1 amino acid sequence of SEQ ID NO: 10, a LCDR2 amino acid sequence of SEQ ID NO: 11, and a LCDR3 amino acid sequence of SEQ ID NO: 32;

(c) a VH comprising a HCDR1 amino acid sequence of SEQ ID NO: 224, a HCDR2 amino acid sequence of SEQ ID NO: 5, and a HCDR3 amino acid sequence of SEQ ID NO: 3; and a VL comprising a LCDR1 amino acid sequence of SEQ ID NO: 13, a LCDR2 amino acid sequence of SEQ ID NO: 14, and a LCDR3 amino acid sequence of SEQ ID NO: 33; or

(d) a VH comprising a HCDR1 amino acid sequence of SEQ ID NO: 224; a HCDR2 amino acid sequence of SEQ ID NO: 2; and a HCDR3 amino acid sequence of SEQ ID NO: 3; and a VL comprising a LCDR1 amino acid sequence of SEQ ID NO: 10, a LCDR2 amino acid sequence of SEQ ID NO: 11, and a LCDR3 amino acid sequence of SEQ ID NO: 32.

In certain embodiments, the anti-PD-1 antibody molecule comprises:

(i) a heavy chain variable region (VH) comprising a HCDR1 amino acid sequence chosen from SEQ ID NO: 1, SEQ ID NO: 4 or SEQ ID NO: 224; a HCDR2 amino acid sequence of SEQ ID NO: 2; and a HCDR3 amino acid sequence of SEQ ID NO: 3; and

(ii) a light chain variable region (VL) comprising a LCDR1 amino acid sequence of SEQ ID NO: 10, a LCDR2 amino acid sequence of SEQ ID NO: 11, and a LCDR3 amino acid sequence of SEQ ID NO: 32.

In other embodiments, the anti-PD-1 antibody molecule comprises:

(i) a heavy chain variable region (VH) comprising a HCDR1 amino acid sequence chosen from SEQ ID NO: 1, SEQ ID NO: 4 or SEQ ID NO: 224; a HCDR2 amino acid sequence of SEQ ID NO: 5, and a HCDR3 amino acid sequence of SEQ ID NO: 3; and

(ii) a light chain variable region (VL) comprising a LCDR1 amino acid sequence of SEQ ID NO: 13, a LCDR2 amino acid sequence of SEQ ID NO: 14, and a LCDR3 amino acid sequence of SEQ ID NO: 33.

In embodiments of the aforesaid antibody molecules, the HCDR1 comprises the amino acid sequence of SEQ ID NO: 1. In other embodiments, the HCDR1 comprises the amino acid sequence of SEQ ID NO: 4. In yet other embodiments, the HCDR1 amino acid sequence of SEQ ID NO: 224.

In embodiments, the aforesaid antibody molecules have a heavy chain variable region comprising at least one framework (FW) region comprising the amino acid sequence of any of SEQ ID NOs: 147, 151, 153, 157, 160, 162, 166, or 169, or an amino acid sequence at least 90% identical thereto, or having no more than two amino acid substitutions, insertions or deletions compared to the amino acid sequence of any of SEQ ID NOs: 147, 151, 153, 157, 160, 162, 166, or 169.

In other embodiments, the aforesaid antibody molecules have a heavy chain variable region comprising at least one framework region comprising the amino acid sequence of any of SEQ ID NOs: 147, 151, 153, 157, 160, 162, 166, or 169.

In yet other embodiments, the aforesaid antibody molecules have a heavy chain variable region comprising at least two, three, or four framework regions comprising the amino acid sequences of any of SEQ ID NOs: 147, 151, 153, 157, 160, 162, 166, or 169.

In other embodiments, the aforesaid antibody molecules comprise a VHFW1 amino acid sequence of SEQ ID NO: 147 or 151, a VHFW2 amino acid sequence of SEQ ID NO: 153, 157, or 160, and a VHFW3 amino acid sequence of SEQ ID NO: 162 or 166, and, optionally, further comprising a VHFW4 amino acid sequence of SEQ ID NO: 169.

In other embodiments, the aforesaid antibody molecules have a light chain variable region comprising at least one framework region comprising the amino acid sequence of any of SEQ ID NOs: 174, 177, 181, 183, 185, 187, 191, 194, 196, 200, 202, 205, or 208, or an amino acid sequence at least 90% identical thereto, or having no more than two amino acid substitutions, insertions or deletions compared to the amino acid sequence of any of 174, 177, 181, 183, 185, 187, 191, 194, 196, 200, 202, 205, or 208.

In other embodiments, the aforesaid antibody molecules have a light chain variable region comprising at least one framework region comprising the amino acid sequence of any of SEQ ID NOs: 174, 177, 181, 183, 185, 187, 191, 194, 196, 200, 202, 205, or 208.

In other embodiments, the aforesaid antibody molecules have a light chain variable region comprising at least two, three, or four framework regions comprising the amino acid sequences of any of SEQ ID NOs: 174, 177, 181, 183, 185, 187, 191, 194, 196, 200, 202, 205, or 208.

In other embodiments, the aforesaid antibody molecules comprise a VLFW1 amino acid sequence of SEQ ID NO: 174, 177, 181, 183, or 185, a VLFW2 amino acid sequence of SEQ ID NO: 187, 191, or 194, and a VLFW3 amino acid sequence of SEQ ID NO: 196, 200, 202, or 205, and, optionally, further comprising a VLFW4 amino acid sequence of SEQ ID NO: 208.

In other embodiments, the aforesaid antibodies comprise a heavy chain variable domain comprising an amino acid sequence at least 85% identical to any of SEQ ID NOs: 38, 50, 82, or 86.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 38, 50, 82, or 86.

In other embodiments, the aforesaid antibody molecules comprise a light chain variable domain comprising an amino acid sequence at least 85% identical to any of SEQ ID NOs: 42, 46, 54, 58, 62, 66, 70, 74, or 78.

In other embodiments, the aforesaid antibody molecules comprise a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 42, 46, 54, 58, 62, 66, 70, 74, or 78.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 38.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 40.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 91.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 50.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 52 or SEQ ID NO: 102.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 82.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 84.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 86.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 88.

In other embodiments, the aforesaid antibody molecules comprise a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 42.

In other embodiments, the aforesaid antibody molecules comprise a light chain comprising the amino acid sequence of SEQ ID NO: 44.

In other embodiments, the aforesaid antibody molecules comprise a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 46.

In other embodiments, the aforesaid antibody molecules comprise a light chain comprising the amino acid sequence of SEQ ID NO: 48.

In other embodiments, the aforesaid antibody molecules comprise a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 54.

In other embodiments, the aforesaid antibody molecules comprise a light chain comprising the amino acid sequence of SEQ ID NO: 56.

In other embodiments, the aforesaid antibody molecules comprise a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 58.

In other embodiments, the aforesaid antibody molecules comprise a light chain comprising the amino acid sequence of SEQ ID NO: 60.

In other embodiments, the aforesaid antibody molecules comprise a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 62.

In other embodiments, the aforesaid antibodies comprise a light chain comprising the amino acid sequence of SEQ ID NO: 64.

In other embodiments, the aforesaid antibody molecules comprise a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 66.

In other embodiments, the aforesaid antibody molecules comprise a light chain comprising the amino acid sequence of SEQ ID NO: 68.

In other embodiments, the aforesaid antibody molecules comprise a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 70.

In other embodiments, the aforesaid antibody molecules comprise a light chain comprising the amino acid sequence of SEQ ID NO: 72.

In other embodiments, the aforesaid antibody molecules comprise a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 74.

In other embodiments, the aforesaid antibody molecules comprise a light chain comprising the amino acid sequence of SEQ ID NO: 76.

In other embodiments, the aforesaid antibody molecules comprise a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 78.

In other embodiments, the aforesaid antibody molecules comprise a light chain comprising the amino acid sequence of SEQ ID NO: 80.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 38 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 42.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 38 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 66.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 38 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 70.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 50 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 70.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 38 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 46.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 50 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 46.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 50 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 54.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 38 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 54.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 38 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 58.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 38 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 62.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 50 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 66.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 38 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 74.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 38 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 78.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 82 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 70.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 82 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 66.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 86 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 66.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 91 and a light chain comprising the amino acid sequence of SEQ ID NO: 44.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 91 and a light chain comprising the amino acid sequence of SEQ ID NO: 56.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 91 and a light chain comprising the amino acid sequence of SEQ ID NO: 68.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 91 and a light chain comprising the amino acid sequence of SEQ ID NO: 72.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 102 and a light chain comprising the amino acid sequence of SEQ ID NO: 72.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 40 and a light chain comprising the amino acid sequence of SEQ ID NO: 44.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 40 and a light chain comprising the amino acid sequence of SEQ ID NO: 48.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 52 and a light chain comprising the amino acid sequence of SEQ ID NO: 48.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 52 and a light chain comprising the amino acid sequence of SEQ ID NO: 56.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 40 and a light chain comprising the amino acid sequence of SEQ ID NO: 56.

In other embodiments, the aforesaid antibodies comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 40 and a light chain comprising the amino acid sequence of SEQ ID NO: 60.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 40 and a light chain comprising the amino acid sequence of SEQ ID NO: 64.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 52 and a light chain comprising the amino acid sequence of SEQ ID NO: 68.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 40 and a light chain comprising the amino acid sequence of SEQ ID NO: 68.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 52 and a light chain comprising the amino acid sequence of SEQ ID NO: 72.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 40 and a light chain comprising the amino acid sequence of SEQ ID NO: 72.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 40 and a light chain comprising the amino acid sequence of SEQ ID NO: 76.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 40 and a light chain comprising the amino acid sequence of SEQ ID NO: 80.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 84 and a light chain comprising the amino acid sequence of SEQ ID NO: 72.

In other embodiments, the aforesaid antibodies comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 84 and a light chain comprising the amino acid sequence of SEQ ID NO: 68.

In other embodiments, the aforesaid antibody molecules comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 88 and a light chain comprising the amino acid sequence of SEQ ID NO: 68.

In other embodiments, the aforesaid antibody molecules are chosen from a Fab, F(ab')2, Fv, or a single chain Fv fragment (scFv).

In other embodiments, the aforesaid antibody molecules comprise a heavy chain constant region selected from IgG1, IgG2, IgG3, and IgG4.

In other embodiments, the aforesaid antibody molecules comprise a light chain constant region chosen from the light chain constant regions of kappa or lambda.

In other embodiments, the aforesaid antibody molecules comprise a human IgG4 heavy chain constant region with a mutation at position 228 according to EU numbering or position 108 of SEQ ID NO: 212 or 214 and a kappa light chain constant region.

In other embodiments, the aforesaid antibody molecules comprise a human IgG4 heavy chain constant region with a Serine to Proline mutation at position 228 according to EU numbering or position 108 of SEQ ID NO: 212 or 214 and a kappa light chain constant region.

In other embodiments, the aforesaid antibody molecules comprise a human IgG1 heavy chain constant region with an Asparagine to Alanine mutation at position 297 according to EU numbering or position 180 of SEQ ID NO: 216 and a kappa light chain constant region.

In other embodiments, the aforesaid antibody molecules comprise a human IgG1 heavy chain constant region with an Aspartate to Alanine mutation at position 265 according to EU numbering or position 148 of SEQ ID NO: 217, and Proline to Alanine mutation at position 329 according to EU numbering or position 212 of SEQ ID NO: 217 and a kappa light chain constant region.

In other embodiments, the aforesaid antibody molecules comprise a human IgG1 heavy chain constant region with a Leucine to Alanine mutation at position 234 according to EU numbering or position 117 of SEQ ID NO: 218, and Leucine to Alanine mutation at position 235 according to EU numbering or position 118 of SEQ ID NO: 218 and a kappa light chain constant region.

In other embodiments, the aforesaid antibody molecules are capable of binding to human PD-1 with a dissociation constant (K_D) of less than about 0.2 nM.

In some embodiments, the aforesaid antibody molecules bind to human PD-1 with a K_D of less than about 0.2 nM, 0.15 nM, 0.1 nM, 0.05 nM, or 0.02 nM, *e.g.,* about 0.13 nM to 0.03 nM, *e.g.,* about 0.077 nM to 0.088 nM, *e.g.,* about 0.083 nM, *e.g.,* as measured by a Biacore method.

In other embodiments, the aforesaid antibody molecules bind to cynomolgus PD-1 with a K_D of less than about 0.2 nM, 0.15 nM, 0.1 nM, 0.05 nM, or 0.02 nM, *e.g.,* about 0.11 nM to 0.08 nM, *e.g.,* about 0.093 nM, *e.g.,* as measured by a Biacore method.

In certain embodiments, the aforesaid antibody molecules bind to both human PD-1 and cynomolgus PD-1 with similar K_D, *e.g.,* in the nM range, *e.g.,* as measured by a Biacore method. In some embodiments, the aforesaid antibody molecules bind to a human PD-1-Ig fusion protein with a K_D of less than about 0.1 nM, 0.075 nM, 0.05 nM, 0.025 nM, or 0.01 nM, *e.g.,* about 0.04 nM, *e.g.,* as measured by ELISA.

In some embodiments, the aforesaid antibody molecules bind to Jurkat cells that express human PD-1 (*e.g.,* human PD-1-transfected Jurkat cells) with a K_D of less than about 0.1 nM, 0.075 nM, 0.05 nM, 0.025 nM, or 0.01 nM, *e.g.,* about 0.06 nM, *e.g.,* as measured by FACS analysis.

In some embodiments, the aforesaid antibody molecules bind to cynomolgus T cells with a K_D of less than about 1nM, 0.75 nM, 0.5 nM, 0.25 nM, or 0.1 nM, *e.g.,* about 0.4 nM, *e.g.,* as measured by FACS analysis.

In some embodiments, the aforesaid antibody molecules bind to cells that express cynomolgus PD-1 (*e.g.,* cells transfected with cynomolgus PD-1) with a K_D of less than about 1nM, 0.75 nM, 0.5 nM, 0.25 nM, or 0.01 nM, *e.g.,* about 0.6 nM, *e.g.,* as measured by FACS analysis.

In certain embodiments, the aforesaid antibody molecules are not cross-reactive with mouse or rat PD-1. In other embodiments, the aforesaid antibodies are cross-reactive with rhesus PD-1. For example, the cross-reactivity can be measured by a Biacore method or a binding assay using cells that expresses PD-1 (*e.g.,* human PD-1-expressing 300.19 cells). In

other embodiments, the aforesaid antibody molecules bind an extracellular Ig-like domain of PD-1.

In other embodiments, the aforesaid antibody molecules are capable of reducing binding of PD-1 to PD-L1, PD-L2, or both, or a cell that expresses PD-L1, PD-L2, or both. In some embodiments, the aforesaid antibody molecules reduce (*e.g.*, block) PD-L1 binding to a cell that expresses PD-1 (*e.g.*, human PD-1-expressing 300.19 cells) with an IC50 of less than about 1.5 nM, 1 nM, 0.8 nM, 0.6 nM, 0.4 nM, 0.2 nM, or 0.1 nM, *e.g.*, between about 0.79 nM and about 1.09 nM, *e.g.*, about 0.94 nM, or about 0.78 nM or less, *e.g.*, about 0.3 nM. In some embodiments, the aforesaid antibodies reduce (*e.g.*, block) PD-L2 binding to a cell that expresses PD-1 (*e.g.*, human PD-1-expressing 300.19 cells) with an IC50 of less than about 2 nM, 1.5 nM, 1 nM, 0.5 nM, or 0.2 nM, *e.g.*, between about 1.05 nM and about 1.55 nM, or about 1.3 nM or less, *e.g.*, about 0.9 nM.

In other embodiments, the aforesaid antibody molecules are capable of enhancing an antigen-specific T cell response.

In embodiments, the antibody molecule is a monospecific antibody molecule or a bispecific antibody molecule. In embodiments, the antibody molecule has a first binding specificity for PD-1 and a second binding specifity for TIM-3, LAG-3, CEACAM (*e.g.*, CEACAM-1, CEACAM-3, and/or CEACAM-5), PD-L1 or PD-L2. In embodiments, the antibody molecule comprises an antigen binding fragment of an antibody, *e.g.*, a half antibody or antigen binding fragment of a half antibody.

In some embodiments, the aforesaid antibody molecules increase the expression of IL-2 from cells activated by Staphylococcal enterotoxin B (SEB) (*e.g.*, at 25 μg/mL) by at least about 2, 3, 4, 5-fold, *e.g.*, about 2 to 3-fold, *e.g.*, about 2 to 2.6-fold, *e.g.*, about 2.3-fold, compared to the expression of IL-2 when an isotype control (*e.g.*, IgG4) is used, *e.g.*, as measured in a SEB T cell activation assay or a human whole blood *ex vivo* assay.

In some embodiments, the aforesaid antibody molecules increase the expression of IFN-γ from T cells stimulated by anti-CD3 (*e.g.*, at 0.1 μg/mL) by at least about 2, 3, 4, 5-fold, *e.g.*, about 1.2 to 3.4-fold, *e.g.*, about 2.3-fold, compared to the expression of IFN-γ when an isotype control (*e.g.*, IgG4) is used, *e.g.*, as measured in an IFN-γ activity assay.

In some embodiments, the aforesaid antibody molecules increase the expression of IFN-γ from T cells activated by SEB (*e.g.*, at 3 pg/mL) by at least about 2, 3, 4, 5-fold, *e.g.*, about 0.5 to 4.5-fold, *e.g.*, about 2.5-fold, compared to the expression of IFN-γ when an isotype control (*e.g.*, IgG4) is used, *e.g.*, as measured in an IFN-γ activity assay.

In some embodiments, the aforesaid antibody molecules increase the expression of IFN-γ from T cells activated with an CMV peptide by at least about 2, 3, 4, 5-fold, *e.g.,* about 2 to 3.6-fold, *e.g.,* about 2.8-fold, compared to the expression of IFN-γ when an isotype control (*e.g.,* IgG4) is used, *e.g.,* as measured in an IFN-γ activity assay.

In some embodiments, the aforesaid antibody molecules increase the proliferation of $CD8^+$ T cells activated with an CMV peptide by at least about 1, 2, 3, 4, 5-fold, *e.g.,* about 1.5-fold, compared to the proliferation of $CD8^+$ T cells when an isotype control (*e.g.,* IgG4) is used, *e.g.,* as measured by the percentage of CD8+ T cells that passed through at least n (*e.g.,* n = 2 or 4) cell divisions.

In certain embodiments, the aforesaid antibody molecules has a Cmax between about 100 μg/mL and about 500 μg/mL, between about 150 μg/mL and about 450 μg/mL, between about 250 μg/mL and about 350 μg/mL, or between about 200 μg/mL and about 400 μg/mL, *e.g.,* about 292.5 μg/mL, *e.g.,* as measured in monkey.

In certain embodiments, the aforesaid antibody molecules has a $T_{1/2}$ between about 250 hours and about 650 hours, between about 300 hours and about 600 hours, between about 350 hours and about 550 hours, or between about 400 hours and about 500 hours, *e.g.,* about 465.5 hours, *e.g.,* as measured in monkey.

In some embodiments, the aforesaid antibody molecules bind to PD-1 with a Kd slower than 5×10^{-4}, 1×10^{-4}, 5×10^{-5}, or 1×10^{-5} s^{-1}, *e.g.,* about 2.13×10^{-4} s^{-1}, *e.g.*, as measured by a Biacore method. In some embodiments, the aforesaid antibody molecules bind to PD-1 with a Ka faster than 1×10^{4}, 5×10^{4}, 1×10^{5}, or 5×10^{5} $M^{-1}s^{-1}$, *e.g.,* about 2.78×10^{5} $M^{-1}s^{-1}$, *e.g.*, as measured by a Biacore method.

In some embodiments, the aforesaid anti-PD-1 antibody molecules bind to one or more residues within the C strand, CC' loop, C' strand and FG loop of PD-1. The domain structure of PD-1 is described, *e.g.*, in Cheng et al., "Structure and Interactions of the Human Programmed Cell Death 1 Receptor" *J. Biol. Chem.* 2013, 288:11771-11785. As described in Cheng *et. al.*, the C strand comprises residues F43-M50, the CC' loop comprises S51-N54, the C' strand comprises residues Q55-F62, and the FG loop comprises residues L108-I114 (amino acid numbering according to Chang *et al. supra*). Accordingly, in some embodiments, an anti-PD-1 antibody as described herein binds to at least one residue in one or more of the ranges F43-M50, S51-N54, Q55-F62, and L108-I114 of PD-1. In some embodiments, an anti-PD-1 antibody as described herein binds to at least one residue in two, three, or all four of the ranges F43-M50, S51-N54, Q55-F62, and L108-I114 of PD-1. In some embodiments,

the anti-PD-1 antibody binds to a residue in PD-1 that is also part of a binding site for one or both of PD-L1 and PD-L2.

In another aspect, the invention provides an isolated nucleic acid molecule encoding any of the aforesaid antibody molecules, vectors and host cells thereof.

An isolated nucleic acid encoding the antibody heavy chain variable region or light chain variable region, or both, of any the aforesaid antibody molecules is also provided.

In one embodiment, the isolated nucleic acid encodes heavy chain CDRs 1-3, wherein said nucleic acid comprises a nucleotide sequence of SEQ ID NO: 108-112, 223, 122-126, 133-137, or 144-146.

In another embodiment, the isolated nucleic acid encodes light chain CDRs 1-3, wherein said nucleic acid comprises a nucleotide sequence of SEQ ID NO: 113-120, 127-132, or 138-143.

In other embodiments, the aforesaid nucleic acid further comprises a nucleotide sequence encoding a heavy chain variable domain, wherein said nucleotide sequence is at least 85% identical to any of SEQ ID NO: 39, 51, 83, 87, 90, 95, or 101.

In other embodiments, the aforesaid nucleic acid further comprises a nucleotide sequence encoding a heavy chain variable domain, wherein said nucleotide sequence comprises any of SEQ ID NO: 39, 51, 83, 87, 90, 95, or 101.

In other embodiments, the aforesaid nucleic acid further comprises a nucleotide sequence encoding a heavy chain, wherein said nucleotide sequence is at least 85% identical to any of SEQ ID NO: 41, 53, 85, 89, 92, 96, or 103.

In other embodiments, the aforesaid nucleic acid further comprises a nucleotide sequence encoding a heavy chain, wherein said nucleotide sequence comprises any of SEQ ID NO: 41, 53, 85, 89, 92, 96, or 103.

In other embodiments, the aforesaid nucleic acid further comprises a nucleotide sequence encoding a light chain variable domain, wherein said nucleotide sequence is at least 85% identical to any of SEQ ID NO: 45, 49, 57, 61, 65, 69, 73, 77, 81, 94, 98, 100, 105, or 107.

In other embodiments, the aforesaid nucleic acid further comprises a nucleotide sequence encoding a light chain variable domain, wherein said nucleotide sequence comprises any of SEQ ID NO: 45, 49, 57, 61, 65, 69, 73, 77, 81, 94, 98, 100, 105, or 107.

In other embodiments, the aforesaid nucleic acid further comprises a nucleotide sequence encoding a light chain, wherein said nucleotide sequence is at least 85% identical to any of SEQ ID NO: 45, 49, 57, 61, 65, 69, 73, 77, 81, 94, 98, 100, 105 or 107.

In other embodiments, the aforesaid nucleic acid further comprises a nucleotide sequence encoding a light chain, wherein said nucleotide sequence comprises any of SEQ ID NO: 45, 49, 57, 61, 65, 69, 73, 77, 81, 94, 98, 100, 105 or 107.

In certain embodiments, one or more expression vectors and host cells comprising the aforesaid nucleic acids are provided.

A method of producing an antibody molecule or fragment thereof, comprising culturing the host cell as described herein under conditions suitable for gene expression is also provided.

In one aspect, the invention features a method of providing an antibody molecule described herein. The method includes: providing a PD-1 antigen (*e.g.*, an antigen comprising at least a portion of a PD-1 epitope); obtaining an antibody molecule that specifically binds to the PD-1 polypeptide; and evaluating if the antibody molecule specifically binds to the PD-1 polypeptide, or evaluating efficacy of the antibody molecule in modulating, *e.g.*, inhibiting, the activity of the PD-1. The method can further include administering the antibody molecule to a subject, *e.g.*, a human or non-human animal.

In another aspect, the invention provides, compositions, *e.g.*, pharmaceutical compositions, which include a pharmaceutically acceptable carrier, excipient or stabilizer, and at least one of the therapeutic agents, *e.g.,* anti-PD-1 antibody molecules described herein. In one embodiment, the composition, *e.g.*, the pharmaceutical composition, includes a combination of the antibody molecule and one or more agents, *e.g.*, a therapeutic agent or other antibody molecule, as described herein. In one embodiment, the antibody molecule is conjugated to a label or a therapeutic agent.

Pharmaceutical Compositions and Kits

In another aspect, the present invention provides compositions, *e.g.*, pharmaceutically acceptable compositions, which include an antibody molecule described herein, formulated together with a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, isotonic and absorption delaying agents, and the like that are physiologically compatible. The carrier can be suitable for intravenous, intramuscular, subcutaneous, parenteral, rectal, spinal or epidermal administration (*e.g.* by injection or infusion).

The compositions of this invention may be in a variety of forms. These include, for example, liquid, semi-solid and solid dosage forms, such as liquid solutions (*e.g.*, injectable

and infusible solutions), dispersions or suspensions, liposomes and suppositories. The preferred form depends on the intended mode of administration and therapeutic application. Typical preferred compositions are in the form of injectable or infusible solutions. The preferred mode of administration is parenteral (*e.g.*, intravenous, subcutaneous, intraperitoneal, intramuscular). In a preferred embodiment, the antibody is administered by intravenous infusion or injection. In another preferred embodiment, the antibody is administered by intramuscular or subcutaneous injection.

The phrases "parenteral administration" and "administered parenterally" as used herein means modes of administration other than enteral and topical administration, usually by injection, and includes, without limitation, intravenous, intramuscular, intraarterial, intrathecal, intracapsular, intraorbital, intracardiac, intradermal, intraperitoneal, transtracheal, subcutaneous, subcuticular, intraarticular, subcapsular, subarachnoid, intraspinal, epidural and intrasternal injection and infusion.

Therapeutic compositions typically should be sterile and stable under the conditions of manufacture and storage. The composition can be formulated as a solution, microemulsion, dispersion, liposome, or other ordered structure suitable to high antibody concentration. Sterile injectable solutions can be prepared by incorporating the active compound (*i.e.,* antibody or antibody portion) 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, the preferred 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. The proper fluidity of a solution 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. Prolonged absorption of injectable compositions can be brought about by including in the composition an agent that delays absorption, for example, monostearate salts and gelatin.

The antibody molecules can be administered by a variety of methods known in the art, although for many therapeutic applications, the preferred route/mode of administration is intravenous injection or infusion. For example, the antibody molecules can be administered by intravenous infusion at a rate of more than 20 mg/min, *e.g.*, 20-40 mg/min, and typically

greater than or equal to 40 mg/min to reach a dose of about 35 to 440 mg/m^2, typically about 70 to 310 mg/m^2, and more typically, about 110 to 130 mg/m^2. In embodiments, the antibody molecules can be administered by intravenous infusion at a rate of less than 10mg/min; preferably less than or equal to 5 mg/min to reach a dose of about 1 to 100 mg/m ^{2}, preferably about 5 to 50 mg/m^2, about 7 to 25 mg/m^2 and more preferably, about 10 mg/m^2. As will be appreciated by the skilled artisan, the route and/or mode of administration will vary depending upon the desired results. In certain embodiments, the active compound may be prepared with a carrier that will protect the compound against rapid release, such as a controlled release formulation, including implants, transdermal patches, and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Many methods for the preparation of such formulations are patented or generally known to those skilled in the art. See, *e.g.*, *Sustained and Controlled Release Drug Delivery Systems*, J. R. Robinson, ed., Marcel Dekker, Inc., New York, 1978.

In certain embodiments, an antibody molecule can be orally administered, for example, with an inert diluent or an assimilable edible carrier. The compound (and other ingredients, if desired) may also be enclosed in a hard or soft shell gelatin capsule, compressed into tablets, or incorporated directly into the subject's diet. For oral therapeutic administration, the compounds may be incorporated with excipients and used in the form of ingestible tablets, buccal tablets, troches, capsules, elixirs, suspensions, syrups, wafers, and the like. To administer a compound of the invention by other than parenteral administration, it may be necessary to coat the compound with, or co-administer the compound with, a material to prevent its inactivation. Therapeutic compositions can also be administered with medical devices known in the art.

Dosage regimens are adjusted to provide the optimum desired response (*e.g.*, a therapeutic response). For example, a single bolus may be administered, several divided doses may be administered over time or the dose may be proportionally reduced or increased as indicated by the exigencies of the therapeutic situation. It is especially advantageous to formulate 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 subjects to be treated; each unit contains 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 (a) the unique characteristics

of the active compound and the particular therapeutic effect to be achieved, and (b) the limitations inherent in the art of compounding such an active compound for the treatment of sensitivity in individuals.

An exemplary, non-limiting range for a therapeutically or prophylactically effective amount of an antibody molecule is 0.1-30 mg/kg, more preferably 1-25 mg/kg. Dosages and therapeutic regimens of the anti-PD-1 antibody molecule can be determined by a skilled artisan. In certain embodiments, the anti-PD-1 antibody molecule is administered by injection (*e.g.*, subcutaneously or intravenously) at a dose of about 1 to 40 mg/kg, *e.g.*, 1 to 30 mg/kg, *e.g.*, about 5 to 25 mg/kg, about 10 to 20 mg/kg, about 1 to 5 mg/kg, 1 to 10 mg/kg, 5 to 15 mg/kg, 10 to 20 mg/kg, 15 to 25 mg/kg, or about 3 mg/kg. The dosing schedule can vary from *e.g.*, once a week to once every 2, 3, or 4 weeks. In one embodiment, the anti-PD-1 antibody molecule is administered at a dose from about 10 to 20 mg/kg every other week.

As another example, non-limiting range for a therapeutically or prophylactically effective amount of an antibody molecule is 200-500 mg, more preferably 300-400 mg/kg. Dosages and therapeutic regimens of the anti-PD-1 antibody molecule can be determined by a skilled artisan. In certain embodiments, the anti-PD-1 antibody molecule is administered by injection (*e.g.*, subcutaneously or intravenously) at a dose (*e.g.,* a flat dose) of about 200 mg to 500 mg, *e.g.,* about 250 mg to 450 mg, about 300 mg to 400 mg, about 250 mg to 350 mg, about 350 mg to 450 mg, or about 300 mg or about 400 mg. The dosing schedule (*e.g.,* flat dosing schedule) can vary from e.g., once a week to once every 2, 3, 4, 5, or 6 weeks. In one embodiment the anti-PD-1 antibody molecule is administered at a dose from about 300 mg to 400 mg once every three or once every four weeks. In one embodiment, the anti-PD-1 antibody molecule is administered at a dose from about 300 mg once every three weeks. In one embodiment, the anti-PD-1 antibody molecule is administered at a dose from about 400 mg once every four weeks. In one embodiment, the anti-PD-1 antibody molecule is administered at a dose from about 300 mg once every four weeks. In one embodiment, the anti-PD-1 antibody molecule is administered at a dose from about 400 mg once every three weeks. While not wishing to be bound by theory, in some embodiments, flat or fixed dosing can be beneficial to patients, for example, to save drug supply and to reduce pharmacy errors.

In some embodiments, the clearance (CL) of the anti-PD-1 antibody molecule is from about 6 to 16 mL/h, *e.g.,* about 7 to 15 mL/h, about 8 to 14 mL/h, about 9 to 12 mL/h, or about 10 to 11 mL/h, *e.g.,* about 8.9 mL/h, 10.9 mL/h, or 13.2 mL/h.

In some embodiments, the exponent of weight on CL of the anti-PD-1 antibody molecule is from about 0.4 to 0.7, about 0.5 to 0.6, or 0.7 or less, *e.g.,* 0.6 or less, or about 0.54.

In some embodiments, the volume of distribution at steady state (Vss) of the anti-PD-1 antibody molecule is from about 5 to 10 V, *e.g.,* about 6 to 9 V, about 7 to 8 V, or about 6.5 to 7.5 V, *e.g.,* about 7.2 V.

In some embodiments, the half-life of the anti-PD-1 antibody molecule is from about 10 to 30 days, *e.g.,* about 15 to 25 days, about 17 to 22 days, about 19 to 24 days, or about 18 to 22 days, *e.g.,* about 20 days.

In some embodiments, the Cmin (*e.g.,* for a 80 kg patient) of the anti-PD-1 antibody molecule is at least about 0.4 μg/mL, *e.g.,* at least about 3.6 μg/mL, *e.g.,* from about 20 to 50 μg/mL, *e.g.,* about 22 to 42 μg/mL, about 26 to 47 μg/mL, about 22 to 26 μg/mL, about 42 to 47 μg/mL, about 25 to 35 μg/mL, about 32 to 38 μg/mL, *e.g.,* about 31 μg/mL or about 35 μg/mL. In one embodiment, the Cmin is determined in a patient receiving the anti-PD-1 antibody molecule at a dose of about 400 mg once every four weeks. In another embodiment, the Cmin is determined in a patient receiving the anti-PD-1 antibody molecule at a dose of about 300 mg once every three weeks. In certain embodiments, the Cmin is at least about 50-fold higher, *e.g.,* at least about 60-fold, 65-fold, 70-fold, 75-fold, 80-fold, 85-fold, 90-fold, 95-fold, or 100-fold, *e.g.,* at least about 77-fold, higher than the EC50 of the anti-PD-1 antibody molecule, *e.g.,* as determined based on IL-2 change in an SEB *ex-vivo* assay. In other embodiments, the Cmin is at least 5-fold higher, *e.g.,* at least 6-fold, 7-fold, 8-fold, 9-fold, or 10-fold, *e.g.,* at least about 8.6-fold, higher than the EC90 of the anti-PD-1 antibody molecule, *e.g.,* as determined based on IL-2 change in an SEB *ex-vivo* assay.

The antibody molecule can be administered by intravenous infusion at a rate of more than 20 mg/min, *e.g.*, 20-40 mg/min, and typically greater than or equal to 40 mg/min to reach a dose of about 35 to 440 mg/m^2, typically about 70 to 310 mg/m^2, and more typically, about 110 to 130 mg/m^2. In embodiments, the infusion rate of about 110 to 130 mg/m^2 achieves a level of about 3 mg/kg. In other embodiments, the antibody molecule can be administered by intravenous infusion at a rate of less than 10 mg/min, *e.g.*, less than or equal to 5 mg/min to reach a dose of about 1 to 100 mg/m^2, *e.g.*, about 5 to 50 mg/m^2, about 7 to 25 mg/m^2, or, about 10 mg/m^2. In some embodiments, the antibody is infused over a period of about 30 min. It is to be noted that dosage values may vary with the type and severity of the condition to be alleviated. It is to be further understood that for any particular subject, specific dosage regimens should be adjusted over time according to the individual need and

the professional judgment of the person administering or supervising the administration of the compositions, and that dosage ranges set forth herein are exemplary only and are not intended to limit the scope or practice of the claimed composition.

The pharmaceutical compositions of the invention may include a "therapeutically effective amount" or a "prophylactically effective amount" of an antibody or antibody portion of the invention. A "therapeutically effective amount" refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired therapeutic result. A therapeutically effective amount of the modified antibody or antibody fragment may vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of the antibody or antibody portion to elicit a desired response in the individual. A therapeutically effective amount is also one in which any toxic or detrimental effects of the modified antibody or antibody fragment is outweighed by the therapeutically beneficial effects. A "therapeutically effective dosage" preferably inhibits a measurable parameter, *e.g.,* tumor growth rate by at least about 20%, more preferably by at least about 40%, even more preferably by at least about 60%, and still more preferably by at least about 80% relative to untreated subjects. The ability of a compound to inhibit a measurable parameter, *e.g.,* cancer, can be evaluated in an animal model system predictive of efficacy in human tumors. Alternatively, this property of a composition can be evaluated by examining the ability of the compound to inhibit, such inhibition in vitro by assays known to the skilled practitioner.

A "prophylactically effective amount" refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired prophylactic result. ypically, since a prophylactic dose is used in subjects prior to or at an earlier stage of disease, the prophylactically effective amount will be less than the therapeutically effective amount.

Also within the scope of the invention is a kit comprising an antibody molecule described herein. The kit can include one or more other elements including: instructions for use; other reagents, *e.g.,* a label, a therapeutic agent, or an agent useful for chelating, or otherwise coupling, an antibody to a label or therapeutic agent, or a radioprotective composition; devices or other materials for preparing the antibody for administration; pharmaceutically acceptable carriers; and devices or other materials for administration to a subject.

Uses of the Combination Therapies

The combinations, *e.g.,* the anti-PD-1 antibody molecules disclosed herein, have in vitro and *in vivo* diagnostic, as well as therapeutic and prophylactic utilities. For example,

these molecules can be administered to cells in culture, in vitro or *ex vivo*, or to a human subject, to treat, prevent, and/or diagnose a variety of disorders, such as cancers and infectious disorders.

Accordingly, in one aspect, the invention provides a method of modifying an immune response in a subject comprising administering to the subject the combination described herein, such that the immune response in the subject is modified. In one embodiment, the immune response is enhanced, stimulated or up-regulated.

As used herein, the term "subject" is a human patient having a disorder or condition characterized by abnormal PD-1 functioning.

Table 1. Amino acid and nucleotide sequences for murine, chimeric and humanized antibody molecules. The antibody molecules include murine mAb BAP049, chimeric mAbs BAP049-chi and BAP049-chi-Y, and humanized mAbs BAP049-hum01 to BAP049-hum16 and BAP049-Clone-A to BAP049-Clone-E. The amino acid and nucleotide sequences of the heavy and light chain CDRs, the heavy and light chain variable regions, and the heavy and light chains are shown.

BAP049 HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH
SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY
SEQ ID NO: 6	VH	QVQLQQPGSELVRPGASVKLSCKASGYTFTTYW MHWVRQRPGQGLEWIGNIYPGTGGSNFDEKFKN RTSLTVDTSSTTAYMHLASLTSEDSAVYYCTRW TTGTGAYWGQGTLVTVSA
SEQ ID NO: 7	DNA VH	CAGGTCCAGCTGCAGCAACCTGGGTCTGAGCTG GTGAGGCCTGGAGCTTCAGTGAAGCTGTCCTGC AAGGCGTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGAGGCAGAGGCCTGGACAAGGC CTTGAGTGGATTGGAAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAAAAC AGGACCTCACTGACTGTAGACACATCCTCCACC ACAGCCTACATGCACCTCGCCAGCCTGACATCT GAGGACTCTGCGGTCTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAAGGG ACTCTGGTCACTGTCTCTGCA
SEQ ID NO: 8	VH	QVQLQQSGSELVRPGASVKLSCKASGYTFTTYW MHWVRQRPGQGLEWIGNIYPGTGGSNFDEKFKN RTSLTVDTSSTTAYMHLASLTSEDSAVYYCTRW TTGTGAYWGQGTLVTVSA
SEQ ID NO: 9	DNA VH	CAGGTCCAGCTGCAGCAGTCTGGGTCTGAGCTG GTGAGGCCTGGAGCTTCAGTGAAGCTGTCCTGC AAGGCGTCTGGCTACACATTCACCACTTACTGG

		ATGCACTGGGTGAGGCAGAGGCCTGGACAAGGC CTTGAGTGGATTGGAAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAAAAC AGGACCTCACTGACTGTAGACACATCCTCCACC ACAGCCTACATGCACCTCGCCAGCCTGACATCT GAGGACTCTGCGGTCTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAAGGG ACTCTGGTCACTGTCTCTGCA
BAP049 LC		
SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT
SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 12 (Kabat)	LCDR3	QNDYSYPCT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 15 (Chothia)	LCDR3	DYSYPC
SEQ ID NO: 16	VL	DIVMTQSPSSLTVTAGEKVTMSCKSSQSLLDSG NQKNFLTWYQQKPGQPPKLLIFWASTRESGVPD RFTGSGSVTDFTLTISSVQAEDLAVYYCQNDYS YPCTFGGGTKLEIK
SEQ ID NO: 17	DNA VL	GACATTGTGATGACCCAGTCTCCATCCTCCCTG ACTGTGACAGCAGGAGAGAAGGTCACTATGAGC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCAGGGCAGCCTCCTAAACTGTTGATCTTC TGGGCATCCACTAGGGAATCTGGGGTCCCTGAT CGCTTCACAGGCAGTGGATCTGTAACAGATTTC ACTCTCACCATCAGCAGTGTGCAGGCTGAAGAC CTGGCAGTTTATTACTGTCAGAATGATTATAGT TATCCGTGCACGTTCGGAGGGGGGACCAAGCTG GAAATAAAA
BAP049-chi HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH
SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY
SEQ ID NO: 18	VH	QVQLQQPGSELVRPGASVKLSCKASGYTFTTYW MHWVRQRPGQGLEWIGNIYPGTGGSNFDEKFKN RTSLTVDTSSTTAYMHLASLTSEDSAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 19	DNA VH	CAGGTCCAGCTGCAGCAGCCTGGGTCTGAGCTG GTGAGGCCTGGAGCTTCAGTGAAGCTGTCCTGC AAGGCGTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGAGGCAGAGGCCTGGACAAGGC CTTGAGTGGATTGGAAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAAAAC AGGACCTCACTGACTGTAGACACATCCTCCACC ACAGCCTACATGCACCTCGCCAGCCTGACATCT GAGGACTCTGCGGTCTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCC
SEQ ID NO: 20	HC	QVQLQQPGSELVRPGASVKLSCKASGYTFTTYW MHWVRQRPGQGLEWIGNIYPGTGGSNFDEKFKN RTSLTVDTSSTTAYMHLASLTSEDSAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS

		RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK
SEQ ID NO: 21	DNA HC	CAGGTCCAGCTGCAGCAGCCTGGGTCTGAGCTG GTGAGGCCTGGAGCTTCAGTGAAGCTGTCCTGC AAGGCGTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGAGGCAGAGGCCTGGACAAGGC CTTGAGTGGATTGGAAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAAAAC AGGACCTCACTGACTGTAGACACATCCTCCACC ACAGCCTACATGCACCTCGCCAGCCTGACATCT GAGGACTCTGCGGTCTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCCGCTTCCACCAAG GGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCC AGGAGCACCTCCGAGAGCACAGCCGCCCTGGGC TGCCTGGTCAAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC GGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACGAAGACCTAC ACCTGCAACGTAGATCACAAGCCCAGCAACACC AAGGTGGACAAGAGAGTTGAGTCCAAATATGGT CCCCCATGCCCACCGTGCCCAGCACCTGAGTTC CTGGGGGGACCATCAGTCTTCCTGTTCCCCCCA AAACCCAAGGACACTCTCATGATCTCCCGGACC CCTGAGGTCACGTGCGTGGTGGTGGACGTGAGC CAGGAAGACCCCGAGGTCCAGTTCAACTGGTAC GTGGATGGCGTGGAGGTGCATAATGCCAAGACA AAGCCGCGGGAGGAGCAGTTCAACAGCACGTAC CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG GACTGGCTGAACGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGGCCTCCCGTCCTCCATCGAG AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAGCCACAGGTGTACACCCTGCCCCCATCCCAG GAGGAGATGACCAAGAACCAGGTCAGCCTGACC TGCCTGGTCAAAGGCTTCTACCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGGAC TCCGACGGCTCCTTCTTCCTCTACAGCAGGCTA ACCGTGGACAAGAGCAGGTGGCAGGAGGGGAAT GTCTTCTCATGCTCCGTGATGCATGAGGCTCTG CACAACCACTACACACAGAAGAGCCTCTCCCTG TCTCTGGGTAAA
SEQ ID NO: 22	VH	QVQLQQSGSELVRPGASVKLSCKASGYTFTTYW MHWVRQRPGQGLEWIGNIYPGTGGSNFDEKFKN RTSLTVDTSSTTAYMHLASLTSEDSAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 23	DNA VH	CAGGTCCAGCTGCAGCAGTCTGGGTCTGAGCTG GTGAGGCCTGGAGCTTCAGTGAAGCTGTCCTGC AAGGCGTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGAGGCAGAGGCCTGGACAAGGC CTTGAGTGGATTGGAAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAAAAC

		AGGACCTCACTGACTGTAGACACATCCTCCACC ACAGCCTACATGCACCTCGCCAGCCTGACATCT GAGGACTCTGCGGTCTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCC
SEQ ID NO: 30	HC	QVQLQQSGSELVRPGASVKLSCKASGYTFTTYW MHWVRQRPGQGLEWIGNIYPGTGGSNFDEKFKN RTSLTVDTSSTTAYMHLASLTSEDSAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK
SEQ ID NO: 31	DNA HC	CAGGTCCAGCTGCAGCAGTCTGGGTCTGAGCTG GTGAGGCCTGGAGCTTCAGTGAAGCTGTCCTGC AAGGCGTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGAGGCAGAGGCCTGGACAAGGC CTTGAGTGGATTGGAAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAAAAC AGGACCTCACTGACTGTAGACACATCCTCCACC ACAGCCTACATGCACCTCGCCAGCCTGACATCT GAGGACTCTGCGGTCTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCCGCTTCCACCAAG GGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCC AGGAGCACCTCCGAGAGCACAGCCGCCCTGGGC TGCCTGGTCAAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC GGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACGAAGACCTAC ACCTGCAACGTAGATCACAAGCCCAGCAACACC AAGGTGGACAAGAGAGTTGAGTCCAAATATGGT CCCCCATGCCCACCGTGCCCAGCACCTGAGTTC CTGGGGGGACCATCAGTCTTCCTGTTCCCCCCA AAACCCAAGGACACTCTCATGATCTCCCGGACC CCTGAGGTCACGTGCGTGGTGGTGGACGTGAGC CAGGAAGACCCCGAGGTCCAGTTCAACTGGTAC GTGGATGGCGTGGAGGTGCATAATGCCAAGACA AAGCCGCGGGAGGAGCAGTTCAACAGCACGTAC CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG GACTGGCTGAACGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGGCCTCCCGTCCTCCATCGAG AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAGCCACAGGTGTACACCCTGCCCCCATCCCAG GAGGAGATGACCAAGAACCAGGTCAGCCTGACC TGCCTGGTCAAAGGCTTCTACCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGGAC TCCGACGGCTCCTTCTTCCTCTACAGCAGGCTA ACCGTGGACAAGAGCAGGTGGCAGGAGGGGAAT GTCTTCTCATGCTCCGTGATGCATGAGGCTCTG CACAACCACTACACACAGAAGAGCCTCTCCCTG TCTCTGGGTAAA
BAP049-chi LC		

SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT
SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 12 (Kabat)	LCDR3	QNDYSYPCT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 15 (Chothia)	LCDR3	DYSYPC
SEQ ID NO: 24	VL	DIVMTQSPSSLTVTAGEKVTMSCKSSQSLLDSG NQKNFLTWYQQKPGQPPKLLIFWASTRESGVPD RFTGSGSVTDFTLTISSVQAEDLAVYYCQNDYS YPCTFGQGTKVEIK
SEQ ID NO: 25	DNA VL	GACATTGTGATGACCCAGTCTCCATCCTCCCTG ACTGTGACAGCAGGAGAGAAGGTCACTATGAGC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCAGGGCAGCCTCCTAAACTGTTGATCTTC TGGGCATCCACTAGGGAATCTGGGGTCCCTGAT CGCTTCACAGGCAGTGGATCTGTAACAGATTTC ACTCTCACCATCAGCAGTGTGCAGGCTGAAGAC CTGGCAGTTTATTACTGTCAGAATGATTATAGT TATCCGTGCACGTTCGGCCAAGGGACCAAGGTG GAAATCAAA
SEQ ID NO: 26	LC	DIVMTQSPSSLTVTAGEKVTMSCKSSQSLLDSG NQKNFLTWYQQKPGQPPKLLIFWASTRESGVPD RFTGSGSVTDFTLTISSVQAEDLAVYYCQNDYS YPCTFGQGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 27	DNA LC	GACATTGTGATGACCCAGTCTCCATCCTCCCTG ACTGTGACAGCAGGAGAGAAGGTCACTATGAGC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCAGGGCAGCCTCCTAAACTGTTGATCTTC TGGGCATCCACTAGGGAATCTGGGGTCCCTGAT CGCTTCACAGGCAGTGGATCTGTAACAGATTTC ACTCTCACCATCAGCAGTGTGCAGGCTGAAGAC CTGGCAGTTTATTACTGTCAGAATGATTATAGT TATCCGTGCACGTTCGGCCAAGGGACCAAGGTG GAAATCAAACGTACGGTGGCTGCACCATCTGTC TTCATCTTCCCGCCATCTGATGAGCAGTTGAAA TCTGGAACTGCCTCTGTTGTGTGCCTGCTGAAT AACTTCTATCCCAGAGAGGCCAAAGTACAGTGG AAGGTGGATAACGCCCTCCAATCGGGTAACTCC CAGGAGAGTGTCACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGCACCCTGACGCTG AGCAAAGCAGACTACGAGAAACACAAAGTCTAC GCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
BAP049-chi-Y HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH
SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY

SEQ ID NO: 18	VH	QVQLQQPGSELVRPGASVKLSCKASGYTFTTYW MHWVRQRPGQGLEWIGNIYPGTGGSNFDEKFKN RTSLTVDTSSTTAYMHLASLTSEDSAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 19	DNA VH	CAGGTCCAGCTGCAGCAGCCTGGGTCTGAGCTG GTGAGGCCTGGAGCTTCAGTGAAGCTGTCCTGC AAGGCGTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGAGGCAGAGGCCTGGACAAGGC CTTGAGTGGATTGGAAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAAAAC AGGACCTCACTGACTGTAGACACATCCTCCACC ACAGCCTACATGCACCTCGCCAGCCTGACATCT GAGGACTCTGCGGTCTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCC
SEQ ID NO: 20	HC	QVQLQQPGSELVRPGASVKLSCKASGYTFTTYW MHWVRQRPGQGLEWIGNIYPGTGGSNFDEKFKN RTSLTVDTSSTTAYMHLASLTSEDSAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK
SEQ ID NO: 21	DNA HC	CAGGTCCAGCTGCAGCAGCCTGGGTCTGAGCTG GTGAGGCCTGGAGCTTCAGTGAAGCTGTCCTGC AAGGCGTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGAGGCAGAGGCCTGGACAAGGC CTTGAGTGGATTGGAAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAAAAC AGGACCTCACTGACTGTAGACACATCCTCCACC ACAGCCTACATGCACCTCGCCAGCCTGACATCT GAGGACTCTGCGGTCTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCCGCTTCCACCAAG GGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCC AGGAGCACCTCCGAGAGCACAGCCGCCCTGGGC TGCCTGGTCAAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC GGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACGAAGACCTAC ACCTGCAACGTAGATCACAAGCCCAGCAACACC AAGGTGGACAAGAGAGTTGAGTCCAAATATGGT CCCCCATGCCCACCGTGCCCAGCACCTGAGTTC CTGGGGGGACCATCAGTCTTCCTGTTCCCCCCA AAACCCAAGGACACTCTCATGATCTCCCGGACC CCTGAGGTCACGTGCGTGGTGGTGGACGTGAGC CAGGAAGACCCCGAGGTCCAGTTCAACTGGTAC GTGGATGGCGTGGAGGTGCATAATGCCAAGACA AAGCCGCGGGAGGAGCAGTTCAACAGCACGTAC CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG GACTGGCTGAACGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGGCCTCCCGTCCTCCATCGAG AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAGCCACAGGTGTACACCCTGCCCCCATCCCAG

		GAGGAGATGACCAAGAACCAGGTCAGCCTGACC TGCCTGGTCAAAGGCTTCTACCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGGAC TCCGACGGCTCCTTCTTCCTCTACAGCAGGCTA ACCGTGGACAAGAGCAGGTGGCAGGAGGGGAAT GTCTTCTCATGCTCCGTGATGCATGAGGCTCTG CACAACCACTACACACAGAAGAGCCTCTCCCTG TCTCTGGGTAAA
SEQ ID NO: 22	VH	QVQLQQSGSELVRPGASVKLSCKASGYTFTTYW MHWVRQRPGQGLEWIGNIYPGTGGSNFDEKFKN RTSLTVDTSSTTAYMHLASLTSEDSAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 23	DNA VH	CAGGTCCAGCTGCAGCAGTCTGGGTCTGAGCTG GTGAGGCCTGGAGCTTCAGTGAAGCTGTCCTGC AAGGCGTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGAGGCAGAGGCCTGGACAAGGC CTTGAGTGGATTGGAAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAAAAC AGGACCTCACTGACTGTAGACACATCCTCCACC ACAGCCTACATGCACCTCGCCAGCCTGACATCT GAGGACTCTGCGGTCTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCC
SEQ ID NO: 30	HC	QVQLQQSGSELVRPGASVKLSCKASGYTFTTYW MHWVRQRPGQGLEWIGNIYPGTGGSNFDEKFKN RTSLTVDTSSTTAYMHLASLTSEDSAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK
SEQ ID NO: 31	DNA HC	CAGGTCCAGCTGCAGCAGTCTGGGTCTGAGCTG GTGAGGCCTGGAGCTTCAGTGAAGCTGTCCTGC AAGGCGTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGAGGCAGAGGCCTGGACAAGGC CTTGAGTGGATTGGAAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAAAAC AGGACCTCACTGACTGTAGACACATCCTCCACC ACAGCCTACATGCACCTCGCCAGCCTGACATCT GAGGACTCTGCGGTCTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCCGCTTCCACCAAG GGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCC AGGAGCACCTCCGAGAGCACAGCCGCCCTGGGC TGCCTGGTCAAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC GGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACGAAGACCTAC ACCTGCAACGTAGATCACAAGCCCAGCAACACC AAGGTGGACAAGAGAGTTGAGTCCAAATATGGT CCCCCATGCCCACCGTGCCCAGCACCTGAGTTC CTGGGGGGACCATCAGTCTTCCTGTTCCCCCCA AAACCCAAGGACACTCTCATGATCTCCCGGACC

		CCTGAGGTCACGTGCGTGGTGGTGGACGTGAGC CAGGAAGACCCCGAGGTCCAGTTCAACTGGTAC GTGGATGGCGTGGAGGTGCATAATGCCAAGACA AAGCCGCGGGAGGAGCAGTTCAACAGCACGTAC CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG GACTGGCTGAACGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGGCCTCCCGTCCTCCATCGAG AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAGCCACAGGTGTACACCCTGCCCCCATCCCAG GAGGAGATGACCAAGAACCAGGTCAGCCTGACC TGCCTGGTCAAAGGCTTCTACCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGGAC TCCGACGGCTCCTTCTTCCTCTACAGCAGGCTA ACCGTGGACAAGAGCAGGTGGCAGGAGGGGAAT GTCTTCTCATGCTCCGTGATGCATGAGGCTCTG CACAACCACTACACACAGAAGAGCCTCTCCCTG TCTCTGGGTAAA
BAP049-chi-Y LC		
SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT
SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 32 (Kabat)	LCDR3	QNDYSYPYT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 33 (Chothia)	LCDR3	DYSYPY
SEQ ID NO: 34	VL	DIVMTQSPSSLTVTAGEKVTMSCKSSQSLLDSG NQKNFLTWYQQKPGQPPKLLIFWASTRESGVPD RFTGSGSVTDFTLTISSVQAEDLAVYYCQNDYS YPYTFGQGTKVEIK
SEQ ID NO: 35	DNA VL	GACATTGTGATGACCCAGTCTCCATCCTCCCTG ACTGTGACAGCAGGAGAGAAGGTCACTATGAGC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCAGGGCAGCCTCCTAAACTGTTGATCTTC TGGGCATCCACTAGGGAATCTGGGGTCCCTGAT CGCTTCACAGGCAGTGGATCTGTAACAGATTTC ACTCTCACCATCAGCAGTGTGCAGGCTGAAGAC CTGGCAGTTTATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAA
SEQ ID NO: 36	LC	DIVMTQSPSSLTVTAGEKVTMSCKSSQSLLDSG NQKNFLTWYQQKPGQPPKLLIFWASTRESGVPD RFTGSGSVTDFTLTISSVQAEDLAVYYCQNDYS YPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 37	DNA LC	GACATTGTGATGACCCAGTCTCCATCCTCCCTG ACTGTGACAGCAGGAGAGAAGGTCACTATGAGC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCAGGGCAGCCTCCTAAACTGTTGATCTTC TGGGCATCCACTAGGGAATCTGGGGTCCCTGAT CGCTTCACAGGCAGTGGATCTGTAACAGATTTC ACTCTCACCATCAGCAGTGTGCAGGCTGAAGAC CTGGCAGTTTATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAACGTACGGTGGCTGCACCATCTGTC

		TTCATCTTCCCGCCATCTGATGAGCAGTTGAAA TCTGGAACTGCCTCTGTTGTGTGCCTGCTGAAT AACTTCTATCCCAGAGAGGCCAAAGTACAGTGG AAGGTGGATAACGCCCTCCAATCGGGTAACTCC CAGGAGAGTGTCACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGCACCCTGACGCTG AGCAAAGCAGACTACGAGAAACACAAAGTCTAC GCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
BAP049-hum01 HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH
SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY
SEQ ID NO: 38	VH	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 39	DNA VH	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGAGTCACGATTACCGCGGACAAATCCACGAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCC
SEQ ID NO: 40	HC	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK
SEQ ID NO: 41	DNA HC	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGAGTCACGATTACCGCGGACAAATCCACGAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCCGCTTCCACCAAG GGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCC AGGAGCACCTCCGAGAGCACAGCCGCCCTGGGC

		TGCCTGGTCAAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC GGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACGAAGACCTAC ACCTGCAACGTAGATCACAAGCCCAGCAACACC AAGGTGGACAAGAGAGTTGAGTCCAAATATGGT CCCCCATGCCCACCGTGCCCAGCACCTGAGTTC CTGGGGGGACCATCAGTCTTCCTGTTCCCCCCA AAACCCAAGGACACTCTCATGATCTCCCGGACC CCTGAGGTCACGTGCGTGGTGGTGGACGTGAGC CAGGAAGACCCCGAGGTCCAGTTCAACTGGTAC GTGGATGGCGTGGAGGTGCATAATGCCAAGACA AAGCCGCGGGAGGAGCAGTTCAACAGCACGTAC CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG GACTGGCTGAACGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGGCCTCCCGTCCTCCATCGAG AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAGCCACAGGTGTACACCCTGCCCCCATCCCAG GAGGAGATGACCAAGAACCAGGTCAGCCTGACC TGCCTGGTCAAAGGCTTCTACCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGGAC TCCGACGGCTCCTTCTTCCTCTACAGCAGGCTA ACCGTGGACAAGAGCAGGTGGCAGGAGGGGAAT GTCTTCTCATGCTCCGTGATGCATGAGGCTCTG CACAACCACTACACACAGAAGAGCCTCTCCCTG TCTCTGGGTAAA
BAP049-hum01 LC		
SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT
SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 32 (Kabat)	LCDR3	QNDYSYPYT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 33 (Chothia)	LCDR3	DYSYPY
SEQ ID NO: 42	VL	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTEFTLTISSLQPDDFATYYCQNDYS YPYTFGQGTKVEIK
SEQ ID NO: 43	DNA VL	GAAATTGTGTTGACACAGTCTCCAGCCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCATCA AGGTTCAGCGGCAGTGGATCTGGGACAGAATTC ACTCTCACCATCAGCAGCCTGCAGCCTGATGAT TTTGCAACTTATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAA
SEQ ID NO: 44	LC	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTEFTLTISSLQPDDFATYYCQNDYS YPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO: 45	DNA LC	GAAATTGTGTTGACACAGTCTCCAGCCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCATCA AGGTTCAGCGGCAGTGGATCTGGGACAGAATTC ACTCTCACCATCAGCAGCCTGCAGCCTGATGAT TTTGCAACTTATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAACGTACGGTGGCTGCACCATCTGTC TTCATCTTCCCGCCATCTGATGAGCAGTTGAAA TCTGGAACTGCCTCTGTTGTGTGCCTGCTGAAT AACTTCTATCCCAGAGAGGCCAAAGTACAGTGG AAGGTGGATAACGCCCTCCAATCGGGTAACTCC CAGGAGAGTGTCACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGCACCCTGACGCTG AGCAAAGCAGACTACGAGAAACACAAAGTCTAC GCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
BAP049-hum02 HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH
SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY
SEQ ID NO: 38	VH	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 39	DNA VH	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGAGTCACGATTACCGCGGACAAATCCACGAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCC
SEQ ID NO: 40	HC	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK
SEQ ID NO: 41	DNA HC	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT

		AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGAGTCACGATTACCGCGGACAAATCCACGAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCCGCTTCCACCAAG GGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCC AGGAGCACCTCCGAGAGCACAGCCGCCCTGGGC TGCCTGGTCAAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC GGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACGAAGACCTAC ACCTGCAACGTAGATCACAAGCCCAGCAACACC AAGGTGGACAAGAGAGTTGAGTCCAAATATGGT CCCCCATGCCCACCGTGCCCAGCACCTGAGTTC CTGGGGGGACCATCAGTCTTCCTGTTCCCCCCA AAACCCAAGGACACTCTCATGATCTCCCGGACC CCTGAGGTCACGTGCGTGGTGGTGGACGTGAGC CAGGAAGACCCCGAGGTCCAGTTCAACTGGTAC GTGGATGGCGTGGAGGTGCATAATGCCAAGACA AAGCCGCGGGAGGAGCAGTTCAACAGCACGTAC CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG GACTGGCTGAACGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGGCCTCCCGTCCTCCATCGAG AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAGCCACAGGTGTACACCCTGCCCCCATCCCAG GAGGAGATGACCAAGAACCAGGTCAGCCTGACC TGCCTGGTCAAAGGCTTCTACCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGGAC TCCGACGGCTCCTTCTTCCTCTACAGCAGGCTA ACCGTGGACAAGAGCAGGTGGCAGGAGGGGAAT GTCTTCTCATGCTCCGTGATGCATGAGGCTCTG CACAACCACTACACACAGAAGAGCCTCTCCCTG TCTCTGGGTAAA
BAP049-hum02 LC		
SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT
SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 32 (Kabat)	LCDR3	QNDYSYPYT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 33 (Chothia)	LCDR3	DYSYPY
SEQ ID NO: 46	VL	DIQMTQSPSSLSASVGDRVTITCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGIPP RFSGSGYGTDFTLTINNIESEDAAYYFCQNDYS YPYTFGQGTKVEIK
SEQ ID NO: 47	DNA VL	GACATCCAGATGACCCAGTCTCCATCCTCCCTG TCTGCATCTGTAGGAGACAGAGTCACCATCACT TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT TGGGCATCCACTAGGGAATCTGGGATCCCACCT CGATTCAGTGGCAGCGGGTATGGAACAGATTTT ACCCTCACAATTAATAACATAGAATCTGAGGAT GCTGCATATTACTTCTGTCAGAATGATTATAGT

		TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAA
SEQ ID NO: 48	LC	DIQMTQSPSSLSASVGDRVTITCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGIPP RFSGSGYGTDFTLTINNIESEDAAYYFCQNDYS YPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 49	DNA LC	GACATCCAGATGACCCAGTCTCCATCCTCCCTG TCTGCATCTGTAGGAGACAGAGTCACCATCACT TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT TGGGCATCCACTAGGGAATCTGGGATCCCACCT CGATTCAGTGGCAGCGGGTATGGAACAGATTTT ACCCTCACAATTAATAACATAGAATCTGAGGAT GCTGCATATTACTTCTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAACGTACGGTGGCTGCACCATCTGTC TTCATCTTCCCGCCATCTGATGAGCAGTTGAAA TCTGGAACTGCCTCTGTTGTGTGCCTGCTGAAT AACTTCTATCCCAGAGAGGCCAAAGTACAGTGG AAGGTGGATAACGCCCTCCAATCGGGTAACTCC CAGGAGAGTGTCACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGCACCCTGACGCTG AGCAAAGCAGACTACGAGAAACACAAAGTCTAC GCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
BAP049-hum03 HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH
SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY
SEQ ID NO: 50	VH	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWIRQSPSRGLEWLGNIYPGTGGSNFDEKFKN RFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 51	DNA VH	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGATCAGGCAGTCCCCATCGAGAGGC CTTGAGTGGCTGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTTCAAATGAACAGCCTGAGAGCC GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCC
SEQ ID NO: 52	HC	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWIRQSPSRGLEWLGNIYPGTGGSNFDEKFKN RFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF

		LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK
SEQ ID NO: 53	DNA HC	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGATCAGGCAGTCCCCATCGAGAGGC CTTGAGTGGCTGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTTCAAATGAACAGCCTGAGAGCC GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCCGCTTCCACCAAG GGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCC AGGAGCACCTCCGAGAGCACAGCCGCCCTGGGC TGCCTGGTCAAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC GGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACGAAGACCTAC ACCTGCAACGTAGATCACAAGCCCAGCAACACC AAGGTGGACAAGAGAGTTGAGTCCAAATATGGT CCCCCATGCCCACCGTGCCCAGCACCTGAGTTC CTGGGGGGACCATCAGTCTTCCTGTTCCCCCCA AAACCCAAGGACACTCTCATGATCTCCCGGACC CCTGAGGTCACGTGCGTGGTGGTGGACGTGAGC CAGGAAGACCCCGAGGTCCAGTTCAACTGGTAC GTGGATGGCGTGGAGGTGCATAATGCCAAGACA AAGCCGCGGGAGGAGCAGTTCAACAGCACGTAC CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG GACTGGCTGAACGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGGCCTCCCGTCCTCCATCGAG AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAGCCACAGGTGTACACCCTGCCCCCATCCCAG GAGGAGATGACCAAGAACCAGGTCAGCCTGACC TGCCTGGTCAAAGGCTTCTACCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGGAC TCCGACGGCTCCTTCTTCCTCTACAGCAGGCTA ACCGTGGACAAGAGCAGGTGGCAGGAGGGGAAT GTCTTCTCATGCTCCGTGATGCATGAGGCTCTG CACAACCACTACACACAGAAGAGCCTCTCCCTG TCTCTGGGTAAA
BAP049-hum03 LC		
SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT
SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 32 (Kabat)	LCDR3	QNDYSYPYT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 33 (Chothia)	LCDR3	DYSYPY
SEQ ID NO: 46	VL	DIQMTQSPSSLSASVGDRVTITCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGIPP RFSGSGYGTDFTLTINNIESEDAAYYFCQNDYS YPYTFGQGTKVEIK

SEQ ID NO: 47	DNA VL	GACATCCAGATGACCCAGTCTCCATCCTCCCTG TCTGCATCTGTAGGAGACAGAGTCACCATCACT TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT TGGGCATCCACTAGGGAATCTGGGATCCCACCT CGATTCAGTGGCAGCGGGTATGGAACAGATTTT ACCCTCACAATTAATAACATAGAATCTGAGGAT GCTGCATATTACTTCTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAA
SEQ ID NO: 48	LC	DIQMTQSPSSLSASVGDRVTITCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGIPP RFSGSGYGTDFTLTINNIESEDAAYYFCQNDYS YPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 49	DNA LC	GACATCCAGATGACCCAGTCTCCATCCTCCCTG TCTGCATCTGTAGGAGACAGAGTCACCATCACT TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT TGGGCATCCACTAGGGAATCTGGGATCCCACCT CGATTCAGTGGCAGCGGGTATGGAACAGATTTT ACCCTCACAATTAATAACATAGAATCTGAGGAT GCTGCATATTACTTCTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAACGTACGGTGGCTGCACCATCTGTC TTCATCTTCCCGCCATCTGATGAGCAGTTGAAA TCTGGAACTGCCTCTGTTGTGTGCCTGCTGAAT AACTTCTATCCCAGAGAGGCCAAAGTACAGTGG AAGGTGGATAACGCCCTCCAATCGGGTAACTCC CAGGAGAGTGTCACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGCACCCTGACGCTG AGCAAAGCAGACTACGAGAAACACAAAGTCTAC GCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
BAP049-hum04 HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH
SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY
SEQ ID NO: 50	VH	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWIRQSPSRGLEWLGNIYPGTGGSNFDEKFKN RFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 51	DNA VH	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGATCAGGCAGTCCCCATCGAGAGGC CTTGAGTGGCTGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTTCAAATGAACAGCCTGAGAGCC GAGGACACGGCCGTGTATTACTGTACAAGATGG

		ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCC
SEQ ID NO: 52	HC	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWIRQSPSRGLEWLGNIYPGTGGSNFDEKFKN RFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK
SEQ ID NO: 53	DNA HC	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGATCAGGCAGTCCCCATCGAGAGGC CTTGAGTGGCTGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTTCAAATGAACAGCCTGAGAGCC GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCCGCTTCCACCAAG GGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCC AGGAGCACCTCCGAGAGCACAGCCGCCCTGGGC TGCCTGGTCAAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC GGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACGAAGACCTAC ACCTGCAACGTAGATCACAAGCCCAGCAACACC AAGGTGGACAAGAGAGTTGAGTCCAAATATGGT CCCCCATGCCCACCGTGCCCAGCACCTGAGTTC CTGGGGGGACCATCAGTCTTCCTGTTCCCCCCA AAACCCAAGGACACTCTCATGATCTCCCGGACC CCTGAGGTCACGTGCGTGGTGGTGGACGTGAGC CAGGAAGACCCCGAGGTCCAGTTCAACTGGTAC GTGGATGGCGTGGAGGTGCATAATGCCAAGACA AAGCCGCGGGAGGAGCAGTTCAACAGCACGTAC CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG GACTGGCTGAACGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGGCCTCCCGTCCTCCATCGAG AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAGCCACAGGTGTACACCCTGCCCCCATCCCAG GAGGAGATGACCAAGAACCAGGTCAGCCTGACC TGCCTGGTCAAAGGCTTCTACCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGGAC TCCGACGGCTCCTTCTTCCTCTACAGCAGGCTA ACCGTGGACAAGAGCAGGTGGCAGGAGGGGAAT GTCTTCTCATGCTCCGTGATGCATGAGGCTCTG CACAACCACTACACACAGAAGAGCCTCTCCCTG TCTCTGGGTAAA
BAP049-hum04 LC		
SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT

SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 32 (Kabat)	LCDR3	QNDYSYPYT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 33 (Chothia)	LCDR3	DYSYPY
SEQ ID NO: 54	VL	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSG NQKNFLTWYQQKPGKAPKLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLQPEDIATYYCQNDYS YPYTFGQGTKVEIK
SEQ ID NO: 55	DNA VL	GAAATTGTGTTGACACAGTCTCCAGCCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTATCAGCAG AAACCAGGGAAAGCTCCTAAGCTCCTGATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCATCA AGGTTCAGTGGAAGTGGATCTGGGACAGATTTT ACTTTCACCATCAGCAGCCTGCAGCCTGAAGAT ATTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAA
SEQ ID NO: 56	LC	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSG NQKNFLTWYQQKPGKAPKLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLQPEDIATYYCQNDYS YPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 57	DNA LC	GAAATTGTGTTGACACAGTCTCCAGCCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTATCAGCAG AAACCAGGGAAAGCTCCTAAGCTCCTGATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCATCA AGGTTCAGTGGAAGTGGATCTGGGACAGATTTT ACTTTCACCATCAGCAGCCTGCAGCCTGAAGAT ATTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAACGTACGGTGGCTGCACCATCTGTC TTCATCTTCCCGCCATCTGATGAGCAGTTGAAA TCTGGAACTGCCTCTGTTGTGTGCCTGCTGAAT AACTTCTATCCCAGAGAGGCCAAAGTACAGTGG AAGGTGGATAACGCCCTCCAATCGGGTAACTCC CAGGAGAGTGTCACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGCACCCTGACGCTG AGCAAAGCAGACTACGAGAAACACAAAGTCTAC GCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
BAP049-hum05 HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH
SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY
SEQ ID NO: 38	VH	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN

		RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 39	DNA VH	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGAGTCACGATTACCGCGGACAAATCCACGAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCC
SEQ ID NO: 40	HC	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK
SEQ ID NO: 41	DNA HC	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGAGTCACGATTACCGCGGACAAATCCACGAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCCGCTTCCACCAAG GGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCC AGGAGCACCTCCGAGAGCACAGCCGCCCTGGGC TGCCTGGTCAAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC GGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACGAAGACCTAC ACCTGCAACGTAGATCACAAGCCCAGCAACACC AAGGTGGACAAGAGAGTTGAGTCCAAATATGGT CCCCCATGCCCACCGTGCCCAGCACCTGAGTTC CTGGGGGGACCATCAGTCTTCCTGTTCCCCCCA AAACCCAAGGACACTCTCATGATCTCCCGGACC CCTGAGGTCACGTGCGTGGTGGTGGACGTGAGC CAGGAAGACCCCGAGGTCCAGTTCAACTGGTAC GTGGATGGCGTGGAGGTGCATAATGCCAAGACA AAGCCGCGGGAGGAGCAGTTCAACAGCACGTAC CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG GACTGGCTGAACGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGGCCTCCCGTCCTCCATCGAG AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAGCCACAGGTGTACACCCTGCCCCCATCCCAG GAGGAGATGACCAAGAACCAGGTCAGCCTGACC TGCCTGGTCAAAGGCTTCTACCCCAGCGACATC

		GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGGAC TCCGACGGCTCCTTCTTCCTCTACAGCAGGCTA ACCGTGGACAAGAGCAGGTGGCAGGAGGGGAAT GTCTTCTCATGCTCCGTGATGCATGAGGCTCTG CACAACCACTACACACAGAAGAGCCTCTCCCTG TCTCTGGGTAAA
BAP049-hum05 LC		
SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT
SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 32 (Kabat)	LCDR3	QNDYSYPYT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 33 (Chothia)	LCDR3	DYSYPY
SEQ ID NO: 54	VL	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSG NQKNFLTWYQQKPGKAPKLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLQPEDIATYYCQNDYS YPYTFGQGTKVEIK
SEQ ID NO: 55	DNA VL	GAAATTGTGTTGACACAGTCTCCAGCCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTATCAGCAG AAACCAGGGAAAGCTCCTAAGCTCCTGATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCATCA AGGTTCAGTGGAAGTGGATCTGGGACAGATTTT ACTTTCACCATCAGCAGCCTGCAGCCTGAAGAT ATTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAA
SEQ ID NO: 56	LC	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSG NQKNFLTWYQQKPGKAPKLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLQPEDIATYYCQNDYS YPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 57	DNA LC	GAAATTGTGTTGACACAGTCTCCAGCCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTATCAGCAG AAACCAGGGAAAGCTCCTAAGCTCCTGATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCATCA AGGTTCAGTGGAAGTGGATCTGGGACAGATTTT ACTTTCACCATCAGCAGCCTGCAGCCTGAAGAT ATTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAACGTACGGTGGCTGCACCATCTGTC TTCATCTTCCCGCCATCTGATGAGCAGTTGAAA TCTGGAACTGCCTCTGTTGTGTGCCTGCTGAAT AACTTCTATCCCAGAGAGGCCAAAGTACAGTGG AAGGTGGATAACGCCCTCCAATCGGGTAACTCC CAGGAGAGTGTCACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGCACCCTGACGCTG AGCAAAGCAGACTACGAGAAACACAAAGTCTAC GCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
BAP049-hum06 HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH

SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY
SEQ ID NO: 38	VH	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 39	DNA VH	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGAGTCACGATTACCGCGGACAAATCCACGAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCC
SEQ ID NO: 40	HC	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK
SEQ ID NO: 41	DNA HC	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGAGTCACGATTACCGCGGACAAATCCACGAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCCGCTTCCACCAAG GGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCC AGGAGCACCTCCGAGAGCACAGCCGCCCTGGGC TGCCTGGTCAAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC GGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACGAAGACCTAC ACCTGCAACGTAGATCACAAGCCCAGCAACACC AAGGTGGACAAGAGAGTTGAGTCCAAATATGGT CCCCCATGCCCACCGTGCCCAGCACCTGAGTTC CTGGGGGGACCATCAGTCTTCCTGTTCCCCCCA AAACCCAAGGACACTCTCATGATCTCCCGGACC CCTGAGGTCACGTGCGTGGTGGTGGACGTGAGC CAGGAAGACCCCGAGGTCCAGTTCAACTGGTAC

		GTGGATGGCGTGGAGGTGCATAATGCCAAGACA AAGCCGCGGGAGGAGCAGTTCAACAGCACGTAC CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG GACTGGCTGAACGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGGCCTCCCGTCCTCCATCGAG AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAGCCACAGGTGTACACCCTGCCCCCATCCCAG GAGGAGATGACCAAGAACCAGGTCAGCCTGACC TGCCTGGTCAAAGGCTTCTACCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGGAC TCCGACGGCTCCTTCTTCCTCTACAGCAGGCTA ACCGTGGACAAGAGCAGGTGGCAGGAGGGGAAT GTCTTCTCATGCTCCGTGATGCATGAGGCTCTG CACAACCACTACACACAGAAGAGCCTCTCCCTG TCTCTGGGTAAA
BAP049-hum06 LC		
SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT
SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 32 (Kabat)	LCDR3	QNDYSYPYT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 33 (Chothia)	LCDR3	DYSYPY
SEQ ID NO: 58	VL	DIVMTQTPLSLPVTPGEPASISCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIK
SEQ ID NO: 59	DNA VL	GATATTGTGATGACCCAGACTCCACTCTCCCTG CCCGTCACCCCTGGAGAGCCGGCCTCCATCTCC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCCTCG AGGTTCAGTGGCAGTGGATCTGGGACAGATTTC ACCTTTACCATCAGTAGCCTGGAAGCTGAAGAT GCTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAA
SEQ ID NO: 60	LC	DIVMTQTPLSLPVTPGEPASISCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 61	DNA LC	GATATTGTGATGACCCAGACTCCACTCTCCCTG CCCGTCACCCCTGGAGAGCCGGCCTCCATCTCC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCCTCG AGGTTCAGTGGCAGTGGATCTGGGACAGATTTC ACCTTTACCATCAGTAGCCTGGAAGCTGAAGAT GCTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAACGTACGGTGGCTGCACCATCTGTC TTCATCTTCCCGCCATCTGATGAGCAGTTGAAA TCTGGAACTGCCTCTGTTGTGTGCCTGCTGAAT

		AACTTCTATCCCAGAGAGGCCAAAGTACAGTGG AAGGTGGATAACGCCCTCCAATCGGGTAACTCC CAGGAGAGTGTCACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGCACCCTGACGCTG AGCAAAGCAGACTACGAGAAACACAAAGTCTAC GCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
BAP049-hum07 HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH
SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY
SEQ ID NO: 38	VH	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 39	DNA VH	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGAGTCACGATTACCGCGGACAAATCCACGAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCC
SEQ ID NO: 40	HC	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK
SEQ ID NO: 41	DNA HC	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGAGTCACGATTACCGCGGACAAATCCACGAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCCGCTTCCACCAAG GGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCC AGGAGCACCTCCGAGAGCACAGCCGCCCTGGGC TGCCTGGTCAAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC

		GGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACGAAGACCTAC ACCTGCAACGTAGATCACAAGCCCAGCAACACC AAGGTGGACAAGAGAGTTGAGTCCAAATATGGT CCCCCATGCCCACCGTGCCCAGCACCTGAGTTC CTGGGGGGACCATCAGTCTTCCTGTTCCCCCCA AAACCCAAGGACACTCTCATGATCTCCCGGACC CCTGAGGTCACGTGCGTGGTGGTGGACGTGAGC CAGGAAGACCCCGAGGTCCAGTTCAACTGGTAC GTGGATGGCGTGGAGGTGCATAATGCCAAGACA AAGCCGCGGGAGGAGCAGTTCAACAGCACGTAC CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG GACTGGCTGAACGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGGCCTCCCGTCCTCCATCGAG AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAGCCACAGGTGTACACCCTGCCCCCATCCCAG GAGGAGATGACCAAGAACCAGGTCAGCCTGACC TGCCTGGTCAAAGGCTTCTACCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGGAC TCCGACGGCTCCTTCTTCCTCTACAGCAGGCTA ACCGTGGACAAGAGCAGGTGGCAGGAGGGGAAT GTCTTCTCATGCTCCGTGATGCATGAGGCTCTG CACAACCACTACACACAGAAGAGCCTCTCCCTG TCTCTGGGTAAA
BAP049-hum07 LC		
SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT
SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 32 (Kabat)	LCDR3	QNDYSYPYT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 33 (Chothia)	LCDR3	DYSYPY
SEQ ID NO: 62	VL	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSG NQKNFLTWYQQKPGKAPKLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIK
SEQ ID NO: 63	DNA VL	GAAATTGTGTTGACACAGTCTCCAGCCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTATCAGCAG AAACCAGGGAAAGCTCCTAAGCTCCTGATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCCTCG AGGTTCAGTGGCAGTGGATCTGGGACAGATTTC ACCTTTACCATCAGTAGCCTGGAAGCTGAAGAT GCTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAA
SEQ ID NO: 64	LC	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSG NQKNFLTWYQQKPGKAPKLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 65	DNA LC	GAAATTGTGTTGACACAGTCTCCAGCCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA

		AATCAAAAGAACTTCTTGACCTGGTATCAGCAG AAACCAGGGAAAGCTCCTAAGCTCCTGATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCCTCG AGGTTCAGTGGCAGTGGATCTGGGACAGATTTC ACCTTTACCATCAGTAGCCTGGAAGCTGAAGAT GCTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAACGTACGGTGGCTGCACCATCTGTC TTCATCTTCCCGCCATCTGATGAGCAGTTGAAA TCTGGAACTGCCTCTGTTGTGTGCCTGCTGAAT AACTTCTATCCCAGAGAGGCCAAAGTACAGTGG AAGGTGGATAACGCCCTCCAATCGGGTAACTCC CAGGAGAGTGTCACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGCACCCTGACGCTG AGCAAAGCAGACTACGAGAAACACAAAGTCTAC GCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
BAP049-hum08 HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH
SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY
SEQ ID NO: 50	VH	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWIRQSPSRGLEWLGNIYPGTGGSNFDEKFKN RFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 51	DNA VH	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGATCAGGCAGTCCCCATCGAGAGGC CTTGAGTGGCTGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTTCAAATGAACAGCCTGAGAGCC GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCC
SEQ ID NO: 52	HC	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWIRQSPSRGLEWLGNIYPGTGGSNFDEKFKN RFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK
SEQ ID NO: 53	DNA HC	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGATCAGGCAGTCCCCATCGAGAGGC CTTGAGTGGCTGGGTAATATTTATCCTGGTACT

		GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTTCAAATGAACAGCCTGAGAGCC GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCCGCTTCCACCAAG GGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCC AGGAGCACCTCCGAGAGCACAGCCGCCCTGGGC TGCCTGGTCAAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC GGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACGAAGACCTAC ACCTGCAACGTAGATCACAAGCCCAGCAACACC AAGGTGGACAAGAGAGTTGAGTCCAAATATGGT CCCCCATGCCCACCGTGCCCAGCACCTGAGTTC CTGGGGGGACCATCAGTCTTCCTGTTCCCCCCA AAACCCAAGGACACTCTCATGATCTCCCGGACC CCTGAGGTCACGTGCGTGGTGGTGGACGTGAGC CAGGAAGACCCCGAGGTCCAGTTCAACTGGTAC GTGGATGGCGTGGAGGTGCATAATGCCAAGACA AAGCCGCGGGAGGAGCAGTTCAACAGCACGTAC CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG GACTGGCTGAACGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGGCCTCCCGTCCTCCATCGAG AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAGCCACAGGTGTACACCCTGCCCCCATCCCAG GAGGAGATGACCAAGAACCAGGTCAGCCTGACC TGCCTGGTCAAAGGCTTCTACCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGGAC TCCGACGGCTCCTTCTTCCTCTACAGCAGGCTA ACCGTGGACAAGAGCAGGTGGCAGGAGGGGAAT GTCTTCTCATGCTCCGTGATGCATGAGGCTCTG CACAACCACTACACACAGAAGAGCCTCTCCCTG TCTCTGGGTAAA
BAP049-hum08 LC		
SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT
SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 32 (Kabat)	LCDR3	QNDYSYPYT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 33 (Chothia)	LCDR3	DYSYPY
SEQ ID NO: 66	VL	EIVLTQSPDFQSVTPKEKVTITCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIK
SEQ ID NO: 67	DNA VL	GAAATTGTGCTGACTCAGTCTCCAGACTTTCAG TCTGTGACTCCAAAGGAGAAAGTCACCATCACC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCCTCG AGGTTCAGTGGCAGTGGATCTGGGACAGATTTC ACCTTTACCATCAGTAGCCTGGAAGCTGAAGAT GCTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAA

SEQ ID NO: 68	LC	EIVLTQSPDFQSVTPKEKVTITCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 69	DNA LC	GAAATTGTGCTGACTCAGTCTCCAGACTTTCAG TCTGTGACTCCAAAGGAGAAAGTCACCATCACC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCCTCG AGGTTCAGTGGCAGTGGATCTGGGACAGATTTC ACCTTTACCATCAGTAGCCTGGAAGCTGAAGAT GCTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAACGTACGGTGGCTGCACCATCTGTC TTCATCTTCCCGCCATCTGATGAGCAGTTGAAA TCTGGAACTGCCTCTGTTGTGTGCCTGCTGAAT AACTTCTATCCCAGAGAGGCCAAAGTACAGTGG AAGGTGGATAACGCCCTCCAATCGGGTAACTCC CAGGAGAGTGTCACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGCACCCTGACGCTG AGCAAAGCAGACTACGAGAAACACAAAGTCTAC GCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
BAP049-hum09 HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH
SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY
SEQ ID NO: 38	VH	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 39	DNA VH	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGAGTCACGATTACCGCGGACAAATCCACGAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCC
SEQ ID NO: 40	HC	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY

		RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK
SEQ ID NO: 41	DNA HC	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGAGTCACGATTACCGCGGACAAATCCACGAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCCGCTTCCACCAAG GGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCC AGGAGCACCTCCGAGAGCACAGCCGCCCTGGGC TGCCTGGTCAAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC GGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACGAAGACCTAC ACCTGCAACGTAGATCACAAGCCCAGCAACACC AAGGTGGACAAGAGAGTTGAGTCCAAATATGGT CCCCCATGCCCACCGTGCCCAGCACCTGAGTTC CTGGGGGGACCATCAGTCTTCCTGTTCCCCCCA AAACCCAAGGACACTCTCATGATCTCCCGGACC CCTGAGGTCACGTGCGTGGTGGTGGACGTGAGC CAGGAAGACCCCGAGGTCCAGTTCAACTGGTAC GTGGATGGCGTGGAGGTGCATAATGCCAAGACA AAGCCGCGGGAGGAGCAGTTCAACAGCACGTAC CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG GACTGGCTGAACGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGGCCTCCCGTCCTCCATCGAG AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAGCCACAGGTGTACACCCTGCCCCCATCCCAG GAGGAGATGACCAAGAACCAGGTCAGCCTGACC TGCCTGGTCAAAGGCTTCTACCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGGAC TCCGACGGCTCCTTCTTCCTCTACAGCAGGCTA ACCGTGGACAAGAGCAGGTGGCAGGAGGGGAAT GTCTTCTCATGCTCCGTGATGCATGAGGCTCTG CACAACCACTACACACAGAAGAGCCTCTCCCTG TCTCTGGGTAAA
BAP049-hum09 LC		
SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT
SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 32 (Kabat)	LCDR3	QNDYSYPYT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 33 (Chothia)	LCDR3	DYSYPY
SEQ ID NO: 66	VL	EIVLTQSPDFQSVTPKEKVTITCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIK

SEQ ID NO: 67	DNA VL	GAAATTGTGCTGACTCAGTCTCCAGACTTTCAG TCTGTGACTCCAAAGGAGAAAGTCACCATCACC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCCTCG AGGTTCAGTGGCAGTGGATCTGGGACAGATTTC ACCTTTACCATCAGTAGCCTGGAAGCTGAAGAT GCTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAA
SEQ ID NO: 68	LC	EIVLTQSPDFQSVTPKEKVTITCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 69	DNA LC	GAAATTGTGCTGACTCAGTCTCCAGACTTTCAG TCTGTGACTCCAAAGGAGAAAGTCACCATCACC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCCTCG AGGTTCAGTGGCAGTGGATCTGGGACAGATTTC ACCTTTACCATCAGTAGCCTGGAAGCTGAAGAT GCTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAACGTACGGTGGCTGCACCATCTGTC TTCATCTTCCCGCCATCTGATGAGCAGTTGAAA TCTGGAACTGCCTCTGTTGTGTGCCTGCTGAAT AACTTCTATCCCAGAGAGGCCAAAGTACAGTGG AAGGTGGATAACGCCCTCCAATCGGGTAACTCC CAGGAGAGTGTCACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGCACCCTGACGCTG AGCAAAGCAGACTACGAGAAACACAAAGTCTAC GCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
BAP049-hum10 HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH
SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY
SEQ ID NO: 50	VH	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWIRQSPSRGLEWLGNIYPGTGGSNFDEKFKN RFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 51	DNA VH	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGATCAGGCAGTCCCCATCGAGAGGC CTTGAGTGGCTGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTTCAAATGAACAGCCTGAGAGCC GAGGACACGGCCGTGTATTACTGTACAAGATGG

		ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCC
SEQ ID NO: 52	HC	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWIRQSPSRGLEWLGNIYPGTGGSNFDEKFKN RFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK
SEQ ID NO: 53	DNA HC	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGATCAGGCAGTCCCCATCGAGAGGC CTTGAGTGGCTGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTTCAAATGAACAGCCTGAGAGCC GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCCGCTTCCACCAAG GGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCC AGGAGCACCTCCGAGAGCACAGCCGCCCTGGGC TGCCTGGTCAAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC GGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACGAAGACCTAC ACCTGCAACGTAGATCACAAGCCCAGCAACACC AAGGTGGACAAGAGAGTTGAGTCCAAATATGGT CCCCCATGCCCACCGTGCCCAGCACCTGAGTTC CTGGGGGGACCATCAGTCTTCCTGTTCCCCCCA AAACCCAAGGACACTCTCATGATCTCCCGGACC CCTGAGGTCACGTGCGTGGTGGTGGACGTGAGC CAGGAAGACCCCGAGGTCCAGTTCAACTGGTAC GTGGATGGCGTGGAGGTGCATAATGCCAAGACA AAGCCGCGGGAGGAGCAGTTCAACAGCACGTAC CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG GACTGGCTGAACGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGGCCTCCCGTCCTCCATCGAG AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAGCCACAGGTGTACACCCTGCCCCCATCCCAG GAGGAGATGACCAAGAACCAGGTCAGCCTGACC TGCCTGGTCAAAGGCTTCTACCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGGAC TCCGACGGCTCCTTCTTCCTCTACAGCAGGCTA ACCGTGGACAAGAGCAGGTGGCAGGAGGGGAAT GTCTTCTCATGCTCCGTGATGCATGAGGCTCTG CACAACCACTACACACAGAAGAGCCTCTCCCTG TCTCTGGGTAAA
BAP049-hum10 LC		
SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT

SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 32 (Kabat)	LCDR3	QNDYSYPYT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 33 (Chothia)	LCDR3	DYSYPY
SEQ ID NO: 70	VL	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIK
SEQ ID NO: 71	DNA VL	GAAATTGTGTTGACACAGTCTCCAGCCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCCTCG AGGTTCAGTGGCAGTGGATCTGGGACAGATTTC ACCTTTACCATCAGTAGCCTGGAAGCTGAAGAT GCTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAA
SEQ ID NO: 72	LC	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 73	DNA LC	GAAATTGTGTTGACACAGTCTCCAGCCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCCTCG AGGTTCAGTGGCAGTGGATCTGGGACAGATTTC ACCTTTACCATCAGTAGCCTGGAAGCTGAAGAT GCTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAACGTACGGTGGCTGCACCATCTGTC TTCATCTTCCCGCCATCTGATGAGCAGTTGAAA TCTGGAACTGCCTCTGTTGTGTGCCTGCTGAAT AACTTCTATCCCAGAGAGGCCAAAGTACAGTGG AAGGTGGATAACGCCCTCCAATCGGGTAACTCC CAGGAGAGTGTCACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGCACCCTGACGCTG AGCAAAGCAGACTACGAGAAACACAAAGTCTAC GCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
BAP049-hum11 HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH
SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY
SEQ ID NO: 38	VH	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN

		RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 39	DNA VH	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGAGTCACGATTACCGCGGACAAATCCACGAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCC
SEQ ID NO: 40	HC	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK
SEQ ID NO: 41	DNA HC	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGAGTCACGATTACCGCGGACAAATCCACGAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCCGCTTCCACCAAG GGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCC AGGAGCACCTCCGAGAGCACAGCCGCCCTGGGC TGCCTGGTCAAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC GGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACGAAGACCTAC ACCTGCAACGTAGATCACAAGCCCAGCAACACC AAGGTGGACAAGAGAGTTGAGTCCAAATATGGT CCCCCATGCCCACCGTGCCCAGCACCTGAGTTC CTGGGGGGACCATCAGTCTTCCTGTTCCCCCCA AAACCCAAGGACACTCTCATGATCTCCCGGACC CCTGAGGTCACGTGCGTGGTGGTGGACGTGAGC CAGGAAGACCCCGAGGTCCAGTTCAACTGGTAC GTGGATGGCGTGGAGGTGCATAATGCCAAGACA AAGCCGCGGGAGGAGCAGTTCAACAGCACGTAC CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG GACTGGCTGAACGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGGCCTCCCGTCCTCCATCGAG AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAGCCACAGGTGTACACCCTGCCCCCATCCCAG GAGGAGATGACCAAGAACCAGGTCAGCCTGACC TGCCTGGTCAAAGGCTTCTACCCCAGCGACATC

		GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGGAC TCCGACGGCTCCTTCTTCCTCTACAGCAGGCTA ACCGTGGACAAGAGCAGGTGGCAGGAGGGGAAT GTCTTCTCATGCTCCGTGATGCATGAGGCTCTG CACAACCACTACACACAGAAGAGCCTCTCCCTG TCTCTGGGTAAA
BAP049-hum11 LC		
SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT
SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 32 (Kabat)	LCDR3	QNDYSYPYT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 33 (Chothia)	LCDR3	DYSYPY
SEQ ID NO: 70	VL	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIK
SEQ ID NO: 71	DNA VL	GAAATTGTGTTGACACAGTCTCCAGCCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCCTCG AGGTTCAGTGGCAGTGGATCTGGGACAGATTTC ACCTTTACCATCAGTAGCCTGGAAGCTGAAGAT GCTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAA
SEQ ID NO: 72	LC	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 73	DNA LC	GAAATTGTGTTGACACAGTCTCCAGCCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCCTCG AGGTTCAGTGGCAGTGGATCTGGGACAGATTTC ACCTTTACCATCAGTAGCCTGGAAGCTGAAGAT GCTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAACGTACGGTGGCTGCACCATCTGTC TTCATCTTCCCGCCATCTGATGAGCAGTTGAAA TCTGGAACTGCCTCTGTTGTGTGCCTGCTGAAT AACTTCTATCCCAGAGAGGCCAAAGTACAGTGG AAGGTGGATAACGCCCTCCAATCGGGTAACTCC CAGGAGAGTGTCACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGCACCCTGACGCTG AGCAAAGCAGACTACGAGAAACACAAAGTCTAC GCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
BAP049-hum12 HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH

SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY
SEQ ID NO: 38	VH	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 39	DNA VH	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGAGTCACGATTACCGCGGACAAATCCACGAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCC
SEQ ID NO: 40	HC	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK
SEQ ID NO: 41	DNA HC	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGAGTCACGATTACCGCGGACAAATCCACGAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCCGCTTCCACCAAG GGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCC AGGAGCACCTCCGAGAGCACAGCCGCCCTGGGC TGCCTGGTCAAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC GGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACGAAGACCTAC ACCTGCAACGTAGATCACAAGCCCAGCAACACC AAGGTGGACAAGAGAGTTGAGTCCAAATATGGT CCCCCATGCCCACCGTGCCCAGCACCTGAGTTC CTGGGGGGACCATCAGTCTTCCTGTTCCCCCCA AAACCCAAGGACACTCTCATGATCTCCCGGACC CCTGAGGTCACGTGCGTGGTGGTGGACGTGAGC CAGGAAGACCCCGAGGTCCAGTTCAACTGGTAC

		GTGGATGGCGTGGAGGTGCATAATGCCAAGACA AAGCCGCGGGAGGAGCAGTTCAACAGCACGTAC CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG GACTGGCTGAACGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGGCCTCCCGTCCTCCATCGAG AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAGCCACAGGTGTACACCCTGCCCCCATCCCAG GAGGAGATGACCAAGAACCAGGTCAGCCTGACC TGCCTGGTCAAAGGCTTCTACCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGGAC TCCGACGGCTCCTTCTTCCTCTACAGCAGGCTA ACCGTGGACAAGAGCAGGTGGCAGGAGGGGAAT GTCTTCTCATGCTCCGTGATGCATGAGGCTCTG CACAACCACTACACACAGAAGAGCCTCTCCCTG TCTCTGGGTAAA
BAP049-hum12 LC		
SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT
SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 32 (Kabat)	LCDR3	QNDYSYPYT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 33 (Chothia)	LCDR3	DYSYPY
SEQ ID NO: 74	VL	DIQMTQSPSSLSASVGDRVTITCKSSQSLLDSG NQKNFLTWYLQKPGQSPQLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIK
SEQ ID NO: 75	DNA VL	GACATCCAGATGACCCAGTCTCCATCCTCCCTG TCTGCATCTGTAGGAGACAGAGTCACCATCACT TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCTGCAG AAGCCAGGGCAGTCTCCACAGCTCCTGATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCCTCG AGGTTCAGTGGCAGTGGATCTGGGACAGATTTC ACCTTTACCATCAGTAGCCTGGAAGCTGAAGAT GCTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAA
SEQ ID NO: 76	LC	DIQMTQSPSSLSASVGDRVTITCKSSQSLLDSG NQKNFLTWYLQKPGQSPQLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 77	DNA LC	GACATCCAGATGACCCAGTCTCCATCCTCCCTG TCTGCATCTGTAGGAGACAGAGTCACCATCACT TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCTGCAG AAGCCAGGGCAGTCTCCACAGCTCCTGATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCCTCG AGGTTCAGTGGCAGTGGATCTGGGACAGATTTC ACCTTTACCATCAGTAGCCTGGAAGCTGAAGAT GCTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAACGTACGGTGGCTGCACCATCTGTC TTCATCTTCCCGCCATCTGATGAGCAGTTGAAA TCTGGAACTGCCTCTGTTGTGTGCCTGCTGAAT

		AACTTCTATCCCAGAGAGGCCAAAGTACAGTGG AAGGTGGATAACGCCCTCCAATCGGGTAACTCC CAGGAGAGTGTCACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGCACCCTGACGCTG AGCAAAGCAGACTACGAGAAACACAAAGTCTAC GCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
BAP049-hum13 HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH
SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY
SEQ ID NO: 38	VH	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 39	DNA VH	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGAGTCACGATTACCGCGGACAAATCCACGAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCC
SEQ ID NO: 40	HC	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK
SEQ ID NO: 41	DNA HC	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGAGTCACGATTACCGCGGACAAATCCACGAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCCGCTTCCACCAAG GGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCC AGGAGCACCTCCGAGAGCACAGCCGCCCTGGGC TGCCTGGTCAAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC

		GGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACGAAGACCTAC ACCTGCAACGTAGATCACAAGCCCAGCAACACC AAGGTGGACAAGAGAGTTGAGTCCAAATATGGT CCCCCATGCCCACCGTGCCCAGCACCTGAGTTC CTGGGGGGACCATCAGTCTTCCTGTTCCCCCCA AAACCCAAGGACACTCTCATGATCTCCCGGACC CCTGAGGTCACGTGCGTGGTGGTGGACGTGAGC CAGGAAGACCCCGAGGTCCAGTTCAACTGGTAC GTGGATGGCGTGGAGGTGCATAATGCCAAGACA AAGCCGCGGGAGGAGCAGTTCAACAGCACGTAC CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG GACTGGCTGAACGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGGCCTCCCGTCCTCCATCGAG AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAGCCACAGGTGTACACCCTGCCCCCATCCCAG GAGGAGATGACCAAGAACCAGGTCAGCCTGACC TGCCTGGTCAAAGGCTTCTACCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGGAC TCCGACGGCTCCTTCTTCCTCTACAGCAGGCTA ACCGTGGACAAGAGCAGGTGGCAGGAGGGGAAT GTCTTCTCATGCTCCGTGATGCATGAGGCTCTG CACAACCACTACACACAGAAGAGCCTCTCCCTG TCTCTGGGTAAA
BAP049-hum13 LC		
SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT
SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 32 (Kabat)	LCDR3	QNDYSYPYT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 33 (Chothia)	LCDR3	DYSYPY
SEQ ID NO: 78	VL	DVVMTQSPLSLPVTLGQPASISCKSSQSLLDSG NQKNFLTWYQQKPGKAPKLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIK
SEQ ID NO: 79	DNA VL	GATGTTGTGATGACTCAGTCTCCACTCTCCCTG CCCGTCACCCTTGGACAGCCGGCCTCCATCTCC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTAACCTGGTATCAGCAG AAACCAGGGAAAGCTCCTAAGCTCCTGATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCCTCG AGGTTCAGTGGCAGTGGATCTGGGACAGATTTC ACCTTTACCATCAGTAGCCTGGAAGCTGAAGAT GCTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAA
SEQ ID NO: 80	LC	DVVMTQSPLSLPVTLGQPASISCKSSQSLLDSG NQKNFLTWYQQKPGKAPKLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 81	DNA LC	GATGTTGTGATGACTCAGTCTCCACTCTCCCTG CCCGTCACCCTTGGACAGCCGGCCTCCATCTCC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA

		AATCAAAAGAACTTCTTAACCTGGTATCAGCAG AAACCAGGGAAAGCTCCTAAGCTCCTGATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCCTCG AGGTTCAGTGGCAGTGGATCTGGGACAGATTTC ACCTTTACCATCAGTAGCCTGGAAGCTGAAGAT GCTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAACGTACGGTGGCTGCACCATCTGTC TTCATCTTCCCGCCATCTGATGAGCAGTTGAAA TCTGGAACTGCCTCTGTTGTGTGCCTGCTGAAT AACTTCTATCCCAGAGAGGCCAAAGTACAGTGG AAGGTGGATAACGCCCTCCAATCGGGTAACTCC CAGGAGAGTGTCACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGCACCCTGACGCTG AGCAAAGCAGACTACGAGAAACACAAAGTCTAC GCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
BAP049-hum14 HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH
SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY
SEQ ID NO: 82	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYW MHWIRQSPSRGLEWLGNIYPGTGGSNFDEKFKN RFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 83	DNA VH	CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGATCAGGCAGTCCCCATCGAGAGGC CTTGAGTGGCTGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTTCAAATGAACAGCCTGAGAGCC GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTACTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCC
SEQ ID NO: 84	HC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYW MHWIRQSPSRGLEWLGNIYPGTGGSNFDEKFKN RFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK
SEQ ID NO: 85	DNA HC	CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGATCAGGCAGTCCCCATCGAGAGGC CTTGAGTGGCTGGGTAATATTTATCCTGGTACT

		GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTTCAAATGAACAGCCTGAGAGCC GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTACTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCCGCTTCCACCAAG GGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCC AGGAGCACCTCCGAGAGCACAGCCGCCCTGGGC TGCCTGGTCAAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC GGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACGAAGACCTAC ACCTGCAACGTAGATCACAAGCCCAGCAACACC AAGGTGGACAAGAGAGTTGAGTCCAAATATGGT CCCCCATGCCCACCGTGCCCAGCACCTGAGTTC CTGGGGGGACCATCAGTCTTCCTGTTCCCCCCA AAACCCAAGGACACTCTCATGATCTCCCGGACC CCTGAGGTCACGTGCGTGGTGGTGGACGTGAGC CAGGAAGACCCCGAGGTCCAGTTCAACTGGTAC GTGGATGGCGTGGAGGTGCATAATGCCAAGACA AAGCCGCGGGAGGAGCAGTTCAACAGCACGTAC CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG GACTGGCTGAACGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGGCCTCCCGTCCTCCATCGAG AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAGCCACAGGTGTACACCCTGCCCCCATCCCAG GAGGAGATGACCAAGAACCAGGTCAGCCTGACC TGCCTGGTCAAAGGCTTCTACCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGGAC TCCGACGGCTCCTTCTTCCTCTACAGCAGGCTA ACCGTGGACAAGAGCAGGTGGCAGGAGGGGAAT GTCTTCTCATGCTCCGTGATGCATGAGGCTCTG CACAACCACTACACACAGAAGAGCCTCTCCCTG TCTCTGGGTAAA
BAP049-hum14 LC		
SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT
SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 32 (Kabat)	LCDR3	QNDYSYPYT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 33 (Chothia)	LCDR3	DYSYPY
SEQ ID NO: 70	VL	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIK
SEQ ID NO: 71	DNA VL	GAAATTGTGTTGACACAGTCTCCAGCCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCCTCG AGGTTCAGTGGCAGTGGATCTGGGACAGATTTC ACCTTTACCATCAGTAGCCTGGAAGCTGAAGAT GCTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAA

SEQ ID NO: 72	LC	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 73	DNA LC	GAAATTGTGTTGACACAGTCTCCAGCCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCCTCG AGGTTCAGTGGCAGTGGATCTGGGACAGATTTC ACCTTTACCATCAGTAGCCTGGAAGCTGAAGAT GCTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAACGTACGGTGGCTGCACCATCTGTC TTCATCTTCCCGCCATCTGATGAGCAGTTGAAA TCTGGAACTGCCTCTGTTGTGTGCCTGCTGAAT AACTTCTATCCCAGAGAGGCCAAAGTACAGTGG AAGGTGGATAACGCCCTCCAATCGGGTAACTCC CAGGAGAGTGTCACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGCACCCTGACGCTG AGCAAAGCAGACTACGAGAAACACAAAGTCTAC GCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
BAP049-hum15 HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH
SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY
SEQ ID NO: 82	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYW MHWIRQSPSRGLEWLGNIYPGTGGSNFDEKFKN RFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 83	DNA VH	CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGATCAGGCAGTCCCCATCGAGAGGC CTTGAGTGGCTGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTTCAAATGAACAGCCTGAGAGCC GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTACTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCC
SEQ ID NO: 84	HC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYW MHWIRQSPSRGLEWLGNIYPGTGGSNFDEKFKN RFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY

		RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK
SEQ ID NO: 85	DNA HC	CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGATCAGGCAGTCCCCATCGAGAGGC CTTGAGTGGCTGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTTCAAATGAACAGCCTGAGAGCC GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTACTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCCGCTTCCACCAAG GGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCC AGGAGCACCTCCGAGAGCACAGCCGCCCTGGGC TGCCTGGTCAAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC GGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACGAAGACCTAC ACCTGCAACGTAGATCACAAGCCCAGCAACACC AAGGTGGACAAGAGAGTTGAGTCCAAATATGGT CCCCCATGCCCACCGTGCCCAGCACCTGAGTTC CTGGGGGGACCATCAGTCTTCCTGTTCCCCCCA AAACCCAAGGACACTCTCATGATCTCCCGGACC CCTGAGGTCACGTGCGTGGTGGTGGACGTGAGC CAGGAAGACCCCGAGGTCCAGTTCAACTGGTAC GTGGATGGCGTGGAGGTGCATAATGCCAAGACA AAGCCGCGGGAGGAGCAGTTCAACAGCACGTAC CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG GACTGGCTGAACGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGGCCTCCCGTCCTCCATCGAG AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAGCCACAGGTGTACACCCTGCCCCCATCCCAG GAGGAGATGACCAAGAACCAGGTCAGCCTGACC TGCCTGGTCAAAGGCTTCTACCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGGAC TCCGACGGCTCCTTCTTCCTCTACAGCAGGCTA ACCGTGGACAAGAGCAGGTGGCAGGAGGGGAAT GTCTTCTCATGCTCCGTGATGCATGAGGCTCTG CACAACCACTACACACAGAAGAGCCTCTCCCTG TCTCTGGGTAAA
BAP049-hum15 LC		
SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT
SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 32 (Kabat)	LCDR3	QNDYSYPYT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 33 (Chothia)	LCDR3	DYSYPY
SEQ ID NO: 66	VL	EIVLTQSPDFQSVTPKEKVTITCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIK

SEQ ID NO: 67	DNA VL	GAAATTGTGCTGACTCAGTCTCCAGACTTTCAG TCTGTGACTCCAAAGGAGAAAGTCACCATCACC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCCTCG AGGTTCAGTGGCAGTGGATCTGGGACAGATTTC ACCTTTACCATCAGTAGCCTGGAAGCTGAAGAT GCTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAA
SEQ ID NO: 68	LC	EIVLTQSPDFQSVTPKEKVTITCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 69	DNA LC	GAAATTGTGCTGACTCAGTCTCCAGACTTTCAG TCTGTGACTCCAAAGGAGAAAGTCACCATCACC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCCTCG AGGTTCAGTGGCAGTGGATCTGGGACAGATTTC ACCTTTACCATCAGTAGCCTGGAAGCTGAAGAT GCTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAACGTACGGTGGCTGCACCATCTGTC TTCATCTTCCCGCCATCTGATGAGCAGTTGAAA TCTGGAACTGCCTCTGTTGTGTGCCTGCTGAAT AACTTCTATCCCAGAGAGGCCAAAGTACAGTGG AAGGTGGATAACGCCCTCCAATCGGGTAACTCC CAGGAGAGTGTCACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGCACCCTGACGCTG AGCAAAGCAGACTACGAGAAACACAAAGTCTAC GCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
BAP049-hum16 HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH
SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY
SEQ ID NO: 86	VH	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQAPGQGLEWMGNIYPGTGGSNFDEKFKN RFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 87	DNA VH	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTTCAAATGAACAGCCTGAGAGCC GAGGACACGGCCGTGTATTACTGTACAAGATGG

		ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCC
SEQ ID NO: 88	HC	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQAPGQGLEWMGNIYPGTGGSNFDEKFKN RFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK
SEQ ID NO: 89	DNA HC	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGGAGTCTCTGAGGATCTCCTGT AAGGGTTCTGGCTACACATTCACCACTTACTGG ATGCACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGTAATATTTATCCTGGTACT GGTGGTTCTAACTTCGATGAGAAGTTCAAGAAC AGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTTCAAATGAACAGCCTGAGAGCC GAGGACACGGCCGTGTATTACTGTACAAGATGG ACTACTGGGACGGGAGCTTATTGGGGCCAGGGC ACCACCGTGACCGTGTCCTCCGCTTCCACCAAG GGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCC AGGAGCACCTCCGAGAGCACAGCCGCCCTGGGC TGCCTGGTCAAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC GGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACGAAGACCTAC ACCTGCAACGTAGATCACAAGCCCAGCAACACC AAGGTGGACAAGAGAGTTGAGTCCAAATATGGT CCCCCATGCCCACCGTGCCCAGCACCTGAGTTC CTGGGGGGACCATCAGTCTTCCTGTTCCCCCCA AAACCCAAGGACACTCTCATGATCTCCCGGACC CCTGAGGTCACGTGCGTGGTGGTGGACGTGAGC CAGGAAGACCCCGAGGTCCAGTTCAACTGGTAC GTGGATGGCGTGGAGGTGCATAATGCCAAGACA AAGCCGCGGGAGGAGCAGTTCAACAGCACGTAC CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG GACTGGCTGAACGGCAAGGAGTACAAGTGCAAG GTGTCCAACAAAGGCCTCCCGTCCTCCATCGAG AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAGCCACAGGTGTACACCCTGCCCCCATCCCAG GAGGAGATGACCAAGAACCAGGTCAGCCTGACC TGCCTGGTCAAAGGCTTCTACCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGGAC TCCGACGGCTCCTTCTTCCTCTACAGCAGGCTA ACCGTGGACAAGAGCAGGTGGCAGGAGGGGAAT GTCTTCTCATGCTCCGTGATGCATGAGGCTCTG CACAACCACTACACACAGAAGAGCCTCTCCCTG TCTCTGGGTAAA
BAP049-hum16 LC		
SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT

SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 32 (Kabat)	LCDR3	QNDYSYPYT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 33 (Chothia)	LCDR3	DYSYPY
SEQ ID NO: 66	VL	EIVLTQSPDFQSVTPKEKVTITCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIK
SEQ ID NO: 67	DNA VL	GAAATTGTGCTGACTCAGTCTCCAGACTTTCAG TCTGTGACTCCAAAGGAGAAAGTCACCATCACC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCCTCG AGGTTCAGTGGCAGTGGATCTGGGACAGATTTC ACCTTTACCATCAGTAGCCTGGAAGCTGAAGAT GCTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAA
SEQ ID NO: 68	LC	EIVLTQSPDFQSVTPKEKVTITCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 69	DNA LC	GAAATTGTGCTGACTCAGTCTCCAGACTTTCAG TCTGTGACTCCAAAGGAGAAAGTCACCATCACC TGCAAGTCCAGTCAGAGTCTGTTAGACAGTGGA AATCAAAAGAACTTCTTGACCTGGTACCAGCAG AAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT TGGGCATCCACTAGGGAATCTGGGGTCCCCTCG AGGTTCAGTGGCAGTGGATCTGGGACAGATTTC ACCTTTACCATCAGTAGCCTGGAAGCTGAAGAT GCTGCAACATATTACTGTCAGAATGATTATAGT TATCCGTACACGTTCGGCCAAGGGACCAAGGTG GAAATCAAACGTACGGTGGCTGCACCATCTGTC TTCATCTTCCCGCCATCTGATGAGCAGTTGAAA TCTGGAACTGCCTCTGTTGTGTGCCTGCTGAAT AACTTCTATCCCAGAGAGGCCAAAGTACAGTGG AAGGTGGATAACGCCCTCCAATCGGGTAACTCC CAGGAGAGTGTCACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGCACCCTGACGCTG AGCAAAGCAGACTACGAGAAACACAAAGTCTAC GCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
BAP049-Clone-A HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH
SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY
SEQ ID NO: 38	VH	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN

		RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 90	DNA VH	GAAGTGCAGCTGGTGCAGTCTGGCGCCGAAGTG AAGAAGCCTGGCGAGTCCCTGCGGATCTCCTGC AAGGGCTCTGGCTACACCTTCACCACCTACTGG ATGCACTGGGTGCGACAGGCTACCGGCCAGGGC CTGGAATGGATGGGCAACATCTATCCTGGCACC GGCGGCTCCAACTTCGACGAGAAGTTCAAGAAC AGAGTGACCATCACCGCCGACAAGTCCACCTCC ACCGCCTACATGGAACTGTCCTCCCTGAGATCC GAGGACACCGCCGTGTACTACTGCACCCGGTGG ACAACCGGCACAGGCGCTTATTGGGGCCAGGGC ACCACAGTGACCGTGTCCTCT
SEQ ID NO: 91	HC	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLG
SEQ ID NO: 92	DNA HC	GAAGTGCAGCTGGTGCAGTCTGGCGCCGAAGTG AAGAAGCCTGGCGAGTCCCTGCGGATCTCCTGC AAGGGCTCTGGCTACACCTTCACCACCTACTGG ATGCACTGGGTGCGACAGGCTACCGGCCAGGGC CTGGAATGGATGGGCAACATCTATCCTGGCACC GGCGGCTCCAACTTCGACGAGAAGTTCAAGAAC AGAGTGACCATCACCGCCGACAAGTCCACCTCC ACCGCCTACATGGAACTGTCCTCCCTGAGATCC GAGGACACCGCCGTGTACTACTGCACCCGGTGG ACAACCGGCACAGGCGCTTATTGGGGCCAGGGC ACCACAGTGACCGTGTCCTCTGCTTCTACCAAG GGGCCCAGCGTGTTCCCCCTGGCCCCCTGCTCC AGAAGCACCAGCGAGAGCACAGCCGCCCTGGGC TGCCTGGTGAAGGACTACTTCCCCGAGCCCGTG ACCGTGTCCTGGAACAGCGGAGCCCTGACCAGC GGCGTGCACACCTTCCCCGCCGTGCTGCAGAGC AGCGGCCTGTACAGCCTGAGCAGCGTGGTGACC GTGCCCAGCAGCAGCCTGGGCACCAAGACCTAC ACCTGTAACGTGGACCACAAGCCCAGCAACACC AAGGTGGACAAGAGGGTGGAGAGCAAGTACGGC CCACCCTGCCCCCCCTGCCCAGCCCCCGAGTTC CTGGGCGGACCCAGCGTGTTCCTGTTCCCCCCC AAGCCCAAGGACACCCTGATGATCAGCAGAACC CCCGAGGTGACCTGTGTGGTGGTGGACGTGTCC CAGGAGGACCCCGAGGTCCAGTTCAACTGGTAC GTGGACGGCGTGGAGGTGCACAACGCCAAGACC AAGCCCAGAGAGGAGCAGTTTAACAGCACCTAC CGGGTGGTGTCCGTGCTGACCGTGCTGCACCAG GACTGGCTGAACGGCAAAGAGTACAAGTGTAAG GTCTCCAACAAGGGCCTGCCAAGCAGCATCGAA AAGACCATCAGCAAGGCCAAGGGCCAGCCTAGA GAGCCCCAGGTCTACACCCTGCCACCCAGCCAA GAGGAGATGACCAAGAACCAGGTGTCCCTGACC TGTCTGGTGAAGGGCTTCTACCCAAGCGACATC

		GCCGTGGAGTGGGAGAGCAACGGCCAGCCCGAG AACAACTACAAGACCACCCCCCCAGTGCTGGAC AGCGACGGCAGCTTCTTCCTGTACAGCAGGCTG ACCGTGGACAAGTCCAGATGGCAGGAGGGCAAC GTCTTTAGCTGCTCCGTGATGCACGAGGCCCTG CACAACCACTACACCCAGAAGAGCCTGAGCCTG TCCCTGGGC
BAP049-Clone-A LC		
SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT
SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 32 (Kabat)	LCDR3	QNDYSYPYT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 33 (Chothia)	LCDR3	DYSYPY
SEQ ID NO: 42	VL	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTEFTLTISSLQPDDFATYYCQNDYS YPYTFGQGTKVEIK
SEQ ID NO: 93	DNA VL	GAGATCGTGCTGACCCAGTCCCCTGCCACCCTG TCACTGTCTCCAGGCGAGAGAGCTACCCTGTCC TGCAAGTCCTCCCAGTCCCTGCTGGACTCCGGC AACCAGAAGAACTTCCTGACCTGGTATCAGCAG AAGCCCGGCCAGGCCCCCAGACTGCTGATCTAC TGGGCCTCCACCCGGGAATCTGGCGTGCCCTCT AGATTCTCCGGCTCCGGCTCTGGCACCGAGTTT ACCCTGACCATCTCCAGCCTGCAGCCCGACGAC TTCGCCACCTACTACTGCCAGAACGACTACTCC TACCCCTACACCTTCGGCCAGGGCACCAAGGTG GAAATCAAG
SEQ ID NO: 44	LC	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTEFTLTISSLQPDDFATYYCQNDYS YPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 94	DNA LC	GAGATCGTGCTGACCCAGTCCCCTGCCACCCTG TCACTGTCTCCAGGCGAGAGAGCTACCCTGTCC TGCAAGTCCTCCCAGTCCCTGCTGGACTCCGGC AACCAGAAGAACTTCCTGACCTGGTATCAGCAG AAGCCCGGCCAGGCCCCCAGACTGCTGATCTAC TGGGCCTCCACCCGGGAATCTGGCGTGCCCTCT AGATTCTCCGGCTCCGGCTCTGGCACCGAGTTT ACCCTGACCATCTCCAGCCTGCAGCCCGACGAC TTCGCCACCTACTACTGCCAGAACGACTACTCC TACCCCTACACCTTCGGCCAGGGCACCAAGGTG GAAATCAAGCGTACGGTGGCCGCTCCCAGCGTG TTCATCTTCCCCCCAAGCGACGAGCAGCTGAAG AGCGGCACCGCCAGCGTGGTGTGTCTGCTGAAC AACTTCTACCCCAGGGAGGCCAAGGTGCAGTGG AAGGTGGACAACGCCCTGCAGAGCGGCAACAGC CAGGAGAGCGTCACCGAGCAGGACAGCAAGGAC TCCACCTACAGCCTGAGCAGCACCCTGACCCTG AGCAAGGCCGACTACGAGAAGCACAAGGTGTAC GCCTGTGAGGTGACCCACCAGGGCCTGTCCAGC CCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC
BAP049-Clone-B HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH

SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY
SEQ ID NO: 38	VH	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 95	DNA VH	GAGGTGCAGCTGGTGCAGTCAGGCGCCGAAGTG AAGAAGCCCGGCGAGTCACTGAGAATTAGCTGT AAAGGTTCAGGCTACACCTTCACTACCTACTGG ATGCACTGGGTCCGCCAGGCTACCGGTCAAGGC CTCGAGTGGATGGGTAATATCTACCCCGGCACC GGCGGCTCTAACTTCGACGAGAAGTTTAAGAAT AGAGTGACTATCACCGCCGATAAGTCTACTAGC ACCGCCTATATGGAACTGTCTAGCCTGAGATCA GAGGACACCGCCGTCTACTACTGCACTAGGTGG ACTACCGGCACAGGCGCCTACTGGGGTCAAGGC ACTACCGTGACCGTGTCTAGC
SEQ ID NO: 91	HC	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLG
SEQ ID NO: 96	DNA HC	GAGGTGCAGCTGGTGCAGTCAGGCGCCGAAGTG AAGAAGCCCGGCGAGTCACTGAGAATTAGCTGT AAAGGTTCAGGCTACACCTTCACTACCTACTGG ATGCACTGGGTCCGCCAGGCTACCGGTCAAGGC CTCGAGTGGATGGGTAATATCTACCCCGGCACC GGCGGCTCTAACTTCGACGAGAAGTTTAAGAAT AGAGTGACTATCACCGCCGATAAGTCTACTAGC ACCGCCTATATGGAACTGTCTAGCCTGAGATCA GAGGACACCGCCGTCTACTACTGCACTAGGTGG ACTACCGGCACAGGCGCCTACTGGGGTCAAGGC ACTACCGTGACCGTGTCTAGCGCTAGCACTAAG GGCCCGTCCGTGTTCCCCCTGGCACCTTGTAGC CGGAGCACTAGCGAATCCACCGCTGCCCTCGGC TGCCTGGTCAAGGATTACTTCCCGGAGCCCGTG ACCGTGTCCTGGAACAGCGGAGCCCTGACCTCC GGAGTGCACACCTTCCCCGCTGTGCTGCAGAGC TCCGGGCTGTACTCGCTGTCGTCGGTGGTCACG GTGCCTTCATCTAGCCTGGGTACCAAGACCTAC ACTTGCAACGTGGACCACAAGCCTTCCAACACT AAGGTGGACAAGCGCGTCGAATCGAAGTACGGC CCACCGTGCCCGCCTTGTCCCGCGCCGGAGTTC CTCGGCGGTCCCTCGGTCTTTCTGTTCCCACCG AAGCCCAAGGACACTTTGATGATTTCCCGCACC CCTGAAGTGACATGCGTGGTCGTGGACGTGTCA CAGGAAGATCCGGAGGTGCAGTTCAATTGGTAC

		GTGGATGGCGTCGAGGTGCACAACGCCAAAACC AAGCCGAGGGAGGAGCAGTTCAACTCCACTTAC CGCGTCGTGTCCGTGCTGACGGTGCTGCATCAG GACTGGCTGAACGGGAAGGAGTACAAGTGCAAA GTGTCCAACAAGGGACTTCCTAGCTCAATCGAA AAGACCATCTCGAAAGCCAAGGGACAGCCCCGG GAACCCCAAGTGTATACCCTGCCACCGAGCCAG GAAGAAATGACTAAGAACCAAGTCTCATTGACT TGCCTTGTGAAGGGCTTCTACCCATCGGATATC GCCGTGGAATGGGAGTCCAACGGCCAGCCGGAA AACAACTACAAGACCACCCCTCCGGTGCTGGAC TCAGACGGATCCTTCTTCCTCTACTCGCGGCTG ACCGTGGATAAGAGCAGATGGCAGGAGGGAAAT GTGTTCAGCTGTTCTGTGATGCATGAAGCCCTG CACAACCACTACACTCAGAAGTCCCTGTCCCTC TCCCTGGGA
BAP049-Clone-B LC		
SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT
SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 32 (Kabat)	LCDR3	QNDYSYPYT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 33 (Chothia)	LCDR3	DYSYPY
SEQ ID NO: 54	VL	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSG NQKNFLTWYQQKPGKAPKLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLQPEDIATYYCQNDYS YPYTFGQGTKVEIK
SEQ ID NO: 97	DNA VL	GAGATCGTCCTGACTCAGTCACCCGCTACCCTG AGCCTGAGCCCTGGCGAGCGGGCTACACTGAGC TGTAAATCTAGTCAGTCACTGCTGGATAGCGGT AATCAGAAGAACTTCCTGACCTGGTATCAGCAG AAGCCCGGTAAAGCCCCTAAGCTGCTGATCTAC TGGGCCTCTACTAGAGAATCAGGCGTGCCCTCT AGGTTTAGCGGTAGCGGTAGTGGCACCGACTTC ACCTTCACTATCTCTAGCCTGCAGCCCGAGGAT ATCGCTACCTACTACTGTCAGAACGACTATAGC TACCCCTACACCTTCGGTCAAGGCACTAAGGTC GAGATTAAG
SEQ ID NO: 56	LC	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSG NQKNFLTWYQQKPGKAPKLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLQPEDIATYYCQNDYS YPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 98	DNA LC	GAGATCGTCCTGACTCAGTCACCCGCTACCCTG AGCCTGAGCCCTGGCGAGCGGGCTACACTGAGC TGTAAATCTAGTCAGTCACTGCTGGATAGCGGT AATCAGAAGAACTTCCTGACCTGGTATCAGCAG AAGCCCGGTAAAGCCCCTAAGCTGCTGATCTAC TGGGCCTCTACTAGAGAATCAGGCGTGCCCTCT AGGTTTAGCGGTAGCGGTAGTGGCACCGACTTC ACCTTCACTATCTCTAGCCTGCAGCCCGAGGAT ATCGCTACCTACTACTGTCAGAACGACTATAGC TACCCCTACACCTTCGGTCAAGGCACTAAGGTC GAGATTAAGCGTACGGTGGCCGCTCCCAGCGTG TTCATCTTCCCCCCCAGCGACGAGCAGCTGAAG AGCGGCACCGCCAGCGTGGTGTGCCTGCTGAAC

		AACTTCTACCCCCGGGAGGCCAAGGTGCAGTGG AAGGTGGACAACGCCCTGCAGAGCGGCAACAGC CAGGAGAGCGTCACCGAGCAGGACAGCAAGGAC TCCACCTACAGCCTGAGCAGCACCCTGACCCTG AGCAAGGCCGACTACGAGAAGCATAAGGTGTAC GCCTGCGAGGTGACCCACCAGGGCCTGTCCAGC CCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC
BAP049-Clone-C HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH
SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY
SEQ ID NO: 38	VH	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 90	DNA VH	GAAGTGCAGCTGGTGCAGTCTGGCGCCGAAGTG AAGAAGCCTGGCGAGTCCCTGCGGATCTCCTGC AAGGGCTCTGGCTACACCTTCACCACCTACTGG ATGCACTGGGTGCGACAGGCTACCGGCCAGGGC CTGGAATGGATGGGCAACATCTATCCTGGCACC GGCGGCTCCAACTTCGACGAGAAGTTCAAGAAC AGAGTGACCATCACCGCCGACAAGTCCACCTCC ACCGCCTACATGGAACTGTCCTCCCTGAGATCC GAGGACACCGCCGTGTACTACTGCACCCGGTGG ACAACCGGCACAGGCGCTTATTGGGGCCAGGGC ACCACAGTGACCGTGTCCTCT
SEQ ID NO: 91	HC	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLG
SEQ ID NO: 92	DNA HC	GAAGTGCAGCTGGTGCAGTCTGGCGCCGAAGTG AAGAAGCCTGGCGAGTCCCTGCGGATCTCCTGC AAGGGCTCTGGCTACACCTTCACCACCTACTGG ATGCACTGGGTGCGACAGGCTACCGGCCAGGGC CTGGAATGGATGGGCAACATCTATCCTGGCACC GGCGGCTCCAACTTCGACGAGAAGTTCAAGAAC AGAGTGACCATCACCGCCGACAAGTCCACCTCC ACCGCCTACATGGAACTGTCCTCCCTGAGATCC GAGGACACCGCCGTGTACTACTGCACCCGGTGG ACAACCGGCACAGGCGCTTATTGGGGCCAGGGC ACCACAGTGACCGTGTCCTCTGCTTCTACCAAG GGGCCCAGCGTGTTCCCCCTGGCCCCCTGCTCC AGAAGCACCAGCGAGAGCACAGCCGCCCTGGGC TGCCTGGTGAAGGACTACTTCCCCGAGCCCGTG ACCGTGTCCTGGAACAGCGGAGCCCTGACCAGC

		GGCGTGCACACCTTCCCCGCCGTGCTGCAGAGC AGCGGCCTGTACAGCCTGAGCAGCGTGGTGACC GTGCCCAGCAGCAGCCTGGGCACCAAGACCTAC ACCTGTAACGTGGACCACAAGCCCAGCAACACC AAGGTGGACAAGAGGGTGGAGAGCAAGTACGGC CCACCCTGCCCCCCCTGCCCAGCCCCCGAGTTC CTGGGCGGACCCAGCGTGTTCCTGTTCCCCCCC AAGCCCAAGGACACCCTGATGATCAGCAGAACC CCCGAGGTGACCTGTGTGGTGGTGGACGTGTCC CAGGAGGACCCCGAGGTCCAGTTCAACTGGTAC GTGGACGGCGTGGAGGTGCACAACGCCAAGACC AAGCCCAGAGAGGAGCAGTTTAACAGCACCTAC CGGGTGGTGTCCGTGCTGACCGTGCTGCACCAG GACTGGCTGAACGGCAAAGAGTACAAGTGTAAG GTCTCCAACAAGGGCCTGCCAAGCAGCATCGAA AAGACCATCAGCAAGGCCAAGGGCCAGCCTAGA GAGCCCCAGGTCTACACCCTGCCACCCAGCCAA GAGGAGATGACCAAGAACCAGGTGTCCCTGACC TGTCTGGTGAAGGGCTTCTACCCAAGCGACATC GCCGTGGAGTGGGAGAGCAACGGCCAGCCCGAG AACAACTACAAGACCACCCCCCCAGTGCTGGAC AGCGACGGCAGCTTCTTCCTGTACAGCAGGCTG ACCGTGGACAAGTCCAGATGGCAGGAGGGCAAC GTCTTTAGCTGCTCCGTGATGCACGAGGCCCTG CACAACCACTACACCCAGAAGAGCCTGAGCCTG TCCCTGGGC
BAP049-Clone-C LC		
SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT
SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 32 (Kabat)	LCDR3	QNDYSYPYT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 33 (Chothia)	LCDR3	DYSYPY
SEQ ID NO: 66	VL	EIVLTQSPDFQSVTPKEKVTITCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIK
SEQ ID NO: 99	DNA VL	GAGATCGTGCTGACCCAGTCCCCCGACTTCCAG TCCGTGACCCCCAAAGAAAAAGTGACCATCACA TGCAAGTCCTCCCAGTCCCTGCTGGACTCCGGC AACCAGAAGAACTTCCTGACCTGGTATCAGCAG AAGCCCGGCCAGGCCCCCAGACTGCTGATCTAC TGGGCCTCCACCCGGGAATCTGGCGTGCCCTCT AGATTCTCCGGCTCCGGCTCTGGCACCGACTTT ACCTTCACCATCTCCAGCCTGGAAGCCGAGGAC GCCGCCACCTACTACTGCCAGAACGACTACTCC TACCCCTACACCTTCGGCCAGGGCACCAAGGTG GAAATCAAG
SEQ ID NO: 68	LC	EIVLTQSPDFQSVTPKEKVTITCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 100	DNA LC	GAGATCGTGCTGACCCAGTCCCCCGACTTCCAG TCCGTGACCCCCAAAGAAAAAGTGACCATCACA TGCAAGTCCTCCCAGTCCCTGCTGGACTCCGGC

		AACCAGAAGAACTTCCTGACCTGGTATCAGCAG AAGCCCGGCCAGGCCCCCAGACTGCTGATCTAC TGGGCCTCCACCCGGGAATCTGGCGTGCCCTCT AGATTCTCCGGCTCCGGCTCTGGCACCGACTTT ACCTTCACCATCTCCAGCCTGGAAGCCGAGGAC GCCGCCACCTACTACTGCCAGAACGACTACTCC TACCCCTACACCTTCGGCCAGGGCACCAAGGTG GAAATCAAGCGTACGGTGGCCGCTCCCAGCGTG TTCATCTTCCCCCCAAGCGACGAGCAGCTGAAG AGCGGCACCGCCAGCGTGGTGTGTCTGCTGAAC AACTTCTACCCCAGGGAGGCCAAGGTGCAGTGG AAGGTGGACAACGCCCTGCAGAGCGGCAACAGC CAGGAGAGCGTCACCGAGCAGGACAGCAAGGAC TCCACCTACAGCCTGAGCAGCACCCTGACCCTG AGCAAGGCCGACTACGAGAAGCACAAGGTGTAC GCCTGTGAGGTGACCCACCAGGGCCTGTCCAGC CCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC
BAP049-Clone-D HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH
SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY
SEQ ID NO: 50	VH	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWIRQSPSRGLEWLGNIYPGTGGSNFDEKFKN RFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 101	DNA VH	GAAGTGCAGCTGGTGCAGTCTGGCGCCGAAGTG AAGAAGCCTGGCGAGTCCCTGCGGATCTCCTGC AAGGGCTCTGGCTACACCTTCACCACCTACTGG ATGCACTGGATCCGGCAGTCCCCCTCTAGGGGC CTGGAATGGCTGGGCAACATCTACCCTGGCACC GGCGGCTCCAACTTCGACGAGAAGTTCAAGAAC AGGTTCACCATCTCCCGGGACAACTCCAAGAAC ACCCTGTACCTGCAGATGAACTCCCTGCGGGCC GAGGACACCGCCGTGTACTACTGTACCAGATGG ACCACCGGAACCGGCGCCTATTGGGGCCAGGGC ACAACAGTGACCGTGTCCTCC
SEQ ID NO: 102	HC	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWIRQSPSRGLEWLGNIYPGTGGSNFDEKFKN RFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLG
SEQ ID NO: 103	DNA HC	GAAGTGCAGCTGGTGCAGTCTGGCGCCGAAGTG AAGAAGCCTGGCGAGTCCCTGCGGATCTCCTGC AAGGGCTCTGGCTACACCTTCACCACCTACTGG ATGCACTGGATCCGGCAGTCCCCCTCTAGGGGC CTGGAATGGCTGGGCAACATCTACCCTGGCACC

		GGCGGCTCCAACTTCGACGAGAAGTTCAAGAAC AGGTTCACCATCTCCCGGGACAACTCCAAGAAC ACCCTGTACCTGCAGATGAACTCCCTGCGGGCC GAGGACACCGCCGTGTACTACTGTACCAGATGG ACCACCGGAACCGGCGCCTATTGGGGCCAGGGC ACAACAGTGACCGTGTCCTCCGCTTCTACCAAG GGGCCCAGCGTGTTCCCCCTGGCCCCCTGCTCC AGAAGCACCAGCGAGAGCACAGCCGCCCTGGGC TGCCTGGTGAAGGACTACTTCCCCGAGCCCGTG ACCGTGTCCTGGAACAGCGGAGCCCTGACCAGC GGCGTGCACACCTTCCCCGCCGTGCTGCAGAGC AGCGGCCTGTACAGCCTGAGCAGCGTGGTGACC GTGCCCAGCAGCAGCCTGGGCACCAAGACCTAC ACCTGTAACGTGGACCACAAGCCCAGCAACACC AAGGTGGACAAGAGGGTGGAGAGCAAGTACGGC CCACCCTGCCCCCCCTGCCCAGCCCCCGAGTTC CTGGGCGGACCCAGCGTGTTCCTGTTCCCCCCC AAGCCCAAGGACACCCTGATGATCAGCAGAACC CCCGAGGTGACCTGTGTGGTGGTGGACGTGTCC CAGGAGGACCCCGAGGTCCAGTTCAACTGGTAC GTGGACGGCGTGGAGGTGCACAACGCCAAGACC AAGCCCAGAGAGGAGCAGTTTAACAGCACCTAC CGGGTGGTGTCCGTGCTGACCGTGCTGCACCAG GACTGGCTGAACGGCAAAGAGTACAAGTGTAAG GTCTCCAACAAGGGCCTGCCAAGCAGCATCGAA AAGACCATCAGCAAGGCCAAGGGCCAGCCTAGA GAGCCCCAGGTCTACACCCTGCCACCCAGCCAA GAGGAGATGACCAAGAACCAGGTGTCCCTGACC TGTCTGGTGAAGGGCTTCTACCCAAGCGACATC GCCGTGGAGTGGGAGAGCAACGGCCAGCCCGAG AACAACTACAAGACCACCCCCCCAGTGCTGGAC AGCGACGGCAGCTTCTTCCTGTACAGCAGGCTG ACCGTGGACAAGTCCAGATGGCAGGAGGGCAAC GTCTTTAGCTGCTCCGTGATGCACGAGGCCCTG CACAACCACTACACCCAGAAGAGCCTGAGCCTG TCCCTGGGC
BAP049-Clone-D LC		
SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT
SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 32 (Kabat)	LCDR3	QNDYSYPYT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 33 (Chothia)	LCDR3	DYSYPY
SEQ ID NO: 70	VL	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIK
SEQ ID NO: 104	DNA VL	GAGATCGTGCTGACCCAGTCCCCTGCCACCCTG TCACTGTCTCCAGGCGAGAGAGCTACCCTGTCC TGCAAGTCCTCCCAGTCCCTGCTGGACTCCGGC AACCAGAAGAACTTCCTGACCTGGTATCAGCAG AAGCCCGGCCAGGCCCCCAGACTGCTGATCTAC TGGGCCTCCACCCGGGAATCTGGCGTGCCCTCT AGATTCTCCGGCTCCGGCTCTGGCACCGACTTT ACCTTCACCATCTCCAGCCTGGAAGCCGAGGAC GCCGCCACCTACTACTGCCAGAACGACTACTCC TACCCCTACACCTTCGGCCAGGGCACCAAGGTG GAAATCAAG

SEQ ID NO: 72	LC	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 105	DNA LC	GAGATCGTGCTGACCCAGTCCCCTGCCACCCTG TCACTGTCTCCAGGCGAGAGAGCTACCCTGTCC TGCAAGTCCTCCCAGTCCCTGCTGGACTCCGGC AACCAGAAGAACTTCCTGACCTGGTATCAGCAG AAGCCCGGCCAGGCCCCCAGACTGCTGATCTAC TGGGCCTCCACCCGGGAATCTGGCGTGCCCTCT AGATTCTCCGGCTCCGGCTCTGGCACCGACTTT ACCTTCACCATCTCCAGCCTGGAAGCCGAGGAC GCCGCCACCTACTACTGCCAGAACGACTACTCC TACCCCTACACCTTCGGCCAGGGCACCAAGGTG GAAATCAAGCGTACGGTGGCCGCTCCCAGCGTG TTCATCTTCCCCCCAAGCGACGAGCAGCTGAAG AGCGGCACCGCCAGCGTGGTGTGTCTGCTGAAC AACTTCTACCCCAGGGAGGCCAAGGTGCAGTGG AAGGTGGACAACGCCCTGCAGAGCGGCAACAGC CAGGAGAGCGTCACCGAGCAGGACAGCAAGGAC TCCACCTACAGCCTGAGCAGCACCCTGACCCTG AGCAAGGCCGACTACGAGAAGCACAAGGTGTAC GCCTGTGAGGTGACCCACCAGGGCCTGTCCAGC CCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC
BAP049-Clone-E HC		
SEQ ID NO: 1 (Kabat)	HCDR1	TYWMH
SEQ ID NO: 2 (Kabat)	HCDR2	NIYPGTGGSNFDEKFKN
SEQ ID NO: 3 (Kabat)	HCDR3	WTTGTGAY
SEQ ID NO: 4 (Chothia)	HCDR1	GYTFTTY
SEQ ID NO: 5 (Chothia)	HCDR2	YPGTGG
SEQ ID NO: 3 (Chothia)	HCDR3	WTTGTGAY
SEQ ID NO: 38	VH	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSS
SEQ ID NO: 95	DNA VH	GAGGTGCAGCTGGTGCAGTCAGGCGCCGAAGTG AAGAAGCCCGGCGAGTCACTGAGAATTAGCTGT AAAGGTTCAGGCTACACCTTCACTACCTACTGG ATGCACTGGGTCCGCCAGGCTACCGGTCAAGGC CTCGAGTGGATGGGTAATATCTACCCCGGCACC GGCGGCTCTAACTTCGACGAGAAGTTTAAGAAT AGAGTGACTATCACCGCCGATAAGTCTACTAGC ACCGCCTATATGGAACTGTCTAGCCTGAGATCA GAGGACACCGCCGTCTACTACTGCACTAGGTGG ACTACCGGCACAGGCGCCTACTGGGGTCAAGGC ACTACCGTGACCGTGTCTAGC
SEQ ID NO: 91	HC	EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYW MHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKN RVTITADKSTSTAYMELSSLRSEDTAVYYCTRW TTGTGAYWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY

		RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLG
SEQ ID NO: 96	DNA HC	GAGGTGCAGCTGGTGCAGTCAGGCGCCGAAGTG AAGAAGCCCGGCGAGTCACTGAGAATTAGCTGT AAAGGTTCAGGCTACACCTTCACTACCTACTGG ATGCACTGGGTCCGCCAGGCTACCGGTCAAGGC CTCGAGTGGATGGGTAATATCTACCCCGGCACC GGCGGCTCTAACTTCGACGAGAAGTTTAAGAAT AGAGTGACTATCACCGCCGATAAGTCTACTAGC ACCGCCTATATGGAACTGTCTAGCCTGAGATCA GAGGACACCGCCGTCTACTACTGCACTAGGTGG ACTACCGGCACAGGCGCCTACTGGGGTCAAGGC ACTACCGTGACCGTGTCTAGCGCTAGCACTAAG GGCCCGTCCGTGTTCCCCCTGGCACCTTGTAGC CGGAGCACTAGCGAATCCACCGCTGCCCTCGGC TGCCTGGTCAAGGATTACTTCCCGGAGCCCGTG ACCGTGTCCTGGAACAGCGGAGCCCTGACCTCC GGAGTGCACACCTTCCCCGCTGTGCTGCAGAGC TCCGGGCTGTACTCGCTGTCGTCGGTGGTCACG GTGCCTTCATCTAGCCTGGGTACCAAGACCTAC ACTTGCAACGTGGACCACAAGCCTTCCAACACT AAGGTGGACAAGCGCGTCGAATCGAAGTACGGC CCACCGTGCCCGCCTTGTCCCGCGCCGGAGTTC CTCGGCGGTCCCTCGGTCTTTCTGTTCCCACCG AAGCCCAAGGACACTTTGATGATTTCCCGCACC CCTGAAGTGACATGCGTGGTCGTGGACGTGTCA CAGGAAGATCCGGAGGTGCAGTTCAATTGGTAC GTGGATGGCGTCGAGGTGCACAACGCCAAAACC AAGCCGAGGGAGGAGCAGTTCAACTCCACTTAC CGCGTCGTGTCCGTGCTGACGGTGCTGCATCAG GACTGGCTGAACGGGAAGGAGTACAAGTGCAAA GTGTCCAACAAGGGACTTCCTAGCTCAATCGAA AAGACCATCTCGAAAGCCAAGGGACAGCCCCGG GAACCCCAAGTGTATACCCTGCCACCGAGCCAG GAAGAAATGACTAAGAACCAAGTCTCATTGACT TGCCTTGTGAAGGGCTTCTACCCATCGGATATC GCCGTGGAATGGGAGTCCAACGGCCAGCCGGAA AACAACTACAAGACCACCCCTCCGGTGCTGGAC TCAGACGGATCCTTCTTCCTCTACTCGCGGCTG ACCGTGGATAAGAGCAGATGGCAGGAGGGAAAT GTGTTCAGCTGTTCTGTGATGCATGAAGCCCTG CACAACCACTACACTCAGAAGTCCCTGTCCCTC TCCCTGGGA
BAP049-Clone-E LC		
SEQ ID NO: 10 (Kabat)	LCDR1	KSSQSLLDSGNQKNFLT
SEQ ID NO: 11 (Kabat)	LCDR2	WASTRES
SEQ ID NO: 32 (Kabat)	LCDR3	QNDYSYPYT
SEQ ID NO: 13 (Chothia)	LCDR1	SQSLLDSGNQKNF
SEQ ID NO: 14 (Chothia)	LCDR2	WAS
SEQ ID NO: 33 (Chothia)	LCDR3	DYSYPY
SEQ ID NO: 70	VL	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIK
SEQ ID NO: 106	DNA VL	GAGATCGTCCTGACTCAGTCACCCGCTACCCTG

		AGCCTGAGCCCTGGCGAGCGGGCTACACTGAGC TGTAAATCTAGTCAGTCACTGCTGGATAGCGGT AATCAGAAGAACTTCCTGACCTGGTATCAGCAG AAGCCCGGTCAAGCCCCTAGACTGCTGATCTAC TGGGCCTCTACTAGAGAATCAGGCGTGCCCTCT AGGTTTAGCGGTAGCGGTAGTGGCACCGACTTC ACCTTCACTATCTCTAGCCTGGAAGCCGAGGAC GCCGCTACCTACTACTGTCAGAACGACTATAGC TACCCCTACACCTTCGGTCAAGGCACTAAGGTC GAGATTAAG
SEQ ID NO: 72	LC	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSG NQKNFLTWYQQKPGQAPRLLIYWASTRESGVPS RFSGSGSGTDFTFTISSLEAEDAATYYCQNDYS YPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 107	DNA LC	GAGATCGTCCTGACTCAGTCACCCGCTACCCTG AGCCTGAGCCCTGGCGAGCGGGCTACACTGAGC TGTAAATCTAGTCAGTCACTGCTGGATAGCGGT AATCAGAAGAACTTCCTGACCTGGTATCAGCAG AAGCCCGGTCAAGCCCCTAGACTGCTGATCTAC TGGGCCTCTACTAGAGAATCAGGCGTGCCCTCT AGGTTTAGCGGTAGCGGTAGTGGCACCGACTTC ACCTTCACTATCTCTAGCCTGGAAGCCGAGGAC GCCGCTACCTACTACTGTCAGAACGACTATAGC TACCCCTACACCTTCGGTCAAGGCACTAAGGTC GAGATTAAGCGTACGGTGGCCGCTCCCAGCGTG TTCATCTTCCCCCCCAGCGACGAGCAGCTGAAG AGCGGCACCGCCAGCGTGGTGTGCCTGCTGAAC AACTTCTACCCCCGGGAGGCCAAGGTGCAGTGG AAGGTGGACAACGCCCTGCAGAGCGGCAACAGC CAGGAGAGCGTCACCGAGCAGGACAGCAAGGAC TCCACCTACAGCCTGAGCAGCACCCTGACCCTG AGCAAGGCCGACTACGAGAAGCATAAGGTGTAC GCCTGCGAGGTGACCCACCAGGGCCTGTCCAGC CCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC
BAP049 HC		
SEQ ID NO: 108 (Kabat)	HCDR1	ACTTACTGGATGCAC
SEQ ID NO: 109 (Kabat)	HCDR2	AATATTTATCCTGGTACTGGTGGTTCTAACTTC GATGAGAAGTTCAAGAAC
SEQ ID NO: 110 (Kabat)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
SEQ ID NO: 111 (Chothia)	HCDR1	GGCTACACATTCACCACTTAC
SEQ ID NO: 112 (Chothia)	HCDR2	TATCCTGGTACTGGTGGT
SEQ ID NO: 110 (Chothia)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
BAP049 LC		
SEQ ID NO: 113 (Kabat)	LCDR1	AAGTCCAGTCAGAGTCTGTTAGACAGTGGAAAT CAAAAGAACTTCTTGACC
SEQ ID NO: 114 (Kabat)	LCDR2	TGGGCATCCACTAGGGAATCT
SEQ ID NO: 115 (Kabat)	LCDR3	CAGAATGATTATAGTTATCCGTGCACG
SEQ ID NO: 116 (Chothia)	LCDR1	AGTCAGAGTCTGTTAGACAGTGGAAATCAAAAG AACTTC
SEQ ID NO: 117 (Chothia)	LCDR2	TGGGCATCC
SEQ ID NO: 118 (Chothia)	LCDR3	GATTATAGTTATCCGTGC
BAP049-chi HC		

SEQ ID NO: 108 (Kabat)	HCDR1	ACTTACTGGATGCAC
SEQ ID NO: 109 (Kabat)	HCDR2	AATATTTATCCTGGTACTGGTGGTTCTAACTTC GATGAGAAGTTCAAGAAC
SEQ ID NO: 110 (Kabat)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
SEQ ID NO: 111 (Chothia)	HCDR1	GGCTACACATTCACCACTTAC
SEQ ID NO: 112 (Chothia)	HCDR2	TATCCTGGTACTGGTGGT
SEQ ID NO: 110 (Chothia)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
BAP049-chi LC		
SEQ ID NO: 113 (Kabat)	LCDR1	AAGTCCAGTCAGAGTCTGTTAGACAGTGGAAAT CAAAAGAACTTCTTGACC
SEQ ID NO: 114 (Kabat)	LCDR2	TGGGCATCCACTAGGGAATCT
SEQ ID NO: 115 (Kabat)	LCDR3	CAGAATGATTATAGTTATCCGTGCACG
SEQ ID NO: 116 (Chothia)	LCDR1	AGTCAGAGTCTGTTAGACAGTGGAAATCAAAAG AACTTC
SEQ ID NO: 117 (Chothia)	LCDR2	TGGGCATCC
SEQ ID NO: 118 (Chothia)	LCDR3	GATTATAGTTATCCGTGC
BAP049-chi Y HC		
SEQ ID NO: 108 (Kabat)	HCDR1	ACTTACTGGATGCAC
SEQ ID NO: 109 (Kabat)	HCDR2	AATATTTATCCTGGTACTGGTGGTTCTAACTTC GATGAGAAGTTCAAGAAC
SEQ ID NO: 110 (Kabat)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
SEQ ID NO: 111 (Chothia)	HCDR1	GGCTACACATTCACCACTTAC
SEQ ID NO: 112 (Chothia)	HCDR2	TATCCTGGTACTGGTGGT
SEQ ID NO: 110 (Chothia)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
BAP049-chi Y LC		
SEQ ID NO: 113 (Kabat)	LCDR1	AAGTCCAGTCAGAGTCTGTTAGACAGTGGAAAT CAAAAGAACTTCTTGACC
SEQ ID NO: 114 (Kabat)	LCDR2	TGGGCATCCACTAGGGAATCT
SEQ ID NO: 119 (Kabat)	LCDR3	CAGAATGATTATAGTTATCCGTACACG
SEQ ID NO: 116 (Chothia)	LCDR1	AGTCAGAGTCTGTTAGACAGTGGAAATCAAAAG AACTTC
SEQ ID NO: 117 (Chothia)	LCDR2	TGGGCATCC
SEQ ID NO: 120 (Chothia)	LCDR3	GATTATAGTTATCCGTAC
BAP049-hum01 HC		
SEQ ID NO: 108 (Kabat)	HCDR1	ACTTACTGGATGCAC
SEQ ID NO: 109 (Kabat)	HCDR2	AATATTTATCCTGGTACTGGTGGTTCTAACTTC GATGAGAAGTTCAAGAAC
SEQ ID NO: 110 (Kabat)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
SEQ ID NO: 111 (Chothia)	HCDR1	GGCTACACATTCACCACTTAC
SEQ ID NO: 112 (Chothia)	HCDR2	TATCCTGGTACTGGTGGT
SEQ ID NO: 110 (Chothia)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
BAP049-hum01 LC		
SEQ ID NO: 113 (Kabat)	LCDR1	AAGTCCAGTCAGAGTCTGTTAGACAGTGGAAAT CAAAAGAACTTCTTGACC
SEQ ID NO: 114 (Kabat)	LCDR2	TGGGCATCCACTAGGGAATCT
SEQ ID NO: 119 (Kabat)	LCDR3	CAGAATGATTATAGTTATCCGTACACG
SEQ ID NO: 116 (Chothia)	LCDR1	AGTCAGAGTCTGTTAGACAGTGGAAATCAAAAG AACTTC
SEQ ID NO: 117 (Chothia)	LCDR2	TGGGCATCC

SEQ ID NO: 120 (Chothia)	LCDR3	GATTATAGTTATCCGTAC
BAP049-hum02 HC		
SEQ ID NO: 108 (Kabat)	HCDR1	ACTTACTGGATGCAC
SEQ ID NO: 109 (Kabat)	HCDR2	AATATTTATCCTGGTACTGGTGGTTCTAACTTC GATGAGAAGTTCAAGAAC
SEQ ID NO: 110 (Kabat)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
SEQ ID NO: 111 (Chothia)	HCDR1	GGCTACACATTCACCACTTAC
SEQ ID NO: 112 (Chothia)	HCDR2	TATCCTGGTACTGGTGGT
SEQ ID NO: 110 (Chothia)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
BAP049-hum02 LC		
SEQ ID NO: 113 (Kabat)	LCDR1	AAGTCCAGTCAGAGTCTGTTAGACAGTGGAAAT CAAAAGAACTTCTTGACC
SEQ ID NO: 114 (Kabat)	LCDR2	TGGGCATCCACTAGGGAATCT
SEQ ID NO: 119 (Kabat)	LCDR3	CAGAATGATTATAGTTATCCGTACACG
SEQ ID NO: 116 (Chothia)	LCDR1	AGTCAGAGTCTGTTAGACAGTGGAAATCAAAAG AACTTC
SEQ ID NO: 117 (Chothia)	LCDR2	TGGGCATCC
SEQ ID NO: 120 (Chothia)	LCDR3	GATTATAGTTATCCGTAC
BAP049-hum03 HC		
SEQ ID NO: 108 (Kabat)	HCDR1	ACTTACTGGATGCAC
SEQ ID NO: 109 (Kabat)	HCDR2	AATATTTATCCTGGTACTGGTGGTTCTAACTTC GATGAGAAGTTCAAGAAC
SEQ ID NO: 110 (Kabat)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
SEQ ID NO: 111 (Chothia)	HCDR1	GGCTACACATTCACCACTTAC
SEQ ID NO: 112 (Chothia)	HCDR2	TATCCTGGTACTGGTGGT
SEQ ID NO: 110 (Chothia)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
BAP049-hum03 LC		
SEQ ID NO: 113 (Kabat)	LCDR1	AAGTCCAGTCAGAGTCTGTTAGACAGTGGAAAT CAAAAGAACTTCTTGACC
SEQ ID NO: 114 (Kabat)	LCDR2	TGGGCATCCACTAGGGAATCT
SEQ ID NO: 119 (Kabat)	LCDR3	CAGAATGATTATAGTTATCCGTACACG
SEQ ID NO: 116 (Chothia)	LCDR1	AGTCAGAGTCTGTTAGACAGTGGAAATCAAAAG AACTTC
SEQ ID NO: 117 (Chothia)	LCDR2	TGGGCATCC
SEQ ID NO: 120 (Chothia)	LCDR3	GATTATAGTTATCCGTAC
BAP049-hum04 HC		
SEQ ID NO: 108 (Kabat)	HCDR1	ACTTACTGGATGCAC
SEQ ID NO: 109 (Kabat)	HCDR2	AATATTTATCCTGGTACTGGTGGTTCTAACTTC GATGAGAAGTTCAAGAAC
SEQ ID NO: 110 (Kabat)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
SEQ ID NO: 111 (Chothia)	HCDR1	GGCTACACATTCACCACTTAC
SEQ ID NO: 112 (Chothia)	HCDR2	TATCCTGGTACTGGTGGT
SEQ ID NO: 110 (Chothia)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
BAP049-hum04 LC		
SEQ ID NO: 113 (Kabat)	LCDR1	AAGTCCAGTCAGAGTCTGTTAGACAGTGGAAAT CAAAAGAACTTCTTGACC
SEQ ID NO: 114 (Kabat)	LCDR2	TGGGCATCCACTAGGGAATCT
SEQ ID NO: 119 (Kabat)	LCDR3	CAGAATGATTATAGTTATCCGTACACG

SEQ ID NO: 116 (Chothia)	LCDR1	AGTCAGAGTCTGTTAGACAGTGGAAATCAAAAG AACTTC
SEQ ID NO: 117 (Chothia)	LCDR2	TGGGCATCC
SEQ ID NO: 120 (Chothia)	LCDR3	GATTATAGTTATCCGTAC
BAP049-hum05 HC		
SEQ ID NO: 108 (Kabat)	HCDR1	ACTTACTGGATGCAC
SEQ ID NO: 109 (Kabat)	HCDR2	AATATTTATCCTGGTACTGGTGGTTCTAACTTC GATGAGAAGTTCAAGAAC
SEQ ID NO: 110 (Kabat)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
SEQ ID NO: 111 (Chothia)	HCDR1	GGCTACACATTCACCACTTAC
SEQ ID NO: 112 (Chothia)	HCDR2	TATCCTGGTACTGGTGGT
SEQ ID NO: 110 (Chothia)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
BAP049-hum05 LC		
SEQ ID NO: 113 (Kabat)	LCDR1	AAGTCCAGTCAGAGTCTGTTAGACAGTGGAAAT CAAAAGAACTTCTTGACC
SEQ ID NO: 114 (Kabat)	LCDR2	TGGGCATCCACTAGGGAATCT
SEQ ID NO: 119 (Kabat)	LCDR3	CAGAATGATTATAGTTATCCGTACACG
SEQ ID NO: 116 (Chothia)	LCDR1	AGTCAGAGTCTGTTAGACAGTGGAAATCAAAAG AACTTC
SEQ ID NO: 117 (Chothia)	LCDR2	TGGGCATCC
SEQ ID NO: 120 (Chothia)	LCDR3	GATTATAGTTATCCGTAC
BAP049-hum06 HC		
SEQ ID NO: 108 (Kabat)	HCDR1	ACTTACTGGATGCAC
SEQ ID NO: 109 (Kabat)	HCDR2	AATATTTATCCTGGTACTGGTGGTTCTAACTTC GATGAGAAGTTCAAGAAC
SEQ ID NO: 110 (Kabat)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
SEQ ID NO: 111 (Chothia)	HCDR1	GGCTACACATTCACCACTTAC
SEQ ID NO: 112 (Chothia)	HCDR2	TATCCTGGTACTGGTGGT
SEQ ID NO: 110 (Chothia)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
BAP049-hum06 LC		
SEQ ID NO: 113 (Kabat)	LCDR1	AAGTCCAGTCAGAGTCTGTTAGACAGTGGAAAT CAAAAGAACTTCTTGACC
SEQ ID NO: 114 (Kabat)	LCDR2	TGGGCATCCACTAGGGAATCT
SEQ ID NO: 119 (Kabat)	LCDR3	CAGAATGATTATAGTTATCCGTACACG
SEQ ID NO: 116 (Chothia)	LCDR1	AGTCAGAGTCTGTTAGACAGTGGAAATCAAAAG AACTTC
SEQ ID NO: 117 (Chothia)	LCDR2	TGGGCATCC
SEQ ID NO: 120 (Chothia)	LCDR3	GATTATAGTTATCCGTAC
BAP049-hum07 HC		
SEQ ID NO: 108 (Kabat)	HCDR1	ACTTACTGGATGCAC
SEQ ID NO: 109 (Kabat)	HCDR2	AATATTTATCCTGGTACTGGTGGTTCTAACTTC GATGAGAAGTTCAAGAAC
SEQ ID NO: 110 (Kabat)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
SEQ ID NO: 111 (Chothia)	HCDR1	GGCTACACATTCACCACTTAC
SEQ ID NO: 112 (Chothia)	HCDR2	TATCCTGGTACTGGTGGT
SEQ ID NO: 110 (Chothia)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
BAP049-hum07 LC		
SEQ ID NO: 113 (Kabat)	LCDR1	AAGTCCAGTCAGAGTCTGTTAGACAGTGGAAAT CAAAAGAACTTCTTGACC

SEQ ID NO: 114 (Kabat)	LCDR2	TGGGCATCCACTAGGGAATCT
SEQ ID NO: 119 (Kabat)	LCDR3	CAGAATGATTATAGTTATCCGTACACG
SEQ ID NO: 116 (Chothia)	LCDR1	AGTCAGAGTCTGTTAGACAGTGGAAATCAAAAG AACTTC
SEQ ID NO: 117 (Chothia)	LCDR2	TGGGCATCC
SEQ ID NO: 120 (Chothia)	LCDR3	GATTATAGTTATCCGTAC
BAP049-hum08 HC		
SEQ ID NO: 108 (Kabat)	HCDR1	ACTTACTGGATGCAC
SEQ ID NO: 109 (Kabat)	HCDR2	AATATTTATCCTGGTACTGGTGGTTCTAACTTC GATGAGAAGTTCAAGAAC
SEQ ID NO: 110 (Kabat)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
SEQ ID NO: 111 (Chothia)	HCDR1	GGCTACACATTCACCACTTAC
SEQ ID NO: 112 (Chothia)	HCDR2	TATCCTGGTACTGGTGGT
SEQ ID NO: 110 (Chothia)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
BAP049-hum08 LC		
SEQ ID NO: 113 (Kabat)	LCDR1	AAGTCCAGTCAGAGTCTGTTAGACAGTGGAAAT CAAAAGAACTTCTTGACC
SEQ ID NO: 114 (Kabat)	LCDR2	TGGGCATCCACTAGGGAATCT
SEQ ID NO: 119 (Kabat)	LCDR3	CAGAATGATTATAGTTATCCGTACACG
SEQ ID NO: 116 (Chothia)	LCDR1	AGTCAGAGTCTGTTAGACAGTGGAAATCAAAAG AACTTC
SEQ ID NO: 117 (Chothia)	LCDR2	TGGGCATCC
SEQ ID NO: 120 (Chothia)	LCDR3	GATTATAGTTATCCGTAC
BAP049-hum09 HC		
SEQ ID NO: 108 (Kabat)	HCDR1	ACTTACTGGATGCAC
SEQ ID NO: 109 (Kabat)	HCDR2	AATATTTATCCTGGTACTGGTGGTTCTAACTTC GATGAGAAGTTCAAGAAC
SEQ ID NO: 110 (Kabat)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
SEQ ID NO: 111 (Chothia)	HCDR1	GGCTACACATTCACCACTTAC
SEQ ID NO: 112 (Chothia)	HCDR2	TATCCTGGTACTGGTGGT
SEQ ID NO: 110 (Chothia)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
BAP049-hum09 LC		
SEQ ID NO: 113 (Kabat)	LCDR1	AAGTCCAGTCAGAGTCTGTTAGACAGTGGAAAT CAAAAGAACTTCTTGACC
SEQ ID NO: 114 (Kabat)	LCDR2	TGGGCATCCACTAGGGAATCT
SEQ ID NO: 119 (Kabat)	LCDR3	CAGAATGATTATAGTTATCCGTACACG
SEQ ID NO: 116 (Chothia)	LCDR1	AGTCAGAGTCTGTTAGACAGTGGAAATCAAAAG AACTTC
SEQ ID NO: 117 (Chothia)	LCDR2	TGGGCATCC
SEQ ID NO: 120 (Chothia)	LCDR3	GATTATAGTTATCCGTAC
BAP049-hum10 HC		
SEQ ID NO: 108 (Kabat)	HCDR1	ACTTACTGGATGCAC
SEQ ID NO: 109 (Kabat)	HCDR2	AATATTTATCCTGGTACTGGTGGTTCTAACTTC GATGAGAAGTTCAAGAAC
SEQ ID NO: 110 (Kabat)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
SEQ ID NO: 111 (Chothia)	HCDR1	GGCTACACATTCACCACTTAC
SEQ ID NO: 112 (Chothia)	HCDR2	TATCCTGGTACTGGTGGT
SEQ ID NO: 110 (Chothia)	HCDR3	TGGACTACTGGGACGGGAGCTTAT

BAP049-hum10 LC		
SEQ ID NO: 113 (Kabat)	LCDR1	AAGTCCAGTCAGAGTCTGTTAGACAGTGGAAAT CAAAAGAACTTCTTGACC
SEQ ID NO: 114 (Kabat)	LCDR2	TGGGCATCCACTAGGGAATCT
SEQ ID NO: 119 (Kabat)	LCDR3	CAGAATGATTATAGTTATCCGTACACG
SEQ ID NO: 116 (Chothia)	LCDR1	AGTCAGAGTCTGTTAGACAGTGGAAATCAAAAG AACTTC
SEQ ID NO: 117 (Chothia)	LCDR2	TGGGCATCC
SEQ ID NO: 120 (Chothia)	LCDR3	GATTATAGTTATCCGTAC
BAP049-hum11 HC		
SEQ ID NO: 108 (Kabat)	HCDR1	ACTTACTGGATGCAC
SEQ ID NO: 109 (Kabat)	HCDR2	AATATTTATCCTGGTACTGGTGGTTCTAACTTC GATGAGAAGTTCAAGAAC
SEQ ID NO: 110 (Kabat)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
SEQ ID NO: 111 (Chothia)	HCDR1	GGCTACACATTCACCACTTAC
SEQ ID NO: 112 (Chothia)	HCDR2	TATCCTGGTACTGGTGGT
SEQ ID NO: 110 (Chothia)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
BAP049-hum11 LC		
SEQ ID NO: 113 (Kabat)	LCDR1	AAGTCCAGTCAGAGTCTGTTAGACAGTGGAAAT CAAAAGAACTTCTTGACC
SEQ ID NO: 114 (Kabat)	LCDR2	TGGGCATCCACTAGGGAATCT
SEQ ID NO: 119 (Kabat)	LCDR3	CAGAATGATTATAGTTATCCGTACACG
SEQ ID NO: 116 (Chothia)	LCDR1	AGTCAGAGTCTGTTAGACAGTGGAAATCAAAAG AACTTC
SEQ ID NO: 117 (Chothia)	LCDR2	TGGGCATCC
SEQ ID NO: 120 (Chothia)	LCDR3	GATTATAGTTATCCGTAC
BAP049-hum12 HC		
SEQ ID NO: 108 (Kabat)	HCDR1	ACTTACTGGATGCAC
SEQ ID NO: 109 (Kabat)	HCDR2	AATATTTATCCTGGTACTGGTGGTTCTAACTTC GATGAGAAGTTCAAGAAC
SEQ ID NO: 110 (Kabat)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
SEQ ID NO: 111 (Chothia)	HCDR1	GGCTACACATTCACCACTTAC
SEQ ID NO: 112 (Chothia)	HCDR2	TATCCTGGTACTGGTGGT
SEQ ID NO: 110 (Chothia)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
BAP049-hum12 LC		
SEQ ID NO: 113 (Kabat)	LCDR1	AAGTCCAGTCAGAGTCTGTTAGACAGTGGAAAT CAAAAGAACTTCTTGACC
SEQ ID NO: 114 (Kabat)	LCDR2	TGGGCATCCACTAGGGAATCT
SEQ ID NO: 119 (Kabat)	LCDR3	CAGAATGATTATAGTTATCCGTACACG
SEQ ID NO: 116 (Chothia)	LCDR1	AGTCAGAGTCTGTTAGACAGTGGAAATCAAAAG AACTTC
SEQ ID NO: 117 (Chothia)	LCDR2	TGGGCATCC
SEQ ID NO: 120 (Chothia)	LCDR3	GATTATAGTTATCCGTAC
BAP049-hum13 HC		
SEQ ID NO: 108 (Kabat)	HCDR1	ACTTACTGGATGCAC
SEQ ID NO: 109 (Kabat)	HCDR2	AATATTTATCCTGGTACTGGTGGTTCTAACTTC GATGAGAAGTTCAAGAAC
SEQ ID NO: 110 (Kabat)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
SEQ ID NO: 111 (Chothia)	HCDR1	GGCTACACATTCACCACTTAC

SEQ ID NO: 112 (Chothia)	HCDR2	TATCCTGGTACTGGTGGT
SEQ ID NO: 110 (Chothia)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
BAP049-hum13 LC		
SEQ ID NO: 121 (Kabat)	LCDR1	AAGTCCAGTCAGAGTCTGTTAGACAGTGGAAAT CAAAAGAACTTCTTAACC
SEQ ID NO: 114 (Kabat)	LCDR2	TGGGCATCCACTAGGGAATCT
SEQ ID NO: 119 (Kabat)	LCDR3	CAGAATGATTATAGTTATCCGTACACG
SEQ ID NO: 116 (Chothia)	LCDR1	AGTCAGAGTCTGTTAGACAGTGGAAATCAAAAG AACTTC
SEQ ID NO: 117 (Chothia)	LCDR2	TGGGCATCC
SEQ ID NO: 120 (Chothia)	LCDR3	GATTATAGTTATCCGTAC
BAP049-hum14 HC		
SEQ ID NO: 108 (Kabat)	HCDR1	ACTTACTGGATGCAC
SEQ ID NO: 109 (Kabat)	HCDR2	AATATTTATCCTGGTACTGGTGGTTCTAACTTC GATGAGAAGTTCAAGAAC
SEQ ID NO: 223 (Kabat)	HCDR3	TGGACTACTGGGACGGGAGCTTAC
SEQ ID NO: 111 (Chothia)	HCDR1	GGCTACACATTCACCACTTAC
SEQ ID NO: 112 (Chothia)	HCDR2	TATCCTGGTACTGGTGGT
SEQ ID NO: 223 (Chothia)	HCDR3	TGGACTACTGGGACGGGAGCTTAC
BAP049-hum14 LC		
SEQ ID NO: 113 (Kabat)	LCDR1	AAGTCCAGTCAGAGTCTGTTAGACAGTGGAAAT CAAAAGAACTTCTTGACC
SEQ ID NO: 114 (Kabat)	LCDR2	TGGGCATCCACTAGGGAATCT
SEQ ID NO: 119 (Kabat)	LCDR3	CAGAATGATTATAGTTATCCGTACACG
SEQ ID NO: 116 (Chothia)	LCDR1	AGTCAGAGTCTGTTAGACAGTGGAAATCAAAAG AACTTC
SEQ ID NO: 117 (Chothia)	LCDR2	TGGGCATCC
SEQ ID NO: 120 (Chothia)	LCDR3	GATTATAGTTATCCGTAC
BAP049-hum15 HC		
SEQ ID NO: 108 (Kabat)	HCDR1	ACTTACTGGATGCAC
SEQ ID NO: 109 (Kabat)	HCDR2	AATATTTATCCTGGTACTGGTGGTTCTAACTTC GATGAGAAGTTCAAGAAC
SEQ ID NO: 223 (Kabat)	HCDR3	TGGACTACTGGGACGGGAGCTTAC
SEQ ID NO: 111 (Chothia)	HCDR1	GGCTACACATTCACCACTTAC
SEQ ID NO: 112 (Chothia)	HCDR2	TATCCTGGTACTGGTGGT
SEQ ID NO: 223 (Chothia)	HCDR3	TGGACTACTGGGACGGGAGCTTAC
BAP049-hum15 LC		
SEQ ID NO: 113 (Kabat)	LCDR1	AAGTCCAGTCAGAGTCTGTTAGACAGTGGAAAT CAAAAGAACTTCTTGACC
SEQ ID NO: 114 (Kabat)	LCDR2	TGGGCATCCACTAGGGAATCT
SEQ ID NO: 119 (Kabat)	LCDR3	CAGAATGATTATAGTTATCCGTACACG
SEQ ID NO: 116 (Chothia)	LCDR1	AGTCAGAGTCTGTTAGACAGTGGAAATCAAAAG AACTTC
SEQ ID NO: 117 (Chothia)	LCDR2	TGGGCATCC
SEQ ID NO: 120 (Chothia)	LCDR3	GATTATAGTTATCCGTAC
BAP049-hum16 HC		
SEQ ID NO: 108 (Kabat)	HCDR1	ACTTACTGGATGCAC
SEQ ID NO: 109 (Kabat)	HCDR2	AATATTTATCCTGGTACTGGTGGTTCTAACTTC GATGAGAAGTTCAAGAAC

SEQ ID NO: 110 (Kabat)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
SEQ ID NO: 111 (Chothia)	HCDR1	GGCTACACATTCACCACTTAC
SEQ ID NO: 112 (Chothia)	HCDR2	TATCCTGGTACTGGTGGT
SEQ ID NO: 110 (Chothia)	HCDR3	TGGACTACTGGGACGGGAGCTTAT
BAP049-hum16 LC		
SEQ ID NO: 113 (Kabat)	LCDR1	AAGTCCAGTCAGAGTCTGTTAGACAGTGGAAAT CAAAAGAACTTCTTGACC
SEQ ID NO: 114 (Kabat)	LCDR2	TGGGCATCCACTAGGGAATCT
SEQ ID NO: 119 (Kabat)	LCDR3	CAGAATGATTATAGTTATCCGTACACG
SEQ ID NO: 116 (Chothia)	LCDR1	AGTCAGAGTCTGTTAGACAGTGGAAATCAAAAG AACTTC
SEQ ID NO: 117 (Chothia)	LCDR2	TGGGCATCC
SEQ ID NO: 120 (Chothia)	LCDR3	GATTATAGTTATCCGTAC
BAP049-Clone-A HC		
SEQ ID NO: 122 (Kabat)	HCDR1	ACCTACTGGATGCAC
SEQ ID NO: 123 (Kabat)	HCDR2	AACATCTATCCTGGCACCGGCGGCTCCAACTTC GACGAGAAGTTCAAGAAC
SEQ ID NO: 124 (Kabat)	HCDR3	TGGACAACCGGCACAGGCGCTTAT
SEQ ID NO: 125 (Chothia)	HCDR1	GGCTACACCTTCACCACCTAC
SEQ ID NO: 126 (Chothia)	HCDR2	TATCCTGGCACCGGCGGC
SEQ ID NO: 124 (Chothia)	HCDR3	TGGACAACCGGCACAGGCGCTTAT
BAP049-Clone-A LC		
SEQ ID NO: 127 (Kabat)	LCDR1	AAGTCCTCCCAGTCCCTGCTGGACTCCGGCAAC CAGAAGAACTTCCTGACC
SEQ ID NO: 128 (Kabat)	LCDR2	TGGGCCTCCACCCGGGAATCT
SEQ ID NO: 129 (Kabat)	LCDR3	CAGAACGACTACTCCTACCCCTACACC
SEQ ID NO: 130 (Chothia)	LCDR1	TCCCAGTCCCTGCTGGACTCCGGCAACCAGAAG AACTTC
SEQ ID NO: 131 (Chothia)	LCDR2	TGGGCCTCC
SEQ ID NO: 132 (Chothia)	LCDR3	GACTACTCCTACCCCTAC
BAP049-Clone-B HC		
SEQ ID NO: 133 (Kabat)	HCDR1	ACCTACTGGATGCAC
SEQ ID NO: 134 (Kabat)	HCDR2	AATATCTACCCCGGCACCGGCGGCTCTAACTTC GACGAGAAGTTTAAGAAT
SEQ ID NO: 135 (Kabat)	HCDR3	TGGACTACCGGCACAGGCGCCTAC
SEQ ID NO: 136 (Chothia)	HCDR1	GGCTACACCTTCACTACCTAC
SEQ ID NO: 137 (Chothia)	HCDR2	TACCCCGGCACCGGCGGC
SEQ ID NO: 135 (Chothia)	HCDR3	TGGACTACCGGCACAGGCGCCTAC
BAP049-Clone-B LC		
SEQ ID NO: 138 (Kabat)	LCDR1	AAATCTAGTCAGTCACTGCTGGATAGCGGTAAT CAGAAGAACTTCCTGACC
SEQ ID NO: 139 (Kabat)	LCDR2	TGGGCCTCTACTAGAGAATCA
SEQ ID NO: 140 (Kabat)	LCDR3	CAGAACGACTATAGCTACCCCTACACC
SEQ ID NO: 141 (Chothia)	LCDR1	AGTCAGTCACTGCTGGATAGCGGTAATCAGAAG AACTTC
SEQ ID NO: 142 (Chothia)	LCDR2	TGGGCCTCT
SEQ ID NO: 143 (Chothia)	LCDR3	GACTATAGCTACCCCTAC
BAP049-Clone-C HC		

SEQ ID NO: 122 (Kabat)	HCDR1	ACCTACTGGATGCAC
SEQ ID NO: 123 (Kabat)	HCDR2	AACATCTATCCTGGCACCGGCGGCTCCAACTTC GACGAGAAGTTCAAGAAC
SEQ ID NO: 124 (Kabat)	HCDR3	TGGACAACCGGCACAGGCGCTTAT
SEQ ID NO: 125 (Chothia)	HCDR1	GGCTACACCTTCACCACCTAC
SEQ ID NO: 126 (Chothia)	HCDR2	TATCCTGGCACCGGCGGC
SEQ ID NO: 124 (Chothia)	HCDR3	TGGACAACCGGCACAGGCGCTTAT
BAP049-Clone-C LC		
SEQ ID NO: 127 (Kabat)	LCDR1	AAGTCCTCCCAGTCCCTGCTGGACTCCGGCAAC CAGAAGAACTTCCTGACC
SEQ ID NO: 128 (Kabat)	LCDR2	TGGGCCTCCACCCGGGAATCT
SEQ ID NO: 129 (Kabat)	LCDR3	CAGAACGACTACTCCTACCCCTACACC
SEQ ID NO: 130 (Chothia)	LCDR1	TCCCAGTCCCTGCTGGACTCCGGCAACCAGAAG AACTTC
SEQ ID NO: 131 (Chothia)	LCDR2	TGGGCCTCC
SEQ ID NO: 132 (Chothia)	LCDR3	GACTACTCCTACCCCTAC
BAP049-Clone-D HC		
SEQ ID NO: 122 (Kabat)	HCDR1	ACCTACTGGATGCAC
SEQ ID NO: 144 (Kabat)	HCDR2	AACATCTACCCTGGCACCGGCGGCTCCAACTTC GACGAGAAGTTCAAGAAC
SEQ ID NO: 145 (Kabat)	HCDR3	TGGACCACCGGAACCGGCGCCTAT
SEQ ID NO: 125 (Chothia)	HCDR1	GGCTACACCTTCACCACCTAC
SEQ ID NO: 146 (Chothia)	HCDR2	TACCCTGGCACCGGCGGC
SEQ ID NO: 145 (Chothia)	HCDR3	TGGACCACCGGAACCGGCGCCTAT
BAP049-Clone-D LC		
SEQ ID NO: 127 (Kabat)	LCDR1	AAGTCCTCCCAGTCCCTGCTGGACTCCGGCAAC CAGAAGAACTTCCTGACC
SEQ ID NO: 128 (Kabat)	LCDR2	TGGGCCTCCACCCGGGAATCT
SEQ ID NO: 129 (Kabat)	LCDR3	CAGAACGACTACTCCTACCCCTACACC
SEQ ID NO: 130 (Chothia)	LCDR1	TCCCAGTCCCTGCTGGACTCCGGCAACCAGAAG AACTTC
SEQ ID NO: 131 (Chothia)	LCDR2	TGGGCCTCC
SEQ ID NO: 132 (Chothia)	LCDR3	GACTACTCCTACCCCTAC
BAP049-Clone-E HC		
SEQ ID NO: 133 (Kabat)	HCDR1	ACCTACTGGATGCAC
SEQ ID NO: 134 (Kabat)	HCDR2	AATATCTACCCCGGCACCGGCGGCTCTAACTTC GACGAGAAGTTTAAGAAT
SEQ ID NO: 135 (Kabat)	HCDR3	TGGACTACCGGCACAGGCGCCTAC
SEQ ID NO: 136 (Chothia)	HCDR1	GGCTACACCTTCACTACCTAC
SEQ ID NO: 137 (Chothia)	HCDR2	TACCCCGGCACCGGCGGC
SEQ ID NO: 135 (Chothia)	HCDR3	TGGACTACCGGCACAGGCGCCTAC
BAP049-Clone-E LC		
SEQ ID NO: 138 (Kabat)	LCDR1	AAATCTAGTCAGTCACTGCTGGATAGCGGTAAT CAGAAGAACTTCCTGACC
SEQ ID NO: 139 (Kabat)	LCDR2	TGGGCCTCTACTAGAGAATCA
SEQ ID NO: 140 (Kabat)	LCDR3	CAGAACGACTATAGCTACCCCTACACC
SEQ ID NO: 141 (Chothia)	LCDR1	AGTCAGTCACTGCTGGATAGCGGTAATCAGAAG AACTTC
SEQ ID NO: 142 (Chothia)	LCDR2	TGGGCCTCT

SEQ ID NO: 143 (Chothia)	LCDR3	GACTATAGCTACCCCTAC

Table 2. Amino acid and nucleotide sequences of the heavy and light chain framework regions for humanized mAbs BAP049-hum01 to BAP049-hum16 and BAP049-Clone-A to BAP049-Clone-E

	Amino Acid Sequence	**Nucleotide Sequence**
VHFW1 (type a)	EVQLVQSGAEVKKPGESLRISCKGS (SEQ ID NO: 147)	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAA GCCCGGGGAGTCTCTGAGGATCTCCTGTAAGGGTTCT (SEQ ID NO: 148) GAAGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAA GCCTGGCGAGTCCCTGCGGATCTCCTGCAAGGGCTCT (SEQ ID NO: 149) GAGGTGCAGCTGGTGCAGTCAGGCGCCGAAGTGAAGAA GCCCGGCGAGTCACTGAGAATTAGCTGTAAAGGTTCA (SEQ ID NO: 150)
VHFW1 (type b)	QVQLVQSGAEVKKPGASVKVSCKAS (SEQ ID NO: 151)	CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAA GCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT (SEQ ID NO: 152)
VHFW2 (type a)	WVRQATGQGLEWMG (SEQ ID NO: 153)	TGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGAT GGGT (SEQ ID NO: 154) TGGGTGCGACAGGCTACCGGCCAGGGCCTGGAATGGAT GGGC (SEQ ID NO: 155) TGGGTCCGCCAGGCTACCGGTCAAGGCCTCGAGTGGAT GGGT (SEQ ID NO: 156)
VHFW2 (type b)	WIRQSPSRGLEWLG (SEQ ID NO: 157)	TGGATCAGGCAGTCCCCATCGAGAGGCCTTGAGTGGCT GGGT (SEQ ID NO: 158) TGGATCCGGCAGTCCCCCTCTAGGGGCCTGGAATGGCT GGGC (SEQ ID NO: 159)
VHFW2 (type c)	WVRQAPGQGLEWMG (SEQ ID NO: 160)	TGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGAT GGGT (SEQ ID NO: 161)
VHFW3 (type a)	RVTITADKSTSTAYMELSSLRSEDTAVY YCTR (SEQ ID NO: 162)	AGAGTCACGATTACCGCGGACAAATCCACGAGCACAGC CTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGG CCGTGTATTACTGTACAAGA (SEQ ID NO: 163) AGAGTGACCATCACCGCCGACAAGTCCACCTCCACCGC CTACATGGAACTGTCCTCCCTGAGATCCGAGGACACCG CCGTGTACTACTGCACCCGG (SEQ ID NO: 164) AGAGTGACTATCACCGCCGATAAGTCTACTAGCACCGC CTATATGGAACTGTCTAGCCTGAGATCAGAGGACACCG CCGTCTACTACTGCACTAGG (SEQ ID NO: 165)
VHFW3 (type b)	RFTISRDNSKNTLYLQMNSLRAEDTAVY YCTR (SEQ ID NO: 166)	AGATTCACCATCTCCAGAGACAATTCCAAGAACACGCT GTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGG CCGTGTATTACTGTACAAGA (SEQ ID NO: 167) AGGTTCACCATCTCCCGGGACAACTCCAAGAACACCCT GTACCTGCAGATGAACTCCCTGCGGGCCGAGGACACCG CCGTGTACTACTGTACCAGA (SEQ ID NO: 168)

VHFW4	WGQGTTVTVSS (SEQ ID NO: 169)	TGGGGCCAGGGCACCACCGTGACCGTGTCCTCC (SEQ ID NO: 170) TGGGGCCAGGGCACCACAGTGACCGTGTCCTCT (SEQ ID NO: 171) TGGGGTCAAGGCACTACCGTGACCGTGTCTAGC (SEQ ID NO: 172) TGGGGCCAGGGCACAACAGTGACCGTGTCCTCC (SEQ ID NO: 173)
VLFW1 (type a)	EIVLTQSPDFQSVTPKEKVTITC (SEQ ID NO: 174)	GAAATTGTGCTGACTCAGTCTCCAGACTTTCAGTCTGT GACTCCAAAGGAGAAAGTCACCATCACCTGC (SEQ ID NO: 175) GAGATCGTGCTGACCCAGTCCCCCGACTTCCAGTCCGT GACCCCCAAAGAAAAAGTGACCATCACATGC (SEQ ID NO: 176)
VLFW1 (type b)	EIVLTQSPATLSLSPGERATLSC (SEQ ID NO: 177)	GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTT GTCTCCAGGGGAAAGAGCCACCCTCTCCTGC (SEQ ID NO: 178) GAGATCGTGCTGACCCAGTCCCCTGCCACCCTGTCACT GTCTCCAGGCGAGAGAGCTACCCTGTCCTGC (SEQ ID NO: 179) GAGATCGTCCTGACTCAGTCACCCGCTACCCTGAGCCT GAGCCCTGGCGAGCGGGCTACACTGAGCTGT (SEQ ID NO: 180)
VLFW1 (type c)	DIVMTQTPLSLPVTPGEPASISC (SEQ ID NO: 181)	GATATTGTGATGACCCAGACTCCACTCTCCCTGCCCGT CACCCCTGGAGAGCCGGCCTCCATCTCCTGC (SEQ ID NO: 182)
VLFW1 (type d)	DVVMTQSPLSLPVTLGQPASISC (SEQ ID NO: 183)	GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGT CACCCTTGGACAGCCGGCCTCCATCTCCTGC (SEQ ID NO: 184)
VLFW1 (type e)	DIQMTQSPSSLSASVGDRVTITC (SEQ ID NO: 185)	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGC ATCTGTAGGAGACAGAGTCACCATCACTTGC (SEQ ID NO: 186)
VLFW2 (type a)	WYQQKPGQAPRLLIY (SEQ ID NO: 187)	TGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTAT (SEQ ID NO: 188) TGGTATCAGCAGAAGCCCGGCCAGGCCCCCAGACTGCT GATCTAC (SEQ ID NO: 189) TGGTATCAGCAGAAGCCCGGTCAAGCCCCTAGACTGCT GATCTAC (SEQ ID NO: 190)
VLFW2 (type b)	WYQQKPGKAPKLLIY (SEQ ID NO: 191)	TGGTATCAGCAGAAACCAGGGAAAGCTCCTAAGCTCCT GATCTAT (SEQ ID NO: 192) TGGTATCAGCAGAAGCCCGGTAAAGCCCCTAAGCTGCT GATCTAC (SEQ ID NO: 193)
VLFW2 (type c)	WYLQKPGQSPQLLIY (SEQ ID NO: 194)	TGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCT GATCTAT (SEQ ID NO: 195)

VLFW3 (type a)	GVPSRFSGSGSGTDFTFTISSLEAEDAA TYYC (SEQ ID NO: 196)	GGGGTCCCCTCGAGGTTCAGTGGCAGTGGATCTGGGAC AGATTTCACCTTTACCATCAGTAGCCTGGAAGCTGAAG ATGCTGCAACATATTACTGT (SEQ ID NO: 197) GGCGTGCCCTCTAGATTCTCCGGCTCCGGCTCTGGCAC CGACTTTACCTTCACCATCTCCAGCCTGGAAGCCGAGG ACGCCGCCACCTACTACTGC (SEQ ID NO: 198) GGCGTGCCCTCTAGGTTTAGCGGTAGCGGTAGTGGCAC CGACTTCACCTTCACTATCTCTAGCCTGGAAGCCGAGG ACGCCGCTACCTACTACTGT (SEQ ID NO: 199)
VLFW3 (type b)	GIPPRFSGSGYGTDFTLTINNIESEDAA YYFC (SEQ ID NO: 200)	GGGATCCCACCTCGATTCAGTGGCAGCGGGTATGGAAC AGATTTTACCCTCACAATTAATAACATAGAATCTGAGG ATGCTGCATATTACTTCTGT (SEQ ID NO: 201)
VLFW3 (type c)	GVPSRFSGSGSGTEFTLTISSLQPDDFA TYYC (SEQ ID NO: 202)	GGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGAC AGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGATG ATTTTGCAACTTATTACTGT (SEQ ID NO: 203) GGCGTGCCCTCTAGATTCTCCGGCTCCGGCTCTGGCAC CGAGTTTACCCTGACCATCTCCAGCCTGCAGCCCGACG ACTTCGCCACCTACTACTGC (SEQ ID NO: 204)
VLFW3 (type d)	GVPSRFSGSGSGTDFTFTISSLQPEDIA TYYC (SEQ ID NO: 205)	GGGGTCCCATCAAGGTTCAGTGGAAGTGGATCTGGGAC AGATTTTACTTTCACCATCAGCAGCCTGCAGCCTGAAG ATATTGCAACATATTACTGT (SEQ ID NO: 206) GGCGTGCCCTCTAGGTTTAGCGGTAGCGGTAGTGGCAC CGACTTCACCTTCACTATCTCTAGCCTGCAGCCCGAGG ATATCGCTACCTACTACTGT (SEQ ID NO: 207)
VLFW4	FGQGTKVEIK (SEQ ID NO: 208)	TTCGGCCAAGGGACCAAGGTGGAAATCAAA (SEQ ID NO: 209) TTCGGCCAGGGCACCAAGGTGGAAATCAAG (SEQ ID NO: 210) TTCGGTCAAGGCACTAAGGTCGAGATTAAG (SEQ ID NO: 211)

Table 3. Constant region amino acid sequences of human IgG heavy chains and human kappa light chain

HC	**IgG4 (S228P) mutant constant region amino acid sequence (EU Numbering)** ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTKT YTCNVDHKPS NTKVDKRVES KYGPPCPPCP APEFLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSQED PEVQFNWYVD GVEVHNAKTK PREEQFNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS SIEKTISKAK GQPREPQVYT LPPSQEEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSRL TVDKSRWQEG NVFSCSVMHE ALHNHYTQKS LSLSLGK (SEQ ID NO: 212)
LC	**Human kappa constant region amino acid sequence** RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK

	SFNRGEC (SEQ ID NO: 213)
HC	**IgG4 (S228P) mutant constant region amino acid sequence lacing C-terminal lysine (K) (EU Numbering)** ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTKT YTCNVDHKPS NTKVDKRVES KYGPPCPPCP APEFLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSQED PEVQFNWYVD GVEVHNAKTK PREEQFNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS SIEKTISKAK GQPREPQVYT LPPSQEEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSRL TVDKSRWQEG NVFSCSVMHE ALHNHYTQKS LSLSLG (SEQ ID NO: 214)
HC	**IgG1 wild type** ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKRVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK (SEQ ID NO: 215)
HC	**IgG1 (N297A) mutant constant region amino acid sequence (EU Numbering)** ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKRVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYA STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK (SEQ ID NO: 216)
HC	**IgG1 (D265A, P329A) mutant constant region amino acid sequence (EU Numbering)** ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKRVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVAVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LAAPIEKTIS KAKGQPREPQ VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK (SEQ ID NO: 217)
HC	**IgG1 (L234A, L235A) mutant constant region amino acid sequence (EU Numbering)** ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKRVEP KSCDKTHTCP PCPAPEAAGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK (SEQ ID NO: 218)

Table 4. Amino acid sequences of the heavy and light chain leader sequences for humanized mAbs BAP049-Clone-A to BAP049-Clone-E

BAP049-Clone-A	HC	MEWSWVFLFFLSVTTGVHS (SEQ ID NO: 219)
	LC	MSVPTQVLGLLLLWLTDARC (SEQ ID NO: 220)
BAP049-Clone-B	HC	MAWVWTLPFLMAAAQSVQA (SEQ ID NO: 221)
	LC	MSVLTQVLALLLLWLTGTRC (SEQ ID NO: 222)
BAP049-Clone-C	HC	MEWSWVFLFFLSVTTGVHS (SEQ ID NO: 219)
	LC	MSVPTQVLGLLLLWLTDARC (SEQ ID NO: 220)
BAP049-Clone-D	HC	MEWSWVFLFFLSVTTGVHS (SEQ ID NO: 219)
	LC	MSVPTQVLGLLLLWLTDARC (SEQ ID NO: 220)
BAP049-Clone-E	HC	MAWVWTLPFLMAAAQSVQA (SEQ ID NO: 221)
	LC	MSVLTQVLALLLLWLTGTRC (SEQ ID NO: 222)

EXAMPLES

The Examples below are set forth to aid in the understanding of the inventions but are not intended to, and should not be construed to, limit its scope in any way.

Example 1: Pharmacokinetics Analysis of Flat Dosing Schedules

Based on pharmacokinetic (PK) modeling, utilizing flat dose is expected provide the exposure to patients at the appropriate Cmin concentrations. Over 99.5% of patients will be above EC50 and over 93% of patients will be above EC90. Predicted steady state mean Cmin for the exemplary anti-PD-1 antibody molecule utilizing either 300mg once every three weeks (Q3W) or 400 mg once every four weeks (Q4W) is expected to be above 20ug/mL (with highest weight, 150 kg) on average.

Table 5. Exemplary PK parameters based on flat dosing schedules

Number of patients in PK dataset	46
CL (mL/h)	10.9 [8.9, 13.2]; IIV: 62%
Exponent of Weight on CL	**0.54 [0.021, 1.06]**

Volume of distribution at SS (L)	7.2 [6.5, 7.9]; IIV: 22%
Half-Life (days)	20 [17, 23]; IIV: 64%
Predicted Cmin (ug/mL) for 80 kg patient	**31 [22, 42] (400mg q4w)** **35 [26, 47] (300mg q3w)**

The expected mean steady state Cmin concentrations for the exemplary anti-PD-1 antibody molecule observed with either doses/regimens (300 mg q3w or 400 mg q4w) will be at least 77 fold higher than the EC50 (0.42ug/mL) and about 8.6 fold higher than the EC90. The *ex vivo* potentcy is based on IL-2 change in SEB *ex-vivo* assay.

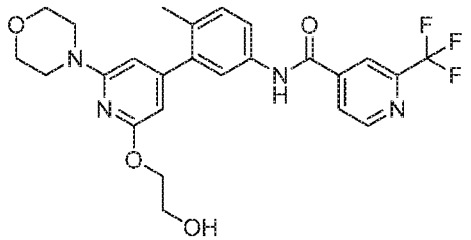
Less than 10% of patients are expected to achieve Cmin concentrations below 3.6ug/mL for either 300 mg Q3W or 400 mg Q4W. Less than 0.5% of patients are expected to achieve Cmin concentrations below 0.4 μg/mL for either 300 mg Q3W or 400 mg Q4W.

Predicted Ctrough (Cmin) concetrations across the different weights for patients while receiving the same dose of the exemplary anti-PD-1 antibody molecule are shown in Figure 12. Body weight based dosing is compared to fixed dose (3.75 mg/kg Q3W vs. 300 mg Q3W and 5 mg/kg Q4W vs. 400 mg Q4W). Figure 12 supports flat dosing of the exemplary anti-PD-1 antibody molecule.

The PK model further is validated. As shown in Figure 13, the observed versus model predicted concentrations lie on the line of unity. Figure 14 shows that the model captures accumulation, time course, and within subject variability.

Example 2: N-(3-(2-(2-hydroxyethoxy)-6-morpholinopyridin-4-yl)-4-methylphenyl)-2-(trifluoromethyl)isonicotinamide

COMPOUND A (Compound A) is a morpholine-substituted biaryl compound of the following structure



Compound A is Example 1156 in published PCT application WO2014/151616, the contents of which are incorporated by reference. The preparation of Compound A, pharmaceutically acceptable salts of Compound A and pharmaceutical compositions comprising compound A are also disclosed in the PCT application, *e.g.*, see pages 739-741.

COMPOUND A is a type II inhibitor of both b-Raf and c-Raf.

Compound	b-Raf IC-50 (μM)	c-Raf FL IC-50 (μM)
COMPOUND A	0.00073	0.00020

COMPOUND A is a potent and selective inhibitor targeting both *BRAF* and CRAF kinases with sub-nM IC50 values in biochemical assays. COMPOUND A has demonstrated efficacy in a wide range of MAPK pathway-driven human cancer cell lines and in vivo tumor xenografts including models harboring activating lesions in the *KRAS*, *NRAS*, and *BRAF* oncogenes.

Example 3: Anti-tumor activity of Compound A in *KRAS*-mutant NSCLC models

H358 model:

SCID beige female tumor bearing NCI-H358 mice, n=8 per group, were randomized into 3 groups 14 days post tumor cell inoculation with an average tumor volume range of 259.44-262.47mm^3.

Animals were administered an oral dose of either vehicle, Compound A at 30mg/kg or 200mg/kg daily for 14 consecutive days at a dosing volume of 10ml/kg of animal body weight during course of treatment. Tumor volumes were measured by digital caliper 3 times a week and body weights of all animals were recorded through the course of treatment.

Calu6 model:

Female nude tumor bearing Calu6 mice, n=6 per group were randomized into treatment groups on day 17 following tumor implantation, when the average tumor volume was 180 mm3. Treatments with compound A were initiated on Day 17 and continued for 16 days. Dosing volume was 10 mL/kg. Tumor volumes were collected at the time of randomization and twice weekly thereafter for the study duration.

H727 model:

Nude female mice tumor bearing NCI-H358, n=8 per group, were randomized into 2 groups with an average tumor volume range of 275.74 mm3. Animals were administered an oral dose of either vehicle or Compound A at 100 mg/kg daily for 14 consecutive days at a dosing volume of 10ml/kg of animal body weight during course of treatment. Tumor volumes were measured by digital caliper 3 times a week and body weights of all animals were recorded through the course of treatment. As shown in Figures 15A, 15B and 15C, Compound A showed single agent activity in KRASmt NSCLC models.

In cell-based assays, Compound A has demonstrated anti-proliferative activity in cell lines that contain a variety of mutations that activate MAPK signaling. For instance, Compound A inhibited the proliferation of the non-small cell lung cancer cell line Calu-6 (*KRAS* Q61K), colorectal cell line HCT116 (*KRAS* G13D) with IC50 values ranging from 0.2 – 1.2μM. *In vivo*, treatment with Compound A generated tumor regressions in several human *KRAS*-mutant models including the NSCLC-derived Calu-6 (*KRAS* Q61K) and NCI-H358 (*KRAS* G12C) xenografts as well as the ovarian Hey-A8 (*KRAS* G12D, *BRAF* G464E) xenografts. In all cases, anti-tumor effects were dose-dependent and well tolerated as judged by lack of significant body weight loss. The Calu-6 model was sensitive to Compound A when implanted in both nude mice and nude rats with regressions observed at doses of 100, 200, and 300 mg/kg once daily (QD) in mice and 75 and 150 mg/kg QD in rats. Tumor stasis in this model was observed at 30 mg/kg QD and 35mg/kg QD in mice and rats, respectively. Regressions were also achieved in a second human NSCLC model, NCI-H358, at the 200

mg/kg QD dose in mice and in the human ovarian Hey-A8 xenograft at doses as low as 30 mg/kg QD in mice. Furthermore, data from a dose fractionation efficacy study in Calu-6 xenografts demonstrated that across different dosing levels, Compound A dosed QD and fractioned twice a day (BID) showed similar levels of anti-tumor activity. These results support exploration of QD or BID dose regimen in the clinic.

Collectively the in vitro and *in vivo* MAPK-pathway suppression and anti-proliferative activity observed for Compound A at well-tolerated doses suggests that Compound A may have anti-tumor activity in patients with tumors harboring activating lesions in the MAPK pathway and in particular may therefore be useful as a single agent or in combination with anti-PD-1 antibody molecule for the treatment of NSCLC patients harboring *KRAS* mutations.

Example 4: Anti-tumor activity of Compound A in *NRAS*-mutant melanoma model

The antitumor efficacy and tolerability of Compound A were determined in an *NRAS*-mutant melanoma xenograft nude mouse model. $5x10^6$ SKMEL30 cells ($NRAS^{Q61K}$ melanoma cells) in 50% Matrigel™ were implanted subcutaneously into the right flank of female nude mice. Mice were randomized into treatment groups on day 12 post implantation, when the average tumor volume was ~200 mm^3. Mice were grouped (n=9) and treated with vehicle or Compound A at 25 and 100 mg/kg bid (twice daily). Treatments began on day 12 and continued until day 21 post implantation. Tumor volume and body weights were collected at the time of randomization and twice per week for the study duration. Tumor volume was determined by measurement with calipers and calculated using a modified ellipsoid formula, where tumor volume (TV) (mm^3) = [((l x w2) x 3.14159)) / 6], where l is the longest axis of the tumor and w is perpendicular to l. Mice were monitored for tumor growth, body weight and body condition. Animal well-being and behavior were monitored twice weekly. General health of mice was monitored daily. The anti-tumor activity was determined by assessing %T/C or % regression on day 21 post-implant (9 days of treatment). Treatment with Compound A with both doses, 25 mg/kg and 100 mg/kg bid, resulted in regression (48% and 59% regression respectively). All doses were well tolerated with no significant body weight loss and no signs of toxicity or mortalities were observed (Figure 16 which shows the efficacy and tolerability of

Compound A in SKMEL30 xenograft in mice. Tumor volumes (A) or percent body weight change from initial (B) treatment groups were plotted vs. vehicle control).

Example 5: A phase I dose finding study of Compound A in adult patients with solid tumors (including solid advanced tumors) harboring MAPK pathway alterations

Compound A single agent

The recommended starting dose and regimen of Compound A single agent in this study is 100 mg QD orally based on the preclinical safety, tolerability data, PK/PD data obtained in preclinical studies, as well as exploratory human efficacious dose range projection. Provisional doses for dose escalation can be found in the Table below.

Table 6 Exemplary Dose levels for Compound A

Dose level (DL)	Proposed daily dose*	Increment from previous dose
-1**	50 mg	-50%
1 (starting dose)	100 mg	(starting dose)
2	200 mg	100%
3	400 mg	100%
4	800 mg	100%
5	1200 mg	50%

*It is possible for additional and/or intermediate dose levels to be added during the course of the study, including doses outside the range of provisional doses shown in this table.
**Dose level -1 represent treatment doses for patients requiring a dose reduction from the starting dose level.

To date, patients have been treated in the study at the dose levels of 100 mg QD, 200 mg QD, 300 mg QD, 400 mg QD, 800 mg QD and 200 mg BID.

In the dose expansion part, patients in Compound A single agent arm are treated with Compound A at the recommended dose and regimen selected based on the dose escalation data. This dose is expected to be safe and tolerated in adult patients in all indications included in the trial. The single agent arm consists of 3 distinct groups: *KRAS*- and/or *BRAF*-mutant NSCLC, *KRAS*- and/or *BRAF*-mutant ovarian cancer, and patients with other solid tumors (which may be advanced) harboring MAPK pathway alteration(s) such as relapsed/refractory melanoma after failure of BRAFi/MEKi combination therapy and *NRAS*-mutant melanoma patients.

Compound A single agent:

- Group 1: patients with confirmed KRAS and/or BRAF-mutated NSCLC.

- Group 2: patients with confirmed KRAS and/or BRAF-mutated ovarian cancer
- Group 3: patients with advanced solid tumors harboring documented MAPK pathway alteration(s) other than those defined in Group 1 and 2. These include but are not limited to:
- patients with relapsed/refractory BRAF V600-mutated melanoma after failure of BRAFi/MEKi combination therapy
- patients with NRAS-mutated melanoma.

The clinical regimen for this first-in-human trial is a continuous once daily dosing schedule for Compound A. The QD regimen has been demonstrated to be efficacious and tolerated in preclinical studies. In Calu6 xenografts, similar levels of efficacy were achieved with either QD or fractionated BID regimens, suggesting efficacy is related to overall exposure. The predicted human PK and the predicted half-life (~9h), also suggest efficacious exposure can be achieved with QD dosing.

This was further confirmed by preliminary results obtained from the clinical trial. A subject with non-small cell lung cancer (NSCLC) treated with 1200 mg QD of COMPOUND A was shown to result in partial response of -35% according to the Response Evaluation Criteria In Solid Tumors (RECIST) criteria.

BID dosing of Compound A (e.g. 200 mg twice daily or 400 mg twice daily) is also envisaged.

Example 6: A phase I dose finding study of Compound A in adult patients with solid tumors and advanced solid tumors harboring MAPK pathway alterations and of Compound A combined with an exemplary antibody molecule (Antibody B) in NSCLC patients harboring *KRAS* mutations and in patients suffering from *NRAS* mutant melanoma.

The exemplary antibody molecule (BAP049-Clone-E, also referred to as Antibody B) tested in this study is a humanized anti-programmed death-1 (PD-1) IgG4 monoclonal antibody (mAb) that blocks binding of programmed cell death ligand-1 (PD-L1) and programmed cell death ligand-2 (PD-L2) to PD-1. It binds to PD-1 with high affinity and inhibits its biological activity. The amino acid sequences of this antibody molecule are described in Table 1 herein

(VH: SEQ ID NO: 38; VL: SEQ ID NO: 70). Results from pre-clinical toxicology studies have shown that it has a favorable safety profile. Its pharmacodynamic activity has also been demonstrated *in vivo*.

Compound A in combination with Antibody B

The dose escalation of Compound A in combination with Antibody B will start once a recommended dose and regimen has been identified for Compound A single agent. The starting dose of Compound A will be a previously tested dose that is lower than the recommended single agent dose. The selection of this dose will be supported by the current available efficacy, safety, PK and/or PD data of Compound A single agent in order to minimize exposure to potentially toxic drug levels while limiting the number of patients that might receive inactive doses.

The regimen for Compound A will be the same as selected for single agent Compound A. In case both regimens for Compound A single agent will be explored during single agent expansion part, then one preferred regimen will be chosen for the combination based on all available data including safety and exposure. Switching Compound A dose regimen in the combination arm at a later stage may be decided based on emerging data.

Antibody B will be administered at a flat dose of 400 mg Q4W i.v. (intravenously) which is the single agent RDE (Recommended dose for expansion). Antibody B may also be administered 300 mg i.v. Q3W for combination treatment regimens for which this may be more convenient.

In the dose expansion part, patients in the combination arm will be treated at the recommended dose and regimen for the drug combination based on the dose escalation data.

KRAS-mutant NSCLC and *NRAS*-mutant melanoma patients will be enrolled in the combination arm of this study. It is also envisaged that in the treatment group of *KRAS*-mutated NSCLC patients patients who have received prior PD-1/PD-L1 inhibitor therapy and patients who are naïve to PD-1- or PD-L1-directed therapy will benefit from the combination therapy and that in the treatment group of *NRAS*-mutated melanoma patients previously treated with immunotherapy including e.g. ipilimumab or prior PD-1/PD-L1 inhibitor, and immunotherapy-naive patients will benefit from the combination therapy.

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INCORPORATION BY REFERENCE

Other embodiments and examples including figures and tables are disclosed in International Patent Application Publication No. WO 2015/112900 and U.S. Patent Application Publication No. US 2015/0210769, entitled "Antibody Molecules to PD-1 and Uses Thereof," which are incorporated by reference in its entirety.

All publications, patents, and Accession numbers mentioned herein are hereby incorporated by reference in their entirety as if each individual publication or patent was specifically and individually indicated to be incorporated by reference.

EQUIVALENTS

While specific embodiments of the subject invention have been discussed, the above specification is illustrative and not restrictive. Many variations of the invention will become apparent to those skilled in the art upon review of this specification and the claims below. The full scope of the invention should be determined by reference to the claims, along with their full scope of equivalents, and the specification, along with such variations.

The reference in this specification to any prior publication (or information derived from it), or to any matter which is known, is not, and should not be taken as an acknowledgment or admission or any form of suggestion that that prior publication (or information derived from it) or known matter forms part of the common general knowledge in the field of endeavour to which this specification relates.

Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and "comprising", will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integers or steps.

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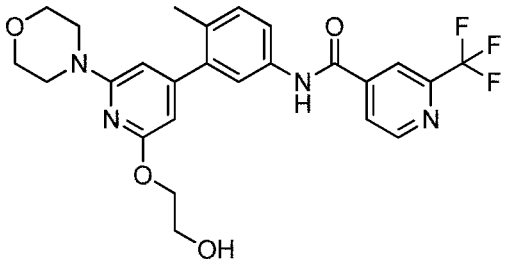
CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. A method for treating a proliferative disease in a subject comprising the separate, simultaneous or sequential administration of a pharmaceutical combination comprising

(A) a c-Raf inhibitor which is COMPOUND A,



,

or a pharmaceutically acceptable salt thereof;

and

(B) an isolated antibody molecule capable of binding to a human Programmed Death-1 (PD-1) comprising a heavy chain variable region (VH) comprising a HCDR1 amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 4, a HCDR2 amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 5, and a HCDR3 amino acid sequence of SEQ ID NO: 3, and a light chain variable region (VL) comprising a LCDR1 amino acid sequence of SEQ ID NO: 10 or SEQ ID NO: 13, a LCDR2 amino acid sequence of SEQ ID NO: 11 or SEQ ID NO: 14, and a LCDR3 amino acid sequence of SEQ ID NO: 32 or SEQ ID NO: 33,

to a subject in need thereof, wherein the anti-PD-1 antibody molecule is administered in a dose of about 300 mg to 400 mg once every three weeks or once every four weeks.

2. The method according claim 1, wherein the proliferative disease is selected from a solid tumor that harbors one or more Mitogen-activated protein kinase (MAPK) alteration(s), *KRAS*-mutant NSCLC (non-small cell lung cancer), *NRAS*-mutant melanoma, *KRAS*- and/or *BRAF*-mutant NSCLC, *KRAS*- and/or *BRAF*-mutant ovarian cancer and *BRAF*-mutant melanoma resistant to BRAFi/MEKi combination treatment.

3. The method according to claim 1 or 2, wherein the proliferative disease is *NRAS*-mutant melanoma or *KRAS*-mutant NSCLC.

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4. The method according to any one of claims 1 to 3, wherein the anti-PD-1 antibody molecule comprises:

(a) a heavy chain variable region (VH) comprising a HCDR1 amino acid sequence of SEQ ID NO: 4, a HCDR2 amino acid sequence of SEQ ID NO: 5, and a HCDR3 amino acid sequence of SEQ ID NO: 3; and a light chain variable region (VL) comprising a LCDR1 amino acid sequence of SEQ ID NO: 13, a LCDR2 amino acid sequence of SEQ ID NO: 14, and a LCDR3 amino acid sequence of SEQ ID NO: 33; or

(b) a VH comprising a HCDR1 amino acid sequence of SEQ ID NO: 1; a HCDR2 amino acid sequence of SEQ ID NO: 2; and a HCDR3 amino acid sequence of SEQ ID NO: 3; and a VL comprising a LCDR1 amino acid sequence of SEQ ID NO: 10, a LCDR2 amino acid sequence of SEQ ID NO: 11, and a LCDR3 amino acid sequence of SEQ ID NO: 32.

5. The method of claim 1 or 4, wherein the c-Raf kinase inhibitor is administered in oral dosage form or wherein the anti-PD-1 antibody molecule is administered in injectable dosage form.

6. The method according to any one of claims 1 to 5, wherein the anti-PD-1 antibody molecule is administered at a dose of about 300 mg once every three weeks.

7. The method according to any one of claims 1 to 5, wherein the anti-PD-1 antibody molecule is administered at a dose of about 400 mg once every four weeks.

8. The method according to any one of claims 1 to 7, wherein the c-Raf kinase inhibitor is administered at a dose of about 5-1200 mg per day; either once per day or twice per day.

9. The method according to claim 8, wherein the c-Raf kinase inhibitor is administered at a dose of about 5-1200 mg per day; once per day.

10. The method according to any one of claims 1 to 9, wherein the c-Raf inhibitor is administered at a dose of about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, or 1200 mg once a day.

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11. The method according to any one of claims 1 to 5, wherein the c-Raf inhibitor is administered at a dose of about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, or 1200 mg once a day and the anti-PD-1 antibody molecule is administered at (i) a dose of about 300 mg once every three weeks or (ii) a dose of about 400 mg once every four weeks.

12. The method according to any one of claims 1 to 11, wherein the anti-PD-1 antibody molecule comprises:

(a) a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 38 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 42;

(b) a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 38 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 66;

(c) a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 38 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 70;

(d) a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 50 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 70;

(e) a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 38 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 46;

(f) a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 50 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 46;

(g) a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 50 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 54;

(h) a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 38 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 54;

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(i) a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 38 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 58;

(j) a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 38 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 62;

(k) a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 50 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 66;

(l) a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 38 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 74;

(m) a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 38 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 78;

(n) a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 82 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 70;

(o) a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 82 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 66; or

(p) a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 86 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 66.

13. A method for treating a solid tumor that harbors at least one Mitogen-activated protein kinase (MAPK) alteration in a subject comprising the separate, simultaneous or sequential administration of a pharmaceutical combination comprising (A) a c-Raf inhibitor which is COMPOUND A,

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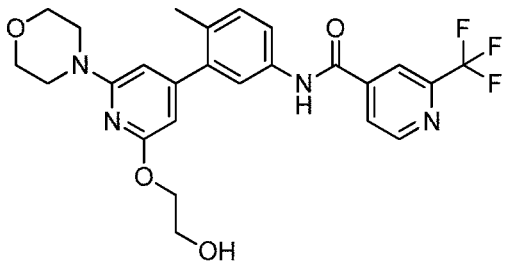


,

or a pharmaceutically acceptable salt thereof;

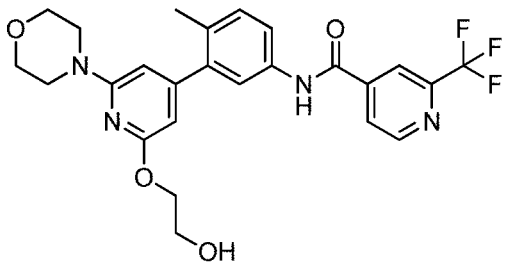
and

(B) an isolated antibody molecule capable of binding to a human Programmed Death-1 (PD-1) comprising a heavy chain variable region (VH) comprising a HCDR1 amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 4, a HCDR2 amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 5, and a HCDR3 amino acid sequence of SEQ ID NO: 3, and a light chain variable region (VL) comprising a LCDR1 amino acid sequence of SEQ ID NO: 10 or SEQ ID NO: 13, a LCDR2 amino acid sequence of SEQ ID NO: 11 or SEQ ID NO: 14, and a LCDR3 amino acid sequence of SEQ ID NO: 32 or SEQ ID NO: 33,

to a subject in need thereof, wherein the anti-PD-1 antibody molecule is administered in a dose of about 300 mg to 400 mg once every three weeks or once every four weeks.

14. A method for treating a cancer which is selected from *NRAS*-mutant melanoma, *KRAS*-mutant NSCLC (non-small cell lung cancer), *BRAF*-mutant NSCLC, *KRAS*- and *BRAF*-mutant NSCLC, *KRAS*-mutant ovarian cncer, *BRAF*-mutant ovarian cancer, and *KRAS*- and *BRAF*- mutant ovarian cancer, and relapsed or refractory *BRAF* V600-mutant melanoma in a subject comprising the separate, simultaneous or sequential administration of a pharmaceutical combination comprising

(A) a c-Raf inhibitor which is COMPOUND A,



,

or a pharmaceutically acceptable salt thereof;

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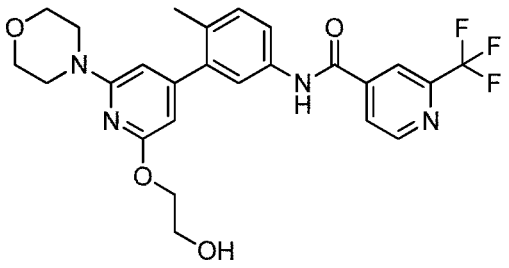
and

(B) an isolated antibody molecule capable of binding to a human Programmed Death-1 (PD-1) comprising a heavy chain variable region (VH) comprising a HCDR1 amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 4, a HCDR2 amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 5, and a HCDR3 amino acid sequence of SEQ ID NO: 3, and a light chain variable region (VL) comprising a LCDR1 amino acid sequence of SEQ ID NO: 10 or SEQ ID NO: 13, a LCDR2 amino acid sequence of SEQ ID NO: 11 or SEQ ID NO: 14, and a LCDR3 amino acid sequence of SEQ ID NO: 32 or SEQ ID NO: 33,

to a subject in need thereof, wherein the anti-PD-1 antibody molecule is administered in a dose of about 300 mg to 400 mg once every three weeks or once every four weeks.

15. Use of (A) a c-Raf inhibitor which is COMPOUND A,



,

or a pharmaceutically acceptable salt thereof;

and

(B) an isolated antibody molecule capable of binding to a human Programmed Death-1 (PD-1) comprising a heavy chain variable region (VH) comprising a HCDR1 amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 4, a HCDR2 amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 5, and a HCDR3 amino acid sequence of SEQ ID NO: 3, and a light chain variable region (VL) comprising a LCDR1 amino acid sequence of SEQ ID NO: 10 or SEQ ID NO: 13, a LCDR2 amino acid sequence of SEQ ID NO: 11 or SEQ ID NO: 14, and a LCDR3 amino acid sequence of SEQ ID NO: 32 or SEQ ID NO: 33,

for the preparation of a medicament for the treatment of a proliferative disease,

wherein the medicament is formulated for separate, simultaneous or sequential administration of the c-Raf inhibitor, or a pharmaceutically acceptable salt thereof, and the anti-PD-1 antibody molecule to a subject, and wherein treatment comprises administration

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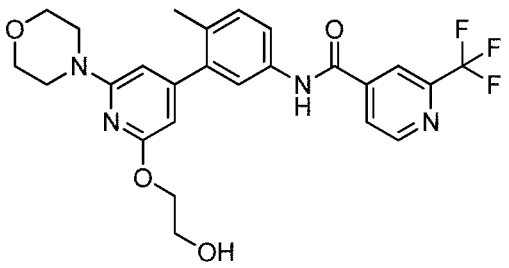
of the anti-PD-1 antibody molecule to the subject in a dose of about 300 mg to 400 mg once every three weeks or once every four weeks.

16. Use according to claim 15, wherein the proliferative disease is selected from a solid tumor that harbors one or more Mitogen-activated protein kinase (MAPK) alteration(s), *KRAS*-mutant NSCLC (non-small cell lung cancer), *NRAS*-mutant melanoma, *KRAS*- and/or *BRAF*-mutant NSCLC, *KRAS*- and/or *BRAF*-mutant ovarian cancer and *BRAF*-mutant melanoma resistant to BRAFi/MEKi combination treatment.

17. Use according to claim 15 or 16, wherein the proliferative disease is *NRAS*-mutant melanoma or *KRAS*-mutant NSCLC.

18. Use of (A) a c-Raf inhibitor which is COMPOUND A,



,

or a pharmaceutically acceptable salt thereof;

and

(B) an isolated antibody molecule capable of binding to a human Programmed Death-1 (PD-1) comprising a heavy chain variable region (VH) comprising a HCDR1 amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 4, a HCDR2 amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 5, and a HCDR3 amino acid sequence of SEQ ID NO: 3, and a light chain variable region (VL) comprising a LCDR1 amino acid sequence of SEQ ID NO: 10 or SEQ ID NO: 13, a LCDR2 amino acid sequence of SEQ ID NO: 11 or SEQ ID NO: 14, and a LCDR3 amino acid sequence of SEQ ID NO: 32 or SEQ ID NO: 33,

for the preparation of a medicament for the treatment of a solid tumor that harbors at least one Mitogen-activated protein kinase (MAPK) alteration,

wherein the medicament is formulated for separate, simultaneous or sequential administration of the c-Raf inhibitor, or a pharmaceutically acceptable salt thereof, and the

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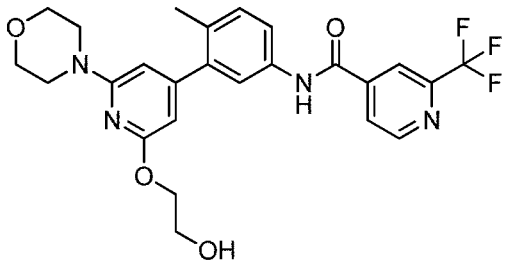
anti-PD-1 antibody molecule to a subject, and wherein treatment comprises administration of the anti-PD-1 antibody molecule to the subject in a dose of about 300 mg to 400 mg once every three weeks or once every four weeks..

19. Use of (A) a c-Raf inhibitor which is COMPOUND A,



,

or a pharmaceutically acceptable salt thereof;

and

(B) an isolated antibody molecule capable of binding to a human Programmed Death-1 (PD-1) comprising a heavy chain variable region (VH) comprising a HCDR1 amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 4, a HCDR2 amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 5, and a HCDR3 amino acid sequence of SEQ ID NO: 3, and a light chain variable region (VL) comprising a LCDR1 amino acid sequence of SEQ ID NO: 10 or SEQ ID NO: 13, a LCDR2 amino acid sequence of SEQ ID NO: 11 or SEQ ID NO: 14, and a LCDR3 amino acid sequence of SEQ ID NO: 32 or SEQ ID NO: 33,

for the preparation of a medicament for the treatment of a cancer which is selected from *NRAS*-mutant melanoma, *KRAS*-mutant NSCLC (non-small cell lung cancer), *BRAF*-mutant NSCLC, *KRAS*- and *BRAF*-mutant NSCLC, *KRAS*-mutant ovarian cncer, *BRAF*-mutant ovarian cancer, and *KRAS*- and *BRAF*- mutant ovarian cancer, and relapsed or refractory *BRAF* V600-mutant melanoma,

wherein the medicament is formulated for separate, simultaneous or sequential administration of the c-Raf inhibitor, or a pharmaceutically acceptable salt thereof, and the anti-PD-1 antibody molecule to a subject, and wherein treatment comprises administration of the anti-PD-1 antibody molecule to the subject in a dose of about 300 mg to 400 mg once every three weeks or once every four weeks.

Heavy Chain (murine IgG1)

FWH1	CDRH1	FWH2	CDRH2
QVQLQQSGSE LVRPGASVKL	SCKAS***GYTFT*** ***TYW***MHWVRQR	PGQGLEWIGN	I***YPGTGG***SNF DEKFKNRTSL
QVQLQQPGSE LVRPGASVKL	SCKAS***GYTFT*** ***TYW***MHWVRQR	PGQGLEWIGN	I***YPGTGG***SNF DEKFKNRTSL

FWH3	CDRH3	FWH4	
TVDTSSTTAY MHLASLTSED	SAVYYCTR***WT*** ***TGTGAY***WGQG	TLVTVSA	
TVDTSSTTAY MHLASLTSED	SAVYYCTR***WT*** ***TGTGAY***WGQG	TLVTVSAAKT	TPPSVYPLAP GSAA

Light Chain (murine κ)

FWL1	CDRL1	FWL2	CDRL2
DIVMTQSPSS LTVTAGEKVT	MSCKS***SQSLL DSGNQKNF***LT	WYQQKPGQPP	KLLIF***WAS***TR ESGVPDRFTG
DIVMTQSPSS LTVTAGEKVT	MSCKS***SQSLL DSGNQKNF***LT	WYQQKPGQPP	KLLIF***WAS***TR ESGVPDRFTG

FWL3	CDRL3	FWL4	
SGSVTDFTLT ISSVQAEDLA	VYYCQN***DYSY P***CTFGGGTKL	EIK	
SGSVTDFTLT ISSVQAEDLA	VYYCQN***DYSY P***CTFGGGTKL	EIKRAD	

FIGURE 1

Heavy Chain

```
GL        QVQLQQPGSE LVRPGASVKL SCKASGYTFT SYWMHWVKQR HGQGLEWIGN IYPGSGSTNY
Mu mAb    ------S--- ---------- ---------- T------R-- P--------- ----T-GS-F

GL        DEKFKSKGTL TVDTSSSTAY MHLSSLTSED SAVYYCTR
Mu mAb    -----NRTS- ------T--- ---A------ ---------WT TGTGAYWGQG TLVTVSA
```

Light Chain

```
GL        DIVMTQSPSS LTVTAGEKVT MSCKSSQSLL NSGNQKNYLT WYQQKPGQPP KLLIYWASTR
Mu mAb    ---------- ---------- ---------- D------F-- ---------- ----F-----

GL        ESGVPDRFTG SGSGTDFTLT ISSVQAEDLA VYYCQNDYSY P
Mu mAb    ---------- ---V------ ---------- ----------- -CTFGGGTKL EIK
```

FIGURE 2A

```
mAb         C   T   F   G   G   G   T   K   L   E   I   K
mAb     g tgc acg ttc gga ggg ggg acc aag ctg gaa ata aaa
J2      - -a- --- --- --- --- --- --- --- --- --- --- ---c
J2          Y
```

FIGURE 2B

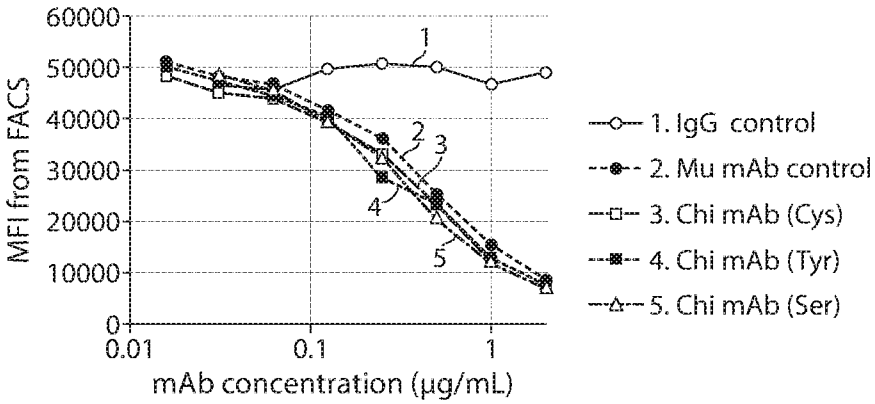


FIGURE 3A

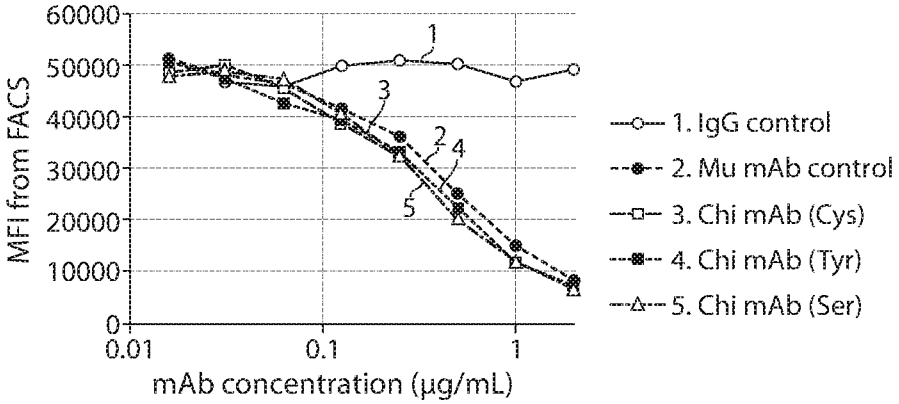


FIGURE 3B

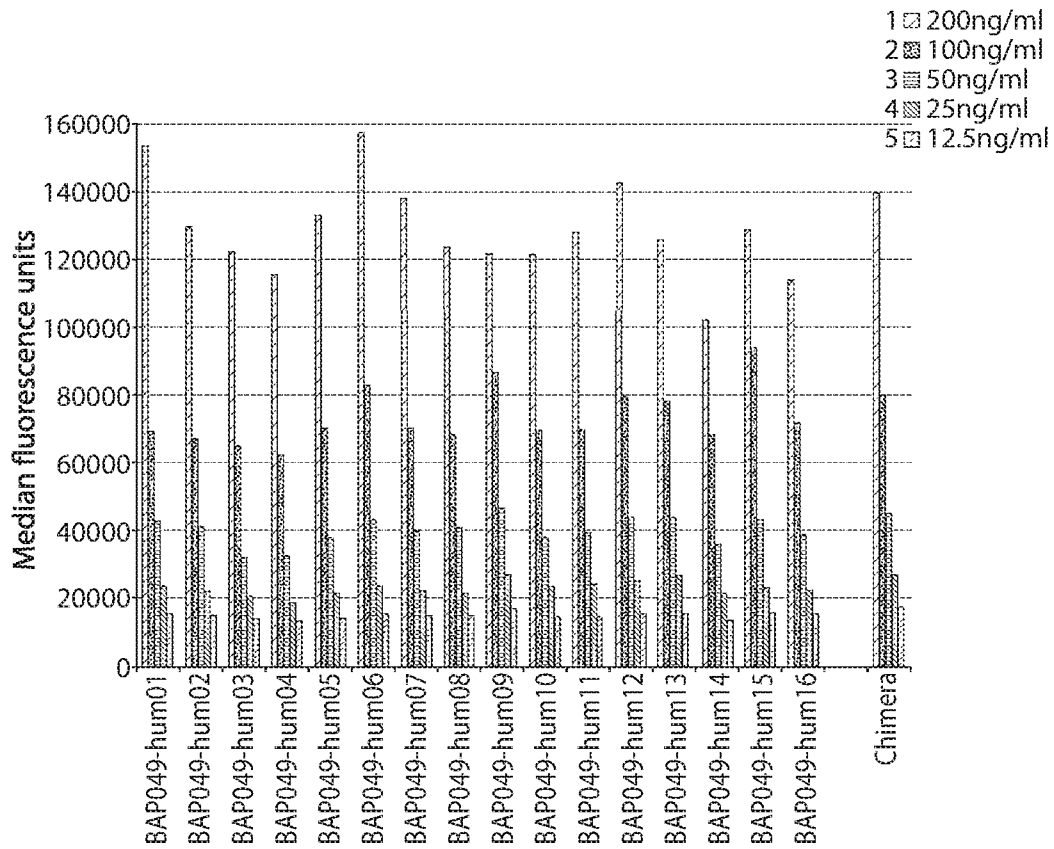

1 200ng/ml
2 100ng/ml
3 50ng/ml
4 25ng/ml
5 12.5ng/ml
Median fluorescence units
160000
140000
120000
100000
80000
60000
40000
20000
0
BAP049-hum01
BAP049-hum02
BAP049-hum03
BAP049-hum04
BAP049-hum05
BAP049-hum06
BAP049-hum07
BAP049-hum08
BAP049-hum09
BAP049-hum10
BAP049-hum11
BAP049-hum12
BAP049-hum13
BAP049-hum14
BAP049-hum15
BAP049-hum16
Chimera

FIGURE 4

Clone No.	Concentration µg/mL	Sequence					
		HC			LC		
		FW1	FW2	FW3	FW1	FW2	FW3
		4 unique HC			9 unique LC		
1	23.3	a	a	a	b	a	c
2	45.5	a	a	a	e	a	b
3	58.4	a	b	b	e	a	b
4	52.9	a	b	b	b	b	d
5	30	a	a	a	b	b	d
6	7.9	a	a	a	c	a	a
7	24.9	a	a	a	b	b	a
8	32.8	a	b	b	a	a	a
9	16.3	a	a	a	a	a	a
10	61.5	a	b	b	b	a	a
11	31.4	a	a	a	b	a	a
12	34.8	a	a	a	e	c	a
13	8.6	a	a	a	d	b	a
14	48.4	b	b	b	b	a	a
15	20.7	b	b	b	a	a	a
16	32.8	a	c	b	a	a	a

FIGURE 5

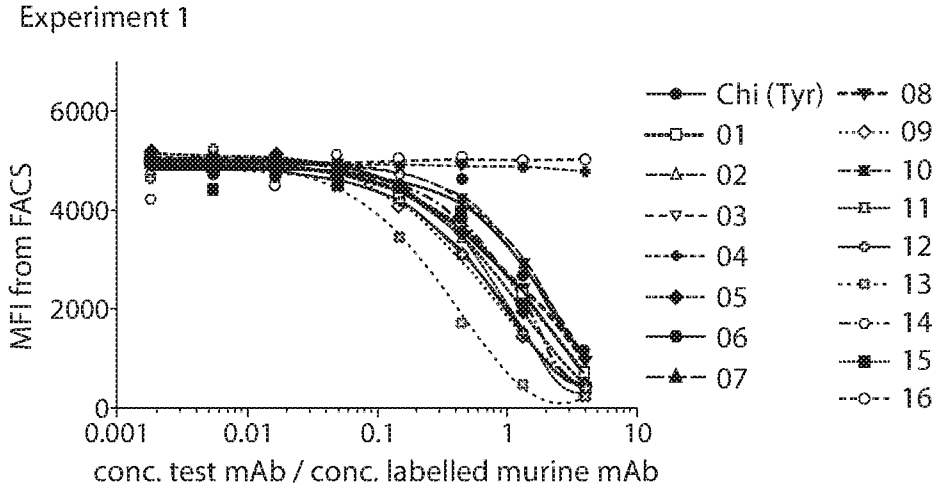


FIGURE 6A

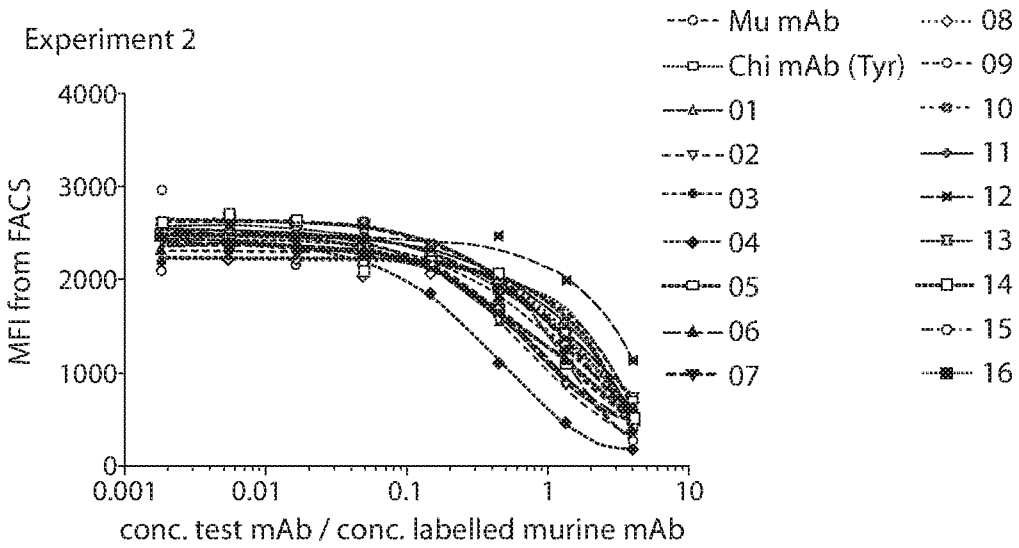


FIGURE 6B

Clone No.	Conc. µg/mL	Sequence						Ranking	Competition Binding		Ranking
		HC			LC			FACS data	1st exp.	2nd exp.*	
		FW1	FW2	FW3	FW1	FW2	FW3				
Chimeric	20.6	4 unique HC			9 unique LC						
1	23.3	a	a	a	b	a	c	2	7	2	A
2	45.5	a	a	a	e	a	b	6	3	2	D
3	58.4	a	b	b	e	a	b	7	8	14	E
4	52.9	a	b	b	b	b	d	14	15	15	B
5	30	a	a	a	b	b	d	5	5		A
6	7.9	a	a	a	c	a	a	1	7	3	D
7	24.9	a	a	a	b	b	a	4	7		D
8	32.8	a	b	b	a	a	a	7	7	4	C
9	16.3	a	a	a	a	a	a	7	2	4	B
10	61.5	a	b	b	b	a	a	7	6		C
11	31.4	a	a	a	b	a	a	6	4		B
12	34.8	a	a	a	e	c	a	3	8	16	D
13	8.6	a	a	a	d	b	a	6	1	1	D
14	48.4	b	b	b	b	a	a	16	7	15	C
15	20.7	b	b	b	a	a	a	6	7	15	C
16	32.8	a	c	b	a	a	a	15	16	15	C

*empty boxes means worse than 4

FIGURE 7

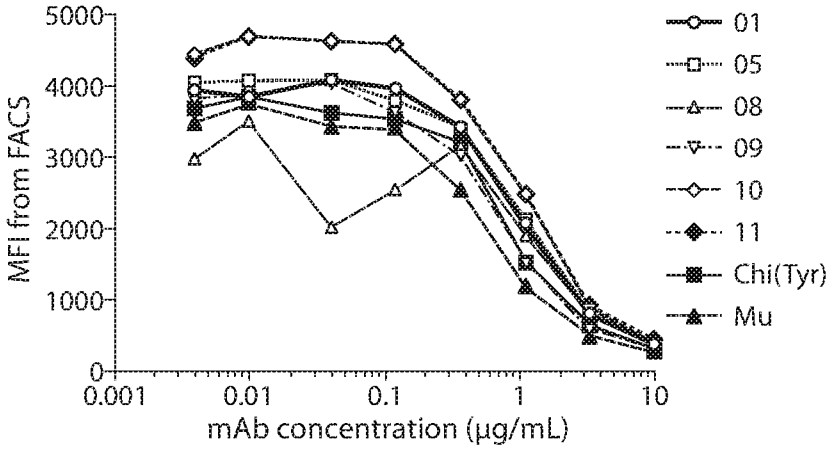


FIGURE 8A

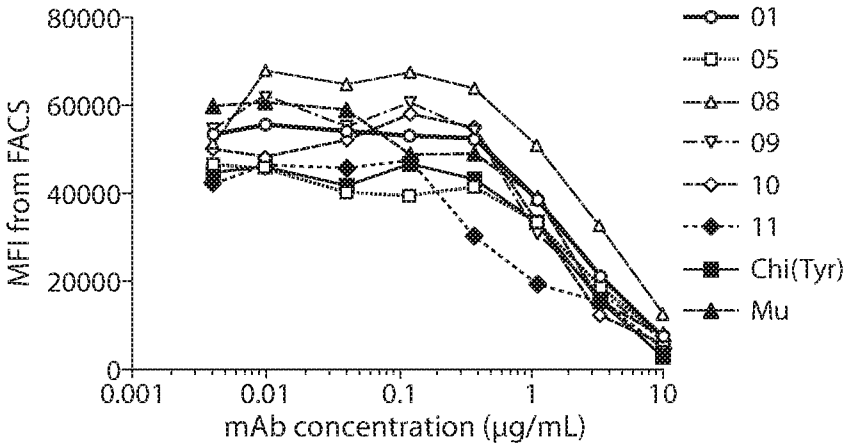


FIGURE 8B

```
                          10        20        30        40        50        60
                   ....|....|....|....|....|....|....|....|....|....|....|....|
BAP049-chi-HC      QVQLQQSGSELVRPGASVKLSCKASGYTFTTYWMHWVRQRPGQGLEWIGNIYPGTGGSNF
BAP049-hum01-HC    EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYWMHWVRQATGQGLEWMGNIYPGTGGSNF
BAP049-hum02-HC    EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYWMHWVRQATGQGLEWMGNIYPGTGGSNF
BAP049-hum05-HC    EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYWMHWVRQATGQGLEWMGNIYPGTGGSNF
BAP049-hum06-HC    EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYWMHWVRQATGQGLEWMGNIYPGTGGSNF
BAP049-hum07-HC    EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYWMHWVRQATGQGLEWMGNIYPGTGGSNF
BAP049-hum09-HC    EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYWMHWVRQATGQGLEWMGNIYPGTGGSNF
BAP049-hum11-HC    EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYWMHWVRQATGQGLEWMGNIYPGTGGSNF
BAP049-hum12-HC    EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYWMHWVRQATGQGLEWMGNIYPGTGGSNF
BAP049-hum13-HC    EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYWMHWVRQATGQGLEWMGNIYPGTGGSNF
BAP049-hum03-HC    EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYWMHWIRQSPSRGLEWLGNIYPGTGGSNF
BAP049-hum04-HC    EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYWMHWIRQSPSRGLEWLGNIYPGTGGSNF
BAP049-hum08-HC    EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYWMHWIRQSPSRGLEWLGNIYPGTGGSNF
BAP049-hum10-HC    EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYWMHWIRQSPSRGLEWLGNIYPGTGGSNF
BAP049-hum14-HC    QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYWMHWIRQSPSRGLEWLGNIYPGTGGSNF
BAP049-hum15-HC    QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYWMHWIRQSPSRGLEWLGNIYPGTGGSNF
BAP049-hum16-HC    EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYWMHWVRQAPGQGLEWMGNIYPGTGGSNF

                          70        80        90       100       110
                   ....|....|....|....|....|....|....|....|....|....|..
BAP049-chi-HC      DEKFKNRTSLTVDTSSTTAYMHLASLTSEDSAVYYCTRWTTGTGAYWGQGTTVTVSS
BAP049-hum01-HC    DEKFKNRVTITADKSTSTAYMELSSLRSEDTAVYYCTRWTTGTGAYWGQGTTVTVSS
BAP049-hum02-HC    DEKFKNRVTITADKSTSTAYMELSSLRSEDTAVYYCTRWTTGTGAYWGQGTTVTVSS
BAP049-hum05-HC    DEKFKNRVTITADKSTSTAYMELSSLRSEDTAVYYCTRWTTGTGAYWGQGTTVTVSS
BAP049-hum06-HC    DEKFKNRVTITADKSTSTAYMELSSLRSEDTAVYYCTRWTTGTGAYWGQGTTVTVSS
BAP049-hum07-HC    DEKFKNRVTITADKSTSTAYMELSSLRSEDTAVYYCTRWTTGTGAYWGQGTTVTVSS
BAP049-hum09-HC    DEKFKNRVTITADKSTSTAYMELSSLRSEDTAVYYCTRWTTGTGAYWGQGTTVTVSS
BAP049-hum11-HC    DEKFKNRVTITADKSTSTAYMELSSLRSEDTAVYYCTRWTTGTGAYWGQGTTVTVSS
BAP049-hum12-HC    DEKFKNRVTITADKSTSTAYMELSSLRSEDTAVYYCTRWTTGTGAYWGQGTTVTVSS
BAP049-hum13-HC    DEKFKNRVTITADKSTSTAYMELSSLRSEDTAVYYCTRWTTGTGAYWGQGTTVTVSS
BAP049-hum03-HC    DEKFKNRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWTTGTGAYWGQGTTVTVSS
BAP049-hum04-HC    DEKFKNRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWTTGTGAYWGQGTTVTVSS
BAP049-hum08-HC    DEKFKNRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWTTGTGAYWGQGTTVTVSS
BAP049-hum10-HC    DEKFKNRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWTTGTGAYWGQGTTVTVSS
BAP049-hum14-HC    DEKFKNRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWTTGTGAYWGQGTTVTVSS
BAP049-hum15-HC    DEKFKNRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWTTGTGAYWGQGTTVTVSS
BAP049-hum16-HC    DEKFKNRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWTTGTGAYWGQGTTVTVSS
```

FIGURE 9A

```
                          10        20        30        40        50        60
                   ....|....|....|....|....|....|....|....|....|....|....|....|
BAP049-chi-HC      QVQLQQSGSELVRPGASVKLSCKASGYTFTTYWMHWVRQRPGQGLEWIGNIYPGTGGSNF
BAP049-hum01-HC    E...V...A.VKK..E.LRI...G..............AT......M............
BAP049-hum02-HC    E...V...A.VKK..E.LRI...G..............AT......M............
BAP049-hum05-HC    E...V...A.VKK..E.LRI...G..............AT......M............
BAP049-hum06-HC    E...V...A.VKK..E.LRI...G..............AT......M............
BAP049-hum07-HC    E...V...A.VKK..E.LRI...G..............AT......M............
BAP049-hum09-HC    E...V...A.VKK..E.LRI...G..............AT......M............
BAP049-hum11-HC    E...V...A.VKK..E.LRI...G..............AT......M............
BAP049-hum12-HC    E...V...A.VKK..E.LRI...G..............AT......M............
BAP049-hum13-HC    E...V...A.VKK..E.LRI...G..............AT......M............
BAP049-hum03-HC    E...V...A.VKK..E.LRI...G............I..S.SR....L............
BAP049-hum04-HC    E...V...A.VKK..E.LRI...G............I..S.SR....L............
BAP049-hum08-HC    E...V...A.VKK..E.LRI...G............I..S.SR....L............
BAP049-hum10-HC    E...V...A.VKK..E.LRI...G............I..S.SR....L............
BAP049-hum14-HC    ....V...A.VKK......V................I..S.SR....L............
BAP049-hum15-HC    ....V...A.VKK......V................I..S.SR....L............
BAP049-hum16-HC    E...V...A.VKK..E.LRI...G..............A.......M............

                          70        80        90       100       110
                   ....|....|....|....|....|....|....|....|....|....|....|..
BAP049-chi-HC      DEKFKNRTSLTVDTSSTTAYMHLASLTSEDSAVYYCTRWTTGTGAYWGQGTTVTVSS
BAP049-hum01-HC    .......VTI.A.K.TS....E.S..R...T.........................
BAP049-hum02-HC    .......VTI.A.K.TS....E.S..R...T.........................
BAP049-hum05-HC    .......VTI.A.K.TS....E.S..R...T.........................
BAP049-hum06-HC    .......VTI.A.K.TS....E.S..R...T.........................
BAP049-hum07-HC    .......VTI.A.K.TS....E.S..R...T.........................
BAP049-hum09-HC    .......VTI.A.K.TS....E.S..R...T.........................
BAP049-hum11-HC    .......VTI.A.K.TS....E.S..R...T.........................
BAP049-hum12-HC    .......VTI.A.K.TS....E.S..R...T.........................
BAP049-hum13-HC    .......VTI.A.K.TS....E.S..R...T.........................
BAP049-hum03-HC    .......FTISR.N.KN.L.LQMN..RA..T.........................
BAP049-hum04-HC    .......FTISR.N.KN.L.LQMN..RA..T.........................
BAP049-hum08-HC    .......FTISR.N.KN.L.LQMN..RA..T.........................
BAP049-hum10-HC    .......FTISR.N.KN.L.LQMN..RA..T.........................
BAP049-hum14-HC    .......FTISR.N.KN.L.LQMN..RA..T.........................
BAP049-hum15-HC    .......FTISR.N.KN.L.LQMN..RA..T.........................
BAP049-hum16-HC    .......FTISR.N.KN.L.LQMN..RA..T.........................
```

FIGURE 9B

```
                          10        20        30        40        50        60
                   ....|....|....|....|....|....|....|....|....|....|....|....|
BAP049-chi-LC      DIVMTQSPSSLTVTAGEKVTMSCKSSQSLLDSGNQKNFLTWYQQKPGQPPKLLIFWASTR
BAP049-hum08-LC    EIVLTQSPDFQSVTPKEKVTITCKSSQSLLDSGNQKNFLTWYQQKPGQAPRLLIYWASTR
BAP049-hum09-LC    EIVLTQSPDFQSVTPKEKVTITCKSSQSLLDSGNQKNFLTWYQQKPGQAPRLLIYWASTR
BAP049-hum15-LC    EIVLTQSPDFQSVTPKEKVTITCKSSQSLLDSGNQKNFLTWYQQKPGQAPRLLIYWASTR
BAP049-hum16-LC    EIVLTQSPDFQSVTPKEKVTITCKSSQSLLDSGNQKNFLTWYQQKPGQAPRLLIYWASTR
BAP049-hum10-LC    EIVLTQSPATLSLSPGERATLSCKSSQSLLDSGNQKNFLTWYQQKPGQAPRLLIYWASTR
BAP049-hum11-LC    EIVLTQSPATLSLSPGERATLSCKSSQSLLDSGNQKNFLTWYQQKPGQAPRLLIYWASTR
BAP049-hum14-LC    EIVLTQSPATLSLSPGERATLSCKSSQSLLDSGNQKNFLTWYQQKPGQAPRLLIYWASTR
BAP049-hum06-LC    DIVMTQTPLSLPVTPGEPASISCKSSQSLLDSGNQKNFLTWYQQKPGQAPRLLIYWASTR
BAP049-hum07-LC    EIVLTQSPATLSLSPGERATLSCKSSQSLLDSGNQKNFLTWYQQKPGKAPKLLIYWASTR
BAP049-hum13-LC    DVVMTQSPLSLPVTLGQPASISCKSSQSLLDSGNQKNFLTWYQQKPGKAPKLLIYWASTR
BAP049-hum12-LC    DIQMTQSPSSLSASVGDRVTITCKSSQSLLDSGNQKNFLTWYLQKPGQSPQLLIYWASTR
BAP049-hum02-LC    DIQMTQSPSSLSASVGDRVTITCKSSQSLLDSGNQKNFLTWYQQKPGQAPRLLIYWASTR
BAP049-hum03-LC    DIQMTQSPSSLSASVGDRVTITCKSSQSLLDSGNQKNFLTWYQQKPGQAPRLLIYWASTR
BAP049-hum01-LC    EIVLTQSPATLSLSPGERATLSCKSSQSLLDSGNQKNFLTWYQQKPGQAPRLLIYWASTR
BAP049-hum04-LC    EIVLTQSPATLSLSPGERATLSCKSSQSLLDSGNQKNFLTWYQQKPGKAPKLLIYWASTR
BAP049-hum05-LC    EIVLTQSPATLSLSPGERATLSCKSSQSLLDSGNQKNFLTWYQQKPGKAPKLLIYWASTR

                          70        80        90        100       110
                   ....|....|....|....|....|....|....|....|....|...
BAP049-chi-LC      ESGVPDRFTGSGSVTDFTLTISSVQAEDLAVYYCQNDYSYPCTFGQGTKVEIK
BAP049-hum08-LC    ESGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQNDYSYPYTFGQGTKVEIK
BAP049-hum09-LC    ESGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQNDYSYPYTFGQGTKVEIK
BAP049-hum15-LC    ESGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQNDYSYPYTFGQGTKVEIK
BAP049-hum16-LC    ESGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQNDYSYPYTFGQGTKVEIK
BAP049-hum10-LC    ESGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQNDYSYPYTFGQGTKVEIK
BAP049-hum11-LC    ESGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQNDYSYPYTFGQGTKVEIK
BAP049-hum14-LC    ESGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQNDYSYPYTFGQGTKVEIK
BAP049-hum06-LC    ESGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQNDYSYPYTFGQGTKVEIK
BAP049-hum07-LC    ESGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQNDYSYPYTFGQGTKVEIK
BAP049-hum13-LC    ESGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQNDYSYPYTFGQGTKVEIK
BAP049-hum12-LC    ESGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQNDYSYPYTFGQGTKVEIK
BAP049-hum02-LC    ESGIPPRFSGSGYGTDFTLTINNIESEDAAYYFCQNDYSYPYTFGQGTKVEIK
BAP049-hum03-LC    ESGIPPRFSGSGYGTDFTLTINNIESEDAAYYFCQNDYSYPYTFGQGTKVEIK
BAP049-hum01-LC    ESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQNDYSYPYTFGQGTKVEIK
BAP049-hum04-LC    ESGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQNDYSYPYTFGQGTKVEIK
BAP049-hum05-LC    ESGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQNDYSYPYTFGQGTKVEIK
```

FIGURE 10A

```
                          10        20        30        40        50        60
                   ....|....|....|....|....|....|....|....|....|....|....|....|
BAP049-chi-LC      DIVMTQSPSSLTVTAGEKVTMSCKSSQSLLDSGNQKNFLTWYQQKPGQPPKLLIFWASTR
BAP049-hum08-LC    E..L....DFQS..PK....IT.........................A.R...Y.....
BAP049-hum09-LC    E..L....DFQS..PK....IT.........................A.R...Y.....
BAP049-hum15-LC    E..L....DFQS..PK....IT.........................A.R...Y.....
BAP049-hum16-LC    E..L....DFQS..PK....IT.........................A.R...Y.....
BAP049-hum10-LC    E..L....AT.SLSP..RA.L..........................A.R...Y.....
BAP049-hum11-LC    E..L....AT.SLSP..RA.L..........................A.R...Y.....
BAP049-hum14-LC    E..L....AT.SLSP..RA.L..........................A.R...Y.....
BAP049-hum06-LC    ......T.L..P..P..PASI..........................A.R...Y.....
BAP049-hum07-LC    E..L....AT.SLSP..RA.L..........................KA.....Y.....
BAP049-hum13-LC    .V......L..P..L.QPASI..........................KA.....Y.....
BAP049-hum12-LC    ..Q........SASV.DR..IT.....................L.....S.Q...Y.....
BAP049-hum02-LC    ..Q........SASV.DR..IT.........................A.R...Y.....
BAP049-hum03-LC    ..Q........SASV.DR..IT.........................A.R...Y.....
BAP049-hum01-LC    E..L....AT.SLSP..RA.L..........................A.R...Y.....
BAP049-hum04-LC    E..L....AT.SLSP..RA.L..........................KA.....Y.....
BAP049-hum05-LC    E..L....AT.SLSP..RA.L..........................KA.....Y.....

                          70        80        90        100       110
                   ....|....|....|....|....|....|....|....|....|....|...
BAP049-chi-LC      ESGVPDRFTGSGSVTDFTLTISSVQAEDLAVYYCQNDYSYPCTFGQGTKVEIK
BAP049-hum08-LC    .....S..S....G....F....LE...A.T..........Y...........
BAP049-hum09-LC    .....S..S....G....F....LE...A.T..........Y...........
BAP049-hum15-LC    .....S..S....G....F....LE...A.T..........Y...........
BAP049-hum16-LC    .....S..S....G....F....LE...A.T..........Y...........
BAP049-hum10-LC    .....S..S....G....F....LE...A.T..........Y...........
BAP049-hum11-LC    .....S..S....G....F....LE...A.T..........Y...........
BAP049-hum14-LC    .....S..S....G....F....LE...A.T..........Y...........
BAP049-hum06-LC    .....S..S....G....F....LE...A.T..........Y...........
BAP049-hum07-LC    .....S..S....G....F....LE...A.T..........Y...........
BAP049-hum13-LC    .....S..S....G....F....LE...A.T..........Y...........
BAP049-hum12-LC    .....S..S....G....F....LE...A.T..........Y...........
BAP049-hum02-LC    ...I.P..S...YG.......NNIES..A.Y.F........Y...........
BAP049-hum03-LC    ...I.P..S...YG.......NNIES..A.Y.F........Y...........
BAP049-hum01-LC    .....S..S....G.E.......L.PD.F.T..........Y...........
BAP049-hum04-LC    .....S..S....G....F....L.P..I.T..........Y...........
BAP049-hum05-LC    .....S..S....G....F....L.P..I.T..........Y...........
```

FIGURE 10B

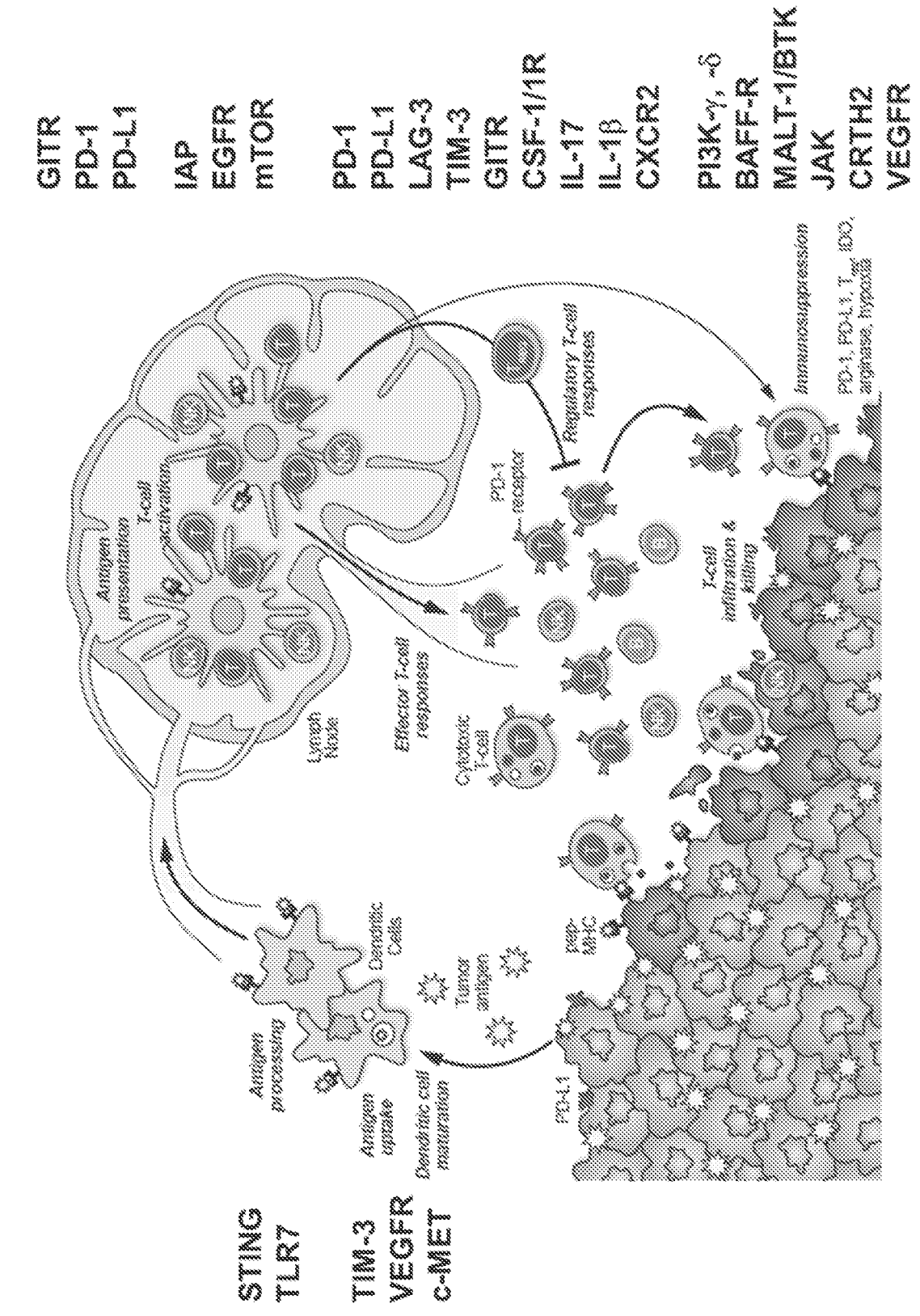

GITR
PD-1
PD-L1
IAP
EGFR
mTOR
PD-1
PD-L1
LAG-3
TIM-3
GITR
CSF-1/1R
IL-17
IL-1β
CXCR2
PI3Kγ, -δ
BAFF-R
MALT-1/BTK
JAK
CRTH2
VEGFR
STING
TLR7
TIM-3
VEGFR
c-MET
Antigen presentation
T-cell activation
Lymph Node
Effector T-cell responses
PD-1 receptor
Regulatory T-cell responses
Cytotoxic T-cell
T-cell infiltration & killing
Immunosuppression
PD-1, PD-L1, T_reg, IDO, arginase, hypoxia
Antigen processing
Antigen uptake
Dendritic cell maturation
Dendritic Cells
Tumor antigen
PD-L1

FIGURE 11

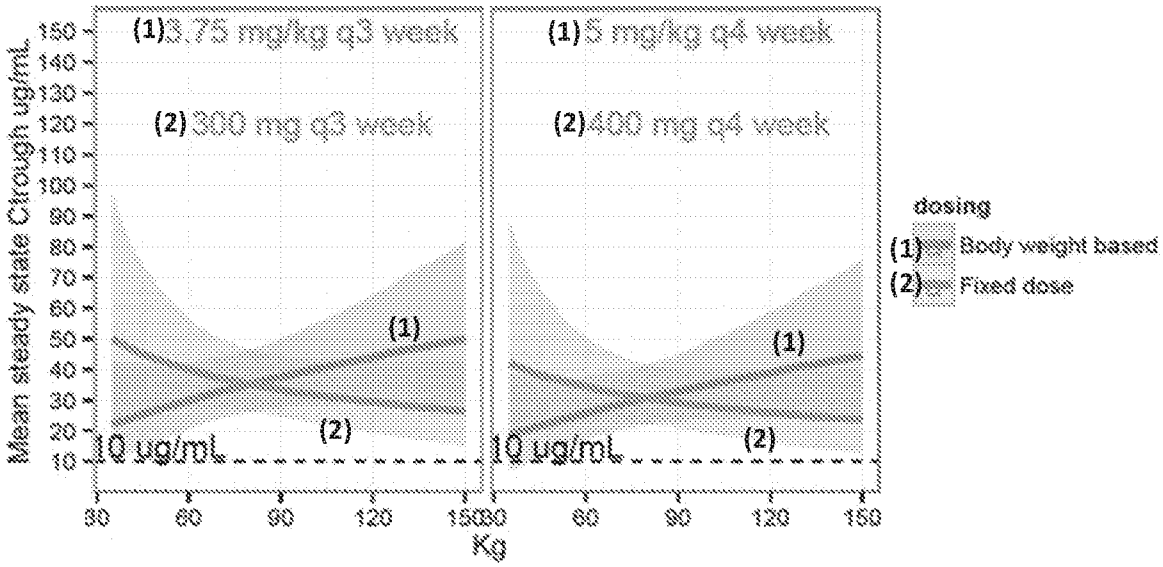


FIGURE 12

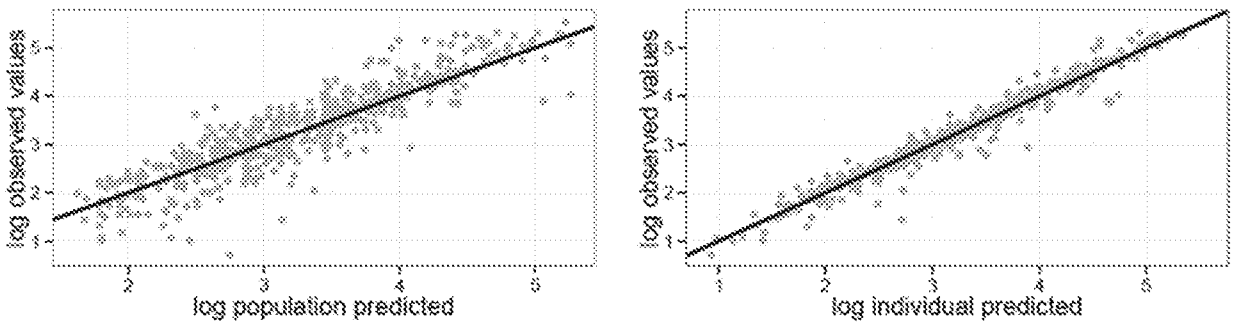


FIGURE 13

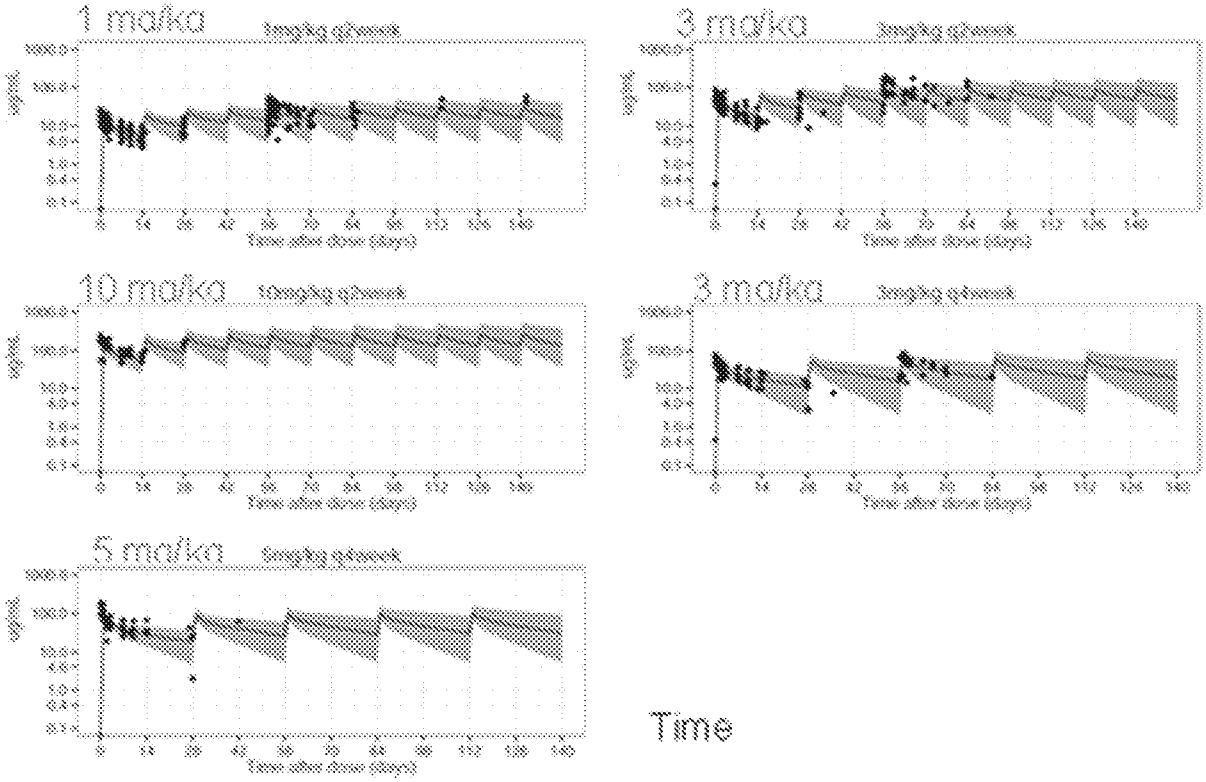
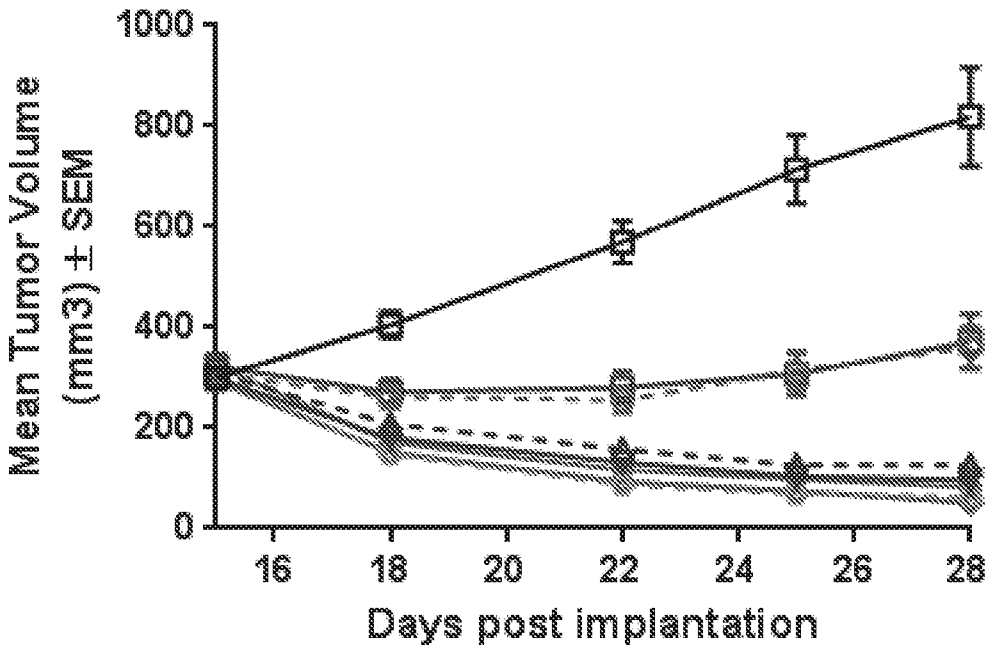


FIGURE 14

FIGURE 15A

Calu6 ($KRAS^{Q61K}$)



Vehicle
Compound A 15mg/kg bid
Compound A 30mg/kg qd
Compound A 50mg/kg bid
Compound A 100mg/kg qd
Compound A 100mg/kg bid
Compound A 200mg/kg qd
Compound A 300mg/kg q2d

FIGURE 15B

NCI-H727 ($KRAS^{G12V}$)

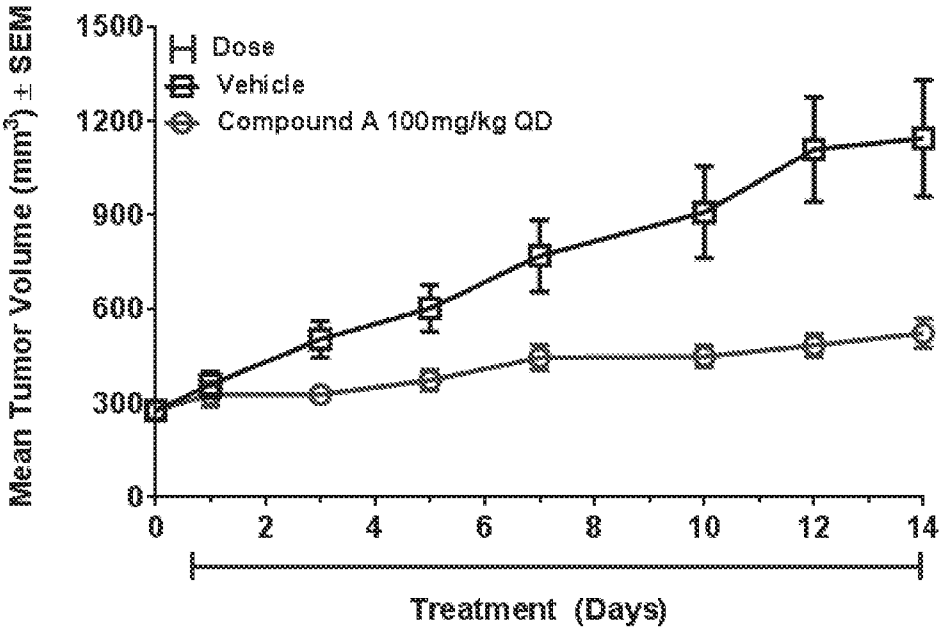


FIGURE 15C

NCI-H358 ($KRAS^{G12C}$)

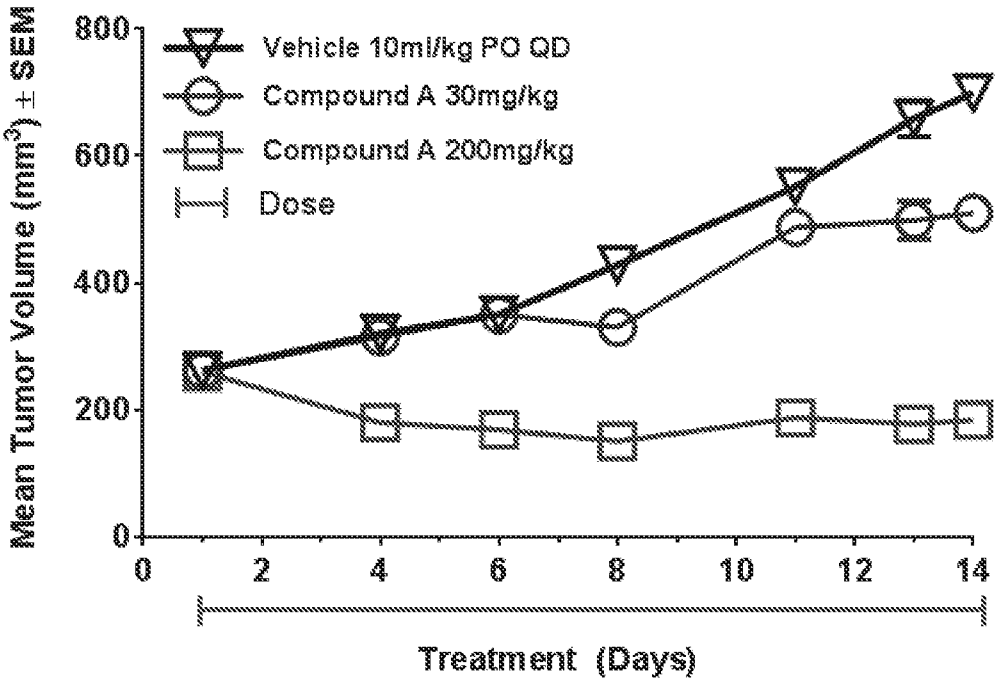
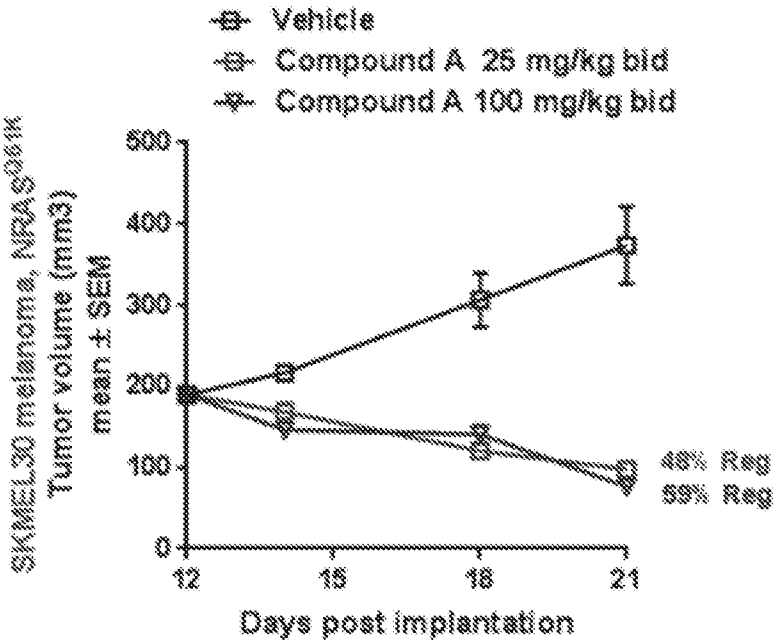
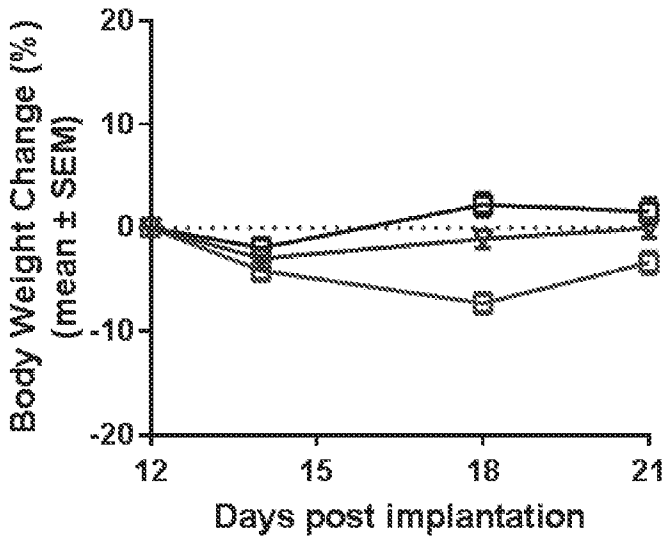


FIGURE 16


Vehicle
Compound A 25 mg/kg bid
Compound A 100 mg/kg bid
SKMEL30 melanoma, NRAS Q61K
Tumor volume (mm3)
mean ± SEM
500
400
300
200
100
0
12
15
18
21
Days post implantation
48% Reg
59% Reg


Body Weight Change (%)
(mean ± SEM)
20
10
0
-10
-20
12
15
18
21
Days post implantation

SEQUENCE LISTING

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<120> THERAPEUTIC USES OF A C-RAF INHIBITOR

<130> PAT057346-WO-PCT

<140>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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Thr Tyr Trp Met His
1 5

<210> 2
<211> 17
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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Asn Ile Tyr Pro Gly Thr Gly Gly Ser Asn Phe Asp Glu Lys Phe Lys
1 5 10 15

Asn

<210> 3
<211> 8
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<213> Artificial Sequence

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Trp Thr Thr Gly Thr Gly Ala Tyr
1 5

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1 5

<210> 5
<211> 6
<212> PRT
<213> Artificial Sequence

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<400> 5
Tyr Pro Gly Thr Gly Gly
1 5

<210> 6
<211> 117
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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

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

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

Gly Asn Ile Tyr Pro Gly Thr Gly Gly Ser Asn Phe Asp Glu Lys Phe
50 55 60

Lys Asn Arg Thr Ser Leu Thr Val Asp Thr Ser Ser Thr Thr Ala Tyr
65 70 75 80

```
Met His Leu Ala Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Thr Arg Trp Thr Thr Gly Thr Gly Ala Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ala
        115
```

<210> 7
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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tcctgcaagg cgtctggcta cacattcacc acttactgga tgcactgggt gaggcagagg 120

cctggacaag gccttgagtg gattggaaat atttatcctg gtactggtgg ttctaacttc 180

gatgagaagt tcaaaaacag gacctcactg actgtagaca catcctccac cacagcctac 240

atgcacctcg ccagcctgac atctgaggac tctgcggtct attactgtac aagatggact 300

actgggacgg gagcttattg gggccaaggg actctggtca ctgtctctgc a 351

<210> 8
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 8
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Gln Val Gln Leu Gln Gln Ser Gly Ser Glu Leu Val Arg Pro Gly Ala
1               5                   10                  15

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

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

Gly Asn Ile Tyr Pro Gly Thr Gly Gly Ser Asn Phe Asp Glu Lys Phe
    50                  55                  60
```

```
Lys Asn Arg Thr Ser Leu Thr Val Asp Thr Ser Ser Thr Thr Ala Tyr
65                  70                  75                  80


Met His Leu Ala Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95


Thr Arg Trp Thr Thr Gly Thr Gly Ala Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ala
        115


<210> 9
<211> 351
<212> DNA
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 9
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tcctgcaagg cgtctggcta cacattcacc acttactgga tgcactgggt gaggcagagg      120

cctggacaag gccttgagtg gattggaaat atttatcctg gtactggtgg ttctaacttc      180

gatgagaagt tcaaaaacag gacctcactg actgtagaca catcctccac cacagcctac      240

atgcacctcg ccagcctgac atctgaggac tctgcggtct attactgtac aagatggact      300

actgggacgg gagcttattg gggccaaggg actctggtca ctgtctctgc a               351


<210> 10
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 10
Lys Ser Ser Gln Ser Leu Leu Asp Ser Gly Asn Gln Lys Asn Phe Leu
1               5                   10                  15


Thr



<210> 11
<211> 7
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<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 11
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 12
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 12
Gln Asn Asp Tyr Ser Tyr Pro Cys Thr
1 5

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

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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Ser Gln Ser Leu Leu Asp Ser Gly Asn Gln Lys Asn Phe
1 5 10

<210> 14
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 14
Trp Ala Ser
1

<210> 15
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 15
Asp Tyr Ser Tyr Pro Cys
1 5

<210> 16
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Phe Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Val Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Cys Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105 110

Lys

<210> 17
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 17
gacattgtga tgacccagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact 60

atgagctgca agtccagtca gagtctgtta gacagtggaa atcaaaagaa cttcttgacc 120

tggtaccagc agaaaccagg gcagcctcct aaactgttga tcttctgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg taacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300

ccgtgcacgt tcggaggggg gaccaagctg gaaataaaa 339

<210> 18
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 18
Gln Val Gln Leu Gln Gln Pro Gly Ser Glu Leu Val Arg Pro Gly Ala
1 5 10 15

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

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

Gly Asn Ile Tyr Pro Gly Thr Gly Gly Ser Asn Phe Asp Glu Lys Phe
50 55 60

Lys Asn Arg Thr Ser Leu Thr Val Asp Thr Ser Ser Thr Thr Ala Tyr
65 70 75 80

Met His Leu Ala Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Trp Thr Thr Gly Thr Gly Ala Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 19
<211> 351
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 19
caggtccagc tgcagcagcc tgggtctgag ctggtgaggc ctggagcttc agtgaagctg 60

tcctgcaagg cgtctggcta cacattcacc acttactgga tgcactgggt gaggcagagg 120

cctggacaag gccttgagtg gattggaaat atttatcctg gtactggtgg ttctaacttc 180

gatgagaagt tcaaaaacag gacctcactg actgtagaca catcctccac cacagcctac 240

atgcacctcg ccagcctgac atctgaggac tctgcggtct attactgtac aagatggact 300

actgggacgg gagcttattg gggccagggc accaccgtga ccgtgtcctc c 351

<210> 20
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 20
Gln Val Gln Leu Gln Gln Pro Gly Ser Glu Leu Val Arg Pro Gly Ala
1 5 10 15

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

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

Gly Asn Ile Tyr Pro Gly Thr Gly Gly Ser Asn Phe Asp Glu Lys Phe
50 55 60

Lys Asn Arg Thr Ser Leu Thr Val Asp Thr Ser Ser Thr Thr Ala Tyr
65 70 75 80

Met His Leu Ala Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Trp Thr Thr Gly Thr Gly Ala Tyr Trp Gly Gln Gly Thr Thr
100 105 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
130 135 140

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

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

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

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
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385 390 395 400

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440

<210> 21
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 21
caggtccagc tgcagcagcc tgggtctgag ctggtgaggc ctggagcttc agtgaagctg 60

tcctgcaagg cgtctggcta cacattcacc acttactgga tgcactgggt gaggcagagg 120

cctggacaag gccttgagtg gattggaaat atttatcctg gtactggtgg ttctaacttc 180

gatgagaagt tcaaaaacag gacctcactg actgtagaca catcctccac cacagcctac 240

atgcacctcg ccagcctgac atctgaggac tctgcggtct attactgtac aagatggact 300

actgggacgg gagcttattg gggccagggc accaccgtga ccgtgtcctc cgcttccacc 360

aagggcccat ccgtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc 600

aacgtagatc acaagcccag caacaccaag gtggacaaga gagttgagtc caaatatggt 660

cccccatgcc caccgtgccc agcacctgag ttcctggggg gaccatcagt cttcctgttc 720

cccccaaaac ccaaggacac tctcatgatc tcccggaccc ctgaggtcac gtgcgtggtg 780

gtggacgtga gccaggaaga ccccgaggtc agttcaact ggtacgtgga tggcgtggag 840

gtgcataatg ccaagacaaa gccgcgggag gagcagttca acagcacgta ccgtgtggtc 900

agcgtcctca ccgtcctgca ccaggactgg ctgaacggca aggagtacaa gtgcaaggtg 960

tccaacaaag gcctcccgtc ctccatcgag aaaaccatct ccaaagccaa agggcagccc 1020

cgagagccac aggtgtacac cctgccccca tcccaggagg agatgaccaa gaaccaggtc 1080

agcctgacct gcctggtcaa aggcttctac cccagcgaca tcgccgtgga gtgggagagc 1140

aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1200

ttcttcctct acagcaggct aaccgtggac aagagcaggt ggcaggaggg gaatgtcttc 1260

tcatgctccg tgatgcatga ggctctgcac aaccactaca cacagaagag cctctccctg 1320

tctctgggta aa 1332

<210> 22
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 22
Gln Val Gln Leu Gln Gln Ser Gly Ser Glu Leu Val Arg Pro Gly Ala
1 5 10 15

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

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

Gly Asn Ile Tyr Pro Gly Thr Gly Gly Ser Asn Phe Asp Glu Lys Phe
50 55 60

Lys Asn Arg Thr Ser Leu Thr Val Asp Thr Ser Ser Thr Thr Ala Tyr
65 70 75 80

Met His Leu Ala Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Trp Thr Thr Gly Thr Gly Ala Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 23
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 23
caggtccagc tgcagcagtc tgggtctgag ctggtgaggc ctggagcttc agtgaagctg 60

tcctgcaagg cgtctggcta cacattcacc acttactgga tgcactgggt gaggcagagg 120

cctggacaag gccttgagtg gattggaaat atttatcctg gtactggtgg ttctaacttc 180

gatgagaagt tcaaaaacag gacctcactg actgtagaca catcctccac cacagcctac 240

atgcacctcg ccagcctgac atctgaggac tctgcggtct attactgtac aagatggact 300

actgggacgg gagcttattg gggccagggc accaccgtga ccgtgtcctc c 351

<210> 24
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 24
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Phe Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Val Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Cys Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 25
<211> 339
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 25
gacattgtga tgacccagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact 60

atgagctgca agtccagtca gagtctgtta gacagtggaa atcaaaagaa cttcttgacc 120

tggtaccagc agaaaccagg gcagcctcct aaactgttga tcttctgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg taacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300

ccgtgcacgt tcggccaagg gaccaaggtg gaaatcaaa 339

<210> 26
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 26
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Phe Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Val Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Cys Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

```
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220
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<210> 27
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 27
gacattgtga tgacccagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact 60

atgagctgca agtccagtca gagtctgtta gacagtggaa atcaaaagaa cttcttgacc 120

tggtaccagc agaaaccagg gcagcctcct aaactgttga tcttctgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg taacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300

ccgtgcacgt tcggccaagg gaccaaggtg gaaatcaaac gtacggtggc tgcaccatct 360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480

caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 28

<400> 28
000

<210> 29

<400> 29
000

<210> 30
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 30
Gln Val Gln Leu Gln Gln Ser Gly Ser Glu Leu Val Arg Pro Gly Ala
1 5 10 15

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

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

Gly Asn Ile Tyr Pro Gly Thr Gly Gly Ser Asn Phe Asp Glu Lys Phe
50 55 60

Lys Asn Arg Thr Ser Leu Thr Val Asp Thr Ser Ser Thr Thr Ala Tyr
65 70 75 80

Met His Leu Ala Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Trp Thr Thr Gly Thr Gly Ala Tyr Trp Gly Gln Gly Thr Thr
100 105 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
130 135 140

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

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

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

```
Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
                405                 410                 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            420                 425                 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440
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<210> 31
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 31
caggtccagc tgcagcagtc tgggtctgag ctggtgaggc ctggagcttc agtgaagctg 60

tcctgcaagg cgtctggcta cacattcacc acttactgga tgcactgggt gaggcagagg 120

cctggacaag gccttgagtg gattggaaat atttatcctg gtactggtgg ttctaacttc 180

gatgagaagt tcaaaaacag gacctcactg actgtagaca catcctccac cacagcctac 240

atgcacctcg ccagcctgac atctgaggac tctgcggtct attactgtac aagatggact 300

actgggacgg gagcttattg gggccagggc accaccgtga ccgtgtcctc cgcttccacc 360

aagggcccat ccgtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc 600

aacgtagatc acaagcccag caacaccaag gtggacaaga gagttgagtc caaatatggt 660

cccccatgcc caccgtgccc agcacctgag ttcctggggg gaccatcagt cttcctgttc 720

cccccaaaac ccaaggacac tctcatgatc tcccggaccc ctgaggtcac gtgcgtggtg 780

gtggacgtga gccaggaaga ccccgaggtc agttcaact ggtacgtgga tggcgtggag 840

gtgcataatg ccaagacaaa gccgcgggag gagcagttca acagcacgta ccgtgtggtc 900

agcgtcctca ccgtcctgca ccaggactgg ctgaacggca aggagtacaa gtgcaaggtg 960

tccaacaaag gcctcccgtc ctccatcgag aaaaccatct ccaaagccaa agggcagccc 1020

cgagagccac aggtgtacac cctgccccca tcccaggagg agatgaccaa gaaccaggtc 1080

agcctgacct gcctggtcaa aggcttctac cccagcgaca tcgccgtgga gtgggagagc 1140

aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1200

ttcttcctct acagcaggct aaccgtggac aagagcaggt ggcaggaggg gaatgtcttc 1260

tcatgctccg tgatgcatga ggctctgcac aaccactaca cacagaagag cctctccctg 1320

tctctgggta aa 1332

<210> 32
<211> 9
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32
Gln Asn Asp Tyr Ser Tyr Pro Tyr Thr
1 5

<210> 33
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 33
Asp Tyr Ser Tyr Pro Tyr
1 5

<210> 34
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 34
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Phe Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Val Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile

100 105 110

Lys

<210> 35
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 35
gacattgtga tgacccagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact 60

atgagctgca agtccagtca gagtctgtta gacagtggaa atcaaaagaa cttcttgacc 120

tggtaccagc agaaaccagg gcagcctcct aaactgttga tcttctgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg taacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300

ccgtacacgt tcggccaagg gaccaaggtg gaaatcaaa 339

<210> 36
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 36
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Phe Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Val Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn

85 90 95

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

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

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

<210> 37
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 37
gacattgtga tgacccagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact 60

atgagctgca agtccagtca gagtctgtta gacagtggaa atcaaaagaa cttcttgacc 120

tggtaccagc agaaaccagg gcagcctcct aaactgttga tcttctgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg taacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300

ccgtacacgt tcggccaagg gaccaaggtg gaaatcaaac gtacggtggc tgcaccatct 360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480

caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 38
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 38
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30

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

Gly Asn Ile Tyr Pro Gly Thr Gly Gly Ser Asn Phe Asp Glu Lys Phe
50 55 60

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

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

Thr Arg Trp Thr Thr Gly Thr Gly Ala Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 39
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 39
gaagtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaggatc 60

tcctgtaagg gttctggcta cacattcacc acttactgga tgcactgggt gcgacaggcc 120

actggacaag ggcttgagtg gatgggtaat atttatcctg gtactggtgg ttctaacttc 180

gatgagaagt tcaagaacag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtac aagatggact 300

actgggacgg gagcttattg gggccagggc accaccgtga ccgtgtcctc c 351

<210> 40
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 40

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

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30

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

Gly Asn Ile Tyr Pro Gly Thr Gly Gly Ser Asn Phe Asp Glu Lys Phe
50 55 60

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

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

Thr Arg Trp Thr Thr Gly Thr Gly Ala Tyr Trp Gly Gln Gly Thr Thr
100 105 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
130 135 140

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

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

```
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
                405                 410                 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
```

420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440

<210> 41
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 41
gaagtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaggatc 60

tcctgtaagg gttctggcta cacattcacc acttactgga tgcactgggt gcgacaggcc 120

actggacaag ggcttgagtg gatgggtaat atttatcctg gtactggtgg ttctaacttc 180

gatgagaagt tcaagaacag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtac aagatggact 300

actgggacgg gagcttattg gggccagggc accaccgtga ccgtgtcctc cgcttccacc 360

aagggcccat ccgtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc 600

aacgtagatc acaagcccag caacaccaag gtggacaaga gagttgagtc caaatatggt 660

cccccatgcc caccgtgccc agcacctgag ttcctggggg gaccatcagt cttcctgttc 720

cccccaaaac ccaaggacac tctcatgatc tcccggaccc ctgaggtcac gtgcgtggtg 780

gtggacgtga gccaggaaga ccccgaggtc agttcaact ggtacgtgga tggcgtggag 840

gtgcataatg ccaagacaaa gccgcgggag gagcagttca acagcacgta ccgtgtggtc 900

agcgtcctca ccgtcctgca ccaggactgg ctgaacggca aggagtacaa gtgcaaggtg 960

tccaacaaag gcctcccgtc ctccatcgag aaaaccatct ccaaagccaa agggcagccc 1020

cgagagccac aggtgtacac cctgccccca tcccaggagg agatgaccaa gaaccaggtc 1080

agcctgacct gcctggtcaa aggcttctac cccagcgaca tcgccgtgga gtgggagagc 1140

aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1200

ttcttcctct acagcaggct aaccgtggac aagagcaggt ggcaggaggg gaatgtcttc 1260

tcatgctccg tgatgcatga ggctctgcac aaccactaca cacagaagag cctctccctg 1320

tctctgggta aa 1332

<210> 42
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 42
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ala Pro Arg Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 43
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 43
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca agtccagtca gagtctgtta gacagtggaa atcaaaagaa cttcttgacc 120

tggtaccagc agaaacctgg ccaggctccc aggctcctca tctattgggc atccactagg 180

gaatctgggg tcccatcaag gttcagcggc agtggatctg ggacagaatt cactctcacc 240

atcagcagcc tgcagcctga tgattttgca acttattact gtcagaatga ttatagttat 300

ccgtacacgt tcggccaagg gaccaaggtg gaaatcaaa 339

<210> 44
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 44
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ala Pro Arg Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

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


Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220
```

<210> 45
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 45

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gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc       60

ctctcctgca agtccagtca gagtctgtta gacagtggaa atcaaaagaa cttcttgacc      120

tggtaccagc agaaacctgg ccaggctccc aggctcctca tctattgggc atccactagg      180

gaatctgggg tcccatcaag gttcagcggc agtggatctg ggacagaatt cactctcacc      240

atcagcagcc tgcagcctga tgattttgca acttattact gtcagaatga ttatagttat      300

ccgtacacgt tcggccaagg gaccaaggtg gaaatcaaac gtacggtggc tgcaccatct      360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc      420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc      480

caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc      540

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc      600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt      660
```

<210> 46
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 46

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


Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
            20                  25                  30
```

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ala Pro Arg Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Ile
50 55 60

Pro Pro Arg Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Asn Asn Ile Glu Ser Glu Asp Ala Ala Tyr Tyr Phe Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 47
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 47
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgca agtccagtca gagtctgtta gacagtggaa atcaaaagaa cttcttgacc 120

tggtaccagc agaaacctgg ccaggctccc aggctcctca tctattgggc atccactagg 180

gaatctggga tcccacctcg attcagtggc agcgggtatg gaacagattt taccctcaca 240

attaataaca tagaatctga ggatgctgca tattacttct gtcagaatga ttatagttat 300

ccgtacacgt tcggccaagg gaccaaggtg gaaatcaaa 339

<210> 48
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 48
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

```
Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
            20                  25                  30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

Ala Pro Arg Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Ile
    50                  55                  60

Pro Pro Arg Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

Ile Asn Asn Ile Glu Ser Glu Asp Ala Ala Tyr Tyr Phe Cys Gln Asn
                85                  90                  95

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
            100                 105                 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

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

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


<210> 49
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 49
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gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgca agtccagtca gagtctgtta gacagtggaa atcaaaagaa cttcttgacc 120

tggtaccagc agaaacctgg ccaggctccc aggctcctca tctattgggc atccactagg 180

gaatctggga tcccacctcg attcagtggc agcgggtatg gaacagattt taccctcaca 240

attaataaca tagaatctga ggatgctgca tattacttct gtcagaatga ttatagttat 300

ccgtacacgt tcggccaagg gaccaaggtg gaaatcaaac gtacggtggc tgcaccatct 360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480

caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 50
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 50
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30

Trp Met His Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
35 40 45

Gly Asn Ile Tyr Pro Gly Thr Gly Gly Ser Asn Phe Asp Glu Lys Phe
50 55 60

Lys Asn 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 Val Tyr Tyr Cys
85 90 95

Thr Arg Trp Thr Thr Gly Thr Gly Ala Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser

115

<210> 51
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 51
gaagtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaggatc 60

tcctgtaagg gttctggcta cacattcacc acttactgga tgcactggat caggcagtcc 120

ccatcgagag gccttgagtg gctgggtaat atttatcctg gtactggtgg ttctaacttc 180

gatgagaagt tcaagaacag attcaccatc tccagagaca attccaagaa cacgctgtat 240

cttcaaatga acagcctgag agccgaggac acggccgtgt attactgtac aagatggact 300

actgggacgg gagcttattg gggccagggc accaccgtga ccgtgtcctc c 351

<210> 52
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 52
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30

Trp Met His Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
35 40 45

Gly Asn Ile Tyr Pro Gly Thr Gly Gly Ser Asn Phe Asp Glu Lys Phe
50 55 60

Lys Asn 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 Val Tyr Tyr Cys
85 90 95

Thr Arg Trp Thr Thr Gly Thr Gly Ala Tyr Trp Gly Gln Gly Thr Thr

```
            100                 105                 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

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

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

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

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
            340                 345                 350
```

```
Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
                405                 410                 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            420                 425                 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440
```

<210> 53
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 53

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gaagtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaggatc       60

tcctgtaagg gttctggcta cacattcacc acttactgga tgcactggat caggcagtcc      120

ccatcgagag gccttgagtg gctgggtaat atttatcctg gtactggtgg ttctaacttc      180

gatgagaagt tcaagaacag attcaccatc tccagagaca attccaagaa cacgctgtat      240

cttcaaatga acagcctgag agccgaggac acggccgtgt attactgtac aagatggact      300

actgggacgg gagcttattg gggccagggc accaccgtga ccgtgtcctc cgcttccacc      360

aagggcccat ccgtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc      420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca      480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac      540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc      600

aacgtagatc acaagcccag caacaccaag gtggacaaga gagttgagtc caaatatggt      660

cccccatgcc caccgtgccc agcacctgag ttcctggggg gaccatcagt cttcctgttc      720

cccccaaaac ccaaggacac tctcatgatc tcccggaccc ctgaggtcac gtgcgtggtg      780

gtggacgtga gccaggaaga ccccgaggtc agttcaact ggtacgtgga tggcgtggag      840
```

gtgcataatg ccaagacaaa gccgcgggag gagcagttca acagcacgta ccgtgtggtc 900

agcgtcctca ccgtcctgca ccaggactgg ctgaacggca aggagtacaa gtgcaaggtg 960

tccaacaaag gcctcccgtc ctccatcgag aaaaccatct ccaaagccaa agggcagccc 1020

cgagagccac aggtgtacac cctgccccca tcccaggagg agatgaccaa gaaccaggtc 1080

agcctgacct gcctggtcaa aggcttctac cccagcgaca tcgccgtgga gtgggagagc 1140

aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1200

ttcttcctct acagcaggct aaccgtggac aagagcaggt ggcaggaggg gaatgtcttc 1260

tcatgctccg tgatgcatga ggctctgcac aaccactaca cacagaagag cctctccctg 1320

tctctgggta aa 1332

<210> 54
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 54
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys
35 40 45

Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
65 70 75 80

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

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 55

<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 55
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca agtccagtca gagtctgtta gacagtggaa atcaaaagaa cttcttgacc 120

tggtatcagc agaaaccagg gaaagctcct aagctcctga tctattgggc atccactagg 180

gaatctgggg tcccatcaag gttcagtgga agtggatctg ggacagattt tactttcacc 240

atcagcagcc tgcagcctga agatattgca acatattact gtcagaatga ttatagttat 300

ccgtacacgt tcggccaagg gaccaaggtg gaaatcaaa 339

<210> 56
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 56
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys
35 40 45

Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
65 70 75 80

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

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp

115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

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

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

<210> 57
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 57
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca agtccagtca gagtctgtta gacagtggaa atcaaaagaa cttcttgacc 120

tggtatcagc agaaaccagg gaaagctcct aagctcctga tctattgggc atccactagg 180

gaatctgggg tcccatcaag gttcagtgga agtggatctg ggacagattt tactttcacc 240

atcagcagcc tgcagcctga agatattgca acatattact gtcagaatga ttatagttat 300

ccgtacacgt tcggccaagg gaccaaggtg gaaatcaaac gtacggtggc tgcaccatct 360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480

caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 58
<211> 113

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 58

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

Glu	Pro	Ala	Ser	Ile	Ser	Cys	Lys	Ser	Ser	Gln	Ser	Leu	Leu	Asp	Ser
			20					25					30		

Gly	Asn	Gln	Lys	Asn	Phe	Leu	Thr	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln
		35					40					45			

Ala	Pro	Arg	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val
	50					55					60				

Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Phe	Thr
65				70				75						80	

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

Asp	Tyr	Ser	Tyr	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile
			100					105					110		

Lys

<210> 59
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 59

gatattgtga tgacccagac tccactctcc ctgcccgtca cccctggaga gccggcctcc 60

atctcctgca agtccagtca gagtctgtta gacagtggaa atcaaaagaa cttcttgacc 120

tggtaccagc agaaacctgg ccaggctccc aggctcctca tctattgggc atccactagg 180

gaatctgggg tcccctcgag gttcagtggc agtggatctg ggacagattt cacctttacc 240

atcagtagcc tggaagctga agatgctgca acatattact gtcagaatga ttatagttat 300

ccgtacacgt tcggccaagg gaccaaggtg gaaatcaaa 339

<210> 60
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 60

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

Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
            20                  25                  30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

Ala Pro Arg Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
65                  70                  75                  80

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

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
            100                 105                 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

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

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

<210> 61
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 61
gatattgtga tgacccagac tccactctcc ctgcccgtca cccctggaga gccggcctcc 60

atctcctgca agtccagtca gagtctgtta gacagtggaa atcaaaagaa cttcttgacc 120

tggtaccagc agaaacctgg ccaggctccc aggctcctca tctattgggc atccactagg 180

gaatctgggg tcccctcgag gttcagtggc agtggatctg ggacagattt caccttacc 240

atcagtagcc tggaagctga agatgctgca acatattact gtcagaatga ttatagttat 300

ccgtacacgt tcggccaagg gaccaaggtg gaaatcaaac gtacggtggc tgcaccatct 360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480

caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 62
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 62
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys
35 40 45

Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
65 70 75 80

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

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 63
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 63
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca agtccagtca gagtctgtta gacagtggaa atcaaaagaa cttcttgacc 120

tggtatcagc agaaaccagg gaaagctcct aagctcctga tctattgggc atccactagg 180

gaatctgggg tcccctcgag gttcagtggc agtggatctg ggacagattt caccttacc 240

atcagtagcc tggaagctga agatgctgca acatattact gtcagaatga ttatagttat 300

ccgtacacgt tcggccaagg gaccaaggtg gaaatcaaa 339

<210> 64
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 64
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

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Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys
        35                  40                  45

Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
65                  70                  75                  80

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

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
            100                 105                 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220
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<210> 65
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 65
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca agtccagtca gagtctgtta gacagtggaa atcaaaagaa cttcttgacc 120

tggtatcagc agaaaccagg gaaagctcct aagctcctga tctattgggc atccactagg 180

gaatctgggg tcccctcgag gttcagtggc agtggatctg ggacagattt cacctttacc 240

atcagtagcc tggaagctga agatgctgca acatattact gtcagaatga ttatagttat 300

ccgtacacgt tcggccaagg gaccaaggtg gaaatcaaac gtacggtggc tgcaccatct 360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480

caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 66
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 66
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1 5 10 15

Glu Lys Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ala Pro Arg Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
65 70 75 80

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

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 67

<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 67
gaaattgtgc tgactcagtc tccagacttt cagtctgtga ctccaaagga gaaagtcacc 60

atcacctgca agtccagtca gagtctgtta gacagtggaa atcaaaagaa cttcttgacc 120

tggtaccagc agaaacctgg ccaggctccc aggctcctca tctattgggc atccactagg 180

gaatctgggg tcccctcgag gttcagtggc agtggatctg ggacagattt caccttacc 240

atcagtagcc tggaagctga agatgctgca acatattact gtcagaatga ttatagttat 300

ccgtacacgt tcggccaagg gaccaaggtg gaaatcaaa 339

<210> 68
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 68
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1 5 10 15

Glu Lys Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ala Pro Arg Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
65 70 75 80

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

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp

115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

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

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

<210> 69
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 69
gaaattgtgc tgactcagtc tccagacttt cagtctgtga ctccaaagga gaaagtcacc 60

atcacctgca agtccagtca gagtctgtta gacagtggaa atcaaaagaa cttcttgacc 120

tggtaccagc agaaacctgg ccaggctccc aggctcctca tctattgggc atccactagg 180

gaatctgggg tcccctcgag gttcagtggc agtggatctg ggacagattt caccttacc 240

atcagtagcc tggaagctga agatgctgca acatattact gtcagaatga ttatagttat 300

ccgtacacgt tcggccaagg gaccaaggtg gaaatcaaac gtacggtggc tgcaccatct 360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480

caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 70
<211> 113

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 70

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

Glu Arg Ala Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ala Pro Arg Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
65 70 75 80

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

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 71
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 71

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca agtccagtca gagtctgtta gacagtggaa atcaaaagaa cttcttgacc 120

tggtaccagc agaaacctgg ccaggctccc aggctcctca tctattgggc atccactagg 180

gaatctgggg tcccctcgag gttcagtggc agtggatctg ggacagattt cacctttacc 240

atcagtagcc tggaagctga agatgctgca acatattact gtcagaatga ttatagttat 300

ccgtacacgt tcggccaagg gaccaaggtg gaaatcaaa 339

<210> 72
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 72

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

Glu Arg Ala Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
            20                  25                  30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

Ala Pro Arg Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
65                  70                  75                  80

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

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
            100                 105                 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

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

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

<210> 73
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 73
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca agtccagtca gagtctgtta gacagtggaa atcaaaagaa cttcttgacc 120

tggtaccagc agaaacctgg ccaggctccc aggctcctca tctattgggc atccactagg 180

gaatctgggg tcccctcgag gttcagtggc agtggatctg ggacagattt caccttacc 240

atcagtagcc tggaagctga agatgctgca acatattact gtcagaatga ttatagttat 300

ccgtacacgt tcggccaagg gaccaaggtg gaaatcaaac gtacggtggc tgcaccatct 360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480

caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 74
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 74
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Leu Gln Lys Pro Gly Gln
35 40 45

Ser Pro Gln Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
65 70 75 80

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

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 75
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 75
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgca agtccagtca gagtctgtta gacagtggaa atcaaaagaa cttcttgacc 120

tggtacctgc agaagccagg gcagtctcca cagctcctga tctattgggc atccactagg 180

gaatctgggg tcccctcgag gttcagtggc agtggatctg ggacagattt caccttacc 240

atcagtagcc tggaagctga agatgctgca acatattact gtcagaatga ttatagttat 300

ccgtacacgt tcggccaagg gaccaaggtg gaaatcaaa 339

<210> 76
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 76
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

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Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Leu Gln Lys Pro Gly Gln
        35                  40                  45

Ser Pro Gln Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
65                  70                  75                  80

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

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
            100                 105                 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220
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<210> 77
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 77
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgca agtccagtca gagtctgtta gacagtggaa atcaaaagaa cttcttgacc 120

tggtacctgc agaagccagg gcagtctcca cagctcctga tctattgggc atccactagg 180

gaatctgggg tcccctcgag gttcagtggc agtggatctg ggacagattt cacctttacc 240

atcagtagcc tggaagctga agatgctgca acatattact gtcagaatga ttatagttat 300

ccgtacacgt tcggccaagg gaccaaggtg gaaatcaaac gtacggtggc tgcaccatct 360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480

caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 78
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 78
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys
35 40 45

Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
65 70 75 80

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

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 79

<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 79
gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc 60

atctcctgca agtccagtca gagtctgtta gacagtggaa atcaaaagaa cttcttaacc 120

tggtatcagc agaaaccagg gaaagctcct aagctcctga tctattgggc atccactagg 180

gaatctgggg tcccctcgag gttcagtggc agtggatctg ggacagattt caccttacc 240

atcagtagcc tggaagctga agatgctgca acatattact gtcagaatga ttatagttat 300

ccgtacacgt tcggccaagg gaccaaggtg gaaatcaaa 339

<210> 80
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 80
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys
35 40 45

Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
65 70 75 80

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

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp

115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

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

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

<210> 81
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 81
gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc 60

atctcctgca agtccagtca gagtctgtta gacagtggaa atcaaaagaa cttcttaacc 120

tggtatcagc agaaaccagg gaaagctcct aagctcctga tctattgggc atccactagg 180

gaatctgggg tcccctcgag gttcagtggc agtggatctg ggacagattt caccttacc 240

atcagtagcc tggaagctga agatgctgca acatattact gtcagaatga ttatagttat 300

ccgtacacgt tcggccaagg gaccaaggtg gaaatcaaac gtacggtggc tgcaccatct 360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480

caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 82
<211> 117

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 82

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1				5				10					15		
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Thr	Tyr
			20					25					30		
Trp	Met	His	Trp	Ile	Arg	Gln	Ser	Pro	Ser	Arg	Gly	Leu	Glu	Trp	Leu
		35					40					45			
Gly	Asn	Ile	Tyr	Pro	Gly	Thr	Gly	Gly	Ser	Asn	Phe	Asp	Glu	Lys	Phe
	50					55					60				
Lys	Asn	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	Val	Tyr	Tyr	Cys
				85					90					95	
Thr	Arg	Trp	Thr	Thr	Gly	Thr	Gly	Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Thr
			100					105					110		
Val	Thr	Val	Ser	Ser											
			115												

<210> 83
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 83

caggttcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggcta cacattcacc acttactgga tgcactggat caggcagtcc 120

ccatcgagag gccttgagtg gctgggtaat atttatcctg gtactggtgg ttctaacttc 180

gatgagaagt tcaagaacag attcaccatc tccagagaca attccaagaa cacgctgtat 240

cttcaaatga acagcctgag agccgaggac acggccgtgt attactgtac aagatggact 300

actgggacgg gagcttactg gggccagggc accaccgtga ccgtgtcctc c 351

<210> 84
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 84
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30

Trp Met His Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
35 40 45

Gly Asn Ile Tyr Pro Gly Thr Gly Gly Ser Asn Phe Asp Glu Lys Phe
50 55 60

Lys Asn 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 Val Tyr Tyr Cys
85 90 95

Thr Arg Trp Thr Thr Gly Thr Gly Ala Tyr Trp Gly Gln Gly Thr Thr
100 105 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
130 135 140

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

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

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

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
195 200 205

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Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
                405                 410                 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            420                 425                 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440
```

<210> 85

<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 85
caggttcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggcta cacattcacc acttactgga tgcactggat caggcagtcc 120

ccatcgagag gccttgagtg gctgggtaat atttatcctg gtactggtgg ttctaacttc 180

gatgagaagt tcaagaacag attcaccatc tccagagaca attccaagaa cacgctgtat 240

cttcaaatga acagcctgag agccgaggac acggccgtgt attactgtac aagatggact 300

actgggacgg gagcttactg gggccagggc accaccgtga ccgtgtcctc cgcttccacc 360

aagggcccat ccgtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc 600

aacgtagatc acaagcccag caacaccaag gtggacaaga gagttgagtc caaatatggt 660

cccccatgcc caccgtgccc agcacctgag ttcctggggg gaccatcagt cttcctgttc 720

cccccaaaac ccaaggacac tctcatgatc tcccggaccc ctgaggtcac gtgcgtggtg 780

gtggacgtga gccaggaaga ccccgaggtc agttcaact ggtacgtgga tggcgtggag 840

gtgcataatg ccaagacaaa gccgcgggag gagcagttca acagcacgta ccgtgtggtc 900

agcgtcctca ccgtcctgca ccaggactgg ctgaacggca aggagtacaa gtgcaaggtg 960

tccaacaaag gcctcccgtc ctccatcgag aaaaccatct ccaaagccaa agggcagccc 1020

cgagagccac aggtgtacac cctgccccca tcccaggagg agatgaccaa gaaccaggtc 1080

agcctgacct gcctggtcaa aggcttctac cccagcgaca tcgccgtgga gtgggagagc 1140

aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1200

ttcttcctct acagcaggct aaccgtggac aagagcaggt ggcaggaggg gaatgtcttc 1260

tcatgctccg tgatgcatga ggctctgcac aaccactaca cacagaagag cctctccctg 1320

tctctgggta aa 1332

<210> 86
<211> 117
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 86

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

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30

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

Gly Asn Ile Tyr Pro Gly Thr Gly Gly Ser Asn Phe Asp Glu Lys Phe
50 55 60

Lys Asn 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 Val Tyr Tyr Cys
85 90 95

Thr Arg Trp Thr Thr Gly Thr Gly Ala Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 87
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 87

gaagtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaggatc 60

tcctgtaagg gttctggcta cacattcacc acttactgga tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggtaat atttatcctg gtactggtgg ttctaacttc 180

gatgagaagt tcaagaacag attcaccatc tccagagaca attccaagaa cacgctgtat 240

cttcaaatga acagcctgag agccgaggac acggccgtgt attactgtac aagatggact 300

actgggacgg gagcttattg gggccagggc accaccgtga ccgtgtcctc c 351

<210> 88
<211> 444

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 88

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

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Thr Tyr
            20                  25                  30

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

Gly Asn Ile Tyr Pro Gly Thr Gly Gly Ser Asn Phe Asp Glu Lys Phe
    50                  55                  60

Lys Asn 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 Val Tyr Tyr Cys
                85                  90                  95

Thr Arg Trp Thr Thr Gly Thr Gly Ala Tyr Trp Gly Gln Gly Thr Thr
            100                 105                 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

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

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

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

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
    210                 215                 220
```

```
Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
                405                 410                 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            420                 425                 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440
```

<210> 89
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 89
gaagtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaggatc 60

tcctgtaagg gttctggcta cacattcacc acttactgga tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggtaat atttatcctg gtactggtgg ttctaacttc 180

gatgagaagt tcaagaacag attcaccatc tccagagaca attccaagaa cacgctgtat 240

cttcaaatga acagcctgag agccgaggac acggccgtgt attactgtac aagatggact 300

actgggacgg gagcttattg gggccagggc accaccgtga ccgtgtcctc cgcttccacc 360

aagggcccat ccgtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc 600

aacgtagatc acaagcccag caacaccaag gtggacaaga gagttgagtc caaatatggt 660

cccccatgcc caccgtgccc agcacctgag ttcctggggg gaccatcagt cttcctgttc 720

cccccaaaac ccaaggacac tctcatgatc tcccggaccc ctgaggtcac gtgcgtggtg 780

gtggacgtga gccaggaaga ccccgaggtc cagttcaact ggtacgtgga tggcgtggag 840

gtgcataatg ccaagacaaa gccgcgggag gagcagttca acagcacgta ccgtgtggtc 900

agcgtcctca ccgtcctgca ccaggactgg ctgaacggca aggagtacaa gtgcaaggtg 960

tccaacaaag gcctcccgtc ctccatcgag aaaaccatct ccaaagccaa agggcagccc 1020

cgagagccac aggtgtacac cctgccccca tcccaggagg agatgaccaa gaaccaggtc 1080

agcctgacct gcctggtcaa aggcttctac cccagcgaca tcgccgtgga gtgggagagc 1140

aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1200

ttcttcctct acagcaggct aaccgtggac aagagcaggt ggcaggaggg gaatgtcttc 1260

tcatgctccg tgatgcatga ggctctgcac aaccactaca cacagaagag cctctccctg 1320

tctctgggta aa 1332

<210> 90
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 90
gaagtgcagc tggtgcagtc tggcgccgaa gtgaagaagc ctggcgagtc cctgcggatc 60

tcctgcaagg gctctggcta caccttcacc acctactgga tgcactgggt gcgacaggct 120

accggccagg gcctggaatg gatgggcaac atctatcctg gcaccggcgg ctccaacttc 180

gacgagaagt tcaagaacag agtgaccatc accgccgaca agtccacctc caccgcctac 240

atggaactgt cctccctgag atccgaggac accgccgtgt actactgcac ccggtggaca 300

accggcacag gcgcttattg gggccagggc accacagtga ccgtgtcctc t 351

<210> 91
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 91
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30

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

Gly Asn Ile Tyr Pro Gly Thr Gly Gly Ser Asn Phe Asp Glu Lys Phe
50 55 60

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

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

Thr Arg Trp Thr Thr Gly Thr Gly Ala Tyr Trp Gly Gln Gly Thr Thr
100 105 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
130 135 140

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

```
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

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

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
```

405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
435 440

<210> 92
<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 92
gaagtgcagc tggtgcagtc tggcgccgaa gtgaagaagc ctggcgagtc cctgcggatc 60

tcctgcaagg gctctggcta caccttcacc acctactgga tgcactgggt gcgacaggct 120

accggccagg gcctggaatg gatgggcaac atctatcctg gcaccggcgg ctccaacttc 180

gacgagaagt tcaagaacag agtgaccatc accgccgaca agtccacctc caccgcctac 240

atggaactgt cctccctgag atccgaggac accgccgtgt actactgcac ccggtggaca 300

accggcacag gcgcttattg gggccagggc accacagtga ccgtgtcctc tgcttctacc 360

aaggggccca gcgtgttccc cctggccccc tgctccagaa gcaccagcga gagcacagcc 420

gccctgggct gcctggtgaa ggactacttc cccgagcccg tgaccgtgtc ctggaacagc 480

ggagccctga ccagcggcgt gcacaccttc cccgccgtgc tgcagagcag cggcctgtac 540

agcctgagca gcgtggtgac cgtgcccagc agcagcctgg gcaccaagac ctacacctgt 600

aacgtggacc acaagcccag caacaccaag gtggacaaga gggtggagag caagtacggc 660

ccaccctgcc ccccctgccc agcccccgag ttcctgggcg gacccagcgt gttcctgttc 720

ccccccaagc ccaaggacac cctgatgatc agcagaaccc ccgaggtgac ctgtgtggtg 780

gtggacgtgt cccaggagga ccccgaggtc cagttcaact ggtacgtgga cggcgtggag 840

gtgcacaacg ccaagaccaa gcccagagag gagcagttta acagcaccta ccgggtggtg 900

tccgtgctga ccgtgctgca ccaggactgg ctgaacggca aagagtacaa gtgtaaggtc 960

tccaacaagg gcctgccaag cagcatcgaa aagaccatca gcaaggccaa gggccagcct 1020

agagagcccc aggtctacac cctgccaccc agccaagagg agatgaccaa gaaccaggtg 1080

tccctgacct gtctggtgaa gggcttctac ccaagcgaca tcgccgtgga gtgggagagc 1140

aacggccagc ccgagaacaa ctacaagacc acccccccag tgctggacag cgacggcagc 1200

ttcttcctgt acagcaggct gaccgtggac aagtccagat ggcaggaggg caacgtcttt 1260

agctgctccg tgatgcacga ggccctgcac aaccactaca cccagaagag cctgagcctg 1320

tccctgggc 1329

<210> 93
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 93
gagatcgtgc tgacccagtc ccctgccacc ctgtcactgt ctccaggcga gagagctacc 60

ctgtcctgca agtcctccca gtccctgctg gactccggca accagaagaa cttcctgacc 120

tggtatcagc agaagcccgg ccaggccccc agactgctga tctactgggc ctccacccgg 180

gaatctggcg tgccctctag attctccggc tccggctctg gcaccgagtt taccctgacc 240

atctccagcc tgcagcccga cgacttcgcc acctactact gccagaacga ctactcctac 300

ccctacacct tcggccaggg caccaaggtg gaaatcaag 339

<210> 94
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 94
gagatcgtgc tgacccagtc ccctgccacc ctgtcactgt ctccaggcga gagagctacc 60

ctgtcctgca agtcctccca gtccctgctg gactccggca accagaagaa cttcctgacc 120

tggtatcagc agaagcccgg ccaggccccc agactgctga tctactgggc ctccacccgg 180

gaatctggcg tgccctctag attctccggc tccggctctg gcaccgagtt taccctgacc 240

atctccagcc tgcagcccga cgacttcgcc acctactact gccagaacga ctactcctac 300

ccctacacct tcggccaggg caccaaggtg gaaatcaagc gtacggtggc cgctcccagc 360

gtgttcatct tccccccaag cgacgagcag ctgaagagcg gcaccgccag cgtggtgtgt 420

ctgctgaaca acttctaccc cagggaggcc aaggtgcagt ggaaggtgga caacgccctg 480

cagagcggca acagccagga gagcgtcacc gagcaggaca gcaaggactc cacctacagc 540

ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgt 600

gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaacag gggcgagtgc 660

<210> 95
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 95
gaggtgcagc tggtgcagtc aggcgccgaa gtgaagaagc ccggcgagtc actgagaatt 60

agctgtaaag gttcaggcta caccttcact acctactgga tgcactgggt ccgccaggct 120

accggtcaag gcctcgagtg gatgggtaat atctaccccg gcaccggcgg ctctaacttc 180

gacgagaagt ttaagaatag agtgactatc accgccgata agtctactag caccgcctat 240

atggaactgt ctagcctgag atcagaggac accgccgtct actactgcac taggtggact 300

accggcacag gcgcctactg gggtcaaggc actaccgtga ccgtgtctag c 351

<210> 96
<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 96
gaggtgcagc tggtgcagtc aggcgccgaa gtgaagaagc ccggcgagtc actgagaatt 60

agctgtaaag gttcaggcta caccttcact acctactgga tgcactgggt ccgccaggct 120

accggtcaag gcctcgagtg gatgggtaat atctaccccg gcaccggcgg ctctaacttc 180

gacgagaagt ttaagaatag agtgactatc accgccgata agtctactag caccgcctat 240

atggaactgt ctagcctgag atcagaggac accgccgtct actactgcac taggtggact 300

accggcacag gcgcctactg gggtcaaggc actaccgtga ccgtgtctag cgctagcact 360

aagggcccgt ccgtgttccc cctggcacct tgtagccgga gcactagcga atccaccgct 420

gccctcggct gcctggtcaa ggattacttc ccggagcccg tgaccgtgtc ctggaacagc 480

ggagccctga cctccggagt gcacaccttc cccgctgtgc tgcagagctc cgggctgtac 540

tcgctgtcgt cggtggtcac ggtgccttca tctagcctgg gtaccaagac ctacacttgc 600

aacgtggacc acaagccttc caacactaag gtggacaagc gcgtcgaatc gaagtacggc 660

ccaccgtgcc cgccttgtcc cgcgccggag ttcctcggcg gtccctcggt ctttctgttc 720

ccaccgaagc ccaaggacac tttgatgatt tcccgcaccc ctgaagtgac atgcgtggtc 780

gtggacgtgt cacaggaaga tccggaggtg cagttcaatt ggtacgtgga tggcgtcgag 840

gtgcacaacg ccaaaaccaa gccgagggag gagcagttca actccactta ccgcgtcgtg 900

tccgtgctga cggtgctgca tcaggactgg ctgaacggga aggagtacaa gtgcaaagtg 960

tccaacaagg gacttcctag ctcaatcgaa aagaccatct cgaaagccaa gggacagccc 1020

cgggaacccc aagtgtatac cctgccaccg agccaggaag aaatgactaa gaaccaagtc 1080

tcattgactt gccttgtgaa gggcttctac ccatcggata tcgccgtgga atgggagtcc 1140

aacggccagc cggaaaacaa ctacaagacc acccctccgg tgctggactc agacggatcc 1200

ttcttcctct actcgcggct gaccgtggat aagagcagat ggcaggaggg aaatgtgttc 1260

agctgttctg tgatgcatga agccctgcac aaccactaca ctcagaagtc cctgtccctc 1320

tccctggga 1329

<210> 97
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 97
gagatcgtcc tgactcagtc acccgctacc ctgagcctga gccctggcga gcgggctaca 60

ctgagctgta aatctagtca gtcactgctg gatagcggta atcagaagaa cttcctgacc 120

tggtatcagc agaagcccgg taaagcccct aagctgctga tctactgggc ctctactaga 180

gaatcaggcg tgccctctag gtttagcggt agcggtagtg gcaccgactt caccttcact 240

atctctagcc tgcagcccga ggatatcgct acctactact gtcagaacga ctatagctac 300

ccctacacct tcggtcaagg cactaaggtc gagattaag 339

<210> 98
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 98
gagatcgtcc tgactcagtc acccgctacc ctgagcctga gccctggcga gcgggctaca 60

ctgagctgta aatctagtca gtcactgctg gatagcggta atcagaagaa cttcctgacc 120

tggtatcagc agaagcccgg taaagcccct aagctgctga tctactgggc ctctactaga 180

gaatcaggcg tgccctctag gtttagcggt agcggtagtg gcaccgactt caccttcact 240

atctctagcc tgcagcccga ggatatcgct acctactact gtcagaacga ctatagctac 300

ccctacacct tcggtcaagg cactaaggtc gagattaagc gtacggtggc cgctcccagc 360

gtgttcatct tccccccag cgacgagcag ctgaagagcg gcaccgccag cgtggtgtgc 420

ctgctgaaca acttctaccc ccgggaggcc aaggtgcagt ggaaggtgga caacgccctg 480

cagagcggca acagccagga gagcgtcacc gagcaggaca gcaaggactc cacctacagc 540

ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcataaggt gtacgcctgc 600

gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaacag gggcgagtgc 660

<210> 99
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 99
gagatcgtgc tgacccagtc ccccgacttc cagtccgtga cccccaaaga aaaagtgacc 60

atcacatgca agtcctccca gtccctgctg gactccggca accagaagaa cttcctgacc 120

tggtatcagc agaagcccgg ccaggccccc agactgctga tctactgggc ctccacccgg 180

gaatctggcg tgccctctag attctccggc tccggctctg gcaccgactt taccttcacc 240

atctccagcc tggaagccga ggacgccgcc acctactact gccagaacga ctactcctac 300

ccctacacct tcggccaggg caccaaggtg gaaatcaag 339

<210> 100
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 100
gagatcgtgc tgacccagtc ccccgacttc cagtccgtga cccccaaaga aaaagtgacc 60

atcacatgca agtcctccca gtccctgctg gactccggca accagaagaa cttcctgacc 120

tggtatcagc agaagcccgg ccaggccccc agactgctga tctactgggc ctccacccgg 180

gaatctggcg tgccctctag attctccggc tccggctctg gcaccgactt taccttcacc 240

atctccagcc tggaagccga ggacgccgcc acctactact gccagaacga ctactcctac 300

ccctacacct tcggccaggg caccaaggtg gaaatcaagc gtacggtggc cgctcccagc 360

gtgttcatct tccccccaag cgacgagcag ctgaagagcg gcaccgccag cgtggtgtgt 420

ctgctgaaca acttctaccc cagggaggcc aaggtgcagt ggaaggtgga caacgccctg 480

cagagcggca acagccagga gagcgtcacc gagcaggaca gcaaggactc cacctacagc 540

ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgt 600

gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaacag gggcgagtgc 660

<210> 101
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 101
gaagtgcagc tggtgcagtc tggcgccgaa gtgaagaagc ctggcgagtc cctgcggatc 60

tcctgcaagg gctctggcta caccttcacc acctactgga tgcactggat ccggcagtcc 120

ccctctaggg gcctggaatg gctgggcaac atctaccctg gcaccggcgg ctccaacttc 180

gacgagaagt tcaagaacag gttcaccatc tcccgggaca actccaagaa caccctgtac 240

ctgcagatga actccctgcg ggccgaggac accgccgtgt actactgtac cagatggacc 300

accggaaccg gcgcctattg gggccagggc acaacagtga ccgtgtcctc c 351

<210> 102
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 102
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30

Trp Met His Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
35 40 45

Gly Asn Ile Tyr Pro Gly Thr Gly Gly Ser Asn Phe Asp Glu Lys Phe
50 55 60

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

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

Thr Arg Trp Thr Thr Gly Thr Gly Ala Tyr Trp Gly Gln Gly Thr Thr
            100                 105                 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

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

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

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

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
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325 330 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
340 345 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385 390 395 400

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
435 440

<210> 103
<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 103
gaagtgcagc tggtgcagtc tggcgccgaa gtgaagaagc ctggcgagtc cctgcggatc 60

tcctgcaagg gctctggcta caccttcacc acctactgga tgcactggat ccggcagtcc 120

ccctctaggg gcctggaatg gctgggcaac atctaccctg gcaccggcgg ctccaacttc 180

gacgagaagt tcaagaacag gttcaccatc tcccgggaca actccaagaa caccctgtac 240

ctgcagatga actccctgcg ggccgaggac accgccgtgt actactgtac cagatggacc 300

accggaaccg gcgcctattg gggccagggc acaacagtga ccgtgtcctc cgcttctacc 360

aaggggccca gcgtgttccc cctggccccc tgctccagaa gcaccagcga gagcacagcc 420

gccctgggct gcctggtgaa ggactacttc cccgagcccg tgaccgtgtc ctggaacagc 480

ggagccctga ccagcggcgt gcacaccttc cccgccgtgc tgcagagcag cggcctgtac 540

agcctgagca gcgtggtgac cgtgcccagc agcagcctgg gcaccaagac ctacacctgt 600

aacgtggacc acaagcccag caacaccaag gtggacaaga gggtggagag caagtacggc 660

ccaccctgcc ccccctgccc agcccccgag ttcctgggcg gacccagcgt gttcctgttc 720

cccccccaagc ccaaggacac cctgatgatc agcagaaccc ccgaggtgac ctgtgtggtg 780

gtggacgtgt cccaggagga ccccgaggtc cagttcaact ggtacgtgga cggcgtggag 840

gtgcacaacg ccaagaccaa gcccagagag gagcagttta acagcaccta ccgggtggtg 900

tccgtgctga ccgtgctgca ccaggactgg ctgaacggca aagagtacaa gtgtaaggtc 960

tccaacaagg gcctgccaag cagcatcgaa aagaccatca gcaaggccaa gggccagcct 1020

agagagcccc aggtctacac cctgccaccc agccaagagg agatgaccaa gaaccaggtg 1080

tccctgacct gtctggtgaa gggcttctac ccaagcgaca tcgccgtgga gtgggagagc 1140

aacggccagc ccgagaacaa ctacaagacc acccccccag tgctggacag cgacggcagc 1200

ttcttcctgt acagcaggct gaccgtggac aagtccagat ggcaggaggg caacgtcttt 1260

agctgctccg tgatgcacga ggccctgcac aaccactaca cccagaagag cctgagcctg 1320

tccctgggc 1329

<210> 104
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 104
gagatcgtgc tgacccagtc ccctgccacc ctgtcactgt ctccaggcga gagagctacc 60

ctgtcctgca agtcctccca gtccctgctg gactccggca accagaagaa cttcctgacc 120

tggtatcagc agaagcccgg ccaggccccc agactgctga tctactgggc ctccacccgg 180

gaatctggcg tgccctctag attctccggc tccggctctg gcaccgactt taccttcacc 240

atctccagcc tggaagccga ggacgccgcc acctactact gccagaacga ctactcctac 300

ccctacacct tcggccaggg caccaaggtg gaaatcaag 339

<210> 105
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 105
gagatcgtgc tgacccagtc ccctgccacc ctgtcactgt ctccaggcga gagagctacc 60

ctgtcctgca agtcctccca gtccctgctg gactccggca accagaagaa cttcctgacc 120

tggtatcagc agaagcccgg ccaggccccc agactgctga tctactgggc ctccacccgg 180

gaatctggcg tgccctctag attctccggc tccggctctg gcaccgactt taccttcacc 240

atctccagcc tggaagccga ggacgccgcc acctactact gccagaacga ctactcctac 300

ccctacacct tcggccaggg caccaaggtg gaaatcaagc gtacggtggc cgctcccagc 360

gtgttcatct tccccccaag cgacgagcag ctgaagagcg gcaccgccag cgtggtgtgt 420

ctgctgaaca acttctaccc cagggaggcc aaggtgcagt ggaaggtgga caacgccctg 480

cagagcggca acagccagga gagcgtcacc gagcaggaca gcaaggactc cacctacagc 540

ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgt 600

gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaacag gggcgagtgc 660

<210> 106
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 106
gagatcgtcc tgactcagtc acccgctacc ctgagcctga gccctggcga gcgggctaca 60

ctgagctgta aatctagtca gtcactgctg gatagcggta atcagaagaa cttcctgacc 120

tggtatcagc agaagcccgg tcaagcccct agactgctga tctactgggc ctctactaga 180

gaatcaggcg tgccctctag gtttagcggt agcggtagtg gcaccgactt caccttcact 240

atctctagcc tggaagccga ggacgccgct acctactact gtcagaacga ctatagctac 300

ccctacacct tcggtcaagg cactaaggtc gagattaag 339

<210> 107
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 107
gagatcgtcc tgactcagtc acccgctacc ctgagcctga gccctggcga gcgggctaca 60

ctgagctgta aatctagtca gtcactgctg gatagcggta atcagaagaa cttcctgacc 120

tggtatcagc agaagcccgg tcaagcccct agactgctga tctactgggc ctctactaga 180

gaatcaggcg tgccctctag gtttagcggt agcggtagtg gcaccgactt caccttcact 240

atctctagcc tggaagccga ggacgccgct acctactact gtcagaacga ctatagctac 300

ccctacacct tcggtcaagg cactaaggtc gagattaagc gtacggtggc cgctcccagc 360

gtgttcatct tccccccag cgacgagcag ctgaagagcg gcaccgccag cgtggtgtgc 420

ctgctgaaca acttctaccc ccgggaggcc aaggtgcagt ggaaggtgga caacgccctg 480

cagagcggca acagccagga gagcgtcacc gagcaggaca gcaaggactc cacctacagc 540

ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcataaggt gtacgcctgc 600

gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaacag gggcgagtgc 660

<210> 108
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 108
acttactgga tgcac 15

<210> 109
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 109
aatatttatc ctggtactgg tggttctaac ttcgatgaga agttcaagaa c 51

<210> 110
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 110
tggactactg ggacgggagc ttat 24

<210> 111
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 111
ggctacacat tcaccactta c 21

<210> 112
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 112
tatcctggta ctggtggt 18

<210> 113
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 113
aagtccagtc agagtctgtt agacagtgga aatcaaaaga acttcttgac c 51

<210> 114
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 114
tgggcatcca ctagggaatc t 21

<210> 115
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 115
cagaatgatt atagttatcc gtgcacg 27

<210> 116
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 116
agtcagagtc tgttagacag tggaaatcaa aagaacttc 39

<210> 117
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 117
tgggcatcc 9

<210> 118
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 118
gattatagtt atccgtgc 18

<210> 119
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 119
cagaatgatt atagttatcc gtacacg 27

<210> 120
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 120
gattatagtt atccgtac 18

<210> 121
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 121
aagtccagtc agagtctgtt agacagtgga aatcaaaaga acttcttaac c 51

<210> 122
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 122
acctactgga tgcac 15

<210> 123
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 123
aacatctatc ctggcaccgg cggctccaac ttcgacgaga agttcaagaa c 51

<210> 124
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 124
tggacaaccg gcacaggcgc ttat 24

<210> 125
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 125
ggctacacct tcaccaccta c 21

<210> 126
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 126
tatcctggca ccggcggc 18

<210> 127
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 127
aagtcctccc agtccctgct ggactccggc aaccagaaga acttcctgac c 51

<210> 128
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 128
tgggcctcca cccgggaatc t 21

<210> 129
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 129
cagaacgact actcctaccc ctacacc 27

<210> 130
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 130
tcccagtccc tgctggactc cggcaaccag aagaacttc 39

<210> 131
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 131
tgggcctcc 9

<210> 132
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 132
gactactcct acccctac 18

<210> 133
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 133
acctactgga tgcac 15

<210> 134
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 134
aatatctacc ccggcaccgg cggctctaac ttcgacgaga agtttaagaa t 51

<210> 135
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 135
tggactaccg gcacaggcgc ctac 24

<210> 136
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 136
ggctacacct tcactaccta c 21

<210> 137
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 137
taccccggca ccggcggc 18

<210> 138
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 138
aaatctagtc agtcactgct ggatagcggt aatcagaaga acttcctgac c 51

<210> 139
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 139
tgggcctcta ctagagaatc a 21

<210> 140
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 140
cagaacgact atagctaccc ctacacc 27

<210> 141
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 141
agtcagtcac tgctggatag cggtaatcag aagaacttc 39

<210> 142
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 142
tgggcctct 9

<210> 143
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 143
gactatagct acccctac 18

<210> 144
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 144
aacatctacc ctggcaccgg cggctccaac ttcgacgaga agttcaagaa c 51

<210> 145
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 145
tggaccaccg gaaccggcgc ctat 24

<210> 146
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 146
taccctggca ccggcggc 18

<210> 147
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 147
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Arg Ile Ser Cys Lys Gly Ser
20 25

<210> 148
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 148
gaagtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaggatc 60

tcctgtaagg gttct 75

<210> 149
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 149
gaagtgcagc tggtgcagtc tggcgccgaa gtgaagaagc ctggcgagtc cctgcggatc 60

tcctgcaagg gctct 75

<210> 150
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 150
gaggtgcagc tggtgcagtc aggcgccgaa gtgaagaagc ccggcgagtc actgagaatt 60

agctgtaaag gttca 75

<210> 151

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

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 151
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 152
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 152
caggttcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttct 75

<210> 153
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 153
Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met Gly
1 5 10

<210> 154
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 154
tgggtgcgac aggccactgg acaagggctt gagtggatgg gt 42

<210> 155
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 155
tgggtgcgac aggctaccgg ccagggcctg gaatggatgg gc 42

<210> 156
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 156
tgggtccgcc aggctaccgg tcaaggcctc gagtggatgg gt 42

<210> 157
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 157
Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu Gly
1 5 10

<210> 158
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 158
tggatcaggc agtccccatc gagaggcctt gagtggctgg gt 42

<210> 159
<211> 42
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 159
tggatccggc agtccccctc taggggcctg gaatggctgg gc 42

<210> 160
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 160
Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 5 10

<210> 161
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 161
tgggtgcgac aggcccctgg acaagggctt gagtggatgg gt 42

<210> 162
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 162
Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Thr Arg
20 25 30

<210> 163
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 163
agagtcacga ttaccgcgga caaatccacg agcacagcct acatggagct gagcagcctg 60

agatctgagg acacggccgt gtattactgt acaaga 96

<210> 164
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 164
agagtgacca tcaccgccga caagtccacc tccaccgcct acatggaact gtcctccctg 60

agatccgagg acaccgccgt gtactactgc acccgg 96

<210> 165
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 165
agagtgacta tcaccgccga taagtctact agcaccgcct atatggaact gtctagcctg 60

agatcagagg acaccgccgt ctactactgc actagg 96

<210> 166
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 166
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Arg
20 25 30

<210> 167
<211> 96
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 167
agattcacca tctccagaga caattccaag aacacgctgt atcttcaaat gaacagcctg 60

agagccgagg acacggccgt gtattactgt acaaga 96

<210> 168
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 168
aggttcacca tctcccggga caactccaag aacaccctgt acctgcagat gaactccctg 60

cgggccgagg acaccgccgt gtactactgt accaga 96

<210> 169
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 169
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 170
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 170
tggggccagg gcaccaccgt gaccgtgtcc tcc 33

<210> 171
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 171
tggggccagg gcaccacagt gaccgtgtcc tct 33

<210> 172
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 172
tggggtcaag gcactaccgt gaccgtgtct agc 33

<210> 173
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 173
tggggccagg gcacaacagt gaccgtgtcc tcc 33

<210> 174
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 174
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1 5 10 15

Glu Lys Val Thr Ile Thr Cys
20

<210> 175
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 175
gaaattgtgc tgactcagtc tccagacttt cagtctgtga ctccaaagga gaaagtcacc 60

atcacctgc 69

<210> 176
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 176
gagatcgtgc tgacccagtc ccccgacttc cagtccgtga cccccaaaga aaaagtgacc 60

atcacatgc 69

<210> 177
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 177
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys
20

<210> 178
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 178
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgc 69

<210> 179
<211> 69
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 179
gagatcgtgc tgacccagtc ccctgccacc ctgtcactgt ctccaggcga gagagctacc 60

ctgtcctgc 69

<210> 180
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 180
gagatcgtcc tgactcagtc acccgctacc ctgagcctga gccctggcga gcgggctaca 60

ctgagctgt 69

<210> 181
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 181
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys
20

<210> 182
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 182
gatattgtga tgacccagac tccactctcc ctgcccgtca cccctggaga gccggcctcc 60

atctcctgc 69

<210> 183
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 183
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys
20

<210> 184
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 184
gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc 60

atctcctgc 69

<210> 185
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 185
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys
20

<210> 186
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

oligonucleotide"

<400> 186
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgc 69

<210> 187
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 187
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 188
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 188
tggtaccagc agaaacctgg ccaggctccc aggctcctca tctat 45

<210> 189
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 189
tggtatcagc agaagcccgg ccaggccccc agactgctga tctac 45

<210> 190
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 190
tggtatcagc agaagcccgg tcaagcccct agactgctga tctac 45

<210> 191
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 191
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 192
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 192
tggtatcagc agaaaccagg gaaagctcct aagctcctga tctat 45

<210> 193
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 193
tggtatcagc agaagcccgg taaagcccct aagctgctga tctac 45

<210> 194
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 194
Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr
1 5 10 15

<210> 195
<211> 45
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 195
tggtacctgc agaagccagg gcagtctcca cagctcctga tctat 45

<210> 196
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 196
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Phe Thr Ile Ser Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
20 25 30

<210> 197
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 197
ggggtcccct cgaggttcag tggcagtgga tctgggacag atttcacctt taccatcagt 60

agcctggaag ctgaagatgc tgcaacatat tactgt 96

<210> 198
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 198
ggcgtgccct ctagattctc cggctccggc tctggcaccg actttacctt caccatctcc 60

agcctggaag ccgaggacgc cgccacctac tactgc 96

<210> 199

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

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 199
ggcgtgccct ctaggtttag cggtagcggt agtggcaccg acttcacctt cactatctct 60

agcctggaag ccgaggacgc cgctacctac tactgt 96

<210> 200
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 200
Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Asn Asn Ile Glu Ser Glu Asp Ala Ala Tyr Tyr Phe Cys
20 25 30

<210> 201
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 201
gggatcccac ctcgattcag tggcagcggg tatggaacag attttaccct cacaattaat 60

aacatagaat ctgaggatgc tgcatattac ttctgt 96

<210> 202
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 202
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
20 25 30

<210> 203
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 203
ggggtcccat caaggttcag cggcagtgga tctgggacag aattcactct caccatcagc 60

agcctgcagc ctgatgattt tgcaacttat tactgt 96

<210> 204
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 204
ggcgtgccct ctagattctc cggctccggc tctggcaccg agtttaccct gaccatctcc 60

agcctgcagc ccgacgactt cgccacctac tactgc 96

<210> 205
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 205
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys
20 25 30

<210> 206
<211> 96
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 206
ggggtcccat caaggttcag tggaagtgga tctgggacag attttacttt caccatcagc 60

agcctgcagc ctgaagatat tgcaacatat tactgt 96

<210> 207
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 207
ggcgtgccct ctaggtttag cggtagcggt agtggcaccg acttcacctt cactatctct 60

agcctgcagc ccgaggatat cgctacctac tactgt 96

<210> 208
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 208
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 209
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 209
ttcggccaag ggaccaaggt ggaaatcaaa 30

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

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

oligonucleotide"

<400> 210
ttcggccagg gcaccaaggt ggaaatcaag 30

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

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 211
ttcggtcaag gcactaaggt cgagattaag 30

<210> 212
<211> 327
<212> PRT
<213> Homo sapiens

<400> 212
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15

Ser Thr Ser Glu Ser 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 Lys Thr
65 70 75 80

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

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

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

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

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp

145 150 155 160

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Leu Gly Lys
325

<210> 213
<211> 107
<212> PRT
<213> Homo sapiens

<400> 213
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> 214
<211> 326
<212> PRT
<213> Homo sapiens

<400> 214

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

Ser Thr Ser Glu Ser 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 Lys Thr
65                  70                  75                  80

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

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

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

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

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145                 150                 155                 160
```

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Leu Gly
                325
```

<210> 215
<211> 330
<212> PRT
<213> Homo sapiens

<400> 215

```
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 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 Lys
325 330

<210> 216
<211> 330
<212> PRT
<213> Homo sapiens

<400> 216
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 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 Lys
                325                 330
```

<210> 217
<211> 330
<212> PRT
<213> Homo sapiens

<400> 217

```
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 Ala 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 Ala 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 Lys
325 330

<210> 218
<211> 330
<212> PRT
<213> Homo sapiens

<400> 218

```
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 Ala Ala 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 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 Lys
325 330

<210> 219
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 219
Met Glu Trp Ser Trp Val Phe Leu Phe Phe Leu Ser Val Thr Thr Gly
1 5 10 15

Val His Ser

<210> 220
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 220
Met Ser Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr
1 5 10 15

Asp Ala Arg Cys
20

<210> 221
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 221
Met Ala Trp Val Trp Thr Leu Pro Phe Leu Met Ala Ala Ala Gln Ser
1 5 10 15

Val Gln Ala

<210> 222
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 222
Met Ser Val Leu Thr Gln Val Leu Ala Leu Leu Leu Leu Trp Leu Thr
1 5 10 15

Gly Thr Arg Cys
20

<210> 223
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 223
tggactactg ggacgggagc ttac 24

<210> 224
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 224
Gly Tyr Thr Phe Thr Thr Tyr Trp Met His
1 5 10

<210> 225

<400> 225
000

<210> 226

<400> 226
000

<210> 227

<400> 227
000

<210> 228
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 228
Gln Val Gln Leu Gln Gln Pro Gly Ser Glu Leu Val Arg Pro Gly Ala
1 5 10 15

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

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

Gly Asn Ile Tyr Pro Gly Thr Gly Gly Ser Asn Phe Asp Glu Lys Phe
50 55 60

Lys Asn Arg Thr Ser Leu Thr Val Asp Thr Ser Ser Thr Thr Ala Tyr
65 70 75 80

Met His Leu Ala Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Trp Thr Thr Gly Thr Gly Ala Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ala Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu
115 120 125

Ala Pro Gly Ser Ala Ala
130

<210> 229
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 229
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Gly Asn Gln Lys Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Phe Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Val Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Cys Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105 110

Lys Arg Ala Asp
115

<210> 230
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 230
Gln Val Gln Leu Gln Gln Pro Gly Ser Glu Leu Val Arg Pro Gly Ala

1 5 10 15

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

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

Gly Asn Ile Tyr Pro Gly Ser Gly Ser Thr Asn Tyr Asp Glu Lys Phe
50 55 60

Lys Ser Lys Gly Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg

<210> 231
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 231
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro

100

<210> 232
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<220>
<221> CDS
<222> (2)..(37)

<400> 232
g tgc acg ttc gga ggg ggg acc aag ctg gaa ata aaa 37
Cys Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 233
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 233
Cys Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 234
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<220>
<221> CDS
<222> (2)..(37)

<400> 234
g tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa c 38
Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 235
<211> 12
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 235
Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
1 5 10