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(54) Title: COMPOSITIONS AND METHODS FOR ANTIBODIES TARGETING STAPHYLOCOCCAL LEUKOTOXINS

(57) Abstract: The disclosure is directed to antibodies that bind to *Staphylococcus aureus* bi-component leukotoxins and/or gamma-hemolysins. Other aspects of the disclosure are directed to pharmaceutical compositions and diagnostic kits containing the leukotoxin and hemolysin antibodies, and therapeutic and diagnostic methods utilizing the leukotoxin and hemolysin antibodies.

COMPOSITIONS AND METHODS FOR ANTIBODIES TARGETING STAPHYLOCOCCAL LEUKOTOXINS

[0001] This application claims the priority benefit of U.S. Provisional Patent Application Serial No. 62/340,019, filed on May 23, 2016, which is hereby incorporated by reference in its entirety.

FIELD OF THE INVENTION

[0002] The present invention relates to *Staphylococcus aureus* leukotoxin antibodies, gamma-hemolysin antibodies, and compositions containing the same. Also disclosed are therapeutic and diagnostic methods using the leukotoxin and gamma hemolysin antibodies.

BACKGROUND

[0003] Bacterial infections caused by staphylococcus bacteria (i.e., a "staph infection") are very common in the general population. About 25% of individuals commonly carry staphylococcus bacteria on their skin or in their nose. Most of the time, these bacteria do not cause a problem or may cause a relatively minor skin infection. However, staph infections can turn deadly if the bacteria invade deeper into an individual's body, for example, entering the bloodstream, joints, bones, lungs or heart. In the past, a lethal staph infection might have occurred in a person who was hospitalized or had a chronic illness or weakened immune system. Now, it is increasingly common for an otherwise healthy individual to develop life-threatening staph infections. Importantly, many staph infections have become antibiotic resistant.

[0004] *Staphylococcus aureus,* often referred to as "staph," Staph. aureus," or "S. aureus," is a major human pathogen, producing a multitude of virulence factors making it able to cause several types of infection, from superficial lesions to toxinoses and life-threatening systemic conditions such as endocarditis, osteomyelitis, pneumonia, meningitis and sepsis (reviewed in Miller and Cho, "Immunity Against Staphylococcus aureus Cutaneous Infections," *Nat. Rev. Immunol.* 11:505-518 (2011)). Although most individuals encounter *S. aureus* shortly after birth (Holtfreter et al., "Towards the Immune Proteome of Staphylococcus aureus - The Anti-S. aureus Antibody Response," *Int. J. Med. Microbiol.* 300:176-192 (2010)) and possess both antibodies against *S. aureus* and the ability to increase anti-*S. aureus* titers after infection, these antibodies are often not protective against recurrent *S. aureus* infections (Foster TJ, "Immune Evasion by Staphylococci," *Nat. Rev. Microbiol.* 3:948-958 (2005)). In the United States alone, an annual mortality of more than 20,000 is attributed to methicillin-resistant *S. aureus* (MRSA), exceeding deaths caused by influenza, viral hepatitis, and HIV/AIDS (Foster,

TJ., "Immune Evasion by Staphylococci," *Nat. Rev. Microbiol.* 3:948-958 (2005); Klevens et al., "The Impact of Antimicrobial-Resistant, Health Care-Associated Infections on Mortality in the United States," *Clin. Infect. Dis.* 47:927-930 (2008)).

[0005] The pathogen produces a variety of molecules that presumably facilitate survival in or on the human host. Bi-component, pore-forming leukotoxins and gamma hemolysins are among the secreted virulence factors produced by *S. aureus*. These toxins are secreted as water soluble monomers which oligomerize, and insert pores into the plasma membrane of host cells, most notably polymorphonuclear leukocytes (PMNs) and mononuclear phagocytes (Alonzo F. and Torres V., "Staphylococcus aureus Bi-component leukotoxins," *Microbiol. Mol. Biol. Rev.* 78(2): 199-230 (2014)). These pores disrupt cellular osmotic balance and membrane potential leading to death of the targeted cells. In the case of Leukotoxin ED (LukED), the targeting, binding, and killing of host phagocytic cells occurs via the cellular target CCR5, CXCR1 and CXCR2 located on the surface of the phagocytes (Alonzo III et al., "Staphylococcus aureus Leucocidin ED Contributes to Systemic Infection by Targeting Neutrophils and Promoting Bacterial Growth In Vivo," *Mol. Microbiol.* 83:423-435 (2012); Alonzo III et al. "CCR5 is a Receptor for Staphylococcus aureus Leukotoxin ED," Nature 493(7430)51-55 (2012); and Reyes-Robles et al., "Staphylococcus aureus Leukotoxin ED Targets the Chemokine Receptors CXCR1 and CXCR2 to Kill Leukocytes and Promote Infection," *Cell Host & Microbe* 14:453-459 (2013)). Indeed, when the cellular target of LukED, CCR5, is not present on host immune cells, the host animal is resistant to the otherwise lethal *S. aureus* infection (Alonzo III et al. "CCR5 is a Receptor for Staphylococcus aureus Leukotoxin ED," *Nature* 493(7430):51-55 (2012)). Leukotoxin AB (LukAB) can also kill host phagocytic cells, and its cytolytic activity can be exerted both from the outside and the inside of the cell, *i.e.*, after the microorganism is phagocytosed into the host cell (Dumont et al., "Staphylococcus aureus LukAB Cytotoxin Kills Human Neutrophils by Targeting the CD11b Subunit of the Integrin Mac-1," *PNAS* 110(26):10794-10799 (2013)). Due to the contribution that both of these leukotoxins as well as related bi-component toxins have to pathogenesis, they have been considered critical *S. aureus* virulence factors and targets for therapeutic intervention (Alonzo III and Torres, "Bacterial Survival Amidst an Immune Onslaught: The Contribution of the Staphylococcus aureus Leukotoxins," *PLOS Path* 9(2):e1003143 (2013)). However, antibody compositions suitable for therapeutic and/or diagnostic applications are currently not available.

[0006] The present invention is directed to overcoming these and other deficiencies in the art.

SUMMARY

[0007] One aspect of the present disclosure relates to antibodies or binding portions thereof that bind *Staphylococcus aureus* Leukocidin AB (LukAB). A LukAB antibody or binding portion thereof as described herein comprises a heavy chain variable region that comprises: a complementarity-determining region 1 (CDR-H1) comprising an amino acid sequence of any one of SEQ ID NOs: 1-20, or a modified amino acid sequence of any one of SEQ ID NOs: 1-20, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 1-20; a complementarity-determining region 2 (CDR-H2) comprising an amino acid sequence of any one of SEQ ID NOs: 21-41, or a modified amino acid sequence of any one of SEQ ID NOs: 21-41, said modified sequences having at least 80% sequence identity to any one of SEQ ID NOs: 21-41; and a complementarity-determining region 3 (CDR-H3) comprising an amino acid sequence of any one of SEQ ID NOs: 42-62, or a modified amino acid sequence of any one of SEQ ID NO:42-62, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 42-62.

[0008] Another aspect of the present disclosure relates to an antibody or binding portion thereof that competes for leukocidin AB binding with a monoclonal antibody, wherein said monoclonal antibody comprises a heavy chain variable region comprising a CDR-H1 of SEQ ID NO: 11, a CDR-H2 of SEQ ID NO: 31, and a CDR-H3 of SEQ ID NO: 53, and a light chain variable region comprising a CDR-L1 of SEQ ID NO: 66, a CDR-L2 of SEQ ID NO: 92, and a CDR-L3 of SEQ ID NO: 117.

[0009] Another aspect of the present disclosure relates to antibodies or binding portions thereof that bind *Staphylococcus aureus* Leukocidin E (LukE). A LukE antibody or binding portion thereof as described herein comprises a heavy chain variable region that comprises: a complementarity-determining region 1 (CDR-H1) comprising an amino acid sequence of any one of SEQ ID NOs: 287-291, or a modified amino acid sequence of any one of SEQ ID NOs: 287-291, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 287-291; a complementarity-determining region 2 (CDR-H2) comprising an amino acid sequence of any one of SEQ ID NOs: 292-296, or a modified amino acid sequence of any one of SEQ ID NOs: 292-296, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 292-296; and a complementarity-determining region 3 (CDR-H3) comprising an amino acid sequence of any one of SEQ ID NOs: 297-302, or a modified amino acid sequence of any one of SEQ ID NO: 297-302 said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 297-302.

[0010] Another aspect of the present disclosure is directed to an antibody or binding portion thereof that competes for leukocidin E binding with a monoclonal antibody, wherein said monoclonal antibody comprises a heavy chain variable region comprising a CDR-H1 of SEQ ID NO: 290, a CDR-H2 of SEQ ID NO: 295, and a CDR-H3 of SEQ ID NO: 301, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 308, the CDR-L2 of SEQ ID NO: 311, and the CDR-L3 of SEQ ID NO: 321.

[0011] Another aspect of the present disclosure relates to antibodies or binding portions thereof that bind *Staphylococcus aureus* Leukocidin D (LukD). A LukD antibody or binding portion thereof of the present disclosure comprises a heavy chain variable region that comprises: a complementarity-determining region 1 (CDR-H1) comprising an amino acid sequence of any one of SEQ ID NOs: 372-374, or a modified amino acid sequence of any one of SEQ ID NOs: 372-374, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 372-374; a complementarity-determining region 2 (CDR-H2) comprising an amino acid sequence of any one of SEQ ID NOs: 375-379, or a modified amino acid sequence of any one of SEQ ID NOs: 375-379, said modified sequences having at least 80% sequence identity to any one of SEQ ID NOs: 375-379; and a complementarity-determining region 3 (CDR-H3) comprising an amino acid sequence of any one of SEQ ID NOs: 380-383, or a modified amino acid sequence of any one of SEQ ID NO: 380-383, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 380-383.

[0012] Another aspect of the present disclosure relates to an antibody or binding portion thereof that competes for leukocidin D binding with a monoclonal antibody, where the monoclonal antibody comprises: (i) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 373, the CDR-H2 of SEQ ID NO: 378, and the CDR-H3 of SEQ ID NO: 382, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 387, the CDR-L2 of SEQ ID NO: 390, and the CDR-L3 of SEQ ID NO: 395; (ii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 372, the CDR-H2 of SEQ ID NO: 375, and the CDR-H3 of SEQ ID NO: 380, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 386, the CDR-L2 of SEQ ID NO: 388, and the CDR-L3 of SEQ ID NO: 396; (iii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 374, the CDR-H2 of SEQ ID NO: 379, and the CDR-H3 of SEQ ID NO: 383, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 386, the CDR-L2 of SEQ ID NO: 391, and the CDR-L3 of SEQ ID NO: 397; or (iv) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 372, the CDR-H2 of SEQ ID NO: 375, and the CDR-H3 of SEQ ID NO: 380, and a light chain variable region comprising

the CDR-L1 of SEQ ID NO: 386, the CDR-L2 of SEQ ID NO: 388, and the CDR-L3 of SEQ ID NO: 392

[0013] Another aspect of the present disclosure is directed to antibodies or binding portions thereof that bind *Staphylococcus aureus* gamma-hemolysin A (HlgA). A HlgA antibody or binding portion thereof as described herein comprises a heavy chain variable region that comprises: a complementarity-determining region 1 (CDR-H1) comprising an amino acid sequence of any one of SEQ ID NOs: 430-432, or a modified amino acid sequence of any one of SEQ ID NOs: 430-432, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 430-432; a complementarity-determining region 2 (CDR-H2) comprising an amino acid sequence of any one of SEQ ID NOs: 433-435, or a modified amino acid sequence of any one of SEQ ID NOs: 433-435, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 433-435; and a complementarity-determining region 3 (CDR-H3) comprising an amino acid sequence of any one of SEQ ID NOs: 436-438, or a modified amino acid sequence of any one of SEQ ID NO: 436-438, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 436-438.

[0014] Another aspect of the present disclosure relates to an antibody or binding portion thereof that competes for HlgA binding to a monoclonal antibody, wherein the monoclonal antibody comprises: a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 432, the CDR-H2 of SEQ ID NO: 435, and the CDR-H3 of SEQ ID NO: 438 and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 439, the CDR-L2 of SEQ ID NO: 441, and the CDR-L3 of SEQ ID NO: 444.

[0015] Another aspect of the present disclosure is directed to antibodies or binding portions thereof that bind *Staphylococcus aureus* gamma-hemolysin C (HlgC). A HlgC antibody or binding portion thereof of the present disclosure comprises a heavy chain variable region that comprises: a complementarity-determining region 1 (CDR-H1) comprising an amino acid sequence of SEQ ID NO: 470, or a modified amino acid sequence of SEQ ID NO: 470, said modified sequence having at least 80% sequence identity to SEQ ID NO: 470; a complementarity-determining region 2 (CDR-H2) comprising an amino acid sequence of SEQ ID NO: 471, or a modified amino acid sequence of SEQ ID NO: 471, said modified sequence having at least 80% sequence identity to SEQ ID NO: 471; and a complementarity-determining region 3 (CDR-H3) comprising an amino acid sequence of SEQ ID NO: 472, or a modified amino acid sequence of SEQ ID NO: 472, said modified sequence having at least 80% sequence identity to SEQ ID NO: 472.

[0016] Another aspect of the present disclosure is directed to an antibody or binding portion thereof that competes for HlgC binding to a monoclonal antibody, where the monoclonal antibody comprises: a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 470, the CDR-H2 of SEQ ID NO: 471, and the CDR-H3 of SEQ ID NO: 472 and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 474, the CDR-L2 of SEQ ID NO: 479, and the CDR-L3 of SEQ ID NO: 484.

[0017] Another aspect of the present disclosure relates to antibodies or binding portions thereof that bind *Staphylococcus aureus* LukE and/or HlgA. A LukE and/or HlgA antibody or binding portion thereof of the present disclosure comprises a heavy chain variable region that comprises: a complementarity-determining region 1 (CDR-H1) comprising an amino acid sequence of any one of SEQ ID NOs: 513-529, or a modified amino acid sequence of any one of SEQ ID NOs: 513-529, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 513-529; a complementarity-determining region 2 (CDR-H2) comprising an amino acid sequence of any one of SEQ ID NOs: 530-548, or a modified amino acid sequence of any one of SEQ ID NOs: 530-548, said modified sequences having at least 80% sequence identity to any one of SEQ ID NOs: 530-548; and a complementarity-determining region 3 (CDR-H3) comprising an amino acid sequence of any one of SEQ ID NOs: 549-568, or a modified amino acid sequence of any one of SEQ ID NO: 549-568, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 549-568.

[0018] Another aspect of the present disclosure relates to an antibody or binding portion thereof that competes for LukE and/or HlgA binding with a monoclonal antibody, where the monoclonal antibody comprises: (i) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 519, the CDR-H2 of SEQ ID NO: 537, and the CDR-H3 of SEQ ID NO: 556, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 576, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 629; (ii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 521, the CDR-H2 of SEQ ID NO: 539, and the CDR-H3 of SEQ ID NO: 558, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 578, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 631; (iii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 522, the CDR-H2 of SEQ ID NO: 540, and the CDR-H3 of SEQ ID NO: 558, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 583, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 631; (iv) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 523, the CDR-H2 of SEQ ID NO: 541, and the CDR-H3 of SEQ ID NO: 559, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 584, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID

NO: 631; (v) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 524, the CDR-H2 of SEQ ID NO: 542, and the CDR-H3 of SEQ ID NO: 560, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 589, the CDR-L2 of SEQ ID NO: 615, and the CDR-L3 of SEQ ID NO:642; (vi) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 525, the CDR-H2 of SEQ ID NO: 543, and the CDR-H3 of SEQ ID NO: 561 and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 590, the CDR-L2 of SEQ ID NO: 601, and the CDR-L3 of SEQ ID NO: 643; and (vii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 527, the CDR-H2 of SEQ ID NO: 545 and the CDR-H3 of SEQ ID NO: 563, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 596, the CDR-L2 of SEQ ID NO: 620, and the CDR-L3 of SEQ ID NO: 649.

[0019] Other aspects of the present disclosure are directed to isolated polynucleotides encoding the various *S. aureus* antibodies described herein, vectors comprising the isolated polynucleotide, and cells comprising these vectors.

[0020] Additional aspects of the present disclosure are directed to pharmaceutical compositions comprising a *S. aureus* antibody as described herein and a pharmaceutical carrier, as well as methods of treating and inhibiting the onset of a staphylococcal infection in a subject using the pharmaceutical compositions described herein.

[0021] Other aspects of the present disclosure are directed to methods of detecting *S. aureus* in a biological sample using a *S. aureus* antibody as described herein and diagnostic kits containing the *S. aureus* antibodies described herein.

[0022] The tremendous success of *S. aureus* as a pathogen is in part due to its ability to express an arsenal of factors that harm the host. Among these factors are a number of bi-component protein toxins that are secreted into the extracellular milieu where they act by killing host cells. The staphylococcal antibodies and binding portions thereof described herein recognize, bind, and neutralize these bi-component staphylococcal toxins, thereby providing unique therapeutic, prophylactic, and diagnostic agents and approaches for combatting staphylococcal infection.

BRIEF DESCRIPTION OF THE DRAWINGS

[0023] FIGs. 1A-E depict the characterization of monoclonal antibodies that bind leukotoxin subunit LukD via non-competing epitopes and exhibit differential LukED neutralization activity. FIG. 1A shows the binding of anti-LukD mAbs SM1B221 and SM1B225 to LukD protein as determined by ELISA. FIG. 1B shows differential activity of anti-LukD

mAbs SM1B221 and SM1B225 in neutralizing the cytolytic activity of the LukED leukotoxin against human primary polymorphonuclear leukocytes. FIG. 1C shows differential activity of anti-LukD mAbs SM1B221 and SM1B225 in neutralizing the cytolytic activity of the LukED leukotoxin against human primary polymorphic nuclear leukocytes. FIG. 1D shows competition binding studies of anti-LukD mAbs SM1B221 and SM1B225 for LukD determined using a bio-layer interferometry assay. FIG. 1E shows competition binding studies of anti-LukD mAbs SM1B221 and SM1B225 for LukD determined using a bio-layer interferometry assay.

[0024] FIGs. 2A-I depict the characterization of monoclonal antibodies that bind the LukAB leukotoxin via non-competing epitopes and exhibit differential effects on LukAB activity. FIG. 2A shows binding of anti-LukAB mAbs SM1B111, SM1B245, SM1B249 and SM1B252 to LukAB protein as determined by ELISA. FIG. 2B shows differential activity of anti-LukAB mAbs SM1B245, SM1B249 and SM1B252 on neutralizing the cytolytic activity of the LukAB leukotoxin against human primary polymorphonuclear leukocytes. FIG. 2C shows differential activity of anti-LukAB mAbs SM1B245, SM1B249 and SM1B252 in neutralizing the cytolytic activity of the LukAB leukotoxin against human primary polymorphonuclear leukocytes. FIGs. 2D-E shows competition binding studies of anti-LukAB mAbs SM1B111, SM1B245 and SM1B249 determined using a bio-layer interferometry assay. FIGs. 2F-G show competition binding studies of anti-LukAB mAbs SM1B111, SM1B245 and SM1B249 determined using a bio-layer interferometry assay. FIGs. 2H-I show competition binding studies of anti-LukAB mAbs SM1B111, SM1B245 and SM1B249 determined using a bio-layer interferometry assay.

[0025] FIGs. 3A-E depict the characterization of monoclonal antibodies that bind leukotoxin subunit LukE via non-competing epitopes. FIG. 3A shows the binding of the anti-LukE mAbs SM1B318 and SM1B332 to purified LukE protein as determined by an ELISA. FIGs. 3B-D show competition binding studies of anti-LukE mAbs SM1B318, SM1B332, and SM1B507 determined using a bio-layer interferometry assay. FIG. 3E shows the differential activity of the anti-LukE mAbs SM1B318, SM1B322 and SM1B507 and the anti-LukD mAb SM1B221 to inhibit the cytolytic activity of LukED against human primary polymorphonuclear leukocytes.

[0026] FIG. 4 shows a tabular summary of data from Hydrogen/Deuterium Exchange Mass Spectrometry analysis of the binding of Fabs SM1B438, SM1B440, and SM1B709 to LukE protein.

DETAILED DESCRIPTION

[0027] *Staphylococcus aureus* possesses virulence factors that afford it the ability to colonize, persist, disseminate, and evade the immune system of an infected host. One such set of virulence factors include the bi-component pore-forming family of hemolysins and leucocidins (also referred to herein as leukotoxins). The pore forming activity of these toxins requires the concerted action of two polypeptides, *i.e.*, an S (slow)-subunit polypeptide and an F (fast)-subunit polypeptide. These bi-component pore-forming toxins include (i) γ-hemolysin comprised of an S-subunit of HlgA or HlgC with an F-subunit of HlgB, (ii) the Pantone-Valentine Leukocidin (PVL), made of leukocidin S-PV (LukS-PV) and LukF-PV, (iii) LukED made of S-subunit LukE and F-subunit LukD, and (iv) LukAB made of S-subunit LukA and F-subunit LukB. The present disclosure relates generally to antibodies and binding portions thereof that bind to, and in some cases neutralize, one or more of these staphylococcal bi-component leukotoxins and/or gamma hemolysin toxins. The present disclosure also relates to therapeutic and diagnostic compositions containing these antibodies or binding portions thereof, and methods of using these antibodies and binding portions thereof.

[0028] The term "antibody" is used in the broadest sense and specifically encompasses monoclonal antibodies (including full length monoclonal antibodies), polyclonal antibodies, multi-specific antibodies (*e.g.*, bispecific antibodies), and antibody fragments so long as they exhibit the desired binding activity, *i.e.*, binding to one or more particular staphylococcal leukotoxins or gamma hemolysins.

[0029] In one embodiment, the antibody of the disclosure is an immunoglobulin (Ig) molecule and may comprise four polypeptide chains, *e.g.*, two heavy (H) chains and two light (L) chains linked by disulfide bonds. Five types of mammalian Ig heavy chains are known: α, δ, ε, γ, and μ, wherein the type of heavy chain defines the class (isotype) of the antibody. Antibodies of the disclosure can be of any class (*e.g.*, IgG, IgE, IgM, IgD, IgA and IgY) and subclass (*e.g.*, IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2). The heavy chain(s) may contain one region, *i.e.*, the variable region (VH), or two regions, *i.e.*, the constant region (CH) and the VH. Like the heavy chain, a light chain(s) may also consist of one region, *i.e.*, the variable region (VL), or two regions, *i.e.*, the constant domain (CL) and the VL. In mammals there are two types of immunoglobulin light chain, lambda (λ) and kappa (κ). The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known in the art. For a review of the antibody structure, *see* Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, eds. Harlow et al., 1988, which is hereby incorporated by reference in its entirety. One of skill in the art will recognize that each subunit structure, *e.g.*, a CH, VH, CL,

VL, structure, comprises active fragments. For example, the active portions of the VH and VL are the portions that bind to the antigen, *i.e.*, the antigen-binding fragment. Likewise, the active portion of the CH subunit is the portion that binds to and/or activates an Fc receptor and/or complement. The interaction of the CH subunit with Fc receptors and ligands imparts an array of important effector functions. As described in more detail *infra*, in some embodiments, the antibodies described herein contain modified or variant Fc regions to enhance or diminish certain effector functions (*see e.g.*, U.S. Patent No. 8,961,967 to Strohl et al., U.S. Patent No. 8,871,294 to Brezski et al., U.S. Patent No. 8,093,357 to Lazar et al., which are hereby incorporated by reference in their entirety

[0030] The unique binding property or epitope binding specificity of a given antibody is determined by the variable (V) regions. In particular, three variable loops in each of the VL and VH regions, known as complementarity determining regions (CDR), are responsible for the antigen binding specificity.

[0031] Typically three CDRs make up the binding character of a light chain variable region (CDRL1, CDRL2 and CDRL3) and three CDRs make up the binding character of a heavy chain variable region (CDRH1, CDRH2 and CDRH3). CDRs contribute to the functional activity of an antibody molecule and are separated by amino acid sequences that comprise scaffolding or framework regions (FR). The exact definitional CDR boundaries and lengths are subject to different classification and numbering systems, *e.g.*, the Kabat system, Chothia system, contact, or any other boundary definitions. Despite differing boundaries, each of these systems has some degree of overlap in what constitutes the so called "hypervariable regions" (i.e., CDRs) within the variable sequences. CDR definitions according to these systems may therefore differ in length and boundary areas with respect to the adjacent framework region. *See* for example Kabat et al., *Sequences of Proteins of Immunological Interest*, 5th ed. NIH Publication No. 91-3242 (1991); Chothia et al., "Canonical Structures For the Hypervariable Regions of Immunoglobulins," *J. Mol. Biol.* 196:901 (1987); and MacCallum et al., "Antibody-Antigen Interactions: Contact Analysis and Binding Site Topography," *J. Mol. Biol.* 262:732 (1996)), each of which is hereby incorporated by reference in its entirety.

[0032] The CDRs form a loop structure that can be classified as a canonical structure. The term "canonical structure" refers to the main chain conformation that is adopted by the antigen binding (CDR) loops. From comparative structural studies, it has been found that five of the six antigen binding loops have only a limited repertoire of available conformations. Each canonical structure can be characterized by the torsion angles of the polypeptide backbone. Correspondent loops between antibodies may, therefore, have very similar three dimensional

structures, despite high amino acid sequence variability in most parts of the loops (Chothia et al., "Canonical Structures For the Hypervariable Regions of Immunoglobulins," *J. Mol. Biol.* 196:901 (1987); Chothia et al., "Conformations of Immunoglobulin Hypervariable Regions," *Nature* 342:877 (1989); Martin and Thornton, "Structural Families in Loops of Homologous Proteins: Automatic Classification, Modelling and Application to Antibodies," *J. Mol. Biol.* 263:800 (1996), each of which is incorporated by reference in its entirety). Furthermore, there is a relationship between the adopted loop structure and the amino acid sequences surrounding it. The conformation of a particular canonical class is determined by the length of the loop and the amino acid residues residing at key positions within the loop, as well as within the conserved framework (i.e., outside of the loop). Assignment to a particular canonical class can therefore be made based on the presence of these key amino acid residues.

[0033] The term "framework region" refers to the art-recognized portions of an antibody variable region that exist between the more divergent (i.e., hypervariable) CDRs. Such framework regions are typically referred to as frameworks 1 through 4 (FR1, FR2, FR3, and FR4) and provide a scaffold for the presentation of the six CDRs (three from the heavy chain and three from the light chain) in three dimensional space, to form an antigen-binding surface.

[0034] An antibody fragment of the disclosure is a portion or domain of the antibody containing an epitope binding region (*e.g.*, the VH region, the VL region, or a combination of both regions). In one embodiment, the antibody fragment comprises a single-chain polypeptide containing one, two, or three of the CDRs of the light-chain variable domain, and/or one, two, or three of the CDRs of the heavy chain variable region. In another embodiment, the antibody fragment of the disclosure is a single domain antibody (also referred to as a nanobody), *e.g.*, a peptide chain of about 110 amino acids long comprising one heavy chain variable region domain or one light chain variable region domain of a full antibody. In another embodiment, the antibody fragment is a fragment antigen-binding (F(ab)) fragment or a F(ab')2 fragment.

[0035] Antibodies and antibody binding fragments of the present disclosure also encompass mutants, variants, or derivatives of the disclosed antibodies or binding fragments thereof which retain the essential epitope binding features of an Ig molecule. For example, the single domain antibodies can be derived from camelid (VHH domains) or cartilaginous fish (V-NAR) variable domains, alone or fused to an Fc domain. In another embodiment, the antibody fragment comprises the heavy chain and light chain variable regions fused together to form a single-chain variable domain antibody (scFv) or a single-chain variable domain with an Fc portion (*i.e.*, a scFv-Fc, *e.g.*, a minibody.). In another embodiment, the antibody fragment is a divalent or bivalent single-chain variable fragment, engineered by linking two scFvs together

either in tandem (*i.e.*, tandem scFv), or such that they dimerize to form diabodies. In yet another embodiment, the antibody is a trivalent single chain variable fragment, engineered by linking three scFvs together, either in tandem or in a trimer formation to form triabodies. In another embodiment, the antibody is a tetrabody single chain variable fragment. In another embodiment, the antibody is a "linear antibody" comprising a pair of tandem Fd segments (VH-CH1-VH-CH1) that form a pair of antigen binding regions (*see* Zapata et al. *Protein Eng.* 8(10):1057-1062 (1995), which is hereby incorporated by reference in its entirety).

[0036] Antibody and binding portions thereof disclosed herein can be mono-valent, bi-valent, or tri-valent with regard to binding domains, and the binding domains may be mono-specific, bi-specific, or tri-specific in binding specificity by design.

[0037] In one embodiment, the antibody or binding portion thereof as described herein is a chimeric antibody. A chimeric antibody is an antibody where one portion of the amino acid sequence of the heavy and/or light chain is homologous to corresponding sequences in an antibody derived from a particular species or belonging to a particular class, while the remaining segment of each chain is homologous to corresponding sequences in another species or class. Typically the variable region of both light and heavy chains mimics the variable regions of antibodies derived from one species of mammals, while the constant portions are homologous to sequences of antibodies derived from another. For example, the variable region can be derived from presently known sources using readily available B- cells or hybridomas from non-human host organisms in combination with constant regions derived from, for example, human cell preparations. Methods of making chimeric antibodies are well known in the art, *see e.g.*, U.S. Pat. No. 4,816,567 to Cabilly; and Morrison et al., "Chimeric human antibody molecules: mouse antigen-binding domains with human constant region domains" *Proc. Natl. Acad. Sci. USA* 81:6851-6855 (1984), which are hereby incorporated by reference in their entirety.

[0038] In another embodiment, the antibody or binding portion thereof is a CDR-grafted antibody. A "CDR-grafted antibody" is an antibody which comprises heavy and light chain variable region sequences of one species, where one or more of the CDR regions are replaced with CDR regions of another species. For example, in one embodiment the CDR grafted antibody comprises human or humanized heavy and light chain variable regions, where one or more of the CDRs within these regions is replaced with one or more CDRs from another species, *e.g.*, murine CDRs.

[0039] In another embodiment, the antibody or binding portion thereof is a humanized antibody. A humanized antibody is an antibody or a variant, derivative, analog or portion thereof which comprises a framework region having substantially the amino acid sequence of a human

antibody and a complementary determining region having substantially the amino acid sequence of a non-human antibody. As used herein, the term "substantially" in the context of a CDR refers to a CDR having an amino acid sequence that is at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98% or at least 99% identical to the amino acid sequence of a non-human antibody CDR. Likewise, the term "substantially" in the context of a framework region refers to a framework having an amino acid sequence that is at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98% or at least 99% identical to the amino acid sequence of a human framework. A humanized antibody comprises substantially all of at least one, and typically two, variable domains (Fab, Fab', F(ab')2, Fv) in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin (*i.e.*, the donor antibody), and all or substantially all of the framework regions are those of a human or humanized immunoglobulin framework sequence (*i.e.*, the acceptor antibody).

[0040] Methods of humanizing antibodies are well known in the art, *see e.g.*, Almagro and Fransson, "Humanization of Antibodies," *Frontiers in Bioscience* 13:1619-1633 (2008), U.S. Patent No. 6,054,297 to Carter et al., U.S. Patent No. 8,343,489, and U.S. Patent Application Publication No. US20100261620 to Almagro et al., which are hereby incorporated by reference in their entirety. The human or humanized framework sequences can be chosen based on known structure, *i.e.*, a fixed framework sequence, sequence homology to the framework sequences of the donor antibody (*e.g.*, the antibody from which the CDRs are derived), *i.e.*, a best-fit framework sequence, or a combination of both approaches. Regardless of the method chosen to select the human framework sequence, the sequences can be selected from mature framework sequences, germline gene sequences, or consensus framework sequences. Compatible human framework sequences are those that are similar in both length and sequence to the framework sequence of the donor antibody sequence (*i.e.*, the antibody from which the CDRs are derived) to ensure proper folding of the antibody and binding domain formation.

[0041] Humanized antibodies or binding fragments thereof as described herein may comprise the light chain as well as at least the variable domain of a heavy chain. The humanized antibody may further comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For example, the humanized antibody comprises the CH1, hinge, CH2, CH3, and CH4 regions of a human heavy chain. In another embodiment, the humanized antibody comprises only a humanized light chain. In another embodiment, the humanized antibody comprises only a humanized heavy chain. In another embodiment, the

humanized antibody comprises only a humanized variable domain of a light chain and/or a humanized variable domain of a heavy chain.

[0042] The antibodies and binding portions thereof described herein can be human antibodies, humanized antibodies (fully or partially humanized), or animal antibodies such as, but not limited to, bird (for example, a duck or a goose), shark, whale, or mammal, including a non-primates (for example, cow, pig, camel, llama, horse, goat, rabbit, sheep, hamster, guinea pig, cat, dog, rat, mouse, etc.) or non-human primates (for example, a monkey, a chimpanzee, etc.).

[0043] Antibody "specificity" refers to selective recognition of the antibody or binding portion thereof as described herein for a particular epitope of an leukotoxin or gamma hemolysin toxin. The term "epitope" includes any protein determinant capable of specific binding to an immunoglobulin or T-cell receptor or otherwise interacting with a molecule. Epitopic determinants generally consist of chemically active surface groupings of molecules such as amino acids or carbohydrate or sugar side chains and generally have specific three dimensional structural characteristics, as well as specific charge characteristics. An epitope may be "linear" or "conformational". In a linear epitope, all of the points of interaction between the protein and the antibody occur linearly along the primary amino acid sequence of the protein. In a conformational epitope, the points of interaction occur across amino acid residues on the protein that are separated from one another, *i.e.*, noncontiguous amino acids juxtaposed by tertiary folding of a protein. Epitopes formed from contiguous amino acids are typically retained on exposure to denaturing solvents, whereas epitopes formed by tertiary folding are typically lost on treatment with denaturing solvents. An epitope typically includes at least 3, and more usually, at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more amino acids in a unique spatial conformation. Antibodies that recognize the same epitope can be verified in a simple immunoassay showing the ability of one antibody to block the binding of another antibody to a target antigen.

[0044] The antibodies and binding portions thereof described herein may be neutralizing antibodies or binding portions thereof. In the context of the present disclosure, a neutralizing antibody is an antibody or binding portion thereof that prevents or inhibits the cytolytic activity exhibited by a particular staphylococcal bi-component toxin, *e.g.*, LukAB, LukED, HlgAB, or HlgBC. Neutralization activity of a particular antibody can be assessed using the methods described herein or other methods known and used in the art. In one embodiment, neutralization activity is assessed by measuring an antibody's capacity to decrease, prevent or inhibit cellular lactate dehydrogenase (LDH) release caused by leukotoxin or hemolysin mediated cellular pore-

formation. In another embodiment, neutralization activity is assessed by measuring an antibody's capacity to decrease, prevent, or inhibit bi-component leukotoxin or hemolysin induced cell death.

[0045] One aspect of the present disclosure relates to antibodies or binding portions thereof that bind *Staphylococcus aureus* Leukocidin AB (LukAB). LukAB in one of several bi-component, pore-forming toxins produced and secreted by *S. aureus*. These toxins are secreted as water soluble monomers which oligomerize, and insert pores into the plasma membrane of host cells. In one embodiment, LukAB antibodies or binding portions thereof as described herein bind a LukA protein having the amino acid sequence of SEQ ID NO: 829 (Table 25) (which corresponds to the native LukA amino acid sequence containing a poly-histidine tag at the N-terminus to facilitate purification), native LukA, or fragments and homologs thereof, and/or a LukB protein having the amino acid sequence of SEQ ID NO: 830 (Table 25) (which corresponds to the native LukB amino acid sequence containing a poly-histidine tag at the N-terminus to facilitate purification), native LukB, or fragments or homologs thereof. The LukAB antibody or binding portion thereof binds LukA, LukB, and/or LukAB with a Kd of less than or equal to about 10^{-6}, 10^{-7}, 10^{-8}, 10^{-9}, 10^{-10}, 10^{-11} or 10^{-12} M. In one embodiment, the LukAB antibody is a neutralizing antibody, *i.e.*, it neutralizes the cytolytic activity (i.e., pore formation and cell lysis) that LukAB exerts on its target immune host cells. Neutralizing LukAB antibodies neutralize LukAB cytolytic activity by binding to an epitope within regions of the LukA and LukB proteins involved in LukA and LukB protein-protein interaction or involved in LukAB binding to its cognitive receptor on target immune cells (*e.g.*, CD11b).

[0046] The LukAB antibody or binding portion thereof as described herein comprises a heavy chain variable region that comprises: a complementarity-determining region 1 (CDR-H1) comprising an amino acid sequence of any one of SEQ ID NOs: 1-20, or a modified amino acid sequence of any one of SEQ ID NOs: 1-20, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 1-20; a complementarity-determining region 2 (CDR-H2) comprising an amino acid sequence of any one of SEQ ID NOs: 21-41, or a modified amino acid sequence of any one of SEQ ID NOs: 21-41, said modified sequences having at least 80% sequence identity to any one of SEQ ID NOs: 21-41; and a complementarity-determining region 3 (CDR-H3) comprising an amino acid sequence of any one of SEQ ID NOs: 42-62 or a modified amino acid sequence of any one of SEQ ID NO:42-62, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 42-62. As described herein, a plurality of LukAB antibodies have been generated and characterized, and the amino acid

sequences of the CDR H1, H2 and H3 regions of these LukAB antibodies are provided in Table 1 below.

Table 1. LukAB Antibody Heavy Chain CDRs

mAb/Fab name	VH name	HCDR1		HCDR2		HCDR3	
		Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
SM1B105	SM1H100	GYTFSTF	001	LPGSGS	021	GGYDGMD	042
SM1B106	SM1H101	GYTFSTF	001	LPGSGS	021	GGYDGMD	042
SM1B107	SM1H102	GYTFSTF	001	LPGSGS	021	GGYDGMD	042
SM1B108	SM1H103	GYAFSSS	002	YPGDGD	022	RNYDGYHYGMD	043
SM1B109	SM1H100	GYTFSTF	001	LPGSGS	021	GGYDGMD	042
SM1B110	SM1H104	GYTFTSY	003	DPSDSY	023	AAYDNSYYFD	044
SM1B111	SM1H106	GYAFSSS	002	YPGDGD	022	YGYDYDGEYYY AMD	045
SM1B112	SM1H105	GYTFTNY	004	KSYTGE	024	GSLFGLD	046
SM1B243	HLGH31	GFNIKDY	005	DPANGN	025	GDYVPGYFD	047
SM1B244	HLGH32	GDSITSD	006	SYSGS	026	DYGSPYAMD	048
SM1B245	HLGH33	GYTFSTY	007	NPNTGY	027	GGSKAFPYYAMD	049
SM1B246	HLGH34	GYSFTGY	008	DPYNGA	028	GLYGDYWYA	050
SM1B247	HLGH35	GFTFSDY	009	SDGGSY	029	GPTYYGLD	051
SM1B248	HLGH36	GYSFTSY	010	HPSDSE	030	LYVDFFD	052
SM1B249	HLGH37	GFTFSSY	011	NSNGGS	031	PDYPYAMD	053
SM1B250	HLGH38	GYTFTNY	012	NTYTGE	032	SPSYGSRGAWFA	054
SM1B251	HLGH39	GYTFTNY	012	NTYTGE	032	SPSYGSRGAWFA	054
SM1B252	HLGH40	GYTFSDY	013	LPGSDK	033	AGDDYV	055
SM1B253	HLGH41	GFNIKDT	014	DPANDI	034	DWAD	056
SM1B254	HLGH42	GFNIKDT	014	NPANDN	035	DWAD	056
SM1B255	HLGH43	GYTFTRY	015	NPNNGH	036	LDGHLYAVD	057
SM1B256	HLGH44	GYTFTTY	016	NPSNDG	037	SYYGYGDFD	058
SM1B257	HLGH45	GFSLTSY	017	GWNDK	038	DGDSSGSWFA	059
SM1B258	HLGH46	GFSLTGY	018	GWDDK	039	DHGDGGFA	060
SM1B259	HLGH47	GYTFTDY	019	NPNNGG	040	ENSGYGGNYFA	061
SM1B260	HLGH30	GFNIKDS	020	DPEDGE	041	SFGV	062
SM1B261	HLGH30	GFNIKDS	020	DPEDGE	041	SFGV	062
SM1B262	HLGH30	GFNIKDS	020	DPEDGE	041	SFGV	062
SM1B263	HLGH30	GFNIKDS	020	DPEDGE	041	SFGV	062
SM1B264	HLGH30	GFNIKDS	020	DPEDGE	041	SFGV	062
SM1B265	HLGH30	GFNIKDS	020	DPEDGE	041	SFGV	062
SM1B266	HLGH30	GFNIKDS	020	DPEDGE	041	SFGV	062
SM1B267	HLGH30	GFNIKDS	020	DPEDGE	041	SFGV	062
SM1B268	HLGH30	GFNIKDS	020	DPEDGE	041	SFGV	062
SM1B269	HLGH30	GFNIKDS	020	DPEDGE	041	SFGV	062

mAb/Fab name	VH name	HCDR1		HCDR2		HCDR3	
		Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
SM1B270	HLGH30	GFNIKDS	020	DPEDGE	041	SFGV	062
SM1B271	HLGH30	GFNIKDS	020	DPEDGE	041	SFGV	062
SM1B272	HLGH30	GFNIKDS	020	DPEDGE	041	SFGV	062
SM1B273	HLGH30	GFNIKDS	020	DPEDGE	041	SFGV	062
SM1B274	HLGH30	GFNIKDS	020	DPEDGE	041	SFGV	062
SM1B275	HLGH30	GFNIKDS	020	DPEDGE	041	SFGV	062

[0047] In another embodiment of the present disclosure, the LukAB antibody or binding portion further comprises a light chain variable region. The light chain variable region of the LukAB antibody or binding portion thereof comprises a complementarity-determining region 1 (CDR-L1) having an amino acid sequence of any one of SEQ ID NOs: 63-87, or a modified amino acid sequence of any one of SEQ ID NO: 63-87, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 63-87; a complementarity-determining region 2 (CDR-L2) having an amino acid sequence of any one of SEQ ID NOs: 88-105, or a modified amino acid sequence of any one of SEQ ID NO: 88-105, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 88-105; and a complementarity-determining region 3 (CDR-L3) having an amino acid sequence of any one of SEQ ID NOs: 106-135, or a modified amino acid sequence of any one of SEQ ID NO: 106-135, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 106-135. The LukAB antibody CDR -L1, -L2 and -L3 amino acid sequences are provided in Table 2 below.

Table 2: LukAB Antibody Light Chain CDRs

mAb/Fab name	VL name	LCDR1		LCDR2		LCDR3	
		Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
SM1B105	SM1L19	SSSVSSSY	063	RTS	088	WSGYPF	106
SM1B106	SM1L20	SESVDNSGISF	064	AAS	089	SKEVPY	107
SM1B107	SM1L21	SESVDNSGISF	064	AAS	089	SKEVPY	107
SM1B108	SM1L22	SQSVSDD	065	YAS	090	DYSSPW	108
SM1B109	SM1L20	SESVDNSGISF	064	AAS	089	SKEVPY	107
SM1B110	SM1L23	SSSVSY	066	STS	091	RSSYPF	109
SM1B111	SM1L25	HSNLISNY	067	RTS	088	GSSIPF	110
SM1B112	SM1L24	SSHVSY	068	DTS	092	YSGYPY	111
SM1B243	HLGL29	SQDINSY	069	RAN	093	YDEFPY	112
SM1B244	HLGL30	SQNVGTN	070	SAS	094	YNSYPF	113

mAb/Fab name	VL name	LCDR1		LCDR2		LCDR3	
		Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
SM1B245	HLGL31	SESVDGYGNSF	071	RAS	095	SNGDPF	114
SM1B246	HLGL32	SQSIVHSNGKTY	072	KVS	096	GSHVPW	115
SM1B247	DARL6	SKSVSISGYSY	073	LAS	097	SRELPF	116
SM1B248	HLGL31	SESVDGYGNSF	071	RAS	095	SNGDPF	114
SM1B249	HLGL33	SSSVSY	066	DTS	092	WISNPP	117
SM1B250	HLGL34	SQSVDYDGDSY	074	AAS	089	SNEDPL	118
SM1B251	HLGL35	SENIYSY	075	NAK	098	HYGSPY	119
SM1B252	HLGL36	SQSIVYSNGNTY	076	KVS	096	GSHVPF	120
SM1B253	HLGL37	SQSLLHSDGKTY	077	LVS	099	GTHFPY	121
SM1B254	HLGL38	SQSLLHSDGKTY	077	LVS	099	GTHFPY	121
SM1B255	HLGL39	SQSLLDSDGETY	078	MVS	100	GTHFPQ	122
SM1B256	HLGL40	SQSLLDSDGETY	078	LVS	099	GTHSPY	123
SM1B257	HLGL41	SQDINKY	079	YTS	101	YDNLR	124
SM1B258	HLGL42	SQSIVHSNGNTY	080	KVS	096	GSHVPF	120
SM1B259	HLGL43	SSSVSY	066	DTS	092	WSSYPP	125
SM1B260	HLGL31	SESVDGYGNSF	071	RAS	095	SNGDPF	114
SM1B261	HLGL44	SENVGTY	081	GAS	102	SYSYPL	126
SM1B262	ATCL189	SQDINSY	069	RAN	093	YDEFPL	127
SM1B263	HLGL45	SQDINKY	079	YTS	101	YDNLW	128
SM1B264	HLGL46	SENIYSN	082	AAT	103	FWGTPW	129
SM1B265	HLGL47	SENIYSY	075	NAK	098	HYGSPY	119
SM1B266	HLGL48	SQNINVW	083	KAS	104	GQSYPL	130
SM1B267	HLGL49	SQNINVW	083	KAS	104	GQSYPY	130
SM1B268	GC5L32	SSSISSNY	084	RTS	088	GSSIPR	131
SM1B269	C27L19	SQSVDYDGDSY	074	AAS	089	SNEDPY	132
SM1B270	HLGL50	SQSVDYDGDSY	074	AAS	089	SYEDPF	133
SM1B271	HLGL43	SSSVSY	066	DTS	092	WSSYPP	125
SM1B272	IFWL448	SQNVGTN	070	SAS	094	YNSYPF	113
SM1B273	HLGL51	SQSLLYSSNQKNY	085	WAS	105	YYSYPY	134
SM1B274	HLGL52	SQSLVHSNGNTY	086	KVS	096	STHVPPY	135
SM1B275	HLGL53	SQSLLYSNGKTY	087	LVS	099	GTHFPQ	122

[0048] The LukAB antibodies disclosed herein comprise the heavy chain CDRs of Table 1 and light chain CDRs of Table 2 or modified CDRs thereof. Encompassed by the present disclosure are CDRs of Table 1 and 2 containing 1, 2, 3, 4, 5, or more amino acid substitutions (depending on the length of the CDR) that maintain or enhance LukAB binding of the antibody. The resulting modified CDRs are at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% similar in sequence to the CDRs of Tables 1 and 2. Suitable amino acid

modifications to the heavy chain CDR sequences of Table 1 and/or the light chain CDR sequences of Table 2 include, for example, conservative substitutions or functionally equivalent amino acid residue substitutions that result in variant CDR sequences having similar or enhanced binding characteristics to those of the CDR sequences of Table 1 and Table 2. Conservative substitutions are those that take place within a family of amino acids that are related in their side chains. Genetically encoded amino acids can be divided into four families: (1) acidic (aspartate, glutamate); (2) basic (lysine, arginine, histidine); (3) nonpolar (alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan); and (4) uncharged polar (glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine). Phenylalanine, tryptophan, and tyrosine are sometimes classified jointly as aromatic amino acids. Alternatively, the amino acid repertoire can be grouped as (1) acidic (aspartate, glutamate); (2) basic (lysine, arginine histidine), (3) aliphatic (glycine, alanine, valine, leucine, isoleucine, serine, threonine), with serine and threonine optionally grouped separately as aliphatic-hydroxyl; (4) aromatic (phenylalanine, tyrosine, tryptophan); (5) amide (asparagine, glutamine); and (6) sulfur-containing (cysteine and methionine) (Stryer (ed.), Biochemistry, 2nd ed, WH Freeman and Co., 1981, which is hereby incorporated by reference in its entirety). Non-conservative substitutions can also be made to the heavy chain CDR sequences of Table 1 and the light chain CDR sequences of Table 2. Non-conservative substitutions involve substituting one or more amino acid residues of the CDR with one or more amino acid residues from a different class of amino acids to improve or enhance the binding properties of CDR. The amino acid sequences of the heavy chain variable region CDRs of Table 1 and/or the light chain variable region CDRs of Table 2 may further comprise one or more internal neutral amino acid insertions or deletions that maintain or enhance LukAB binding.

[0049] In one embodiment, the LukAB antibody or binding portion thereof, comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 1, the CDR-H2 of SEQ ID NO: 21, and the CDR-H3 of SEQ ID NO: 42. In another embodiment, the LukAB antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 2, the CDR-H2 of SEQ ID NO: 22, and the CDR-H3 of SEQ ID NO: 43. In another embodiment, the LukAB antibody of binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 2, the CDR-H2 of SEQ ID NO: 22, and the CDR-H3 of SEQ ID NO: 45. In another embodiment, the LukAB antibody of binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 3, the CDR-H2 of SEQ ID NO: 23, and the CDR-H3 of SEQ ID NO: 44. In another embodiment, the LukAB antibody or binding portion thereof comprises a heavy chain variable region comprising

the CDR-H1 of SEQ ID NO: 4, the CDR-H2 of SEQ ID NO: 24, and the CDR-H3 of SEQ ID NO: 46. In another embodiment, the LukAB antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 5, the CDR-H2 of SEQ ID NO: 25, and the CDR-H3 of SEQ ID NO: 47. In another embodiment, the LukAB antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 6, the CDR-H2 of SEQ ID NO: 26, and the CDR-H3 of SEQ ID NO: 48. In another embodiment, the LukAB antibody of binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 7, the CDR-H2 of SEQ ID NO: 27, and the CDR-H3 of SEQ ID NO: 49. In another embodiment, the LukAB antibody of binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 8, the CDR-H2 of SEQ ID NO: 28, and the CDR-H3 of SEQ ID NO: 50. In another embodiment, the LukAB antibody of binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO:9 , the CDR-H2 of SEQ ID NO: 29, and the CDR-H3 of SEQ ID NO: 51. In another embodiment, the LukAB antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 10, the CDR-H2 of SEQ ID NO: 30, and the CDR-H3 of SEQ ID NO: 52. In another embodiment, the LukAB antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 11, the CDR-H2 of SEQ ID NO: 31, and the CDR-H3 of SEQ ID NO: 53. In another embodiment, the LukAB antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 12, the CDR-H2 of SEQ ID NO: 32, and the CDR-H3 of SEQ ID NO: 54. In another embodiment, the LukAB antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 13, the CDR-H2 of SEQ ID NO: 33, and the CDR-H3 of SEQ ID NO: 55. In another embodiment, the LukAB antibody of binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 14, the CDR-H2 of SEQ ID NO: 34, and the CDR-H3 of SEQ ID NO: 56. In another embodiment, the LukAB antibody of binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 14, the CDR-H2 of SEQ ID NO: 35, and the CDR-H3 of SEQ ID NO: 56. In another embodiment, the LukAB antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 15, the CDR-H2 of SEQ ID NO: 36, and the CDR-H3 of SEQ ID NO: 57. In another embodiment, the LukAB antibody of binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 16, the CDR-H2 of SEQ ID NO: 37, and the CDR-H3 of SEQ ID NO: 58. In another embodiment, the LukAB antibody of binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of

SEQ ID NO: 17, the CDR-H2 of SEQ ID NO: 38, and the CDR-H3 of SEQ ID NO: 59. In another embodiment, the LukAB antibody of binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 18, the CDR-H2 of SEQ ID NO:39, and the CDR-H3 of SEQ ID NO: 60. In another embodiment, the LukAB antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 19, the CDR-H2 of SEQ ID NO: 40, and the CDR-H3 of SEQ ID NO: 61. In another embodiment, the LukAB antibody of binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 20, the CDR-H2 of SEQ ID NO: 41, and the CDR-H3 of SEQ ID NO: 62.

[0050] In one embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 63, the CDR-L2 of SEQ ID NO: 88, and the CDR-L3 of SEQ ID NO: 106. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 64, the CDR-L2 of SEQ ID NO: 89, and the CDR-L3 of SEQ ID NO: 107. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 65, the CDR-L2 of SEQ ID NO: 90, and the CDR-L3 of SEQ ID NO: 108. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 66, the CDR-L2 of SEQ ID NO: 91, and the CDR-L3 of SEQ ID NO: 109. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 67, the CDR-L2 of SEQ ID NO: 88, and the CDR-L3 of SEQ ID NO: 110. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 68, the CDR-L2 of SEQ ID NO: 92, and the CDR-L3 of SEQ ID NO: 111. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 69, the CDR-L2 of SEQ ID NO: 93, and the CDR-L3 of SEQ ID NO: 112. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 70, the CDR-L2 of SEQ ID NO: 94, and the CDR-L3 of SEQ ID NO: 113. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 71, the CDR-L2 of SEQ ID NO: 95, and the CDR-L3 of SEQ ID NO: 114. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 72, the CDR-L2 of SEQ ID NO: 96, and the CDR-L3 of SEQ ID NO: 115. In another embodiment, the LukAB antibody or binding portion thereof comprises a

light chain variable region comprising the CDR-L1 of SEQ ID NO: 73, the CDR-L2 of SEQ ID NO: 97, and the CDR-L3 of SEQ ID NO: 116. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 66, the CDR-L2 of SEQ ID NO: 92, and the CDR-L3 of SEQ ID NO: 117. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 74, the CDR-L2 of SEQ ID NO: 89, and the CDR-L3 of SEQ ID NO: 118. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 75, the CDR-L2 of SEQ ID NO: 98, and the CDR-L3 of SEQ ID NO: 119. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 76, the CDR-L2 of SEQ ID NO: 96, and the CDR-L3 of SEQ ID NO: 120. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 77, the CDR-L2 of SEQ ID NO: 99, and the CDR-L3 of SEQ ID NO: 121. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 78, the CDR-L2 of SEQ ID NO: 100, and the CDR-L3 of SEQ ID NO: 122. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 78, the CDR-L2 of SEQ ID NO: 99, and the CDR-L3 of SEQ ID NO: 123. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 79, the CDR-L2 of SEQ ID NO: 101, and the CDR-L3 of SEQ ID NO: 124. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 80, the CDR-L2 of SEQ ID NO: 96, and the CDR-L3 of SEQ ID NO: 120. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 66, the CDR-L2 of SEQ ID NO: 92, and the CDR-L3 of SEQ ID NO: 125. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 71, the CDR-L2 of SEQ ID NO: 95, and the CDR-L3 of SEQ ID NO: 114. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 81, the CDR-L2 of SEQ ID NO: 102, and the CDR-L3 of SEQ ID NO: 126. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 69, the CDR-L2 of SEQ ID NO: 93, and the CDR-L3 of SEQ ID NO: 127 a light chain variable region comprising the CDR-L1 of SEQ ID NO: 79, the CDR-L2 of SEQ ID NO: 101, and the CDR-L3

of SEQ ID NO: 128. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 82, the CDR-L2 of SEQ ID NO: 103, and the CDR-L3 of SEQ ID NO: 129. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 75, the CDR-L2 of SEQ ID NO: 98, and the CDR-L3 of SEQ ID NO: 119. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 83, the CDR-L2 of SEQ ID NO: 104, and the CDR-L3 of SEQ ID NO: 130. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 84, the CDR-L2 of SEQ ID NO: 88, and the CDR-L3 of SEQ ID NO: 131. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 74, the CDR-L2 of SEQ ID NO: 89, and the CDR-L3 of SEQ ID NO: 132. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 74, the CDR-L2 of SEQ ID NO: 89, and the CDR-L3 of SEQ ID NO: 133. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 66, the CDR-L2 of SEQ ID NO: 92, and the CDR-L3 of SEQ ID NO: 125. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 70, the CDR-L2 of SEQ ID NO: 94, and the CDR-L3 of SEQ ID NO: 113. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 85, the CDR-L2 of SEQ ID NO: 105, and the CDR-L3 of SEQ ID NO: 134. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 86, the CDR-L2 of SEQ ID NO: 96, and the CDR-L3 of SEQ ID NO: 135. In another embodiment, the LukAB antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 87, the CDR-L2 of SEQ ID NO: 99, and the CDR-L3 of SEQ ID NO: 122.

[0051] In another embodiment, the LukAB antibody or binding portion thereof comprises the heavy chain CDRs of SEQ ID NOs: 1, 21, and 42 together with the light chain CDRs of SEQ ID NOs: 63, 88, and 106; the heavy chain CDRs of SEQ ID NOs: 1, 21, and 42 together with the light chain CDRs of SEQ ID NOs: 64, 89, and 107; the heavy chain CDRs of SEQ ID NOs: 2, 22, and 43, together with the light chain CDRs of SEQ ID NOs: 65, 90, and 108; the heavy chain CDRs of SEQ ID NOs: 3, 23, and 44 together with the light chain CDRs of SEQ ID NOs: 66, 91, and 109; the heavy chain CDRs of SEQ ID NOs: 2, 22, and 45, together with the light

chain CDRs of SEQ ID NOs: 67, 88, and 110; the heavy chain CDRs of SEQ ID NOs:4, 24, and 46 together with the light chain CDRs of SEQ ID NOs: 68, 92, and 111; the heavy chain CDRs of SEQ ID NOs: 5, 25, and 47 together with the light chain CDRs of SEQ ID NOs: 69, 93, and 112; the heavy chain CDRs of SEQ ID NOs: 6, 26, and 48 together with the light chain CDRs of SEQ ID NOs: 70, 94, and 113; the heavy chain CDRs of SEQ ID NOs: 7, 27, and 49 together with the light chain CDRs of SEQ ID NOs: 71, 95, and 114; the heavy chain CDRs of SEQ ID NOs: 8, 28, and 50 together with the light chain CDRs of SEQ ID NOs: 72, 96 and 115; the heavy chain CDRs of SEQ ID NOs: 9, 29, and 51 together with the light chain CDRs of SEQ ID NOs: 73, 97, and 116; the heavy chain CDRs of SEQ ID NOs: 10, 30, and 52 together with the light chain CDRs of SEQ ID NOs: 71, 95 and 114; the heavy chain CDRs of SEQ ID NOs: 11, 31, and 53 together with the light chain CDRs of SEQ ID NOs: 66, 92 and 117; the heavy chain CDRs of SEQ ID NOs: 12, 32, and 54 together with the light chain CDRs of SEQ ID NOs: 74, 89 and 118; the heavy chain CDRs of SEQ ID NOs: 12, 32, and 54 together with the light chain CDRs of SEQ ID NOs: 75, 98 and 119; the heavy chain CDRs of SEQ ID NOs: 13, 33, and 55 together with the light chain CDRs of SEQ ID NOs: 76, 96, and 120; the heavy chain CDRs of SEQ ID NOs: 14, 34, and 56 together with the light chain CDRs of SEQ ID NOs: 77, 99, and 121; the heavy chain CDRs of SEQ ID NOs: 14, 35, and 56 together with the light chain CDRs of SEQ ID NOs: 77, 99, and 121; the heavy chain CDRs of SEQ ID NOs: 15, 36, and 57 together with the light chain CDRs of SEQ ID NOs: 78, 100, and 122; the heavy chain CDRs of SEQ ID NOs: 16, 37, and 58 together with the light chain CDRs of SEQ ID NOs: 78, 99 and 123; the heavy chain CDRs of SEQ ID NOs: 17, 38, and 59 together with the light chain CDRs of SEQ ID NOs: 79, 101 and 124; the heavy chain CDRs of SEQ ID NOs: 18, 39, and 60 together with the light chain CDRs of SEQ ID NOs: 80, 96, and 120; the heavy chain CDRs of SEQ ID NOs: 19, 40, and 61 together with the light chain CDRs of SEQ ID NOs: 66, 92, and 125; the heavy chain CDRs of SEQ ID NOs: 20, 41, and 62 together with the light chain CDRs of SEQ ID NOs: 71, 95 and 114; the heavy chain CDRs of SEQ ID NOs: 20, 41, and 62 together with the light chain CDRs of SEQ ID NOs: 81, 102 and 126 ; the heavy chain CDRs of SEQ ID NOs: 20, 41, and 62 together with the light chain CDRs of SEQ ID NOs: 69, 93, and 127; the heavy chain CDRs of SEQ ID NOs: 20, 41, and 62 together with the light chain CDRs of SEQ ID NOs: 79, 101, and 128; the heavy chain CDRs of SEQ ID NOs: 20, 41, and 62 together with the light chain CDRs of SEQ ID NOs: 82, 103, and 129; the heavy chain CDRs of SEQ ID NOs: 20, 41, and 62 together with the light chain CDRs of SEQ ID NOs: 75, 98, and 119; the heavy chain CDRs of SEQ ID NOs: 20, 41, and 62 together with the light chain CDRs of SEQ ID NOs: 83, 104, and 130; the heavy chain CDRs of SEQ ID NOs: 20, 41, and 62 together with the light

chain CDRs of SEQ ID NOs: 84, 88, and 131; the heavy chain CDRs of SEQ ID NOs: 20, 41, and 62 together with the light chain CDRs of SEQ ID NOs: 74, 89, and 132; the heavy chain CDRs of SEQ ID NOs: 20, 41, and 62 together with the light chain CDRs of SEQ ID NOs: 74, 89, and 133; the heavy chain CDRs of SEQ ID NOs: 20, 41, and 62 together with the light chain CDRs of SEQ ID NOs: 85, 105, and 134; the heavy chain CDRs of SEQ ID NOs: 20, 41, and 62 together with the light chain CDRs of SEQ ID NOs: 86, 96, and 135; the heavy chain CDRs of SEQ ID NOs: 20, 41, and 62 together with the light chain CDRs of SEQ ID NOs: 87, 99 and 122.

[0052] The LukAB antibody or binding portion thereof as described herein may comprises a variable light (VL) chain, a variable heavy (VH) chain, or a combination of VL and VH chains. The VL chain of the LukAB antibody comprises an amino acid sequence selected from SEQ ID NOs: 136-176 or an amino acid sequence that is at least 80% identical to any one of the amino acid sequence selected from SEQ ID NOs: 136-176. The VH chain of the LukAB antibody as disclosed herein comprises an amino acid sequence selected from SEQ ID NOs: 177-217 or an amino acid sequence that is at least 80% identical to any one of the amino acid sequence selected from SEQ ID NOs: 177-217. The sequences of the LukAB VL and VH chains are shown in Table 3A below.

Table 3A. LukAB Antibody Variable Light (VL) and Variable Heavy (VH) Chain Sequences

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B105	VL	SM1L19	DIVLTQSPAIMAASLGQKVTMTCSASSSVSSSY LHWYQQKSGASPKPLIHRTSNLASGVPARFSGS GSGTSYSLTISSVEAEDDATYYCQQWSGYPFTF GAGTKLELK	136
SM1B106	VL	SM1L20	DIVMTQSPASLAVSLGQRATISCRASESVDNSGI SFMNWFQQKPGQPPKLLIYAASNQGSGVPARF SGSGSGTDFSLNIHPMEEDDTAMYFCQQSKEVP YTFGGGTKLEIK	137
SM1B107	VL	SM1L21	DIVLTQSPASLAVSLGQRATISCRASESVDNSGI SFMNWFQQKPGQPPKLLIYAASNQGSGVPARF SGSGSGTDFSLNIHPMEEDDTAMYFCQQSKEVP YTFGGGTKLEIK	138
SM1B108	VL	SM1L22	DVVMTQTPKFLLVSAGDRVTITCKASQSVSDD VTWYQQKSGQSPKLLIYYASNRYTGVPDRFTG SGYGTDFTFTISTVQAEDLAVYFCQQDYSSPWT FGGGTKLEIK	139
SM1B109	VL	SM1L20	DIVMTQSPASLAVSLGQRATISCRASESVDNSGI SFMNWFQQKPGQPPKLLIYAASNQGSGVPARF SGSGSGTDFSLNIHPMEEDDTAMYFCQQSKEVP YTFGGGTKLEIK	140

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B110	VL	SM1L23	DIVLTQSPAIMSASPGEKVTITCSASSSVSYMH WFQQKPGTSPKLWIYSTSNLASGVPARFSGSGS GTSYSLTISRMEAEDAATYYCQQRSSYPFTFGS GTKLEIK	141
SM1B111	VL	SM1L25	DIVMTQSPTTMAASPGERITITCSAHSNLISNYL HWYQQKPGFSPKLLIYRTSNLASGVPARFSGSG SGTSYSLTIGTMEAEDVATYFCQQGSSIPFTFGS GTKLEIK	142
SM1B112	VL	SM1L24	QIVLTQSPTIMSASPGEKVTMTCSASSHVSYIY WYQQKPGSSPRLWIYDTSNLVSGVPARFSGSRS GTSYSLTISSMEAEDAATYYCQQYSGYPYTFGG GTKLEIK	143
SM1B243	VL	HLGL29	DIKMTQSPSSMYASLGERVTITCKASQDINSYLS WFQQKPGKSPKTLIYRANRLVDGVPSRFSGSGS GQDYSPTISSLEYEDMGIYYCLQYDEFPYTFGG GTKLEIK	144
SM1B244	VL	HLGL30	DIVMTQSQKFMSTSVGDRVSVTCKASQNVGTN VAWYQQKPGQSPKTLIYSASYRYSGVPDSFTGS GSGTDFTLTISNVQSEDWAEYFCQQYNSYPFTF GSGTKLEIK	145
SM1B245	VL	HLGL31	DIVLTQSPASLAVSLGQRATMSCRASESVDGYG NSFLHWYQQKPGQPPKLLIYRASNLESGIPARF SGTGSRTDFTLTITPVEADDVATYYCQQSNGDP FTFGSGTKLEIK	146
SM1B246	VL	HLGL32	DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNG KTYLEWYLQKPGQSPKLLIYKVSNRFSGVPDRF SGSGSGTDFTLKISRVEAEDLGVYYCLQGSHVP WTFGGGTKLELK	147
SM1B247	VL	DARL6	DIVLTQSPASLAVSLGQRATISCRASKSVSISGY SYMHWYQQKPGQPPKLLIDLASNLESGVPARF SGSGSGTDFTLNIHPVEEEDAATYYCQHSRELP FTFGSGTKLEIK	148
SM1B248	VL	HLGL31	DIVLTQSPASLAVSLGQRATMSCRASESVDGYG NSFLHWYQQKPGQPPKLLIYRASNLESGIPARF SGTGSRTDFTLTITPVEADDVATYYCQQSNGDP FTFGSGTKLEIK	149
SM1B249	VL	HLGL33	QIVLTQSPAIMSASPGEKVTMTCSASSSVSYMH WYQQKSGTSPKRWIYDTSKLASGVPARFSGSG SGTSYSLTISSMEAEDAATYYCQQWISNPPTFG GGTKLEIK	150
SM1B250	VL	HLGL34	DIVLTQSPASLAVSLEQRATISCKASQSVDYDG DSYMNWYQQKPGQPPKLLIYAASNLESGIPARF SGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDP LTFGAGTKLELK	151
SM1B251	VL	HLGL35	DIQMTQSPASLSASVGETVTITCRASENIYSYLA WYQQKQGKSPQLLVYNAKTLVEGVPSRFSGSG SGTQFSLKINSLQPEDFGSYYCQHHYGSPYTFG GGTKLELK	152

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B252	VL	HLGL36	DVLMTQTPLSLPVSLGDQASISCRSSQSIVYSNG NTYLEWYLQKPGQSPKLLIYKVSNRFSGVPDRF SGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVP FTFGSGTKLEIK	153
SM1B253	VL	HLGL37	DVVMTQTPLTLSVTIGQAASISCKSSQSLLHSD GKTYLNWLLQRPGQSPKRLIYLVSKLDSGVPD RFTGSGSGTDFTLKISRVEAEDLGVYYCWQGT HFPYTFGGGTKLEIK	154
SM1B254	VL	HLGL38	DVVMTQTPLTLSVTVGQPASISCKSSQSLLHSD GKTYLNWLLQRPGQSPKRLIYLVSKLDSGVPD RFTGSGSGTDFTLKISRVEAEDLGVYYCWQGT HFPYTFGGGTKLEIK	155
SM1B255	VL	HLGL39	DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDG ETYLNWLLQRPGQSPKRLIYMVSKLDSGVPDR FTGSGSGTDFTLKISRVEAEDLGVYYCWQGTH FPQTFGGGTKLELK	156
SM1B256	VL	HLGL40	DVVMTQTPLTLSVTNGQPASISCKSSQSLLDSD GETYLNWLLQRPGQSPKRLIYLVSKLDSGVPDR FIGSGSGTDFTLKISRVEAEDLGVYFCWQGTHS PYTFGGGTKLEIK	157
SM1B257	VL	HLGL41	DIQMTQSPSSLSASLGGKVTITCKASQDINKYIA WYQHKPGKGPRLLIHYTSTLQPGIPSRFSGSGS GRDYSFSISNLEPEDIATYYCLQYDNLRTFGGG TKVEIK	158
SM1B258	VL	HLGL42	DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNG NTYLEWYLQKPGQSPKLLIYKVSNRFSGVPDRF SGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVP FTFGSGTKLEIK	159
SM1B259	VL	HLGL43	QIVLTQSPAIMSASPGEKVTMTCSASSSVSYMY WYQQKPGSSPRLLIYDTSNLASGVPVRFSGSGS GTSYSLTISRMEAEDAATYYCQQWSSYPPTFGG GTKLEIK	160
SM1B260	VL	HLGL31	DIVLTQSPASLAVSLGQRATMSCRASESVDGYG NSFLHWYQQKPGQPPKLLIYRASNLESGIPARF SGTGSRTDFTLTITPVEADDVATYYCQQSNGDP FTFGSGTKLEIK	161
SM1B261	VL	HLGL44	NIVMTQSPKSMSMSVGERVTLSCKASENVGTY VSWYQQKPEQSPKLLIYGASNRYTGVPERFTGS GSATDFTLTISSVQAEDLADYHCGQSYSYPLTF GAGTKLELK	162
SM1B262	VL	ATCL189	DIKMTQSPSSMYASLGERVTITCKASQDINSYLS WFQQKPGKSPKTLIYRANRLVDGVPSRFSGSGS GQDYSLTISSLEYEDMGIYYCLQYDEFPLTFGA GTKLELK	163
SM1B263	VL	HLGL45	DIQMTQSPSSLSASLGGKVTITCKASQDINKYIA WYQHKPGKGPRLLIHYTSTLQPGIPSRFSGSGS GRDYSFSISNLEPEDIATYYCLQYDNLWTFGGG TKVEIK	164

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B264	VL	HLGL46	DIQMTQSPASLSASVGETVTIICRASENIYSNLA WYQQKQGKSPQLLVYAATNLADGMPSRFSGS GSGTQYSLKINSLQSEDFGSYYCQHFWGTPWT FGGGTKLEIK	165
SM1B265	VL	HLGL47	DIQMTQSPASLSASVGETVTIICRASENIYSYLA WYQQKQGKSPQLLFYNAKTLVEGVPSRFSGSG SGTQFSLKINSLQPEDFGSYYCQHHYGSPYTFG GGTKLELK	166
SM1B266	VL	HLGL48	DIQMTQSPSTLSASLGDTITITCHASQNINVWLS WYQQKPGNIPKLLIYKASNLHTGVPSRFSGSGS GTGFTLTISSLQPEDIATYYCQQGQSYPLTFGAG TKVEIK	167
SM1B267	VL	HLGL49	DIQMTQSPSTLSASLGDTITITCHASQNINVWLS WYQQKPGNIPKLLIYKASNLHTGVPSRFSGSGS GTGFTLTISSLQPEDIATYYCQQGQSYPYTFGG GTKLEIK	168
SM1B268	VL	GC5L32	EIVLTQSPTTMAASPGEKITITCSASSSISSNYLH WYQQKPGFSPKLLIYRTSNLASGVPARFSGSGS GTSYSLTIGTMEAEDVATYYCQQGSSIPRTFGG GTKLEIK	169
SM1B269	VL	C27L19	DIVLTQSPASLAVSLGQRATISCKASQSVDYDG DSYMNWYQQKPGQPPKLLIYAASNLESGIPARF SGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDP YTFGGGTKLEIK	170
SM1B270	VL	HLGL50	DIVLTQSPASLAVSLGQRASISCKASQSVDYDG DSYMNWYQQKPGQPPKLLIYAASNLESGIPARF SGSGSGTDFTLNIHPVEEEDAATYYCQQSYEDP FTFGSGTKLEIK	171
SM1B271	VL	HLGL43	QIVLTQSPAIMSASPGEKVTMTCSASSSVSYMY WYQQKPGSSPRLLIYDTSNLASGVPVRFSGSGS GTSYSLTISRMEAEDAATYYCQQWSSYPPTFGG GTKLEIK	172
SM1B272	VL	IFWL448	DIVMTQSQKFMSTSVGDRVSVTCKASQNVGTN VAWYQQKPGQSPKALIYSASYRYSGVPDRFTG SGSGTDFTLTISNVQSEDLAEYFCQQYNSYPFTF GSGTKLEIK	173
SM1B273	VL	HLGL51	DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSS NQKNYLAWYQQKPGQSPKLLIYWASTRESGVP DRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYY SYPYTFGGGTKLEIK	174
SM1B274	VL	HLGL52	DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSN GNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPD RFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTH VPPYTFGGGTKLELK	175
SM1B275	VL	HLGL53	DVVMTQTPLTLSVTIGQPASISCKSSQSLLYSNG KTYLNWLLQRPGQSPKRLIYLVSKLDSGVPDRF TGSGSGTDFTLKISRVEAEDLGVFYCVQGTHFP QTFGGGTKLELK	176

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B105	VH	SM1H100	EVQLQQSGAELMTPGASVKISCKATGYTFSTF WIEWIKQRPGHGLEWIGEILPGSGSTKYNEKFK GKATFTADTSSNTAYMQLSSLTSEDSAVYYCA RGGYDGMDYWGQGTSVTVSS	177
SM1B106	VH	SM1H101	EVQLQQSGAELMTPGASVKISCKATGYTFSTF WIEWIKQRPGHGLEWIGEILPGSGSTKYNEKFK GKATFTADTSSNTAYMQLSSLSSEDSAVYYCA RGGYDGMDYWGQGTSVTVSS	178
SM1B107	VH	SM1H102	EVQLQQSEAELMTPGASVKISCKATGYTFSTFW IEWIKQRPGHGLEWIGEILPGSGSTKYNEKFKG KATFTADTSSNTAYMQLSSLTSEDSAVYYCAR GGYDGMDYWGQGTSVTVSS	179
SM1B108	VH	SM1H103	EVQLQQSGAELVKPGASVKISCKASGYAFSSS WMNWVKQRPGKGLEWIGRIYPGDGDTNYHG KFKGKATLTADKSSSTAYMQLSSLTSEDSAVYF CARRNYDGYHYGMDYWGQGTSVTVSS	180
SM1B109	VH	SM1H100	EVQLQQSGAELMTPGASVKISCKATGYTFSTF WIEWIKQRPGHGLEWIGEILPGSGSTKYNEKFK GKATFTADTSSNTAYMQLSSLTSEDSAVYYCA RGGYDGMDYWGQGTSVTVSS	181
SM1B110	VH	SM1H104	EVQLQQSGAELVKPGTSVKMSCKASGYTFTSY WMHWVKLRPGQGLEWIGVIDPSDSYTNYNQK FKGRATLTGDTSSSTAYMQLSSLTSEDSAVYYC TRAAYDNSYYFDYWGQGTTLTVSS	182
SM1B111	VH	SM1H106	EVQLQQSGAELVKPGASVKISCKASGYAFSSS WMNWLKQRPGKGLEWIGRIYPGDGDTNYNGK FKGKATLTADKSSSTAYMQLSSLTSEDSAVYFC ARYGYDYDGEYYYAMDYWGQGTSVTVSS	183
SM1B112	VH	SM1H105	QVQLKESGPELKKPGETVRISCKASGYTFTNYG MNWVKQTPGKGLKWIDWLKSYTGEPTHTGDF KGRFDLSLETSANTAYLQINNLKNEDTATYFCA RGSLFGLDYWGQGTSVTVSS	184
SM1B243	VH	HLGH31	EVQLQQSGAELVKSGASVKLSCTASGFNIKDY YMHWVKQRPEQGLEWIGRIDPANGNTKYDPK FQDKATITSDTSSNTAYLQLSSLTSEDTAVYYC AEGDYVPGYFDVWGAGTTVTVSS	185
SM1B244	VH	HLGH32	EVQLQESGPSLVKPSQTLSLTCSVTGDSITSDY WNWIRKFPGNKLEYMGYISYSGSTYYNPSLKS RISITRDTSKNQYYLQLNSVTTEDTATYYCAGD YGSPYAMDYWGQGTSVTVSS	186
SM1B245	VH	HLGH33	QVQLQQSGAELAKPGASVKMSCKSSGYTFSTY WMHWVKQRPGQGLEWIGYINPNTGYTEYNQK FKDTATLTADKSSSTAYMQLSSLTSEDSAVYYC ARGGSKAFPYYAMDYWGQGTSVTVSS	187
SM1B246	VH	HLGH34	EIQLQQSGPELVKPGASVKMSCKASGYSFTGY NMHWVKQSHGKSLEWIGYIDPYNGATSHNQK FKGKATLTVEKSSSTAYMQLNSLTSEDSAVYY CARGLYGDYWYAYWGQGTLVTVSS	188

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B247	VH	HLGH35	EVQLVESGGGLVKPGGSLKLSCAASGFTFSDY YMYWVRQTPEKRLEWVATISDGGSYTFYPDSV KGRFTISRDNAKNNLYLQMSSLKSEDTAMYYC ARGPTYYGLDYWGQGTTLTVSS	189
SM1B248	VH	HLGH36	QVQLQQPGAELVRPGASVRLSCKASGYSFTSY WMSWVKVRPGQGLEWIGMIHPSDSETRLNQK FKDKATLTVDKSSSTAYMQLSSPTSEDSAVYY CARLYVDFFDYWGQGTTLTVSS	190
SM1B249	VH	HLGH37	DVKLVESGGGLVKLGGSLKLSCAASGFTFSSY YMSWVRQTPEKRLELVAAINSNGGSTYYPDTV KGRFTISRDNAKNTLYLQMSSLKSEDTALYYC ARPDYPYAMDYWGQGTSVTVSS	191
SM1B250	VH	HLGH38	QIQLVQSGPELKKPGETVKISCKASGYTFTNYG MNWVKQAPGKGLKWMGWINTYTGEPTYADD FKGRFAFSLETSASTAYLQINNLKNEDTATYFC ARSPSYGSRGAWFAYWSQGTLVTVSA	192
SM1B251	VH	HLGH39	QIQLVQSGPELKKPGETVKISCKASGYTFTNYG MNWVKQAPGKGLKWMGWINTYTGEPTYADD FKGRFAFSLETSASTAYLQINNLKNEDTATYFC ARSPSYGSRGAWFAYWGQGTLVTVSA	193
SM1B252	VH	HLGH40	QVQLQQSGAELMKPGASVKISCKASGYTFSDY WIEWIKQRPGHGLEWMGEILPGSDKTNYNEKF KGKATFTADSSSNTAYMQLNSLTSEDSAVFYC ATAGDDYVKWGQGTLVTVSA	194
SM1B253	VH	HLGH41	EVQLQQSGAELVKPGASVKLSCTASGFNIKDTY MHWVRQRPEQGLEWIGRIDPANDITKYDPKFQ GKATITADTSSNTAYLQLSSLTSEDTAVYYCGR DWADYWGQGTTLTVSS	195
SM1B254	VH	HLGH42	EVQLQQSGAELVKPGASVKLSCTASGFNIKDTY MHWVKQRSEQGLEWIGRINPANDNTKYDPKF QGKATITADTSSNTAYLQLSSLTSEDTAVYYCG RDWADYWGQGTTLTVSS	196
SM1B255	VH	HLGH43	QVQLQQPGAELVKPGASVKLSCKASGYTFTRY WMHWVKQRPGQGLEWIGEINPNNGHTNYNEK FESRATLTVDKSSSTAYMQFNSLTSEDSAVYYC GRLDGHLYAVDYWGQGTSVTVSS	197
SM1B256	VH	HLGH44	QVQLQQPGTELKMPGTSVKLSCKASGYTFTTY WMHWVKLRPGQGFEWIGEINPSNDGTNYNEK FKRKATLTVDKPSSTAYMQLSSLTSEDSTIYYC TISYYGYGDFDYWGQGTTLTVSS	198
SM1B257	VH	HLGH45	QVQLKESGPDLVQPSQTLSLTCTVSGFSLTSYG VHWVRQPPGKGLEWVGTMGWNDKKYYNSAL KSRLSISRNTSKNQVFLKLSSLQTEDTAMYYCT RDGDSSGSWFAYWGQGTLVTVSS	199
SM1B258	VH	HLGH46	QVQLKESGPDLVQPSQTLSLTCTVSGFSLTGYA VHWVRQPPGKGVEWVGTMGWDDKKFYNSAL KSRLSISRDPSKNQVFFKLSSLQTEDTAMYYCT RDHGDGGFAYWGQGTLVTVSS	200

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B259	VH	HLGH47	EVQLQQSGPELVKPGASVKIPCKASGYTFTDYN MDWVKQSHGKSLEWIGNINPNNGGTIYNQNFK DRATLTVDKSSSTAYMELRSLTSEDTAVYYCT RENSGYGGNYFAYWGQGTTLTVSS	201
SM1B260	VH	HLGH30	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLI YWVKQRPEQGLEWIGWIDPEDGETKFAPRFQD KATITSDTSSNTAYLRLSSLTSEDTAIYYCTRSF GVCWGQGTLVTVSA	202
SM1B261	VH	HLGH30	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLI YWVKQRPEQGLEWIGWIDPEDGETKFAPRFQD KATITSDTSSNTAYLRLSSLTSEDTAIYYCTRSF GVCWGQGTLVTVSA	203
SM1B262	VH	HLGH30	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLI YWVKQRPEQGLEWIGWIDPEDGETKFAPRFQD KATITSDTSSNTAYLRLSSLTSEDTAIYYCTRSF GVCWGQGTLVTVSA	204
SM1B263	VH	HLGH30	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLI YWVKQRPEQGLEWIGWIDPEDGETKFAPRFQD KATITSDTSSNTAYLRLSSLTSEDTAIYYCTRSF GVCWGQGTLVTVSA	205
SM1B264	VH	HLGH30	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLI YWVKQRPEQGLEWIGWIDPEDGETKFAPRFQD KATITSDTSSNTAYLRLSSLTSEDTAIYYCTRSF GVCWGQGTLVTVSA	206
SM1B265	VH	HLGH30	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLI YWVKQRPEQGLEWIGWIDPEDGETKFAPRFQD KATITSDTSSNTAYLRLSSLTSEDTAIYYCTRSF GVCWGQGTLVTVSA	207
SM1B266	VH	HLGH30	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLI YWVKQRPEQGLEWIGWIDPEDGETKFAPRFQD KATITSDTSSNTAYLRLSSLTSEDTAIYYCTRSF GVCWGQGTLVTVSA	208
SM1B267	VH	HLGH30	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLI YWVKQRPEQGLEWIGWIDPEDGETKFAPRFQD KATITSDTSSNTAYLRLSSLTSEDTAIYYCTRSF GVCWGQGTLVTVSA	209
SM1B268	VH	HLGH30	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLI YWVKQRPEQGLEWIGWIDPEDGETKFAPRFQD KATITSDTSSNTAYLRLSSLTSEDTAIYYCTRSF GVCWGQGTLVTVSA	210
SM1B269	VH	HLGH30	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLI YWVKQRPEQGLEWIGWIDPEDGETKFAPRFQD KATITSDTSSNTAYLRLSSLTSEDTAIYYCTRSF GVCWGQGTLVTVSA	211
SM1B270	VH	HLGH30	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLI YWVKQRPEQGLEWIGWIDPEDGETKFAPRFQD KATITSDTSSNTAYLRLSSLTSEDTAIYYCTRSF GVCWGQGTLVTVSA	212

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B271	VH	HLGH30	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLI YWVKQRPEQGLEWIGWIDPEDGETKFAPRFQD KATITSDTSSNTAYLRLSSLTSEDTAIYYCTRSF GVCWGQGTLVTVSA	213
SM1B272	VH	HLGH30	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLI YWVKQRPEQGLEWIGWIDPEDGETKFAPRFQD KATITSDTSSNTAYLRLSSLTSEDTAIYYCTRSF GVCWGQGTLVTVSA	214
SM1B273	VH	HLGH30	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLI YWVKQRPEQGLEWIGWIDPEDGETKFAPRFQD KATITSDTSSNTAYLRLSSLTSEDTAIYYCTRSF GVCWGQGTLVTVSA	215
SM1B274	VH	HLGH30	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLI YWVKQRPEQGLEWIGWIDPEDGETKFAPRFQD KATITSDTSSNTAYLRLSSLTSEDTAIYYCTRSF GVCWGQGTLVTVSA	216
SM1B275	VH	HLGH30	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLI YWVKQRPEQGLEWIGWIDPEDGETKFAPRFQD KATITSDTSSNTAYLRLSSLTSEDTAIYYCTRSF GVCWGQGTLVTVSA	217

[0053] In another embodiment, the antibody or binding fragment thereof comprises a VH region having an amino acid sequence that shares at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity to any one of SEQ ID NOs: 177-217 as shown in Table 3A, and/or a VL region having an amino acid sequence that shares at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity to any one of SEQ ID NOs: 136-176 as shown in Table 3A.

[0054] In one embodiment, the antibody or binding fragment thereof of the present disclosure comprises a humanized VH variant of any one of SEQ ID NOs: 177-217 and/or a humanized VL variant of any one of SEQ ID NOs: 136-176, where the framework regions are humanized or replaced with human immunoglobulin framework sequences. As noted *supra*, suitable human or humanized framework sequences can be chosen based on their known structure, a consensus sequence, sequence homology to the framework sequences of donor antibody (*e.g.*, the framework sequences of SEQ ID NOs: 136-217), or a combination of these approaches. The humanized framework regions are designed to be similar in length and sequence to the parental framework sequences of SEQ ID NOs: 136-217, respectively. In one

embodiment, the humanized framework regions share 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more sequence identity to the framework regions of any one of SEQ ID NOs: 136-217, respectively. In another embodiment, the humanized framework regions are 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more similar in length to the framework regions of any one of SEQ ID NOs: 136-217, respectively. Humanized variants of the VH of any one of SEQ ID NOs: 177-217 and the VL of any one of SEQ ID NOs: 136-176 share at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% sequence identity along the entire length of SEQ ID NOs: 177-217 and SEQ ID NOs: 136-176, respectively.

[0055] Suitable LukAB antibodies or binding portions thereof as disclosed herein comprise a VL of SEQ ID NO: 136 and a VH of SEQ ID NO: 177, a VL of SEQ ID NO: 137 and a VH of SEQ ID NO: 178, a VL of SEQ ID NO: 138 and a VH of SEQ ID NO: 179, a VL of SEQ ID NO:139 and a VH of SEQ ID NO: 180, a VL of SEQ ID NO: 140 and a VH of SEQ ID NO: 181, a VL of SEQ ID NO: 141 and a VH of SEQ ID NO: 182, a VL of SEQ ID NO: 142 and a VH of SEQ ID NO: 183, a VL of SEQ ID NO: 143 and a VH of SEQ ID NO: 184, a VL of SEQ ID NO: 144 and a VH of SEQ ID NO: 185, a VL of SEQ ID NO: 145 and a VH of SEQ ID NO: 186, a VL of SEQ ID NO: 146 and a VH of SEQ ID NO: 187, a VL of SEQ ID NO: 147 and a VH of SEQ ID NO: 188, a VL of SEQ ID NO: 148 and a VH of SEQ ID NO: 189, a VL of SEQ ID NO: 149 and a VH of SEQ ID NO: 190, a VL of SEQ ID NO: 150 and a VH of SEQ ID NO: 191, a VL of SEQ ID NO: 151 and a VH of SEQ ID NO: 192, a VL of SEQ ID NO: 152 and a VH of SEQ ID NO: 193, a VL of SEQ ID NO: 153 and a VH of SEQ ID NO: 194, a VL of SEQ ID NO: 154 and a VH of SEQ ID NO: 195, a VL of SEQ ID NO: 155 and a VH of SEQ ID NO: 196, a VL of SEQ ID NO: 156 and a VH of SEQ ID NO: 197, a VL of SEQ ID NO: 157 and a VH of SEQ ID NO: 198, a VL of SEQ ID NO: 158 and a VH of SEQ ID NO: 199, a VL of SEQ ID NO: 159 and a VH of SEQ ID NO: 200, a VL of SEQ ID NO: 160 and a VH of SEQ ID NO: 201, a VL of SEQ ID NO: 161 and a VH of SEQ ID NO: 202, a VL of SEQ ID NO: 162 and a VH of SEQ ID NO: 203, a VL of SEQ ID NO: 163 and a VH of SEQ ID NO: 204, a VL of SEQ ID NO: 164 and a VH of SEQ ID NO: 205, a VL of SEQ ID NO: 165 and a VH of SEQ ID NO: 206, a VL of SEQ ID NO: 166 and a VH of SEQ ID NO: 207, a VL of SEQ ID NO: 167 and a VH of SEQ ID NO: 208, a VL of SEQ ID NO: 168 and a VH of SEQ ID NO: 209, a VL of SEQ ID NO: 169 and a VH of SEQ ID NO: 210, a VL of SEQ ID NO: 170 and a VH of SEQ ID NO: 211, a VL of SEQ ID NO: 171 and a VH of SEQ ID NO: 212, a VL of SEQ ID NO: 172 and a VH of SEQ ID NO:213, a VL of SEQ ID NO: 173 and a VH of SEQ ID NO: 214, a VL of

SEQ ID NO: 174 and a VH of SEQ ID NO: 215, a VL of SEQ ID NO: 175 and a VH of SEQ ID NO: 216, or a VL of SEQ ID NO: 176 and a VH of SEQ ID NO: 217.

[0056] In one embodiment, the LukAB antibody is a LukAB antigen-binding fragment, *i.e.*, a Fab, comprising the heavy chain variable region (VH) and first heavy chain constant domain (CH1) of an antibody coupled to the light chain variable region (VL) and light chain constant region (CL) of the antibody. In another embodiment, the LukAB antibody is a $F(ab')_2$ fragment, which comprises both LukAB antigen-binding fragments of the full-length antibody coupled by the hinge region. The heavy chain and light chain portions of exemplary LukAB Fab fragments are provided in Table 3B below. Exemplary LukAB Fab or $F(ab')_2$ fragments comprise as disclosed herein, a HC region of SEQ ID NO: 1282 and a LC region OF SEQ ID NO: 1290 (SM1B214); a HC region of SEQ ID NO: 1283 and a LC region of SEQ ID NO: 1291 (SM1B245); a HC region of SEQ ID NO: 1284 and a LC region of SEQ ID NO: 1292 (SM1B255); a HC region of SEQ ID NO: 1285 and a LC region of SEQ ID NO: 1293 (SM1B249); a HC region of SEQ ID NO: 1286 and a LC region of SEQ ID NO: 1294 (SM1B253); a HC region of SEQ ID NO: 1287 and a LC region of SEQ ID NO: 1295 (SM1B254); a HC region of SEQ ID NO: 1288 and a LC region of SEQ ID NO: 1296 (SM1B252); a HC region of SEQ ID NO: 1289 and a LC region of SEQ ID NO: 1297 (SM1B256).

Table 3B. LukAB Fab Amino Acid Heavy Chain (HC) and Light Chain (LC) Sequences

Protein AA ID	Fab of	Region	Fab Amino Acid Sequence	SEQ ID NO:
SM1B214	SM1B111	HC	EVQLQQSGAELVKPGASVKISCKASGYAFS SSWMNWLKQRPGKGLEWIGRIYPGDGDTN YNGKFKGKATLTADKSSSTAYMQLSSLTSE DSAVYFCARYGYDYDGEYYYAMDYWGQG TSVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCHHHHHH	1282
SM1B435	SM1B245	HC	QVQLQQSGAELAKPGASVKMSCKSSGYTFS TYWMHWVKQRPGQGLEWIGYINPNTGYTE YNQKFKDTATLTADKSSSTAYMQLSSLTSE DSAVYYCARGGSKAFPYYAMDYWGQGTS VTVSSASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCHHHHHH	1283

Protein AA ID	Fab of	Region	Fab Amino Acid Sequence	SEQ ID NO:
SM1B436	SM1B255	HC	QVQLQQPGAELVKPGASVKLSCKASGYTFT RYWMHWVKQRPGQGLEWIGEINPNNGHT NYNEKFESRATLTVDKSSSTAYMQFNSLTS EDSAVYYCGRLDGHLYAVDYWGQGTSVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCHHHHHH	1284
SM1B441	SM1B249	HC	DVKLVESGGGLVKLGGSLKLSCAASGFTFS SYYMSWVRQTPEKRLELVAAINSNGGSTYY PDTVKGRFTISRDNAKNTLYLQMSSLKSED TALYYCARPDYPYAMDYWGQGTSVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCHHHHHH	1285
SM1B442	SM1B253	HC	EVQLQQSGAELVKPGASVKLSCTASGFNIK DTYMHWVRQRPEQGLEWIGRIDPANDITKY DPKFQGKATITADTSSNTAYLQLSSLTSEDT AVYYCGRDWADYWGQGTTLTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCHHHHHH	1286
SM1B443	SM1B254	HC	EVQLQQSGAELVKPGASVKLSCTASGFNIK DTYMHWVKQRSEQGLEWIGRINPANDNTK YDPKFQGKATITADTSSNTAYLQLSSLTSED TAVYYCGRDWADYWGQGTTLTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCHHHHHH	1287
SM1B712	SM1B252	HC	QVQLQQSGAELMKPGASVKISCKASGYTFS DYWIEWIKQRPGHGLEWMGEILPGSDKTN YNEKFKGKATFTADSSSNTAYMQLNSLTSE DSAVFYCATAGDDYVKWGQGTLVTVSAAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCHHHHHH	1288
SM1B791	SM1B256	HC	QVQLQQPGTELKMPGTSVKLSCKASGYTFT TYWMHWVKLRPGQGFEWIGEINPSNDGTN YNEKFKRKATLTVDKPSSTAYMQLSSLTSE DSTIYYCTISYYGYGDFDYWGQGTTLTVSS ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCHHHHHH	1289

Protein AA ID	Fab of	Region	Fab Amino Acid Sequence	SEQ ID NO:
SM1B214	SM1B111	LC	DIVMTQSPTTMAASPGERITITCSAHSNLISN YLHWYQQKPGFSPKLLIYRTSNLASGVPAR FSGSGSGTSYSLTIGTMEAEDVATYFCQQGS SIPFTFGSGTKLEIKRTVAAPSVFIFPPSDEQL KSGTASVVCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLSSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKSFNRGEC	1290
SM1B435	SM1B245	LC	DIVLTQSPASLAVSLGQRATMSCRASESVD GYGNSFLHWYQQKPGQPPKLLIYRASNLES GIPARFSGTGSRTDFTLTITPVEADDVATYY CQQSNGDPFTFGSGTKLEIKRTVAAPSVFIFP PSDEQLKSGTASVVCLLNNFYPREAKVQW KVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKS FNRGEC	1291
SM1B436	SM1B255	LC	DVVMTQTPLTLSVTIGQPASISCKSSQSLLDS DGETYLNWLLQRPGQSPKRLIYMVSKLDSG VPDRFTGSGSGTDFTLKISRVEAEDLGVYYC WQGTHFPQTFGGGTKLELKRTVAAPSVFIFP PSDEQLKSGTASVVCLLNNFYPREAKVQW KVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKS FNRGEC	1292
SM1B441	SM1B249	LC	QIVLTQSPAIMSASPGEKVTMTCSASSSVSY MHWYQQKSGTSPKRWIYDTSKLASGVPAR FSGSGSGTSYSLTISSMEAEDAATYYCQQWI SNPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQ LKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1293
SM1B442	SM1B253	LC	DVVMTQTPLTLSVTIGQAASISCKSSQSLLH SDGKTYLNWLLQRPGQSPKRLIYLVSKLDS GVPDRFTGSGSGTDFTLKISRVEAEDLGVY YCWQGTHFPYTFGGGTKLEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQ WKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTK SFNRGEC	1294
SM1B443	SM1B254	LC	DVVMTQTPLTLSVTVGQPASISCKSSQSLLH SDGKTYLNWLLQRPGQSPKRLIYLVSKLDS GVPDRFTGSGSGTDFTLKISRVEAEDLGVY YCWQGTHFPYTFGGGTKLEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQ WKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTK SFNRGEC	1295

Protein AA ID	Fab of	Region	Fab Amino Acid Sequence	SEQ ID NO:
SM1B712	SM1B252	LC	DVLMTQTPLSLPVSLGDQASISCRSSQSIVYS NGNTYLEWYLQKPGQSPKLLIYKVSNRFSG VPDRFSGSGSGTDFTLKISRVEAEDLGVYYC FQGSHVPFTFGSGTKLEIKRTVAAPSVFIFPP SDEQLKSGTASVVCLLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	1296
SM1B791	SM1B256	LC	DVVMTQTPLTLSVTNGQPASISCKSSQSLLD SDGETYLNWLLQRPGQSPKRLIYLVSKLDS GVPDRFIGSGSGTDFTLKISRVEAEDLGVYF CWQGTHSPYTFGGGTKLEIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQW KVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKS FNRGEC	1297

[0057] In another embodiment, the LukAB Fab or F(ab')$_2$ fragments as disclosed above comprise a heavy chain region having an amino acid sequence that shares at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity to any one of SEQ ID NOs: 1282-1289 as shown in Table 3B, and/or a light chain region having an amino acid sequence that shares at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity to any one of SEQ ID NOs: 1290-1297 as shown in Table 3B. Additional LukAB Fab or F(ab')2 fragments of the present disclosure include those derived from the full-length LukAB light chain and heavy chain sequences disclosed in Table 19 below (*i.e.*, full length LukAB light chain sequences of SEQ ID NO: 218-258 and heavy chain sequences of SEQ ID NOs: 259-286 and 811-823).

[0058] Exemplary LukAB antibodies of the present disclosure comprising the VL and VH chains as enumerated above are provided in Table 19 by their respective full-length LC and HC sequences. In particular, the amino acid sequences of the full-length light chain corresponding to and comprising the VL of SEQ ID NOs: 136-176 are provided as SEQ ID NO: 218-258 in Table 19, respectfully. The amino acid sequences of the full-length heavy chains corresponding to and comprising the VH of SEQ ID NOs: 177-217 are provided as SEQ ID NOs: 259-286 and 811-823 in Table 19, respectively.

[0059] Another aspect of the present disclosure relates to an antibody or binding portion thereof that competes for leukocidin AB binding with a monoclonal antibody, wherein said monoclonal antibody comprises a heavy chain variable region comprising a CDR-H1 of SEQ ID NO: 11, a CDR-H2 of SEQ ID NO: 31, and a CDR-H3 of SEQ ID NO: 53, and a light chain variable region comprising a CDR-L1 of SEQ ID NO: 66, a CDR-L2 of SEQ ID NO: 92, and a CDR-L3 of SEQ ID NO: 117. In accordance with this aspect of the disclosure, a competitive binding assay, such as Bio-Layer Interferometry (BLI) as described *infra* in Examples 2 and 3 can be utilized to identify a LukAB antibody or binding portion thereof that competes for LukAB binding with the enumerated monoclonal antibody. Other competitive binding assays known in the art can also be utilized to identify a LukAB antibody in accordance with this aspect of the disclosure.

[0060] Another aspect of the present disclosure relates to antibodies or binding portions thereof that bind *Staphylococcus aureus* Leukocidin E (LukE). LukE is an S-class subunit of another bi-component, pore-forming toxin produced and secreted by *S. aureus*. LukE, acts synergistically together with Leukocidin D (LukD), the F-class subunit of the bi-component toxin, to target and kill host immune cells expressing CCR5, CXCR1/CXCR2, or DARC receptors. In one embodiment, LukE antibodies or binding portions thereof as described herein bind a LukE protein having the amino acid sequence of SEQ ID NO: 826 (which corresponds to the native LukE amino acid sequence containing a poly-histidine tag at the N-terminus to facilitate purification), native LukE, or fragments or homologs thereof. The LukE antibody or binding portion thereof binds LukE with a Kd less than or equal to about 10^{-6}, 10^{-7}, 10^{-8}, 10^{-9}, 10^{-10}, 10^{-11} or 10^{-12} M. In one embodiment, the LukE antibody is a neutralizing antibody, *i.e.*, it neutralizes or prevents the cytolytic activity of LukED on its target immune host cells. Neutralizing LukE antibodies neutralize LukED cytolytic activity by binding to an epitope within regions of the LukE protein involved in LukE and LukD protein-protein interaction or involved in LukED binding to one of its cognitive receptors on target immune cells (e.g., CCR5, CXCR1/CXCR2, or DARC).

[0061] A LukE antibody or binding portion thereof as described herein comprises a heavy chain variable region that comprises: a complementarity-determining region 1 (CDR-H1) comprising an amino acid sequence of any one of SEQ ID NOs: 287-291, or a modified amino acid sequence of any one of SEQ ID NOs: 287-291, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 287-291; a complementarity-determining region 2 (CDR-H2) comprising an amino acid sequence of any one of SEQ ID NOs: 292-296, or a modified amino acid sequence of any one of SEQ ID NOs: 292-296, said modified sequence

having at least 80% sequence identity to any one of SEQ ID NOs: 292-296; and a complementarity-determining region 3 (CDR-H3) comprising an amino acid sequence of any one of SEQ ID NOs: 297-302 or a modified amino acid sequence of any one of SEQ ID NO: 297-302 said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 297-302. The LukE antibody heavy chain CDR1, CDR2 and CDR3 amino acid sequences are provided in Table 4 below.

Table 4. LukE Antibody Heavy Chain CDRs

mAb/Fab name	VH name	HCDR1		HCDR2		HCDR3	
		Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
SM1B507	LKEH1	GYTFTDY	287	NPYNGD	292	GNFFD	297
SM1B508	LKEH2	GYSFTGY	288	NPYNGD	292	SYGYAMD	298
SM1B509	LKEH3	GFSLTGY	289	WGDGS	293	KGGNSPYAMD	299
SM1B510	LKEH3	GFSLTGY	289	WGDGS	293	KGGNSPYAMD	299
SM1B511	LKEH6	GYSFTGY	288	NPYNGD	292	SYGYAMD	298
SM1B512	LKEH6	GYSFTGY	288	NPYNGD	292	SYGYAMD	298
SM1B513	LKEH7	GYSFTGY	288	NPYNGD	292	SYGYAMD	298
SM1B514	LKEH9	GYSFTGY	288	SCYSGA	294	GESYYVMD	300
SM1B208	SM1H118	GFTFSSF	290	SSGSSF	295	EGIYFYDSRYFD	301
SM1B209	SM1H118	GFTFSSF	290	SSGSSF	295	EGIYFYDSRYFD	301
SM1B210	SM1H119	GYSFTGY	288	SCYSGA	294	GESYYVMD	300
SM1B211	SM1H120	GYSITNGNH	291	SSSGS	296	GHYYDGSSYAMD	302

[0062] The LukE antibody or binding portion thereof may further comprise a light chain variable region. Exemplary LukE light chain variable regions comprise a complementarity-determining region 1 (CDR-L1) having an amino acid sequence of any one of SEQ ID NOs: 303-309, or a modified amino acid sequence of any one of SEQ ID NO: 303-309, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 303-309; a complementarity-determining region 2 (CDR-L2) having an amino acid sequence of any one of SEQ ID NOs: 310-313, or a modified amino acid sequence of any one of SEQ ID NO: 310-313, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 310-313; and a complementarity-determining region 3 (CDR-L3) having an amino acid sequence of any one of SEQ ID NOs: 314-323, or a modified amino acid sequence of any one of SEQ ID

NO: 314-323, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 314-323. The LukE antibody light chain CDR1, CDR2 and CDR3 amino acid sequences are provided in Table 5 below.

Table 5. LukE Antibody Light Chain CDRs

mAb/Fab name	VL name	LCDR1		LCDR2		LCDR3	
		Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
SM1B507	LKEL1	SSSVSY	303	STS	310	RSNYPL	314
SM1B508	LKEL2	SQTIVHSNGNTY	304	KVS	311	GSHVPF	315
SM1B509	LKEL3	SSSVSSSY	305	STS	310	WTTFPP	316
SM1B510	IFWL470	SQSLVHSNGNTY	306	KVS	311	STHVPP	317
SM1B511	ATCL19	SQSLVHSNGNTY	306	KVS	311	STHVPL	318
SM1B512	LKEL5	SQTIVHSNGNTY	304	KVS	311	GSHVPF	315
SM1B513	LKEL6	SSSVSY	303	STS	310	RSSYPW	319
SM1B514	LKEL9	SQDINSY	307	RAN	312	YDEFPY	320
SM1B208	SM1L38	SQDIVHSNGNTY	308	KVS	311	SSHFPW	321
SM1B209	SM1L39	SQDIVHSNGNTY	308	KVS	311	SSHFPW	321
SM1B210	SM1L40	SQSLVHSNGNTY	306	KVS	311	STHVPF	322
SM1B211	SM1L41	SESVDSYGNSF	309	RAS	313	SNEDPL	323

[0063] The LukE antibodies disclosed herein comprise the heavy chain CDRs of Table 4 and light chain CDRs of Table 5 or modified CDRs thereof. Encompassed by the present disclosure are CDRs of Table 4 and 5 containing 1, 2, 3, 4, 5, or more amino acid substitutions (depending on the length of the particular CDR) that maintain or enhance LukE or LukED binding of the antibody. The resulting modified CDRs are at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% similar in sequence to the CDRs of Tables 4 and 5. Suitable amino acid modifications and insertion to the heavy chain CDR sequences of Table 4 and/or the light chain CDR sequences of Table 5 are described *supra*.

[0064] In one embodiment, the LukE antibody or binding portion thereof of the present disclosure comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 287, the CDR-H2 of SEQ ID NO: 292, and the CDR-H3 of SEQ ID NO: 297. In another embodiment, the LukE antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 288, the CDR-H2 of SEQ ID NO: 292, and the CDR-H3 of SEQ ID NO: 298. In another embodiment, the LukE antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 289, the CDR-H2 of SEQ ID NO: 293, and the CDR-H3 of SEQ ID NO: 299. In another

embodiment, the LukE antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 288, the CDR-H2 of SEQ ID NO: 294, and the CDR-H3 of SEQ ID NO: 300. In another embodiment, the LukE antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 290, the CDR-H2 of SEQ ID NO: 295, and the CDR-H3 of SEQ ID NO: 301. In another embodiment, the LukE antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 288, the CDR-H2 of SEQ ID NO: 294, and the CDR-H3 of SEQ ID NO: 300. In another embodiment, the LukE antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 291, the CDR-H2 of SEQ ID NO: 296, and the CDR-H3 of SEQ ID NO: 302.

[0065] In one embodiment, the LukE antibody or binding portion thereof of the present disclosure comprises a light chain variable region, where the light chain variable region comprises the CDR-L1 of SEQ ID NO: 303, the CDR-L2 of SEQ ID NO: 310, and the CDR-L3 of SEQ ID NO: 314. In another embodiment, the LukE antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 304, the CDR-L2 of SEQ ID NO: 311, and the CDR-L3 of SEQ ID NO: 315. In another embodiment, the LukE antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 305, the CDR-L2 of SEQ ID NO: 310, and the CDR-L3 of SEQ ID NO: 316. In another embodiment, the LukE antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 306, the CDR-L2 of SEQ ID NO: 311, and the CDR-L3 of SEQ ID NO: 317. In another embodiment, the LukE antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 306, the CDR-L2 of SEQ ID NO: 311, and the CDR L3 of SEQ ID NO: 318. In another embodiment, the LukE antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 303, the CDR-L2 of SEQ ID NO: 310, and the CDR-L3 of SEQ ID NO: 319. In another embodiment, the LukE antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 307, the CDR-L2 of SEQ ID NO: 312, and the CDR-L3 of SEQ ID NO: 320. In another embodiment, the LukE antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 308, the CDR-L2 of SEQ ID NO: 311, and the CDR-L3 of SEQ ID NO: 321. In another embodiment, the LukE antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 306, the CDR-L2 of SEQ ID NO: 311, and the CDR-L3 of SEQ ID NO: 322. In another embodiment, the LukE antibody or

binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 309, the CDR-L2 of SEQ ID NO: 313, and the CDR-L3 of SEQ ID NO: 323.

[0066] In another embodiment, the LukE antibody or binding portion thereof comprises the heavy chain CDRs of SEQ ID NOs: 287, 292 and 297 together with the light chain CDRs of SEQ ID NOs: 303, 310, and 314; the heavy chain CDRs of SEQ ID NOs: 288, 292, and 298 together with the light chain CDRs of SEQ ID NOs: 304, 211, and 315; the heavy chain CDRs of SEQ ID NOs: 289, 293, 299 together with the light chain CDRs of SEQ ID NOs: 305, 310, and 316; the heavy chain CDRs of SEQ ID NOs: 289, 293, and 299 together with the light chain CDRs of SEQ ID NOs: 306, 311, and 317; the heavy chain CDRs of SEQ ID NOs: 288, 292, and 298 together with the light chain CDRs of SEQ ID NOs: 306, 311, and 318; the heavy chain CDRs of SEQ ID NOs: 288, 292, and 298 together with the light chain CDRs of SEQ ID NOs: 304, 311, and 315; the heavy chain CDRs of SEQ ID NOs: 288, 292, and 298 together with the light chain CDRs of SEQ ID NOs: 303, 310, and 319; the heavy chain CDRs of SEQ ID NOs: 288, 294, and 300 together with the light chain CDRs of SEQ ID NOs: 307, 312, and 320; the heavy chain CDRs of SEQ ID NOs: 290, 295, and 301 together with the light chain CDRs of SEQ ID NOs: 308, 311, and 321; the heavy chain CDRs of SEQ ID NOs: 288, 294, and 300 together with the light chain CDRs of SEQ ID NOs: 306, 311, and 322; and the heavy chain CDRs of SEQ ID NOs: 291, 296, and 302 together with the light chain CDRs of SEQ ID NOs: 309, 313, and 323.

[0067] The LukE antibody or binding portion thereof as described herein may comprises a variable light (VL) chain, a variable heavy (VH) chain, or a combination of a VL and VH chain. The VL chain of the LukE antibody as disclosed herein may comprise an amino acid sequence selected from SEQ ID NOs: 324-335 or an amino acid sequence that is at least 80% identical to any one of the amino acid sequence selected from SEQ ID NOs: 324-335. The VH chain of the LukE antibody as disclosed herein may comprise an amino acid sequence selected from SEQ ID NOs: 336-347 or an amino acid sequence that is at least 80% identical to any one of the amino acid sequence selected from SEQ ID NOs: 336-347. The amino acid sequences of the LukE VL and VH chains are provided in Table 6A below.

Table 6A. LukE Antibody Variable Light (VL) and Variable Heavy (VH) Chain Sequences

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B507	VL	LKEL1	DIVMTQSPAIMSASPGEKVTIPCSASSSVSYMHWF QQKPGTSPKLWIYSTSNLASGVPGRFSGSGSGTSY SLTISRMEAEDAATYYCQQRSNYPLTFGAGTKLE LK	324

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B508	VL	LKEL2	DVVMTQTPLSLPVSLGDQASISCRSSQTIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPFTFGGGTKLEIR	325
SM1B509	VL	LKEL3	DIVMTQAAAIMSASPGEKVTLTCSASSSVSSSYLYWYQQKPGSSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISSMEAEDAASYFCHQWTTFPPTFGGGTKLEIK	326
SM1B510	VL	IFWL470	DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPTFGGGTKLEIK	327
SM1B511	VL	ATCL19	DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPLTFGAGTKLELK	328
SM1B512	VL	LKEL5	DIKMTQSPLSLPVSLGDQASISCRSSQTIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPFTFGGGTKLEIR	329
SM1B513	VL	LKEL6	DIVLTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPWTFGGGTKLEIK	330
SM1B514	VL	LKEL9	DIVMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPSRFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK	331
SM1B208	VL	SM1L38	DIVMTQSPLSLPVSLGDQASISCRSSQDIVHSNGNTYLGWYLQKPGRSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQSSHFPWTFGGGTRLEIK	332
SM1B209	VL	SM1L39	DVVMTQTPLSLPVSLGDQASISCRSSQDIVHSNGNTYLGWYLQKPGRSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQSSHFPWTFGGGTRLEIK	333
SM1B210	VL	SM1L40	DIVLTQSPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPFTFGSGTKLEIK	334
SM1B211	VL	SM1L41	DIVLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYRASNLESGIPARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGAGTKLELK	335
SM1B507	VH	LKEH1	EVQLQQSGAELVKPGASVKMSCKASGYTFTDYYMDWVKQSHGKSFEWIGHVNPYNGDTRYNQKFKGKATLTVDKSSTTAYMELNSLTSEDSAVYYCARGNFFDYWGQGTTLSVSS	336

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B508	VH	LKEH2	EVQLQQSGAELVKPGASVKISCKTSGYSFTGYFM NWVMQSHGKSLEWIGRINPYNGDTFYNQKFKGK ATLTVDKSSSTAHMELRSLASEDSAVYYCARSYG YAMDYWGQGTSVTVSS	337
SM1B509	VH	LKEH3	QVQLKESGPGLVAPSQSLSITCTVSGFSLTGYGVN WVRQPPGKGLEWLGLMWGDGSTDYNSALNSRL RINKDNSKSQVFLKMSSLQTDDTAIYYCVRKGGN SPYAMDYWGQGTSVTVSS	338
SM1B510	VH	LKEH3	QVQLKESGPGLVAPSQSLSITCTVSGFSLTGYGVN WVRQPPGKGLEWLGLMWGDGSTDYNSALNSRL RINKDNSKSQVFLKMSSLQTDDTAIYYCVRKGGN SPYAMDYWGQGTSVTVSS	339
SM1B511	VH	LKEH6	EVKLVESGPELVKPGASVKISCKTSGYSFTGYFM NWVMQSHGKSLEWIGRINPYNGDTFYNQKFKGK ATLTVDKSSSTAHMELRSLASEDSAVYYCARSYG YAMDYWGQGTSVTVSS	340
SM1B512	VH	LKEH6	EVKLVESGPELVKPGASVKISCKTSGYSFTGYFM NWVMQSHGKSLEWIGRINPYNGDTFYNQKFKGK ATLTVDKSSSTAHMELRSLASEDSAVYYCARSYG YAMDYWGQGTSVTVSS	341
SM1B513	VH	LKEH7	EVQLQQSGPELVKPGASVKISCKASGYSFTGYFM NWVMQSHGKSLEWIGRINPYNGDTFYNQKFKAK ATLTVDKSSNTAHMELRSLASEDSAVYFCARSYG YAMDYWGLGTSVTVSS	342
SM1B514	VH	LKEH9	EVQLQQSGPELVKTGASVKISCKASGYSFTGYYM HWVKQSHGKSLEWIGYLSCYSGATSYNQKFKGK ATFTVDTSSTTAYMQFNSLTSEDSAVYYCARGES YYVMDYWGQGTSVTVSS	343
SM1B208	VH	SM1H118	EVQLQQSGGGSVQPGGSRKLSCAASGFTFSSFGM HWVRQAPEKGLEWVAYISSGSSFIYYGDTVKGRF TISRDNPNNTLFLQMTSLRSEDTAIYYCAREGIYF YDSRYFDVWGAGTTVTVSS	344
SM1B209	VH	SM1H118	EVQLQQSGGGSVQPGGSRKLSCAASGFTFSSFGM HWVRQAPEKGLEWVAYISSGSSFIYYGDTVKGRF TISRDNPNNTLFLQMTSLRSEDTAIYYCAREGIYF YDSRYFDVWGAGTTVTVSS	345
SM1B210	VH	SM1H119	EFQLQQSGPELVKTGASVKISCKASGYSFTGYYM HWVKQSHGRSLEWIGYLSCYSGATSYNQKFKGK ATFTVDTSSTTAYMQFNSLTSEDSAVYYCARGES YYVMDYWGQGTSVTVSS	346
SM1B211	VH	SM1H120	EVQLQQSGPGLVKPSQTVSLTCTVTGYSITNGNH WWNWIRQVSGSKLEWIGYISSSGSTDSNPSLKSRI SITRDTSKNQLFLQLNSVTTEDIATYYCARGHYY DGSSYAMDYWGQGTSVTVSS	347

[0068] In another embodiment, the antibody or binding fragment thereof comprises a VH region having an amino acid sequence that shares at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at

least 94% at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity to any one of SEQ ID NOs: 336-347 as shown in Table 6A, and/or a VL region having an amino acid sequence that shares at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity to any one of SEQ ID NOs: 324-335 as shown in Table 6A.

[0069] In one embodiment, the antibody or binding fragment thereof of the present disclosure comprises a humanized VH variant of any one of SEQ ID NOs: 336-347 and/or a humanized VL variant of any one of SEQ ID NOs: 324-335, where the framework regions are humanized or replaced with human immunoglobulin framework sequences. The humanized framework regions are designed to be similar in length and sequence to the parental framework sequences within SEQ ID NOs: 324-347, respectively. In one embodiment, the humanized framework regions share 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more sequence identity to the framework regions of any one of SEQ ID NOs: 324-347, respectively. In another embodiment, the humanized framework regions are 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more similar in length to the framework regions of any one of SEQ ID NOs: 324-347, respectively. Humanized variants of the VH of any one of SEQ ID NOs: 336-347 and the VL of any one of SEQ ID NOs: 324-335 share at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% sequence identity along the entire length of SEQ ID NOs: 336-347 and SEQ ID NOs: 324-335, respectively.

[0070] Suitable LukE antibodies as disclosed herein comprise a VL of SEQ ID NO: 324 and a VH of SEQ ID NO: 336; a VL of SEQ ID NO: 325 and a VH of SEQ ID NO: 337; a VL of SEQ ID NO: 326 and a VH of SEQ ID NO: 338; a VL of SEQ ID NO: 327 and a VH of SEQ ID NO: 339; a VL of SEQ ID NO: 328 and a VH of SEQ ID NO: 340; a VL of SEQ ID NO: 329 and a VH of SEQ ID NO: 341; a VL of SEQ ID NO: 330 and a VH of SEQ ID NO: 342; a VL of SEQ ID NO: 331 and a VH of SEQ ID NO: 343; a VL of SEQ ID NO: 332 and a VH of SEQ ID NO: 344; a VL of SEQ ID NO: 333 and a VH of SEQ ID NO: 345; a VL of SEQ ID NO: 334 and a VH of SEQ ID NO: 346; or a VL of SEQ ID NO: 335 and a VH of SEQ ID NO: 347.

[0071] In one embodiment, the LukE antibody is a LukE antigen-binding fragment, *i.e.*, a Fab, comprising the heavy chain variable region (VH) and first heavy chain constant domain (CH1) of an antibody coupled to the light chain variable region (VL) and light chain constant region (CL) of the antibody. In another embodiment, the LukE antibody is a $F(ab')_2$ fragment, which comprises both LukE antigen-binding fragments of the full-length antibody coupled by the

hinge region. The heavy chain and light chain portions of exemplary LukE Fab fragments are provided in Table 6B below. Exemplary LukE Fab or $F(ab')_2$ fragments comprise as disclosed herein, a HC region of SEQ ID NO: 1298 and a LC region OF SEQ ID NO: 1301 (SM1B507); a HC region of SEQ ID NO: 1299 and a LC region of SEQ ID NO: 1302 (SM1B508); a HC region of SEQ ID NO: 1300 and a LC region of SEQ ID NO: 1303 (SM1B512).

Table 6B. LukE Fab Amino Acid Heavy Chain (HC) and Light Chain (LC) Sequences

Protein AA ID	Fab of	Region	Fab Amino Acid Sequence	SEQ ID NO:
SM1B709	SM1B507	HC	EVQLQQSGAELVKPGASVKMSCKASGYTF TDYYMDWVKQSHGKSFEWIGHVNPYNGD TRYNQKFKGKATLTVDKSSTTAYMELNSLT SEDSAVYYCARGNFFDYWGQGTTLSVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCHHHHHH	1298
SM1B710	SM1B508	HC	EVQLQQSGAELVKPGASVKISCKTSGYSFT GYFMNWVMQSHGKSLEWIGRINPYNGDTF YNQKFKGKATLTVDKSSSTAHMELRSLASE DSAVYYCARSYGYAMDYWGQGTSVTVSS ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCHHHHHH	1299
SM1B711	SM1B512	HC	EVKLVESGPELVKPGASVKISCKTSGYSFTG YFMNWVMQSHGKSLEWIGRINPYNGDTFY NQKFKGKATLTVDKSSSTAHMELRSLASED SAVYYCARSYGYAMDYWGQGTSVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCHHHHHH	1300
SM1B709	SM1B507	LC	DIVMTQSPAIMSASPGEKVTIPCSASSSVSY MHWFQQKPGTSPKLWIYSTSNLASGVPGRF SGSGSGTSYSLTISRMEAEDAATYYCQQRS NYPLTFGAGTKLELKRTVAAPSVFIFPPSDE QLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGE C	1301

Protein AA ID	Fab of	Region	Fab Amino Acid Sequence	SEQ ID NO:
SM1B710	SM1B508	LC	DVVMTQTPLSLPVSLGDQASISCRSSQTIVH SNGNTYLEWYLQKPGQSPKLLIYKVSNRFS GVPDRFSGSGSGTDFTLKISRVEAEDLGVYY CFQGSHVPFTFGGGTKLEIRRTVAAPSVFIFP PSDEQLKSGTASVVCLLNNFYPREAKVQW KVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKS FNRGEC	1302
SM1B711	SM1B512	LC	DIKMTQSPLSLPVSLGDQASISCRSSQTIVHS NGNTYLEWYLQKPGQSPKLLIYKVSNRFSG VPDRFSGSGSGTDFTLKISRVEAEDLGVYYC FQGSHVPFTFGGGTKLEIRRTVAAPSVFIFPP SDEQLKSGTASVVCLLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	1303

[0072] In another embodiment, the LukE Fab or F(ab')$_2$ fragments as disclosed above comprise a heavy chain region having an amino acid sequence that shares at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity to any one of SEQ ID NOs: 1298-1300 as shown in Table 6B, and/or a light chain region having an amino acid sequence that shares at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity to any one of SEQ ID NOs: 1301-1303 as shown in Table 6B. Additional LukE Fab or F(ab')2 fragments of the present disclosure include those derived from the full-length LukE light chain and heavy chain sequences disclosed in Table 20 below (*i.e.*, full length LukE light chain sequences of SEQ ID NO: 348-359 and heavy chain sequences of SEQ ID NOs: 360-371).

[0073] Exemplary LukE antibodies of the present disclosure comprising the VL and VH chains as enumerated above are provided in Table 20 by their respective full-length LC and HC sequences. In particular, the amino acid sequences of the full-length light chain corresponding to and comprising the VL of SEQ ID NOs: 324-335 are provided as SEQ ID NO: 348-359 in Table 20, respectfully. The amino acid sequences of the full-length heavy chains corresponding to and comprising the VH of SEQ ID NOs: 336-347 are provided as SEQ ID NOs: 360-371 in Table 20, respectively.

[0074] Another aspect of the present disclosure is directed to an antibody or binding portion thereof that competes for leukocidin E binding with a monoclonal antibody, wherein said monoclonal antibody comprises a heavy chain variable region comprising a CDR-H1 of SEQ ID NO: 290, a CDR-H2 of SEQ ID NO: 295, and a CDR-H3 of SEQ ID NO: 301, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 308, the CDR-L2 of SEQ ID NO: 311, and the CDR-L3 of SEQ ID NO: 321. In accordance with this aspect of the disclosure, a competitive binding assay, such as BLI as described *infra* in Examples 2 and 3 can be utilized to identify a LukE antibody or binding portion thereof that competes for LukE binding with the enumerated monoclonal antibody. Other competitive binding assays known in the art can also be utilized to identify a LukE antibody in accordance with this aspect of the disclosure.

[0075] Another aspect of the present disclosure relates to antibodies or binding portions thereof that bind *Staphylococcus aureus* Leukocidin D (LukD). In one embodiment, LukD antibodies or binding portions thereof as described herein bind a LukD protein having the amino acid sequence of SEQ ID NO: 825 (which corresponds to the native LukD amino acid sequence containing a poly-histidine tag at the N-terminus to facilitate purification), native LukD protein, or fragments or homologs thereof. In one embodiment, the LukD antibody is a neutralizing antibody, *i.e.*, it neutralizes or prevents the cytolytic activity of LukED on its target immune host cells. The LukD antibody or binding portion thereof binds LukD with a Kd less than or equal to about 10^{-6}, 10^{-7}, 10^{-8}, 10^{-9}, 10^{-10}, 10^{-11} or 10^{-12} M. Neutralizing LukD antibodies neutralize LukED cytolytic activity by binding to an epitope within regions of the LukD protein involved in LukD and LukE protein-protein interaction or involved in LukED binding to one of its cognitive receptors on target immune cells (e.g., CCR5, CXCR1/CXCR2, or DARC).

[0076] A LukD antibody or binding portion thereof of the present disclosure comprises a heavy chain variable region that comprises: a complementarity-determining region 1 (CDR-H1) comprising an amino acid sequence of any one of SEQ ID NOs: 372-374, or a modified amino acid sequence of any one of SEQ ID NOs: 372-374, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 372-374; a complementarity-determining region 2 (CDR-H2) comprising an amino acid sequence of any one of SEQ ID NOs: 375-379, or a modified amino acid sequence of any one of SEQ ID NOs: 375-379, said modified sequences having at least 80% sequence identity to any one of SEQ ID NOs: 375-379; and a complementarity-determining region 3 (CDR-H3) comprising an amino acid sequence of any one of SEQ ID NOs: 380-383, or a modified amino acid sequence of any one of SEQ ID NO: 380-383, said modified sequence having at least 80% sequence identity to any one of SEQ ID

NOs: 380-383. The LukD antibody heavy chain CDR1, CDR2 and CDR3 amino acid sequences are provided in Table 7 below.

Table 7. LukD Antibody Heavy Chain CDRs

mAb/Fab name	VH name	HCDR1		HCDR2		HCDR3	
		Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
SM1B221	LKDH1	GYTFTDY	372	DTSDSY	375	DYGYAMD	380
SM1B222	LKDH2	GYTFTDY	372	FPGNSD	376	TELD	381
SM1B223	LKDH3	GYTFTDY	372	DTSDSY	375	DYGYAMD	380
SM1B224	LKDH4	GYTFTDY	372	DASDSY	377	DFGYAMD	380
SM1B225	LKDH5	GFTFSSY	373	TGGGTY	378	HRDGNYGCFD	382
SM1B226	LKDH6	GYTFTDY	372	DTSDSY	375	DYGYAMD	380
SM1B227	LKDH7	GYTFTSY	374	NPYNAD	379	SAMD	383
SM1B228	LKDH8	GYTFTDY	372	DTSDSY	375	DYGYAMD	380

[0077] The LukD antibody or binding portion thereof may further comprise a light chain variable region. Exemplary LukD light chain variable regions comprise a complementarity-determining region 1 (CDR-L1) having an amino acid sequence of any one of SEQ ID NOs: 384-387, or a modified amino acid sequence of any one of SEQ ID NO: 384-387, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 384-387; a complementarity-determining region 2 (CDR-L2) having an amino acid sequence of any one of SEQ ID NOs: 388-391, or a modified amino acid sequence of any one of SEQ ID NO: 388-391, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 388-391; and a complementarity-determining region 3 (CDR-L3) having an amino acid sequence of any one of SEQ ID NOs: 392-397, or a modified amino acid sequence of any one of SEQ ID NO: 392-397, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 392-397. The LukD antibody light chain CDR1, CDR2 and CDR3 amino acid sequences are provided in Table 8 below.

Table 8. LukD Antibody Light Chain CDRs

mAb/Fab name	VL name	LCDR1		LCDR2		LCDR3	
		Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
SM1B221	LKDL1	SLSVSY	384	SAS	388	RSSYPF	392
SM1B222	LKDL2	SQSLIHNDGNTY	385	KVS	389	STHVPF	393

mAb/Fab name	VL name	LCDR1		LCDR2		LCDR3	
		Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
SM1B223	LKDL3	SLSVSF	384	SAS	388	RSSYPF	392
SM1B224	LKDL4	SSSVSF	386	STS	390	RSTYPY	394
SM1B225	LKDL5	SSSVSSSY	387	STS	390	YHRSPQ	395
SM1B226	LKDL6	SSSVSF	386	SAS	388	RSSYPY	396
SM1B227	LKDL7	SSSVSY	386	DTS	391	GSGYPL	397
SM1B228	LKDL8	SSSVSY	386	SAS	388	RSSYPF	392

[0078] The LukD antibodies disclosed herein comprise the heavy chain CDRs of Table 7 and light chain CDRs of Table 8 or modified CDRs thereof. Encompassed by the present disclosure are CDRs of Table 7 and 8 containing 1, 2, 3, 4, 5, or more amino acid substitutions that maintain or enhance LukD or LukED binding of the antibody. The resulting modified CDRs are at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% similar in sequence to the CDRs of Tables 7 and 8. Suitable amino acid modifications and insertion to the heavy chain CDR sequences of Table 7 and/or the light chain CDR sequences of Table 8are described *supra*.

[0079] In one embodiment, the LukD antibody or binding portion thereof of the present disclosure comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 372, the CDR-H2 of SEQ ID NO: 375, and the CDR-H3 of SEQ ID NO: 380. In another embodiment, the LukD antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 372, the CDR-H2 of SEQ ID NO: 376, and the CDR-H3 of SEQ ID NO: 381. In another embodiment, the LukD antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 372, the CDR-H2 of SEQ ID NO: 377, and the CDR-H3 of SEQ ID NO: 380. In another embodiment, the LukD antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 373, the CDR-H2 of SEQ ID NO: 378, and the CDR-H3 of SEQ ID NO: 382. In another embodiment, the LukD antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 374, the CDR-H2 of SEQ ID NO: 379, and the CDR-H3 of SEQ ID NO: 383.

[0080] In another embodiment, the LukD antibody or binding portion thereof of the present disclosure comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 384, the CDR-L2 of SEQ ID NO: 388, and the CDR-L3 of SEQ ID NO: 392. In another embodiment, the LukD antibody or binding portion thereof comprises a light chain variable

region comprising the CDR-L1 of SEQ ID NO: 385, the CDR-L2 of SEQ ID NO: 389, and the CDR-L3 of SEQ ID NO: 393. In another embodiment, the LukD antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 386, the CDR-L2 of SEQ ID NO: 390, and the CDR-L3 of SEQ ID NO: 394. In another embodiment, the LukD antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 387, the CDR-L2 of SEQ ID NO: 390, and the CDR-L3 of SEQ ID NO: 395. In another embodiment, the LukD antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 386, the CDR-L2 of SEQ ID NO: 388, and the CDR-L3 of SEQ ID NO: 396. In another embodiment, the LukD antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 386, the CDR-L2 of SEQ ID NO: 391, and the CDR-L3 of SEQ ID NO: 397. In another embodiment, the LukD antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 386, the CDR-L2 of SEQ ID NO: 388, and the CDR-L3 of SEQ ID NO: 392.

[0081] In another embodiment, the LukD antibody or binding portion thereof comprises the heavy chain CDRs of SEQ ID NOs: 372, 375 and 380 together with the light chain CDRs of SEQ ID NOs: 384, 388, and 392; the heavy chain CDRs of SEQ ID NOs: 372, 376, and 381 together with the light chain CDRs of SEQ ID NOs: 385, 389, and 393; the heavy chain CDRs of SEQ ID NOs: 372, 377, and 380 together with the light chain CDRs of SEQ ID NOs: 386, 390, and 394; the heavy chain CDRs of SEQ ID NOs: 373, 378, and 382 together with the light chain CDRs of SEQ ID NOs: 387, 390, and 395; the heavy chain CDRs of SEQ ID NOs: 372, 375, and 380 together with the light chain CDRs of SEQ ID NOs: 386, 388 and 396; the heavy chain CDRs of SEQ ID NOs: 374, 379, and 383 together with the light chain CDRs of SEQ ID NOs: 386, 391, and 397; the heavy chain CDRs of SEQ ID NOs: 372, 375, and 380 together with the light chain CDRs of SEQ ID NOs: 386, 388, and 392.

[0082] The LukD antibody or binding portion thereof as described herein may comprises a variable light (VL) chain, a variable heavy (VH) chain, or a combination of a VL and VH chain. The VL chain of the LukD antibody as disclosed herein may comprise an amino acid sequence selected from SEQ ID NOs: 398-405 or an amino acid sequence that is at least 80% identical to any one of the amino acid sequence selected from SEQ ID NOs: 398-405. The VH chain of the LukD antibody as disclosed herein may comprise an amino acid sequence selected from SEQ ID NOs: 406-413 or an amino acid sequence that is at least 80% identical to any one of the amino acid sequence selected from SEQ ID NOs: 406-413. The amino acid sequences of the LukD VL and VH chains are provided in Table 9A below.

Table 9A. LukD Antibody Variable Light (VL) and Variable Heavy (VH) Chain Sequences

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B221	VL	LKDL1	QIVLTQSPAIMSASPGEKVTITCSASLSVSYMHWF QQKPGTSPKLWIYSASNLASGVPARFSGSGSGTS YSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKL EIK	398
SM1B222	VL	LKDL2	DVVMTQTPLSLPVSLGDQASISCRSSQSLIHNDGN TYLHWYLQKPGQSPKLLIYKVSNRFSGVPDRFSG SGSGTDFTVKISRVEAEDLGVYFCSQSTHVPFTFG AGTKLELK	399
SM1B223	VL	LKDL3	QIVLSQSPAIMSASPGEKVTITCSASLSVSFMHWF QQKPGTSPKLWIYSASNLASGVPARFSGSGSGTS YSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKL EIK	400
SM1B224	VL	LKDL4	QIVLTQSPAIMSASPGEKVTITCSASSSVSFMHWF QQKPGTSPKLWIYSTSNLASGVPARFSGSGSGTSY SLTISRMEAEDAATYYCQQRSTYPYTFGGGTKME IK	401
SM1B225	VL	LKDL5	DIVLTQSPAIMSASLGERVTMTCTASSSVSSSYLH WYQQKPGSSPKLWVYSTSNLASGVPARFSGSGS GSSYSLTISSMEPEDTATYYCHQYHRSPQTFGGG TKLEIK	402
SM1B226	VL	LKDL6	QIVLTQSPAIMSASPGEKVTITCSASSSVSFMHWF QQKPGTSPKLWIYSASNLASGVPARFSGSGSGTS YSLTISRMEAEDAATYYCQQRSSYPYTFGGGTKL EIK	403
SM1B227	VL	LKDL7	DIVLTQSPAIMSASPGEKVTMTCSASSSVSYMHW YQQKSSTSPKLWIYDTSKLASGVPGRFSGSGSGN SYSLTISSMEAEDVATYYCFQGSGYPLTFGSGTKL EIK	404
SM1B228	VL	LKDL8	QIVLTQSPAIMSASPGEKVTITCSASSSVSYMHWF QQKPGTSPKLWIYSASNLASGVPARFSGSGSGTS YSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKL EIK	405
SM1B221	VH	LKDH1	QVQLQQSGAELVMPGASVKMSCKASGYTFTDY WMHWVKQRPGQGLEWIGAIDTSDSYTSYNQKF KGKATLTVDESSSTAYMQLSSLTSEDSAVYYCAR DYGYAMDYWGQGTSVTVSS	406
SM1B222	VH	LKDH2	EVQLQQSGAMLARPGASVTMSCKASGYTFTDY WMHWVRQGPGQGLEWIGAIFPGNSDTTYNQKFR GKAKLTAVTSAITAYMEVSSLTNIDSAVYYCTVT ELDYWGQGTTLTVSS	407
SM1B223	VH	LKDH3	EVQLQQSGADLVMPGTSMKLSCKASGYTFTDY WIHWVKQGPGQGLEWIGAIDTSDSYINYNQKFT DKATLTVDESSSTAYMHLSSLTSEDSAVYYCARD YGYAMDYWGQGTSVTVSS	408
SM1B224	VH	LKDH4	QVQLQQPGAELVMPGSSVKMSCKASGYTFTDY WMHWVKQRPGQGLEWIGAIDASDSYTSYDQKF KGKATLTVDDSSSTAYIHLNSLTSEDSAVYYCAR DFGYAMDYWGQGTSVTVSS	409

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B225	VH	LKDH5	EVQLQQSGGGLVKPGGSLKLSCAASGFTFSSYAM SWVRQTPEKRLEWVATITGGGTYTYYLDSVKGR FTISRDNAKTSLYLQMSSLRSEDTAMYYCARHRD GNYGCFDVWGAGTTVTVSS	410
SM1B226	VH	LKDH6	EVQLQQSGAELVMPGASVKMSCKASGYTFTDY WMHWVLQRPGQGLEWIGAIDTSDSYTTYNQKFK GKATLTVDESSSTAYMLLSSLTSEDSAVYYCARD YGYAMDYWGQGSSVTVSS	411
SM1B227	VH	LKDH7	EFQLQQSGPELVKPGASVKMSCKASGYTFTSYFI HWVKQKPGQGLEWIGFINPYNADTNYNEKFKGK ATLTSDKSSSTAYMELSSLTSEDSAVYYCTPSAM DYWGQGTSVTVSS	412
SM1B228	VH	LKDH8	QVQLQQSGAELVMPGASVKMSCKASGYTFTDY WMHWVKQRPGQGLEWIGAIDTSDSYTTYNQKF KGKATLTVDESSSTAYMQLSSLTSEDSAVYYCAR DYGYAMDYWGQGTSVTVSS	413

[0083] In another embodiment, the LukD antibody or binding fragment thereof comprises a VH region having an amino acid sequence that shares at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity to any one of SEQ ID NOs: 406-413 as shown in Table 9A, and/or a VL region having an amino acid sequence that shares at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity to any one of SEQ ID NOs: 398-405 as shown in Table 9A.

[0084] In one embodiment, the antibody or binding fragment thereof of the present disclosure comprises a humanized VH variant of any one of SEQ ID NOs: 406-413 and/or a humanized VL variant of any one of SEQ ID NOs: 398-405, where the framework regions are humanized or replaced with human immunoglobulin framework sequences. The humanized framework regions are designed to be similar in length and sequence to the parental framework sequences within SEQ ID NOs: 398-413, respectively. In one embodiment, the humanized framework regions share 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more sequence identity to the framework regions of any one of SEQ ID NOs: 398-413, respectively. In another embodiment, the humanized framework regions are 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more similar in length to the framework regions of any one of SEQ ID NOs: 398-413, respectively. Humanized variants of the VH of any one of SEQ ID NOs: 406-413 and the VL of any one of SEQ ID NOs: 398-405 share at least 50%, at least 55%, at least 60%, at least

65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% sequence identity along the entire length of SEQ ID NOs: 406-413 and SEQ ID NOs: 398-405, respectively.

[0085] Exemplary LukD antibodies as disclosed herein comprise a VL of SEQ ID NO: 398 and a VH of SEQ ID NO: 406; a VL of SEQ ID NO: 399 and a VH of SEQ ID NO: 407; a VL of SEQ ID NO: 400 and a VH of SEQ ID NO: 408; a VL of SEQ ID NO: 401 and a VH of SEQ ID NO: 409; a VL of SEQ ID NO: 402 and a VH of SEQ ID NO: 410; a VL of SEQ ID NO: 403 and a VH of SEQ ID NO: 411; a VL of SEQ ID NO: 404 and a VH of SEQ ID NO: 412; a VL of SEQ ID NO: 405 and a VH of SEQ ID NO: 413.

[0086] In one embodiment, the LukD antibody is a LukD antigen-binding fragment, *i.e.*, a Fab, comprising the heavy chain variable region (VH) and first heavy chain constant domain (CH1) of an antibody coupled to the light chain variable region (VL) and light chain constant region (CL) of the antibody. In another embodiment, the LukD antibody is a $F(ab')_2$ fragment, which comprises both LukD antigen-binding fragments of the full-length antibody coupled by the hinge region. Heavy chain and light chain portions of exemplary LukD Fab fragments are provided in Table 9B below. Exemplary LukD Fab or $F(ab')_2$ fragments comprise a HC region of SEQ ID NO: 1304 and a LC region OF SEQ ID NO: 1306 (SM1B225); a HC region of SEQ ID NO: 1305 and a LC region of SEQ ID NO: 1307 (SM1B221).

Table 9B. LukD Fab Amino Acid Heavy Chain (HC) and Light Chain (LC) Sequences

Protein AA ID	Fab of	Region	Fab Amino Acid Sequence	SEQ ID NO:
SM1B434	SM1B225	HC	EVQLQQSGGGLVKPGGSLKLSCAASGFTFS SYAMSWVRQTPEKRLEWVATITGGGTYTY YLDSVKGRFTISRDNAKTSLYLQMSSLRSED TAMYYCARHRDGNYGCFDVWGAGTTVTV SSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCHHHHHH	1304
SM1B790	SM1B221	HC	QVQLQQSGAELVMPGASVKMSCKASGYTF TDYWMHWVKQRPGQGLEWIGAIDTSDSYT SYNQKFKGKATLTVDESSSTAYMQLSSLTS EDSAVYYCARDYGYAMDYWGQGTSVTVS SASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCHHHHHH	1305

Protein AA ID	Fab of	Region	Fab Amino Acid Sequence	SEQ ID NO:
SM1B434	SM1B225	LC	DIVLTQSPAIMSASLGERVTMTCTASSSVSS SYLHWYQQKPGSSPKLWVYSTSNLASGVP ARFSGSGSGSSYSLTISSMEPEDTATYYCHQ YHRSPQTFGGGTKLEIKRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSTYSLSSTLTLS KADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	1306
SM1B790	SM1B221	LC	QIVLTQSPAIMSASPGEKVTITCSASLSVSYM HWFQQKPGTSPKLWIYSASNLASGVPARFS GSGSGTSYSLTISRMEAEDAATYYCQQRSS YPFTFGSGTKLEIKRTVAAPSVFIFPPSDEQL KSGTASVVCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLSSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKSFNRGEC	1307

[0087] In another embodiment, the LukAB Fab or F(ab')$_2$ fragments as disclosed above comprise a heavy chain region having an amino acid sequence that shares at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity to any one of SEQ ID NOs: 1304-1305 as shown in Table 9B, and/or a light chain region having an amino acid sequence that shares at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity to any one of SEQ ID NOs: 1306-1307 as shown in Table 9B. Additional LukD Fab or F(ab')2 fragments of the present disclosure include those derived from the full-length LukD light chain and heavy chain sequences disclosed in Table 21 below (*i.e.*, full length LukD light chain sequences of SEQ ID NO: 414-421 and heavy chain sequences of SEQ ID NOs: 422-429).

[0088] Exemplary LukD antibodies of the present disclosure comprising the VL and VH chains as enumerated above are provided in Table 21 by their respective full-length LC and HC sequences. In particular, the amino acid sequences of the full-length light chain corresponding to and comprising the VL of SEQ ID NOs: 398-405 are provided as SEQ ID NO: 414-421 in Table 21, respectfully. The amino acid sequences of the full-length heavy chains corresponding to and comprising the VH of SEQ ID NOs: 406-413 are provided as SEQ ID NOs: 422-429 in Table 21, respectively.

[0089] Another aspect of the present disclosure relates to an antibody or binding portion thereof that competes for leukocidin D binding with a monoclonal LukD antibody as described

herein. In particular the disclosure herein encompasses antibodies and binding portions thereof that compete for LukD binding with a monoclonal antibody having (i) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 373, the CDR-H2 of SEQ ID NO: 378, and the CDR-H3 of SEQ ID NO: 382, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 387, the CDR-L2 of SEQ ID NO: 390, and the CDR-L3 of SEQ ID NO: 395; (ii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 372, the CDR-H2 of SEQ ID NO: 375, and the CDR-H3 of SEQ ID NO: 380, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 386, the CDR-L2 of SEQ ID NO: 388, and the CDR-L3 of SEQ ID NO: 396; (iii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 374, the CDR-H2 of SEQ ID NO: 379, and the CDR-H3 of SEQ ID NO: 383, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 386, the CDR-L2 of SEQ ID NO: 391, and the CDR-L3 of SEQ ID NO: 397; or (iv) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 372, the CDR-H2 of SEQ ID NO: 375, and the CDR-H3 of SEQ ID NO: 380, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 386, the CDR-L2 of SEQ ID NO: 388, and the CDR-L3 of SEQ ID NO: 392.

[0090] In accordance with this aspect of the disclosure, a competitive binding assay, such as BLI as described *infra* in Examples 2 and 3 can be utilized to identify a LukD antibody or binding portion thereof that competes for LukD binding with the enumerated monoclonal antibodies. Other competitive binding assays known in the art can also be utilized to identify a LukD antibody in accordance with this aspect of the disclosure.

[0091] Another aspect of the present disclosure is directed to antibodies or binding portions thereof that bind *Staphylococcus aureus* gamma-hemolysin A (HlgA). HlgA is another member of the *S. aureus* bi-component toxin family. HlgA, an S-class subunit, functions in conjunction with its partner, HlgB, an F-class subunit, to target and lyse host erythrocytes during *S. aureus* infection. In one embodiment, HlgA antibodies or binding portions thereof as described herein bind a HlgA protein having the amino acid sequence of SEQ ID NO: 832 (which corresponds to the native HlgA amino acid sequence containing a poly-histidine tag at the N-terminus to facilitate purification), native HlgA, or fragments or homologs thereof. The HlgA antibody or binding portion thereof binds HlgA with a Kd less than or equal to about 10^{-6}, 10^{-7}, 10^{-8}, 10^{-9}, 10^{-10}, 10^{-11} or 10^{-12} M. In one embodiment, the HlgA antibody is a neutralizing antibody, *i.e.*, it neutralizes or prevents the cytolytic activity of HlgAB on its target host cells. Neutralizing HlgA antibodies neutralize HlgAB cytolytic activity by binding to an epitope within regions of the HlgA protein involved in HlgA and HlgB protein-protein interaction or involved in HlgAB binding to its cognitive receptor on target cells (*e.g.*, DARC)

[0092] An HlgA antibody or binding portion thereof as described herein comprises a heavy chain variable region that comprises: a complementarity-determining region 1 (CDR-H1) comprising an amino acid sequence of any one of SEQ ID NOs: 430-432, or a modified amino acid sequence of any one of SEQ ID NOs: 430-432, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 430-432; a complementarity-determining region 2 (CDR-H2) comprising an amino acid sequence of any one of SEQ ID NOs: 433-435, or a modified amino acid sequence of any one of SEQ ID NOs: 433-435, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 433-435; and a complementarity-determining region 3 (CDR-H3) comprising an amino acid sequence of any one of SEQ ID NOs: 436-438, or a modified amino acid sequence of any one of SEQ ID NO: 436-438, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 436-438. The HlgA antibody heavy chain CDR1, CDR2 and CDR3 amino acid sequences are provided in Table 10 below.

Table 10. HlgA Antibody Heavy Chain CDRs

mAb/Fab name	VH name	HCDR1		HCDR2		HCDR3	
		Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
SM1B215	HLGH2	GYTFTIY	430	NTYTGE	433	CYYKYEDYAMD	436
SM1B216	HLGH1	GFTFSSY	431	NGNGGS	434	HRADGPWFT	437
SM1B217	SM1H116	GFTFSNY	432	SRRGS	435	VYYDNPWFV	438
SM1B218	SM1H121	GYTFTIY	430	NTYTGE	433	CYYKYEDYAMD	436
SM1B219	SM1H122	GFTFSSY	431	NGNGGS	434	HRADGPWFT	437
SM1B220	SM1H116	GFTFSNY	432	SRRGS	435	VYYDNPWFV	438

[0093] The HlgA antibody or binding portion thereof may further comprise a light chain variable region. Exemplary HlgA light chain variable regions comprise: a complementarity-determining region 1 (CDR-L1) having an amino acid sequence of any one of SEQ ID NOs: 439-440, or a modified amino acid sequence of any one of SEQ ID NO: 439-440, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 439-440; a complementarity-determining region 2 (CDR-L2) having an amino acid sequence of any one of SEQ ID NOs: 441-443, or a modified amino acid sequence of any one of SEQ ID NO: 441-443, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 441-443; and a complementarity-determining region 3 (CDR-L3) having an amino acid sequence of any one of SEQ ID NOs: 444-445 or a modified amino acid sequence of any one of SEQ ID NO: 444-445, said modified sequence having at least 80% sequence identity to any one of SEQ ID

NO: 444-445. The HlgA antibody light chain CDR1, CDR2 and CDR3 amino acid sequences are provided in Table 11 below.

Table 11. HlgA Antibody Light Chain CDRs

mAb/Fab name	VL name	LCDR1		LCDR2		LCDR3	
		Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
SM1B215	HLGL2	SQSLLDSDGKTY	439	VVS	441	GTHFPL	444
SM1B216	HLGL1	SEDIYIR	440	GAT	442	YWRTPL	445
SM1B217	SM1L42	SQSLLDSDGKTY	439	LVS	443	GTHFPL	444
SM1B218	SM1L42	SQSLLDSDGKTY	439	LVS	443	GTHFPL	444
SM1B219	HLGL2	SQSLLDSDGKTY	439	VVS	441	GTHFPL	444
SM1B220	HLGL2	SQSLLDSDGKTY	439	VVS	441	GTHFPL	444

[0094] In one embodiment, the HlgA antibodies disclosed herein comprise the heavy chain CDRs of Table 10 and light chain CDRs of Table 11 or modified CDRs thereof. Encompassed by the present disclosure are CDRs of Table 10 and 11 containing 1, 2, 3, 4, 5, or more amino acid substitutions that maintain or enhance HlgA or HlgAB binding of the antibody. The resulting modified CDRs are at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% similar in sequence to the CDRs of Tables 10 and 11. Suitable amino acid modifications and insertion to the heavy chain CDR sequences of Table 10 and/or the light chain CDR sequences of Table 11are described *supra*.

[0095] In one embodiment, the HlgA antibody or binding portion thereof of the present disclosure comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 430, the CDR-H2 of SEQ ID NO: 433, and the CDR-H3 of SEQ ID NO: 436. In another embodiment, the HlgA antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 431, the CDR-H2 of SEQ ID NO: 434, and the CDR-H3 of SEQ ID NO: 437. In another embodiment, the HlgA antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 432, the CDR-H2 of SEQ ID NO: 435, and the CDR-H3 of SEQ ID NO: 438.

[0096] In one embodiment, the HlgA antibody or binding portion thereof of the present disclosure comprises a light chain variable region, where the light chain variable region comprises the CDR-L1 of SEQ ID NO: 439 , the CDR-L2 of SEQ ID NO: 441 , and the CDR-L3 of SEQ ID NO: 444. In another embodiment, the HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 440, the CDR-L2 of SEQ ID NO: 442, and the CDR-L3 of SEQ ID NO: 445. In another embodiment, the

HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 439, the CDR-L2 of SEQ ID NO: 443, and the CDR-L3 of SEQ ID NO: 444.

[0097] In another embodiment, the HlgA antibody or binding portion thereof comprises the heavy chain CDRs of SEQ ID NOs: 430, 433, and 436 together with the light chain CDRs of SEQ ID NOs: 439, 441, and 444; the heavy chain CDRs of SEQ ID NOs: 431, 434, and 437 together with the light chain CDRs of SEQ ID NOs: 440, 442, and 445; the heavy chain CDRs of SEQ ID NOs: 432, 435, and 438 together with the light chain CDRs of SEQ ID NOs: 439, 443, and 444; the heavy chain CDRs of SEQ ID NOs: 430, 433, and 436 together with the light chain CDRs of SEQ ID NOs: 439, 443, and 444; the heavy chain CDRs of SEQ ID NOs: 431, 434, and 437 together with the light chain CDRs of SEQ ID NOs: 439, 441, and 444; or the heavy chain CDRs of SEQ ID NOs: 432, 435, and 438 together with the light chain CDRs of SEQ ID NOs: 439, 441, and 444.

[0098] The HlgA antibody or binding portion thereof as described herein may comprise a variable light (VL) chain, a variable heavy (VH) chain, or a combination of a VL and VH chain. The VL chain of the HlgA antibody as disclosed herein may comprise an amino acid sequence selected from SEQ ID NOs: 446-451 or an amino acid sequence that is at least 80% identical to any one of the amino acid sequence selected from SEQ ID NOs: 446-451. The VH chain of the HlgA antibody as disclosed herein may comprise an amino acid sequence selected from SEQ ID NOs: 452-457 or an amino acid sequence that is at least 80% identical to any one of the amino acid sequence selected from SEQ ID NOs: 452-457. The amino acid sequences of the HlgA VL and VH chains are provided in Table 12 below.

Table 12. HlgA Antibody Variable Light (VL) and Variable Heavy (VH) Chain Sequences

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B215	VL	HLGL2	DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDG KTYLNWLLQRPGQSPKRLIYVVSKLDSGVPDRF TGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFP LTFGAGTKLELK	446
SM1B216	VL	HLGL1	DVVMTQTPSSFSVSLGDGVTITCKASEDIYIRLA WYQQKPGNAPRLLIFGATSLETGVPSRFSGSGSG KDYTLSITSLQTEDVATYYCQQYWRTPLTFGAG TKLELK	447
SM1B217	VL	SM1L42	DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDG KTYLNWLLQRPGQSPKRLIYLVSKLDSGVPDRF TGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFP LTFGAGTKLELK	448

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B218	VL	SM1L42	DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDG KTYLNWLLQRPGQSPKRLIYLVSKLDSGVPDRF TGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFP LTFGAGTKLELK	449
SM1B219	VL	HLGL2	DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDG KTYLNWLLQRPGQSPKRLIYVVSKLDSGVPDRF TGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFP LTFGAGTKLELK	450
SM1B220	VL	HLGL2	DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDG KTYLNWLLQRPGQSPKRLIYVVSKLDSGVPDRF TGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFP LTFGAGTKLELK	451
SM1B215	VH	HLGH2	EVQLQQSGPELKKPGETVKISCKTSGYTFTIYGM NWMKQAPGKGLKWMGWINTYTGEPTYADDFK GRFAFSLETSASTAYLQINNLKNEDTATYFCARC YYKYEDYAMDYWGQGTSVTVSS	452
SM1B216	VH	HLGH1	EVKLVESGGGLVKPGGSLKLSCAASGFTFSSYA MSWVRQTPEKRLEWVAAINGNGGSTYYPDTVK DRFTISRDNAKNTLYLQMSSLRSEDTALYYCAR HRADGPWFTYWGQGTLVTVSA	453
SM1B217	VH	SM1H116	EVKLVESGGGLVKPGGSLKLSCAASGFTFSNYA MSWVRQTPEKRLEWVASISRRGSTYYPDSVKGR FTISRDNARNILYLQMSSLRSEDTALYYCATVYY DNPWFVYWGQGTLVTVSA	454
SM1B218	VH	SM1H121	QIQLVQSGPELKKPGETVKISCKTSGYTFTIYGM NWTKQAPGKGLKWMGWINTYTGEPTYADDFK GRFAFSLETSASTAYLQINNLKNEDTATYFCARC YYKYEDYAMDYWGQGTSVTVSS	455
SM1B219	VH	SM1H122	DVKLVESGGGLVKPGGSLKLSCAASGFTFSSYA MSWVRQTPEKRLEWVAAINGNGGSTYYPDTVK DRFTISRDNAKNTLYLQMSSLRSEDTALYYCAR HRADGPWFTYWGQGTLVTVSA	456
SM1B220	VH	SM1H116	EVKLVESGGGLVKPGGSLKLSCAASGFTFSNYA MSWVRQTPEKRLEWVASISRRGSTYYPDSVKGR FTISRDNARNILYLQMSSLRSEDTALYYCATVYY DNPWFVYWGQGTLVTVSA	457

[0099] In another embodiment, the HlgA antibody or binding fragment thereof comprises a VH region having an amino acid sequence that shares at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity to any one of SEQ ID NOs: 452-457 as shown in Table 12, and/or a VL region having an amino acid sequence that shares at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95%, at

least 96%, at least 97%, at least 98%, at least 99% sequence identity to any one of SEQ ID NOs: 446-451 as shown in Table 12.

[0100] In one embodiment, the antibody or binding fragment thereof of the present disclosure comprises a humanized VH variant of any one of SEQ ID NOs: 452-457 and/or a humanized VL variant of any one of SEQ ID NOs: 446-451, where the framework regions are humanized or replaced with human immunoglobulin framework sequences. The humanized framework regions are designed to be similar in length and sequence to the parental framework sequences within SEQ ID NOs: 446-457, respectively. In one embodiment, the humanized framework regions share 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more sequence identity to the framework regions of any one of SEQ ID NOs: 446-457, respectively. In another embodiment, the humanized framework regions are 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more similar in length to the framework regions of any one of SEQ ID NOs: 446-457, respectively. Humanized variants of the VH of any one of SEQ ID NOs: 452-457 and the VL of any one of SEQ ID NOs: 446-451 share at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% sequence identity along the entire length of SEQ ID NOs: 452-457 and SEQ ID NOs: 446-451, respectively.

[0101] Suitable HlgA antibodies as disclosed herein may comprise a VL of SEQ ID NO: 446 and a VH of SEQ ID NO: 452; a VL of SEQ ID NO: 447 and a VH of SEQ ID NO: 453; a VL of SEQ ID NO: 448 and a VH of SEQ ID NO: 454; a VL of SEQ ID NO: 449 and a VH of SEQ ID NO: 455; a VL of SEQ ID NO: 450 and a VH of SEQ ID NO: 456; or a VL of SEQ ID NO: 451 and a VH of SEQ ID NO: 457.

[0102] Exemplary HlgA antibodies of the present disclosure comprising the VL and VH chains as enumerated above are provided in Table 22 by their respective full-length LC and HC sequences. In particular, the amino acid sequences of the full-length light chain corresponding to and comprising the VL of SEQ ID NOs: 446-451 are provided as SEQ ID NO: 458-463 in Table 22 , respectfully. The amino acid sequences of the full-length heavy chains corresponding to and comprising the VH of SEQ ID NOs: 452-457 are provided as SEQ ID NOs: 464-469 in Table 22, respectively.

[0103] In another embodiment, the HlgA antibody is a HlgA antigen-binding fragment, *i.e.*, a Fab, comprising the heavy chain variable region (VH) and first heavy chain constant domain (CH1) of an antibody coupled to the light chain variable region (VL) and light chain constant region (CL) of the antibody. In another embodiment, the HlgA antibody is a $F(ab')_2$ fragment, which comprises both HlgA antigen-binding fragments of the full-length antibody

coupled by the hinge region. The heavy chain and light chain portions of HlgA Fab fragments can readily be derived from the full-length HlgA light chain and heavy chain sequences disclosed in Table 22 below (*i.e.*, full length HlgA light chain sequences of SEQ ID NO: 458-463 and heavy chain sequences of SEQ ID NOs: 464-469).

[0104] Another aspect of the present disclosure relates to an antibody or binding portion thereof that competes for HlgA binding with a monoclonal HlgA antibody disclosed herein. In particular, the disclosure encompasses an antibody or binding portion thereof that competes for binding to HlgA with a monoclonal antibody having heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 432, the CDR-H2 of SEQ ID NO: 435, and the CDR-H3 of SEQ ID NO: 438 and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 439, the CDR-L2 of SEQ ID NO: 441, and the CDR-L3 of SEQ ID NO: 444. In accordance with this aspect of the disclosure, a competitive binding assay, such as BLI as described *infra* in Examples 2 and 3 can be utilized to identify an HlgA antibody or binding portion thereof that competes for HlgA binding with the enumerated monoclonal antibody. Other competitive binding assays known in the art can also be utilized to identify an HlgA antibody in accordance with this aspect of the disclosure.

[0105] Another aspect of the present disclosure is directed to antibodies or binding portions thereof that bind *Staphylococcus aureus* gamma-hemolysin C (HlgC). HlgC is another S-class subunit toxin that, in conjunction with HlgB, targets and lyses host erythrocytes during S. aureus infection. In one embodiment, HlgC antibodies or binding portions thereof as described herein bind a HlgC protein having the amino acid sequence of SEQ ID NO: 833 (which corresponds to the native HlgC amino acid sequence containing a poly-histidine tag at the N-terminus to facilitate purification), native HlgC protein, or fragments or homologs thereof. The HlgC antibody or binding portion thereof binds HlgC with a Kd less than or equal to about 10^{-6}, 10^{-7}, 10^{-8}, 10^{-9}, 10^{-10}, 10^{-11} or 10^{-12} M. In one embodiment, the HlgC antibody is a neutralizing antibody, *i.e.*, it neutralizes or prevents the cytolytic activity of HlgCB on its target immune host cells. Neutralizing HlgC antibodies neutralize HlgCB cytolytic activity by binding to an epitope within regions of the HlgC protein involved in HlgC and HlgB protein-protein interaction or involved in HlgCB binding to its cognitive receptor on target immune cells.

[0106] A HlgC antibody or binding portion thereof of the present disclosure comprises a heavy chain variable region that comprises: a complementarity-determining region 1 (CDR-H1) comprising an amino acid sequence of SEQ ID NO: 470, or a modified amino acid sequence of SEQ ID NO: 470, said modified sequence having at least 80% sequence identity to SEQ ID NO: 470; a complementarity-determining region 2 (CDR-H2) comprising an amino acid sequence of

SEQ ID NO: 471, or a modified amino acid sequence of SEQ ID NO: 471, said modified sequence having at least 80% sequence identity to SEQ ID NO: 471; and a complementarity-determining region 3 (CDR-H3) comprising an amino acid sequence of SEQ ID NO: 472 or a modified amino acid sequence of SEQ ID NO: 472, said modified sequence having at least 80% sequence identity to SEQ ID NO: 472. The HlgC antibody heavy chain CDR1, CDR2 and CDR3 amino acid sequences are provided in Table 13 below.

Table 13. HlgC Antibody Heavy Chain CDRs

mAb/Fab name	VH name	HCDR1		HCDR2		HCDR3	
		Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
SM1B202	SM1H117	GFTFSNY	470	SRRGS	471	VYYDNPWFV	472
SM1B203	SM1H115	GFTFSNY	470	SRRGS	471	VYYDNPWFV	472
SM1B204	SM1H116	GFTFSNY	470	SRRGS	471	VYYDNPWFV	472
SM1B205	SM1H116	GFTFSNY	470	SRRGS	471	VYYDNPWFV	472
SM1B206	SM1H116	GFTFSNY	470	SRRGS	471	VYYDNPWFV	472
SM1B207	SM1H115	GFTFSNY	470	SRRGS	471	VYYDNPWFV	472

[0107] The HlgC antibody or binding portion thereof may further comprise a light chain variable region. Exemplary HlgC light chain variable regions comprise a complementarity-determining region 1 (CDR-L1) having an amino acid sequence of any one of SEQ ID NOs: 473-477, or a modified amino acid sequence of any one of SEQ ID NO: 473-477, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 473-477; a complementarity-determining region 2 (CDR-L2) having an amino acid sequence of any one of SEQ ID NOs: 478-482, or a modified amino acid sequence of any one of SEQ ID NO: 478-482, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 478-482; and a complementarity-determining region 3 (CDR-L3) having an amino acid sequence of any one of SEQ ID NOs: 483-487, or a modified amino acid sequence of any one of SEQ ID NO: 483-487, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 483-487. The HlgC antibody light chain CDR1, CDR2 and CDR3 amino acid sequences are provided in Table 14 below.

Table 14. HlgC Antibody Light Chain CDRs

mAb/Fab name	VL name	LCDR1		LCDR2		LCDR3	
		Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
SM1B202	SM1L37	STDIDDD	473	EGN	478	SDNMPY	483
SM1B203	VSTL368	SQSISDY	474	YDS	479	GHRFPF	484
SM1B204	SM1L36	SQSVLYSSNQKNY	475	WAS	480	YLSSY	485
SM1B205	SM1L35	SKSVSTSGYSY	476	LVS	481	IRELT	486
SM1B206	DARL5	SQSISDY	474	YAS	482	GHSFPL	487
SM1B207	SM1L34	SESVSFAGTSL	477	WAS	480	YLSSY	485

[0108] The HlgC antibodies disclosed herein comprise the heavy chain CDRs of Table 13 and light chain CDRs of Table 14 or modified CDRs thereof. Encompassed by the present disclosure are CDRs of Table 13 and 14 containing 1, 2, 3, 4, 5, or more amino acid substitutions that maintain or enhance HlgC or HlgCB binding of the antibody. The resulting modified CDRs are at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% similar in sequence to the CDRs of Tables 13 and 14. Suitable amino acid modifications and insertion to the heavy chain CDR sequences of Table 13 and/or the light chain CDR sequences of Table 14 are described *supra*.

[0109] In one embodiment, the HlgC antibody or binding portion thereof of the present disclosure comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 473 the CDR-L2 of SEQ ID NO: 478, and the CDR-L3 of SEQ ID NO: 483. In another embodiment, the HlgC antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 474, the CDR-L2 of SEQ ID NO: 479, and the CDR-L3 of SEQ ID NO: 484. In another embodiment, the HlgC antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 475, the CDR-L2 of SEQ ID NO: 480, and the CDR-L3 of SEQ ID NO: 485. In another embodiment, the HlgC antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 476, the CDR-L2 of SEQ ID NO: 481, and the CDR-L3 of SEQ ID NO: 486. In another embodiment, the HlgC antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 474, the CDR-L2 of SEQ ID NO: 482, and the CDR-L3 of SEQ ID NO: 487. In another embodiment, the HlgC antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 477, the CDR-L2 of SEQ ID NO: 480, and the CDR-L3 of SEQ ID NO: 485.

[0110] In another embodiment, the HlgC antibody or binding portion thereof comprises the heavy chain CDRs of SEQ ID NOs: 470, 471, and 472 together with the light chain CDRs of SEQ ID NOs: 473, 478, and 483; the heavy chain CDRs of SEQ ID NOs: 470, 471, and 472 together with the light chain CDRs of SEQ ID NOs: 474, 479 and 484; the heavy chain CDRs of SEQ ID NOs: 470, 471, and 472 together with the light chain CDRs of SEQ ID NOs: 475, 480, and 485; the heavy chain CDRs of SEQ ID NOs: 470, 471, and 472 together with the light chain CDRs of SEQ ID NOs: 476, 481, and 486; the heavy chain CDRs of SEQ ID NOs: 470, 471, and 472 together with the light chain CDRs of SEQ ID NOs: 474, 482, and 487; the heavy chain CDRs of SEQ ID NOs: 470, 471, and 472 together with the light chain CDRs of SEQ ID NOs: 477, 480, and 485.

[0111] The HlgC antibody or binding portion thereof as described herein may comprises a variable light (VL) chain, a variable heavy (VH) chain, or a combination of a VL and VH chain. The VL chain of the HlgC antibody as disclosed herein may comprise an amino acid sequence selected from SEQ ID NOs: 488-493 or an amino acid sequence that is at least 80% identical to any one of the amino acid sequence selected from SEQ ID NOs: 488-493. The VH chain of the HlgC antibody as disclosed herein may comprise an amino acid sequence selected from SEQ ID NOs: 494-499 or an amino acid sequence that is at least 80% identical to any one of the amino acid sequence selected from SEQ ID NOs: 494-499. The amino acid sequences of the HlgC VL and VH chains are provided in Table 15 below.

Table 15: HlgC Antibody Variable Light (VL) and Variable Heavy (VH) Chain Sequences

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B202	VL	SM1L37	ETTVTQSPASLSVATGEKVTIRCITSTDIDDDMS WYQQKPGEPPKLLISEGNTLRPGVPSRFSSSGCG TDFVFTIENTLSEDVADYYCLQSDNMPYTFGGG TKLEIK	488
SM1B203	VL	VSTL368	DIVMTQSPATLSVTPGDRVSLSCRASQSISDYLH WYQQKSHESPRLLIKYDSQSISGIPSRFSGSGSGS DFTLSINSVEPEDVGVYYCQNGHRFPFTFGGGTK LEIK	489
SM1B204	VL	SM1L36	NIMMTQSPSSLTVSAGEKVTMSCKSSQSVLYSSN QKNYLAWYQQKPGQSPKLLIYWASTRESGVPD RFAGSGSGTDFTLSISSVQAEDLAVYYCHQYLSS YTFGGGTKLEIK	490
SM1B205	VL	SM1L35	DIVLTQSPASLAVSLGQRATISYRASKSVSTSGYS YMHWNQQKPGQPPRLLIYLVSNLESGVPARFSG SGSGTDFTLNIHPVEEEDAATYYCQHIRELTRSE GGTKLEIK	491

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B206	VL	DARL5	DIVMTQSPATLSVTPGDRVSLSCRASQSISDYLH WYQQKSHESPRLLIKYASQSISGIPSRFSGSGSGS DFTLSINSVEPEDVGVYYCQNGHSFPLTFGAGTK LELK	492
SM1B207	VL	SM1L34	DIVLTQSPASLAVSLGQRATISCQASESVSFAGTS LMHWYQQKPGQSPKLLIYWASTRESGVPDRFA GSGSGTDFTLSISSVQAEDLAVYYCHQYLSSYTF GGGTKLEIK	493
SM1B202	VH	SM1H117	EVMLVESGGGLVKPGGSLKLSCAASGFTFSNYA MSWVRQTPEKRLEWVASISRRGSTYYPDSGKGR FTISRDNARNIPYLQMSSLRSEDTALYYCATVYY DNPWFVYWGQGTLVTVSA	494
SM1B203	VH	SM1H115	EVMLVESGGGLVKPGGSLKLSCAASGFTFSNYA MSWVRQTPEKRLEWVASISRRGSTYYPDSVKGR FTISRDNARNILYLQMSSLRSEDTALYYCATVYY DNPWFVYWGQGTLVTVSA	495
SM1B204	VH	SM1H116	EVKLVESGGGLVKPGGSLKLSCAASGFTFSNYA MSWVRQTPEKRLEWVASISRRGSTYYPDSVKGR FTISRDNARNILYLQMSSLRSEDTALYYCATVYY DNPWFVYWGQGTLVTVSA	496
SM1B205	VH	SM1H116	EVKLVESGGGLVKPGGSLKLSCAASGFTFSNYA MSWVRQTPEKRLEWVASISRRGSTYYPDSVKGR FTISRDNARNILYLQMSSLRSEDTALYYCATVYY DNPWFVYWGQGTLVTVSA	497
SM1B206	VH	SM1H116	EVKLVESGGGLVKPGGSLKLSCAASGFTFSNYA MSWVRQTPEKRLEWVASISRRGSTYYPDSVKGR FTISRDNARNILYLQMSSLRSEDTALYYCATVYY DNPWFVYWGQGTLVTVSA	498
SM1B207	VH	SM1H115	EVMLVESGGGLVKPGGSLKLSCAASGFTFSNYA MSWVRQTPEKRLEWVASISRRGSTYYPDSVKGR FTISRDNARNILYLQMSSLRSEDTALYYCATVYY DNPWFVYWGQGTLVTVSA	499

[0112] In another embodiment, the antibody or binding fragment thereof comprises a VH region having an amino acid sequence that shares at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity to any one of SEQ ID NOs: 494-499 as shown in Table 15, and/or a VL region having an amino acid sequence that shares at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity to any one of SEQ ID NOs: 488-493 as shown in Table 15.

[0113] In one embodiment, the antibody or binding fragment thereof of the present disclosure comprises a humanized VH variant of any one of SEQ ID NOs: 494-499 and/or a humanized VL variant of any one of SEQ ID NOs: 488-493, where the framework regions are humanized or replaced with human immunoglobulin framework sequences. The humanized framework regions are designed to be similar in length and sequence to the parental framework sequences within SEQ ID NOs: 488-499, respectively. In one embodiment, the humanized framework regions share 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more sequence identity to the framework regions of any one of SEQ ID NOs: 488-499, respectively. In another embodiment, the humanized framework regions are 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more similar in length to the framework regions of any one of SEQ ID NOs: 488-499, respectively. Humanized variants of the VH of any one of SEQ ID NOs: 494-499 and the VL of any one of SEQ ID NOs: 488-493 share at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% sequence identity along the entire length of SEQ ID NOs: 494-499 and SEQ ID NOs: 488-493, respectively.

[0114] Suitable HlgC antibodies as disclosed herein comprise a VL of SEQ ID NO: 488 and a VH of SEQ ID NO: 494; a VL of SEQ ID NO: 489 and a VH of SEQ ID NO: 495; a VL of SEQ ID NO: 490 and a VH of SEQ ID NO: 496; a VL of SEQ ID NO: 491 and a VH of SEQ ID NO:497; a VL of SEQ ID NO: 492 and a VH of SEQ ID NO: 498; or a VL of SEQ ID NO: 493 and a VH of SEQ ID NO: 499.

[0115] Exemplary HlgC antibodies of the present disclosure comprising the VL and VH chains as enumerated above are provided in Table 23 by their respective full-length LC and HC sequences. In particular, the amino acid sequences of the full-length light chain corresponding to and comprising the VL of SEQ ID NOs: 488-493 are provided as SEQ ID NO: 500-505 in Table 23, respectfully. The amino acid sequences of the full-length heavy chains corresponding to and comprising the VH of SEQ ID NOs: 494-499 are provided as SEQ ID NOs: 506-511 in Table 23, respectively.

[0116] In another embodiment, the HlgC antibody is a HlgC antigen-binding fragment, *i.e.*, a Fab, comprising the heavy chain variable region (VH) and first heavy chain constant domain (CH1) of an antibody coupled to the light chain variable region (VL) and light chain constant region (CL) of the antibody. In another embodiment, the HlgC antibody is a $F(ab')_2$ fragment, which comprises both HlgC antigen-binding fragments of the full-length antibody coupled by the hinge region. The heavy chain and light chain portions of HlgC Fab fragments can readily be derived from the full-length HlgC light chain and heavy chain sequences disclosed

in Table 23 below (*i.e.*, full length HlgC light chain sequences of SEQ ID NO: 500-505 and heavy chain sequences of SEQ ID NOs: 506-511).

[0117] Another aspect of the present disclosure is directed to an antibody or binding portion thereof that competes for HlgC binding to a monoclonal antibody as described herein. In particular, the present disclosure encompasses an antibody or binding fragment thereof that competes for HlgC binding with a monoclonal antibody having a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 470, the CDR-H2 of SEQ ID NO: 471, and the CDR-H3 of SEQ ID NO: 472 and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 474, the CDR-L2 of SEQ ID NO: 479, and the CDR-L3 of SEQ ID NO: 484. In accordance with this aspect of the disclosure, a competitive binding assay, such as BLI as described *infra* in Examples 2 and 3 can be utilized to identify an HlgC antibody or binding portion thereof that competes for HlgC binding with the enumerated monoclonal antibody. Other competitive binding assays known in the art can also be utilized to identify an HlgC antibody in accordance with this aspect of the disclosure.

[0118] Another aspect of the present disclosure relates to antibodies or binding portions thereof that bind *Staphylococcus aureus* LukE and/or HlgA. In one embodiment, LukE/HlgA antibodies or binding portions thereof as described herein bind a LukE protein having the amino acid sequence of SEQ ID NO: 826 and/or an HlgA protein having the amino acid sequence of SEQ ID NO: 832 including native LukE and HlgA proteins, fragments, and/or homologs thereof. The LukE/HlgA antibody or binding portion thereof binds LukE and/or HlgA with a Kd less than or equal to about 10^{-6}, 10^{-7}, 10^{-8}, 10^{-9}, 10^{-10}, 10^{-11} or 10^{-12} M. In one embodiment, the LukE/HlgA antibody is a neutralizing antibody, *i.e.*, it neutralizes or prevents the cytolytic activity of LukED on its target immune host cells. Neutralizing LukE antibodies neutralize LukED cytolytic activity by binding to and inhibiting LukE and LukD protein-protein interaction or by inhibiting LukED binding to its cognitive receptor on target immune cells.

[0119] A LukE and/or HlgA antibody or binding portion thereof of the present disclosure comprises a heavy chain variable region that comprises: a complementarity-determining region 1 (CDR-H1) comprising an amino acid sequence of any one of SEQ ID NOs: 513-529, or a modified amino acid sequence of any one of SEQ ID NOs: 513-529, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 513-529; a complementarity-determining region 2 (CDR-H2) comprising an amino acid sequence of any one of SEQ ID NOs: 530-548, or a modified amino acid sequence of any one of SEQ ID NOs: 530-548, said modified sequences having at least 80% sequence identity to any one of SEQ ID NOs: 530-548; and a complementarity-determining region 3 (CDR-H3) comprising an amino acid sequence of any

one of SEQ ID NOs: 549-568 or a modified amino acid sequence of any one of SEQ ID NO: 549-568 said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 549-568. The heavy chain CDR1, CDR2 and CDR3 amino acid sequences are provided in Table 16 below.

Table 16. LukE/HlgA Antibody Heavy Chain CDRs

mAb/Fab name	VH name	HCDR1		HCDR2		HCDR3	
		Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
SM1B302	HLGH3	GFTFSSF	513	SRTDN	530	ADYDGPWFA	549
SM1B303	HLGH4	GYSFTGY	514	NPNNGG	531	DDYSFA	550
SM1B304	HLGH5	GFTFTDF	515	RNKANGYT	532	DVGDYD	551
SM1B305	HLGH6	GFTFTNY	516	NTYTGE	533	DYRDGDALD	552
SM1B306	HLGH7	GYSFTSN	517	HPSDSE	534	GDGGFA	553
SM1B307	HLGH8	GYSFTGY	514	NPYNGG	535	GYPRGWFA	554
SM1B308	HLGH9	GFTFRNH	518	NVNAGS	536	HRAYYNYDENAMD	555
SM1B309	HLGH10	GYTFTDY	519	YPNNGG	537	LTYYAKVD	556
SM1B310	HLGH11	GFTFSSY	520	NSNGGS	538	LYYGD	557
SM1B311	HLGH12	GFSLTTY	521	WRGGT	539	TD	558
SM1B312	HLGH12	GFSLTTY	521	WRGGT	539	TD	558
SM1B313	HLGH12	GFSLTTY	521	WRGGT	539	TD	558
SM1B314	HLGH13	GFSLTTY	521	WRGGT	539	TD	558
SM1B315	HLGH14	GFSLTTY	521	WRGGT	539	TD	558
SM1B316	HLGH12	GFSLTTY	521	WRGGT	539	TD	558
SM1B317	HLGH15	GFSLTSY	522	WSGGI	540	TD	558
SM1B318	HLGH16	GYKFSSY	523	LPGSGS	541	TISTATDWFA	559
SM1B319	HLGH16	GYKFSSY	523	LPGSGS	541	TISTATDWFA	559
SM1B320	HLGH17	GYKFSSY	523	LPGSGS	541	TISTATDWFA	559
SM1B321	HLGH18	GYKFSSY	523	LPGSGS	541	TISTATDWFA	559
SM1B322	HLGH17	GYKFSSY	523	LPGSGS	541	TISTATDWFA	559
SM1B323	HLGH19	GYKFSSY	523	LPGSGS	541	TISTATDWFA	559
SM1B324	HLGH20	GFNIKDY	524	DPENGN	542	YDGYAMD	560
SM1B325	HLGH21	GYTFTNY	525	YPGGGY	543	ND	561
SM1B326	HLGH22	GFSITSY	526	WSGGS	544	FYYDYDEGFD	562
SM1B327	HLGH23	GFSITSY	526	WSGGS	544	FYYDYDEGFD	562
SM1B328	HLGH23	GFSITSY	526	WSGGS	544	FYYDYDEGFD	562
SM1B329	HLGH23	GFSITSY	526	WSGGS	544	FYYDYDEGFD	562

mAb/Fab name	VH name	HCDR1		HCDR2		HCDR3	
		Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
SM1B330	HLGH23	GFSITSY	526	WSGGS	544	FYYDYDEGFD	562
SM1B331	HLGH23	GFSITSY	526	WSGGS	544	FYYDYDEGFD	562
SM1B332	HLGH24	GLSLTSY	527	WGDGS	545	RGDYGSYAMD	563
SM1B333	HLGH25	GFNIKDS	528	DPEDGE	546	GGLILD	564
SM1B334	HLGH26	GYTFTNY	525	NTYTGE	533	DYREGDAMD	565
SM1B335	HLGH27	GFTFSSY	520	STSGSY	547	HGDHDGFD	566
SM1B336	HLGH28	GFSFSNY	529	NSGGSF	548	HWDHPWFA	567
SM1B337	HLGH28	GFSFSNY	529	NSGGSF	548	HWDHPWFA	567
SM1B338	HLGH28	GFSFSNY	529	NSGGSF	548	HWDHPWFA	567
SM1B339	HLGH29	GFNIKDS	528	DPEDGE	546	SFGV	568
SM1B340	HLGH30	GFNIKDS	528	DPEDGE	546	SFGV	568

[0120] The LukE/HlgA antibody or binding portion thereof may further comprise a light chain variable region. Exemplary light chain variable regions comprise a complementarity-determining region 1 (CDR-L1) having an amino acid sequence of any one of SEQ ID NOs: 569-600, or a modified amino acid sequence of any one of SEQ ID NO: 569-600, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 569-600; a complementarity-determining region 2 (CDR-L2) having an amino acid sequence of any one of SEQ ID NOs: 601-621, or a modified amino acid sequence of any one of SEQ ID NO: 601-621, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 601-621; and a complementarity-determining region 3 (CDR-L3) having an amino acid sequence of any one of SEQ ID NOs: 622-654, or a modified amino acid sequence of any one of SEQ ID NO: 622-654, said having at least 80% sequence identity to any one of SEQ ID NO: 622-654. The light chain CDR1, CDR2 and CDR3 amino acid sequences are provided in Table 17 below.

Table 17. LukE/HlgA Light Chain CDRs

mAb/Fab name	VL name	LCDR1		LCDR2		LCDR3	
		Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
SM1B302	C47L104	SQDIGSS	569	ATS	601	YASSPW	622
SM1B303	HLGL3	SQDIRSY	570	YTS	602	GNTLPY	623
SM1B304	HLGL4	SQEISGY	571	AAS	603	YASYPR	624

mAb/Fab name	VL name	LCDR1		LCDR2		LCDR3	
		Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
SM1B305	HLGL5	SQIIVHSNGNTY	572	KIS	604	GSHVPW	625
SM1B306	HLGL6	SQSLANSYGNTY	573	GIS	605	GTHQPP	626
SM1B307	HLGL7	SESVDSYGNSF	574	RAS	606	SNEDPPW	627
SM1B308	HLGL8	SQSLLNSRTRKNY	575	WAS	607	SYNLW	628
SM1B309	HLGL9	SQSLLHSNGKTY	576	KVS	608	STHVPL	629
SM1B310	HLGL10	SQDVSAA	577	WAS	607	HYSTPG	630
SM1B311	HLGL11	SQTIVHSSGNTY	578	KVS	608	GSHVPY	631
SM1B312	GC5L29	SQGISNY	579	YTS	602	YSKLPF	632
SM1B313	HLGL12	SQSLLYSSNQKNY	580	WAS	607	YYSYPY	633
SM1B314	OSML437	SENIYSN	581	AAT	609	FWGTPY	634
SM1B315	TM3L53	SQDINSY	582	RAN	610	YDEFPY	635
SM1B316	HLGL13	SQGISNY	579	YTS	602	YSKLPW	636
SM1B317	HLGL14	SQTIVYSDGNTY	583	KVS	608	GSHVPY	631
SM1B318	HLGL14	SQTIVYSDGNTY	584	KVS	608	GSHVPY	631
SM1B319	HLGL15	SKSLLHSNGNTY	585	RMS	611	HLEYPF	637
SM1B320	ATCL1	SQGISNY	579	YTS	602	YSKLPY	638
SM1B321	VSTL360	SENIYSY	586	NAK	612	HYGSPY	639
SM1B322	ATCL3	SQDVSTA	587	SAS	613	HYSTPW	640
SM1B323	HLGL16	STDIDDD	588	EGN	614	SDNLPY	641
SM1B324	HLGL17	SQSLLNSGNQKNY	589	GAS	615	DHSYPP	642
SM1B325	HLGL18	SQDIGNS	590	ATS	601	FASSPL	643
SM1B326	OSML437	SENIYSN	581	AAT	609	FWGTPY	634
SM1B327	HLGL19	SSNVSY	591	DTS	616	WSSNPR	644
SM1B328	VSTL342	SQDIGSY	592	ATS	601	YATSPW	645
SM1B329	HLGL20	SDHINNW	593	GAT	617	YWSTPY	646
SM1B330	HLGL21	SSSVSY	594	YAS	618	WSSNPPI	647
SM1B331	VSTL368	SQSISDY	595	YDS	619	GHRFPF	648
SM1B332	HLGL22	SSSVSSSY	596	STS	620	WSSYPP	649
SM1B333	HLGL23	SESVDSYGNSF	574	LAS	621	NNEDPY	650
SM1B334	HLGL24	SQSIVYSNGNTY	597	KVS	608	GSHVPW	625
SM1B335	HLGL25	SQSLANSYGNTY	573	GIS	605	GTHQPY	651
SM1B336	HLGL26	SQSVLYNSNQRNY	598	WAS	607	YLSSY	652
SM1B337	HLGL27	SQDVGTA	599	WAS	607	YSSYPL	653
SM1B338	HLGL7	SESVDSYGNSF	574	RAS	606	SNEDPPW	627
SM1B339	HLGL7	SESVDSYGNSF	574	RAS	606	SNEDPPW	627
SM1B340	HLGL28	SQDIDNY	600	YTS	602	GYTLPW	654

[0121] The LukE/HlgA antibodies disclosed herein comprise the heavy chain CDRs of Table 16 and light chain CDRs of Table 17 or modified CDRs thereof. Encompassed by the present disclosure are CDRs of Table 16 and 17 containing 1, 2, 3, 4, 5, or more amino acid

substitutions that maintain or enhance LukE or LukED binding of the antibody. The resulting modified CDRs are at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% similar in sequence to the CDRs of Tables 16 and 17. Suitable amino acid modifications and insertion to the heavy chain CDR sequences of Table 16 and/or the light chain CDR sequences of Table 17 are described *supra*.

[0122] In one embodiment, the LukE/HlgA antibody or binding portion thereof of the present disclosure comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 513, the CDR-H2 of SEQ ID NO: 530, and the CDR-H3 of SEQ ID NO: 549. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 514, the CDR-H2 of SEQ ID NO: 531, and the CDR-H3 of SEQ ID NO: 550. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 515, the CDR-H2 of SEQ ID NO: 532, and the CDR-H3 of SEQ ID NO: 551. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 516, the CDR-H2 of SEQ ID NO: 533, and the CDR-H3 of SEQ ID NO: 552. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 517, the CDR-H2 of SEQ ID NO: 534, and the CDR-H3 of SEQ ID NO: 553. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 514, the CDR-H2 of SEQ ID NO: 535, and the CDR-H3 of SEQ ID NO: 554. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 518, the CDR-H2 of SEQ ID NO: 536, and the CDR-H3 of SEQ ID NO: 555. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 519, the CDR-H2 of SEQ ID NO: 537, and the CDR-H3 of SEQ ID NO: 556. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 520, the CDR-H2 of SEQ ID NO: 538, and the CDR-H3 of SEQ ID NO: 557. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 521, the CDR-H2 of SEQ ID NO: 539, and the CDR-H3 of SEQ ID NO: 558. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 522, the CDR-H2 of SEQ ID NO: 540, and the CDR-H3 of SEQ ID NO: 558. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a heavy chain

variable region comprising the CDR-H1 of SEQ ID NO: 523, the CDR-H2 of SEQ ID NO: 541, and the CDR-H3 of SEQ ID NO: 559. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 524, the CDR-H2 of SEQ ID NO: 542, and the CDR-H3 of SEQ ID NO: 560. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 525, the CDR-H2 of SEQ ID NO: 543, and the CDR-H3 of SEQ ID NO: 561. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 526, the CDR-H2 of SEQ ID NO: 544, and the CDR-H3 of SEQ ID NO: 562. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 527, the CDR-H2 of SEQ ID NO: 545, and the CDR-H3 of SEQ ID NO: 563. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 528, the CDR-H2 of SEQ ID NO: 546, and the CDR-H3 of SEQ ID NO: 564. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 525, the CDR-H2 of SEQ ID NO: 533, and the CDR-H3 of SEQ ID NO: 565. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 520, the CDR-H2 of SEQ ID NO: 547, and the CDR-H3 of SEQ ID NO: 566. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 529, the CDR-H2 of SEQ ID NO: 548, and the CDR-H3 of SEQ ID NO: 567. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 528, the CDR-H2 of SEQ ID NO: 546, and the CDR-H3 of SEQ ID NO: 568.

[0123] In another embodiment, the LukE/HlgA antibody or binding portion thereof of the present disclosure comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 569, the CDR-L2 of SEQ ID NO: 601, and the CDR-L3 of SEQ ID NO: 622. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 570, the CDR-L2 of SEQ ID NO: 602, and the CDR-L3 of SEQ ID NO: 623. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 571, the CDR-L2 of SEQ ID NO: 603, and the CDR-L3 of SEQ ID NO: 624. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 572, the CDR-L2 of SEQ ID NO:604 ,

and the CDR-L3 of SEQ ID NO: 625. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 573, the CDR-L2 of SEQ ID NO: 605, and the CDR-L3 of SEQ ID NO: 626. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 574, the CDR-L2 of SEQ ID NO: 606, and the CDR-L3 of SEQ ID NO: 627. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 575, the CDR-L2 of SEQ ID NO: 607, and the CDR-L3 of SEQ ID NO: 628. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 576, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 629. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 577, the CDR-L2 of SEQ ID NO: 607, and the CDR-L3 of SEQ ID NO: 630. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 578, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 631. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 579, the CDR-L2 of SEQ ID NO: 602, and the CDR-L3 of SEQ ID NO: 632. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 580, the CDR-L2 of SEQ ID NO: 607, and the CDR-L3 of SEQ ID NO: 633. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 581, the CDR-L2 of SEQ ID NO: 609, and the CDR-L3 of SEQ ID NO: 634. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 582, the CDR-L2 of SEQ ID NO: 610, and the CDR-L3 of SEQ ID NO: 635. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 579, the CDR-L2 of SEQ ID NO: 602, and the CDR-L3 of SEQ ID NO: 636. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 583, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 631. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 584, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 631. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain

variable region comprising the CDR-L1 of SEQ ID NO: 585, the CDR-L2 of SEQ ID NO: 611, and the CDR-L3 of SEQ ID NO: 637. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 579, the CDR-L2 of SEQ ID NO: 602, and the CDR-L3 of SEQ ID NO: 638. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 586, the CDR-L2 of SEQ ID NO: 612, and the CDR-L3 of SEQ ID NO: 639. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 587, the CDR-L2 of SEQ ID NO: 613, and the CDR-L3 of SEQ ID NO: 640. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 588, the CDR-L2 of SEQ ID NO: 614, and the CDR-L3 of SEQ ID NO: 641. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 589, the CDR-L2 of SEQ ID NO: 615, and the CDR-L3 of SEQ ID NO: 642. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 590, the CDR-L2 of SEQ ID NO: 601, and the CDR-L3 of SEQ ID NO: 64. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 581, the CDR-L2 of SEQ ID NO: 609, and the CDR-L3 of SEQ ID NO: 634. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 591, the CDR-L2 of SEQ ID NO: 616, and the CDR-L3 of SEQ ID NO: 644. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 592, the CDR-L2 of SEQ ID NO: 601, and the CDR-L3 of SEQ ID NO: 645. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 593, the CDR-L2 of SEQ ID NO: 617, and the CDR-L3 of SEQ ID NO: 646. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 594, the CDR-L2 of SEQ ID NO: 618, and the CDR-L3 of SEQ ID NO: 647. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 595, the CDR-L2 of SEQ ID NO: 619, and the CDR-L3 of SEQ ID NO: 648. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 596, the CDR-L2 of SEQ ID NO: 620, and the CDR-L3 of SEQ ID NO: 649. In another

embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 574, the CDR-L2 of SEQ ID NO: 621, and the CDR-L3 of SEQ ID NO: 650. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 597, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 625. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 573, the CDR-L2 of SEQ ID NO: 605, and the CDR-L3 of SEQ ID NO: 651. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 598, the CDR-L2 of SEQ ID NO: 607, and the CDR-L3 of SEQ ID NO: 652. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 599, the CDR-L2 of SEQ ID NO: 607, and the CDR-L3 of SEQ ID NO: 653. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 574, the CDR-L2 of SEQ ID NO: 606, and the CDR-L3 of SEQ ID NO: 627. In another embodiment, the LukE/HlgA antibody or binding portion thereof comprises a light chain variable region comprising the CDR-L1 of SEQ ID NO: 600, the CDR-L2 of SEQ ID NO: 602, and the CDR-L3 of SEQ ID NO: 654.

[0124] In another embodiment, the LukE/HlgA antibody comprises the heavy chain CDRs of SEQ ID NOs: 513, 530, and 549 together with the light chain CDRs of SEQ ID NOs: 569, 601 and, 622; the heavy chain CDRs of SEQ ID NOs: 514, 531, and 550 together with the light chain CDRs of SEQ ID NOs: 570, 602, and 623; the heavy chain CDRs of SEQ ID NOs: 515, 532, and 551 together with the light chain CDRs of SEQ ID NOs: 571, 603, and 624; the heavy chain CDRs of SEQ ID NOs: 516, 533, and 552 together with the light chain CDRs of SEQ ID NOs: 572, 604, and 625; the heavy chain CDRs of SEQ ID NOs: 517, 534, and 553 together with the light chain CDRs of SEQ ID NOs: 573, 605, and 626; the heavy chain CDRs of SEQ ID NOs: 514, 535, and 554 together with the light chain CDRs of SEQ ID NOs: 574, 606, and 627; the heavy chain CDRs of SEQ ID NOs: 518, 536, and 555 together with the light chain CDRs of SEQ ID NOs: 575, 607, and 628; the heavy chain CDRs of SEQ ID NOs: 519, 537, and 556 together with the light chain CDRs of SEQ ID NOs: 576, 608, and 629; the heavy chain CDRs of SEQ ID NOs: 520, 538, and 557 together with the light chain CDRs of SEQ ID NOs: 577, 607, and 630; the heavy chain CDRs of SEQ ID NOs: 521, 539, and 558 together with the light chain CDRs of SEQ ID NOs: 578, 608, and 631; the heavy chain CDRs of SEQ ID NOs: 521, 539, and 558 together with the light chain CDRs of SEQ ID NOs: 579, 602, and 632; the

heavy chain CDRs of SEQ ID NOs: 521, 539, and 558 together with the light chain CDRs of SEQ ID NOs: 580, 607, and 633; the heavy chain CDRs of SEQ ID NOs: 521, 539, and 558 together with the light chain CDRs of SEQ ID NOs:581, 609, and 634; the heavy chain CDRs of SEQ ID NOs: 521, 539, and 558 together with the light chain CDRs of SEQ ID NOs: 582, 610, and 635; the heavy chain CDRs of SEQ ID NOs: 521, 539, and 558 together with the light chain CDRs of SEQ ID NOs: 579, 602, and 636; the heavy chain CDRs of SEQ ID NOs: 522, 540, and 558 together with the light chain CDRs of SEQ ID NOs: 583, 608, and 631; the heavy chain CDRs of SEQ ID NOs: 523, 541, and 559 together with the light chain CDRs of SEQ ID NOs: 584, 608, and 631; the heavy chain CDRs of SEQ ID NOs: 523, 541, and 559 together with the light chain CDRs of SEQ ID NOs: 585, 611, and 637; the heavy chain CDRs of SEQ ID NOs: 523, 541, and 559 together with the light chain CDRs of SEQ ID NOs: 579, 602, and 638; the heavy chain CDRs of SEQ ID NOs: 523, 541, and 559 together with the light chain CDRs of SEQ ID NOs: 586, 612, and 639; the heavy chain CDRs of SEQ ID NOs: 523, 541, and 559 together with the light chain CDRs of SEQ ID NOs: 587, 613, and 640; the heavy chain CDRs of SEQ ID NOs: 523, 541, and 559 together with the light chain CDRs of SEQ ID NOs: 588, 614, and 641; the heavy chain CDRs of SEQ ID NOs: 524, 542, and 560 together with the light chain CDRs of SEQ ID NOs: 589, 615, and 642; the heavy chain CDRs of SEQ ID NOs: 525, 543, and 561 together with the light chain CDRs of SEQ ID NOs: 590, 601, and 643; the heavy chain CDRs of SEQ ID NOs: 526, 544, and 562 together with the light chain CDRs of SEQ ID NOs: 581, 609, and 634; the heavy chain CDRs of SEQ ID NOs: 526, 544, and 562 together with the light chain CDRs of SEQ ID NOs: 591, 616, and 644; the heavy chain CDRs of SEQ ID NOs: 526, 544, and 562 together with the light chain CDRs of SEQ ID NOs: 592, 601, and 645; the heavy chain CDRs of SEQ ID NOs: 526, 544, and 562 together with the light chain CDRs of SEQ ID NOs: 593, 617, and 646; the heavy chain CDRs of SEQ ID NOs: 526, 544, and 562 together with the light chain CDRs of SEQ ID NOs: 594, 618, and 647 ; the heavy chain CDRs of SEQ ID NOs: 526, 544, and 562 together with the light chain CDRs of SEQ ID NOs: 595, 619, and 648; the heavy chain CDRs of SEQ ID NOs: 527, 545, and 563 together with the light chain CDRs of SEQ ID NOs: 596, 620, and 649; the heavy chain CDRs of SEQ ID NOs: 528, 546, and 564 together with the light chain CDRs of SEQ ID NOs: 574, 621, and 650; the heavy chain CDRs of SEQ ID NOs: 525, 533, and 565 together with the light chain CDRs of SEQ ID NOs: 597, 608, and 625; the heavy chain CDRs of SEQ ID NOs: 520, 547, and 566 together with the light chain CDRs of SEQ ID NOs: 573, 605, and 651; the heavy chain CDRs of SEQ ID NOs: 529, 548, and 567 together with the light chain CDRs of SEQ ID NOs: 598, 607, and 652; the heavy chain CDRs of SEQ ID NOs: 529, 548, and 567 together with the light chain CDRs of

SEQ ID NOs: 599, 607, and 653; the heavy chain CDRs of SEQ ID NOs: 529, 548, and 567 together with the light chain CDRs of SEQ ID NOs: 574, 606, and 627; the heavy chain CDRs of SEQ ID NOs: 528, 546, and 568 together with the light chain CDRs of SEQ ID NOs: 574, 606, and 627; the heavy chain CDRs of SEQ ID NOs: 528, 546, and 568 together with the light chain CDRs of SEQ ID NOs: 600, 602, and 654.

[0125] The LukE/HlgA antibody or binding portion thereof as described herein may comprises a variable light (VL) chain, a variable heavy (VH) chain, or a combination of a VL and VH chain. The VL chain of the LukE/HlgA antibody or binding portion thereof as disclosed herein may comprise an amino acid sequence selected from SEQ ID NOs: 655-693 or an amino acid sequence that is at least 80% identical to any one of the amino acid sequence selected from SEQ ID NOs: 655-693. The VH chain of the LukE/HlgA antibody of binding portion thereof may comprise an amino acid sequence selected from SEQ ID NOs: 694-732 or an amino acid sequence that is at least 80% identical to anyone of the amino acid sequence selected from SEQ ID NOs: 694-732. The amino acid sequences of the LukE/HlgA VL and VH chains are provided in Table 18A below.

Table 18A. LukE/HlgA Antibody Variable Light (VL) and Variable Heavy (VH) Chain Sequences

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B302	VL	C47L104	DIQMTQSPSSLSASLGERVSLTCRASQDIGSSLN WLQQEPDGTIKRLIYATSSLDSGVPKRFSGSRSG SDYSLTISSLESEDFVDYYCLQYASSPWTFGGG TKLEIK	655
SM1B303	VL	HLGL3	DIQMTQTTSSLSASLGDRVTISCWASQDIRSYLN WYQQKPDGTVKLLIYYTSRLHSGVPSRFSGSGS GTDFSLTISNLEQEDIATYFCQQGNTLPYTFGGG TKLEIK	656
SM1B304	VL	HLGL4	DIQMTQSPSSLSASLGERVSLTCRASQEISGYLS WLQQKPDGTIKRLIYAASTLDSGVPKRFSGSRS GSDYSLTISSLESEDFADYYCLQYASYPRTFGG GTKLEIK	657
SM1B305	VL	HLGL5	DVLMTQTPLSLPVSLGDQASISCRSSQIIVHSNG NTYLDWYLQKPGQSPKLLIYKISNRFSGVPDRF SGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVP WTFGGGTKLEIK	658
SM1B306	VL	HLGL6	DVVVTQTPLSLPVSFGDQVSISCRSSQSLANSYG NTYLSWYLHKPGQSPQLLIYGISNRFSGVPDRFS GSGSGTDFTLKISTIKPEGLGMYYCLQGTHQPPT FGAGTKLELK	659

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B307	VL	HLGL7	DIVLTQSPASLAVSLGQRATISCRASESVDSYGN SFMHWYQQKPGQPPKLLIYRASNLESGIPARFS GSGSRTDFTLTINPVEADDVATYYCQQSNEDPP WTFGGGTKLEIK	660
SM1B308	VL	HLGL8	DIVMSQSPSSLAVSAGEKVTMSCKSSQSLLNSR TRKNYLAWYQQKPGQSPKLLIYWASTRESGVP DRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSY NLWTFGGGTKLEIK	661
SM1B309	VL	HLGL9	DVVMTQTPLSLPVSLGDQASISCRSSQSLLHSN GKTYLHWYLQKPGQSPKLLIYKVSNRFSGVPD RFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHV PLTFGAGTKLELK	662
SM1B310	VL	HLGL10	DIVMTQSHKFMSTSVGDRVSITCKASQDVSAA VAWYQQKPGQSPKLLIYWASTRHTGVPDRFTG SGSGTDYTLTISSVQAEDLALYYCQQHYSTPGT FGGGTKLEIK	663
SM1B311	VL	HLGL11	DVLMTQTPLSLPVSLGDQASISCRSSQTIVHSSG NTYLEWYLQRPGQSPKLLIYKVSNRFSGVPDRF SGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVP YTFGGGTKLEIK	664
SM1B312	VL	GC5L29	DIQMTQTTSSLSASLGDRVTISCSASQGISNYLN WYQQKPDGTVKLLIYYTSSLHSGVPSRFSGSGS GTDYSLTISNLEPEDIATYYCQQYSKLPFTFGSG TKLEIK	665
SM1B313	VL	HLGL12	DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSS NQKNYLAWYQQKPGQSPKLLIYWASTRESGVP DRLTGSGSGTDFTLTISSVKAEDLAVYYCQQYY SYPYTFGGGTKLEIK	666
SM1B314	VL	OSML437	DIQMTQSPASLSVSVGETVTITCRASENIYSNLA WYQQKQGKSPQLLVYAATNLADGVPSRFSGSG SGTQYSLKINSLQSEDFGSYYCQHFWGTPYTFG GGTKLEIK	667
SM1B315	VL	TM3L53	DIKMTQSPSSMYASLGERVTITCKASQDINSYLS WFQQKPGKSPKTLIYRANRLVDGVPSRFSGSGS GQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGG GTKLEIK	668
SM1B316	VL	HLGL13	DIQMTQTTSSLSASLGDRVTISCSASQGISNYLN WYQQKPDGTVKLLIHYTSSLHSGVPSRFSGSGS GTDYSLTISNLEPEDIATYYCQQYSKLPWTFGG GTKLEIK	669
SM1B317	VL	HLGL14	DVLMTQTPLSLPVSLGDQASISCRSSQTIVYSDG NTYLEWYLQKPGQSPKLLIYKVSNRFSGVPDRV SGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVP YTFGGGTKLEIK	670
SM1B318	VL	HLGL14	DVLMTQTPLSLPVSLGDQASISCRSSQTIVYSDG NTYLEWYLQKPGQSPKLLIYKVSNRFSGVPDRV SGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVP YTFGGGTKLEIK	671

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B319	VL	HLGL15	DIVMTQAAPSVPVTPGESVSISCRSSKSLLHSNG NTYLYWFLQRPGQSPQLLIYRMSNLASGVPDRF SGSGSGTAFTLRISRVEAEDVGVYYCMQHLEYP FTFGSGTKLEIK	672
SM1B320	VL	ATCL1	DIQMTQTTSSLSASLGDRVTISCSASQGISNYLN WYQQKPDGTVKLLIYYTSSLHSGVPSRFSGSGS GTDYSLTISNLEPEDIATYYCQQYSKLPYTFGGG TKLEIK	673
SM1B321	VL	VSTL360	DIQMTQSPASLSASVGETVTIICRASENIYSYLA WYQQKQGKSPQLLVYNAKTLVEGVPSRFSGSG SGTQFSLKINSLQPEDFGSYYCQHHYGSPYTFG GGTKLEIK	674
SM1B322	VL	ATCL3	DIVMTQSHKFMSTSVGDRVSITCKASQDVSTAV AWYQQKPGQSPKLLIYSASYRYTGVPDRFTGS GSGTDFTFTISSVQAEDLAVYYCQQHYSTPWTF GGGTKLEIK	675
SM1B323	VL	HLGL16	ETTVTQSPASLSMAIGEKVTIRCITSTDIDDDMN WYQQKPGEPPKLLISEGNTLRPGVPSRFSSSGY GTDFVFTIENMLSEDVADYYCLQSDNLPYTFGG GTKLEIK	676
SM1B324	VL	HLGL17	DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSG NQKNYLAWYQQKPGQPPKLLIYGASTRESGVP DRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDH SYPPTFGGGTKLEIK	677
SM1B325	VL	HLGL18	DIQMTQSPSSLSASLGERVSLTCRASQDIGNSLN WLQQKPDGTIKRLIYATSNLDSGVPKRFSGSRS GSDYSLTISSLESEDFVNYYCLQFASSPLTFGTG TKLEIK	678
SM1B326	VL	OSML437	DIQMTQSPASLSVSVGETVTITCRASENIYSNLA WYQQKQGKSPQLLVYAATNLADGVPSRFSGSG SGTQYSLKINSLQSEDFGSYYCQHFWGTPYTFG GGTKLEIK	679
SM1B327	VL	HLGL19	QIVLTQSPAIMSASPGEKVTMTCSASSNVSYMH WFQQKSGTSPKRWIYDTSKLASGVPARFSGSGS GTSYSLTVSSMEAEDAATYYCQQWSSNPRTFG GGTKLEIK	680
SM1B328	VL	VSTL342	DIQMTQSPSSLSASLGERVSLTCRASQDIGSYLN WLQQEPDGTIKRLIYATSSLDSGVPKRFSGSRSG ADYSLTISSLESEDFVDYYCLQYATSPWTFGGG TKLEIK	681
SM1B329	VL	HLGL20	DIQMTQSSSYLSVSLGGRVTITCKASDHINNWL AWYQQKPGNAPRLLISGATSLETGVPSRFSGSG SGKDYTLSITSLQTEDVATYYCQQYWSTPYTFG GGTKLEIK	682
SM1B330	VL	HLGL21	QIVLTQSPALMSASPGEKVTMTCSASSSVSYMY WYQQKPRSSPKLKYASNLASGVPARFSGSGSG TSYSLTISSMEAEDAATYYCQQWSSNPPITFGA GTKLELK	683

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B331	VL	VSTL368	DIVMTQSPATLSVTPGDRVSLSCRASQSISDYLH WYQQKSHESPRLLIKYDSQSISGIPSRFSGSGSGS DFTLSINSVEPEDVGVYYCQNGHRFPFTFGGGT KLEIK	684
SM1B332	VL	HLGL22	QIVLTQSPAIMSASPGEKVTLTCSASSSVSSSYLF WYQQKPGSSPKLWIYSTSNLASGVPVRFSGSGF GTSYSLTISRMEAEDAASYFCHQWSSYPPTFGA GTKLELK	685
SM1B333	VL	HLGL23	DIVLTQSPASLAVSLGQRATISCRASESVDSYGN SFMHWYQQKPGQPPKLLIYLASNLESGVPARFS GSGSRTDFTLTIDPVEADDAATYYCQQNNEDPY TFGGGTKLEIK	686
SM1B334	VL	HLGL24	DVLMTQTPLSLPVSLGDQASISCRSSQSIVYSNG NTYLDWYLQKPGQPPKLLIYKVSNRFSGVPDRF SGSGSGTDFILKISRVEAEDLGVYYCFQGSHVP WTFGGGTKLEIK	687
SM1B335	VL	HLGL25	DVVVTQTPLSLPVSFGDQVSISCRSSQSLANSYG NTYLSWYLHKPGQSPQLLIYGISNRFSGVPDRFS GSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPY TFGGGTKLEIK	688
SM1B336	VL	HLGL26	DIVMSQSPSSLAVSVGEKVTMSCKSSQSVLYNS NQRNYLAWYQQKPGQSPKLLIYWASTRESGVP DRSTGSGSGTDFTLTISSVQAEDLAVYYCHQYL SSYTFGGGTKLEIK	689
SM1B337	VL	HLGL27	DIVMTQSHKFMSTSVGDRVSITCKASQDVGTA VAWYQQKPGQSPKLLIYWASTRHTGVPDRFTG SGSGTDFTLTISNVQSEDLADYFCQQYSSYPLTF GAGTKLELK	690
SM1B338	VL	HLGL7	DIVLTQSPASLAVSLGQRATISCRASESVDSYGN SFMHWYQQKPGQPPKLLIYRASNLESGIPARFS GSGSRTDFTLTINPVEADDVATYYCQQSNEDPP WTFGGGTKLEIK	691
SM1B339	VL	HLGL7	DIVLTQSPASLAVSLGQRATISCRASESVDSYGN SFMHWYQQKPGQPPKLLIYRASNLESGIPARFS GSGSRTDFTLTINPVEADDVATYYCQQSNEDPP WTFGGGTKLEIK	692
SM1B340	VL	HLGL28	DIQMTQTTSSLSASLGDRVTISCRASQDIDNYLN WYQQKPDGTVKLLISYTSRLHSGVPSRFSGSGS GTDYSLTISNLEQEDFATYFCQQGYTLPWTFGG GTKLEIK	693
SM1B302	VH	HLGH3	EVKLVESGGDLVKPGGSLKLSCAASGFTFSSFA MSWVRQTPEKRLEWVASISRTDNTYYPDSMKG QFTISRDNARNILYLQMSSLRSENTAIYYCARA DYDGPWFAYWGQGTLVTVSA	694
SM1B303	VH	HLGH4	EVQLQQSGPDLVKPGTSVKMSCKASGYSFTGY YMHWVKQSHGKSLEWIGRVNPNNGGTSYNQK FKGKAILTVDKSSSTAYMELRSLTSEDSAVYYC ARDDYSFAYWGQGTLVTVSA	695

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B304	VH	HLGH5	EVKLVESGGGLVQPGGSLRLSCATSGFTFTDFY MSWVRQPPGKALEWLAFIRNKANGYTTEYSSS VRGRFTISRDNSQSILYLQMNTLRAEDSGTYYC ARDVGDYDYWGQGSTLTVSS	696
SM1B305	VH	HLGH6	QIQLVQSGPELKKPGETVKISCKASGFTFTNYG MNWVKQAPGKDLKWMGWINTYTGEPTYADD FKGRFAFSLETSASTAYLQINNLKDEDTASYFC ARDYRDGDALDYWGQGTSVTVSS	697
SM1B306	VH	HLGH7	QVQLQQPGAELVRPGASVKLSCKASGYSFTSN WMNWMKQRPGQGLEWIGMIHPSDSESRLNQK FKDKATLTVDKSSSTAYMQLSSPTSEDSAVYYC ARGDGGFAYWGQGTLVTVSA	698
SM1B307	VH	HLGH8	EVKLQQSGPELVKPGASMKISCKASGYSFTGYT MNWAKQSHGKNLEWIGLINPYNGGTSYNQKF KGKATLTVDKSSSTAYMELLSLTSEDSAVYYC ARGYPRGWFAYWGQGTLVTVSA	699
SM1B308	VH	HLGH9	DVKLVESGGGLVKPGGSLKLSCAASGFTFRNH AMSWVRQTPEKRLEWVAAINVNAGSTYYPDT VKDRFTISRDNAKNTLYLQMSSLRSEDTALYYC ARHRAYYNYDENAMDYWGQGTSVTVSS	700
SM1B309	VH	HLGH10	EVQLQQSGPELVKPGDSVKMSCKASGYTFTDY YIDWMKQSHGKSLEWIGYIYPNNGGTSYNQNF KDKATLTVDKSSSTAYMELHSLTSEDSAVYYC ARLTYYAKVDSWGQGTSVTVSS	701
SM1B310	VH	HLGH11	DVKLVESGGGLVEWEGVLKLSCAASGFTFSSY AMSWVRQTPEKRLEWVAAINSNGGSTYYPDTV KDRFTISRDNAKNTLYLQMSSLRSEDTALYYCA RLYYGDYWGQGTTLTVSS	702
SM1B311	VH	HLGH12	QVQLKQSGPSLVQPSQSLSITCTVSGFSLTTYGL HWIRQSPGKGLEWLGVIWRGGTTDYNAAFMS RLTITKDNSKSQVFFKMNSLQADDTAIYYCART DIWGAGTTVTVSS	703
SM1B312	VH	HLGH12	QVQLKQSGPSLVQPSQSLSITCTVSGFSLTTYGL HWIRQSPGKGLEWLGVIWRGGTTDYNAAFMS RLTITKDNSKSQVFFKMNSLQADDTAIYYCART DIWGAGTTVTVSS	704
SM1B313	VH	HLGH12	QVQLKQSGPSLVQPSQSLSITCTVSGFSLTTYGL HWIRQSPGKGLEWLGVIWRGGTTDYNAAFMS RLTITKDNSKSQVFFKMNSLQADDTAIYYCART DIWGAGTTVTVSS	705
SM1B314	VH	HLGH13	QVQLKQSGPGLVQPSQSLPITCTVSGFSLTTYGL HWIRQSPGKGLEWLGVIWRGGTTDYNAAFMS RLTITKDNSKSQVFFKMNSLQADDTAIYYCART DIWGAGTTVTVSS	706
SM1B315	VH	HLGH14	QVQLKQSGPGLVQPSQSLSITCTVSGFSLTTYGL HWIRQSPGKGLEWLGVIWRGGTTDYNAAFMS RLTITKDNSKSQVFFKMNSLQADDTAIYYCART DIWGAGTTVTVSS	707

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B316	VH	HLGH12	QVQLKQSGPSLVQPSQSLSITCTVSGFSLTTYGL HWIRQSPGKGLEWLGVIWRGGTTDYNAAFMS RLTITKDNSKSQVFFKMNSLQADDTAIYYCART DIWGAGTTVTVSS	708
SM1B317	VH	HLGH15	QVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGV HWVRQPPGKGLEWLGVIWSGGITDYNAAFISR LSISKDNSKSQVFFKMNSLQADDTAIYYCARTD LWGQGTLVTVSA	709
SM1B318	VH	HLGH16	QVQLQQSGAELMNPGASVKISCKSTGYKFSSY WIEWVKQRPGHGLEWMGEILPGSGSTNHNEKF KGKAIFTADASSNTAYMELSSLTSEDSAVYYCA RTISTATDWFAYWGQGTLVTVSA	710
SM1B319	VH	HLGH16	QVQLQQSGAELMNPGASVKISCKSTGYKFSSY WIEWVKQRPGHGLEWMGEILPGSGSTNHNEKF KGKAIFTADASSNTAYMELSSLTSEDSAVYYCA RTISTATDWFAYWGQGTLVTVSA	711
SM1B320	VH	HLGH17	QVQLQQSGAELMKPGASVKMSCKATGYKFSS YWIEWVKQRPGHGLEWMGEILPGSGSTNHNEK FKGKAIFTADASSNTAYMELSSLTSEDSAVYYC ARTISTATDWFAYWGQGTLVTVSA	712
SM1B321	VH	HLGH18	QVQLQQSGAELMKPGASVKMSCKATGYKFSS YWIEWVKQRPGHGLEWMGEILPGSGSTNHNEK FTGRAIFTADASSNTAYMELSSLTSEDSAVYYC ARTISTATDWFAYWGQGTLVTVSA	713
SM1B322	VH	HLGH17	QVQLQQSGAELMKPGASVKMSCKATGYKFSS YWIEWVKQRPGHGLEWMGEILPGSGSTNHNEK FKGKAIFTADASSNTAYMELSSLTSEDSAVYYC ARTISTATDWFAYWGQGTLVTVSA	714
SM1B323	VH	HLGH19	QVQLQQSGAELMKPGASVKMPCKATGYKFSS YWIEWVKQRPGHGLEWMGEILPGSGSTNHNEK FKGKAIFTADASSNTAYMELSSLTSEDSAVYYC ARTISTATDWFAYWGQGTLVTVSA	715
SM1B324	VH	HLGH20	EVQLQQSGAELVRPGALVKLSCKASGFNIKDY YMHWVKQRPEQGLEWIGWIDPENGNTIYDPKF QGKASITADTSSNTAYLQLSSLTSEDTAVYYCA RYDGYAMDYWGQGTSVTVSS	716
SM1B325	VH	HLGH21	QVQLQQSGAELVRPGTSVKMSCKAAGYTFTNY WIGWVKQRPGHGLEWIGDIYPGGGYTNYNEKF KDKTTLTADTSSNTAYMQLSSLTSEDSAIYYCA SNDCWGQGTTLTVSS	717
SM1B326	VH	HLGH22	QVQLKQSGPGLVQPSQSLSITCTVSGFSITSYGV HWIRQSPGKGLEWLGVIWSGGSTDYNAAFISRL SISEDNSKSQVFFKMNSLQANDTAIYYCATFYY DYDEGFDYWGQGTTLTVSS	718
SM1B327	VH	HLGH23	QVQLKQSGPGLVQPSQSLSITCTVSGFSITSYGV HWIRQSPGKGLEWLGVIWSGGSTDYNAAFISRL SISKDNSKSQVFFKMNSLQANDTAIYYCATFYY DYDEGFDYWGQGTTLTVSS	719

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B328	VH	HLGH23	QVQLKQSGPGLVQPSQSLSITCTVSGFSITSYGV HWIRQSPGKGLEWLGVIWSGGSTDYNAAFISRL SISKDNSKSQVFFKMNSLQANDTAIYYCATFYY DYDEGFDYWGQGTTLTVSS	720
SM1B329	VH	HLGH23	QVQLKQSGPGLVQPSQSLSITCTVSGFSITSYGV HWIRQSPGKGLEWLGVIWSGGSTDYNAAFISRL SISKDNSKSQVFFKMNSLQANDTAIYYCATFYY DYDEGFDYWGQGTTLTVSS	721
SM1B330	VH	HLGH23	QVQLKQSGPGLVQPSQSLSITCTVSGFSITSYGV HWIRQSPGKGLEWLGVIWSGGSTDYNAAFISRL SISKDNSKSQVFFKMNSLQANDTAIYYCATFYY DYDEGFDYWGQGTTLTVSS	722
SM1B331	VH	HLGH23	QVQLKQSGPGLVQPSQSLSITCTVSGFSITSYGV HWIRQSPGKGLEWLGVIWSGGSTDYNAAFISRL SISKDNSKSQVFFKMNSLQANDTAIYYCATFYY DYDEGFDYWGQGTTLTVSS	723
SM1B332	VH	HLGH24	QVQLKESGPGLVAPSQSLSITCTVSGLSLTSYGL SWVRQPPGKGLEWLGVIWGDGSTNYHSALISR LSISKDNSKSQVFLKLNSLQSDDTATYYCATRG DYGSYAMDYWGQGTSVTVSS	724
SM1B333	VH	HLGH25	EVQLQQSGAELVRPGASVKLSCTASGFNIKDSLI HWVKQRPEQGLEWIGWIDPEDGETKYAPKFQD KAALTTDTSSNTAYLHLNSLTSEDTAIYYCGRG GLILDYWGQGTTLTVSS	725
SM1B334	VH	HLGH26	QIQLVQSGPELKKPGETVKISCRSSGYTFTNYGL NWVKQAPGKDLKWMGWLNTYTGEPTYADDF KGRFAFSLETSAGTAYLQINNLKNEDTATYFCS RDYREGDAMDYWSQGTSVTVSS	726
SM1B335	VH	HLGH27	EVQLVESGGGLVKPGGSLKLSCAASGFTFSSYA MSWVRQTPEKRLEWVATISTSGSYTYYRDSVK GRLTISRDNAKNTLYLQMTSLRSEDTAMYYCT RHGDHDGFDYWGQGTTLTVSS	727
SM1B336	VH	HLGH28	EVQLVESGGGLVKPGGSLKLSCVASGFSFSNYA MSWVRQTPERRLEWVATINSGGSFSFFPDSVKG RFTISRDSAKNTLYLQMSSLRSDDTAMYYCTRH WDHPWFAYWGQGTLVTVSA	728
SM1B337	VH	HLGH28	EVQLVESGGGLVKPGGSLKLSCVASGFSFSNYA MSWVRQTPERRLEWVATINSGGSFSFFPDSVKG RFTISRDSAKNTLYLQMSSLRSDDTAMYYCTRH WDHPWFAYWGQGTLVTVSA	729
SM1B338	VH	HLGH28	EVQLVESGGGLVKPGGSLKLSCVASGFSFSNYA MSWVRQTPERRLEWVATINSGGSFSFFPDSVKG RFTISRDSAKNTLYLQMSSLRSDDTAMYYCTRH WDHPWFAYWGQGTLVTVSA	730
SM1B339	VH	HLGH29	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLI YWVKQRPEQGLEWIGWIDPEDGETKFAPRFQD KATITSDTSSNTAYLRLSSLTSKDTAIYYCTRSF GVCWGQGTLVTVSA	731

mAb/Fab name	Region	Name	Sequence	SEQ ID NO:
SM1B340	VH	HLGH30	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLI YWVKQRPEQGLEWIGWIDPEDGETKFAPRFQD KATITSDTSSNTAYLRLSSLTSEDTAIYYCTRSF GVCWGQGTLVTVSA	732

[0126] In another embodiment, the antibody or binding fragment thereof comprises a VH region having an amino acid sequence that shares at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity to any one of SEQ ID NOs: 694-732 as shown in Table 18A, and/or a VL region having an amino acid sequence that shares at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity to any one of SEQ ID NOs: 655-693 as shown in Table 18A.

[0127] In one embodiment, the antibody or binding fragment thereof of the present disclosure comprises a humanized VH variant of any one of SEQ ID NOs: 694-732 and/or a humanized VL variant of any one of SEQ ID NOs: 655-693, where the framework regions are humanized or replaced with human immunoglobulin framework sequences. The humanized framework regions are designed to be similar in length and sequence to the parental framework sequences within SEQ ID NOs: 655-732, respectively. In one embodiment, the humanized framework regions share 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more sequence identity to the framework regions of any one of SEQ ID NOs: 655-732, respectively. In another embodiment, the humanized framework regions are 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more similar in length to the framework regions of any one of SEQ ID NOs: 655-732, respectively. Humanized variants of the VH of any one of SEQ ID NOs: 694-732 and the VL of any one of SEQ ID NOs: 655-693 share at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% sequence identity along the entire length of SEQ ID NOs: 694-732 and SEQ ID NOs: 655-693, respectively.

[0128] Suitable LukE/HlgA antibodies as disclosed herein comprise a VL of SEQ ID NO: 655 and a VH of SEQ ID NO:694; a VL of SEQ ID NO: 656 and a VH of SEQ ID NO: 695; a VL of SEQ ID NO: 657 and a VH of SEQ ID NO:696; a VL of SEQ ID NO: 658 and a VH of SEQ ID NO:697; a VL of SEQ ID NO: 659 and a VH of SEQ ID NO: 698; a VL of SEQ ID NO: 660 and a VH of SEQ ID NO: 699; a VL of SEQ ID NO: 661 and a VH of SEQ ID NO: 700; a

VL of SEQ ID NO: 662 and a VH of SEQ ID NO: 701; a VL of SEQ ID NO: 663 and a VH of SEQ ID NO: 702; a VL of SEQ ID NO: 664 and a VH of SEQ ID NO: 703; a VL of SEQ ID NO: 665 and a VH of SEQ ID NO: 704; a VL of SEQ ID NO: 666 and a VH of SEQ ID NO: 705; a VL of SEQ ID NO: 667 and a VH of SEQ ID NO: 706; a VL of SEQ ID NO: 668 and a VH of SEQ ID NO: 707; a VL of SEQ ID NO: 669 and a VH of SEQ ID NO: 708; a VL of SEQ ID NO: 670 and a VH of SEQ ID NO: 709; a VL of SEQ ID NO: 671 and a VH of SEQ ID NO: 710; a VL of SEQ ID NO: 672 and a VH of SEQ ID NO: 711; a VL of SEQ ID NO: 673 and a VH of SEQ ID NO: 712; a VL of SEQ ID NO: 674 and a VH of SEQ ID NO: 713; a VL of SEQ ID NO: 675 and a VH of SEQ ID NO: 714; a VL of SEQ ID NO: 676 and a VH of SEQ ID NO: 715; a VL of SEQ ID NO: 677 and a VH of SEQ ID NO: 716; a VL of SEQ ID NO: 678 and a VH of SEQ ID NO: 717; a VL of SEQ ID NO: 679 and a VH of SEQ ID NO: 718; a VL of SEQ ID NO: 680 and a VH of SEQ ID NO: 719; a VL of SEQ ID NO: 681 and a VH of SEQ ID NO: 720; a VL of SEQ ID NO: 682 and a VH of SEQ ID NO: 721; a VL of SEQ ID NO: 683 and a VH of SEQ ID NO: 722; a VL of SEQ ID NO: 684 and a VH of SEQ ID NO: 723; a VL of SEQ ID NO: 685 and a VH of SEQ ID NO: 724; a VL of SEQ ID NO: 686 and a VH of SEQ ID NO: 725; a VL of SEQ ID NO: 687 and a VH of SEQ ID NO: 726; a VL of SEQ ID NO: 688 and a VH of SEQ ID NO: 727; a VL of SEQ ID NO: 689 and a VH of SEQ ID NO: 728; a VL of SEQ ID NO: 690 and a VH of SEQ ID NO: 729; a VL of SEQ ID NO: 691 and a VH of SEQ ID NO: 730; a VL of SEQ ID NO: 692 and a VH of SEQ ID NO: 731; or a VL of SEQ ID NO: 693 and a VH of SEQ ID NO: 732.

[0129] In one embodiment, the LukE/HlgA antibody is a LukE/HlgA antigen-binding fragment, *i.e.*, a Fab, comprising the heavy chain variable region (VH) and first heavy chain constant domain (CH1) of an antibody coupled to the light chain variable region (VL) and light chain constant region (CL) of the antibody. In another embodiment, the LukE/HlgA antibody is a $F(ab')_2$ fragment, which comprises both LukE/HlgA antigen-binding fragments of the full-length antibody coupled by the hinge region. The heavy chain and light chain portions of exemplary LukE/HlgA Fab fragments are provided in Table 18B below. Exemplary LukE/HlgA Fab or $F(ab')_2$ fragments comprise as disclosed herein, a HC region of SEQ ID NO: 1308 and a LC region OF SEQ ID NO: 1312 (SM1B309); a HC region of SEQ ID NO: 1309 and a LC region of SEQ ID NO: 1313 (SM1B318); a HC region of SEQ ID NO: 1310 and a LC region of SEQ ID NO: 1314 (SM1B325); a HC region of SEQ ID NO: 1311 and a LC region of SEQ ID NO: 1315 (SM1B440).

Table 18B. LukE/HlgA Fab Amino Acid Heavy Chain (HC) and Light Chain (LC) Sequences

Protein AA ID	Fab of	Region	Fab Amino Acid Sequence	SEQ ID NO:
SM1B437	SM1B309	HC	EVQLQQSGPELVKPGDSVKMSCKASGYTFT DYYIDWMKQSHGKSLEWIGYIYPNNGGTS YNQNFKDKATLTVDKSSSTAYMELHSLTSE DSAVYYCARLTYYAKVDSWGQGTSVTVSS ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCHHHHHH	1308
SM1B438	SM1B318	HC	QVQLQQSGAELMNPGASVKISCKSTGYKFS SYWIEWVKQRPGHGLEWMGEILPGSGSTN HNEKFKGKAIFTADASSNTAYMELSSLTSE DSAVYYCARTISTATDWFAYWGQGTLVTV SAASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCHHHHHH	1309
SM1B439	SM1B325	HC	QVQLQQSGAELVRPGTSVKMSCKAAGYTF TNYWIGWVKQRPGHGLEWIGDIYPGGGYT NYNEKFKDKTTLTADTSSNTAYMQLSSLTS EDSAIYYCASNDCWGQGTTLTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCHHHHHH	1310
SM1B440	SM1B332	HC	QVQLKESGPGLVAPSQSLSITCTVSGLSLTS YGLSWVRQPPGKGLEWLGVIWGDGSTNYH SALISRLSISKDNSKSQVFLKLNSLQSDDTAT YYCATRGDYGSYAMDYWGQGTSVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCHHHHHH	1311
SM1B437	SM1B309	LC	DVVMTQTPLSLPVSLGDQASISCRSSQSLLH SNGKTYLHWYLQKPGQSPKLLIYKVSNRFS GVPDRFSGSGSGTDFTLKISRVEAEDLGVYF CSQSTHVPLTFGAGTKLELKRTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQW KVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKS FNRGEC	1312
SM1B438	SM1B318	LC	DVLMTQTPLSLPVSLGDQASISCRSSQTIVY SDGNTYLEWYLQKPGQSPKLLIYKVSNRFS GVPDRVSGSGSGTDFTLKISRVEAEDLGVY YCFQGSHVPYTFGGGTKLEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQ	1313

Protein AA ID	Fab of	Region	Fab Amino Acid Sequence	SEQ ID NO:
			WKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTK SFNRGEC	
SM1B439	SM1B325	LC	DIQMTQSPSSLSASLGERVSLTCRASQDIGN SLNWLQQKPDGTIKRLIYATSNLDSGVPKRF SGSRSGSDYSLTISSLESEDFVNYYCLQFASS PLTFGTGTKLEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDSTYSLSSTLTLSKADY EKHKVYACEVTHQGLSSPVTKSFNRGEC	1314
SM1B440	SM1B332	LC	QIVLTQSPAIMSASPGEKVTLTCSASSSVSSS YLFWYQQKPGSSPKLWIYSTSNLASGVPVR FSGSGFGTSYSLTISRMEAEDAASYFCHQWS SYPPTFGAGTKLELKRTVAAPSVFIFPPSDEQ LKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1315

[0130] In another embodiment, the LukE/HlgA Fab or F(ab')$_2$ fragments as disclosed above comprise a heavy chain region having an amino acid sequence that shares at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity to any one of SEQ ID NOs: 1308-1311 as shown in Table 18B, and/or a light chain region having an amino acid sequence that shares at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity to any one of SEQ ID NOs: 1312-1315 as shown in Table 18B. Additional LukE/HlgA Fab or F(ab')2 fragments of the present disclosure include those derived from the full-length LukE/HlgA light chain and heavy chain sequences disclosed in Table 24 below (*i.e.*, full length LukE/HlgA light chain sequences of SEQ ID NO: 733-771 and heavy chain sequences of SEQ ID NOs: 772- 810).

[0131] Exemplary LukE/HlgA antibodies of the present disclosure comprising the VL and VH chains as enumerated above are provided in Table 24 by their respective full-length LC and HC sequences. In particular, the amino acid sequences of the full-length light chain corresponding to and comprising the VL of SEQ ID NOs: 655-693 are provided as SEQ ID NO: 733-771 in Table 24, respectfully. The amino acid sequences of the full-length heavy chains corresponding to and comprising the VH of SEQ ID NOs: 694-732 are provided as SEQ ID NOs: 772- 810 in Table 24, respectively.

[0132] Another aspect of the present disclosure relates to an antibody or binding portion thereof that competes for LukE and/or HlgA binding with a monoclonal antibody as disclosed herein. In particular, the present disclosure encompasses an antibody or binding portion thereof that competes for binding to LukE and/or HlgA with a monoclonal antibody comprising: (i) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 519, the CDR-H2 of SEQ ID NO: 537, and the CDR-H3 of SEQ ID NO: 556, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 576, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 629; (ii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 521, the CDR-H2 of SEQ ID NO: 539, and the CDR-H3 of SEQ ID NO: 558, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 578, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 631; (iii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 522, the CDR-H2 of SEQ ID NO: 540, and the CDR-H3 of SEQ ID NO: 558, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 583, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 631; (iv) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 523, the CDR-H2 of SEQ ID NO: 541, and the CDR-H3 of SEQ ID NO: 559, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 584, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 631; (v) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 524, the CDR-H2 of SEQ ID NO: 542, and the CDR-H3 of SEQ ID NO: 560, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 589, the CDR-L2 of SEQ ID NO: 615, and the CDR-L3 of SEQ ID NO:642; (vi) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 525, the CDR-H2 of SEQ ID NO: 543, and the CDR-H3 of SEQ ID NO: 561 and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 590, the CDR-L2 of SEQ ID NO: 601, and the CDR-L3 of SEQ ID NO: 643; and (vii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 527, the CDR-H2 of SEQ ID NO: 545 and the CDR-H3 of SEQ ID NO: 563, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 596, the CDR-L2 of SEQ ID NO: 620, and the CDR-L3 of SEQ ID NO: 649.

[0133] Another aspect of the present disclosure is directed to nucleic acid molecules encoding the *S. aureus* antibodies or binding portions thereof as described herein. The nucleic acid molecules described herein include isolated polynucleotides, recombinant polynucleotide sequences, portions of expression vectors or portions of linear DNA sequences, including linear DNA sequences used for *in vitro* or *in vivo* transcription/translation, and vectors compatible with prokaryotic, eukaryotic or filamentous phage expression, secretion, and/or display of the antibodies or binding fragments thereof described herein.

[0134] In one embodiment, exemplary nucleic acid molecules include those encoding the V_H and V_L regions of the staphylococcal LukAB, LukD, LukD, HlgA, HlgC, and LukE/HlgA antibodies as described *supra* or humanized versions of the VH and VL chains described *supra*. In another embodiment, exemplary recombinant nucleic acid molecules include those encoding the heavy chain and light chain components of the staphylococcal LukAB, LukD, LukD, HlgA, HlgC, and LukE/HlgA Fabs described herein. In another embodiment, exemplary recombinant nucleic acid molecules include those encoding the heavy chain and light chain components of the staphylococcal LukAB, LukD, LukD, HlgA, HlgC, and LukE/HlgA antibodies described herein.

[0135] Suitable nucleic acid sequences (*i.e.*, primary transcripts and coding DNA sequences (CDS)) encoding the LukAB antibody heavy chain polypeptides and light chain polypeptides described herein are enumerated in Tables 26-29 and include SEQ ID NOs: 834-997. Nucleic acid molecules having nucleotide sequences that differ from SEQ ID NOs: 834-997, which as a result of the degeneracy of the genetic code, also encode the LukAB antibody heavy chain and light chain polypeptides described herein are also encompassed by the present disclosure. Such nucleic acid molecules may share 80%, 85%, 90%, or 95% sequence identity to the sequences of SEQ ID NOs: 834-997.

[0136] Suitable nucleic acid sequences (*i.e.*, primary transcripts and coding DNA sequences (CDS)) encoding the LukE antibody heavy chain polypeptides and light chain polypeptides described herein are enumerated in Tables 30-33 and include SEQ ID NOs: 998-1045. Nucleic acid molecules having nucleotide sequences that differ from SEQ ID NOs: 998-1045, which as a result of the degeneracy of the genetic code, also encode the LukE antibody heavy chain and light chain polypeptides described herein are also encompassed by the present disclosure. Such nucleic acid molecules may share 80%, 85%, 90%, or 95% sequence identity to the sequences of SEQ ID NOs: 998-1045.

[0137] Suitable nucleic acid sequences (*i.e.*, primary transcripts and coding DNA sequences (CDS)) encoding the LukD antibody heavy chain polypeptides and light chain polypeptides described herein are enumerated in Tables 34-37 and include SEQ ID NOs: 1046-1077. Nucleic acid molecules having nucleotide sequences that differ from SEQ ID NOs: 1046-1077, which as a result of the degeneracy of the genetic code, also encode the LukD antibody heavy chain and light chain polypeptides described herein are also encompassed by the present disclosure. Such nucleic acid molecules may share 80%, 85%, 90%, or 95% sequence identity to the sequences of SEQ ID NOs: 1046-1077.

[0138] Suitable nucleic acid sequences (*i.e.*, primary transcripts and coding DNA sequences (CDS)) encoding the HlgA antibody heavy chain polypeptides and light chain

polypeptides described herein are enumerated in Tables 38-41 and include SEQ ID NOs: 1078-1101. Nucleic acid molecules having nucleotide sequences that differ from SEQ ID NOs: 1078-1101, which as a result of the degeneracy of the genetic code, also encode the HlgA antibody heavy chain and light chain polypeptides described herein are also encompassed by the present disclosure. Such nucleic acid molecules may share 80%, 85%, 90%, or 95% sequence identity to the sequences of SEQ ID NOs: 1078-1101.

[0139] Suitable nucleic acid sequences (*i.e.*, primary transcripts and coding DNA sequences (CDS)) encoding the HlgC antibody heavy chain polypeptides and light chain polypeptides described herein are enumerated in Tables 42-45 and include SEQ ID NOs: 1102-1125. Nucleic acid molecules having nucleotide sequences that differ from SEQ ID NOs: 1102-1125, which as a result of the degeneracy of the genetic code, also encode the HlgC antibody heavy chain and light chain polypeptides described herein are also encompassed by the present disclosure. Such nucleic acid molecules may share 80%, 85%, 90%, or 95% sequence identity to the sequences of SEQ ID NOs: 1102-1125.

[0140] Suitable nucleic acid sequences (*i.e.*, primary transcripts and coding DNA sequences (CDS)) encoding LukE/HlgA antibody heavy chain polypeptides and light chain polypeptides described herein are enumerated in Tables 46-49 and include SEQ ID NOs: 1126-1281. Nucleic acid molecules having nucleotide sequences that differ from SEQ ID NOs: 1126-1281, which as a result of the degeneracy of the genetic code, also encode the LukE/HlgA antibody heavy chain and light chain polypeptides described herein are also encompassed by the present disclosure. Such nucleic acid molecules may share 80%, 85%, 90%, or 95% sequence identity to the sequences of SEQ ID NOs: 1126-1281.

[0141] Another embodiment of the disclosure is directed to one or more vectors comprising nucleic acid sequence(s) encoding the *S. aureus* antibodies or binding portions thereof as described herein. The nucleotide sequences encoding the heavy and light chain variable domains, Fab fragments, or full-length chains of the antibodies disclosed herein are combined with sequences of promoter, translation initiation, 3′ untranslated region, polyadenylation, and transcription termination to form one or more expression vector constructs.

[0142] In accordance with this embodiment, the expression vector construct encoding the *S. aureus* antibody or binding portion thereof can include the nucleic acid encoding the heavy chain polypeptide, a fragment thereof, a variant thereof, or combinations thereof. The heavy chain polypeptide can include a variable heavy chain (VH) region and/or at least one constant heavy chain (CH) region. The at least one constant heavy chain region can include a constant heavy chain region 1 (CH1), a constant heavy chain region 2 (CH2), and a constant heavy chain

region 3 (CH3), and/or a hinge region. In some embodiments, the heavy chain polypeptide can include a VH region and a CH1 region. In other embodiments, the heavy chain polypeptide can include a VH region, a CH1 region, a hinge region, a CH2 region, and a CH3 region.

[0143] The expression construct can also include a nucleic acid sequence encoding the light chain polypeptide, a fragment thereof, a variant thereof, or combinations thereof. The light chain polypeptide can include a variable light chain (VL) region and/or a constant light chain (CL) region.

[0144] In one embodiment, the expression construct includes a nucleic acid sequence encoding a LukAB antibody or binding fragment thereof as described herein. Suitable nucleic acid sequences (*i.e.*, primary transcripts and coding DNA sequences (CDS)) encoding the LukAB antibody heavy chain polypeptides and light chain polypeptides described herein are enumerated in Tables 26-29 and include SEQ ID NOs: 834-997.

[0145] In one embodiment, the expression construct includes a nucleic acid sequence encoding a LukE antibody or binding fragment thereof as described herein. Suitable nucleic acid sequences (*i.e.*, primary transcripts and coding DNA sequences (CDS)) encoding the LukE antibody heavy chain polypeptides and light chain polypeptides described herein are enumerated in Tables 30-33 and include SEQ ID NOs: 998-1045.

[0146] In one embodiment, the expression construct includes a nucleic acid sequence encoding a LukD antibody or binding fragment thereof as described herein. Suitable nucleic acid sequences (*i.e.*, primary transcripts and coding DNA sequences (CDS)) encoding the LukD antibody heavy chain polypeptides and light chain polypeptides described herein are enumerated in Tables 34-37 and include SEQ ID NOs: 1046-1077.

[0147] In one embodiment, the expression construct includes a nucleic acid sequence encoding a HlgA antibody or binding fragment thereof as described herein. Suitable nucleic acid sequences (*i.e.*, primary transcripts and coding DNA sequences (CDS)) encoding the HlgA antibody heavy chain polypeptides and light chain polypeptides described herein are enumerated in Tables 38-41 and include SEQ ID NOs: 1078-1101

[0148] In one embodiment, the expression construct includes a nucleic acid sequence encoding a HlgC antibody or binding fragment thereof as described herein. Suitable nucleic acid sequences (*i.e.*, primary transcripts and coding DNA sequences (CDS)) encoding the HlgC antibody heavy chain polypeptides and light chain polypeptides described herein are enumerated in Tables 42-45 and include SEQ ID NOs: 1102-1125.

[0149] In one embodiment, the expression construct includes a nucleic acid sequence encoding a LukE/HlgA antibody or binding fragment thereof as described herein. Suitable

nucleic acid sequences (*i.e.*, primary transcripts and coding DNA sequences (CDS)) encoding LukE/HlgA antibody heavy chain polypeptides and light chain polypeptides described herein are enumerated in Tables 46-49 and include SEQ ID NOs: 1126-1281.

[0150] The expression construct also typically comprises a promoter sequence suitable for driving expression of the antibody or binding fragment thereof. Suitable promoter sequences include, without limitation, the elongation factor 1-alpha promoter (EF1a) promoter, a phosphoglycerate kinase-1 promoter (PGK) promoter, a cytomegalovirus immediate early gene promoter (CMV), a chimeric liver-specific promoter (LSP) a cytomegalovirus enhancer/chicken beta-actin promoter (CAG), a tetracycline responsive promoter (TRE), a transthyretin promoter (TTR), a simian virus 40 promoter (SV40) and a CK6 promoter. Other promoters suitable for driving gene expression in mammalian cells that are known in the art are also suitable for incorporation into the expression constructs disclosed herein.

[0151] The expression construct can further encode a protease cleavage site. The protease cleavage site can be recognized by a protease or peptidase. The protease can be an endopeptidase or endoprotease, for example, but not limited to, furin, elastase, HtrA, calpain, trypsin, chymotrypsin, trypsin, and pepsin. In other embodiments, the protease can be a serine protease, a threonine protease, cysteine protease, aspartate protease, metalloprotease, glutamic acid protease, or any protease that cleaves an internal peptide bond (i.e., does not cleave the N-terminal or C-terminal peptide bond). The protease cleavage site can include one or more amino acid sequences that promote or increase the efficiency of cleavage.

[0152] The expression construct can further encode a linker sequence. The linker sequence can encode an amino acid sequence that spatially separates and/or links the one or more components of the expression construct (heavy chain and light chain components of the encoded antibody).

[0153] In one embodiment, a first expression vector construct encodes the heavy chain polypeptide that includes VH and CH1, and a second expression vector construct encodes the light chain polypeptide that includes VL and CL. An alternative arrangement include a first vector encoding the heavy chain polypeptide that includes VH, CH1, hinge region, CH2, and CH3, and the second vector encoding the light chain polypeptide that includes VL and CL.

[0154] In another embodiment, the expression vector construct encodes the heavy chain polypeptide that includes VH and CH1, and the light chain polypeptide that includes VL and CL, and a linker sequence is positioned between the nucleic acid sequence encoding the heavy chain polypeptide and the nucleic acid sequence encoding the light chain polypeptide.

[0155] In an alternative embodiment, the expression vector construct encodes the heavy chain polypeptide that includes VH and CH1, and the light chain polypeptide that includes VL and CL, and a nucleic acid sequence encoding a protease cleavage site is positioned between the nucleic acid sequence encoding the heavy chain polypeptide and the nucleic acid sequence encoding the light chain polypeptide.

[0156] In a further embodiment, the expression vector construct encodes the heavy chain polypeptide that includes VH, CH1, hinge region, CH2, and CH3, and the light chain polypeptide that includes VL and CL, and a linker sequence is positioned between the nucleic acid sequence encoding the heavy chain polypeptide and the nucleic acid sequence encoding the light chain polypeptide.

[0157] In yet another embodiment, the expression vector construct encodes the heavy chain polypeptide that includes VH, CH1, hinge region, CH2, and CH3, and the light chain polypeptide that includes VL and CL, and a heterologous nucleic acid sequence encoding the protease cleavage site is positioned between the nucleic acid sequence encoding the heavy chain polypeptide and the nucleic acid sequence encoding the light chain polypeptide.

[0158] In accordance with this aspect of the disclosure, the nucleic acid molecules encoding the *S. aureus* antibodies and binding fragments thereof can be incorporated into any expression vector capable of expressing the heavy chain polypeptide and/or light chain polypeptide encoded by the nucleic acid sequence construct. Suitable vectors include, *e.g.* a plasmid, a linear nucleic acid, and a viral vector.

[0159] In one embodiment, the expression vector is a circular plasmid (see, e.g., Muthumani et al., "Optimized and Enhanced DNA Plasmid Vector Based In vivo Construction of a Neutralizing anti-HIV-1 Envelope Glycoprotein Fab," *Hum. Vaccin. Immunother*. 9: 2253-2262 (2013), which is hereby incorporated by reference in its entirety). Plasmids can transform a target cell by integration into the cellular genome or exist extrachromosomally (e.g., autonomous replicating plasmid with an origin of replication). Exemplary plasmid vectors include, without limitation, pCEP4, pREP4, pVAX, pcDNA3.0, provax, or any other expression vector capable of expressing the heavy chain polypeptide and/or light chain polypeptide encoded by the recombinant nucleic acid sequence construct.

[0160] In another embodiment, the expression vector is a linear expression cassette ("LEC"). LECs are capable of being efficiently delivered to a subject via electroporation to express the heavy chain polypeptide and/or light chain polypeptide encoded by the recombinant nucleic acid sequence construct. The LEC may be any linear DNA devoid of a phosphate backbone. In one embodiment, the LEC does not contain any antibiotic resistance genes and/or a

phosphate backbone. In another embodiment, the LEC does not contain other nucleic acid sequences unrelated to the desired gene expression.

[0161] The LEC may be derived from any plasmid capable of being linearized. The plasmid may be capable of expressing the heavy chain polypeptide and/or light chain polypeptide encoded by the recombinant nucleic acid sequence construct. Exemplary plasmids include, without limitation, pNP (Puerto Rico/34), pM2 (New Caledonia/99), WLV009, pVAX, pcDNA3.0, or provax, or any other expression vector capable of expressing the heavy chain polypeptide and/or light chain polypeptide encoded by the recombinant nucleic acid sequence construct.

[0162] In another embodiment, the expression vector is a viral vector. Suitable viral vectors that are capable of expressing full length antibodies or binding portions thereof include, for example, an adeno-associated virus (AAV) vector (*See, e.g.*, Lewis et al., "Generation of Neutralizing Activity against Human Immunodeficiency Virus Type I in Serum by Antibody Gene Transfer," *J. Virol.* 76:8769-775 (2002); Fang et al., "An Antibody Delivery System for Regulated Expression of Therapeutic Levels of Monoclonal Antibodies *In vivo*," *Mol. Ther.* 15(6): 1153-9 (2007); Buning et al, "Recent Developments in Adeno- associated Virus Vector Technology," *J. Gene Med.* 10:717-733 (2008), each of which is incorporated herein by reference in its entirety), a lentivirus vector (*See, e.g.*, U.S. Patent No. 748,529 to Fang et al.; Joseph et al., "Inhibition of *In vivo* HIV Infection in Humanized Mice by Gene Therapy of Human Hematopoietic Stem Cells with a Lentiviral Vector Encoding a Broadly Neutralizing anti-HIV Antibody," *J. Virol.*, 84: 6645-53 (2010); and Luo et al., "Engineering Human Hematopoietic Stem/Progenitor Cells to Produce a Broadly Neutralizing anti-HIV Antibody after *In vivo* Maturation to Human B Lymphocytes," *Blood* 113: 1422-1431 (2009), which are hereby incorporated by reference in their entirety), a retrovirus vector (*See e.g.*, U.S. Patent No. 748,529 to Fang et al., which is hereby incorporated by reference in its entirety), a replication deficient adenovirus vector and a gutless adenovirus vector (*See e.g.*, U.S. Pat. No. 5,872,005, which is incorporated herein by reference in its entirety). Methods for generating and isolating adeno-associated viruses (AAVs) suitable for use as vectors are known in the art (*see, e.g.,* Grieger & Samulski, "Adeno-associated Virus as a Gene Therapy Vector: Vector Development, Production and Clinical Applications," *Adv. Biochem. Engin/Biotechnol.* 99: 119-145 (2005); Buning et al, "Recent Developments in Adeno- associated Virus Vector Technology," *J. Gene Med.* 10:717-733 (2008), each of which is incorporated herein by reference in its entirety.

[0163] Another aspect of the present disclosure is directed to a host cell comprising a vector containing a polynucleotide encoding an antibody or binding portion thereof as described

herein. The heavy and light chain expression constructs can be co-transfected, serially transfected, or separately transfected into host cells which are then fused to form a single host cell expressing both chains. The antibodies and binding portions thereof described herein can optionally be produced by a cell line, a mixed cell line, an immortalized cell or clonal population of immortalized cells, as well known in the art (*see e.g.*, Ausubel et al., ed., Current Protocols in Molecular Biology, John Wiley & Sons, Inc., NY, N.Y. (1987-2001); Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Edition, Cold Spring Harbor, N.Y. (1989); Harlow and Lane, Antibodies, a Laboratory Manual, Cold Spring Harbor, N.Y. (1989); Colligan et al., eds., Current Protocols in Immunology, John Wiley & Sons, Inc., NY (1994-2001); Colligan et al., Current Protocols in Protein Science, John Wiley & Sons, NY, N.Y., (1997-2001), which are hereby incorporated by reference in their entirety). Such host cells may be eukaryotic cells, bacterial cells, plant cells or archeal cells. Exemplary eukaryotic cells may be of mammalian, insect, avian or other animal origins. Mammalian eukaryotic cells include immortalized cell lines such as hybridomas or myeloma cell lines such as SP2/0 (American Type Culture Collection (ATCC), Manassas, Va., CRL-1581), NSO (European Collection of Cell Cultures (ECACC), Salisbury, Wiltshire, UK, ECACC No. 85110503), FO (ATCC CRL-1646) and Ag653 (ATCC CRL-1580) murine cell lines. An exemplary human myeloma cell line is U266 (ATTC CRL-TIB-196). Other useful cell lines include those derived from Chinese Hamster Ovary (CHO) cells such as CHO-K1SV (Lonza Biologics, Walkersville, Md.), CHO-K1 (ATCC CRL-61) or DG44.

[0164] The antibodies described herein can be prepared by any of a variety of techniques using the isolated polynucleotides, vectors, and host cells described *supra*. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies via conventional techniques, or via transfection of antibody genes, heavy chains and/or light chains into suitable bacterial or mammalian cell hosts, in order to allow for the production of antibodies, wherein the antibodies may be recombinant. Standard molecular biology techniques are used to prepare the recombinant expression vector, transfect the host cells, select for transformants, culture the host cells and recover the antibody from the culture medium. Transfecting the host cell can be carried out using a variety of techniques commonly used for the introduction of exogenous DNA into a prokaryotic or eukaryotic host cell, e.g., by electroporation, calcium- phosphate precipitation, DEAE-dextran transfection and the like. Although it is possible to express the antibodies described herein in either prokaryotic or eukaryotic host cells, expression of antibodies in eukaryotic cells is sometimes preferable, and sometimes preferable in mammalian host cells, because such eukaryotic cells (and in particular

mammalian cells) are more likely than prokaryotic cells to assemble and secrete a properly folded and immunologically active antibody.

[0165] As noted above, exemplary mammalian host cells for expressing the recombinant antibodies of the invention include Chinese Hamster Ovary (CHO cells) (including dhfr-CHO cells, described in Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77: 4216-4220 (1980), which is hereby incorporated by reference in its entirety). Other suitable mammalian host cells include, without limitation, NS0 myeloma cells, COS cells, and SP2 cells. When recombinant expression vectors encoding antibody genes are introduced into mammalian host cells, the antibodies are produced by culturing the host cells for a period of time sufficient to allow for expression of the antibody in the host cells or, more preferably, secretion of the antibody into the culture medium in which the host cells are grown.

[0166] Host cells can also be used to produce functional antibody fragments, such as Fab fragments or scFv molecules. It is understood that variations on the above procedure are within the scope of the present disclosure. For example, it may be desirable to transfect a host cell with DNA encoding functional fragments of either the light chain and/or the heavy chain of an antibody described herein. Recombinant DNA technology may also be used to remove some or all of the DNA encoding either or both of the light and heavy chains that is not necessary for binding to the antigens of interest. The molecules expressed from such truncated DNA molecules are also encompassed by the antibodies described herein.

[0167] The antibodies and binding portions thereof as described herein can be post-translationally modified by processes such as glycosylation, isomerization, deglycosylation or non-naturally occurring covalent modification such as the addition of polyethylene glycol (PEG) moieties (pegylation) and lipidation. Such modifications may occur *in vivo* or *in vitro*. For example, the antibodies or binding portions thereof described herein can be conjugated to polyethylene glycol (PEGylated) to improve their pharmacokinetic profiles. Conjugation can be carried out by techniques known to those skilled in the art. Conjugation of therapeutic antibodies with PEG has been shown to enhance pharmacodynamics while not interfering with function (see e.g., Deckert et al., *Int. J. Cancer* 87:382-390 (2000); Knight et al., *Platelets* 15:409-418 (2004); Leong et al., *Cytokine* 16:106-119 (2001); Yang et al., *Protein Eng.* 16:761-770 (2003), which are hereby incorporated by reference in their entirety).

[0168] Pharmacokinetic properties of the antibodies of the invention can also be enhanced through Fc modifications by techniques known to those skilled in the art. As described supra, the "Fc" region of an antibody is not involved directly in binding of an antibody to an antigen, but exhibits various effector functions. An antibody "Fc" region is a term well known

and is defined on the basis of papain cleavage of antibodies. The Fc region of an antibody is directly involved in ADCC (antibody-dependent cell-mediated cytotoxicity) and CDC (complement-dependent cytotoxicity) based on complement activation, Clq binding and Fc receptor binding. Complement activation (CDC) is initiated by binding of complement factor Clq to the Fc of most IgG antibody subclasses. While the influence of an antibody on the complement system is dependent on certain conditions, binding to Clq is caused by defined binding sites in the Fc region of the antibody. Such binding sites are known in art, and include, e.g., amino acid residues L234, L235, D270, N297, E318, K320, K322, P331, and P329 (numbering according to EU index of Kabat) (*see e.g.*, Boakle et al., *Nature* 282: 742-43 (1979); Lukas et al., J. *Immunol.* 127: 2555-60 (1981); Brunhouse and Cebra, *Mol. Immunol.* 16: 907-17 (1979); Burton et al., *Nature* 288:338-44 (1980); Thommesen et al., *Mol. Immunol.* 37: 995-1004 (2000); Idusogie et al., *J. Immunol.* 164:4178-84 (2000); Hezareh et al., *J. Virology* 75:12161-68 (2001); Morgan et al., *Immunology* 86:319-24 (1995), which are hereby incorporated by reference in their entirety). Modifications to one or more of these binding sites can be made to modify the effector functions of the antibodies or binding portions thereof as desired.

[0169] *S. aureus* can adversely affect standard IgG1-based monoclonal antibody (mAb) therapeutics either by directly cleaving the mAb, sequestering the mAb by Protein A or Sbi binding, or by killing off the very effector cells required for therapeutic efficacy. Therefore, in one embodiment, an antibody or binding fragment thereof as described herein, comprises one or more amino acid substitutions, insertions, and/or deletions that protect the antibody or binding fragment thereof from staph mediated cleavage and/or sequestration. For example, human IgG1 is susceptible to staph mediated cleavage in the lower hinge region, and this cleavage can result in a loss of Fc mediated effector function both *in vitro* and *in vivo* (Brezski et al., "Tumor-Associated and Microbial Proteases Compromise Host IgG Effector Functions by a Single Cleavage Proximal to the Hinge," *PNAS* 106:17864-17869 (2009), which is hereby incorporated by reference in its entirety. The *S. aureus* protease, GluV8, cleaves human IgG1 in the lower hinge region between amino acids E233 and L234, and it was previously demonstrated that this cleavage abrogates both ADCC and CDC function (Brezski et al., "Human Anti-IgG1 Hinge Autoantibodies Reconstitute the Effector Functions of Proteolytically Inactivated IgGs," *J. Immunol.* 181:3183-3192 (2008), which is hereby incorporated by reference in its entirety). Therefore, in one embodiment, the hinge region of an antibody disclosed herein is engineered to have increased resistance to proteolysis by GluV8. Suitable modifications include mutating the lower hinge region (E233P/L234V/L235A with G236 deleted) as disclosed in U.S. Patent

Application Publication No. US20150210756 to Torres et al., which is hereby incorporated by reference in its entirety.

[0170] In another embodiment, the antibodies or binding fragments thereof comprise one or more amino acid substitutions, insertion, and/or deletions to decrease or prevent non-specific binding to other staphylococcal or host (e.g., human) protein antigens. For example, in one aspect, the antibody or binding fragment thereof is not capable of specific binding to staphylococcal Protein A or second binding protein for immunoglobulins (Sbi). In another aspect, the binding molecule is not capable of specific binding to FcγRI, in particular human FcγRI. In another aspect, the binding molecule does retain specific binding capacity to FcRn.

[0171] The antibodies and binding fragments thereof as described herein are preferably "isolated" antibodies. "Isolated" when used to describe the antibodies disclosed herein, means an antibody that has been identified, separated and/or recovered from a component of its production environment. Preferably, the isolated antibody is free of association with all other components from its production environment. Contaminant components of its production environment, such as that resulting from recombinant transfected cells, are materials that would typically interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. The antibodies and antibody binding fragments are recovered and purified from recombinant cell cultures by known methods including, but not limited to, protein A purification, ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. High performance liquid chromatography ("HPLC") can also be used for purification.

Antibody Compositions

[0172] Another aspect of the present disclosure is directed to a pharmaceutical composition comprising one or more *S. aureus* antibodies as described herein, or one or more nucleic acid molecules or expression vector constructs encoding the one or more *S. aureus* antibodies described herein, and a pharmaceutical carrier, as well as methods of treating and inhibiting the onset of a staphylococcal infection in a subject using these pharmaceutical compositions.

[0173] In one embodiment, the pharmaceutical composition of the present disclosure comprises a single antibody composition, i.e., the composition contains one type of an antibody binding to a particular epitope on a particular protein, e.g., a LukE antibody composition. In

another embodiment, the pharmaceutical composition contains two or more different antibodies, each antibody binding to a different epitope of the same protein or to different epitopes of different staphylococcal bi-component toxin proteins. In another embodiment, the pharmaceutical composition comprises one or more antibodies as described herein in combination with one or more prophylactic or therapeutic agents other than the antibodies described herein that are useful for preventing or treating a staphylococcal infection.

[0174] The therapeutically effective amount of antibody present in the pharmaceutical composition or formulation is determined by taking into account the desired dose volumes and mode(s) of administration. Exemplary antibody concentrations in the pharmaceutical compositions of the present disclosure include from about 0.1 mg/mL to about 50 mg/mL, from about 0.5 mg/mL to about 25 mg/mL, and from about 2 mg/mL to about 10 mg/mL.

[0175] An aqueous formulation is prepared comprising the antibody in a pH-buffered solution. The buffer has a pH in the range from about 4.5 to about 10, from about 5 to about 9, or from about 6 to 8. Examples of buffers include phosphate buffers (e.g., phosphate buffered saline), acetate (e.g. sodium acetate), succinate (such as sodium succinate), gluconate, histidine, citrate and other organic acid buffers. A polyol, which acts as a tonicifier and may stabilize the antibody, may be included in the formulation. In one embodiment, the tonicifying polyol is a salt such as sodium chloride. In another embodiment, the polyol is a nonreducing sugar, such as sucrose or trehalose. The polyol is added to the formulation in an amount which may vary with respect to the desired isotonicity of the formulation. Preferably the aqueous formulation is isotonic, in which case suitable concentrations of the polyol in the formulation are in the range from about 1% to about 15% w/v, or in the range from about 2% to about 10% w/v, for example. However, hypertonic or hypotonic formulations may also be suitable. The amount of polyol added may also alter with respect to the molecular weight of the polyol. For example, a lower amount of a monosaccharide (e.g. mannitol) may be added, compared to a disaccharide (such as trehalose).

[0176] In one embodiment, the pharmaceutical composition contains the above-identified agents (i.e. antibody, buffer, polyol) and is essentially free of one or more preservatives, such as benzyl alcohol, phenol, m-cresol, chlorobutanol and benzethonium Cl. In another embodiment, a preservative may be included in the pharmaceutical composition, particularly where the formulation is a multidose formulation. Suitable preservatives include, without limitation phenol, m-cresol, p-cresol, o-cresol, chlorocresol, benzyl alcohol, phenylmercuric nitrite, phenoxyethanol, formaldehyde, chlorobutanol, magnesium chloride (e.g., hexahydrate), alkylparaben (methyl, ethyl, propyl, butyl and the like), benzalkonium chloride, benzethonium

chloride, sodium dehydroacetate and thimerosal, or mixtures thereof in an aqueous diluent. The concentration of preservative may be in the range from about 0.01% to about 5%, from about 0.5% to about 2% and any range or value therein. One or more other pharmaceutically acceptable carriers, excipients or stabilizers such as those described in Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980) may be included in the composition provided that they do not adversely affect the desired characteristics of the formulation. Acceptable carriers, excipients or stabilizers are nontoxic to recipients at the dosages and concentrations employed and include; additional buffering agents; co-solvents; antioxidants including ascorbic acid and methionine; chelating agents such as EDTA; metal complexes (e.g. Zn-protein complexes); biodegradable polymers such as polyesters; and/or salt-forming counterions such as sodium.

Methods of Use

[0177] The staphylococcal bi-component antibodies and binding portions thereof, or pharmaceutical compositions containing the same, can be used for the treatment, prevention or amelioration of a staphylococcal infection. The staphylococcal infection may be caused by any *Staphylococcus spp*. In one aspect, the staphylococcal infection is caused by *Staphylococcus aureus,* including methicillin-resistant *S. aureus* (MRSA) and methicillin-sensitive *S. aureus* (MSSA). Accordingly, the present disclosure provides a method for the treatment, prevention or amelioration of a staphylococcal infection that involves administering to a subject in need thereof a one or more of the antibodies or binding portions described herein or a pharmaceutical composition containing the same as described herein.

[0178] In accordance with this aspect, a "subject" suitable for treatment with the antibodies and compositions described herein includes any animal, for example, a mammal, such as a human. In the context of administering an antibody composition as described herein for purposes of preventing or inhibiting the onset of a staphylococcal infection in a subject, the subject encompasses any subject that is at risk of becoming infected with staphylococcus or developing a staphylococcal infection. Susceptible subjects include infants and juveniles, as well as immunocompromised juvenile, adults, and elderly adults. However, any infant, juvenile, adult, or elderly adult or immunocompromised individual at risk for developing a staphylococcal infection can be treated in accordance with the methods described herein. In the context of administering an antibody composition as described herein for purposes of treating a staphylococcal infection in a subject, the subject encompasses any subject infected with

staphylococcus. Particularly suitable subjects include those at risk of infection, susceptible to infection, or those infected with methicillin-resistant *S. aureus* (MRSA) or methicillin sensitive S. aureus (MSSA). Other suitable subjects include those subjects which may have or are at risk for developing a condition resulting from a staphylococcus infection, *i.e.*, a staphylococcal associated condition, such as, for example, skin wounds and infections, tissue abscesses, folliculitis, osteomyelitis, pneumonia, scalded skin syndrome, septicemia, septic arthritis, myocarditis, endocarditis, and toxic shock syndrome.

[0179] In one embodiment, the antibodies or binding portions thereof, or pharmaceutical compositions containing the same, are administered prophylactically to prevent, delay, or inhibit the onset or development of staphylococcal infection in a subject at risk of developing a staphylococcal infection or associated condition. In one aspect, prophylactic administration of one or antibodies or binding portions thereof as described herein is effective to fully prevent *S. aureus* infection in an individual. In other embodiments, prophylactic administration is effective to prevent the full extent of infection that would otherwise develop in the absence of such administration, *i.e.*, substantially prevent, inhibit, or minimize staphylococcal infection in an individual.

[0180] In another embodiment, the antibodies, binding portions thereof, or pharmaceutical compositions containing the same as described herein are administered therapeutically to an individual having a staphylococcal infection to inhibit the progression and further development of the infection, *i.e.*, to inhibit and/or prevent the spread of the infection to other cells in an individual, decrease infection, and to treat or alleviate one or more symptoms of infection.

[0181] Therapeutically effective amounts of the antibodies or binding portions thereof as described herein are determined in accordance with standard procedures, which take numerous factors into account, including, for example, the concentrations of the antibodies or binding portions thereof in a pharmaceutical composition, the mode and frequency of administration, the severity of the staphylococcus infection to be treated (or prevented), and subject details, such as age, weight and overall health and immune condition. General guidance can be found, for example, in the publications of the International Conference on Harmonization and in REMINGTON'S PHARMACEUTICAL SCIENCES (Mack Publishing Company 1990), which is hereby incorporated by reference in its entirety. A clinician may administer a composition comprising the antibodies or binding portions thereof as described herein in a single dose or in accordance with a multi-dosing protocol until a dosage is reached that provides the desired or required prophylactic or therapeutic effect. The progress of this therapy can be easily monitored

by conventional assays. In prophylactic applications, a relatively low dosage is administered at relatively infrequent intervals over a long period of time. In therapeutic applications, a relatively high dosage at relatively short intervals (e.g., as little as 15 minutes, 30 minutes, 60 minutes, 90 minutes or even 2 or 3 hours) is sometimes required until progression of the infection is reduced or terminated, and preferably until the subject shows partial or complete amelioration of symptoms of infection.

[0182] The therapeutically effective amount, *i.e.*, the dosage that is sufficient to slow or prevent the spread or severity of staphylococcal infection in a subject, and/or the dosage sufficient to prevent, alleviate (either partially or completely) a staphylococcal infection associated condition. Such therapeutically effective amounts vary by individual, but may range from 0.1 to 10 mg/kg body weight, for example 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 mg/kg, but may be even higher, for example 15, 20, 30, 40, 50, 60, 70, 80, 90 or 100 mg/kg. A fixed unit dose may also be given, for example, 50, 100, 200, 500 or 1000 mg, or the dose may be based on the patient's surface area, e.g., 400, 300, 250, 200, or 100 mg/m^2. Usually between 1 and 8 doses, (e.g., 1, 2, 3, 4, 5, 6, 7 or 8) may be administered to treat infection, but 10, 15, 20 or more doses may be given depending on the severity of infection. Administration of antibodies or binding portions thereof of the present invention may be repeated after one day, two days, three days, four days, five days, six days, one week, two weeks, three weeks, one month, five weeks, six weeks, seven weeks, two months, three months, four months, five months, six months or longer. Repeated courses of treatment are also possible, as is chronic administration. The repeated administration may be at the same dose or at a different dose.

[0183] The therapeutic compositions of the present invention can be administered alone or as part of a combination therapy in conjunction with one or more other active agents, depending upon the nature of the staphylococcus infection that is being treated. Such additional active agents include anti-infective agents, antibiotic agents, and antimicrobial agents that are readily known in the art.

[0184] The mode of administration of the antibodies or binding portions thereof or pharmaceutical compositions described herein may be any suitable route that delivers the antibodies or binding portions thereof to the host, such as parenteral administration, e.g., intradermal, intramuscular, intraperitoneal, intravenous or subcutaneous; inhalation administration; transmucosal administration (oral, intranasal, intravaginal, rectal); or enteral administration. The pharmaceutical composition can be formulated in a tablet, capsule, solution, powder, gel, particle; and/or contained in a syringe, an implanted device, osmotic pump, cartridge, micropump; or other means appreciated by the skilled artisan, as well known in the art.

Site specific administration may be achieved by, for example, intrarticular, intrabronchial, intraabdominal, intracapsular, intracartilaginous, intracavitary, intracelial, intracerebellar, intracerebroventricular, intracolic, intracervical, intragastric, intrahepatic, intracardial, intraosteal, intrapelvic, intrapericardiac, intraperitoneal, intrapleural, intraprostatic, intrapulmonary, intrarectal, intrarenal, intraretinal, intraspinal, intrasynovial, intrathoracic, intrauterine, intravascular, intravesical, intralesional, vaginal, rectal, buccal, sublingual, intranasal, or transdermal delivery.

[0185] In another embodiment, a pharmaceutical composition comprising a recombinant nucleic acid sequence encoding an antibody or binding portion thereof as described herein, is administered to a subject to facilitate *in vivo* expression and formation of the antibody as a prophylactic therapy for the treatment or prevention of staphylococcal infection in a subject. Expression vector constructs suitable for use in this embodiment of the disclosure are described *supra*, and nucleic acid sequences encoding the staphylococcal antibodies described herein are provided herein in Tables 26-49 (SEQ ID NOs: 834-1281).

[0186] The composition can result in the generation of the antibody in the subject within at least about 1 hour, 2 hours, 3 hours, 4 hours, 5 hours, 6 hours, 7 hours, 8 hours, 9 hours, 10 hours, 11 hours, 12 hours, 13 hours, 14 hours, 15 hours, 20 hours, 25 hours, 30 hours, 35 hours, 40 hours, 45 hours, 50 hours, or 60 hours of administration of the composition to the subject. The composition can result in generation of the synthetic antibody in the subject within at least about 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, or 10 days of administration of the composition to the subject. The composition can result in generation of the antibody in the subject within about 1 hour to about 6 days, about 1 hour to about 5 days, about 1 hour to about 4 days, about 1 hour to about 3 days, about 1 hour to about 2 days, about 1 hour to about 1 day, about 1 hour to about 72 hours, about 1 hour to about 60 hours, about 1 hour to about 48 hours, about 1 hour to about 36 hours, about 1 hour to about 24 hours, about 1 hour to about 12 hours, or about 1 hour to about 6 hours of administration of the composition to the subject.

[0187] The composition, when administered to the subject in need thereof, can result in the persistent generation of the antibody in the subject. The composition can result in the generation of the antibody in the subject for at least about 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days, 11 days, 12 days, 13 days, 14 days, 15 days, 16 days, 17 days, 18 days, 19 days, 20 days, 21 days, 22 days, 23 days, 24 days, 25 days, 26 days, 27 days, 28 days, 29 days, 30 days, 31 days, 32 days, 33 days, 34 days, 35 days, 36 days, 37 days, 38 days, 39 days, 40 days, 41 days, 42 days, 43 days, 44 days, 45 days, 46 days, 47 days, 48 days,

49 days, 50 days, 51 days, 52 days, 53 days, 54 days, 55 days, 56 days, 57 days, 58 days, 59 days, or 60 days.

[0188] As described *supra*, the expression vector construct can include the nucleic acid encoding a staphylococcal antibody heavy chain polypeptide, a fragment thereof, a variant thereof, or a combination thereof. The heavy chain polypeptide can include a variable heavy chain (VH) region and/or at least one constant heavy chain (CH) region. The at least one constant heavy chain region can include a constant heavy chain region 1 (CH1), a constant heavy chain region 2 (CH2), and a constant heavy chain region 3 (CH3), and/or a hinge region.

[0189] The expression vector construct can also include the nucleic acid sequence encoding the corresponding staphylococcal antibody light chain polypeptide, a fragment thereof, a variant thereof, or a combination thereof. The light chain polypeptide can include a variable light chain (VL) region and/or a constant light chain (CL) region.

[0190] In one embodiment, the composition comprises an expression vector construct encoding a LukAB antibody or binding fragment thereof as described herein. Suitable nucleic acid sequences encoding the LukAB antibody heavy chain polypeptides and light chain polypeptides described herein are enumerated in Tables 26-29 and include SEQ ID NOs: 834-997.

[0191] In one embodiment, the composition comprises an expression vector construct encoding a LukE antibody or binding fragment thereof as described herein. Suitable nucleic acid sequences encoding the LukE antibody heavy chain polypeptides and light chain polypeptides described herein are enumerated in Tables 30-33 and include SEQ ID NOs: 998-1045.

[0192] In one embodiment, the composition comprises an expression vector construct encoding a LukD antibody or binding fragment thereof as described herein. Suitable nucleic acid sequences encoding the LukD antibody heavy chain polypeptides and light chain polypeptides described herein are enumerated in Tables 34-37 and include SEQ ID NOs: 1046-1077.

[0193] In one embodiment, the composition comprises an expression construct encoding a HlgA antibody or binding fragment thereof as described herein. Suitable nucleic acid sequences encoding the HlgA antibody heavy chain polypeptides and light chain polypeptides described herein are enumerated in Tables 38-41 and include SEQ ID NOs: 1078-1101.

[0194] In one embodiment, the composition comprises an expression construct encoding a HlgC antibody or binding fragment thereof as described herein. Suitable nucleic acid sequences encoding the HlgC antibody heavy chain polypeptides and light chain polypeptides described herein are enumerated in Tables 42-45 and include SEQ ID NOs: 1102-1125.

[0195] In one embodiment, the composition comprises an expression construct encoding a LukE/HlgA antibody or binding fragment thereof as described herein. Suitable nucleic acid sequences encoding LukE/HlgA antibody heavy chain polypeptides and light chain polypeptides described herein are enumerated in Tables 46-49 and include SEQ ID NOs: 1126-1281.

[0196] Upon expression of the first and/or second vectors described above, in, for example, but not limited to, a mammalian subject, the heavy chain polypeptide and the light chain polypeptide assemble into the antibody. In particular, the heavy chain polypeptide and the light chain polypeptide interact with one another such that assembly results in the antibody being capable of binding the desired staphylococcal bi-component toxin (*i.e.*, LukAB, LukE, LukD, HlgA, HlgC, or LukE/HlgA), and exerting its desired biological effect, *e.g.*, neutralization. In still other embodiments, the heavy chain polypeptide and the light chain polypeptide interact with one another such that assembly results in the antibody being capable of eliciting or inducing an immune response against the antigen.

[0197] The expression vector constructs of the invention may be introduced into cells *in vitro* or *ex vivo* using standard methodology known in the art. Such techniques include transfection using calcium phosphate, micro-injection into cells (*see, e.g.,* Capecchi, *Cell* 22:479-488 (1980), which is hereby incorporated by reference in its entirety), electroporation (*see, e.g.,* Shigekawa et al., *BioTechn.* 6:742-751 (1988), which is hereby incorporated by reference in its entirety), liposome-mediated gene transfer (*see, e.g.,* Mannino et al., *BioTechn.* 6:682-690 (1988), which is hereby incorporated by reference in its entirety), lipid-mediated transduction (*see, e.g.,* Felgner et al., *Proc. Natl. Acad. Sci. USA* 84:7413-7417 (1987), which is hereby incorporated by reference in its entirety), and nucleic acid delivery using high-velocity microprojectiles (*see, e.g.,* Klein et al., *Nature* 327:70-73 (1987), which is hereby incorporated by reference in its entirety).

[0198] The vectors may be administered *in vivo* via various routes (e.g., intradermally, intravenously, intraportally, intraperitoneally, intramuscularly, etc.), to deliver the expression vector construct for antibody expression. Dependent upon the route of administration, the antibodies elicit their effect locally or systemically.

[0199] Another aspect of the present disclosure is directed to the use of the antibodies and binding portions thereof as provided herein to detect staphylococcus in a biological sample, such as a blood, tissue, cell, serum, sputum, or other biological sample. In accordance with this embodiment, the antibodies or binding portions thereof can be used in methods of diagnosing a staphylococcal infection in a subject (animal or human). In one aspect, the method for diagnosing a staphylococcal infection involves contacting an antibody or binding portion thereof

as described herein with a sample from the subject to be diagnosed, and detecting at least the presence or the absence of one or more staphylococcal bi-component toxins in the sample. The subject is diagnosed as having a staphylococcal infection based on detecting the presence of one or more bi-component toxins in the sample.

[0200] Methods described herein involving the detection of a staphylococcal leukotoxin and/or gamma hemolysin alone or in combination with each other, in a sample from a subject or elsewhere, involve the use of a detectably labeled antibody or binding portion thereof. Accordingly, in one aspect the antibody or binding portion thereof as described herein may be coupled to a detectable label. Suitable detectable labels are well known in the art and include detectable tags (e.g., a poly-histidine (His6–) tag, a glutathione-S-transferase (GST–) tag, or a maltose-binding protein (MBP–) tag); radioactive labels (e.g., carbon (14C) or phosphorous (32P)); fluorescent labels (e.g., fluorescein and derivatives thereof, fluorescein isothiocyanate, rhodamine and derivatives thereof, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin); luminescent labels (e.g., luminol); bioluminescent labels (e.g., luciferase, luciferin, and aequorin); or enzymatic labels (e.g., luciferin, 2,3-dihydrophthalazinediones, malate dehydrogenase, urease, peroxidases (e.g., horseradish peroxidase), alkaline phosphatase, β-galactosidase, glucoamylase, lysozyme, saccharide oxidases (e.g., glucose oxidase, galactose oxidase, and glucose-6-phosphate dehydrogenase), heterocyclic oxidases (e.g., uricase and xanthine oxidase), lactoperoxidase, microperoxidase). Alternatively, these diagnostic methods involve the use of secondary reagents useful for detectably labeling the antibody or binding portion thereof. In these embodiments, the secondary antibody, which binds to the anti-leukotoxin antibody or binding portion thereof, is coupled to a detectable label, such as any of the aforementioned detectable labels.

[0201] Detection assays for detecting the labeled antibody or a binding portion thereof bound to a staphylococcal leukotoxin and/or gamma hemolysin in a sample are well known in the art and include, for example, immunoprecipitation, direct and indirect sandwich assays, competitive binding assays, enzyme-linked immunosorbent assays (ELISA), radioimmunoassays (RIA), or fluorescent activated cell sorting (FACS).

[0202] The presence or the absence of one or more staphylococcal bi-component toxins in a sample can also be detected using two antibodies or binding portions thereof as described herein, which bind to non-competing epitopes on the staphylococcal bi-component toxin. For example, a double-sandwich ELISA allows for the detection of multiple epitopes using a first antibody as a capture antibody and a second antibody as a detection antibody (see, e.g., Ding et al., “Development of a Double Antibody Sandwich ELISA for West Nile Virus Detection Using

Monoclonal Antibodies against Non-Structural Protein 1," *PLoS One* 9(10):e108623, which is hereby incorporated by reference in its entirety).

[0203] The diagnostic antibodies and binding fragments thereof may be used to detect S. aureus bi-component toxins in any biological samples, including, without limitation tissue extracts, urine, blood, serum, stool, and phlegm. Biological samples that S. aureus leukotoxins may be detected using the antibodies or binding fragments thereof.

[0204] Another aspect of the present disclosure is directed to a diagnostic kit containing one or more of the *S. aureus* bi-component toxin antibodies as described herein. The kit can also include a detectable label. The diagnostic antibody itself may contain the detectable label (*e.g.*, fluorescent molecule, biotin, etc.) which is directly detectable or detectable via a secondary reaction (*e.g.*, reaction with strepavidin). Alternatively, a second reagent containing the detectable label may be utilized, where the second reagent has binding specificity for the primary antibody. In a diagnostic kit suitable for measuring *S. aureus* in a biological sample, the antibodies of the kit may be supplied prebound to a solid phase, such as to the wells of a microtiter dish.

EXAMPLES

[0205] Examples are provided below to illustrate the present invention. These examples are not meant to constrain the present invention to any particular application or theory of operation

Examples 1 - Antibody Generation

[0206] Immunizations were performed with five antigens in six mouse immunization campaigns as described herein.

[0207] **LukAB Antibody Generation.** Two separate cohorts of Balb/c and C3H mice received three or four intraperitoneal (i.p.) injections of a recombinant toxoid variant of the LukAB protein (LukA E323A) (DuMont et al., "Identification of a Crucial Residue Required for Staphylococcus aureus LukAB Cytotoxicity and Receptor Recognition," *Infect Immun.* 82(3):1268-76 (2014), which is hereby incorporated by reference in its entirety) - herein referred to as LukA'B protein) mixed with either Complete (Sigma catalog #F5881) or Incomplete (Sigma catalog #F5506) Freund's adjuvant over the course of 7 to 8 weeks. Immune titers were tested at an intermediate time point, and all mice had titers of at least 128,000. Titer is defined as the greatest sera dilution at which anti-LukA'B antibodies could be detected above background by ELISA. At the end of the 7-8 week period, animals were injected subcutaneously (s.q.) at the

base of the tail (B.O.T.) with LukA'B protein and an agonistic anti-mouse-CD40 mAb (R&D Systems catalog #MAB440) diluted in DPBS. Four days after the B.O.T injection, spleens were harvested, homogenized, and a B cell enriched fraction was isolated by Magnetic Activated Cell Sorting (MACS). B cells and FO mouse myeloma cells were co-incubated in a polyethylene glycol (PEG)-4000 solution to generate mAb secreting hybridomas cell lines. Following 10 days of hybridoma growth, hybridoma conditioned media was added to assay plates coated with LukA'B protein, and ELISA was performed to identify hybridomas that produce LukA'B binding mAbs. Hybridoma media samples positive for binding to LukA'B were subsequently screened by ELISA to identify samples specific to LukA'B, which exhibited no detectable binding to LukD, LukS-PV, LukE, HlgA, or HlgC.

[0208] The immunoglobulin heavy chain (HC) and (LC) genes were cloned from the hybridoma cells by RT-PCR, followed by cDNA synthesis. For HC and LC RT-PCR, pools of primers complementary to v-region framework 1 (FR1) and single primers complementary to a region of constant domain 1 (CD1) were used. From this point, HC and LC expression plasmids were made by one of two methods. For the first method, double stranded HC and LC cDNA fragments were ligated into plasmids to enable sequencing and expression of full length murine LC and HC (IgG1 isotype). LC and HC plasmids were transformed into competent *E. coli*, multiple colonies per chain were picked, and the LC and HC genes were sequenced. Plasmid DNA for the consensus sequence for each chain was prepared for mAb protein expression. For the second method of HC and LC expression plasmid generation, cDNA fragments were sequenced by Next Generation Sequencing. Following sequencing, a panel of mAb HC and LC sequences were selected for de novo gene synthesis based upon quality of the sequencing data, sequence redundancy, and predicted mAb expression risks (i.e. mAb sequences with known post-translational liabilities were excluded). *De novo* gene synthesis was performed to generate plasmid DNA for mAb protein expression.

[0209] Expi293F cells were co-transfected with cognate LC and HC expressing plasmid pairs using Gibco's Expifectamine transfection fit. Culture supernatants were harvested 5 days later, and the mAb concentrations were determined. The recombinantly expressed mAbs were re-tested by ELISA for binding to all six of the aforementioned leukotoxins or subunits thereof to validate mAbs that specifically bind to LukA'B and not the other five toxins.

[0210] **LukD Antibody Generation.** A cohort of Balb/c and C3H mice received three intraperitoneal (i.p.) injections of recombinant LukD protein mixed with either Complete (Sigma catalog #F5881) or Incomplete (Sigma catalog #F5506) Freund's adjuvant over the course of 6 weeks. Immune titers were tested at an intermediate time point, and all mice had titers of at least

64,000. Titer is defined as the greatest sera dilution at which anti-LukD antibodies could be detected above background by ELISA. At the end of the 6 week period, animals were injected subcutaneously (s.q.) at the base of the tail (B.O.T.) with LukD protein and an agonistic anti-mouse-CD40 mAb (R&D Systems catalog #MAB440) diluted in DPBS. Four days after the B.O.T injection, spleens were harvested, homogenized, and a B cell enriched fraction was isolated by Magnetic Activated Cell Sorting (MACS). B cells and FO mouse myeloma cells were co-incubated in a polyethylene glycol (PEG)-4000 solution to generate mAb secreting hybridomas cell lines. Following 10 days of hybridoma growth, hybridoma conditioned media was added to assay plates coated with LukD protein, and ELISA was performed to identify hybridomas that produce LukD binding mAbs. Hybridoma media samples positive for binding to LukD were subsequently screened by ELISA to identify samples specific to LukD, which exhibited no detectable binding to LukA'B, LukS-PV, LukE, HlgA, or HlgC.

[0211] The immunoglobulin heavy chain (HC) and (LC) genes were cloned from the hybridoma cells by RT-PCR, followed by cDNA synthesis. For HC and LC RT-PCR, pools of primers complementary to v-region framework 1 (FR1) and single primers complementary to a region of constant domain 1 (CD1) were used. Double stranded HC and LC cDNA fragments were ligated into plasmids to enable sequencing and expression of full length murine LC and HC (IgG1 isotype). LC and HC plasmids were transformed into competent *E. coli*, multiple colonies per chain were picked, and the LC and HC genes were sequenced. Plasmid DNA for the consensus sequence for each chain was prepared for mAb protein expression.

[0212] Expi293F cells were co-transfected with cognate LC and HC expressing plasmid pairs using Gibco's Expifectamine transfection fit. Culture supernatants were harvested 5 days later, and the mAb concentrations were determined. The recombinantly expressed mAbs were re-tested by ELISA for binding to LukD to validate binding.

[0213] **LukE Antibody Generation**. A cohort of Balb/c and C3H mice received three intraperitoneal (i.p.) injections of recombinant LukE protein mixed with either Complete (Sigma catalog #F5881) or Incomplete (Sigma catalog #F5506) Freund's adjuvant over the course of 8 weeks. Immune titers were tested at an intermediate time point, and all mice had titers of at least 72,000. Titer is defined as the greatest sera dilution at which anti-LukE antibodies could be detected above background by ELISA. At the end of the 8 week period, animals were injected subcutaneously (s.q.) at the base of the tail (B.O.T.) with LukE protein and an agonistic anti-mouse-CD40 mAb (R&D Systems catalog #MAB440) diluted in DPBS.

[0214] Four days after the B.O.T injection, spleens were harvested, homogenized, and a B cell enriched fraction was isolated by Magnetic Activated Cell Sorting (MACS). B cells and

FO mouse myeloma cells were co-incubated in a polyethylene glycol (PEG)-4000 solution to generate mAb secreting hybridomas cell lines. Following 10 days of hybridoma growth, hybridoma conditioned media was added to assay plates coated with LukE protein, and ELISA was performed to identify hybridomas that produce LukE binding mAbs. Hybridoma media samples positive for binding to LukE were subsequently screened by ELISA to identify samples specific to LukE, which exhibited no detectable binding to LukA'B, LukD, LukS-PV, HlgA, or HlgC.

[0215] The immunoglobulin heavy chain (HC) and (LC) genes were cloned from the hybridoma cells by RT-PCR, followed by cDNA synthesis. For HC and LC RT-PCR, pools of primers complementary to v-region framework 1 (FR1) and single primers complementary to a region of constant domain 1 (CD1) were used. Double stranded HC and LC cDNA fragments were ligated into plasmids to enable sequencing and expression of full length murine LC and HC (IgG1 isotype). LC and HC plasmids were transformed into competent *E. coli*, multiple colonies per chain were picked, and the LC and HC genes were sequenced. Plasmid DNA for the consensus sequence for each chain was prepared for mAb protein expression.

[0216] Expi293F cells were co-transfected with cognate LC and HC expressing plasmid pairs using Gibco's Expifectamine transfection fit. Culture supernatants were harvested 5 days later, and the mAb concentrations were determined. The recombinantly expressed mAbs were re-tested by ELISA for binding to all five of the aforementioned leukotoxins or subunits thereof to validate mAbs that specifically bind to LukE and not the other five toxins.

[0217] **HlgA Antibody Generation**. A cohort of Balb/c and C3H mice received three intraperitoneal (i.p.) injections of recombinant HlgA protein mixed with either Complete (Sigma catalog #F5881) or Incomplete (Sigma catalog #F5506) Freund's adjuvant over the course of 8 weeks. Immune titers were tested at an intermediate time point, and all mice had titers of at least 72,000. Titer is defined as the greatest sera dilution at which anti-HlgA antibodies could be detected above background by ELISA. At the end of the 8 week period, animals were injected subcutaneously (s.q.) at the base of the tail (B.O.T.) with HlgA protein and an agonistic anti-mouse-CD40 mAb (R&D Systems catalog #MAB440) diluted in DPBS.

[0218] Four days after the B.O.T injection, spleens were harvested, homogenized, and a B cell enriched fraction was isolated by Magnetic Activated Cell Sorting (MACS). B cells and FO mouse myeloma cells were co-incubated in a polyethylene glycol (PEG)-4000 solution to generate mAb secreting hybridomas cell lines. Following 10 days of hybridoma growth, hybridoma conditioned media was added to assay plates coated with HlgA protein, and ELISA was performed to identify hybridomas that produce HlgA binding mAbs. Hybridoma media

samples positive for binding to HlgA were subsequently screened by ELISA to identify samples specific to HlgA, which exhibited no detectable binding to LukA'B, LukD, LukS-PV, LukE or HlgC.

[0219] The immunoglobulin heavy chain (HC) and (LC) genes were cloned from the hybridoma cells by RT-PCR, followed by cDNA synthesis. For HC and LC RT-PCR, pools of primers complementary to v-region framework 1 (FR1) and single primers complementary to a region of constant domain 1 (CD1) were used. Double stranded HC and LC cDNA fragments were ligated into plasmids to enable sequencing and expression of full length murine LC and HC (IgG1 isotype). LC and HC plasmids were transformed into competent *E. coli*, multiple colonies per chain were picked, and the LC and HC genes were sequenced. Plasmid DNA for the consensus sequence for each chain was prepared for mAb protein expression.

[0220] Expi293F cells were co-transfected with cognate LC and HC expressing plasmid pairs using Gibco's Expifectamine transfection fit. Culture supernatants were harvested 5 days later, and the mAb concentrations were determined. The recombinantly expressed mAbs were re-tested by ELISA for binding to all six of the aforementioned leukotoxins or subunits thereof to validate mAbs that specifically bind to HlgA and not the other five toxins.

[0221] **HlgC Antibody Generation**. A cohort of Balb/c and C3H mice received five intraperitoneal (i.p.) injections of recombinant HlgC protein mixed with either Complete (Sigma catalog #F5881) or Incomplete (Sigma catalog #F5506) Freund's adjuvant over the course of 3 months. Immune titers were tested at an intermediate time point, and all mice had titers between 72,000 to 218,000. Titer is defined as the greatest sera dilution at which anti-HlgC antibodies could be detected above background by ELISA. At the end of the 3 month period, animals were injected subcutaneously (s.q.) at the base of the tail (B.O.T.) with HlgC protein and an agonistic anti-mouse-CD40 mAb (R&D Systems catalog #MAB440) diluted in DPBS.

[0222] Four days after the B.O.T injection, spleens were harvested, homogenized, and a B cell enriched fraction was isolated by Magnetic Activated Cell Sorting (MACS). B cells and FO mouse myeloma cells were co-incubated in a polyethylene glycol (PEG)-4000 solution to generate mAb secreting hybridomas cell lines. Following 10 days of hybridoma growth, hybridoma conditioned media was added to assay plates coated with HlgC protein, and ELISA was performed to identify hybridomas that produce HlgC binding mAbs. Hybridoma media samples positive for binding to HlgC were subsequently screened by ELISA to identify samples specific to HlgC, which exhibited no detectable binding to LukA'B, LukD, LukS-PV, LukE, or HlgA.

[0223] The immunoglobulin heavy chain (HC) and (LC) genes were cloned from the hybridoma cells by RT-PCR, followed by cDNA synthesis. For HC and LC RT-PCR, pools of primers complementary to v-region framework 1 (FR1) and single primers complementary to a region of constant domain 1 (CD1) were used. From this point, HC and LC expression plasmids were made by one of two methods. In the first method, double stranded HC and LC cDNA fragments were ligated into plasmids to enable sequencing and expression of full length murine LC and HC (IgG1 isotype). LC and HC plasmids were transformed into competent *E. coli*, multiple colonies per chain were picked, and the LC and HC genes were sequenced. Plasmid DNA for the consensus sequence for each chain was prepared for mAb protein expression. In the second method, cDNA fragments were sequenced by Next Generation Sequencing. Following sequencing, a panel of mAb HC and LC sequences were selected for de novo gene synthesis based upon quality of the sequencing data, sequence redundancy, and predicted mAb expression risks (i.e. mAb sequences with known post-translational liabilities were excluded). *De novo* gene synthesis was performed to generate plasmid DNA for mAb protein expression.

[0224] Expi293F cells were co-transfected with cognate LC and HC expressing plasmid pairs using Gibco's Expifectamine transfection fit. Culture supernatants were harvested 5 days later, and the mAb concentrations were determined. The recombinantly expressed mAbs were re-tested by ELISA for binding to all six of the aforementioned leukotoxins or subunits thereof to validate mAbs that specifically bind to HlgC and not the other five toxins.

[0225] **LukE/HlgA Antibody Generation**. A cohort of Balb/c and C3H mice received three intraperitoneal (i.p.) injections of recombinant LukE plus HlgA protein mixed with either Complete (Sigma catalog #F5881) or Incomplete (Sigma catalog #F5506) Freund's adjuvant over the course of 6 weeks. Immune titers to both LukE and HlgA were tested at an intermediate time point. All C3H mice had titers to both antigens of at least 128,000. Four out of five Balb/c mice exhibited titers, ranging from 4000 - 64,000 to HlgA and 8000 – 64,000 to LukE. Titer is defined as the greatest sera dilution at which anti-HlgA and anti-LukE antibodies could be detected above background by ELISA. At the end of the 6 week period, animals were injected subcutaneously (s.q.) at the base of the tail (B.O.T.) with LukE plus HlgA proteins and an agonistic anti-mouse-CD40 mAb (R&D Systems catalog #MAB440) diluted in DPBS.

[0226] Four days after the B.O.T injection, spleens were harvested, homogenized, and a B cell enriched fraction was isolated by Magnetic Activated Cell Sorting (MACS). B cells and FO mouse myeloma cells were co-incubated in a polyethylene glycol (PEG)-4000 solution to generate mAb secreting hybridomas cell lines. Following 10 days of hybridoma growth, hybridoma conditioned media was added to assay plates coated with a combination of LukE and

HlgA protein, and ELISA was performed to identify hybridomas that produce LukE and/or HlgA binding mAbs. Hybridoma media samples positive for binding to LukE and/or HlgA were subsequently screened by ELISA to identify samples specific to LukE and/or HlgA, which exhibited no detectable binding to LukA'B, LukD, LukS-PV or HlgC.

[0227] The immunoglobulin heavy chain (HC) and (LC) genes were cloned from the hybridoma cells by RT-PCR, followed by cDNA synthesis. For HC and LC RT-PCR, pools of primers complementary to v-region framework 1 (FR1) and single primers complementary to a region of constant domain 1 (CD1) were used. cDNA fragments were sequenced by Next Generation Sequencing. Following sequencing, a panel of mAb HC and LC sequences were selected for de novo gene synthesis based upon quality of the sequencing data, sequence redundancy, and predicted mAb expression risks (i.e. mAb sequences with known post-translational liabilities were excluded). De novo gene synthesis was performed to generate plasmid DNA for mAb protein expression.

[0228] Expi293F cells were co-transfected with cognate LC and HC expressing plasmid pairs using Gibco's Expifectamine transfection fit. Culture supernatants were harvested 5 days later, and the mAb concentrations were determined. The recombinantly expressed mAbs were re-tested by ELISA for binding to all six of the aforementioned leukotoxins or subunits thereof to validate mAbs that specifically bind to LukE and/or HlgA and not the other toxins.

Example 2 - Characterization of Monoclonal Antibodies that Bind Leukotoxin Subunit LukD via Non-Competing Epitopes and Exhibit Differential LukED Neutralization Activity

[0229] A series of monoclonal antibodies (mAbs) were identified from hybridoma cell lines derived from the spleens of mice following immunization with recombinant LukD protein as described in Example 1. Herein is described the characterization of the interaction of two such anti-LukD mAbs, antibody SM1B221 (SEQ ID NOs: 422 HC plus SEQ ID NO: 414 LC) and antibody SM1B225 (SEQ ID NOs: 426 HC plus SEQ ID NO: 418 LC), with the LukD protein. These experiments demonstrate that the LukD antigen is able to engage with both mAbs simultaneously indicating that they bind different epitopes. Further, while SM1B225 neutralizes the cytolytic activity of the LukED leukotoxin against human polymorphonuclear leukocytes (PMNs), SM1B221 exhibits no detectable neutralization activity. These data substantiate the notion that mAbs can be identified that bind leukotoxin subunits through alternate epitopes, and that only a subset of these correspond to neutralizing epitopes wherein mAb binding inhibits the cytolytic activity of the targeted leukotoxin.

[0230] **Procedures.** *Proteins.* mAbs SM1B221 and SM1B225 were purified from transiently transfected Expi293F cells (ThermoFisher Scientific Inc.) and purified by standard chromatographic methods with Protein G Sepharose (GE Healthcare Life Sciences Inc.) as the primary capture resin. A recombinant derivative of the LukD protein (SEQ ID NO: 824) that bears an amino-terminal polyhistidine affinity tag and was purified from *E. coli* by Nickel affinity chromatography. For LukED neutralization assays, recombinant LukD and LukE subunits bearing polyhistidine affinity tags (SEQ ID NOs: 826 (LukE) and 825 (LukD)) were individually purified from *S. aureus* and combined at the time of the assay (as indicated below).

[0231] *ELISA assays.* Binding of the mAbs to purified, recombinant LukD protein that was chemically biotinylated *in vitro* was determined by ELISA. Briefly, 100µl of a 5µg/mL solution of streptavidin (in PBS) was added per well of a 96 well White Maxisorp plate (Nunc-cat# 436110) and incubated overnight at 4°C. Wells were then washed 3X with TBST (50 mM Tris HCl, pH 7.4, 150 mM NaCl, 0.1% Tween 20), blocked with 300µL/well StartingBlock T20 (Pierce cat# 37543), and incubated 45-60 minutes at room temperature (RT). The plate was washed 3 times with TBST and 0.2µg of a biotinylated preparation of LukD protein (in 100µL) was added to each test well. The plate was incubated 45-60 minutes at RT with gentle shaking. The plate was then washed 3 times with TBST. In separate dilution plates, the mAb test articles were serially diluted four-fold in blocking buffer starting at 10µg/mL. Titrated test articles (100µL) were added to test wells and the plate incubated 45-60 minutes at RT with gentle shaking. The plate was then washed 3 times with TBST. For detection of bound test articles, 100µL/well of a peroxidase-conjugated, F(ab')2 fragment of a goat anti-mouse IgG, FC-γ fragment specific antibody (Jackson Immuno Research product 115-036-071) diluted 1:5000 in Starting block T20 was added and the plate incubated for 45-60min at RT with gentle shaking. The plate was then washed 3 times with TBST. To detect bound F(ab')2 fragment of the goat anti-mouse antibody, 100µL/well of the POD Chemiluminescence substrate (Roche-cat# 11582950001) was added immediately prior to reading plates and the plates read using an Envision reader within 15 minutes of the substrate addition. The data were analyzed using GraphPad Prism. Values were transformed to a log scale and fit using a non-linear regression sigmoidal dose-response equation resulting in an eleven point binding curve for each antibody against each antigen.

[0232] *LukED neutralization studies.* For LukED neutralization studies, the anti-LukD mAb test articles (0.625µg/mL) in 100µL reactions were incubated with purified, recombinant LukED (2.5µg/mL per subunit; 72.5nM) for 30 mins at 4°C. Freshly isolated human primary polymorphonuclear leukocytes (hPMNs, 200,000 cells in RPMI+ 10mM HEPES + 0.1% HSA)

were added to the mixture of LukED and mAb protein to a final volume of 100µl. Ethidium bromide was then added to the cells at 1:2000 final dilution and plates were read 30 and 60 mins post toxin addition. Following 1 hour intoxication in a 37°C CO_2 incubator, 25µl of supernatant was carefully transferred to a new plate after spinning the plate down at 1500 RPM for 10mins. Cell Titer reagent (Promega) was added to the remaining cells and incubated for 1.5 hours. The 25µl of supernatant were mixed with equal amounts of CytoTox-ONE™ Assay reagent (Promega) that rapidly measures the release of lactate dehydrogenase (LDH) from cells with a damaged membrane. LDH released into the culture medium was measured with a 10-minute coupled enzymatic assay that results in the conversion of resazurin into a fluorescent resorufin product. For the neutralization experiments, LukED was used at a concentration of 72.5nM (2.5µg/mL per subunit).

[0233] *Determination of affinity (K_D) constants.* K_D values for LukD were determined by Bio-Layer Interferometry (BLI) using an Octet^{RED} 384 instrument (forteBIO Inc.) running the basic kinetics protocol ("Biomolecular Binding Kinetics Assays on the Octet Platform", as outlined in Application Note 14 from Pall forteBIO Corp. accessible via the FortBIO website). Briefly, biotinylated LukD protein was loaded onto Dip and Read™ Streptavidin (SA) Biosensor pins at a 10µg/mL concentration in PBS pH7.2 for 5 minutes. A baseline was set by washing with phosphate buffered saline (PBS, pH 7.2) for 1 minute. The association rates for mAbs SM1B221 and SM1B225 were measured by addition of a 10µg/mL concentration in PBS (pH7.2) over a period of 5 minutes. Following initial binding of either the SM1B221 or the SM1B225 mAb, a baseline was reset by washing with phosphate buffered saline (PBS, pH 7.2) for 1 minute. Binding of the second mAb was measured by addition of a 10ug/mL concentration in PBS (pH7.2) over a period of 5 minutes. Curve fitting to determine K_D values used the initial 120 seconds of association and 60 seconds of dissociation to analyze on and off rates.

[0234] **Results.** The binding of the anti-LukD mAbs SM1B221 and SM1B225 to purified LukD protein as determined by an ELISA assay is shown in FIG. 1A. For each, saturation binding is apparent at a concentration of ~1µg/mL under these conditions with half maximal binding in the 0.01 to 0.2µg/mL range with slightly higher affinity apparent for the SM1B221 mAb.

[0235] The ability of the anti-LukD mAbs SM1B221 and SM1B225 to inhibit cytolytic activity of LukED against hPMNs was determined by measuring (i) LDH release from lysed cells using the CytoTox-ONE™ assay reagent (Promega), and (ii) by quantitation of ATP present - an indicator of metabolically active cells – using the Cell Titer reagent (Promega). As is shown in FIGs. 1B-C, SM1B221 does not inhibit LukED mediated cytolysis of hPMNs as

determined either by LDH release (FIG. 1C) or ATP levels (FIG. 1B). In contrast, minimal if any cytolysis of hPMNs is apparent with SM1B225. These data clearly indicate that the anti-LukD mAbs SM1B221 and SM1B225 have differential activity in neutralizing the cytolytic activity of the LukED leukotoxin and imply that they interact with the LukD protein through distinct binding epitopes.

[0236] If the anti-LukD mAbs SM1B221 and SM1B225 bind LukD through distinct binding sites, then it would be expected that they would not exhibit competition in binding and this was assessed by Bio-Layer Interferometry (BLI). FIG. 1D shows the BLI trace for an experiment wherein a biotinylated variant of LukD was first loaded to apparent saturation onto a streptavidin-coated biosensor pin followed by near saturation binding of the SM1B221 mAb. After a PBS wash, either SM1B221 or SM1B225 was then added and binding measured for a further five minutes. As expected, minimal additional binding of SM1B221 was detected. However, addition of SM1B225 resulted in a further increase in the BLI signal indicating that the LukD protein immobilized on the pin displays the SM1B225 binding epitope in the presence of saturation binding of the SM1B221 mAb.

[0237] FIG. 1E shows the BLI trace for an experiment wherein a biotinylated variant of LukD was first loaded to apparent saturation onto a streptavidin-coated biosensor pin followed by near saturation binding of the SM1B225 mAb. After a PBS wash, either SM1B221 or SM1B225 was then added and binding measured for a further five minutes. As expected, minimal additional binding of SM1B225 was detected. However, addition of SM1B221 resulted in a further increase in the BLI signal indicating that the LukD protein immobilized on the pin displays the SM1B221 binding epitope in the presence of saturation binding of the SM1B221 mAb. These BLI data clearly indicate that the anti-LukD mAbs SM1B221 and SM1B225 bind LukD through distinct and non-competing binding sites.

[0238] **Summary.** Analysis of the LukED neutralization activity of the anti-LukD mAbs SM1B221 and SM1B225 clearly indicates that only the SM1B225 mAb exhibits activity in blocking LukED mediated cytolysis of hPMNs (FIGs. 1B-C) despite both antibodies exhibiting potent LukD binding activity (FIG. 1A). The notion that they bind LukD via different binding epitopes is further substantiated by data from BLI studies indicating that SM1B221 and SM1B225 do not compete with each other in binding LukD.

Example 3 - Characterization of Monoclonal Antibodies that Bind the LukAB Leukotoxin via Non-Competing Epitopes and Exhibit Differential Effects on LukAB Activity

[0239] A series of monoclonal antibodies (mAbs) were identified from hybridoma cell lines derived from the spleens of mice following immunization with recombinant LukAB protein (see Example 1). Herein is described the characterization of the interaction of four such anti-LukAB mAbs (SM1B111 - SEQ ID NO: 265 HC plus SEQ ID NO: 224 LC; SM1B245 - SEQ ID NO: 269 HC plus SEQ ID NO: 228 LC; SM1B249 - SEQ ID NO: 273 HC plus SEQ ID NO: 237 LC; and SM1B252 - SEQ ID NO: 276 HC plus SEQ ID NO: 235 LC) with the LukAB protein. As demonstrated herein these four LukAB mAbs exhibit both differences in binding characteristics and apparent differences in their impact on LukAB activities. These data further substantiate the notion that mAbs can be identified that bind leukotoxins (or subunits thereof) via alternate epitopes and that such differential binding impacts leukotoxin activity in distinct ways.

[0240] **Procedures.** *Proteins.* mAbs SM1B111, SM1B245, SM1B249 and SM1B252 were purified from transiently transfected Expi293F cells (ThermoFisher Scientific Inc.) and purified by standard chromatographic methods with Protein G Sepharose (GE Healthcare Life Sciences Inc.) as the primary capture resin. For LukAB binding studies conducted by ELISA assay or Bio-Layer Interferometry (BLI), a recombinant toxoid variant of the LukAB protein (LukA E323A) was used (DuMont et al., "Identification of a Crucial Residue Required for Staphylococcus aureus LukAB Cytotoxicity and Receptor Recognition,", *Infect Immun.* 82(3):1268-76 (2014), which is hereby incorporated by reference in its entirety) that further bears poly-histidine and streptavidin binding sequences at the amino-terminus of the LukA sequence (SEQ ID NOs: 827 LukA and 828 LukB). Recombinant LukAB toxoid protein (LukA E323A) protein was purified by nickel affinity chromatography as soluble heterodimers from an *E. coli* strain expressing biotin ligase. For LukAB neutralization and human CD11b I-domain interaction studies, a recombinant form of the LukAB protein (SEQ ID Nos: 829 LukA and 830 LukB) that bears an amino-terminal polyhistidine affinity tag on the LukA subunit was purified from *S. aureus* by nickel affinity chromatography. For studies of the impact of anti-LukAB mAbs on LukAB interaction with the human CD11b protein, a recombinant form of the human CD11b I-domain (SEQ ID NO: 831) was purified from *E. coli* (Dumont *et al.*, "*Staphylococcus aureus* LukAB Cytotoxin Kills Human Neutrophils by Targeting the CD11b Subunit of the Integrin Mac-1," *PNAS* 110: 10794-99 (2013), which is hereby incorporated by reference in its entirety).

[0241] *LukAB binding assays by ELISA.* Binding of the anti-LukAB mAbs to purified, recombinant LukAB protein was determined by ELISA. Briefly, 100µl of a 5µg/mL solution of

streptavidin (in PBS) was added per well of a 96 well White Maxisorp plate (Nunc-cat# 436110) and incubated overnight at 4°C. Wells were washed 3X with TBST (50 mM Tris HCl, pH 7.4, 150 mM NaCl, 0.1% Tween 20), blocked with 300µL/well StartingBlock T20 (Pierce cat# 37543), and incubated 45-60 minutes at room temperature (RT). The plate was washed 3 times with TBST, and 0.2µg of a biotinylated preparation of LukAB protein (in 100µL) was added to each test well. The plate was incubated 45-60 minutes at RT with gentle shaking and then washed 3 times with TBST. In separate dilution plates, the mAb test articles were serially diluted four-fold in blocking buffer starting at 10µg/mL. 100µL of titrated test articles were added to test wells and the plate incubated 45-60 minutes at RT with gentle shaking. The plate was then washed 3 times with TBST. For detection of bound test articles, 100µL/well of a peroxidase-conjugated, F(ab')2 fragment of a goat anti-mouse IgG, FC-g fragment specific antibody (Jackson Immuno Research product 115-036-071) diluted 1:5000 in Starting block T20 was added and the plate incubated for 45-60min at RT with gentle shaking. The plate was then washed 3 times with TBST. To detect bound F(ab')2 fragment of the goat anti-mouse antibody, 100µL/well of the POD Chemiluminescence substrate (Roche-cat# 11582950001) was added immediately prior to reading plates and the plates read using an Envision reader within 15 minutes of the substrate addition. The data were analyzed using GraphPad Prism. Values were transformed to a log scale and fit using a non-linear regression sigmoidal dose-response equation resulting in an eleven point binding curve for each antibody against each antigen.

[0242] *LukAB neutralization studies*. For LukAB neutralization studies, the anti-LukAB mAb test articles in 100µL reactions were incubated with purified, recombinant LukAB for 30 mins at 4°C at a mAb/LukAB molar ration of 10:1. Freshly isolated human primary polymorphonuclear leukocytes (hPMNs, 200,000 cells in RPMI+ 10mM HEPES + 0.1% HSA) were added to the mixture of LukAB and mAb protein to a final volume of 100µL. Ethidium bromide was then added to the cells at 1:2000 final dilution and plates were read 30 and 60 mins post toxin addition. Following 1 hour intoxication in a 37°C CO_2 incubator, 25µL of supernatant was carefully transferred to a new plate after spinning the plate down at 1500 RPM for 10mins. Cell Titer reagent (Promega) was added to the remaining cells and incubated for 1.5 hours. The 25µL of supernatant were mixed with equal amounts of CytoTox-ONE™ Assay reagent (Promega) that rapidly measures the release of lactate dehydrogenase (LDH) from cells with a damaged membrane. LDH released into the culture medium was measured with a 10-minute coupled enzymatic assay that results in the conversion of resazurin into a fluorescent resorufin product.

[0243] *Determination of mAb affinity (K_D) constants and competition binding studies.* K_D values for LukAB were determined by Bio-Layer Interferometry (BLI) using an Octet^{RED} 384 instrument (forteBIO Inc.) running the basic kinetics protocol ("Biomolecular Binding Kinetics Assays on the Octet Platform", at outlined in Application Note 14 from Pall ForteBIO Corp. accessible via the ForteBIO website). Briefly, biotinylated LukAB protein was loaded onto Dip and Read™ Streptavidin (SA) Biosensor pins at a 10μg/mL concentration in PBS pH7.2 for5 minutes. A baseline was set by washing with phosphate buffered saline (PBS, pH 7.2) for 1 minute. The association rates for the test article mAbs were measured by addition of a 10ug/mL concentration in PBS (pH7.2) over a period of 5 minutes. Following initial binding of a mAb, a baseline was reset by washing with phosphate buffered saline (PBS, pH 7.2) for 1 minute. Binding of the second mAb was measured by addition of a 10ug/mL concentration in PBS (pH7.2) over a period of 5 minutes. Curve fitting to determine K_D values used the initial 60 seconds of association and dissociation steps to analyze on and off rates.

[0244] **Results.** The binding of the anti-LukAB mAbs SM1B111, SM1B245, SM1B249 and SM1B252 to purified LukAB protein as determined by an ELISA assay is shown in FIG. 2A. In this format, apparent saturation binding and half maximal saturation binding is observed over a broad concentration range with the SM1B245 exhibiting the highest apparent binding affinity and SM1B249 exhibiting the weakest apparent binding affinity.

[0245] The ability of the anti-LukAB mAbs SM1B245, SM1B249 and SM1B252 to neutralize the cytolytic activity of LukAB against hPMNs was determined by measuring (i) LDH release from lysed cells using the CytoTox-ONE™ assay reagent (Promega), and (ii) by quantitation of ATP present - an indicator of metabolically active cells – using the Cell Titer reagent (Promega). As is shown in FIGs. 2B-C, SM1B249 exhibits the most potent inhibition of cytolysis of hPMNs as determined either by LDH release (FIG. 2C) or ATP levels (FIG. 2B). In contrast, only minimal impact on cytolysis of hPMNs is apparent with SM1B245 and SM1B252. These data clearly indicate that the anti-LukAB mAbs have differential activity in neutralizing the cytolytic activity of the LukAB leukotoxin and imply that they interact with the LukAB protein through distinct binding epitopes.

[0246] If the anti-LukAB mAbs SM1B245, SM1B249 and SM1B252 bind LukAB through distinct binding sites, then it would be expected that they would not exhibit competition for LukAB binding. Competitive binding studies were carried out using Bio-Layer Interferometry (BLI). FIGs. 2D-E show the BLI trace for an experiment wherein a biotinylated variant of LukAB was first loaded to apparent saturation onto a streptavidin-coated biosensor pin followed by near saturation binding of the SM1B111 mAb. After a PBS wash, either SM1B111,

SM1B245, or SM1B249 were then added and binding measured for a further five minutes. As expected, minimal additional binding of SM1B111 was detected (grey, lower line trace). However, addition of either SM1B245 (black, upper line trace in FIG. 2D) or SM1B249 (black, upper line trace in FIG. 2E) resulted in a further increase in the BLI signal indicating that the LukAB protein immobilized on the pin displays the SM1B245 and SM1B249 binding epitopes in the presence of saturation binding of the SM1B111 mAb.

[0247] FIGs. 2F-G show the BLI trace for an experiment wherein a biotinylated variant of LukAB was first loaded to apparent saturation onto a streptavidin-coated biosensor pin followed by near saturation binding of the SM1B245 mAb. After a PBS wash, either SM1B245, SM1B111, or SM1B249 were added and binding measured for a further five minutes. As expected, minimal additional binding of SM1B245 was detected (grey, lower line trace). However, addition of either SM1B111 (black, upper line trace in FIG. 2F) or SM1B249 (black, upper line trace in FIG. 2G) resulted in a further increase in the BLI signal indicating that the LukAB protein immobilized on the pin displays the SM1B111 and SM1B249 binding epitopes in the presence of saturation binding of the SM1B245 mAb.

[0248] FIGs. 2H-I show the BLI trace for an experiment wherein a biotinylated variant of LukAB was first loaded to apparent saturation onto a streptavidin-coated biosensor pin followed by near saturation binding of the SM1B249 mAb. After a PBS wash, either SM1B249, SM1B111, or SM1B245 were then added and binding measured for a further five minutes. As expected, minimal additional binding of SM1B249 was detected (grey, lower line trace). However, addition of either SM1B111 (black, upper line trace in FIG. 2H) or SM1B245 (black, upper line trace in FIG. 2I) resulted in a further increase in the BLI signal indicating that the LukAB protein immobilized on the pin displays the SM1B111 and SM1B245 binding epitopes in the presence of saturation binding of the SM1B249 mAb.

[0249] **Summary**. Analysis of the LukAB neutralization activity of the anti-LukAB mAbs SM1B111, SM1B245 and SM1B249 indicates that only the SM1B249 mAb exhibits potent activity in blocking LukAB mediated cytolysis of hPMNs (FIGs. 2B-C) despite all three antibodies exhibiting LukAB binding activity (FIG. 2A). The notion that they bind LukAB via different binding epitopes is further substantiated by data from BLI studies indicating that SM1B111, SM1B245, and SM1B249 do not compete with each other in binding LukAB.

Example 4 - Characterization of Monoclonal Antibodies that Bind Leukotoxin Subunit LukE via Non-Competing Epitopes

[0250] A series of monoclonal antibodies (mAbs) were identified from hybridoma cell lines derived from the spleens of mice following immunization with recombinant LukE protein as described in Example 1. Herein is described the characterization of the interaction of three such anti-LukE mAbs (SM1B318; SEQ ID NOs: 788 HC plus SEQ ID NO: 749 LC, SM1B332; SEQ ID NOs: 802 HC plus SEQ ID NO: 763 LC and SM1B507; SEQ ID NOs: 360 HC plus SEQ ID NO: 348 LC) with the LukE protein and demonstrate that the LukE antigen is able to engage (i) with the SM1B 318 and SM1B332 mAbs simultaneously indicating that they bind different epitopes, and (ii) with the SM1B 332 and SM1B507 mAbs simultaneously indicating that they bind different epitopes.

[0251] **Procedures.** *Proteins.* mAbs SM1B318, SM1B332 and SM1B507 were purified from transiently transfected Expi293F cells (ThermoFisher Scientific Inc.) and purified by standard chromatographic methods with Protein A Sepharose (GE Healthcare Life Sciences Inc.) as the primary capture resin. A recombinant derivative of the LukE protein (SEQ ID NO: 826) that bears an amino-terminal poly-histidine affinity tag and was purified from *E. coli* by Nickel affinity chromatography.

[0252] *ELISA assays.* Binding of select mAbs to purified, recombinant LukE protein that was chemically biotinylated *in vitro* was determined by ELISA. Briefly, 100µl of a 5µg/mL solution of streptavidin (in PBS) was added per well of a 96 well White Maxisorp plate (Nunc-cat# 436110) and incubated overnight at 4˚C. Wells were then washed 3X with TBST (50 mM Tris HCl, pH 7.4, 150 mM NaCl, 0.1% Tween 20), blocked with 300µL/well StartingBlock T20 (Pierce cat# 37543), and incubated 45-60 minutes at room temperature (RT). The plate was washed 3 times with TBST and 0.2µg of a biotinylated preparation of LukE protein (in 100µL) was added to each test well. The plate was incubated 45-60 minutes at RT with gentle shaking. The plate was then washed 3 times with TBST. In separate dilution plates, the mAb test articles were serially diluted four-fold in blocking buffer starting at 10µg/mL. Titrated test articles (100µL) were added to test wells and the plate incubated 45-60 minutes at RT with gentle shaking. The plate was then washed 3 times with TBST. For detection of bound test articles, 100µL/well of a peroxidase-conjugated, F(ab')2 fragment of a goat anti-mouse IgG, FC-γ fragment specific antibody (Jackson Immuno Research product 115-036-071) diluted 1:5000 in Starting block T20 was added and the plate incubated for 45-60min at RT with gentle shaking. The plate was then washed 3 times with TBST. To detect bound F(ab')2 fragment of the goat anti-mouse antibody, 100µL/well of the POD Chemiluminescence substrate (Roche-cat#

11582950001) was added immediately prior to reading plates and the plates read using an Envision reader within 15 minutes of the substrate addition. The data were analyzed using GraphPad Prism. Values were transformed to a log scale and fit using a non-linear regression sigmoidal dose-response equation resulting in an 12-point binding curve for each antibody against each antigen.

[0253] *Determination of affinity (K_D) constants.* K_D values for LukE were determined by Bio-Layer Interferometry (BLI) using an Octet^{RED} 384 instrument (forteBIO Inc.) running the basic kinetics protocol ("Biomolecular Binding Kinetics Assays on the Octet Platform", as outlined in Application Note 14 from Pall forteBIO Corp. accessible via the ForteBIO website). Briefly, biotinylated LukE protein was loaded onto Dip and Read™ Streptavidin (SA) Biosensor pins at a 10µg/mL concentration in PBS pH7.2 for 5 minutes. A baseline was set by washing with phosphate buffered saline (PBS, pH 7.2) for 1 minute. The association rates for mAbs SM1B318, SM1B332 and SM1B507 were measured by addition of a 10µg/mL concentration in PBS (pH7.2) over a period of 5 minutes. Following initial binding of either the SM1B318, SM1B332 or the SM1B507 mAb, a baseline was reset by washing with phosphate buffered saline (PBS, pH 7.2) for 1 minute. Binding of the second mAb was measured by addition of a 10ug/mL concentration in PBS (pH7.2) over a period of 5 minutes. Curve fitting to determine K_D values used the initial 30 seconds of association and 30 seconds of dissociation to analyze on and off rates.

[0254] *LukED neutralization studies.* For LukED neutralization studies, the anti-LukE mAbs plus the anti-LukD mAb (each 0.625µg/mL) were incubated with purified, recombinant LukED (2.5µg/mL per subunit; 72.5nM) for 30 mins at 4°C. Freshly isolated human primary polymorphonuclear leukocytes (hPMNs, 200,000 cells in RPMI+ 10mM HEPES + 0.1% HSA) were then added to the mixture of LukED and mAb protein to a final volume of 100µl. Ethidium bromide was then added to the cells at 1:2000 final dilution and plates were read 30 and 60 mins post toxin addition. Following 1 hour intoxication in a 37°C CO2 incubator, 25µl of supernatant was carefully transferred to a new plate after spinning the plate down at 1500 RPM for 10mins. Cell Titer reagent (Promega) was added to the remaining cells and incubated for 1.5 hours. LDH released into the culture medium was measured with a 10-minute coupled enzymatic assay that results in the conversion of resazurin into a fluorescent resorufin product. For the neutralization experiments, LukED was used at a concentration of 72.5nM (2.5µg/mL per subunit).

[0255] **Results.** The binding of the anti-LukE mAbs SM1B318 and SM1B332 to purified LukE protein as determined by an ELISA assay is shown in FIG. 3A. For SM1B332, saturation binding is apparent at a concentration of ~1µg/mL under these conditions with half

maximal binding at ~0.05μg/mL. Under these conditions, lower relative affinity is apparent for the SM1B318 mAb compared to SM1B332.

[0256] If the anti-LukE mAbs SM1B318, SM1B332 and SM1B507 bind LukE through distinct binding sites, then it would be expected that they would not exhibit competition in binding and this was assessed by Bio-Layer Interferometry (BLI). FIG. 3B shows the BLI trace for an experiment wherein a biotinylated variant of LukE was first loaded to apparent saturation onto a streptavidin-coated biosensor pin followed by near saturation binding of the SM1B318 mAb. After a PBS wash, either SM1B318, SM1B332 or SM1B507 was then added and binding measured for a further five minutes. As expected, minimal additional binding of SM1B318 was detected. However, addition of SM1B332 resulted in a further increase in the BLI signal indicating that the LukE protein immobilized on the pin displays the SM1B332 binding epitope in the presence of saturation binding of the SM1B318 mAb.

[0257] FIG. 3C shows the BLI trace for an experiment wherein a biotinylated variant of LukE was first loaded to apparent saturation onto a streptavidin-coated biosensor pin followed by near saturation binding of the SM1B332 mAb. After a PBS wash, either SM1B318 or SM1B507 was then added and binding measured for a further five minutes. As expected, minimal additional binding of SM1B332 was detected. However, addition of SM1B318 or SM1B507 resulted in a further increase in the BLI signal indicating that the LukE protein immobilized on the pin displays the SM1B318 and SM1B507 binding epitopes in the presence of saturation binding of the SM1B332 mAb. These BLI data clearly indicate that the anti-LukE mAbs SM1B318 and SM1B507 bind LukE through distinct and non-competing binding sites in comparison to the SM1B332 mAb.

[0258] FIG. 3D shows the BLI trace for an experiment wherein a biotinylated variant of LukE was first loaded to apparent saturation onto a streptavidin-coated biosensor pin followed by near saturation binding of the SM1B507 mAb. After a PBS wash, either SM1B318 or SM1B332 was then added and binding measured for a further five minutes. As expected, minimal additional binding of SM1B507 was detected. However, addition of SM1B318 or SM1B332 resulted in a further increase in the BLI signal indicating that the LukE protein immobilized on the pin displays the SM1B318 and SM1B332 binding epitopes in the presence of saturation binding of the SM1B507 mAb. These BLI data clearly indicate that the anti-LukE mAbs SM1B318 and SM1B332 bind LukE through distinct and non-competing binding sites in comparison to the SM1B507 mAb.

[0259] The relative ability of the anti-LukE mAbs SM1B318, SM1B332 and SM1B507 plus the anti-LukD mAb SM1B221 to inhibit the cytolytic activity of LukED against hPMNs

was as determined by LDH release from lysed cells is shown in FIG. 3E. In contrast to the minimal protection from cytolysis of hPMNs that is apparent with SM1B221 (targeting LukD), each of the anti-LukE mAbs exhibited potent LukED neutralization activity.

[0260] **Summary.** These data indicate that anti-LukE mAbs that exhibit functional LukED neutralization activity can be identified that bind the target antigen via different, discrete epitopes and imply that alternate mechanisms of target neutralization can be achieved.

Example 5 - Characterization of Monoclonal Antibodies that Bind Leukotoxin Subunit LukD and Exhibit Differential LukED Neutralization Activity

[0261] To identify the specific epitopes of the three distinct anti-LukE monoclonal antibodies (mAbs) described in Example 4, Fabs were prepared that include the HC variable domain sequences of each mAb and employed in solution phase hydrogen/deuterium exchange-Mass Spectrometry (HDX-MS) studies with recombinant, purified LukE protein. Herein we describe the identification of both distinct and overlapping components of the epitopes recognized by SM1B438 (SEQ ID NOs: 1309 HC plus SEQ ID NO: 1313 LC the Fab corresponding to mAb SM1B318), SM1B440 (SEQ ID NOs: 1311 HC plus SEQ ID NO: 1315 LC the Fab corresponding to mAb SM1B332) and SM1B709 (SEQ ID NOs: 1298 HC plus SEQ ID NO: 1301 LC the Fab corresponding to mAb SM1B507).

[0262] **Procedures.** *Proteins.* Fab proteins SM1B438, SM1B440 and SM1B709, each bearing a poly-histidine affinity tag on the carboxyl-terminus of the HC component, were purified from transiently transfected Expi293F cells (ThermoFisher Scientific Inc.) by Nickel affinity chromatography. A recombinant derivative of the LukE protein (SEQ ID NO: 826) that bears an amino-terminal poly-histidine affinity tag and was purified from *E. coli* by Nickel affinity chromatography.

[0263] HDX-MS epitope mapping HDX-MS studies were conducting using published methods (Hamuro, Y., *et al.,* 'Rapid Analysis of Protein Structure and Dynamics by Hydrogen/Deuterium Exchange Mass Spectrometry', Journal of Biomolecular Techniques 14(3): 171-182 (2003) and Horn, J.R., *et al.,* 'The Role of Protein Dynamics in Increasing Binding Affinity for an Engineered Protein-Protein Interaction Established by H/D Exchange Mass Spectrometry', Biochemistry 45: 8488-8498 (2006), which are hereby incorporated by reference in their entirety). Briefly, the recombinant LukE protein in the absence or presence of Fabs were incubated in a deuterated water solution for predetermined times resulting in deuterium incorporation at exchangeable hydrogen atoms. Regions bound to the Fab proteins were inferred to be those sites relatively protected from exchange and thus contain a lower fraction of

deuterium than the reference LukE protein. The deuterium exchange was carried at room temperature for 0s, 60sec, 300sec, 1800sec, 7200sec, and 14400 sec. Following proteolysis, deuterium levels of the identified LukE peptides were monitored by the corresponding mass shift as determined by LC/MS.

[0264] **Results.** FIG. 4 shows data from HDX-MS analysis of the binding of Fabs SM1B438, SM1B440 and SM1B709 to LukE protein with the regions of LukE that were protected from Hydrogen/Deuterium exchange identified (as per the LukE numbering of SEQ ID NO: 826). In accord with the data generated from the afore described BLI studies undertaken with the corresponding mAb proteins (as described in Example 4, FIGs. 3B, 3C and 3D), it is apparent that the non-linear epitopes recognized by each Fab (and presumably therein the corresponding mAbs) are distinct with only one overlapping linear epitope component in the C-terminus of LukE (corresponding to amino acid residues 207-219 of SEQ ID NO: 826).

[0265] **Summary.** These data further exemplify that mAbs capable of neutralizing the cytolytic activity of leukotoxin ED can do so through the recognition of distinct epitopes on LukE and support the notion that neutralization can be achieved via discrete mechanisms.

Table 19. LukAB Light Chain (LC) and Heavy Chain (HC) Amino Acid Sequences

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B105	LC	DIVLTQSPAIMAASLGQKVTMTCSASSSVSSSYLHWYQQKS GASPKPLIHRTSNLASGVPARFSGSGSGTSYSLTISSVEAEDD ATYYCQQWSGYPFTFGAGTKLELKRADAAPTVSIFPPSSEQL TSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTD QDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVK SFNRNEC	218
SM1B106	LC	DIVMTQSPASLAVSLGQRATISCRASESVDNSGISFMNWFQQ KPGQPPKLLIYAASNQGSGVPARFSGSGSGTDFSLNIHPMEE DDTAMYFCQQSKEVPYTFGGGTKLEIKRADAAPTVSIFPPSS EQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	219
SM1B107	LC	DIVLTQSPASLAVSLGQRATISCRASESVDNSGISFMNWFQQ KPGQPPKLLIYAASNQGSGVPARFSGSGSGTDFSLNIHPMEE DDTAMYFCQQSKEVPYTFGGGTKLEIKRADAAPTVSIFPPSS EQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	220

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B108	LC	DVVMTQTPKFLLVSAGDRVTITCKASQSVSDDVTWYQQKS GQSPKLLIYYASNRYTGVPDRFTGSGYGTDFTFTISTVQAED LAVYFCQQDYSSPWTFGGGTKLEIKRADAAPTVSIFSPSSEQ LTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWT DQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIV KSFNRNEC	221
SM1B109	LC	DIVMTQSPASLAVSLGQRATISCRASESVDNSGISFMNWFQQ KPGQPPKLLIYAASNQGSGVPARFSGSGSGTDFSLNIHPMEE DDTAMYFCQQSKEVPYTFGGGTKLEIKRADAAPTVSIFPPSS EQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	222
SM1B110	LC	DIVLTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTS PKLWIYSTSNLASGVPARFSGSGSGTSYSLTISRMEAEDAAT YYCQQRSSYPFTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSG GASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDS KDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFN RNEC	223
SM1B111	LC	DIVMTQSPTTMAASPGERITITCSAHSNLISNYLHWYQQKPG FSPKLLIYRTSNLASGVPARFSGSGSGTSYSLTIGTMEAEDVA TYFCQQGSSIPFTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSG GASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDS KDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFN RNEC	224
SM1B112	LC	QIVLTQSPTIMSASPGEKVTMTCSASSHVSYIYWYQQKPGSS PRLWIYDTSNLVSGVPARFSGSRSGTSYSLTISSMEAEDAAT YYCQQYSGYPYTFGGGTKLEIKRADAAPTVSIFPPSSEQLTS GGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD SKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSF NRNEC	225
SM1B243	LC	DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPG KSPKTLIYRANRLVDGVPSRFSGSGSGQDYSPTISSLEYEDM GIYYCLQYDEFPYTFGGGTKLEIKRADAAPTVSIFPPSSEQLT SGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQ DSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKS FNRNEC	226
SM1B244	LC	DIVMTQSQKFMSTSVGDRVSVTCKASQNVGTNVAWYQQK PGQSPKTLIYSASYRYSGVPDSFTGSGSGTDFTLTISNVQSED WAEYFCQQYNSYPFTFGSGTKLEIKRADAAPTVSIFPPSSEQ LTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWT DQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIV KSFNRNEC	227
SM1B245	LC	DIVLTQSPASLAVSLGQRATMSCRASESVDGYGNSFLHWYQ QKPGQPPKLLIYRASNLESGIPARFSGTGSRTDFTLTITPVEA DDVATYYCQQSNGDPFTFGSGTKLEIKRADAAPTVSIFPPSS EQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	228

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B246	LC	DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGKTYLEWYL QKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVE AEDLGVYYCLQGSHVPWTFGGGTKLELKRADAAPTVSIFPP SSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLN SWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTST SPIVKSFNRNEC	229
SM1B247	LC	DIVLTQSPASLAVSLGQRATISCRASKSVSISGYSYMHWYQQ KPGQPPKLLIDLASNLESGVPARFSGSGSGTDFTLNIHPVEEE DAATYYCQHSRELPFTFGSGTKLEIKRADAAPTVSIFPPSSEQ LTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWT DQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIV KSFNRNEC	230
SM1B248	LC	DIVLTQSPASLAVSLGQRATMSCRASESVDGYGNSFLHWYQ QKPGQPPKLLIYRASNLESGIPARFSGTGSRTDFTLTITPVEA DDVATYYCQQSNGDPFTFGSGTKLEIKRADAAPTVSIFPPSS EQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	231
SM1B249	LC	QIVLTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGT SPKRWIYDTSKLASGVPARFSGSGSGTSYSLTISSMEAEDAA TYYCQQWISNPPTFGGGTKLEIKRADAAPTVSIFPPSSEQLTS GGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD SKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSF NRNEC	232
SM1B250	LC	DIVLTQSPASLAVSLEQRATISCKASQSVDYDGDSYMNWYQ QKPGQPPKLLIYAASNLESGIPARFSGSGSGTDFTLNIHPVEE EDAATYYCQQSNEDPLTFGAGTKLELKRADAAPTVSIFPPSS EQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	233
SM1B251	LC	DIQMTQSPASLSASVGETVTTICRASENIYSYLAWYQQKQG KSPQLLVYNAKTLVEGVPSRFSGSGSGTQFSLKINSLQPEDF GSYYCQHHYGSPYTFGGGTKLELKRADAAPTVSIFPPSSEQL TSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTD QDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVK SFNRNEC	234
SM1B252	LC	DVLMTQTPLSLPVSLGDQASISCRSSQSIVYSNGNTYLEWYL QKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVE AEDLGVYYCFQGSHVPFTFGSGTKLEIKRADAAPTVSIFPPSS EQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	235
SM1B253	LC	DVVMTQTPLTLSVTIGQAASISCKSSQSLLHSDGKTYLNWLL QRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVE AEDLGVYYCWQGTHFPYTFGGGTKLEIKRADAAPTVSIFPP SSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLN SWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTST SPIVKSFNRNEC	236

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B254	LC	DVVMTQTPLTLSVTVGQPASISCKSSQSLLHSDGKTYLNWL LQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVE AEDLGVYYCWQGTHFPYTFGGGTKLEIKRADAAPTVSIFPP SSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLN SWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTST SPIVKSFNRNEC	237
SM1B255	LC	DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGETYLNWLL QRPGQSPKRLIYMVSKLDSGVPDRFTGSGSGTDFTLKISRVE AEDLGVYYCWQGTHFPQTFGGGTKLELKRADAAPTVSIFPP SSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLN SWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTST SPIVKSFNRNEC	238
SM1B256	LC	DVVMTQTPLTLSVTNGQPASISCKSSQSLLDSDGETYLNWL LQRPGQSPKRLIYLVSKLDSGVPDRFIGSGSGTDFTLKISRVE AEDLGVYFCWQGTHSPYTFGGGTKLEIKRADAAPTVSIFPPS SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	239
SM1B257	LC	DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGK GPRLLIHYTSTLQPGIPSRFSGSGSGRDYSFSISNLEPEDIATY YCLQYDNLRTFGGGTKVEIKRADAAPTVSIFPPSSEQLTSGG ASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSK DSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNR NEC	240
SM1B258	LC	DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYL QKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVE AEDLGVYYCFQGSHVPFTFGSGTKLEIKRADAAPTVSIFPPSS EQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	241
SM1B259	LC	QIVLTQSPAIMSASPGEKVTMTCSASSSVSYMYWYQQKPGS SPRLLIYDTSNLASGVPVRFSGSGSGTSYSLTISRMEAEDAAT YYCQQWSSYPPTFGGGTKLEIKRADAAPTVSIFPPSSEQLTS GGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD SKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSF NRNEC	242
SM1B260	LC	DIVLTQSPASLAVSLGQRATMSCRASESVDGYGNSFLHWYQ QKPGQPPKLLIYRASNLESGIPARFSGTGSRTDFTLTITPVEA DDVATYYCQQSNGDPFTFGSGTKLEIKRADAAPTVSIFPPSS EQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	243
SM1B261	LC	NIVMTQSPKSMSMSVGERVTLSCKASENVGTYVSWYQQKP EQSPKLLIYGASNRYTGVPERFTGSGSATDFTLTISSVQAEDL ADYHCGQSYSYPLTFGAGTKLELKRADAAPTVSIFPPSSEQL TSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTD QDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVK SFNRNEC	244

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B262	LC	DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPG KSPKTLIYRANRLVDGVPSRFSGSGSGQDYSLTISSLEYEDM GIYYCLQYDEFPLTFGAGTKLELKRADAAPTVSIFPPSSEQLT SGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQ DSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKS FNRNEC	245
SM1B263	LC	DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGK GPRLLIHYTSTLQPGIPSRFSGSGSGRDYSFSISNLEPEDIATY YCLQYDNLWTFGGGTKVEIKRADAAPTVSIFPPSSEQLTSGG ASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSK DSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNR NEC	246
SM1B264	LC	DIQMTQSPASLSASVGETVTIICRASENIYSNLAWYQQKQGK SPQLLVYAATNLADGMPSRFSGSGSGTQYSLKINSLQSEDFG SYYCQHFWGTPWTFGGGTKLEIKRADAAPTVSIFPPSSEQLT SGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQ DSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKS FNRNEC	247
SM1B265	LC	DIQMTQSPASLSASVGETVTIICRASENIYSYLAWYQQKQGK SPQLLFYNAKTLVEGVPSRFSGSGSGTQFSLKINSLQPEDFGS YYCQHHYGSPYTFGGGTKLELKRADAAPTVSIFPPSSEQLTS GGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD SKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSF NRNEC	248
SM1B266	LC	DIQMTQSPSTLSASLGDTITITCHASQNINVWLSWYQQKPGN IPKLLIYKASNLHTGVPSRFSGSGSGTGFTLTISSLQPEDIATY YCQQGQSYPLTFGAGTKVEIKRADAAPTVSIFPPSSEQLTSG GASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDS KDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFN RNEC	249
SM1B267	LC	DIQMTQSPSTLSASLGDTITITCHASQNINVWLSWYQQKPGN IPKLLIYKASNLHTGVPSRFSGSGSGTGFTLTISSLQPEDIATY YCQQGQSYPYTFGGGTKLEIKRADAAPTVSIFPPSSEQLTSG GASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDS KDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFN RNEC	250
SM1B268	LC	EIVLTQSPTTMAASPGEKITITCSASSSISSNYLHWYQQKPGF SPKLLIYRTSNLASGVPARFSGSGSGTSYSLTIGTMEAEDVA TYYCQQGSSIPRTFGGGTKLEIKRADAAPTVSIFPPSSEQLTS GGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD SKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSF NRNEC	251
SM1B269	LC	DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQ QKPGQPPKLLIYAASNLESGIPARFSGSGSGTDFTLNIHPVEE EDAATYYCQQSNEDPYTFGGGTKLEIKRADAAPTVSIFPPSS EQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	252

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B270	LC	DIVLTQSPASLAVSLGQRASISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLESGIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSYEDPFTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC	253
SM1B271	LC	QIVLTQSPAIMSASPGEKVTMTCSASSSVSYMYWYQQKPGSSPRLLIYDTSNLASGVPVRFSGSGSGTSYSLTISRMEAEDAATYYCQQWSSYPPTFGGGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC	254
SM1B272	LC	DIVMTQSQKFMSTSVGDRVSVTCKASQNVGTNVAWYQQKPGQSPKALIYSASYRYSGVPDRFTGSGSGTDFTLTISNVQSEDLAEYFCQQYNSYPFTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC	255
SM1B273	LC	DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYSYPYTFGGGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC	256
SM1B274	LC	DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPYTFGGGTKLELKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC	257
SM1B275	LC	DVVMTQTPLTLSVTIGQPASISCKSSQSLLYSNGKTYLNWLLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVFYCVQGTHFPQTFGGGTKLELKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC	258
SM1B105	HC	EVQLQQSGAELMTPGASVKISCKATGYTFSTFWIEWIKQRPGHGLEWIGEILPGSGSTKYNEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCARGGYDGMDYWGQGTSVTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK	259

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B106	HC	EVQLQQSGAELMTPGASVKISCKATGYTFSTFWIEWIKQRP GHGLEWIGEILPGSGSTKYNEKFKGKATFTADTSSNTAYMQ LSSLSSEDSAVYYCARGGYDGMDYWGQGTSVTVSSAKTTP PSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSL SSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVAHPAS STKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITLT PKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFN STFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKT KGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEW QWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSNWEAG NTFTCSVLHEGLHNHHTEKSLSHSPGK	260
SM1B107	HC	EVQLQQSEAELMTPGASVKISCKATGYTFSTFWIEWIKQRPG HGLEWIGEILPGSGSTKYNEKFKGKATFTADTSSNTAYMQL SSLTSEDSAVYYCARGGYDGMDYWGQGTSVTVSSAKTTPP SVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLS SGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVAHPASS TKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITLTP KVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNS TFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTK GRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQ WNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSNWEAGN TFTCSVLHEGLHNHHTEKSLSHSPGK	261
SM1B108	HC	EVQLQQSGAELVKPGASVKISCKASGYAFSSSWMNWVKQR PGKGLEWIGRIYPGDGDTNYHGKFKGKATLTADKSSSTAY MQLSSLTSEDSAVYFCARRNYDGYHYGMDYWGQGTSVTV SSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTV TWNSGSLSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTC NVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPK DVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQT QPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPA PIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFF PEDITVEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQ KSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK	262
SM1B109	HC	EVQLQQSGAELMTPGASVKISCKATGYTFSTFWIEWIKQRP GHGLEWIGEILPGSGSTKYNEKFKGKATFTADTSSNTAYMQ LSSLTSEDSAVYYCARGGYDGMDYWGQGTSVTVSSAKTTP PSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSL SSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVAHPAS STKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITLT PKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFN STFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKT KGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEW QWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSNWEAG NTFTCSVLHEGLHNHHTEKSLSHSPGK	263

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B110	HC	EVQLQQSGAELVKPGTSVKMSCKASGYTFTSYWMHWVKL RPGQGLEWIGVIDPSDSYTNYNQKFKGRATLTGDTSSSTAY MQLSSLTSEDSAVYYCTRAAYDNSYYFDYWGQGTTLTVSS AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTW NSGSLSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNV AHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDV LTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQP REEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIE KTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPE DITVEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKS NWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK	264
SM1B111	HC	EVQLQQSGAELVKPGASVKISCKASGYAFSSSWMNWLKQR PGKGLEWIGRIYPGDGDTNYNGKFKGKATLTADKSSSTAY MQLSSLTSEDSAVYFCARYGYDYDGEYYYAMDYWGQGTS VTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEP VTVTWNSGSLSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSET VTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPP KPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHT AQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAA FPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMIT DFFPEDITVEWQWNGQPAENYKNTQPIMNTNGSYFVYSKL NVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK	265
SM1B112	HC	QVQLKESGPELKKPGETVRISCKASGYTFTNYGMNWVKQT PGKGLKWIDWLKSYTGEPTHTGDFKGRFDLSLETSANTAYL QINNLKNEDTATYFCARGSLFGLDYWGQGTSVTVSSAKTTP PSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSL SSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVAHPAS STKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITLT PKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFN STFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKT KGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEW QWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSNWEAG NTFTCSVLHEGLHNHHTEKSLSHSPGK	266
SM1B243	HC	EVQLQQSGAELVKSGASVKLSCTASGFNIKDYYMHWVKQR PEQGLEWIGRIDPANGNTKYDPKFQDKATITSDTSSNTAYLQ LSSLTSEDTAVYYCAEGDYVPGYFDVWGAGTTVTVSSAKT TAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSG SLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	267

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B244	HC	EVQLQESGPSLVKPSQTLSLTCSVTGDSITSDYWNWIRKFPG NKLEYMGYISYSGSTYYNPSLKSRISITRDTSKNQYYLQLNS VTTEDTATYYCAGDYGSPYAMDYWGQGTSVTVSSAKTTAP SVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSS GVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASS TKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVL MISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTH REDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIE RTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMP EDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEK KNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	268
SM1B245	HC	QVQLQQSGAELAKPGASVKMSCKSSGYTFSTYWMHWVKQ RPGQGLEWIGYINPNTGYTEYNQKFKDTATLTADKSSSTAY MQLSSLTSEDSAVYYCARGGSKAFPYYAMDYWGQGTSVT VSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTL TWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSIT CNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSV FIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVE VHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKV NNKDLPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTL TCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYF MYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTP GK	269
SM1B246	HC	EIQLQQSGPELVKPGASVKMSCKASGYSFTGYNMHWVKQS HGKSLEWIGYIDPYNGATSHNQKFKGKATLTVEKSSSTAYM QLNSLTSEDSAVYYCARGLYGDYWYAYWGQGTLVTVSSA KTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVA HPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPK IKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTA QTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKD LPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMV TDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSK LRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	270
SM1B247	HC	EVQLVESGGGLVKPGGSLKLSCAASGFTFSDYYMYWVRQT PEKRLEWVATISDGGSYTFYPDSVKGRFTISRDNAKNNLYL QMSSLKSEDTAMYYCARGPTYYGLDYWGQGTTLTVSSAKT TAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSG SLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	271

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B248	HC	QVQLQQPGAELVRPGASVRLSCKASGYSFTSYWMSWVKVR PGQGLEWIGMIHPSDSETRLNQKFKDKATLTVDKSSSTAYM QLSSPTSEDSAVYYCARLYVDFFDYWGQGTTLTVSSAKTTA PSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLS SGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPAS STKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDV LMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQT HREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPI ERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFM PEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVE KKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	272
SM1B249	HC	DVKLVESGGGLVKLGGSLKLSCAASGFTFSSYYMSWVRQT PEKRLELVAAINSNGGSTYYPDTVKGRFTISRDNAKNTLYL QMSSLKSEDTALYYCARPDYPYAMDYWGQGTSVTVSSAKT TAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSG SLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	273
SM1B250	HC	QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAP GKGLKWMGWINTYTGEPTYADDFKGRFAFSLETSASTAYL QINNLKNEDTATYFCARSPSYGSRGAWFAYWSQGTLVTVS AAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITC NVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFI FPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEV HTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVN NKDLPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLT CMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFM YSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG K	274
SM1B251	HC	QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAP GKGLKWMGWINTYTGEPTYADDFKGRFAFSLETSASTAYL QINNLKNEDTATYFCARSPSYGSRGAWFAYWGQGTLVTVS AAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITC NVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFI FPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEV HTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVN NKDLPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLT CMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFM YSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG K	275

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B252	HC	QVQLQQSGAELMKPGASVKISCKASGYTFSDYWIEWIKQRP GHGLEWMGEILPGSDKTNYNEKFKGKATFTADSSSNTAYM QLNSLTSEDSAVFYCATAGDDYVKWGQGTLVTVSAAKTTA PSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLS SGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPAS STKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDV LMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQT HREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPI ERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFM PEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVE KKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	276
SM1B253	HC	EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVRQR PEQGLEWIGRIDPANDITKYDPKFQGKATITADTSSNTAYLQ LSSLTSEDTAVYYCGRDWADYWGQGTTLTVSSAKTTAPSV YPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSG VHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASST KVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVL MISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTH REDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIE RTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMP EDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEK KNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	277
SM1B254	HC	EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQR SEQGLEWIGRINPANDNTKYDPKFQGKATITADTSSNTAYL QLSSLTSEDTAVYYCGRDWADYWGQGTTLTVSSAKTTAPS VYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSS GVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASS TKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVL MISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTH REDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIE RTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMP EDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEK KNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	278
SM1B255	HC	QVQLQQPGAELVKPGASVKLSCKASGYTFTRYWMHWVKQ RPGQGLEWIGEINPNNGHTNYNEKFESRATLTVDKSSSTAY MQFNSLTSEDSAVYYCGRLDGHLYAVDYWGQGTSVTVSSA KTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVA HPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPK IKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTA QTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKD LPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMV TDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSK LRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	279

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B256	HC	QVQLQQPGTELKMPGTSVKLSCKASGYTFTTYWMHWVKL RPGQGFEWIGEINPSNDGTNYNEKFKRKATLTVDKPSSTAY MQLSSLTSEDSTIYYCTISYYGYGDFDYWGQGTTLTVSSAK TTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNS GSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVA HPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPK IKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTA QTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKD LPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMV TDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSK LRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	280
SM1B257	HC	QVQLKESGPDLVQPSQTLSLTCTVSGFSLTSYGVHWVRQPP GKGLEWVGTMGWNDKKYYNSALKSRLSISRNTSKNQVFLK LSSLQTEDTAMYYCTRDGDSSGSWFAYWGQGTLVTVSSAK TTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNS GSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVA HPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPK IKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTA QTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKD LPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMV TDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSK LRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	281
SM1B258	HC	QVQLKESGPDLVQPSQTLSLTCTVSGFSLTGYAVHWVRQPP GKGVEWVGTMGWDDKKFYNSALKSRLSISRDPSKNQVFFK LSSLQTEDTAMYYCTRDHGDGGFAYWGQGTLVTVSSAKTT APSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	282
SM1B259	HC	EVQLQQSGPELVKPGASVKIPCKASGYTFTDYNMDWVKQS HGKSLEWIGNINPNNGGTIYNQNFKDRATLTVDKSSSTAYM ELRSLTSEDTAVYYCTRENSGYGGNYFAYWGQGTTLTVSS AKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTW NSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNV AHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPP KIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHT AQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNK DLPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCM VTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYS KLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	283

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B260	HC	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLIYWVKQRP EQGLEWIGWIDPEDGETKFAPRFQDKATITSDTSSNTAYLRL SSLTSEDTAIYYCTRSFGVCWGQGTLVTVSAAKTTAPSVYP LAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVH TFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKV DKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMIS LSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTI SKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDI YVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKN WVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	284
SM1B261	HC	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLIYWVKQRP EQGLEWIGWIDPEDGETKFAPRFQDKATITSDTSSNTAYLRL SSLTSEDTAIYYCTRSFGVCWGQGTLVTVSAAKTTAPSVYP LAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVH TFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKV DKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMIS LSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTI SKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDI YVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKN WVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	285
SM1B262	HC	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLIYWVKQRP EQGLEWIGWIDPEDGETKFAPRFQDKATITSDTSSNTAYLRL SSLTSEDTAIYYCTRSFGVCWGQGTLVTVSAAKTTAPSVYP LAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVH TFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKV DKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMIS LSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTI SKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDI YVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKN WVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	286
SM1B263	HC	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLIYWVKQRP EQGLEWIGWIDPEDGETKFAPRFQDKATITSDTSSNTAYLRL SSLTSEDTAIYYCTRSFGVCWGQGTLVTVSAAKTTAPSVYP LAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVH TFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKV DKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMIS LSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTI SKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDI YVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKN WVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	811

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B264	HC	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLIYWVKQRP EQGLEWIGWIDPEDGETKFAPRFQDKATITSDTSSNTAYLRL SSLTSEDTAIYYCTRSFGVCWGQGTLVTVSAAKTTAPSVYP LAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVH TFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKV DKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMIS LSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTI SKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDI YVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKN WVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	812
SM1B265	HC	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLIYWVKQRP EQGLEWIGWIDPEDGETKFAPRFQDKATITSDTSSNTAYLRL SSLTSEDTAIYYCTRSFGVCWGQGTLVTVSAAKTTAPSVYP LAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVH TFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKV DKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMIS LSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTI SKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDI YVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKN WVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	813
SM1B266	HC	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLIYWVKQRP EQGLEWIGWIDPEDGETKFAPRFQDKATITSDTSSNTAYLRL SSLTSEDTAIYYCTRSFGVCWGQGTLVTVSAAKTTAPSVYP LAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVH TFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKV DKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMIS LSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTI SKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDI YVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKN WVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	814
SM1B267	HC	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLIYWVKQRP EQGLEWIGWIDPEDGETKFAPRFQDKATITSDTSSNTAYLRL SSLTSEDTAIYYCTRSFGVCWGQGTLVTVSAAKTTAPSVYP LAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVH TFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKV DKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMIS LSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTI SKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDI YVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKN WVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	815

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B268	HC	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLIYWVKQRP EQGLEWIGWIDPEDGETKFAPRFQDKATITSDTSSNTAYLRL SSLTSEDTAIYYCTRSFGVCWGQGTLVTVSAAKTTAPSVYP LAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVH TFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKV DKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMIS LSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTI SKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDI YVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKN WVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	816
SM1B269	HC	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLIYWVKQRP EQGLEWIGWIDPEDGETKFAPRFQDKATITSDTSSNTAYLRL SSLTSEDTAIYYCTRSFGVCWGQGTLVTVSAAKTTAPSVYP LAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVH TFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKV DKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMIS LSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTI SKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDI YVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKN WVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	817
SM1B270	HC	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLIYWVKQRP EQGLEWIGWIDPEDGETKFAPRFQDKATITSDTSSNTAYLRL SSLTSEDTAIYYCTRSFGVCWGQGTLVTVSAAKTTAPSVYP LAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVH TFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKV DKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMIS LSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTI SKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDI YVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKN WVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	818
SM1B271	HC	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLIYWVKQRP EQGLEWIGWIDPEDGETKFAPRFQDKATITSDTSSNTAYLRL SSLTSEDTAIYYCTRSFGVCWGQGTLVTVSAAKTTAPSVYP LAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVH TFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKV DKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMIS LSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTI SKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDI YVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKN WVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	819

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B272	HC	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLIYWVKQRP EQGLEWIGWIDPEDGETKFAPRFQDKATITSDTSSNTAYLRL SSLTSEDTAIYYCTRSFGVCWGQGTLVTVSAAKTTAPSVYP LAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVH TFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKV DKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMIS LSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTI SKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDI YVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKN WVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	820
SM1B273	HC	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLIYWVKQRP EQGLEWIGWIDPEDGETKFAPRFQDKATITSDTSSNTAYLRL SSLTSEDTAIYYCTRSFGVCWGQGTLVTVSAAKTTAPSVYP LAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVH TFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKV DKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMIS LSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTI SKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDI YVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKN WVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	821
SM1B274	HC	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLIYWVKQRP EQGLEWIGWIDPEDGETKFAPRFQDKATITSDTSSNTAYLRL SSLTSEDTAIYYCTRSFGVCWGQGTLVTVSAAKTTAPSVYP LAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVH TFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKV DKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMIS LSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTI SKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDI YVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKN WVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	822
SM1B275	HC	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLIYWVKQRP EQGLEWIGWIDPEDGETKFAPRFQDKATITSDTSSNTAYLRL SSLTSEDTAIYYCTRSFGVCWGQGTLVTVSAAKTTAPSVYP LAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVH TFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKV DKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMIS LSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTI SKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDI YVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKN WVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	823

Table 20. LukE Light Chain (LC) and Heavy Chain (HC) Amino Acid Sequences

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B507	LC	DIVMTQSPAIMSASPGEKVTIPCSASSSVSYMHWFQQKPGTS PKLWIYSTSNLASGVPGRFSGSGSGTSYSLTISRMEAEDAAT YYCQQRSNYPLTFGAGTKLELKRADAAPTVSIFPPSSEQLTS GGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD SKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSF NRNEC	348
SM1B508	LC	DVVMTQTPLSLPVSLGDQASISCRSSQTIVHSNGNTYLEWYL QKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVE AEDLGVYYCFQGSHVPFTFGGGTKLEIRRADAAPTVSIFPPS SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	349
SM1B509	LC	DIVMTQAAAIMSASPGEKVTLTCSASSSVSSSYLYWYQQKP GSSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISSMEAEDA ASYFCHQWTTFPPTFGGGTKLEIKRADAAPTVSIFPPSSEQLT SGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQ DSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKS FNRNEC	350
SM1B510	LC	DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWY LQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVE AEDLGVYFCSQSTHVPPTFGGGTKLEIKRADAAPTVSIFPPSS EQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	351
SM1B511	LC	DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWY LQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVE AEDLGVYFCSQSTHVPLTFGAGTKLELKRADAAPTVSIFPPS SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	352
SM1B512	LC	DIKMTQSPLSLPVSLGDQASISCRSSQTIVHSNGNTYLEWYL QKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVE AEDLGVYYCFQGSHVPFTFGGGTKLEIRRADAAPTVSIFPPS SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	353
SM1B513	LC	DIVLTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTS PKLWIYSTSNLASGVPARFSGSGSGTSYSLTISRMEAEDAAT YYCQQRSSYPWTFGGGTKLEIKRADAAPTVSIFPPSSEQLTS GGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD SKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSF NRNEC	354
SM1B514	LC	DIVMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPG KSPKTLIYRANRLVDGVPSRFSGSGSGQDYSLTISSLEYEDM GIYYCLQYDEFPYTFGGGTKLEIKRADAAPTVSIFPPSSEQLT SGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQ DSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKS FNRNEC	355

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B208	LC	DIVMTQSPLSLPVSLGDQASISCRSSQDIVHSNGNTYLGWYL QKPGRSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEA EDLGVYYCFQSSHFPWTFGGGTRLEIKRADAAPTVSIFPPSS EQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	356
SM1B209	LC	DVVMTQTPLSLPVSLGDQASISCRSSQDIVHSNGNTYLGWY LQKPGRSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVE AEDLGVYYCFQSSHFPWTFGGGTRLEIKRADAAPTVSIFPPS SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	357
SM1B210	LC	DIVLTQSPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYL QKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVE AEDLGVYFCSQSTHVPFTFGSGTKLEIKRADAAPTVSIFPPSS EQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	358
SM1B211	LC	DIVLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQ QKPGQPPKLLIYRASNLESGIPARFSGSGSRTDFTLTINPVEA DDVATYYCQQSNEDPLTFGAGTKLELKRADAAPTVSIFPPSS EQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	359
SM1B507	HC	EVQLQQSGAELVKPGASVKMSCKASGYTFTDYYMDWVKQ SHGKSFEWIGHVNPYNGDTRYNQKFKGKATLTVDKSSTTA YMELNSLTSEDSAVYYCARGNFFDYWGQGTTLSVSSAKTT PPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGS LSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVAHPA SSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITL TPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQF NSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISK TKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVE WQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSNWEA GNTFTCSVLHEGLHNHHTEKSLSHSPGK	360
SM1B508	HC	EVQLQQSGAELVKPGASVKISCKTSGYSFTGYFMNWVMQS HGKSLEWIGRINPYNGDTFYNQKFKGKATLTVDKSSSTAHM ELRSLASEDSAVYYCARSYGYAMDYWGQGTSVTVSSAKTT PPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGS LSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVAHPA SSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITL TPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQF NSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISK TKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVE WQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSNWEA GNTFTCSVLHEGLHNHHTEKSLSHSPGK	361

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B509	HC	QVQLKESGPGLVAPSQSLSITCTVSGFSLTGYGVNWVRQPP GKGLEWLGLMWGDGSTDYNSALNSRLRINKDNSKSQVFLK MSSLQTDDTAIYYCVRKGGNSPYAMDYWGQGTSVTVSSAK TTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNS GSLSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVAH PASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTI TLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREE QFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTI SKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDIT VEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSNW EAGNTFTCSVLHEGLHNHHTEKSLSHSPGK	362
SM1B510	HC	QVQLKESGPGLVAPSQSLSITCTVSGFSLTGYGVNWVRQPP GKGLEWLGLMWGDGSTDYNSALNSRLRINKDNSKSQVFLK MSSLQTDDTAIYYCVRKGGNSPYAMDYWGQGTSVTVSSAK TTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNS GSLSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVAH PASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTI TLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREE QFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTI SKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDIT VEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSNW EAGNTFTCSVLHEGLHNHHTEKSLSHSPGK	363
SM1B511	HC	EVKLVESGPELVKPGASVKISCKTSGYSFTGYFMNWVMQS HGKSLEWIGRINPYNGDTFYNQKFKGKATLTVDKSSSTAHM ELRSLASEDSAVYYCARSYGYAMDYWGQGTSVTVSSAKTT PPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGS LSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVAHPA SSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITL TPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQF NSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISK TKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVE WQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSNWEA GNTFTCSVLHEGLHNHHTEKSLSHSPGK	364
SM1B512	HC	EVKLVESGPELVKPGASVKISCKTSGYSFTGYFMNWVMQS HGKSLEWIGRINPYNGDTFYNQKFKGKATLTVDKSSSTAHM ELRSLASEDSAVYYCARSYGYAMDYWGQGTSVTVSSAKTT PPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGS LSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVAHPA SSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITL TPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQF NSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISK TKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVE WQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSNWEA GNTFTCSVLHEGLHNHHTEKSLSHSPGK	365

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B513	HC	EVQLQQSGPELVKPGASVKISCKASGYSFTGYFMNWVMQS HGKSLEWIGRINPYNGDTFYNQKFKAKATLTVDKSSNTAH MELRSLASEDSAVYFCARSYGYAMDYWGLGTSVTVSSAKT TPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSG SLSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVAHP ASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTI TLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREE QFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTI SKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDIT VEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSNW EAGNTFTCSVLHEGLHNHHTEKSLSHSPGK	366
SM1B514	HC	EVQLQQSGPELVKTGASVKISCKASGYSFTGYYMHWVKQS HGKSLEWIGYLSCYSGATSYNQKFKGKATFTVDTSSTTAYM QFNSLTSEDSAVYYCARGESYYVMDYWGQGTSVTVSSAKT TPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSG SLSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVAHP ASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTI TLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREE QFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTI SKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDIT VEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSNW EAGNTFTCSVLHEGLHNHHTEKSLSHSPGK	367
SM1B208	HC	EVQLQQSGGGSVQPGGSRKLSCAASGFTFSSFGMHWVRQA PEKGLEWVAYISSGSSFIYYGDTVKGRFTISRDNPNNTLFLQ MTSLRSEDTAIYYCAREGIYFYDSRYFDVWGAGTTVTVSSA KTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVA HPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVL TITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPR EEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEK TISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDI TVEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSN WEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK	368
SM1B209	HC	EVQLQQSGGGSVQPGGSRKLSCAASGFTFSSFGMHWVRQA PEKGLEWVAYISSGSSFIYYGDTVKGRFTISRDNPNNTLFLQ MTSLRSEDTAIYYCAREGIYFYDSRYFDVWGAGTTVTVSSA KTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVA HPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVL TITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPR EEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEK TISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDI TVEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSN WEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK	369

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B210	HC	DVQLQESGPGHSMVTLGCLVGQSIQAEFQLQQSGPELVKTG ASVKISCKASGYSFTGYYMHWVKQSHGRSLEWIGYLSCYS GATSYNQKFKGKATFTVDTSSTTAYMQFNSLTSEDSAVYYC ARGESYYVMDYWGQGTSVTVSSAKTTPPSVYPLAPGSAAQ TNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLES DLYTLSSSVTVPSSPRPSETVTCNVAHPASSTKVDKKIVPRD CGCKPCICTVPEVSSVFIFPPKPKDVLTITLTPKVTCVVVDISK DDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIM HQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTI PPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENY KNTQPIMNTNGSYFVYSKLNVQKSNWEAGNTFTCSVLHEG LHNHHTEKSLSHSPGK	370
SM1B211	HC	EVQLQQSGPGLVKPSQTVSLTCTVTGYSITNGNHWWNWIR QVSGSKLEWIGYISSSGSTDSNPSLKSRISITRDTSKNQLFLQL NSVTTEDIATYYCARGHYYDGSSYAMDYWGQGTSVTVSSA KTTAPSVYPLAPVCGDTSDSMVTLGCLVKGYFPEPVTVTW NSGSLSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNV AHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDV LTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQP REEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIE KTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPE DITVEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKS NWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK	371

Table 21. LukD Light Chain (LC) and Heavy Chain (HC) Amino Acid Sequences

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B221	LC	QIVLTQSPAIMSASPGEKVTITCSASLSVSYMHWFQQKPGTS PKLWIYSASNLASGVPARFSGSGSGTSYSLTISRMEAEDAAT YYCQQRSSYPFTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSG GASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDS KDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFN RNEC	414
SM1B222	LC	DVVMTQTPLSLPVSLGDQASISCRSSQSLIHNDGNTYLHWY LQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTVKISRV EAEDLGVYFCSQSTHVPFTFGAGTKLELKRADAAPTVSIFPP SSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLN SWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTST SPIVKSFNRNEC	415
SM1B223	LC	QIVLSQSPAIMSASPGEKVTITCSASLSVSFMHWFQQKPGTSP KLWIYSASNLASGVPARFSGSGSGTSYSLTISRMEAEDAATY YCQQRSSYPFTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSGG ASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSK DSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNR NEC	416

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B224	LC	QIVLTQSPAIMSASPGEKVTITCSASSSVSFMHWFQQKPGTSP KLWIYSTSNLASGVPARFSGSGSGTSYSLTISRMEAEDAATY YCQQRSTYPYTFGGGTKMEIKRADAAPTVSIFPPSSEQLTSG GASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDS KDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFN RNEC	417
SM1B225	LC	DIVLTQSPAIMSASLGERVTMTCTASSSVSSSYLHWYQQKP GSSPKLWVYSTSNLASGVPARFSGSGSGSSYSLTISSMEPED TATYYCHQYHRSPQTFGGGTKLEIKRADAAPTVSIFPPSSEQ LTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWT DQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIV KSFNRNEC	418
SM1B226	LC	QIVLTQSPAIMSASPGEKVTITCSASSSVSFMHWFQQKPGTSP KLWIYSASNLASGVPARFSGSGSGTSYSLTISRMEAEDAATY YCQQRSSYPYTFGGGTKLEIKRADAAPTVSIFPPSSEQLTSGG ASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSK DSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNR NEC	419
SM1B227	LC	DIVLTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSST SPKLWIYDTSKLASGVPGRFSGSGSGNSYSLTISSMEAEDVA TYYCFQGSGYPLTFGSGTKLEIKRADAAPTVSIFPPSSEQLTS GGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD SKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSF NRNEC	420
SM1B228	LC	QIVLTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTS PKLWIYSASNLASGVPARFSGSGSGTSYSLTISRMEAEDAAT YYCQQRSSYPFTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSG GASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDS KDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFN RNEC	421
SM1B221	HC	QVQLQQSGAELVMPGASVKMSCKASGYTFTDYWMHWVK QRPGQGLEWIGAIDTSDSYTSYNQKFKGKATLTVDESSSTA YMQLSSLTSEDSAVYYCARDYGYAMDYWGQGTSVTVSSA KTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVA HPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVL TITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPR EEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEK TISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDI TVEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSN WEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK	422

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B222	HC	EVQLQQSGAMLARPGASVTMSCKASGYTFTDYWMHWVR QGPGQGLEWIGAIFPGNSDTTYNQKFRGKAKLTAVTSAITA YMEVSSLTNIDSAVYYCTVTELDYWGQGTTLTVSSAKTTPP SVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLS SGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVAHPASS TKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITLTP KVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNS TFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTK GRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQ WNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSNWEAGN TFTCSVLHEGLHNHHTEKSLSHSPGK	423
SM1B223	HC	EVQLQQSGADLVMPGTSMKLSCKASGYTFTDYWIHWVKQ GPGQGLEWIGAIDTSDSYINYNQKFTDKATLTVDESSSTAY MHLSSLTSEDSAVYYCARDYGYAMDYWGQGTSVTVSSAK TTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNS GSLSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVAH PASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTI TLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREE QFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTI SKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDIT VEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSNW EAGNTFTCSVLHEGLHNHHTEKSLSHSPGK	424
SM1B224	HC	QVQLQQPGAELVMPGSSVKMSCKASGYTFTDYWMHWVK QRPGQGLEWIGAIDASDSYTSYDQKFKGKATLTVDDSSSTA YIHLNSLTSEDSAVYYCARDFGYAMDYWGQGTSVTVSSAK TTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNS GSLSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVAH PASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTI TLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREE QFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTI SKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDIT VEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSNW EAGNTFTCSVLHEGLHNHHTEKSLSHSPGK	425
SM1B225	HC	EVQLQQSGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQT PEKRLEWVATITGGGTYTYYLDSVKGRFTISRDNAKTSLYL QMSSLRSEDTAMYYCARHRDGNYGCFDVWGAGTTVTVSS AKTTPPSVYPLAPGSAAQTNPMVTLGCLVKGYFPEPVTVTW NSGSLSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNV AHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDV LTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQP REEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIE KTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPE DITVEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKS NWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK	426

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B226	HC	EVQLQQSGAELVMPGASVKMSCKASGYTFTDYWMHWVL QRPGQGLEWIGAIDTSDSYTTYNQKFKGKATLTVDESSSTA YMLLSSLTSEDSAVYYCARDYGYAMDYWGQGSSVTVSSA KTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVA HPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVL TITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPR EEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEK TISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDI TVEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSN WEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK	427
SM1B227	HC	EFQLQQSGPELVKPGASVKMSCKASGYTFTSYFIHWVKQKP GQGLEWIGFINPYNADTNYNEKFKGKATLTSDKSSSTAYME LSSLTSEDSAVYYCTPSAMDYWGQGTSVTVSSAKTTPPSVY PLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGV HTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITLTPKVT CVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFR SVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRP KAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWN GQPAENYKNTQPIMNTNGSYFVYSKLNVQKSNWEAGNTFT CSVLHEGLHNHHTEKSLSHSPGK	428
SM1B228	HC	QVQLQQSGAELVMPGASVKMSCKASGYTFTDYWMHWVK QRPGQGLEWIGAIDTSDSYTTYNQKFKGKATLTVDESSSTA YMQLSSLTSEDSAVYYCARDYGYAMDYWGQGTSVTVSSA KTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVA HPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVL TITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPR EEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEK TISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDI TVEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSN WEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK	429

Table 22. HlgA Light Chain (LC) and Heavy Chain (HC) Amino Acid Sequences

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B215	LC	DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLL QRPGQSPKRLIYVVSKLDSGVPDRFTGSGSGTDFTLKISRVE AEDLGVYYCWQGTHFPLTFGAGTKLELKRADAAPTVSIFPP SSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLN SWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTST SPIVKSFNRNEC	458
SM1B216	LC	DVVMTQTPSSFSVSLGDGVTITCKASEDIYIRLAWYQQKPG NAPRLLIFGATSLETGVPSRFSGSGSGKDYTLSITSLQTEDVA TYYCQQYWRTPLTFGAGTKLELKRADAAPTVSIFPPSSEQLT	459

mAb/Fab name	Region	Sequence	SEQ ID NO:
		SGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQ DSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKS FNRNEC	
SM1B217	LC	DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLL QRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVE AEDLGVYYCWQGTHFPLTFGAGTKLELKRADAAPTVSIFPP SSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLN SWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTST SPIVKSFNRNEC	460
SM1B218	LC	DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLL QRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVE AEDLGVYYCWQGTHFPLTFGAGTKLELKRADAAPTVSIFPP SSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLN SWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTST SPIVKSFNRNEC	461
SM1B219	LC	DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLL QRPGQSPKRLIYVVSKLDSGVPDRFTGSGSGTDFTLKISRVE AEDLGVYYCWQGTHFPLTFGAGTKLELKRADAAPTVSIFPP SSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLN SWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTST SPIVKSFNRNEC	462
SM1B220	LC	DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLL QRPGQSPKRLIYVVSKLDSGVPDRFTGSGSGTDFTLKISRVE AEDLGVYYCWQGTHFPLTFGAGTKLELKRADAAPTVSIFPP SSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLN SWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTST SPIVKSFNRNEC	463
SM1B215	HC	EVQLQQSGPELKKPGETVKISCKTSGYTFTIYGMNWMKQAP GKGLKWMGWINTYTGEPTYADDFKGRFAFSLETSASTAYL QINNLKNEDTATYFCARCYYKYEDYAMDYWGQGTSVTVS SAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVT WNSGSLSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTC NVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPK DVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQT QPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPA PIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFF PEDITVEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQ KSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK	464
SM1B216	HC	EVKLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTP EKRLEWVAAINGNGGSTYYPDTVKDRFTISRDNAKNTLYLQ MSSLRSEDTALYYCARHRADGPWFTYWGQGTLVTVSAAK TTPPSVYPLAPGSAAQTNPMVTLGCLVKGYFPEPVTVTWNS GSLSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVAH PASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTI TLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREE QFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTI SKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDIT VEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSNW EAGNTFTCSVLHEGLHNHHTEKSLSHSPGK	465

mAb/Fab name	Region	Sequence	SEQ ID NO:
SM1B217	HC	EVKLVESGGGLVKPGGSLKLSCAASGFTFSNYAMSWVRQT PEKRLEWVASISRRGSTYYPDSVKGRFTISRDNARNILYLQM SSLRSEDTALYYCATVYYDNPWFVYWGQGTLVTVSAAKTT PPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGS LSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVAHPA SSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITL TPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQF NSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISK TKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVE WQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSNWEA GNTFTCSVLHEGLHNHHTEKSLSHSPGK	466
SM1B218	HC	QIQLVQSGPELKKPGETVKISCKTSGYTFTIYGMNWTKQAP GKGLKWMGWINTYTGEPTYADDFKGRFAFSLETSASTAYL QINNLKNEDTATYFCARCYYKYEDYAMDYWGQGTSVTVS SAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVT WNSGSLSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTC NVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPK DVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQT QPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPA PIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFF PEDITVEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQ KSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK	467
SM1B219	HC	DVKLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQT PEKRLEWVAAINGNGGSTYYPDTVKDRFTISRDNAKNTLYL QMSSLRSEDTALYYCARHRADGPWFTYWGQGTLVTVSAA KTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVA HPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVL TITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPR EEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEK TISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDI TVEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSN WEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK	468
SM1B220	HC	EVKLVESGGGLVKPGGSLKLSCAASGFTFSNYAMSWVRQT PEKRLEWVASISRRGSTYYPDSVKGRFTISRDNARNILYLQM SSLRSEDTALYYCATVYYDNPWFVYWGQGTLVTVSAAKTT PPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGS LSSGVHTFPAVLESDLYTLSSSVTVPSSPRPSETVTCNVAHPA SSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITL TPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQF NSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISK TKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVE WQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSNWEA GNTFTCSVLHEGLHNHHTEKSLSHSPGK	469

Table 23. HlgC Light Chain (LC) and Heavy Chain (HC) Amino Acid Sequences

mAb/Fab name	Region	sequence	SEQ ID NO:
SM1B202	LC	ETTVTQSPASLSVATGEKVTIRCITSTDIDDDMSWYQQKPGE PPKLLISEGNTLRPGVPSRFSSSGCGTDFVFTIENTLSEDVAD YYCLQSDNMPYTFGGGTKLEIKRADAAPTVSIFPPSSEQLTS GGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD SKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSF NRNEC	500
SM1B203	LC	DIVMTQSPATLSVTPGDRVSLSCRASQSISDYLHWYQQKSH ESPRLLIKYDSQSISGIPSRFSGSGSGSDFTLSINSVEPEDVGV YYCQNGHRFPFTFGGGTKLEIKRADAAPTVSIFPPSSEQLTSG GASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDS KDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFN RNEC	501
SM1B204	LC	NIMMTQSPSSLTVSAGEKVTMSCKSSQSVLYSSNQKNYLA WYQQKPGQSPKLLIYWASTRESGVPDRFAGSGSGTDFTLSIS SVQAEDLAVYYCHQYLSSYTFGGGTKLEIKRADAAPTVSIFP PSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVL NSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTS TSPIVKSFNRNEC	502
SM1B205	LC	DIVLTQSPASLAVSLGQRATISYRASKSVSTSGYSYMHWNQ QKPGQPPRLLIYLVSNLESGVPARFSGSGSGTDFTLNIHPVEE EDAATYYCQHIRELTRSEGGTKLEIKRADAAPTVSIFPPSSEQ LTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWT DQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIV KSFNRNEC	503
SM1B206	LC	DIVMTQSPATLSVTPGDRVSLSCRASQSISDYLHWYQQKSH ESPRLLIKYASQSISGIPSRFSGSGSGSDFTLSINSVEPEDVGV YYCQNGHSFPLTFGAGTKLELKRADAAPTVSIFPPSSEQLTS GGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD SKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSF NRNEC	504
SM1B207	LC	DIVLTQSPASLAVSLGQRATISCQASESVSFAGTSLMHWYQ QKPGQSPKLLIYWASTRESGVPDRFAGSGSGTDFTLSISSVQ AEDLAVYYCHQYLSSYTFGGGTKLEIKRADAAPTVSIFPPSS EQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	505
SM1B202	HC	EVMLVESGGGLVKPGGSLKLSCAASGFTFSNYAMSWVRQT PEKRLEWVASISRRGSTYYPDSGKGRFTISRDNARNIPYLQM SSLRSEDTALYYCATVYYDNPWFVYWGQGTLVTVSAAKTT APSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	506

mAb/Fab name	Region	sequence	SEQ ID NO:
SM1B203	HC	EVMLVESGGGLVKPGGSLKLSCAASGFTFSNYAMSWVRQT PEKRLEWVASISRRGSTYYPDSVKGRFTISRDNARNILYLQM SSLRSEDTALYYCATVYYDNPWFVYWGQGTLVTVSAAKTT APSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	507
SM1B204	HC	EVKLVESGGGLVKPGGSLKLSCAASGFTFSNYAMSWVRQT PEKRLEWVASISRRGSTYYPDSVKGRFTISRDNARNILYLQM SSLRSEDTALYYCATVYYDNPWFVYWGQGTLVTVSAAKTT APSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	508
SM1B205	HC	EVKLVESGGGLVKPGGSLKLSCAASGFTFSNYAMSWVRQT PEKRLEWVASISRRGSTYYPDSVKGRFTISRDNARNILYLQM SSLRSEDTALYYCATVYYDNPWFVYWGQGTLVTVSAAKTT APSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	509
SM1B206	HC	EVKLVESGGGLVKPGGSLKLSCAASGFTFSNYAMSWVRQT PEKRLEWVASISRRGSTYYPDSVKGRFTISRDNARNILYLQM SSLRSEDTALYYCATVYYDNPWFVYWGQGTLVTVSAAKTT APSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	510

mAb/Fab name	Region	sequence	SEQ ID NO:
SM1B207	HC	EVMLVESGGGLVKPGGSLKLSCAASGFTFSNYAMSWVRQT PEKRLEWVASISRRGSTYYPDSVKGRFTISRDNARNILYLQM SSLRSEDTALYYCATVYYDNPWFVYWGQGTLVTVSAAKTT APSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	511

Table 24. LukE/HlgA Light Chain (LC) and Heavy Chain (HC) Amino Acid Sequences

mAb/Fab name	region	sequence	SEQ ID NO:
SM1B302	LC	DIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEPDG TIKRLIYATSSLDSGVPKRFSGSRSGSDYSLTISSLESEDFVDY YCLQYASSPWTFGGGTKLEIKRADAAPTVSIFPPSSEQLTSG GASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDS KDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFN RNEC	733
SM1B303	LC	DIQMTQTTSSLSASLGDRVTISCWASQDIRSYLNWYQQKPD GTVKLLIYYTSRLHSGVPSRFSGSGSGTDFSLTISNLEQEDIA TYFCQQGNTLPYTFGGGTKLEIKRADAAPTVSIFPPSSEQLTS GGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD SKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSF NRNEC	734
SM1B304	LC	DIQMTQSPSSLSASLGERVSLTCRASQEISGYLSWLQQKPDG TIKRLIYAASTLDSGVPKRFSGSRSGSDYSLTISSLESEDFAD YYCLQYASYPRTFGGGTKLEIKRADAAPTVSIFPPSSEQLTS GGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD SKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSF NRNEC	735
SM1B305	LC	DVLMTQTPLSLPVSLGDQASISCRSSQIIVHSNGNTYLDWYL QKPGQSPKLLIYKISNRFSGVPDRFSGSGSGTDFTLKISRVEA EDLGVYYCFQGSHVPWTFGGGTKLEIKRADAAPTVSIFPPSS EQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	736
SM1B306	LC	DVVVTQTPLSLPVSFGDQVSISCRSSQSLANSYGNTYLSWYL HKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPE GLGMYYCLQGTHQPPTFGAGTKLELKRADAAPTVSIFPPSSE QLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSW TDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPI VKSFNRNEC	737

mAb/Fab name	region	sequence	SEQ ID NO:
SM1B307	LC	DIVLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQ QKPGQPPKLLIYRASNLESGIPARFSGSGSRTDFTLTINPVEA DDVATYYCQQSNEDPPWTFGGGTKLEIKRADAAPTVSIFPPS SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	738
SM1B308	LC	DIVMSQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAW YQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISS VQAEDLAVYYCKQSYNLWTFGGGTKLEIKRADAAPTVSIFP PSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVL NSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTS TSPIVKSFNRNEC	739
SM1B309	LC	DVVMTQTPLSLPVSLGDQASISCRSSQSLLHSNGKTYLHWY LQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVE AEDLGVYFCSQSTHVPLTFGAGTKLELKRADAAPTVSIFPPS SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	740
SM1B310	LC	DIVMTQSHKFMSTSVGDRVSITCKASQDVSAAVAWYQQKP GQSPKLLIYWASTRHTGVPDRFTGSGSGTDYTLTISSVQAED LALYYCQQHYSTPGTFGGGTKLEIKRADAAPTVSIFPPSSEQ LTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWT DQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIV KSFNRNEC	741
SM1B311	LC	DVLMTQTPLSLPVSLGDQASISCRSSQTIVHSSGNTYLEWYL QRPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEA EDLGVYYCFQGSHVPYTFGGGTKLEIKRADAAPTVSIFPPSS EQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	742
SM1B312	LC	DIQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDG TVKLLIYYTSSLHSGVPSRFSGSGSGTDYSLTISNLEPEDIATY YCQQYSKLPFTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSGG ASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSK DSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNR NEC	743
SM1B313	LC	DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKNYLAW YQQKPGQSPKLLIYWASTRESGVPDRLTGSGSGTDFTLTISS VKAEDLAVYYCQQYYSYPYTFGGGTKLEIKRADAAPTVSIF PPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGV LNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKT STSPIVKSFNRNEC	744
SM1B314	LC	DIQMTQSPASLSVSVGETVTITCRASENIYSNLAWYQQKQG KSPQLLVYAATNLADGVPSRFSGSGSGTQYSLKINSLQSEDF GSYYCQHFWGTPYTFGGGTKLEIKRADAAPTVSIFPPSSEQL TSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTD QDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVK SFNRNEC	745

mAb/Fab name	region	sequence	SEQ ID NO:
SM1B315	LC	DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPG KSPKTLIYRANRLVDGVPSRFSGSGSGQDYSLTISSLEYEDM GIYYCLQYDEFPYTFGGGTKLEIKRADAAPTVSIFPPSSEQLT SGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQ DSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKS FNRNEC	746
SM1B316	LC	DIQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDG TVKLLIHYTSSLHSGVPSRFSGSGSGTDYSLTISNLEPEDIATY YCQQYSKLPWTFGGGTKLEIKRADAAPTVSIFPPSSEQLTSG GASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDS KDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFN RNEC	747
SM1B317	LC	DVLMTQTPLSLPVSLGDQASISCRSSQTIVYSDGNTYLEWYL QKPGQSPKLLIYKVSNRFSGVPDRVSGSGSGTDFTLKISRVE AEDLGVYYCFQGSHVPYTFGGGTKLEIKRADAAPTVSIFPPS SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	748
SM1B318	LC	DVLMTQTPLSLPVSLGDQASISCRSSQTIVYSDGNTYLEWYL QKPGQSPKLLIYKVSNRFSGVPDRVSGSGSGTDFTLKISRVE AEDLGVYYCFQGSHVPYTFGGGTKLEIKRADAAPTVSIFPPS SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	749
SM1B319	LC	DIVMTQAAPSVPVTPGESVSISCRSSKSLLHSNGNTYLYWFL QRPGQSPQLLIYRMSNLASGVPDRFSGSGSGTAFTLRISRVE AEDVGVYYCMQHLEYPFTFGSGTKLEIKRADAAPTVSIFPPS SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	750
SM1B320	LC	DIQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDG TVKLLIYYTSSLHSGVPSRFSGSGSGTDYSLTISNLEPEDIATY YCQQYSKLPYTFGGGTKLEIKRADAAPTVSIFPPSSEQLTSG GASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDS KDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFN RNEC	751
SM1B321	LC	DIQMTQSPASLSASVGETVTIICRASENIYSYLAWYQQKQGK SPQLLVYNAKTLVEGVPSRFSGSGSGTQFSLKINSLQPEDFG SYYCQHHYGSPYTFGGGTKLEIKRADAAPTVSIFPPSSEQLT SGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQ DSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKS FNRNEC	752
SM1B322	LC	DIVMTQSHKFMSTSVGDRVSITCKASQDVSTAVAWYQQKP GQSPKLLIYSASYRYTGVPDRFTGSGSGTDFTFTISSVQAEDL AVYYCQQHYSTPWTFGGGTKLEIKRADAAPTVSIFPPSSEQL TSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTD QDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVK SFNRNEC	753

mAb/Fab name	region	sequence	SEQ ID NO:
SM1B323	LC	ETTVTQSPASLSMAIGEKVTIRCITSTDIDDDMNWYQQKPGE PPKLLISEGNTLRPGVPSRFSSSGYGTDFVFTIENMLSEDVAD YYCLQSDNLPYTFGGGTKLEIKRADAAPTVSIFPPSSEQLTSG GASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDS KDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFN RNEC	754
SM1B324	LC	DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSGNQKNYLAW YQQKPGQPPKLLIYGASTRESGVPDRFTGSGSGTDFTLTISSV QAEDLAVYYCQNDHSYPPTFGGGTKLEIKRADAAPTVSIFPP SSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLN SWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTST SPIVKSFNRNEC	755
SM1B325	LC	DIQMTQSPSSLSASLGERVSLTCRASQDIGNSLNWLQQKPDG TIKRLIYATSNLDSGVPKRFSGSRSGSDYSLTISSLESEDFVN YYCLQFASSPLTFGTGTKLEIKRADAAPTVSIFPPSSEQLTSG GASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDS KDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFN RNEC	756
SM1B326	LC	DIQMTQSPASLSVSVGETVTITCRASENIYSNLAWYQQKQG KSPQLLVYAATNLADGVPSRFSGSGSGTQYSLKINSLQSEDF GSYYCQHFWGTPYTFGGGTKLEIKRADAAPTVSIFPPSSEQL TSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTD QDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVK SFNRNEC	757
SM1B327	LC	QIVLTQSPAIMSASPGEKVTMTCSASSNVSYMHWFQQKSGT SPKRWIYDTSKLASGVPARFSGSGSGTSYSLTVSSMEAEDA ATYYCQQWSSNPRTFGGGTKLEIKRADAAPTVSIFPPSSEQL TSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTD QDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVK SFNRNEC	758
SM1B328	LC	DIQMTQSPSSLSASLGERVSLTCRASQDIGSYLNWLQQEPDG TIKRLIYATSSLDSGVPKRFSGSRSGADYSLTISSLESEDFVD YYCLQYATSPWTFGGGTKLEIKRADAAPTVSIFPPSSEQLTS GGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD SKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSF NRNEC	759
SM1B329	LC	DIQMTQSSSYLSVSLGGRVTITCKASDHINNWLAWYQQKPG NAPRLLISGATSLETGVPSRFSGSGSGKDYTLSITSLQTEDVA TYYCQQYWSTPYTFGGGTKLEIKRADAAPTVSIFPPSSEQLT SGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQ DSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKS FNRNEC	760
SM1B330	LC	QIVLTQSPALMSASPGEKVTMTCSASSSVSYMYWYQQKPRS SPKLKYASNLASGVPARFSGSGSGTSYSLTISSMEAEDAATY YCQQWSSNPPITFGAGTKLELKRADAAPTVSIFPPSSEQLTSG GASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDS KDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFN RNEC	761

mAb/Fab name	region	sequence	SEQ ID NO:
SM1B331	LC	DIVMTQSPATLSVTPGDRVSLSCRASQSISDYLHWYQQKSH ESPRLLIKYDSQSISGIPSRFSGSGSGSDFTLSINSVEPEDVGV YYCQNGHRFPFTFGGGTKLEIKRADAAPTVSIFPPSSEQLTSG GASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDS KDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFN RNEC	762
SM1B332	LC	QIVLTQSPAIMSASPGEKVTLTCSASSSVSSSYLFWYQQKPG SSPKLWIYSTSNLASGVPVRFSGSGFGTSYSLTISRMEAEDA ASYFCHQWSSYPPTFGAGTKLELKRADAAPTVSIFPPSSEQL TSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTD QDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVK SFNRNEC	763
SM1B333	LC	DIVLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQ QKPGQPPKLLIYLASNLESGVPARFSGSGSRTDFTLTIDPVEA DDAATYYCQQNNEDPYTFGGGTKLEIKRADAAPTVSIFPPSS EQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	764
SM1B334	LC	DVLMTQTPLSLPVSLGDQASISCRSSQSIVYSNGNTYLDWYL QKPGQPPKLLIYKVSNRFSGVPDRFSGSGSGTDFILKISRVEA EDLGVYYCFQGSHVPWTFGGGTKLEIKRADAAPTVSIFPPSS EQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	765
SM1B335	LC	DVVVTQTPLSLPVSFGDQVSISCRSSQSLANSYGNTYLSWYL HKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPE DLGMYYCLQGTHQPYTFGGGTKLEIKRADAAPTVSIFPPSSE QLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSW TDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPI VKSFNRNEC	766
SM1B336	LC	DIVMSQSPSSLAVSVGEKVTMSCKSSQSVLYNSNQRNYLA WYQQKPGQSPKLLIYWASTRESGVPDRSTGSGSGTDFTLTIS SVQAEDLAVYYCHQYLSSYTFGGGTKLEIKRADAAPTVSIFP PSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVL NSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTS TSPIVKSFNRNEC	767
SM1B337	LC	DIVMTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKP GQSPKLLIYWASTRHTGVPDRFTGSGSGTDFTLTISNVQSED LADYFCQQYSSYPLTFGAGTKLELKRADAAPTVSIFPPSSEQ LTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWT DQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIV KSFNRNEC	768
SM1B338	LC	DIVLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQ QKPGQPPKLLIYRASNLESGIPARFSGSGSRTDFTLTINPVEA DDVATYYCQQSNEDPPWTFGGGTKLEIKRADAAPTVSIFPPS SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	769

mAb/Fab name	region	sequence	SEQ ID NO:
SM1B339	LC	DIVLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQ QKPGQPPKLLIYRASNLESGIPARFSGSGSRTDFTLTINPVEA DDVATYYCQQSNEDPPWTFGGGTKLEIKRADAAPTVSIFPPS SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSFNRNEC	770
SM1B340	LC	DIQMTQTTSSLSASLGDRVTISCRASQDIDNYLNWYQQKPD GTVKLLISYTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDFA TYFCQQGYTLPWTFGGGTKLEIKRADAAPTVSIFPPSSEQLT SGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQ DSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKS FNRNEC	771
SM1B302	HC	EVKLVESGGDLVKPGGSLKLSCAASGFTFSSFAMSWVRQTP EKRLEWVASISRTDNTYYPDSMKGQFTISRDNARNILYLQM SSLRSENTAIYYCARADYDGPWFAYWGQGTLVTVSAAKTT APSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	772
SM1B303	HC	EVQLQQSGPDLVKPGTSVKMSCKASGYSFTGYYMHWVKQ SHGKSLEWIGRVNPNNGGTSYNQKFKGKAILTVDKSSSTAY MELRSLTSEDSAVYYCARDDYSFAYWGQGTLVTVSAAKTT APSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	773
SM1B304	HC	EVKLVESGGGLVQPGGSLRLSCATSGFTFTDFYMSWVRQPP GKALEWLAFIRNKANGYTTEYSSSVRGRFTISRDNSQSILYL QMNTLRAEDSGTYYCARDVGDYDYWGQGSTLTVSSAKTT APSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	774

mAb/Fab name	region	sequence	SEQ ID NO:
SM1B305	HC	QIQLVQSGPELKKPGETVKISCKASGFTFTNYGMNWVKQAP GKDLKWMGWINTYTGEPTYADDFKGRFAFSLETSASTAYL QINNLKDEDTASYFCARDYRDGDALDYWGQGTSVTVSSAK TTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNS GSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVA HPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPK IKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTA QTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKD LPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMV TDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSK LRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	775
SM1B306	HC	QVQLQQPGAELVRPGASVKLSCKASGYSFTSNWMNWMKQ RPGQGLEWIGMIHPSDSESRLNQKFKDKATLTVDKSSSTAY MQLSSPTSEDSAVYYCARGDGGFAYWGQGTLVTVSAAKTT APSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	776
SM1B307	HC	EVKLQQSGPELVKPGASMKISCKASGYSFTGYTMNWAKQS HGKNLEWIGLINPYNGGTSYNQKFKGKATLTVDKSSSTAY MELLSLTSEDSAVYYCARGYPRGWFAYWGQGTLVTVSAA KTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVA HPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPK IKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTA QTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKD LPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMV TDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSK LRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	777
SM1B308	HC	DVKLVESGGGLVKPGGSLKLSCAASGFTFRNHAMSWVRQT PEKRLEWVAAINVNAGSTYYPDTVKDRFTISRDNAKNTLYL QMSSLRSEDTALYYCARHRAYYNYDENAMDYWGQGTSVT VSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTL TWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSIT CNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSV FIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVE VHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKV NNKDLPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTL TCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYF MYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTP GK	778

mAb/Fab name	region	sequence	SEQ ID NO:
SM1B309	HC	EVQLQQSGPELVKPGDSVKMSCKASGYTFTDYYIDWMKQS HGKSLEWIGYIYPNNGGTSYNQNFKDKATLTVDKSSSTAY MELHSLTSEDSAVYYCARLTYYAKVDSWGQGTSVTVSSAK TTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNS GSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVA HPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPK IKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTA QTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKD LPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMV TDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSK LRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	779
SM1B310	HC	DVKLVESGGGLVEWEGVLKLSCAASGFTFSSYAMSWVRQT PEKRLEWVAAINSNGGSTYYPDTVKDRFTISRDNAKNTLYL QMSSLRSEDTALYYCARLYYGDYWGQGTTLTVSSAKTTAP SVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSS GVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASS TKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVL MISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTH REDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIE RTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMP EDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEK KNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	780
SM1B311	HC	QVQLKQSGPSLVQPSQSLSITCTVSGFSLTTYGLHWIRQSPG KGLEWLGVIWRGGTTDYNAAFMSRLTITKDNSKSQVFFKM NSLQADDTAIYYCARTDIWGAGTTVTVSSAKTTAPSVYPLA PVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFP AVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKK IEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPI VTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNS TLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKP KGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVE WTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVE RNSYSCSVVHEGLHNHHTTKSFSRTPGK	781
SM1B312	HC	QVQLKQSGPSLVQPSQSLSITCTVSGFSLTTYGLHWIRQSPG KGLEWLGVIWRGGTTDYNAAFMSRLTITKDNSKSQVFFKM NSLQADDTAIYYCARTDIWGAGTTVTVSSAKTTAPSVYPLA PVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFP AVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKK IEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPI VTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNS TLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKP KGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVE WTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVE RNSYSCSVVHEGLHNHHTTKSFSRTPGK	782

mAb/Fab name	region	sequence	SEQ ID NO:
SM1B313	HC	QVQLKQSGPSLVQPSQSLSITCTVSGFSLTTYGLHWIRQSPG KGLEWLGVIWRGGTTDYNAAFMSRLTITKDNSKSQVFFKM NSLQADDTAIYYCARTDIWGAGTTVTVSSAKTTAPSVYPLA PVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFP AVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKK IEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPI VTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNS TLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKP KGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVE WTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVE RNSYSCSVVHEGLHNHHTTKSFSRTPGK	783
SM1B314	HC	QVQLKQSGPGLVQPSQSLPITCTVSGFSLTTYGLHWIRQSPG KGLEWLGVIWRGGTTDYNAAFMSRLTITKDNSKSQVFFKM NSLQADDTAIYYCARTDIWGAGTTVTVSSAKTTAPSVYPLA PVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFP AVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKK IEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPI VTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNS TLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKP KGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVE WTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVE RNSYSCSVVHEGLHNHHTTKSFSRTPGK	784
SM1B315	HC	QVQLKQSGPGLVQPSQSLSITCTVSGFSLTTYGLHWIRQSPG KGLEWLGVIWRGGTTDYNAAFMSRLTITKDNSKSQVFFKM NSLQADDTAIYYCARTDIWGAGTTVTVSSAKTTAPSVYPLA PVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFP AVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKK IEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPI VTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNS TLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKP KGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVE WTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVE RNSYSCSVVHEGLHNHHTTKSFSRTPGK	785
SM1B316	HC	QVQLKQSGPSLVQPSQSLSITCTVSGFSLTTYGLHWIRQSPG KGLEWLGVIWRGGTTDYNAAFMSRLTITKDNSKSQVFFKM NSLQADDTAIYYCARTDIWGAGTTVTVSSAKTTAPSVYPLA PVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFP AVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKK IEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPI VTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNS TLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKP KGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVE WTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVE RNSYSCSVVHEGLHNHHTTKSFSRTPGK	786

mAb/Fab name	region	sequence	SEQ ID NO:
SM1B317	HC	QVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQPP GKGLEWLGVIWSGGITDYNAAFISRLSISKDNSKSQVFFKM NSLQADDTAIYYCARTDLWGQGTLVTVSAAKTTAPSVYPL APVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHT FPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVD KKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISL SPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDY NSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTIS KPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIY VEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNW VERNSYSCSVVHEGLHNHHTTKSFSRTPGK	787
SM1B318	HC	QVQLQQSGAELMNPGASVKISCKSTGYKFSSYWIEWVKQR PGHGLEWMGEILPGSGSTNHNEKFKGKAIFTADASSNTAYM ELSSLTSEDSAVYYCARTISTATDWFAYWGQGTLVTVSAAK TTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNS GSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVA HPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPK IKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTA QTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKD LPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMV TDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSK LRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	788
SM1B319	HC	QVQLQQSGAELMNPGASVKISCKSTGYKFSSYWIEWVKQR PGHGLEWMGEILPGSGSTNHNEKFKGKAIFTADASSNTAYM ELSSLTSEDSAVYYCARTISTATDWFAYWGQGTLVTVSAAK TTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNS GSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVA HPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPK IKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTA QTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKD LPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMV TDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSK LRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	789
SM1B320	HC	QVQLQQSGAELMKPGASVKMSCKATGYKFSSYWIEWVKQ RPGHGLEWMGEILPGSGSTNHNEKFKGKAIFTADASSNTAY MELSSLTSEDSAVYYCARTISTATDWFAYWGQGTLVTVSA AKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTW NSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNV AHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPP KIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHT AQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNK DLPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCM VTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYS KLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	790

mAb/Fab name	region	sequence	SEQ ID NO:
SM1B321	HC	QVQLQQSGAELMKPGASVKMSCKATGYKFSSYWIEWVKQ RPGHGLEWMGEILPGSGSTNHNEKFTGRAIFTADASSNTAY MELSSLTSEDSAVYYCARTISTATDWFAYWGQGTLVTVSA AKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTW NSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNV AHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPP KIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHT AQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNK DLPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCM VTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYS KLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	791
SM1B322	HC	QVQLQQSGAELMKPGASVKMSCKATGYKFSSYWIEWVKQ RPGHGLEWMGEILPGSGSTNHNEKFKGKAIFTADASSNTAY MELSSLTSEDSAVYYCARTISTATDWFAYWGQGTLVTVSA AKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTW NSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNV AHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPP KIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHT AQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNK DLPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCM VTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYS KLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	792
SM1B323	HC	QVQLQQSGAELMKPGASVKMPCKATGYKFSSYWIEWVKQ RPGHGLEWMGEILPGSGSTNHNEKFKGKAIFTADASSNTAY MELSSLTSEDSAVYYCARTISTATDWFAYWGQGTLVTVSA AKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTW NSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNV AHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPP KIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHT AQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNK DLPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCM VTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYS KLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	793
SM1B324	HC	EVQLQQSGAELVRPGALVKLSCKASGFNIKDYYMHWVKQR PEQGLEWIGWIDPENGNTIYDPKFQGKASITADTSSNTAYLQ LSSLTSEDTAVYYCARYDGYAMDYWGQGTSVTVSSAKTTA PSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLS SGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPAS STKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDV LMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQT HREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPI ERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFM PEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVE KKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	794

mAb/Fab name	region	sequence	SEQ ID NO:
SM1B325	HC	QVQLQQSGAELVRPGTSVKMSCKAAGYTFTNYWIGWVKQ RPGHGLEWIGDIYPGGGYTNYNEKFKDKTTLTADTSSNTAY MQLSSLTSEDSAIYYCASNDCWGQGTTLTVSSAKTTAPSVY PLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGV HTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTK VDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMI SLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRE DYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERT ISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPED IYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKN WVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	795
SM1B326	HC	QVQLKQSGPGLVQPSQSLSITCTVSGFSITSYGVHWIRQSPG KGLEWLGVIWSGGSTDYNAAFISRLSISEDNSKSQVFFKMNS LQANDTAIYYCATFYYDYDEGFDYWGQGTTLTVSSAKTTA PSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLS SGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPAS STKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDV LMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQT HREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPI ERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFM PEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVE KKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	796
SM1B327	HC	QVQLKQSGPGLVQPSQSLSITCTVSGFSITSYGVHWIRQSPG KGLEWLGVIWSGGSTDYNAAFISRLSISKDNSKSQVFFKMN SLQANDTAIYYCATFYYDYDEGFDYWGQGTTLTVSSAKTT APSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	797
SM1B328	HC	QVQLKQSGPGLVQPSQSLSITCTVSGFSITSYGVHWIRQSPG KGLEWLGVIWSGGSTDYNAAFISRLSISKDNSKSQVFFKMN SLQANDTAIYYCATFYYDYDEGFDYWGQGTTLTVSSAKTT APSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	798

mAb/Fab name	region	sequence	SEQ ID NO:
SM1B329	HC	QVQLKQSGPGLVQPSQSLSITCTVSGFSITSYGVHWIRQSPG KGLEWLGVIWSGGSTDYNAAFISRLSISKDNSKSQVFFKMN SLQANDTAIYYCATFYYDYDEGFDYWGQGTTLTVSSAKTT APSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	799
SM1B330	HC	QVQLKQSGPGLVQPSQSLSITCTVSGFSITSYGVHWIRQSPG KGLEWLGVIWSGGSTDYNAAFISRLSISKDNSKSQVFFKMN SLQANDTAIYYCATFYYDYDEGFDYWGQGTTLTVSSAKTT APSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	800
SM1B331	HC	QVQLKQSGPGLVQPSQSLSITCTVSGFSITSYGVHWIRQSPG KGLEWLGVIWSGGSTDYNAAFISRLSISKDNSKSQVFFKMN SLQANDTAIYYCATFYYDYDEGFDYWGQGTTLTVSSAKTT APSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	801
SM1B332	HC	QVQLKESGPGLVAPSQSLSITCTVSGLSLTSYGLSWVRQPPG KGLEWLGVIWGDGSTNYHSALISRLSISKDNSKSQVFLKLNS LQSDDTATYYCATRGDYGSYAMDYWGQGTSVTVSSAKTT APSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	802

mAb/Fab name	region	sequence	SEQ ID NO:
SM1B333	HC	EVQLQQSGAELVRPGASVKLSCTASGFNIKDSLIHWVKQRP EQGLEWIGWIDPEDGETKYAPKFQDKAALTTDTSSNTAYLH LNSLTSEDTAIYYCGRGGLILDYWGQGTTLTVSSAKTTAPSV YPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSG VHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASST KVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVL MISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTH REDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIE RTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMP EDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEK KNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	803
SM1B334	HC	QIQLVQSGPELKKPGETVKISCRSSGYTFTNYGLNWVKQAP GKDLKWMGWLNTYTGEPTYADDFKGRFAFSLETSAGTAYL QINNLKNEDTATYFCSRDYREGDAMDYWSQGTSVTVSSAK TTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNS GSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVA HPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPK IKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTA QTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKD LPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMV TDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSK LRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	804
SM1B335	HC	EVQLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTP EKRLEWVATISTSGSYTYYRDSVKGRLTISRDNAKNTLYLQ MTSLRSEDTAMYYCTRHGDHDGFDYWGQGTTLTVSSAKTT APSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGS LSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	805
SM1B336	HC	EVQLVESGGGLVKPGGSLKLSCVASGFSFSNYAMSWVRQT PERRLEWVATINSGGSFSFFPDSVKGRFTISRDSAKNTLYLQ MSSLRSDDTAMYYCTRHWDHPWFAYWGQGTLVTVSAAKT TAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSG SLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	806

mAb/Fab name	region	sequence	SEQ ID NO:
SM1B337	HC	EVQLVESGGGLVKPGGSLKLSCVASGFSFSNYAMSWVRQT PERRLEWVATINSGGSFSFFPDSVKGRFTISRDSAKNTLYLQ MSSLRSDDTAMYYCTRHWDHPWFAYWGQGTLVTVSAAKT TAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSG SLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	807
SM1B338	HC	EVQLVESGGGLVKPGGSLKLSCVASGFSFSNYAMSWVRQT PERRLEWVATINSGGSFSFFPDSVKGRFTISRDSAKNTLYLQ MSSLRSDDTAMYYCTRHWDHPWFAYWGQGTLVTVSAAKT TAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSG SLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIK DVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT QTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP APIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	808
SM1B339	HC	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLIYWVKQRP EQGLEWIGWIDPEDGETKFAPRFQDKATITSDTSSNTAYLRL SSLTSKDTAIYYCTRSFGVCWGQGTLVTVSAAKTTAPSVYP LAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVH TFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKV DKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMIS LSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTI SKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDI YVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKN WVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	809
SM1B340	HC	EVQLQQSGAELVRPGASVKLSCTTSGFNIKDSLIYWVKQRP EQGLEWIGWIDPEDGETKFAPRFQDKATITSDTSSNTAYLRL SSLTSEDTAIYYCTRSFGVCWGQGTLVTVSAAKTTAPSVYP LAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVH TFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKV DKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMIS LSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTI SKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDI YVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKN WVERNSYSCSVVHEGLHNHHTTKSFSRTPGK	810

Table 25. Staphylococcal Protein Sequence

SEQ ID No.	Type	Species	Description	Sequence
824	PRT	S. aureus	LukD (E.coli expressed, chemically biotinylated used for binding studies)	MGSSHHHHHHSSGLVPAGSHMLAQHITPVSEKKV DDKITLYKTTATSDNDKLNISQILTFNFIKDKSYDK DTLVLKAAGNINSGYKKPNPKDYNYSQFYWGGK YNVSVSSESNDAVNVVDYAPKNQNEEFQVQQTL GYSYGGDINISNGLSGGLNGSKSFSETINYKQESYR TTIDRKTNHKSIGWGVEAHKIMNNGWGPYGRDS YDPTYGNELFLGGRQSSSNAGQNFLPTHQMPLLA RGNFNPEFISVLSHKQNDTKKSKIKVTYQREMDR YTNQWNRLHWVGNNYKNQNTVTFTSTYEVDWQ NHTVKLIGTDSKETNPGV
825	PRT	S. aureus	LukD (S. Aureus expressed, used for neutralization studies)	NSAHHHHHHGSAQHITPVSEKKVDDKITLYKTTA TSDNDKLNISQILTFNFIKDKSYDKDTLVLKAAGNI NSGYKKPNPKDYNYSQFYWGGKYNVSVSSESND AVNVVDYAPKNQNEEFQVQQTLGYSYGGDINISN GLSGGLNGSKSFSETINYKQESYRTTIDRKTNHKSI GWGVEAHKIMNNGWGPYGRDSYDPTYGNELFLG GRQSSSNAGQNFLPTHQMPLLARGNFNPEFISVLS HKQNDTKKSKIKVTYQREMDRYTNQWNRLHWV GNNYKNQNTVTFTSTYEVDWQNHTVKLIGTDSKE TNPGV
826	PRT	S. aureus	LukE (S. Aureus expressed, used for neutralization studies)	NSAHHHHHHGSNTNIENIGDGAEVIKRTEDVSSKK WGVTQNVQFDFVKDKKYNKDALIVKMQGFINSR TSFSDVKGSGYELTKRMIWPFQYNIGLTTKDPNVS LINYLPKNKIETTDVGQTLGYNIGGNFQSAPSIGGN GSFNYSKTISYTQKSYVSEVDKQNSKSVKWGVKA NEFVTPDGKKSAHDRYLFVQSPNGPTGSAREYFA PDNQLPPLVQSGFNPSFITTLSHEKGSSDTSEFEISY GRNLDITYATLFPRTGIYAERKHNAFVNRNFVVRY EVNWKTHEIKVKGHN
827	PRT	S. aureus	LukA (E.coli expressed, in vivo biotinylation, used for binding studies)	MNSAHHHHHHHHHHGGGLNDIFEAQKIEWHEGS HKDSQDQNKKEHVDKSQQKDKRNVTNKDKNST APDDIGKNGKITKRTETVYDEKTNILQNLQFDFID DPTYDKNVLLVKKQGSIHSNLKFESHKEEKNSNW LKYPSEYHVDFQVKRNRKTEILDQLPKNKISTAKV DSTFSYSSGGKFDSTKGIGRTSSNSYSKTISYNQQN YDTIASGKNNNWHVHWSVIANDLKYGGEVKNRN DELLFYRNTRIATVENPELSFASKYRYPALVRSGF NPEFLTYLSNEKSNEKTQFEVTYTRNQDILKNRPGI HYAPPILEKNKDGQRLIVTYEVDWKNKTVKVVD KYSDDNKPYKAG
828	PRT	S. aureus	LukB (E.coli expressed, used for binding studies)	MKINSEIKQVSEKNLDGDTKMYTRTATTSDSQKNI TQSLQFNFLTEPNYDKETVFIKAKGTIGSGLRILDP NGYWNSTLRWPGSYSVSIQNVDDNNNTNVTDFA PKNQDESREVKYTYGYKTGGDFSINRGGLTGNIT KESNYSETISYQQPSYRTLLDQSTSHKGVGWKVE AHLINNMGHDHTRQLTNDSDNRTKSEIFSLTRNG NLWAKDNFTPKDKMPVTVSEGFNPEFLAVMSHD

				KKDKGKSQFVVHYKRSMDEFKIDWNRHGFWGY WSGENHVDKKEEKLSALYEVDWKTHNVKFVKVL NDNEKK
829	PRT	S. aureus	LukA (S. aureus expressed, used for neutralizati on studies)	NSAHHHHHHGSHKDSQDQNKKEHVDKSQQKDK RNVTNKDKNSTAPDDIGKNGKITKRTETVYDEKT NILQNLQFDFIDDPTYDKNVLLVKKQGSIHSNLKF ESHKEEKNSNWLKYPSEYHVDFQVKRNRKTEILD QLPKNKISTAKVDSTFSYSSGGKFDSTKGIGRTSSN SYSKTISYNQQNYDTIASGKNNNWHVHWSVIAND LKYGGEVKNRNDELLFYRNTRIATVENPELSFASK YRYPALVRSGFNPEFLTYLSNEKSNEKTQFEVTYT RNQDILKNRPGIHYAPPILEKNKDGQRLIVTYEVD WKNKTVKVVDKYSDDNKPYKEG
830	PRT	S. aureus	LukB (S. aureus expressed, used for neutralizati on studies)	KINSEIKQVSEKNLDGDTKMYTRTATTSDSQKNIT QSLQFNFLTEPNYDKETVFIKAKGTIGSGLRILDPN GYWNSTLRWPGSYSVSIQNVDDNNNTNVTDFAP KNQDESREVKYTYGYKTGGDFSINRGGLTGNITK ESNYSETISYQQPSYRTLLDQSTSHKGVGWKVEA HLINNMGHDHTRQLTNDSDNRTKSEIFSLTRNGNL WAKDNFTPKDKMPVTVSEGFNPEFLAVMSHDKK DKGKSQFVVHYKRSMDEFKIDWNRHGFWGYWS GENHVDKKEEKLSALYEVDWKTHNVKFVKVLND NEKK
831	PRT	Human	CD11b I-domain	MGSSHHHHHHSSGLVPRGSHMGSNLRQQPQKFPE ALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVST VMEQLKKSKTLFSLMQYSEEFRIHFTFKEFQNNPN PRSLVKPITQLLGRTHTATGIRKVVRELFNITNGAR KNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIR YVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNN FEALKTIQNQLREKIFAGGGGGDYKDHDGDYKD HDIDYKDDDDK
832	PRT	S. aureus	HlgA	NSAHHHHHHGSENKIEDIGQGAEIIKRTQDITSKRL AITQNIQFDFVKDKKYNKDALVVKMQGFISSRTT YSDLKKYPYIKRMIWPFQYNISLKTKDSNVDLINY LPKNKIDSADVSQKLGYNIGGNFQSAPSIGGSGSF NYSKTISYNQKNYVTEVESQNSKGVKWGVKANS FVTPNGQVSAYDQYLFAQDPTGPAARDYFVPDNQ LPPLIQSGFNPSFITTLSHERGKGDKSEFEITYGRN MDATYAYVTRHRLAVDRKHDAFKNRNVTVKYE VNWKTHEVKIKSITPK
833	PRT	S. aureus	HlgC	NSAHHHHHHGSANDTEDIGKGSDIEIIKRTEDKTS NKWGVTQNIQFDFVKDKKYNKDALILKMQGFISS RTTYYNYKKTNHVKAMRWPFQYNIGLKTNDKYV SLINYLPKNKIESTNVSQTLGYNIGGNFQSAPSLGG NGSFNYSKSISYTQQNYVSEVEQQNSKSVLWGVK ANSFATESGQKSAFDSDLFVGYKPHSKDPRDYFVP DSELPPLVQSGFNPSFIATVSHEKGSSDTSEFEITYG RNMDVTHAIKRSTHYGNSYLDGHRVHNAFVNRN YTVKYEVNWKTHEIKVKGQN

Table 26. LukAB Antibody Heavy Chain CDSs

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
SM1B105	pDR000023596	GAGGTTCAGCTGCAGCAGTCTGGGGCTGAGC TGATGACGCCTGGGGCCTCAGTGAAGATATC CTGCAAGGCTACTGGCTACACATTCAGTACC TTTTGGATAGAGTGGATCAAGCAGAGGCCTG GACATGGCCTTGAGTGGATTGGAGAGATTTT ACCTGGAAGTGGTAGTACTAAGTACAATGAG AAGTTCAAGGGCAAGGCCACATTCACTGCAG ATACATCCTCCAACACAGCCTACATGCAACT CAGCAGCCTGACATCTGAGGACTCTGCCGTC TATTATTGTGCAAGAGGTGGTTACGATGGTA TGGACTACTGGGGTCAAGGAACCTCAGTCAC CGTCTCCTCAGCCAAAACGACACCCCCATCT GTCTATCCACTGGCCCCTGGATCTGCTGCCCA AACTAACTCCATGGTGACCCTGGGATGCCTG GTCAAGGGCTATTTCCCTGAGCCAGTGACAG TGACCTGGAACTCTGGATCCCTGTCCAGCGG TGTGCACACCTTCCCAGCTGTCCTGGAGTCTG ACCTCTACACTCTGAGCAGCTCAGTGACTGT CCCCTCCAGCCCTCGGCCCAGCGAGACCGTC ACCTGCAACGTTGCCCACCCGGCCAGCAGCA CCAAGGTGGACAAGAAAATTGTGCCCAGGG ATTGTGGTTGTAAGCCTTGCATATGTACAGTC CCAGAAGTATCATCTGTCTTCATCTTCCCCCC AAAGCCCAAGGATGTGCTCACCATTACTCTG ACTCCTAAGGTCACGTGTGTTGTGGTAGACA TCAGCAAGGATGATCCCGAGGTCCAGTTCAG CTGGTTTGTAGATGATGTGGAGGTGCACACA GCTCAGACGCAACCCCGGGAGGAGCAGTTCA ACAGCACTTTCCGCTCAGTCAGTGAACTTCC CATCATGCACCAGGACTGGCTCAATGGCAAG GAGTTCAAATGCAGGGTCAACAGTGCAGCTT TCCCTGCCCCCATCGAGAAAACCATCTCCAA AACCAAAGGCAGACCGAAGGCTCCACAGGT GTACACCATTCCACCTCCCAAGGAGCAGATG GCCAAGGATAAAGTCAGTCTGACCTGCATGA TAACAGACTTCTTCCCTGAAGACATTACTGT GGAGTGGCAGTGGAATGGGCAGCCAGCGGA GAACTACAAGAACACTCAGCCCATCATGAAC ACGAATGGCTCTTACTTCGTCTACAGCAAGC TCAATGTGCAGAAGAGCAACTGGGAGGCAG GAAATACTTTCACCTGCTCTGTGTTACATGAG GGCCTGCACAACCACCATACTGAGAAGAGCC TCTCCCACTCTCCTGGTAAA	834
SM1B106	pDR000023618	GAGGTTCAGCTGCAGCAGTCTGGGGCTGAGC TGATGACGCCTGGGGCCTCAGTGAAGATATC CTGCAAGGCTACTGGCTACACATTCAGTACC	835

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		TTTTGGATAGAGTGGATCAAGCAGAGGCCTG GACATGGCCTTGAGTGGATTGGAGAGATTTT ACCTGGAAGTGGTAGTACTAAGTACAATGAG AAGTTCAAGGGCAAGGCCACATTCACTGCAG ATACATCCTCCAACACAGCCTACATGCAACT CAGCAGCCTGTCATCTGAGGACTCTGCCGTC TATTATTGTGCAAGAGGTGGTTACGATGGTA TGGACTACTGGGGTCAAGGAACCTCAGTCAC CGTCTCCTCAGCCAAAACGACACCCCCATCT GTCTATCCACTGGCCCCTGGATCTGCTGCCCA AACTAACTCCATGGTGACCCTGGGATGCCTG GTCAAGGGCTATTTCCCTGAGCCAGTGACAG TGACCTGGAACTCTGGATCCCTGTCCAGCGG TGTGCACACCTTCCCAGCTGTCCTGGAGTCTG ACCTCTACACTCTGAGCAGCTCAGTGACTGT CCCCTCCAGCCCTCGGCCCAGCGAGACCGTC ACCTGCAACGTTGCCCACCCGGCCAGCAGCA CCAAGGTGGACAAGAAAATTGTGCCCAGGG ATTGTGGTTGTAAGCCTTGCATATGTACAGTC CCAGAAGTATCATCTGTCTTCATCTTCCCCCC AAAGCCCAAGGATGTGCTCACCATTACTCTG ACTCCTAAGGTCACGTGTGTTGTGGTAGACA TCAGCAAGGATGATCCCGAGGTCCAGTTCAG CTGGTTTGTAGATGATGTGGAGGTGCACACA GCTCAGACGCAACCCCGGGAGGAGCAGTTCA ACAGCACTTTCCGCTCAGTCAGTGAACTTCC CATCATGCACCAGGACTGGCTCAATGGCAAG GAGTTCAAATGCAGGGTCAACAGTGCAGCTT TCCCTGCCCCCATCGAGAAAACCATCTCCAA AACCAAAGGCAGACCGAAGGCTCCACAGGT GTACACCATTCCACCTCCCAAGGAGCAGATG GCCAAGGATAAAGTCAGTCTGACCTGCATGA TAACAGACTTCTTCCCTGAAGACATTACTGT GGAGTGGCAGTGGAATGGGCAGCCAGCGGA GAACTACAAGAACACTCAGCCCATCATGAAC ACGAATGGCTCTTACTTCGTCTACAGCAAGC TCAATGTGCAGAAGAGCAACTGGGAGGCAG GAAATACTTTCACCTGCTCTGTGTTACATGAG GGCCTGCACAACCACCATACTGAGAAGAGCC TCTCCCACTCTCCTGGTAAA	
SM1B107	pDR000023619	GAGGTTCAGCTGCAGCAGTCTGAGGCTGAGC TGATGACGCCTGGGGCCTCAGTGAAGATATC CTGCAAGGCTACTGGCTACACATTCAGTACC TTTTGGATAGAGTGGATCAAGCAGAGGCCTG GACATGGCCTTGAGTGGATTGGAGAGATTTT ACCTGGAAGTGGTAGTACTAAGTACAATGAG AAGTTCAAGGGCAAGGCCACATTCACTGCAG ATACATCCTCCAACACAGCCTACATGCAACT	836

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		CAGCAGCCTGACATCTGAGGACTCTGCCGTC TATTATTGTGCAAGAGGTGGTTACGATGGTA TGGACTACTGGGGTCAAGGAACCTCAGTCAC CGTCTCCTCAGCCAAAACGACACCCCCATCT GTCTATCCACTGGCCCCTGGATCTGCTGCCCA AACTAACTCCATGGTGACCCTGGGATGCCTG GTCAAGGGCTATTTCCCTGAGCCAGTGACAG TGACCTGGAACTCTGGATCCCTGTCCAGCGG TGTGCACACCTTCCCAGCTGTCCTGGAGTCTG ACCTCTACACTCTGAGCAGCTCAGTGACTGT CCCCTCCAGCCCTCGGCCCAGCGAGACCGTC ACCTGCAACGTTGCCCACCCGGCCAGCAGCA CCAAGGTGGACAAGAAAATTGTGCCCAGGG ATTGTGGTTGTAAGCCTTGCATATGTACAGTC CCAGAAGTATCATCTGTCTTCATCTTCCCCCC AAAGCCCAAGGATGTGCTCACCATTACTCTG ACTCCTAAGGTCACGTGTGTTGTGGTAGACA TCAGCAAGGATGATCCCGAGGTCCAGTTCAG CTGGTTTGTAGATGATGTGGAGGTGCACACA GCTCAGACGCAACCCCGGGAGGAGCAGTTCA ACAGCACTTTCCGCTCAGTCAGTGAACTTCC CATCATGCACCAGGACTGGCTCAATGGCAAG GAGTTCAAATGCAGGGTCAACAGTGCAGCTT TCCCTGCCCCCATCGAGAAAACCATCTCCAA AACCAAAGGCAGACCGAAGGCTCCACAGGT GTACACCATTCCACCTCCCAAGGAGCAGATG GCCAAGGATAAAGTCAGTCTGACCTGCATGA TAACAGACTTCTTCCCTGAAGACATTACTGT GGAGTGGCAGTGGAATGGGCAGCCAGCGGA GAACTACAAGAACACTCAGCCCATCATGAAC ACGAATGGCTCTTACTTCGTCTACAGCAAGC TCAATGTGCAGAAGAGCAACTGGGAGGCAG GAAATACTTTCACCTGCTCTGTGTTACATGAG GGCCTGCACAACCACCATACTGAGAAGAGCC TCTCCCACTCTCCTGGTAAA	
SM1B108	pDR000023620	GAGGTTCAGCTGCAGCAGTCTGGGGCTGAGC TGGTGAAGCCTGGGGCCTCAGTGAAGATTTC CTGCAAGGCTTCTGGCTATGCATTCAGTAGC TCCTGGATGAACTGGGTGAAGCAGAGGCCTG GAAAGGGTCTTGAGTGGATTGGACGGATTTA TCCTGGAGATGGAGATACTAACTACCATGGG AAGTTCAAGGGCAAGGCCACACTGACTGCAG ACAAATCCTCCAGCACAGCCTACATGCAACT CAGCAGCCTGACATCTGAGGACTCTGCGGTC TACTTCTGTGCAAGAAGGAACTATGATGGTT ACCACTATGGTATGGACTACTGGGGTCAAGG AACCTCAGTCACCGTCTCCTCAGCCAAAACG ACACCCCCATCTGTCTATCCACTGGCCCCTGG	837

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		ATCTGCTGCCCAAACTAACTCCATGGTGACC CTGGGATGCCTGGTCAAGGGCTATTTCCCTG AGCCAGTGACAGTGACCTGGAACTCTGGATC CCTGTCCAGCGGTGTGCACACCTTCCCAGCT GTCCTGGAGTCTGACCTCTACACTCTGAGCA GCTCAGTGACTGTCCCCTCCAGCCCTCGGCC CAGCGAGACCGTCACCTGCAACGTTGCCCAC CCGGCCAGCAGCACCAAGGTGGACAAGAAA ATTGTGCCCAGGGATTGTGGTTGTAAGCCTT GCATATGTACAGTCCCAGAAGTATCATCTGT CTTCATCTTCCCCCCAAAGCCCAAGGATGTG CTCACCATTACTCTGACTCCTAAGGTCACGTG TGTTGTGGTAGACATCAGCAAGGATGATCCC GAGGTCCAGTTCAGCTGGTTTGTAGATGATG TGGAGGTGCACACAGCTCAGACGCAACCCCG GGAGGAGCAGTTCAACAGCACTTTCCGCTCA GTCAGTGAACTTCCCATCATGCACCAGGACT GGCTCAATGGCAAGGAGTTCAAATGCAGGGT CAACAGTGCAGCTTTCCCTGCCCCCATCGAG AAAACCATCTCCAAAACCAAAGGCAGACCG AAGGCTCCACAGGTGTACACCATTCCACCTC CCAAGGAGCAGATGGCCAAGGATAAAGTCA GTCTGACCTGCATGATAACAGACTTCTTCCCT GAAGACATTACTGTGGAGTGGCAGTGGAATG GGCAGCCAGCGGAGAACTACAAGAACACTC AGCCCATCATGAACACGAATGGCTCTTACTT CGTCTACAGCAAGCTCAATGTGCAGAAGAGC AACTGGGAGGCAGGAAATACTTTCACCTGCT CTGTGTTACATGAGGGCCTGCACAACCACCA TACTGAGAAGAGCCTCTCCCACTCTCCTGGT AAA	
SM1B109	pDR000023596	GAGGTTCAGCTGCAGCAGTCTGGGGCTGAGC TGATGACGCCTGGGGCCTCAGTGAAGATATC CTGCAAGGCTACTGGCTACACATTCAGTACC TTTTGGATAGAGTGGATCAAGCAGAGGCCTG GACATGGCCTTGAGTGGATTGGAGAGATTTT ACCTGGAAGTGGTAGTACTAAGTACAATGAG AAGTTCAAGGGCAAGGCCACATTCACTGCAG ATACATCCTCCAACACAGCCTACATGCAACT CAGCAGCCTGACATCTGAGGACTCTGCCGTC TATTATTGTGCAAGAGGTGGTTACGATGGTA TGGACTACTGGGGTCAAGGAACCTCAGTCAC CGTCTCCTCAGCCAAAACGACACCCCCATCT GTCTATCCACTGGCCCCTGGATCTGCTGCCCA AACTAACTCCATGGTGACCCTGGGATGCCTG GTCAAGGGCTATTTCCCTGAGCCAGTGACAG TGACCTGGAACTCTGGATCCCTGTCCAGCGG TGTGCACACCTTCCCAGCTGTCCTGGAGTCTG	838

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		ACCTCTACACTCTGAGCAGCTCAGTGACTGT CCCCTCCAGCCCTCGGCCCAGCGAGACCGTC ACCTGCAACGTTGCCCACCCGGCCAGCAGCA CCAAGGTGGACAAGAAAATTGTGCCCAGGG ATTGTGGTTGTAAGCCTTGCATATGTACAGTC CCAGAAGTATCATCTGTCTTCATCTTCCCCCC AAAGCCCAAGGATGTGCTCACCATTACTCTG ACTCCTAAGGTCACGTGTGTTGTGGTAGACA TCAGCAAGGATGATCCCGAGGTCCAGTTCAG CTGGTTTGTAGATGATGTGGAGGTGCACACA GCTCAGACGCAACCCCGGGAGGAGCAGTTCA ACAGCACTTTCCGCTCAGTCAGTGAACTTCC CATCATGCACCAGGACTGGCTCAATGGCAAG GAGTTCAAATGCAGGGTCAACAGTGCAGCTT TCCCTGCCCCCATCGAGAAAACCATCTCCAA AACCAAAGGCAGACCGAAGGCTCCACAGGT GTACACCATTCCACCTCCCAAGGAGCAGATG GCCAAGGATAAAGTCAGTCTGACCTGCATGA TAACAGACTTCTTCCCTGAAGACATTACTGT GGAGTGGCAGTGGAATGGGCAGCCAGCGGA GAACTACAAGAACACTCAGCCCATCATGAAC ACGAATGGCTCTTACTTCGTCTACAGCAAGC TCAATGTGCAGAAGAGCAACTGGGAGGCAG GAAATACTTTCACCTGCTCTGTGTTACATGAG GGCCTGCACAACCACCATACTGAGAAGAGCC TCTCCCACTCTCCTGGTAAA	
SM1B110	pDR000023622	GAGGTTCAGCTGCAGCAGTCTGGGGCTGAGC TGGTCAAGCCTGGGACTTCAGTGAAGATGTC CTGCAAGGCTTCTGGCTACACCTTCACCAGC TACTGGATGCACTGGGTGAAACTTAGGCCTG GACAAGGCCTTGAGTGGATCGGAGTGATTGA TCCTTCTGATAGTTATACTAACTATAATCAAA AGTTCAAGGGCAGGGCCACATTGACTGGAGA CACATCCTCCAGCACAGCCTACATGCAGCTC AGCAGCCTGACATCTGAGGACTCTGCGGTCT ATTACTGTACAAGAGCAGCATATGATAACTC GTACTACTTTGACTACTGGGGCCAAGGCACC ACTCTCACAGTCTCCTCAGCCAAAACGACAC CCCCATCTGTCTATCCACTGGCCCCTGGATCT GCTGCCCAAACTAACTCCATGGTGACCCTGG GATGCCTGGTCAAGGGCTATTTCCCTGAGCC AGTGACAGTGACCTGGAACTCTGGATCCCTG TCCAGCGGTGTGCACACCTTCCCAGCTGTCCT GGAGTCTGACCTCTACACTCTGAGCAGCTCA GTGACTGTCCCCTCCAGCCCTCGGCCCAGCG AGACCGTCACCTGCAACGTTGCCCACCCGGC CAGCAGCACCAAGGTGGACAAGAAAATTGT GCCCAGGGATTGTGGTTGTAAGCCTTGCATA	839

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		TGTACAGTCCCAGAAGTATCATCTGTCTTCAT CTTCCCCCCAAAGCCCAAGGATGTGCTCACC ATTACTCTGACTCCTAAGGTCACGTGTGTTGT GGTAGACATCAGCAAGGATGATCCCGAGGTC CAGTTCAGCTGGTTTGTAGATGATGTGGAGG TGCACACAGCTCAGACGCAACCCCGGGAGG AGCAGTTCAACAGCACTTTCCGCTCAGTCAG TGAACTTCCCATCATGCACCAGGACTGGCTC AATGGCAAGGAGTTCAAATGCAGGGTCAAC AGTGCAGCTTTCCCTGCCCCCATCGAGAAAA CCATCTCCAAAACCAAAGGCAGACCGAAGG CTCCACAGGTGTACACCATTCCACCTCCCAA GGAGCAGATGGCCAAGGATAAAGTCAGTCT GACCTGCATGATAACAGACTTCTTCCCTGAA GACATTACTGTGGAGTGGCAGTGGAATGGGC AGCCAGCGGAGAACTACAAGAACACTCAGC CCATCATGAACACGAATGGCTCTTACTTCGT CTACAGCAAGCTCAATGTGCAGAAGAGCAAC TGGGAGGCAGGAAATACTTTCACCTGCTCTG TGTTACATGAGGGCCTGCACAACCACCATAC TGAGAAGAGCCTCTCCCACTCTCCTGGTAAA	
SM1B111	pDR000023624	GAGGTTCAGCTGCAGCAGTCTGGGGCTGAGC TGGTGAAGCCTGGGGCCTCAGTGAAGATTTC CTGCAAGGCTTCTGGCTATGCATTCAGTAGTT CCTGGATGAACTGGTTGAAGCAGAGGCCTGG AAAGGGTCTTGAGTGGATTGGACGGATTTAT CCTGGAGATGGAGATACTAATTACAATGGGA AGTTCAAGGGCAAGGCCACACTGACTGCAGA CAAGTCCTCCAGTACAGCCTACATGCAACTC AGCAGCCTGACATCTGAGGACTCTGCGGTCT ACTTCTGTGCAAGATACGGCTATGATTACGA CGGGGAATATTACTATGCTATGGACTACTGG GGTCAAGGAACCTCAGTCACCGTCTCCTCAG CCAAAACGACACCCCCATCTGTCTATCCACT GGCCCCTGGATCTGCTGCCCAAACTAACTCC ATGGTGACCCTGGGATGCCTGGTCAAGGGCT ATTTCCCTGAGCCAGTGACAGTGACCTGGAA CTCTGGATCCCTGTCCAGCGGTGTGCACACC TTCCCAGCTGTCCTGGAGTCTGACCTCTACAC TCTGAGCAGCTCAGTGACTGTCCCCTCCAGC CCTCGGCCCAGCGAGACCGTCACCTGCAACG TTGCCCACCCGGCCAGCAGCACCAAGGTGGA CAAGAAAATTGTGCCCAGGGATTGTGGTTGT AAGCCTTGCATATGTACAGTCCCAGAAGTAT CATCTGTCTTCATCTTCCCCCCAAAGCCCAAG GATGTGCTCACCATTACTCTGACTCCTAAGGT CACGTGTGTTGTGGTAGACATCAGCAAGGAT GATCCCGAGGTCCAGTTCAGCTGGTTTGTAG	840

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		ATGATGTGGAGGTGCACACAGCTCAGACGCA ACCCCGGGAGGAGCAGTTCAACAGCACTTTC CGCTCAGTCAGTGAACTTCCCATCATGCACC AGGACTGGCTCAATGGCAAGGAGTTCAAATG CAGGGTCAACAGTGCAGCTTTCCCTGCCCCC ATCGAGAAAACCATCTCCAAAACCAAAGGC AGACCGAAGGCTCCACAGGTGTACACCATTC CACCTCCCAAGGAGCAGATGGCCAAGGATA AAGTCAGTCTGACCTGCATGATAACAGACTT CTTCCCTGAAGACATTACTGTGGAGTGGCAG TGGAATGGGCAGCCAGCGGAGAACTACAAG AACACTCAGCCCATCATGAACACGAATGGCT CTTACTTCGTCTACAGCAAGCTCAATGTGCA GAAGAGCAACTGGGAGGCAGGAAATACTTT CACCTGCTCTGTGTTACATGAGGGCCTGCAC AACCACCATACTGAGAAGAGCCTCTCCCACT CTCCTGGTAAA	
SM1B112	pDR000023623	CAGGTGCAGCTGAAGGAGTCAGGACCTGAA CTGAAGAAGCCTGGAGAGACAGTCAGGATCT CCTGCAAGGCTTCTGGGTATACTTTCACAAA TTATGGAATGAACTGGGTGAAGCAGACTCCA GGAAAGGGTTTAAAGTGGATAGACTGGTTAA AGTCCTACACTGGAGAGCCAACACATACTGG TGACTTCAAGGGACGGTTTGACCTCTCTTTGG AAACCTCTGCCAACACTGCCTATTTGCAGAT CAACAACCTCAAAAATGAGGACACGGCTAC ATATTTCTGTGCAAGAGGGTCCCTCTTTGGTT TGGACTACTGGGGTCAAGGAACCTCAGTCAC CGTCTCCTCAGCCAAAACGACACCCCCATCT GTCTATCCACTGGCCCCTGGATCTGCTGCCCA AACTAACTCCATGGTGACCCTGGGATGCCTG GTCAAGGGCTATTTCCCTGAGCCAGTGACAG TGACCTGGAACTCTGGATCCCTGTCCAGCGG TGTGCACACCTTCCCAGCTGTCCTGGAGTCTG ACCTCTACACTCTGAGCAGCTCAGTGACTGT CCCCTCCAGCCCTCGGCCCAGCGAGACCGTC ACCTGCAACGTTGCCCACCCGGCCAGCAGCA CCAAGGTGGACAAGAAAATTGTGCCCAGGG ATTGTGGTTGTAAGCCTTGCATATGTACAGTC CCAGAAGTATCATCTGTCTTCATCTTCCCCCC AAAGCCCAAGGATGTGCTCACCATTACTCTG ACTCCTAAGGTCACGTGTGTTGTGGTAGACA TCAGCAAGGATGATCCCGAGGTCCAGTTCAG CTGGTTTGTAGATGATGTGGAGGTGCACACA GCTCAGACGCAACCCCGGGAGGAGCAGTTCA ACAGCACTTTCCGCTCAGTCAGTGAACTTCC CATCATGCACCAGGACTGGCTCAATGGCAAG GAGTTCAAATGCAGGGTCAACAGTGCAGCTT	841

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		TCCCTGCCCCCATCGAGAAAACCATCTCCAA AACCAAAGGCAGACCGAAGGCTCCACAGGT GTACACCATTCCACCTCCCAAGGAGCAGATG GCCAAGGATAAAGTCAGTCTGACCTGCATGA TAACAGACTTCTTCCCTGAAGACATTACTGT GGAGTGGCAGTGGAATGGGCAGCCAGCGGA GAACTACAAGAACACTCAGCCCATCATGAAC ACGAATGGCTCTTACTTCGTCTACAGCAAGC TCAATGTGCAGAAGAGCAACTGGGAGGCAG GAAATACTTTCACCTGCTCTGTGTTACATGAG GGCCTGCACAACCACCATACTGAGAAGAGCC TCTCCCACTCTCCTGGTAAA	
SM1B243	pDR000030109	GAAGTCCAGCTGCAGCAGAGCGGAGCCGAG CTGGTCAAAAGCGGAGCCAGCGTGAAGCTG AGCTGCACCGCCAGCGGCTTCAACATCAAGG ACTACTACATGCACTGGGTCAAGCAGCGGCC CGAGCAGGGCCTGGAATGGATCGGAAGAAT CGACCCCGCCAACGGCAACACCAAATACGAC CCCAAGTTCCAGGACAAGGCCACCATCACCA GCGACACCAGCAGCAACACCGCCTACCTGCA GCTGAGCAGCCTGACCAGCGAGGACACCGCC GTGTACTACTGCGCCGAGGGCGATTACGTGC CCGGCTACTTTGATGTGTGGGGAGCCGGCAC CACCGTGACCGTGTCATCTGCCAAAACAACA GCACCAAGTGTCTATCCACTGGCCCCTGTGT GTGGAGATACAACTGGCTCCTCGGTGACTCT AGGATGCCTGGTCAAGGGTTATTTCCCTGAG CCAGTGACCTTGACCTGGAACTCTGGATCCC TGTCCAGTGGTGTGCACACCTTCCCAGCTGTC CTGCAGTCTGACCTCTACACCCTCAGCAGCT CAGTGACTGTAACCTCGAGCACCTGGCCCAG CCAGTCCATCACCTGCAATGTGGCCCACCCG GCAAGCAGCACCAAGGTGGACAAGAAAATT GAGCCCAGAGGGCCCACAATCAAGCCCTGTC CTCCATGCAAATGCCCAGCACCTAACCTCTT GGGTGGACCATCCGTCTTCATCTTCCCTCCAA AGATCAAGGATGTACTCATGATCTCCCTGAG CCCCATAGTCACATGTGTGGTGGTGGATGTG AGCGAGGATGACCCAGATGTCCAGATCAGCT GGTTTGTGAACAACGTGGAAGTACACACAGC TCAGACACAAACCCATAGAGAGGATTACAAC AGTACTCTCCGGGTGGTCAGTGCCCTCCCCA TCCAGCACCAGGACTGGATGAGTGGCAAGG AGTTCAAATGCAAGGTCAACAACAAAGACCT CCCAGCGCCCATCGAGAGAACCATCTCAAAA CCCAAAGGGTCAGTAAGAGCTCCACAGGTAT ATGTCTTGCCTCCACCAGAAGAAGAGATGAC TAAGAAACAGGTCACTCTGACCTGCATGGTC	842

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		ACAGACTTCATGCCTGAAGACATTTACGTGG AGTGGACCAACAACGGGAAAACAGAGCTAA ACTACAAGAACACTGAACCAGTCCTGGACTC TGATGGTTCTTACTTCATGTACAGCAAGCTG AGAGTGGAAAAGAAGAACTGGGTGGAAAGA AATAGCTACTCCTGTTCAGTGGTCCACGAGG GTCTGCACAATCACCACACGACTAAGAGCTT CTCCCGGACTCCGGGTAAA	
SM1B244	pDR000030218	GAGGTCCAGCTGCAGGAATCTGGCCCTAGCC TGGTCAAGCCCAGCCAGACCCTGAGCCTGAC CTGTAGCGTGACCGGCGACAGCATCACCAGC GACTACTGGAACTGGATCCGGAAGTTCCCCG GCAACAAGCTCGAGTACATGGGCTACATCAG CTACAGCGGCAGCACCTACTACAACCCCAGC CTGAAGTCCCGGATCTCCATCACCCGGGACA CCAGCAAGAACCAGTACTATCTGCAGCTGAA CAGCGTGACCACCGAGGACACCGCCACCTAC TATTGTGCCGGCGACTACGGCAGCCCCTACG CCATGGATTATTGGGGCCAGGGCACCTCCGT GACCGTGTCTAGTGCCAAAACAACAGCACCA AGTGTCTATCCACTGGCCCCTGTGTGTGGAG ATACAACTGGCTCCTCGGTGACTCTAGGATG CCTGGTCAAGGGTTATTTCCCTGAGCCAGTG ACCTTGACCTGGAACTCTGGATCCCTGTCCA GTGGTGTGCACACCTTCCCAGCTGTCCTGCA GTCTGACCTCTACACCCTCAGCAGCTCAGTG ACTGTAACCTCGAGCACCTGGCCCAGCCAGT CCATCACCTGCAATGTGGCCCACCCGGCAAG CAGCACCAAGGTGGACAAGAAAATTGAGCC CAGAGGGCCCACAATCAAGCCCTGTCCTCCA TGCAAATGCCCAGCACCTAACCTCTTGGGTG GACCATCCGTCTTCATCTTCCCTCCAAAGATC AAGGATGTACTCATGATCTCCCTGAGCCCCA TAGTCACATGTGTGGTGGTGGATGTGAGCGA GGATGACCCAGATGTCCAGATCAGCTGGTTT GTGAACAACGTGGAAGTACACACAGCTCAG ACACAAACCCATAGAGAGGATTACAACAGT ACTCTCCGGGTGGTCAGTGCCCTCCCCATCC AGCACCAGGACTGGATGAGTGGCAAGGAGT TCAAATGCAAGGTCAACAACAAAGACCTCCC AGCGCCCATCGAGAGAACCATCTCAAAACCC AAAGGGTCAGTAAGAGCTCCACAGGTATATG TCTTGCCTCCACCAGAAGAAGAGATGACTAA GAAACAGGTCACTCTGACCTGCATGGTCACA GACTTCATGCCTGAAGACATTTACGTGGAGT GGACCAACAACGGGAAAACAGAGCTAAACT ACAAGAACACTGAACCAGTCCTGGACTCTGA TGGTTCTTACTTCATGTACAGCAAGCTGAGA	843

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		GTGGAAAAGAAGAACTGGGTGGAAAGAAAT AGCTACTCCTGTTCAGTGGTCCACGAGGGTC TGCACAATCACCACACGACTAAGAGCTTCTC CCGGACTCCGGGTAAA	
SM1B245	pDR000030219	CAGGTCCAGCTGCAGCAGTCTGGCGCTGAAC TGGCCAAGCCTGGGGCCAGCGTGAAGATGA GCTGCAAGAGCAGCGGCTACACCTTCAGCAC CTACTGGATGCACTGGGTCAAGCAGAGGCCA GGCCAGGGCCTGGAATGGATCGGCTACATCA ACCCCAACACCGGCTACACAGAGTACAACCA GAAGTTCAAGGACACCGCCACCCTGACCGCC GACAAGTCTAGCAGCACCGCCTACATGCAGC TGAGCAGCCTGACCAGCGAGGACAGCGCCGT GTACTATTGTGCCAGAGGCGGCAGCAAGGCC TTCCCCTACTACGCCATGGACTATTGGGGCC AGGGCACCAGCGTGACCGTGTCTAGTGCCAA AACAACAGCACCAAGTGTCTATCCACTGGCC CCTGTGTGTGGAGATACAACTGGCTCCTCGG TGACTCTAGGATGCCTGGTCAAGGGTTATTT CCCTGAGCCAGTGACCTTGACCTGGAACTCT GGATCCCTGTCCAGTGGTGTGCACACCTTCC CAGCTGTCCTGCAGTCTGACCTCTACACCCTC AGCAGCTCAGTGACTGTAACCTCGAGCACCT GGCCCAGCCAGTCCATCACCTGCAATGTGGC CCACCCGGCAAGCAGCACCAAGGTGGACAA GAAAATTGAGCCCAGAGGGCCCACAATCAA GCCCTGTCCTCCATGCAAATGCCCAGCACCT AACCTCTTGGGTGGACCATCCGTCTTCATCTT CCCTCCAAAGATCAAGGATGTACTCATGATC TCCCTGAGCCCCATAGTCACATGTGTGGTGG TGGATGTGAGCGAGGATGACCCAGATGTCCA GATCAGCTGGTTTGTGAACAACGTGGAAGTA CACACAGCTCAGACACAAACCCATAGAGAG GATTACAACAGTACTCTCCGGGTGGTCAGTG CCCTCCCCATCCAGCACCAGGACTGGATGAG TGGCAAGGAGTTCAAATGCAAGGTCAACAAC AAAGACCTCCCAGCGCCCATCGAGAGAACCA TCTCAAAACCCAAAGGGTCAGTAAGAGCTCC ACAGGTATATGTCTTGCCTCCACCAGAAGAA GAGATGACTAAGAAACAGGTCACTCTGACCT GCATGGTCACAGACTTCATGCCTGAAGACAT TTACGTGGAGTGGACCAACAACGGGAAAAC AGAGCTAAACTACAAGAACACTGAACCAGTC CTGGACTCTGATGGTTCTTACTTCATGTACAG CAAGCTGAGAGTGGAAAAGAAGAACTGGGT GGAAAGAAATAGCTACTCCTGTTCAGTGGTC CACGAGGGTCTGCACAATCACCACACGACTA AGAGCTTCTCCCGGACTCCGGGTAAA	844

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
SM1B246	pDR000030220	GAGATCCAGCTGCAGCAGTCTGGCCCTGAGC TGGTCAAGCCTGGGGCCAGCGTGAAGATGAG CTGCAAGGCCAGCGGCTACAGCTTCACCGGC TACAACATGCACTGGGTCAAGCAGAGCCACG GCAAGAGCCTGGAATGGATCGGCTACATCGA CCCCTACAACGGGGCCACCAGCCACAACCAG AAGTTCAAGGGCAAGGCCACCCTGACCGTGG AAAAGAGCAGCAGCACCGCCTACATGCAGCT GAACAGCCTGACCAGCGAGGACAGCGCCGT GTACTACTGCGCCAGAGGCCTGTACGGCGAC TATTGGTACGCCTATTGGGGCCAGGGCACCC TGGTCACCGTGTCTAGTGCCAAAACAACAGC ACCAAGTGTCTATCCACTGGCCCCTGTGTGT GGAGATACAACTGGCTCCTCGGTGACTCTAG GATGCCTGGTCAAGGGTTATTTCCCTGAGCC AGTGACCTTGACCTGGAACTCTGGATCCCTG TCCAGTGGTGTGCACACCTTCCCAGCTGTCCT GCAGTCTGACCTCTACACCCTCAGCAGCTCA GTGACTGTAACCTCGAGCACCTGGCCCAGCC AGTCCATCACCTGCAATGTGGCCCACCCGGC AAGCAGCACCAAGGTGGACAAGAAAATTGA GCCCAGAGGGCCCACAATCAAGCCCTGTCCT CCATGCAAATGCCCAGCACCTAACCTCTTGG GTGGACCATCCGTCTTCATCTTCCCTCCAAAG ATCAAGGATGTACTCATGATCTCCCTGAGCC CCATAGTCACATGTGTGGTGGTGGATGTGAG CGAGGATGACCCAGATGTCCAGATCAGCTGG TTTGTGAACAACGTGGAAGTACACACAGCTC AGACACAAACCCATAGAGAGGATTACAACA GTACTCTCCGGGTGGTCAGTGCCCTCCCCATC CAGCACCAGGACTGGATGAGTGGCAAGGAG TTCAAATGCAAGGTCAACAACAAAGACCTCC CAGCGCCCATCGAGAGAACCATCTCAAAACC CAAAGGGTCAGTAAGAGCTCCACAGGTATAT GTCTTGCCTCCACCAGAAGAAGAGATGACTA AGAAACAGGTCACTCTGACCTGCATGGTCAC AGACTTCATGCCTGAAGACATTTACGTGGAG TGGACCAACAACGGGAAAACAGAGCTAAAC TACAAGAACACTGAACCAGTCCTGGACTCTG ATGGTTCTTACTTCATGTACAGCAAGCTGAG AGTGGAAAAGAAGAACTGGGTGGAAAGAAA TAGCTACTCCTGTTCAGTGGTCCACGAGGGT CTGCACAATCACCACACGACTAAGAGCTTCT CCCGGACTCCGGGTAAA	845
SM1B247	pDR000030221	GAGGTGCAGCTGGTGGAATCTGGCGGAGGA CTGGTCAAGCCTGGCGGCAGCCTGAAACTGT CTTGCGCCGCCAGCGGCTTCACCTTCAGCGA CTACTACATGTACTGGGTCCGACAGACCCCT	846

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		GAGAAGCGGCTGGAATGGGTGGCCACAATC AGCGACGGCGGCAGCTACACCTTCTACCCCG ACAGCGTGAAGGGCCGGTTCACCATCAGCCG GGACAACGCCAAGAACAACCTGTACCTGCAG ATGTCCAGCCTGAAGTCCGAGGACACCGCCA TGTACTACTGCGCCAGAGGCCCCACCTACTA CGGCCTGGATTATTGGGGCCAGGGCACCACC CTGACCGTGTCTAGTGCCAAAACAACAGCAC CAAGTGTCTATCCACTGGCCCCTGTGTGTGG AGATACAACTGGCTCCTCGGTGACTCTAGGA TGCCTGGTCAAGGGTTATTTCCCTGAGCCAG TGACCTTGACCTGGAACTCTGGATCCCTGTCC AGTGGTGTGCACACCTTCCCAGCTGTCCTGC AGTCTGACCTCTACACCCTCAGCAGCTCAGT GACTGTAACCTCGAGCACCTGGCCCAGCCAG TCCATCACCTGCAATGTGGCCCACCCGGCAA GCAGCACCAAGGTGGACAAGAAAATTGAGC CCAGAGGGCCCACAATCAAGCCCTGTCCTCC ATGCAAATGCCCAGCACCTAACCTCTTGGGT GGACCATCCGTCTTCATCTTCCCTCCAAAGAT CAAGGATGTACTCATGATCTCCCTGAGCCCC ATAGTCACATGTGTGGTGGTGGATGTGAGCG AGGATGACCCAGATGTCCAGATCAGCTGGTT TGTGAACAACGTGGAAGTACACACAGCTCAG ACACAAACCCATAGAGAGGATTACAACAGT ACTCTCCGGGTGGTCAGTGCCCTCCCCATCC AGCACCAGGACTGGATGAGTGGCAAGGAGT TCAAATGCAAGGTCAACAACAAAGACCTCCC AGCGCCCATCGAGAGAACCATCTCAAAACCC AAAGGGTCAGTAAGAGCTCCACAGGTATATG TCTTGCCTCCACCAGAAGAAGAGATGACTAA GAAACAGGTCACTCTGACCTGCATGGTCACA GACTTCATGCCTGAAGACATTTACGTGGAGT GGACCAACAACGGGAAAACAGAGCTAAACT ACAAGAACACTGAACCAGTCCTGGACTCTGA TGGTTCTTACTTCATGTACAGCAAGCTGAGA GTGGAAAAGAAGAACTGGGTGGAAAGAAAT AGCTACTCCTGTTCAGTGGTCCACGAGGGTC TGCACAATCACCACACGACTAAGAGCTTCTC CCGGACTCCGGGTAAA	
SM1B248	pDR000030222	CAGGTCCAGCTGCAGCAGCCTGGCGCTGAAC TCGTCAGACCTGGCGCTTCTGTGCGGCTGAG CTGCAAGGCCAGCGGCTACAGCTTCACCAGC TACTGGATGAGCTGGGTCAAAGTGCGGCCAG GCCAGGGCCTGGAATGGATCGGAATGATCCA CCCCAGCGACAGCGAGACACGGCTGAACCA GAAGTTCAAGGACAAGGCCACCCTGACCGTG GACAAGAGCAGCAGCACCGCCTACATGCAG	847

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		CTGTCCAGCCCCACAAGCGAGGACAGCGCCG TGTACTACTGCGCCAGACTGTACGTGGACTT CTTCGACTACTGGGGCCAGGGCACCACACTG ACAGTGTCCTCTGCCAAAACAACAGCACCAA GTGTCTATCCACTGGCCCCTGTGTGTGGAGA TACAACTGGCTCCTCGGTGACTCTAGGATGC CTGGTCAAGGGTTATTTCCCTGAGCCAGTGA CCTTGACCTGGAACTCTGGATCCCTGTCCAGT GGTGTGCACACCTTCCCAGCTGTCCTGCAGT CTGACCTCTACACCCTCAGCAGCTCAGTGAC TGTAACCTCGAGCACCTGGCCCAGCCAGTCC ATCACCTGCAATGTGGCCCACCCGGCAAGCA GCACCAAGGTGGACAAGAAAATTGAGCCCA GAGGGCCCACAATCAAGCCCTGTCCTCCATG CAAATGCCCAGCACCTAACCTCTTGGGTGGA CCATCCGTCTTCATCTTCCCTCCAAAGATCAA GGATGTACTCATGATCTCCCTGAGCCCCATA GTCACATGTGTGGTGGTGGATGTGAGCGAGG ATGACCCAGATGTCCAGATCAGCTGGTTTGT GAACAACGTGGAAGTACACACAGCTCAGAC ACAAACCCATAGAGAGGATTACAACAGTACT CTCCGGGTGGTCAGTGCCCTCCCCATCCAGC ACCAGGACTGGATGAGTGGCAAGGAGTTCA AATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAAA GGGTCAGTAAGAGCTCCACAGGTATATGTCT TGCCTCCACCAGAAGAAGAGATGACTAAGA AACAGGTCACTCTGACCTGCATGGTCACAGA CTTCATGCCTGAAGACATTTACGTGGAGTGG ACCAACAACGGGAAAACAGAGCTAAACTAC AAGAACACTGAACCAGTCCTGGACTCTGATG GTTCTTACTTCATGTACAGCAAGCTGAGAGT GGAAAAGAAGAACTGGGTGGAAAGAAATAG CTACTCCTGTTCAGTGGTCCACGAGGGTCTG CACAATCACCACACGACTAAGAGCTTCTCCC GGACTCCGGGTAAA	
SM1B249	pDR000030223	GACGTGAAGCTGGTGGAATCTGGCGGCGGAC TGGTCAAGCTGGGCGGCAGCCTGAAACTGTC TTGCGCCGCCAGCGGCTTCACCTTCAGCAGC TACTACATGAGCTGGGTCCGACAGACCCCTG AGAAGCGGCTGGAACTGGTGGCCGCCATCAA CAGCAATGGCGGCAGCACCTACTACCCCGAC ACCGTGAAGGGCCGGTTCACCATCTCCCGGG ACAACGCCAAGAACACCCTGTACCTGCAGAT GTCCAGCCTGAAGTCCGAGGACACCGCCCTG TACTACTGCGCCAGACCCGACTACCCCTACG CCATGGATTACTGGGGCCAGGGCACCAGCGT GACCGTGTCATCTGCCAAAACAACAGCACCA	848

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		AGTGTCTATCCACTGGCCCCTGTGTGTGGAG ATACAACTGGCTCCTCGGTGACTCTAGGATG CCTGGTCAAGGGTTATTTCCCTGAGCCAGTG ACCTTGACCTGGAACTCTGGATCCCTGTCCA GTGGTGTGCACACCTTCCCAGCTGTCCTGCA GTCTGACCTCTACACCCTCAGCAGCTCAGTG ACTGTAACCTCGAGCACCTGGCCCAGCCAGT CCATCACCTGCAATGTGGCCCACCCGGCAAG CAGCACCAAGGTGGACAAGAAAATTGAGCC CAGAGGGCCCACAATCAAGCCCTGTCCTCCA TGCAAATGCCCAGCACCTAACCTCTTGGGTG GACCATCCGTCTTCATCTTCCCTCCAAAGATC AAGGATGTACTCATGATCTCCCTGAGCCCCA TAGTCACATGTGTGGTGGTGGATGTGAGCGA GGATGACCCAGATGTCCAGATCAGCTGGTTT GTGAACAACGTGGAAGTACACACAGCTCAG ACACAAACCCATAGAGAGGATTACAACAGT ACTCTCCGGGTGGTCAGTGCCCTCCCCATCC AGCACCAGGACTGGATGAGTGGCAAGGAGT TCAAATGCAAGGTCAACAACAAAGACCTCCC AGCGCCCATCGAGAGAACCATCTCAAAACCC AAAGGGTCAGTAAGAGCTCCACAGGTATATG TCTTGCCTCCACCAGAAGAAGAGATGACTAA GAAACAGGTCACTCTGACCTGCATGGTCACA GACTTCATGCCTGAAGACATTTACGTGGAGT GGACCAACAACGGGAAAACAGAGCTAAACT ACAAGAACACTGAACCAGTCCTGGACTCTGA TGGTTCTTACTTCATGTACAGCAAGCTGAGA GTGGAAAAGAAGAACTGGGTGGAAAGAAAT AGCTACTCCTGTTCAGTGGTCCACGAGGGTC TGCACAATCACCACACGACTAAGAGCTTCTC CCGGACTCCGGGTAAA	
SM1B250	pDR000030224	CAGATCCAGCTGGTGCAGAGCGGCCCTGAGC TGAAGAAACCCGGCGAGACAGTGAAGATCA GCTGCAAGGCCAGCGGCTACACCTTCACCAA CTACGGCATGAACTGGGTCAAGCAGGCCCCT GGCAAGGGCCTGAAGTGGATGGGCTGGATC AACACCTACACCGGCGAGCCCACCTACGCCG ACGACTTCAAGGGCAGATTCGCCTTCAGCCT GGAAACCAGCGCCAGCACCGCCTACCTGCAG ATCAACAACCTGAAGAACGAGGACACCGCC ACCTACTTTTGCGCCAGAAGCCCCAGCTACG GCAGCAGAGGCGCTTGGTTTGCCTATTGGAG CCAGGGCACCCTGGTCACCGTGTCTGCTGCC AAAACAACAGCACCAAGTGTCTATCCACTGG CCCCTGTGTGTGGAGATACAACTGGCTCCTC GGTGACTCTAGGATGCCTGGTCAAGGGTTAT TTCCCTGAGCCAGTGACCTTGACCTGGAACT	849

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		CTGGATCCCTGTCCAGTGGTGTGCACACCTTC CCAGCTGTCCTGCAGTCTGACCTCTACACCCT CAGCAGCTCAGTGACTGTAACCTCGAGCACC TGGCCCAGCCAGTCCATCACCTGCAATGTGG CCCACCCGGCAAGCAGCACCAAGGTGGACA AGAAAATTGAGCCCAGAGGGCCCACAATCA AGCCCTGTCCTCCATGCAAATGCCCAGCACC TAACCTCTTGGGTGGACCATCCGTCTTCATCT TCCCTCCAAAGATCAAGGATGTACTCATGAT CTCCCTGAGCCCCATAGTCACATGTGTGGTG GTGGATGTGAGCGAGGATGACCCAGATGTCC AGATCAGCTGGTTTGTGAACAACGTGGAAGT ACACACAGCTCAGACACAAACCCATAGAGA GGATTACAACAGTACTCTCCGGGTGGTCAGT GCCCTCCCCATCCAGCACCAGGACTGGATGA GTGGCAAGGAGTTCAAATGCAAGGTCAACA ACAAAGACCTCCCAGCGCCCATCGAGAGAAC CATCTCAAAACCCAAAGGGTCAGTAAGAGCT CCACAGGTATATGTCTTGCCTCCACCAGAAG AAGAGATGACTAAGAAACAGGTCACTCTGAC CTGCATGGTCACAGACTTCATGCCTGAAGAC ATTTACGTGGAGTGGACCAACAACGGGAAA ACAGAGCTAAACTACAAGAACACTGAACCA GTCCTGGACTCTGATGGTTCTTACTTCATGTA CAGCAAGCTGAGAGTGGAAAAGAAGAACTG GGTGGAAAGAAATAGCTACTCCTGTTCAGTG GTCCACGAGGGTCTGCACAATCACCACACGA CTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B251	pDR000030225	CAGATCCAGCTGGTGCAGAGCGGCCCTGAGC TGAAGAAACCCGGCGAGACAGTGAAGATCA GCTGCAAGGCCAGCGGCTACACCTTCACCAA CTACGGCATGAACTGGGTCAAGCAGGCCCCT GGCAAGGGCCTGAAGTGGATGGGCTGGATC AACACCTACACCGGCGAGCCCACCTACGCCG ACGACTTCAAGGGCAGATTCGCCTTCAGCCT GGAAACCAGCGCCAGCACCGCCTACCTGCAG ATCAACAACCTGAAGAACGAGGACACCGCC ACCTACTTTTGCGCCAGAAGCCCCAGCTACG GCAGCAGAGGCGCTTGGTTTGCCTACTGGGG CCAGGGCACCCTGGTCACAGTGTCTGCTGCC AAAACAACAGCACCAAGTGTCTATCCACTGG CCCCTGTGTGTGGAGATACAACTGGCTCCTC GGTGACTCTAGGATGCCTGGTCAAGGGTTAT TTCCCTGAGCCAGTGACCTTGACCTGGAACT CTGGATCCCTGTCCAGTGGTGTGCACACCTTC CCAGCTGTCCTGCAGTCTGACCTCTACACCCT CAGCAGCTCAGTGACTGTAACCTCGAGCACC TGGCCCAGCCAGTCCATCACCTGCAATGTGG	850

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		CCCACCCGGCAAGCAGCACCAAGGTGGACA AGAAAATTGAGCCCAGAGGGCCCACAATCA AGCCCTGTCCTCCATGCAAATGCCCAGCACC TAACCTCTTGGGTGGACCATCCGTCTTCATCT TCCCTCCAAAGATCAAGGATGTACTCATGAT CTCCCTGAGCCCCATAGTCACATGTGTGGTG GTGGATGTGAGCGAGGATGACCCAGATGTCC AGATCAGCTGGTTTGTGAACAACGTGGAAGT ACACACAGCTCAGACACAAACCCATAGAGA GGATTACAACAGTACTCTCCGGGTGGTCAGT GCCCTCCCCATCCAGCACCAGGACTGGATGA GTGGCAAGGAGTTCAAATGCAAGGTCAACA ACAAAGACCTCCCAGCGCCCATCGAGAGAAC CATCTCAAAACCCAAAGGGTCAGTAAGAGCT CCACAGGTATATGTCTTGCCTCCACCAGAAG AAGAGATGACTAAGAAACAGGTCACTCTGAC CTGCATGGTCACAGACTTCATGCCTGAAGAC ATTTACGTGGAGTGGACCAACAACGGGAAA ACAGAGCTAAACTACAAGAACACTGAACCA GTCCTGGACTCTGATGGTTCTTACTTCATGTA CAGCAAGCTGAGAGTGGAAAAGAAGAACTG GGTGGAAAGAAATAGCTACTCCTGTTCAGTG GTCCACGAGGGTCTGCACAATCACCACACGA CTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B252	pDR000030226	CAGGTCCAGCTGCAGCAGAGCGGAGCCGAA CTGATGAAGCCTGGGGCCAGCGTGAAGATCA GCTGCAAGGCCAGCGGCTACACCTTCAGCGA CTACTGGATCGAGTGGATCAAGCAGCGGCCT GGCCACGGCCTGGAATGGATGGGAGAGATC CTGCCCGGCAGCGACAAGACCAACTACAACG AGAAGTTCAAGGGCAAGGCCACCTTCACCGC CGACAGCAGCAGCAACACCGCCTACATGCAG CTGAACAGCCTGACCAGCGAGGACAGCGCC GTGTTCTATTGTGCCACAGCCGGCGACGACT ACGTGAAGTGGGGACAGGGCACCCTGGTCAC CGTGTCTGCTGCCAAAACAACAGCACCAAGT GTCTATCCACTGGCCCCTGTGTGTGGAGATA CAACTGGCTCCTCGGTGACTCTAGGATGCCT GGTCAAGGGTTATTTCCCTGAGCCAGTGACC TTGACCTGGAACTCTGGATCCCTGTCCAGTG GTGTGCACACCTTCCCAGCTGTCCTGCAGTCT GACCTCTACACCCTCAGCAGCTCAGTGACTG TAACCTCGAGCACCTGGCCCAGCCAGTCCAT CACCTGCAATGTGGCCCACCCGGCAAGCAGC ACCAAGGTGGACAAGAAAATTGAGCCCAGA GGGCCCACAATCAAGCCCTGTCCTCCATGCA AATGCCCAGCACCTAACCTCTTGGGTGGACC ATCCGTCTTCATCTTCCCTCCAAAGATCAAGG	851

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		ATGTACTCATGATCTCCCTGAGCCCCATAGTC ACATGTGTGGTGGTGGATGTGAGCGAGGATG ACCCAGATGTCCAGATCAGCTGGTTTGTGAA CAACGTGGAAGTACACACAGCTCAGACACA AACCCATAGAGAGGATTACAACAGTACTCTC CGGGTGGTCAGTGCCCTCCCCATCCAGCACC AGGACTGGATGAGTGGCAAGGAGTTCAAAT GCAAGGTCAACAACAAAGACCTCCCAGCGCC CATCGAGAGAACCATCTCAAAACCCAAAGG GTCAGTAAGAGCTCCACAGGTATATGTCTTG CCTCCACCAGAAGAAGAGATGACTAAGAAA CAGGTCACTCTGACCTGCATGGTCACAGACT TCATGCCTGAAGACATTTACGTGGAGTGGAC CAACAACGGGAAAACAGAGCTAAACTACAA GAACACTGAACCAGTCCTGGACTCTGATGGT TCTTACTTCATGTACAGCAAGCTGAGAGTGG AAAAGAAGAACTGGGTGGAAAGAAATAGCT ACTCCTGTTCAGTGGTCCACGAGGGTCTGCA CAATCACCACACGACTAAGAGCTTCTCCCGG ACTCCGGGTAAA	
SM1B253	pDR000030227	GAAGTCCAGCTGCAGCAGAGCGGAGCCGAA CTGGTCAAGCCTGGCGCTTCCGTGAAGCTGA GCTGCACCGCCAGCGGCTTCAACATCAAGGA CACCTACATGCACTGGGTCCGACAGAGGCCC GAGCAGGGCCTGGAATGGATCGGCAGAATC GACCCCGCCAACGACATCACCAAATACGACC CCAAGTTCCAGGGCAAGGCCACCATCACCGC CGACACCAGCAGCAACACAGCCTACCTGCAG CTGAGCAGCCTGACCAGCGAGGACACCGCCG TGTACTACTGCGGCAGAGACTGGGCCGATTA CTGGGGCCAGGGCACCACCCTGACAGTGTCT AGTGCCAAAACAACAGCACCAAGTGTCTATC CACTGGCCCCTGTGTGTGGAGATACAACTGG CTCCTCGGTGACTCTAGGATGCCTGGTCAAG GGTTATTTCCCTGAGCCAGTGACCTTGACCTG GAACTCTGGATCCCTGTCCAGTGGTGTGCAC ACCTTCCCAGCTGTCCTGCAGTCTGACCTCTA CACCCTCAGCAGCTCAGTGACTGTAACCTCG AGCACCTGGCCCAGCCAGTCCATCACCTGCA ATGTGGCCCACCCGGCAAGCAGCACCAAGGT GGACAAGAAAATTGAGCCCAGAGGGCCCAC AATCAAGCCCTGTCCTCCATGCAAATGCCCA GCACCTAACCTCTTGGGTGGACCATCCGTCTT CATCTTCCCTCCAAAGATCAAGGATGTACTC ATGATCTCCCTGAGCCCCATAGTCACATGTG TGGTGGTGGATGTGAGCGAGGATGACCCAGA TGTCCAGATCAGCTGGTTTGTGAACAACGTG GAAGTACACACAGCTCAGACACAAACCCATA	852

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		GAGAGGATTACAACAGTACTCTCCGGGTGGT CAGTGCCCTCCCCATCCAGCACCAGGACTGG ATGAGTGGCAAGGAGTTCAAATGCAAGGTCA ACAACAAAGACCTCCCAGCGCCCATCGAGAG AACCATCTCAAAACCCAAAGGGTCAGTAAGA GCTCCACAGGTATATGTCTTGCCTCCACCAG AAGAAGAGATGACTAAGAAACAGGTCACTC TGACCTGCATGGTCACAGACTTCATGCCTGA AGACATTTACGTGGAGTGGACCAACAACGGG AAAACAGAGCTAAACTACAAGAACACTGAA CCAGTCCTGGACTCTGATGGTTCTTACTTCAT GTACAGCAAGCTGAGAGTGGAAAAGAAGAA CTGGGTGGAAAGAAATAGCTACTCCTGTTCA GTGGTCCACGAGGGTCTGCACAATCACCACA CGACTAAGAGCTTCTCCCGGACTCCGGGTAA A	
SM1B254	pDR000030228	GAAGTCCAGCTGCAGCAGAGCGGAGCCGAA CTGGTCAAGCCTGGCGCTTCCGTGAAGCTGA GCTGCACCGCCAGCGGCTTCAACATCAAGGA CACCTACATGCACTGGGTCAAGCAGCGGAGC GAGCAGGGCCTGGAATGGATCGGCAGAATC AACCCCGCCAACGACAACACCAAATACGACC CCAAGTTCCAGGGCAAGGCCACCATCACCGC CGACACCAGCAGCAACACAGCCTACCTGCAG CTGAGCAGCCTGACCAGCGAGGACACCGCCG TGTACTACTGCGGCAGAGACTGGGCCGATTA CTGGGGCCAGGGCACCACCCTGACAGTGTCT AGTGCCAAAACAACAGCACCAAGTGTCTATC CACTGGCCCCTGTGTGTGGAGATACAACTGG CTCCTCGGTGACTCTAGGATGCCTGGTCAAG GGTTATTTCCCTGAGCCAGTGACCTTGACCTG GAACTCTGGATCCCTGTCCAGTGGTGTGCAC ACCTTCCCAGCTGTCCTGCAGTCTGACCTCTA CACCCTCAGCAGCTCAGTGACTGTAACCTCG AGCACCTGGCCCAGCCAGTCCATCACCTGCA ATGTGGCCCACCCGGCAAGCAGCACCAAGGT GGACAAGAAAATTGAGCCCAGAGGGCCCAC AATCAAGCCCTGTCCTCCATGCAAATGCCCA GCACCTAACCTCTTGGGTGGACCATCCGTCTT CATCTTCCCTCCAAAGATCAAGGATGTACTC ATGATCTCCCTGAGCCCCATAGTCACATGTG TGGTGGTGGATGTGAGCGAGGATGACCCAGA TGTCCAGATCAGCTGGTTTGTGAACAACGTG GAAGTACACACAGCTCAGACACAAACCCATA GAGAGGATTACAACAGTACTCTCCGGGTGGT CAGTGCCCTCCCCATCCAGCACCAGGACTGG ATGAGTGGCAAGGAGTTCAAATGCAAGGTCA ACAACAAAGACCTCCCAGCGCCCATCGAGAG	853

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		AACCATCTCAAAACCCAAAGGGTCAGTAAGA GCTCCACAGGTATATGTCTTGCCTCCACCAG AAGAAGAGATGACTAAGAAACAGGTCACTC TGACCTGCATGGTCACAGACTTCATGCCTGA AGACATTTACGTGGAGTGGACCAACAACGGG AAAACAGAGCTAAACTACAAGAACACTGAA CCAGTCCTGGACTCTGATGGTTCTTACTTCAT GTACAGCAAGCTGAGAGTGGAAAAGAAGAA CTGGGTGGAAAGAAATAGCTACTCCTGTTCA GTGGTCCACGAGGGTCTGCACAATCACCACA CGACTAAGAGCTTCTCCCGGACTCCGGGTAA A	
SM1B255	pDR000030229	CAGGTCCAGCTGCAGCAGCCTGGCGCTGAAC TGGTCAAGCCAGGCGCTTCCGTGAAGCTGAG CTGCAAGGCCAGCGGCTACACCTTCACCCGG TACTGGATGCACTGGGTCAAGCAGAGGCCAG GCCAGGGCCTGGAATGGATCGGCGAGATCA ACCCCAACAACGGCCACACCAACTACAACGA GAAGTTCGAGAGCCGGGCCACCCTGACCGTG GACAAGAGCAGCAGCACCGCCTACATGCAGT TCAACAGCCTGACCAGCGAGGACAGCGCCGT GTACTACTGCGGCAGACTGGATGGCCACCTG TACGCCGTGGATTACTGGGGCCAGGGCACCA GCGTGACCGTGTCATCTGCCAAAACAACAGC ACCAAGTGTCTATCCACTGGCCCCTGTGTGT GGAGATACAACTGGCTCCTCGGTGACTCTAG GATGCCTGGTCAAGGGTTATTTCCCTGAGCC AGTGACCTTGACCTGGAACTCTGGATCCCTG TCCAGTGGTGTGCACACCTTCCCAGCTGTCCT GCAGTCTGACCTCTACACCCTCAGCAGCTCA GTGACTGTAACCTCGAGCACCTGGCCCAGCC AGTCCATCACCTGCAATGTGGCCCACCCGGC AAGCAGCACCAAGGTGGACAAGAAAATTGA GCCCAGAGGGCCCACAATCAAGCCCTGTCCT CCATGCAAATGCCCAGCACCTAACCTCTTGG GTGGACCATCCGTCTTCATCTTCCCTCCAAAG ATCAAGGATGTACTCATGATCTCCCTGAGCC CCATAGTCACATGTGTGGTGGTGGATGTGAG CGAGGATGACCCAGATGTCCAGATCAGCTGG TTTGTGAACAACGTGGAAGTACACACAGCTC AGACACAAACCCATAGAGAGGATTACAACA GTACTCTCCGGGTGGTCAGTGCCCTCCCCATC CAGCACCAGGACTGGATGAGTGGCAAGGAG TTCAAATGCAAGGTCAACAACAAAGACCTCC CAGCGCCCATCGAGAGAACCATCTCAAAACC CAAAGGGTCAGTAAGAGCTCCACAGGTATAT GTCTTGCCTCCACCAGAAGAAGAGATGACTA AGAAACAGGTCACTCTGACCTGCATGGTCAC	854

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		AGACTTCATGCCTGAAGACATTTACGTGGAG TGGACCAACAACGGGAAAACAGAGCTAAAC TACAAGAACACTGAACCAGTCCTGGACTCTG ATGGTTCTTACTTCATGTACAGCAAGCTGAG AGTGGAAAAGAAGAACTGGGTGGAAAGAAA TAGCTACTCCTGTTCAGTGGTCCACGAGGGT CTGCACAATCACCACACGACTAAGAGCTTCT CCCGGACTCCGGGTAAA	
SM1B256	pDR000030230	CAGGTCCAGCTGCAGCAGCCTGGCACAGAGC TGAAGATGCCCGGCACCAGCGTGAAGCTGAG CTGCAAGGCCAGCGGCTACACCTTCACCACC TACTGGATGCACTGGGTCAAGCTGCGGCCAG GCCAGGGCTTTGAGTGGATCGGCGAGATCAA CCCCAGCAACGACGGCACCAACTACAACGA GAAGTTCAAGCGGAAGGCCACCCTGACCGTG GACAAGCCTAGCAGCACCGCCTACATGCAGC TGTCCAGCCTGACCAGCGAGGACAGCACCAT CTACTACTGCACCATCAGCTACTACGGCTAC GGCGACTTCGACTACTGGGGCCAGGGCACCA CACTGACAGTGTCCTCTGCCAAAACAACAGC ACCAAGTGTCTATCCACTGGCCCCTGTGTGT GGAGATACAACTGGCTCCTCGGTGACTCTAG GATGCCTGGTCAAGGGTTATTTCCCTGAGCC AGTGACCTTGACCTGGAACTCTGGATCCCTG TCCAGTGGTGTGCACACCTTCCCAGCTGTCCT GCAGTCTGACCTCTACACCCTCAGCAGCTCA GTGACTGTAACCTCGAGCACCTGGCCCAGCC AGTCCATCACCTGCAATGTGGCCCACCCGGC AAGCAGCACCAAGGTGGACAAGAAAATTGA GCCCAGAGGGCCCACAATCAAGCCCTGTCCT CCATGCAAATGCCCAGCACCTAACCTCTTGG GTGGACCATCCGTCTTCATCTTCCCTCCAAAG ATCAAGGATGTACTCATGATCTCCCTGAGCC CCATAGTCACATGTGTGGTGGTGGATGTGAG CGAGGATGACCCAGATGTCCAGATCAGCTGG TTTGTGAACAACGTGGAAGTACACACAGCTC AGACACAAACCCATAGAGAGGATTACAACA GTACTCTCCGGGTGGTCAGTGCCCTCCCCATC CAGCACCAGGACTGGATGAGTGGCAAGGAG TTCAAATGCAAGGTCAACAACAAAGACCTCC CAGCGCCCATCGAGAGAACCATCTCAAAACC CAAAGGGTCAGTAAGAGCTCCACAGGTATAT GTCTTGCCTCCACCAGAAGAAGAGATGACTA AGAAACAGGTCACTCTGACCTGCATGGTCAC AGACTTCATGCCTGAAGACATTTACGTGGAG TGGACCAACAACGGGAAAACAGAGCTAAAC TACAAGAACACTGAACCAGTCCTGGACTCTG ATGGTTCTTACTTCATGTACAGCAAGCTGAG	855

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		AGTGGAAAAGAAGAACTGGGTGGAAAGAAA TAGCTACTCCTGTTCAGTGGTCCACGAGGGT CTGCACAATCACCACACGACTAAGAGCTTCT CCCGGACTCCGGGTAAA	
SM1B257	pDR000030231	CAGGTGCAGCTGAAAGAGTCCGGCCCTGATC TGGTGCAGCCCAGCCAGACCCTGAGCCTGAC CTGTACCGTGTCCGGCTTCAGCCTGACCAGC TACGGCGTGCACTGGGTCCGACAGCCACCTG GCAAAGGCCTGGAATGGGTCGGAACCATGG GCTGGAACGACAAGAAGTACTACAACAGCG CCCTGAAGTCCCGGCTGAGCATCAGCAGAAA CACCAGCAAGAACCAGGTGTTCCTGAAGCTG AGCAGCCTGCAGACCGAGGACACCGCCATGT ACTACTGCACCAGGGACGGCGATAGCAGCG GCAGTTGGTTCGCCTATTGGGGCCAGGGCAC CCTGGTCACCGTGTCTAGTGCCAAAACAACA GCACCAAGTGTCTATCCACTGGCCCCTGTGT GTGGAGATACAACTGGCTCCTCGGTGACTCT AGGATGCCTGGTCAAGGGTTATTTCCCTGAG CCAGTGACCTTGACCTGGAACTCTGGATCCC TGTCCAGTGGTGTGCACACCTTCCCAGCTGTC CTGCAGTCTGACCTCTACACCCTCAGCAGCT CAGTGACTGTAACCTCGAGCACCTGGCCCAG CCAGTCCATCACCTGCAATGTGGCCCACCCG GCAAGCAGCACCAAGGTGGACAAGAAAATT GAGCCCAGAGGGCCCACAATCAAGCCCTGTC CTCCATGCAAATGCCCAGCACCTAACCTCTT GGGTGGACCATCCGTCTTCATCTTCCCTCCAA AGATCAAGGATGTACTCATGATCTCCCTGAG CCCCATAGTCACATGTGTGGTGGTGGATGTG AGCGAGGATGACCCAGATGTCCAGATCAGCT GGTTTGTGAACAACGTGGAAGTACACACAGC TCAGACACAAACCCATAGAGAGGATTACAAC AGTACTCTCCGGGTGGTCAGTGCCCTCCCCA TCCAGCACCAGGACTGGATGAGTGGCAAGG AGTTCAAATGCAAGGTCAACAACAAAGACCT CCCAGCGCCCATCGAGAGAACCATCTCAAAA CCCAAAGGGTCAGTAAGAGCTCCACAGGTAT ATGTCTTGCCTCCACCAGAAGAAGAGATGAC TAAGAAACAGGTCACTCTGACCTGCATGGTC ACAGACTTCATGCCTGAAGACATTTACGTGG AGTGGACCAACAACGGGAAAACAGAGCTAA ACTACAAGAACACTGAACCAGTCCTGGACTC TGATGGTTCTTACTTCATGTACAGCAAGCTG AGAGTGGAAAAGAAGAACTGGGTGGAAAGA AATAGCTACTCCTGTTCAGTGGTCCACGAGG GTCTGCACAATCACCACACGACTAAGAGCTT CTCCCGGACTCCGGGTAAA	856

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
SM1B258	pDR000030232	CAGGTGCAGCTGAAAGAGTCCGGCCCTGATC TGGTGCAGCCCAGCCAGACCCTGAGCCTGAC CTGTACCGTGTCCGGCTTCAGCCTGACAGGC TACGCTGTGCATTGGGTCCGACAGCCTCCAG GCAAGGGCGTGGAATGGGTCGGAACCATGG GCTGGGACGACAAGAAGTTCTACAACAGCGC CCTGAAGTCCCGGCTGAGCATCTCCAGGGAC CCCAGCAAGAACCAGGTGTTCTTCAAGCTGA GCAGCCTGCAGACCGAGGACACCGCCATGTA CTACTGCACCAGGGATCACGGCGACGGCGGC TTTGCCTATTGGGGCCAGGGAACCCTGGTCA CCGTGTCCTCTGCCAAAACAACAGCACCAAG TGTCTATCCACTGGCCCCTGTGTGTGGAGAT ACAACTGGCTCCTCGGTGACTCTAGGATGCC TGGTCAAGGGTTATTTCCCTGAGCCAGTGAC CTTGACCTGGAACTCTGGATCCCTGTCCAGT GGTGTGCACACCTTCCCAGCTGTCCTGCAGT CTGACCTCTACACCCTCAGCAGCTCAGTGAC TGTAACCTCGAGCACCTGGCCCAGCCAGTCC ATCACCTGCAATGTGGCCCACCCGGCAAGCA GCACCAAGGTGGACAAGAAAATTGAGCCCA GAGGGCCCACAATCAAGCCCTGTCCTCCATG CAAATGCCCAGCACCTAACCTCTTGGGTGGA CCATCCGTCTTCATCTTCCCTCCAAAGATCAA GGATGTACTCATGATCTCCCTGAGCCCCATA GTCACATGTGTGGTGGTGGATGTGAGCGAGG ATGACCCAGATGTCCAGATCAGCTGGTTTGT GAACAACGTGGAAGTACACACAGCTCAGAC ACAAACCCATAGAGAGGATTACAACAGTACT CTCCGGGTGGTCAGTGCCCTCCCCATCCAGC ACCAGGACTGGATGAGTGGCAAGGAGTTCA AATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAAA GGGTCAGTAAGAGCTCCACAGGTATATGTCT TGCCTCCACCAGAAGAAGAGATGACTAAGA AACAGGTCACTCTGACCTGCATGGTCACAGA CTTCATGCCTGAAGACATTTACGTGGAGTGG ACCAACAACGGGAAAACAGAGCTAAACTAC AAGAACACTGAACCAGTCCTGGACTCTGATG GTTCTTACTTCATGTACAGCAAGCTGAGAGT GGAAAAGAAGAACTGGGTGGAAAGAAATAG CTACTCCTGTTCAGTGGTCCACGAGGGTCTG CACAATCACCACACGACTAAGAGCTTCTCCC GGACTCCGGGTAAA	857
SM1B259	pDR000030233	GAAGTCCAGCTGCAGCAGTCTGGCCCTGAGC TGGTCAAGCCTGGGGCCAGCGTGAAGATCCC ATGCAAGGCCAGCGGCTACACCTTCACCGAC TACAACATGGACTGGGTCAAGCAGAGCCACG	858

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		GCAAGAGCCTGGAATGGATCGGCAACATCA ACCCCAACAACGGCGGCACCATCTACAACCA GAACTTCAAGGACCGGGCCACCCTGACCGTG GACAAGAGCAGCAGCACCGCCTACATGGAA CTGCGGAGCCTGACCAGCGAGGACACCGCCG TGTACTACTGCACCAGAGAGAACTCCGGCTA CGGCGGCAACTACTTCGCCTATTGGGGCCAG GGCACCACACTGACAGTGTCCTCTGCCAAAA CAACAGCACCAAGTGTCTATCCACTGGCCCC TGTGTGTGGAGATACAACTGGCTCCTCGGTG ACTCTAGGATGCCTGGTCAAGGGTTATTTCC CTGAGCCAGTGACCTTGACCTGGAACTCTGG ATCCCTGTCCAGTGGTGTGCACACCTTCCCA GCTGTCCTGCAGTCTGACCTCTACACCCTCAG CAGCTCAGTGACTGTAACCTCGAGCACCTGG CCCAGCCAGTCCATCACCTGCAATGTGGCCC ACCCGGCAAGCAGCACCAAGGTGGACAAGA AAATTGAGCCCAGAGGGCCCACAATCAAGCC CTGTCCTCCATGCAAATGCCCAGCACCTAAC CTCTTGGGTGGACCATCCGTCTTCATCTTCCC TCCAAAGATCAAGGATGTACTCATGATCTCC CTGAGCCCCATAGTCACATGTGTGGTGGTGG ATGTGAGCGAGGATGACCCAGATGTCCAGAT CAGCTGGTTTGTGAACAACGTGGAAGTACAC ACAGCTCAGACACAAACCCATAGAGAGGATT ACAACAGTACTCTCCGGGTGGTCAGTGCCCT CCCCATCCAGCACCAGGACTGGATGAGTGGC AAGGAGTTCAAATGCAAGGTCAACAACAAA GACCTCCCAGCGCCCATCGAGAGAACCATCT CAAAACCCAAAGGGTCAGTAAGAGCTCCAC AGGTATATGTCTTGCCTCCACCAGAAGAAGA GATGACTAAGAAACAGGTCACTCTGACCTGC ATGGTCACAGACTTCATGCCTGAAGACATTT ACGTGGAGTGGACCAACAACGGGAAAACAG AGCTAAACTACAAGAACACTGAACCAGTCCT GGACTCTGATGGTTCTTACTTCATGTACAGCA AGCTGAGAGTGGAAAAGAAGAACTGGGTGG AAAGAAATAGCTACTCCTGTTCAGTGGTCCA CGAGGGTCTGCACAATCACCACACGACTAAG AGCTTCTCCCGGACTCCGGGTAAA	
SM1B260	pDR000030234	GAAGTCCAGCTGCAGCAGAGCGGAGCCGAA CTCGTCAGACCTGGCGCTTCCGTGAAGCTGA GCTGCACCACCAGCGGCTTCAACATCAAGGA CAGCCTGATCTACTGGGTCAAGCAGCGGCCC GAGCAGGGCCTGGAATGGATCGGCTGGATTG ACCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAGC GACACCAGCAGCAACACCGCCTACCTGAGAC	859

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		TGAGCAGCCTGACCAGCGAGGACACCGCCAT CTACTACTGCACCCGGTCCTTCGGCGTGTGTT GGGGCCAGGGAACCCTGGTCACAGTGTCTGC TGCCAAAACAACAGCACCAAGTGTCTATCCA CTGGCCCCTGTGTGTGGAGATACAACTGGCT CCTCGGTGACTCTAGGATGCCTGGTCAAGGG TTATTTCCCTGAGCCAGTGACCTTGACCTGGA ACTCTGGATCCCTGTCCAGTGGTGTGCACAC CTTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAG CACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTG GACAAGAAAATTGAGCCCAGAGGGCCCACA ATCAAGCCCTGTCCTCCATGCAAATGCCCAG CACCTAACCTCTTGGGTGGACCATCCGTCTTC ATCTTCCCTCCAAAGATCAAGGATGTACTCA TGATCTCCCTGAGCCCCATAGTCACATGTGT GGTGGTGGATGTGAGCGAGGATGACCCAGAT GTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAG AGAGGATTACAACAGTACTCTCCGGGTGGTC AGTGCCCTCCCCATCCAGCACCAGGACTGGA TGAGTGGCAAGGAGTTCAAATGCAAGGTCAA CAACAAAGACCTCCCAGCGCCCATCGAGAGA ACCATCTCAAAACCCAAAGGGTCAGTAAGAG CTCCACAGGTATATGTCTTGCCTCCACCAGA AGAAGAGATGACTAAGAAACAGGTCACTCT GACCTGCATGGTCACAGACTTCATGCCTGAA GACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAAC CAGTCCTGGACTCTGATGGTTCTTACTTCATG TACAGCAAGCTGAGAGTGGAAAAGAAGAAC TGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACAC GACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B261	pDR000030234	GAAGTCCAGCTGCAGCAGAGCGGAGCCGAA CTCGTCAGACCTGGCGCTTCCGTGAAGCTGA GCTGCACCACCAGCGGCTTCAACATCAAGGA CAGCCTGATCTACTGGGTCAAGCAGCGGCCC GAGCAGGGCCTGGAATGGATCGGCTGGATTG ACCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAGC GACACCAGCAGCAACACCGCCTACCTGAGAC TGAGCAGCCTGACCAGCGAGGACACCGCCAT CTACTACTGCACCCGGTCCTTCGGCGTGTGTT GGGGCCAGGGAACCCTGGTCACAGTGTCTGC TGCCAAAACAACAGCACCAAGTGTCTATCCA CTGGCCCCTGTGTGTGGAGATACAACTGGCT	860

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		CCTCGGTGACTCTAGGATGCCTGGTCAAGGG TTATTTCCCTGAGCCAGTGACCTTGACCTGGA ACTCTGGATCCCTGTCCAGTGGTGTGCACAC CTTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAG CACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTG GACAAGAAAATTGAGCCCAGAGGGCCCACA ATCAAGCCCTGTCCTCCATGCAAATGCCCAG CACCTAACCTCTTGGGTGGACCATCCGTCTTC ATCTTCCCTCCAAAGATCAAGGATGTACTCA TGATCTCCCTGAGCCCCATAGTCACATGTGT GGTGGTGGATGTGAGCGAGGATGACCCAGAT GTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAG AGAGGATTACAACAGTACTCTCCGGGTGGTC AGTGCCCTCCCCATCCAGCACCAGGACTGGA TGAGTGGCAAGGAGTTCAAATGCAAGGTCAA CAACAAAGACCTCCCAGCGCCCATCGAGAGA ACCATCTCAAAACCCAAAGGGTCAGTAAGAG CTCCACAGGTATATGTCTTGCCTCCACCAGA AGAAGAGATGACTAAGAAACAGGTCACTCT GACCTGCATGGTCACAGACTTCATGCCTGAA GACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAAC CAGTCCTGGACTCTGATGGTTCTTACTTCATG TACAGCAAGCTGAGAGTGGAAAAGAAGAAC TGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACAC GACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B262	pDR000030234	GAAGTCCAGCTGCAGCAGAGCGGAGCCGAA CTCGTCAGACCTGGCGCTTCCGTGAAGCTGA GCTGCACCACCAGCGGCTTCAACATCAAGGA CAGCCTGATCTACTGGGTCAAGCAGCGGCCC GAGCAGGGCCTGGAATGGATCGGCTGGATTG ACCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAGC GACACCAGCAGCAACACCGCCTACCTGAGAC TGAGCAGCCTGACCAGCGAGGACACCGCCAT CTACTACTGCACCCGGTCCTTCGGCGTGTGTT GGGGCCAGGGAACCCTGGTCACAGTGTCTGC TGCCAAAACAACAGCACCAAGTGTCTATCCA CTGGCCCCTGTGTGTGGAGATACAACTGGCT CCTCGGTGACTCTAGGATGCCTGGTCAAGGG TTATTTCCCTGAGCCAGTGACCTTGACCTGGA ACTCTGGATCCCTGTCCAGTGGTGTGCACAC CTTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAG	861

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		CACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTG GACAAGAAAATTGAGCCCAGAGGGCCCACA ATCAAGCCCTGTCCTCCATGCAAATGCCCAG CACCTAACCTCTTGGGTGGACCATCCGTCTTC ATCTTCCCTCCAAAGATCAAGGATGTACTCA TGATCTCCCTGAGCCCCATAGTCACATGTGT GGTGGTGGATGTGAGCGAGGATGACCCAGAT GTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAG AGAGGATTACAACAGTACTCTCCGGGTGGTC AGTGCCCTCCCCATCCAGCACCAGGACTGGA TGAGTGGCAAGGAGTTCAAATGCAAGGTCAA CAACAAAGACCTCCCAGCGCCCATCGAGAGA ACCATCTCAAAACCCAAAGGGTCAGTAAGAG CTCCACAGGTATATGTCTTGCCTCCACCAGA AGAAGAGATGACTAAGAAACAGGTCACTCT GACCTGCATGGTCACAGACTTCATGCCTGAA GACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAAC CAGTCCTGGACTCTGATGGTTCTTACTTCATG TACAGCAAGCTGAGAGTGGAAAAGAAGAAC TGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACAC GACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B263	pDR000030234	GAAGTCCAGCTGCAGCAGAGCGGAGCCGAA CTCGTCAGACCTGGCGCTTCCGTGAAGCTGA GCTGCACCACCAGCGGCTTCAACATCAAGGA CAGCCTGATCTACTGGGTCAAGCAGCGGCCC GAGCAGGGCCTGGAATGGATCGGCTGGATTG ACCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAGC GACACCAGCAGCAACACCGCCTACCTGAGAC TGAGCAGCCTGACCAGCGAGGACACCGCCAT CTACTACTGCACCCGGTCCTTCGGCGTGTGTT GGGGCCAGGGAACCCTGGTCACAGTGTCTGC TGCCAAAACAACAGCACCAAGTGTCTATCCA CTGGCCCCTGTGTGTGGAGATACAACTGGCT CCTCGGTGACTCTAGGATGCCTGGTCAAGGG TTATTTCCCTGAGCCAGTGACCTTGACCTGGA ACTCTGGATCCCTGTCCAGTGGTGTGCACAC CTTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAG CACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTG GACAAGAAAATTGAGCCCAGAGGGCCCACA ATCAAGCCCTGTCCTCCATGCAAATGCCCAG CACCTAACCTCTTGGGTGGACCATCCGTCTTC	862

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		ATCTTCCCTCCAAAGATCAAGGATGTACTCA TGATCTCCCTGAGCCCCATAGTCACATGTGT GGTGGTGGATGTGAGCGAGGATGACCCAGAT GTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAG AGAGGATTACAACAGTACTCTCCGGGTGGTC AGTGCCCTCCCCATCCAGCACCAGGACTGGA TGAGTGGCAAGGAGTTCAAATGCAAGGTCAA CAACAAAGACCTCCCAGCGCCCATCGAGAGA ACCATCTCAAAACCCAAAGGGTCAGTAAGAG CTCCACAGGTATATGTCTTGCCTCCACCAGA AGAAGAGATGACTAAGAAACAGGTCACTCT GACCTGCATGGTCACAGACTTCATGCCTGAA GACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAAC CAGTCCTGGACTCTGATGGTTCTTACTTCATG TACAGCAAGCTGAGAGTGGAAAAGAAGAAC TGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACAC GACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B264	pDR000030234	GAAGTCCAGCTGCAGCAGAGCGGAGCCGAA CTCGTCAGACCTGGCGCTTCCGTGAAGCTGA GCTGCACCACCAGCGGCTTCAACATCAAGGA CAGCCTGATCTACTGGGTCAAGCAGCGGCCC GAGCAGGGCCTGGAATGGATCGGCTGGATTG ACCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAGC GACACCAGCAGCAACACCGCCTACCTGAGAC TGAGCAGCCTGACCAGCGAGGACACCGCCAT CTACTACTGCACCCGGTCCTTCGGCGTGTGTT GGGGCCAGGGAACCCTGGTCACAGTGTCTGC TGCCAAAACAACAGCACCAAGTGTCTATCCA CTGGCCCCTGTGTGTGGAGATACAACTGGCT CCTCGGTGACTCTAGGATGCCTGGTCAAGGG TTATTTCCCTGAGCCAGTGACCTTGACCTGGA ACTCTGGATCCCTGTCCAGTGGTGTGCACAC CTTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAG CACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTG GACAAGAAAATTGAGCCCAGAGGGCCCACA ATCAAGCCCTGTCCTCCATGCAAATGCCCAG CACCTAACCTCTTGGGTGGACCATCCGTCTTC ATCTTCCCTCCAAAGATCAAGGATGTACTCA TGATCTCCCTGAGCCCCATAGTCACATGTGT GGTGGTGGATGTGAGCGAGGATGACCCAGAT GTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAG	863

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		AGAGGATTACAACAGTACTCTCCGGGTGGTC AGTGCCCTCCCCATCCAGCACCAGGACTGGA TGAGTGGCAAGGAGTTCAAATGCAAGGTCAA CAACAAAGACCTCCCAGCGCCCATCGAGAGA ACCATCTCAAAACCCAAAGGGTCAGTAAGAG CTCCACAGGTATATGTCTTGCCTCCACCAGA AGAAGAGATGACTAAGAAACAGGTCACTCT GACCTGCATGGTCACAGACTTCATGCCTGAA GACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAAC CAGTCCTGGACTCTGATGGTTCTTACTTCATG TACAGCAAGCTGAGAGTGGAAAAGAAGAAC TGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACAC GACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B265	pDR000030234	GAAGTCCAGCTGCAGCAGAGCGGAGCCGAA CTCGTCAGACCTGGCGCTTCCGTGAAGCTGA GCTGCACCACCAGCGGCTTCAACATCAAGGA CAGCCTGATCTACTGGGTCAAGCAGCGGCCC GAGCAGGGCCTGGAATGGATCGGCTGGATTG ACCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAGC GACACCAGCAGCAACACCGCCTACCTGAGAC TGAGCAGCCTGACCAGCGAGGACACCGCCAT CTACTACTGCACCCGGTCCTTCGGCGTGTGTT GGGGCCAGGGAACCCTGGTCACAGTGTCTGC TGCCAAAACAACAGCACCAAGTGTCTATCCA CTGGCCCCTGTGTGTGGAGATACAACTGGCT CCTCGGTGACTCTAGGATGCCTGGTCAAGGG TTATTTCCCTGAGCCAGTGACCTTGACCTGGA ACTCTGGATCCCTGTCCAGTGGTGTGCACAC CTTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAG CACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTG GACAAGAAAATTGAGCCCAGAGGGCCCACA ATCAAGCCCTGTCCTCCATGCAAATGCCCAG CACCTAACCTCTTGGGTGGACCATCCGTCTTC ATCTTCCCTCCAAAGATCAAGGATGTACTCA TGATCTCCCTGAGCCCCATAGTCACATGTGT GGTGGTGGATGTGAGCGAGGATGACCCAGAT GTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAG AGAGGATTACAACAGTACTCTCCGGGTGGTC AGTGCCCTCCCCATCCAGCACCAGGACTGGA TGAGTGGCAAGGAGTTCAAATGCAAGGTCAA CAACAAAGACCTCCCAGCGCCCATCGAGAGA ACCATCTCAAAACCCAAAGGGTCAGTAAGAG	864

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		CTCCACAGGTATATGTCTTGCCTCCACCAGA AGAAGAGATGACTAAGAAACAGGTCACTCT GACCTGCATGGTCACAGACTTCATGCCTGAA GACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAAC CAGTCCTGGACTCTGATGGTTCTTACTTCATG TACAGCAAGCTGAGAGTGGAAAAGAAGAAC TGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACAC GACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B266	pDR000030234	GAAGTCCAGCTGCAGCAGAGCGGAGCCGAA CTCGTCAGACCTGGCGCTTCCGTGAAGCTGA GCTGCACCACCAGCGGCTTCAACATCAAGGA CAGCCTGATCTACTGGGTCAAGCAGCGGCCC GAGCAGGGCCTGGAATGGATCGGCTGGATTG ACCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAGC GACACCAGCAGCAACACCGCCTACCTGAGAC TGAGCAGCCTGACCAGCGAGGACACCGCCAT CTACTACTGCACCCGGTCCTTCGGCGTGTGTT GGGGCCAGGGAACCCTGGTCACAGTGTCTGC TGCCAAAACAACAGCACCAAGTGTCTATCCA CTGGCCCCTGTGTGTGGAGATACAACTGGCT CCTCGGTGACTCTAGGATGCCTGGTCAAGGG TTATTTCCCTGAGCCAGTGACCTTGACCTGGA ACTCTGGATCCCTGTCCAGTGGTGTGCACAC CTTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAG CACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTG GACAAGAAAATTGAGCCCAGAGGGCCCACA ATCAAGCCCTGTCCTCCATGCAAATGCCCAG CACCTAACCTCTTGGGTGGACCATCCGTCTTC ATCTTCCCTCCAAAGATCAAGGATGTACTCA TGATCTCCCTGAGCCCCATAGTCACATGTGT GGTGGTGGATGTGAGCGAGGATGACCCAGAT GTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAG AGAGGATTACAACAGTACTCTCCGGGTGGTC AGTGCCCTCCCCATCCAGCACCAGGACTGGA TGAGTGGCAAGGAGTTCAAATGCAAGGTCAA CAACAAAGACCTCCCAGCGCCCATCGAGAGA ACCATCTCAAAACCCAAAGGGTCAGTAAGAG CTCCACAGGTATATGTCTTGCCTCCACCAGA AGAAGAGATGACTAAGAAACAGGTCACTCT GACCTGCATGGTCACAGACTTCATGCCTGAA GACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAAC	865

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		CAGTCCTGGACTCTGATGGTTCTTACTTCATG TACAGCAAGCTGAGAGTGGAAAAGAAGAAC TGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACAC GACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B267	pDR000030234	GAAGTCCAGCTGCAGCAGAGCGGAGCCGAA CTCGTCAGACCTGGCGCTTCCGTGAAGCTGA GCTGCACCACCAGCGGCTTCAACATCAAGGA CAGCCTGATCTACTGGGTCAAGCAGCGGCCC GAGCAGGGCCTGGAATGGATCGGCTGGATTG ACCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAGC GACACCAGCAGCAACACCGCCTACCTGAGAC TGAGCAGCCTGACCAGCGAGGACACCGCCAT CTACTACTGCACCCGGTCCTTCGGCGTGTGTT GGGGCCAGGGAACCCTGGTCACAGTGTCTGC TGCCAAAACAACAGCACCAAGTGTCTATCCA CTGGCCCCTGTGTGTGGAGATACAACTGGCT CCTCGGTGACTCTAGGATGCCTGGTCAAGGG TTATTTCCCTGAGCCAGTGACCTTGACCTGGA ACTCTGGATCCCTGTCCAGTGGTGTGCACAC CTTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAG CACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTG GACAAGAAAATTGAGCCCAGAGGGCCCACA ATCAAGCCCTGTCCTCCATGCAAATGCCCAG CACCTAACCTCTTGGGTGGACCATCCGTCTTC ATCTTCCCTCCAAAGATCAAGGATGTACTCA TGATCTCCCTGAGCCCCATAGTCACATGTGT GGTGGTGGATGTGAGCGAGGATGACCCAGAT GTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAG AGAGGATTACAACAGTACTCTCCGGGTGGTC AGTGCCCTCCCCATCCAGCACCAGGACTGGA TGAGTGGCAAGGAGTTCAAATGCAAGGTCAA CAACAAAGACCTCCCAGCGCCCATCGAGAGA ACCATCTCAAAACCCAAAGGGTCAGTAAGAG CTCCACAGGTATATGTCTTGCCTCCACCAGA AGAAGAGATGACTAAGAAACAGGTCACTCT GACCTGCATGGTCACAGACTTCATGCCTGAA GACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAAC CAGTCCTGGACTCTGATGGTTCTTACTTCATG TACAGCAAGCTGAGAGTGGAAAAGAAGAAC TGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACAC GACTAAGAGCTTCTCCCGGACTCCGGGTAAA	866

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
SM1B268	pDR000030234	GAAGTCCAGCTGCAGCAGAGCGGAGCCGAA CTCGTCAGACCTGGCGCTTCCGTGAAGCTGA GCTGCACCACCAGCGGCTTCAACATCAAGGA CAGCCTGATCTACTGGGTCAAGCAGCGGCCC GAGCAGGGCCTGGAATGGATCGGCTGGATTG ACCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAGC GACACCAGCAGCAACACCGCCTACCTGAGAC TGAGCAGCCTGACCAGCGAGGACACCGCCAT CTACTACTGCACCCGGTCCTTCGGCGTGTGTT GGGGCCAGGGAACCCTGGTCACAGTGTCTGC TGCCAAAACAACAGCACCAAGTGTCTATCCA CTGGCCCCTGTGTGTGGAGATACAACTGGCT CCTCGGTGACTCTAGGATGCCTGGTCAAGGG TTATTTCCCTGAGCCAGTGACCTTGACCTGGA ACTCTGGATCCCTGTCCAGTGGTGTGCACAC CTTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAG CACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTG GACAAGAAAATTGAGCCCAGAGGGCCCACA ATCAAGCCCTGTCCTCCATGCAAATGCCCAG CACCTAACCTCTTGGGTGGACCATCCGTCTTC ATCTTCCCTCCAAAGATCAAGGATGTACTCA TGATCTCCCTGAGCCCCATAGTCACATGTGT GGTGGTGGATGTGAGCGAGGATGACCCAGAT GTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAG AGAGGATTACAACAGTACTCTCCGGGTGGTC AGTGCCCTCCCCATCCAGCACCAGGACTGGA TGAGTGGCAAGGAGTTCAAATGCAAGGTCAA CAACAAAGACCTCCCAGCGCCCATCGAGAGA ACCATCTCAAAACCCAAAGGGTCAGTAAGAG CTCCACAGGTATATGTCTTGCCTCCACCAGA AGAAGAGATGACTAAGAAACAGGTCACTCT GACCTGCATGGTCACAGACTTCATGCCTGAA GACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAAC CAGTCCTGGACTCTGATGGTTCTTACTTCATG TACAGCAAGCTGAGAGTGGAAAAGAAGAAC TGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACAC GACTAAGAGCTTCTCCCGGACTCCGGGTAAA	867
SM1B269	pDR000030234	GAAGTCCAGCTGCAGCAGAGCGGAGCCGAA CTCGTCAGACCTGGCGCTTCCGTGAAGCTGA GCTGCACCACCAGCGGCTTCAACATCAAGGA CAGCCTGATCTACTGGGTCAAGCAGCGGCCC GAGCAGGGCCTGGAATGGATCGGCTGGATTG	868

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		ACCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAGC GACACCAGCAGCAACACCGCCTACCTGAGAC TGAGCAGCCTGACCAGCGAGGACACCGCCAT CTACTACTGCACCCGGTCCTTCGGCGTGTGTT GGGGCCAGGGAACCCTGGTCACAGTGTCTGC TGCCAAAACAACAGCACCAAGTGTCTATCCA CTGGCCCCTGTGTGTGGAGATACAACTGGCT CCTCGGTGACTCTAGGATGCCTGGTCAAGGG TTATTTCCCTGAGCCAGTGACCTTGACCTGGA ACTCTGGATCCCTGTCCAGTGGTGTGCACAC CTTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAG CACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTG GACAAGAAAATTGAGCCCAGAGGGCCCACA ATCAAGCCCTGTCCTCCATGCAAATGCCCAG CACCTAACCTCTTGGGTGGACCATCCGTCTTC ATCTTCCCTCCAAAGATCAAGGATGTACTCA TGATCTCCCTGAGCCCCATAGTCACATGTGT GGTGGTGGATGTGAGCGAGGATGACCCAGAT GTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAG AGAGGATTACAACAGTACTCTCCGGGTGGTC AGTGCCCTCCCCATCCAGCACCAGGACTGGA TGAGTGGCAAGGAGTTCAAATGCAAGGTCAA CAACAAAGACCTCCCAGCGCCCATCGAGAGA ACCATCTCAAAACCCAAAGGGTCAGTAAGAG CTCCACAGGTATATGTCTTGCCTCCACCAGA AGAAGAGATGACTAAGAAACAGGTCACTCT GACCTGCATGGTCACAGACTTCATGCCTGAA GACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAAC CAGTCCTGGACTCTGATGGTTCTTACTTCATG TACAGCAAGCTGAGAGTGGAAAAGAAGAAC TGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACAC GACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B270	pDR000030234	GAAGTCCAGCTGCAGCAGAGCGGAGCCGAA CTCGTCAGACCTGGCGCTTCCGTGAAGCTGA GCTGCACCACCAGCGGCTTCAACATCAAGGA CAGCCTGATCTACTGGGTCAAGCAGCGGCCC GAGCAGGGCCTGGAATGGATCGGCTGGATTG ACCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAGC GACACCAGCAGCAACACCGCCTACCTGAGAC TGAGCAGCCTGACCAGCGAGGACACCGCCAT CTACTACTGCACCCGGTCCTTCGGCGTGTGTT	869

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		GGGGCCAGGGAACCCTGGTCACAGTGTCTGC TGCCAAAACAACAGCACCAAGTGTCTATCCA CTGGCCCCTGTGTGTGGAGATACAACTGGCT CCTCGGTGACTCTAGGATGCCTGGTCAAGGG TTATTTCCCTGAGCCAGTGACCTTGACCTGGA ACTCTGGATCCCTGTCCAGTGGTGTGCACAC CTTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAG CACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTG GACAAGAAAATTGAGCCCAGAGGGCCCACA ATCAAGCCCTGTCCTCCATGCAAATGCCCAG CACCTAACCTCTTGGGTGGACCATCCGTCTTC ATCTTCCCTCCAAAGATCAAGGATGTACTCA TGATCTCCCTGAGCCCCATAGTCACATGTGT GGTGGTGGATGTGAGCGAGGATGACCCAGAT GTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAG AGAGGATTACAACAGTACTCTCCGGGTGGTC AGTGCCCTCCCCATCCAGCACCAGGACTGGA TGAGTGGCAAGGAGTTCAAATGCAAGGTCAA CAACAAAGACCTCCCAGCGCCCATCGAGAGA ACCATCTCAAAACCCAAAGGGTCAGTAAGAG CTCCACAGGTATATGTCTTGCCTCCACCAGA AGAAGAGATGACTAAGAAACAGGTCACTCT GACCTGCATGGTCACAGACTTCATGCCTGAA GACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAAC CAGTCCTGGACTCTGATGGTTCTTACTTCATG TACAGCAAGCTGAGAGTGGAAAAGAAGAAC TGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACAC GACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B271	pDR000030234	GAAGTCCAGCTGCAGCAGAGCGGAGCCGAA CTCGTCAGACCTGGCGCTTCCGTGAAGCTGA GCTGCACCACCAGCGGCTTCAACATCAAGGA CAGCCTGATCTACTGGGTCAAGCAGCGGCCC GAGCAGGGCCTGGAATGGATCGGCTGGATTG ACCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAGC GACACCAGCAGCAACACCGCCTACCTGAGAC TGAGCAGCCTGACCAGCGAGGACACCGCCAT CTACTACTGCACCCGGTCCTTCGGCGTGTGTT GGGGCCAGGGAACCCTGGTCACAGTGTCTGC TGCCAAAACAACAGCACCAAGTGTCTATCCA CTGGCCCCTGTGTGTGGAGATACAACTGGCT CCTCGGTGACTCTAGGATGCCTGGTCAAGGG TTATTTCCCTGAGCCAGTGACCTTGACCTGGA	870

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		ACTCTGGATCCCTGTCCAGTGGTGTGCACAC CTTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAG CACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTG GACAAGAAAATTGAGCCCAGAGGGCCCACA ATCAAGCCCTGTCCTCCATGCAAATGCCCAG CACCTAACCTCTTGGGTGGACCATCCGTCTTC ATCTTCCCTCCAAAGATCAAGGATGTACTCA TGATCTCCCTGAGCCCCATAGTCACATGTGT GGTGGTGGATGTGAGCGAGGATGACCCAGAT GTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAG AGAGGATTACAACAGTACTCTCCGGGTGGTC AGTGCCCTCCCCATCCAGCACCAGGACTGGA TGAGTGGCAAGGAGTTCAAATGCAAGGTCAA CAACAAAGACCTCCCAGCGCCCATCGAGAGA ACCATCTCAAAACCCAAAGGGTCAGTAAGAG CTCCACAGGTATATGTCTTGCCTCCACCAGA AGAAGAGATGACTAAGAAACAGGTCACTCT GACCTGCATGGTCACAGACTTCATGCCTGAA GACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAAC CAGTCCTGGACTCTGATGGTTCTTACTTCATG TACAGCAAGCTGAGAGTGGAAAAGAAGAAC TGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACAC GACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B272	pDR000030234	GAAGTCCAGCTGCAGCAGAGCGGAGCCGAA CTCGTCAGACCTGGCGCTTCCGTGAAGCTGA GCTGCACCACCAGCGGCTTCAACATCAAGGA CAGCCTGATCTACTGGGTCAAGCAGCGGCCC GAGCAGGGCCTGGAATGGATCGGCTGGATTG ACCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAGC GACACCAGCAGCAACACCGCCTACCTGAGAC TGAGCAGCCTGACCAGCGAGGACACCGCCAT CTACTACTGCACCCGGTCCTTCGGCGTGTGTT GGGGCCAGGGAACCCTGGTCACAGTGTCTGC TGCCAAAACAACAGCACCAAGTGTCTATCCA CTGGCCCCTGTGTGTGGAGATACAACTGGCT CCTCGGTGACTCTAGGATGCCTGGTCAAGGG TTATTTCCCTGAGCCAGTGACCTTGACCTGGA ACTCTGGATCCCTGTCCAGTGGTGTGCACAC CTTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAG CACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTG	871

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		GACAAGAAAATTGAGCCCAGAGGGCCCACA ATCAAGCCCTGTCCTCCATGCAAATGCCCAG CACCTAACCTCTTGGGTGGACCATCCGTCTTC ATCTTCCCTCCAAAGATCAAGGATGTACTCA TGATCTCCCTGAGCCCCATAGTCACATGTGT GGTGGTGGATGTGAGCGAGGATGACCCAGAT GTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAG AGAGGATTACAACAGTACTCTCCGGGTGGTC AGTGCCCTCCCCATCCAGCACCAGGACTGGA TGAGTGGCAAGGAGTTCAAATGCAAGGTCAA CAACAAAGACCTCCCAGCGCCCATCGAGAGA ACCATCTCAAAACCCAAAGGGTCAGTAAGAG CTCCACAGGTATATGTCTTGCCTCCACCAGA AGAAGAGATGACTAAGAAACAGGTCACTCT GACCTGCATGGTCACAGACTTCATGCCTGAA GACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAAC CAGTCCTGGACTCTGATGGTTCTTACTTCATG TACAGCAAGCTGAGAGTGGAAAAGAAGAAC TGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACAC GACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B273	pDR000030234	GAAGTCCAGCTGCAGCAGAGCGGAGCCGAA CTCGTCAGACCTGGCGCTTCCGTGAAGCTGA GCTGCACCACCAGCGGCTTCAACATCAAGGA CAGCCTGATCTACTGGGTCAAGCAGCGGCCC GAGCAGGGCCTGGAATGGATCGGCTGGATTG ACCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAGC GACACCAGCAGCAACACCGCCTACCTGAGAC TGAGCAGCCTGACCAGCGAGGACACCGCCAT CTACTACTGCACCCGGTCCTTCGGCGTGTGTT GGGGCCAGGGAACCCTGGTCACAGTGTCTGC TGCCAAAACAACAGCACCAAGTGTCTATCCA CTGGCCCCTGTGTGTGGAGATACAACTGGCT CCTCGGTGACTCTAGGATGCCTGGTCAAGGG TTATTTCCCTGAGCCAGTGACCTTGACCTGGA ACTCTGGATCCCTGTCCAGTGGTGTGCACAC CTTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAG CACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTG GACAAGAAAATTGAGCCCAGAGGGCCCACA ATCAAGCCCTGTCCTCCATGCAAATGCCCAG CACCTAACCTCTTGGGTGGACCATCCGTCTTC ATCTTCCCTCCAAAGATCAAGGATGTACTCA TGATCTCCCTGAGCCCCATAGTCACATGTGT	872

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		GGTGGTGGATGTGAGCGAGGATGACCCAGAT GTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAG AGAGGATTACAACAGTACTCTCCGGGTGGTC AGTGCCCTCCCCATCCAGCACCAGGACTGGA TGAGTGGCAAGGAGTTCAAATGCAAGGTCAA CAACAAAGACCTCCCAGCGCCCATCGAGAGA ACCATCTCAAAACCCAAAGGGTCAGTAAGAG CTCCACAGGTATATGTCTTGCCTCCACCAGA AGAAGAGATGACTAAGAAACAGGTCACTCT GACCTGCATGGTCACAGACTTCATGCCTGAA GACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAAC CAGTCCTGGACTCTGATGGTTCTTACTTCATG TACAGCAAGCTGAGAGTGGAAAAGAAGAAC TGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACAC GACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B274	pDR000030234	GAAGTCCAGCTGCAGCAGAGCGGAGCCGAA CTCGTCAGACCTGGCGCTTCCGTGAAGCTGA GCTGCACCACCAGCGGCTTCAACATCAAGGA CAGCCTGATCTACTGGGTCAAGCAGCGGCCC GAGCAGGGCCTGGAATGGATCGGCTGGATTG ACCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAGC GACACCAGCAGCAACACCGCCTACCTGAGAC TGAGCAGCCTGACCAGCGAGGACACCGCCAT CTACTACTGCACCCGGTCCTTCGGCGTGTGTT GGGGCCAGGGAACCCTGGTCACAGTGTCTGC TGCCAAAACAACAGCACCAAGTGTCTATCCA CTGGCCCCTGTGTGTGGAGATACAACTGGCT CCTCGGTGACTCTAGGATGCCTGGTCAAGGG TTATTTCCCTGAGCCAGTGACCTTGACCTGGA ACTCTGGATCCCTGTCCAGTGGTGTGCACAC CTTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAG CACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTG GACAAGAAAATTGAGCCCAGAGGGCCCACA ATCAAGCCCTGTCCTCCATGCAAATGCCCAG CACCTAACCTCTTGGGTGGACCATCCGTCTTC ATCTTCCCTCCAAAGATCAAGGATGTACTCA TGATCTCCCTGAGCCCCATAGTCACATGTGT GGTGGTGGATGTGAGCGAGGATGACCCAGAT GTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAG AGAGGATTACAACAGTACTCTCCGGGTGGTC AGTGCCCTCCCCATCCAGCACCAGGACTGGA	873

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		TGAGTGGCAAGGAGTTCAAATGCAAGGTCAA CAACAAAGACCTCCCAGCGCCCATCGAGAGA ACCATCTCAAAACCCAAAGGGTCAGTAAGAG CTCCACAGGTATATGTCTTGCCTCCACCAGA AGAAGAGATGACTAAGAAACAGGTCACTCT GACCTGCATGGTCACAGACTTCATGCCTGAA GACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAAC CAGTCCTGGACTCTGATGGTTCTTACTTCATG TACAGCAAGCTGAGAGTGGAAAAGAAGAAC TGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACAC GACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B275	pDR000030234	GAAGTCCAGCTGCAGCAGAGCGGAGCCGAA CTCGTCAGACCTGGCGCTTCCGTGAAGCTGA GCTGCACCACCAGCGGCTTCAACATCAAGGA CAGCCTGATCTACTGGGTCAAGCAGCGGCCC GAGCAGGGCCTGGAATGGATCGGCTGGATTG ACCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAGC GACACCAGCAGCAACACCGCCTACCTGAGAC TGAGCAGCCTGACCAGCGAGGACACCGCCAT CTACTACTGCACCCGGTCCTTCGGCGTGTGTT GGGGCCAGGGAACCCTGGTCACAGTGTCTGC TGCCAAAACAACAGCACCAAGTGTCTATCCA CTGGCCCCTGTGTGTGGAGATACAACTGGCT CCTCGGTGACTCTAGGATGCCTGGTCAAGGG TTATTTCCCTGAGCCAGTGACCTTGACCTGGA ACTCTGGATCCCTGTCCAGTGGTGTGCACAC CTTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAG CACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTG GACAAGAAAATTGAGCCCAGAGGGCCCACA ATCAAGCCCTGTCCTCCATGCAAATGCCCAG CACCTAACCTCTTGGGTGGACCATCCGTCTTC ATCTTCCCTCCAAAGATCAAGGATGTACTCA TGATCTCCCTGAGCCCCATAGTCACATGTGT GGTGGTGGATGTGAGCGAGGATGACCCAGAT GTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAG AGAGGATTACAACAGTACTCTCCGGGTGGTC AGTGCCCTCCCCATCCAGCACCAGGACTGGA TGAGTGGCAAGGAGTTCAAATGCAAGGTCAA CAACAAAGACCTCCCAGCGCCCATCGAGAGA ACCATCTCAAAACCCAAAGGGTCAGTAAGAG CTCCACAGGTATATGTCTTGCCTCCACCAGA AGAAGAGATGACTAAGAAACAGGTCACTCT	874

mAb/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		GACCTGCATGGTCACAGACTTCATGCCTGAA GACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAAC CAGTCCTGGACTCTGATGGTTCTTACTTCATG TACAGCAAGCTGAGAGTGGAAAAGAAGAAC TGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACAC GACTAAGAGCTTCTCCCGGACTCCGGGTAAA	

Table 27. LukAB Antibody Heavy Chain Primary Transcripts

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
SM1B105	pDR000023596	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAGG TTCAGCTGCAGCAGTCTGGGGCTGAGCTGAT GACGCCTGGGGCCTCAGTGAAGATATCCTGC AAGGCTACTGGCTACACATTCAGTACCTTTT GGATAGAGTGGATCAAGCAGAGGCCTGGAC ATGGCCTTGAGTGGATTGGAGAGATTTTACC TGGAAGTGGTAGTACTAAGTACAATGAGAA GTTCAAGGGCAAGGCCACATTCACTGCAGA TACATCCTCCAACACAGCCTACATGCAACTC AGCAGCCTGACATCTGAGGACTCTGCCGTCT ATTATTGTGCAAGAGGTGGTTACGATGGTAT GGACTACTGGGGTCAAGGAACCTCAGTCAC CGTCTCCTCAGCCAAAACGACACCCCCATCT GTCTATCCACTGGCCCCTGGATCTGCTGCCC AAACTAACTCCATGGTGACCCTGGGATGCCT GGTCAAGGGCTATTTCCCTGAGCCAGTGACA GTGACCTGGAACTCTGGATCCCTGTCCAGCG GTGTGCACACCTTCCCAGCTGTCCTGGAGTC TGACCTCTACACTCTGAGCAGCTCAGTGACT GTCCCCTCCAGCCCTCGGCCCAGCGAGACCG TCACCTGCAACGTTGCCCACCCGGCCAGCAG CACCAAGGTGGACAAGAAAATTGTGCCCAG GGATTGTGGTTGTAAGCCTTGCATATGTACA GTCCCAGAAGTATCATCTGTCTTCATCTTCC CCCCAAAGCCCAAGGATGTGCTCACCATTAC TCTGACTCCTAAGGTCACGTGTGTTGTGGTA GACATCAGCAAGGATGATCCCGAGGTCCAG TTCAGCTGGTTTGTAGATGATGTGGAGGTGC ACACAGCTCAGACGCAACCCCGGGAGGAGC AGTTCAACAGCACTTTCCGCTCAGTCAGTGA	875

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		ACTTCCCATCATGCACCAGGACTGGCTCAAT GGCAAGGAGTTCAAATGCAGGGTCAACAGT GCAGCTTTCCCTGCCCCCATCGAGAAAACCA TCTCCAAAACCAAAGGCAGACCGAAGGCTC CACAGGTGTACACCATTCCACCTCCCAAGGA GCAGATGGCCAAGGATAAAGTCAGTCTGAC CTGCATGATAACAGACTTCTTCCCTGAAGAC ATTACTGTGGAGTGGCAGTGGAATGGGCAG CCAGCGGAGAACTACAAGAACACTCAGCCC ATCATGAACACGAATGGCTCTTACTTCGTCT ACAGCAAGCTCAATGTGCAGAAGAGCAACT GGGAGGCAGGAAATACTTTCACCTGCTCTGT GTTACATGAGGGCCTGCACAACCACCATACT GAGAAGAGCCTCTCCCACTCTCCTGGTAAAT GA	
SM1B106	pDR000023618	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAGG TTCAGCTGCAGCAGTCTGGGGCTGAGCTGAT GACGCCTGGGGCCTCAGTGAAGATATCCTGC AAGGCTACTGGCTACACATTCAGTACCTTTT GGATAGAGTGGATCAAGCAGAGGCCTGGAC ATGGCCTTGAGTGGATTGGAGAGATTTTACC TGGAAGTGGTAGTACTAAGTACAATGAGAA GTTCAAGGGCAAGGCCACATTCACTGCAGA TACATCCTCCAACACAGCCTACATGCAACTC AGCAGCCTGTCATCTGAGGACTCTGCCGTCT ATTATTGTGCAAGAGGTGGTTACGATGGTAT GGACTACTGGGGTCAAGGAACCTCAGTCAC CGTCTCCTCAGCCAAAACGACACCCCCATCT GTCTATCCACTGGCCCCTGGATCTGCTGCCC AAACTAACTCCATGGTGACCCTGGGATGCCT GGTCAAGGGCTATTTCCCTGAGCCAGTGACA GTGACCTGGAACTCTGGATCCCTGTCCAGCG GTGTGCACACCTTCCCAGCTGTCCTGGAGTC TGACCTCTACACTCTGAGCAGCTCAGTGACT GTCCCCTCCAGCCCTCGGCCCAGCGAGACCG TCACCTGCAACGTTGCCCACCCGGCCAGCAG CACCAAGGTGGACAAGAAAATTGTGCCCAG GGATTGTGGTTGTAAGCCTTGCATATGTACA GTCCCAGAAGTATCATCTGTCTTCATCTTCC CCCCAAAGCCCAAGGATGTGCTCACCATTAC TCTGACTCCTAAGGTCACGTGTGTTGTGGTA GACATCAGCAAGGATGATCCCGAGGTCCAG TTCAGCTGGTTTGTAGATGATGTGGAGGTGC ACACAGCTCAGACGCAACCCCGGGAGGAGC AGTTCAACAGCACTTTCCGCTCAGTCAGTGA ACTTCCCATCATGCACCAGGACTGGCTCAAT GGCAAGGAGTTCAAATGCAGGGTCAACAGT	876

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GCAGCTTTCCCTGCCCCCATCGAGAAAACCA TCTCCAAAACCAAAGGCAGACCGAAGGCTC CACAGGTGTACACCATTCCACCTCCCAAGGA GCAGATGGCCAAGGATAAAGTCAGTCTGAC CTGCATGATAACAGACTTCTTCCCTGAAGAC ATTACTGTGGAGTGGCAGTGGAATGGGCAG CCAGCGGAGAACTACAAGAACACTCAGCCC ATCATGAACACGAATGGCTCTTACTTCGTCT ACAGCAAGCTCAATGTGCAGAAGAGCAACT GGGAGGCAGGAAATACTTTCACCTGCTCTGT GTTACATGAGGGCCTGCACAACCACCATACT GAGAAGAGCCTCTCCCACTCTCCTGGTAAAT GA	
SM1B107	pDR000023619	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAGG TTCAGCTGCAGCAGTCTGAGGCTGAGCTGAT GACGCCTGGGGCCTCAGTGAAGATATCCTGC AAGGCTACTGGCTACACATTCAGTACCTTTT GGATAGAGTGGATCAAGCAGAGGCCTGGAC ATGGCCTTGAGTGGATTGGAGAGATTTTACC TGGAAGTGGTAGTACTAAGTACAATGAGAA GTTCAAGGGCAAGGCCACATTCACTGCAGA TACATCCTCCAACACAGCCTACATGCAACTC AGCAGCCTGACATCTGAGGACTCTGCCGTCT ATTATTGTGCAAGAGGTGGTTACGATGGTAT GGACTACTGGGGTCAAGGAACCTCAGTCAC CGTCTCCTCAGCCAAAACGACACCCCCATCT GTCTATCCACTGGCCCCTGGATCTGCTGCCC AAACTAACTCCATGGTGACCCTGGGATGCCT GGTCAAGGGCTATTTCCCTGAGCCAGTGACA GTGACCTGGAACTCTGGATCCCTGTCCAGCG GTGTGCACACCTTCCCAGCTGTCCTGGAGTC TGACCTCTACACTCTGAGCAGCTCAGTGACT GTCCCCTCCAGCCCTCGGCCCAGCGAGACCG TCACCTGCAACGTTGCCCACCCGGCCAGCAG CACCAAGGTGGACAAGAAAATTGTGCCCAG GGATTGTGGTTGTAAGCCTTGCATATGTACA GTCCCAGAAGTATCATCTGTCTTCATCTTCC CCCCAAAGCCCAAGGATGTGCTCACCATTAC TCTGACTCCTAAGGTCACGTGTGTTGTGGTA GACATCAGCAAGGATGATCCCGAGGTCCAG TTCAGCTGGTTTGTAGATGATGTGGAGGTGC ACACAGCTCAGACGCAACCCCGGGAGGAGC AGTTCAACAGCACTTTCCGCTCAGTCAGTGA ACTTCCCATCATGCACCAGGACTGGCTCAAT GGCAAGGAGTTCAAATGCAGGGTCAACAGT GCAGCTTTCCCTGCCCCCATCGAGAAAACCA TCTCCAAAACCAAAGGCAGACCGAAGGCTC	877

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CACAGGTGTACACCATTCCACCTCCCAAGGA GCAGATGGCCAAGGATAAAGTCAGTCTGAC CTGCATGATAACAGACTTCTTCCCTGAAGAC ATTACTGTGGAGTGGCAGTGGAATGGGCAG CCAGCGGAGAACTACAAGAACACTCAGCCC ATCATGAACACGAATGGCTCTTACTTCGTCT ACAGCAAGCTCAATGTGCAGAAGAGCAACT GGGAGGCAGGAAATACTTTCACCTGCTCTGT GTTACATGAGGGCCTGCACAACCACCATACT GAGAAGAGCCTCTCCCACTCTCCTGGTAAAT GA	
SM1B108	pDR000023620	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAGG TTCAGCTGCAGCAGTCTGGGGCTGAGCTGGT GAAGCCTGGGGCCTCAGTGAAGATTTCCTGC AAGGCTTCTGGCTATGCATTCAGTAGCTCCT GGATGAACTGGGTGAAGCAGAGGCCTGGAA AGGGTCTTGAGTGGATTGGACGGATTTATCC TGGAGATGGAGATACTAACTACCATGGGAA GTTCAAGGGCAAGGCCACACTGACTGCAGA CAAATCCTCCAGCACAGCCTACATGCAACTC AGCAGCCTGACATCTGAGGACTCTGCGGTCT ACTTCTGTGCAAGAAGGAACTATGATGGTTA CCACTATGGTATGGACTACTGGGGTCAAGG AACCTCAGTCACCGTCTCCTCAGCCAAAACG ACACCCCCATCTGTCTATCCACTGGCCCCTG GATCTGCTGCCCAAACTAACTCCATGGTGAC CCTGGGATGCCTGGTCAAGGGCTATTTCCCT GAGCCAGTGACAGTGACCTGGAACTCTGGA TCCCTGTCCAGCGGTGTGCACACCTTCCCAG CTGTCCTGGAGTCTGACCTCTACACTCTGAG CAGCTCAGTGACTGTCCCCTCCAGCCCTCGG CCCAGCGAGACCGTCACCTGCAACGTTGCCC ACCCGGCCAGCAGCACCAAGGTGGACAAGA AAATTGTGCCCAGGGATTGTGGTTGTAAGCC TTGCATATGTACAGTCCCAGAAGTATCATCT GTCTTCATCTTCCCCCCAAAGCCCAAGGATG TGCTCACCATTACTCTGACTCCTAAGGTCAC GTGTGTTGTGGTAGACATCAGCAAGGATGAT CCCGAGGTCCAGTTCAGCTGGTTTGTAGATG ATGTGGAGGTGCACACAGCTCAGACGCAAC CCCGGGAGGAGCAGTTCAACAGCACTTTCC GCTCAGTCAGTGAACTTCCCATCATGCACCA GGACTGGCTCAATGGCAAGGAGTTCAAATG CAGGGTCAACAGTGCAGCTTTCCCTGCCCCC ATCGAGAAAACCATCTCCAAAACCAAAGGC AGACCGAAGGCTCCACAGGTGTACACCATT CCACCTCCCAAGGAGCAGATGGCCAAGGAT	878

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		AAAGTCAGTCTGACCTGCATGATAACAGACT TCTTCCCTGAAGACATTACTGTGGAGTGGCA GTGGAATGGGCAGCCAGCGGAGAACTACAA GAACACTCAGCCCATCATGAACACGAATGG CTCTTACTTCGTCTACAGCAAGCTCAATGTG CAGAAGAGCAACTGGGAGGCAGGAAATACT TTCACCTGCTCTGTGTTACATGAGGGCCTGC ACAACCACCATACTGAGAAGAGCCTCTCCC ACTCTCCTGGTAAATGA	
SM1B109	pDR000023596	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAGG TTCAGCTGCAGCAGTCTGGGGCTGAGCTGAT GACGCCTGGGGCCTCAGTGAAGATATCCTGC AAGGCTACTGGCTACACATTCAGTACCTTTT GGATAGAGTGGATCAAGCAGAGGCCTGGAC ATGGCCTTGAGTGGATTGGAGAGATTTTACC TGGAAGTGGTAGTACTAAGTACAATGAGAA GTTCAAGGGCAAGGCCACATTCACTGCAGA TACATCCTCCAACACAGCCTACATGCAACTC AGCAGCCTGACATCTGAGGACTCTGCCGTCT ATTATTGTGCAAGAGGTGGTTACGATGGTAT GGACTACTGGGGTCAAGGAACCTCAGTCAC CGTCTCCTCAGCCAAAACGACACCCCCATCT GTCTATCCACTGGCCCCTGGATCTGCTGCCC AAACTAACTCCATGGTGACCCTGGGATGCCT GGTCAAGGGCTATTTCCCTGAGCCAGTGACA GTGACCTGGAACTCTGGATCCCTGTCCAGCG GTGTGCACACCTTCCCAGCTGTCCTGGAGTC TGACCTCTACACTCTGAGCAGCTCAGTGACT GTCCCCTCCAGCCCTCGGCCCAGCGAGACCG TCACCTGCAACGTTGCCCACCCGGCCAGCAG CACCAAGGTGGACAAGAAAATTGTGCCCAG GGATTGTGGTTGTAAGCCTTGCATATGTACA GTCCCAGAAGTATCATCTGTCTTCATCTTCC CCCCAAAGCCCAAGGATGTGCTCACCATTAC TCTGACTCCTAAGGTCACGTGTGTTGTGGTA GACATCAGCAAGGATGATCCCGAGGTCCAG TTCAGCTGGTTTGTAGATGATGTGGAGGTGC ACACAGCTCAGACGCAACCCCGGGAGGAGC AGTTCAACAGCACTTTCCGCTCAGTCAGTGA ACTTCCCATCATGCACCAGGACTGGCTCAAT GGCAAGGAGTTCAAATGCAGGGTCAACAGT GCAGCTTTCCCTGCCCCCATCGAGAAAACCA TCTCCAAAACCAAAGGCAGACCGAAGGCTC CACAGGTGTACACCATTCCACCTCCCAAGGA GCAGATGGCCAAGGATAAAGTCAGTCTGAC CTGCATGATAACAGACTTCTTCCCTGAAGAC ATTACTGTGGAGTGGCAGTGGAATGGGCAG	879

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CCAGCGGAGAACTACAAGAACACTCAGCCC ATCATGAACACGAATGGCTCTTACTTCGTCT ACAGCAAGCTCAATGTGCAGAAGAGCAACT GGGAGGCAGGAAATACTTTCACCTGCTCTGT GTTACATGAGGGCCTGCACAACCACCATACT GAGAAGAGCCTCTCCCACTCTCCTGGTAAAT GA	
SM1B110	pDR000023622	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAGG TTCAGCTGCAGCAGTCTGGGGCTGAGCTGGT CAAGCCTGGGACTTCAGTGAAGATGTCCTGC AAGGCTTCTGGCTACACCTTCACCAGCTACT GGATGCACTGGGTGAAACTTAGGCCTGGAC AAGGCCTTGAGTGGATCGGAGTGATTGATCC TTCTGATAGTTATACTAACTATAATCAAAAG TTCAAGGGCAGGGCCACATTGACTGGAGAC ACATCCTCCAGCACAGCCTACATGCAGCTCA GCAGCCTGACATCTGAGGACTCTGCGGTCTA TTACTGTACAAGAGCAGCATATGATAACTCG TACTACTTTGACTACTGGGGCCAAGGCACCA CTCTCACAGTCTCCTCAGCCAAAACGACACC CCCATCTGTCTATCCACTGGCCCCTGGATCT GCTGCCCAAACTAACTCCATGGTGACCCTGG GATGCCTGGTCAAGGGCTATTTCCCTGAGCC AGTGACAGTGACCTGGAACTCTGGATCCCTG TCCAGCGGTGTGCACACCTTCCCAGCTGTCC TGGAGTCTGACCTCTACACTCTGAGCAGCTC AGTGACTGTCCCCTCCAGCCCTCGGCCCAGC GAGACCGTCACCTGCAACGTTGCCCACCCGG CCAGCAGCACCAAGGTGGACAAGAAAATTG TGCCCAGGGATTGTGGTTGTAAGCCTTGCAT ATGTACAGTCCCAGAAGTATCATCTGTCTTC ATCTTCCCCCCAAAGCCCAAGGATGTGCTCA CCATTACTCTGACTCCTAAGGTCACGTGTGT TGTGGTAGACATCAGCAAGGATGATCCCGA GGTCCAGTTCAGCTGGTTTGTAGATGATGTG GAGGTGCACACAGCTCAGACGCAACCCCGG GAGGAGCAGTTCAACAGCACTTTCCGCTCAG TCAGTGAACTTCCCATCATGCACCAGGACTG GCTCAATGGCAAGGAGTTCAAATGCAGGGT CAACAGTGCAGCTTTCCCTGCCCCCATCGAG AAAACCATCTCCAAAACCAAAGGCAGACCG AAGGCTCCACAGGTGTACACCATTCCACCTC CCAAGGAGCAGATGGCCAAGGATAAAGTCA GTCTGACCTGCATGATAACAGACTTCTTCCC TGAAGACATTACTGTGGAGTGGCAGTGGAA TGGGCAGCCAGCGGAGAACTACAAGAACAC TCAGCCCATCATGAACACGAATGGCTCTTAC	880

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		TTCGTCTACAGCAAGCTCAATGTGCAGAAGA GCAACTGGGAGGCAGGAAATACTTTCACCT GCTCTGTGTTACATGAGGGCCTGCACAACCA CCATACTGAGAAGAGCCTCTCCCACTCTCCT GGTAAATGA	
SM1B111	pDR000023624	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAGG TTCAGCTGCAGCAGTCTGGGGCTGAGCTGGT GAAGCCTGGGGCCTCAGTGAAGATTTCCTGC AAGGCTTCTGGCTATGCATTCAGTAGTTCCT GGATGAACTGGTTGAAGCAGAGGCCTGGAA AGGGTCTTGAGTGGATTGGACGGATTTATCC TGGAGATGGAGATACTAATTACAATGGGAA GTTCAAGGGCAAGGCCACACTGACTGCAGA CAAGTCCTCCAGTACAGCCTACATGCAACTC AGCAGCCTGACATCTGAGGACTCTGCGGTCT ACTTCTGTGCAAGATACGGCTATGATTACGA CGGGGAATATTACTATGCTATGGACTACTGG GGTCAAGGAACCTCAGTCACCGTCTCCTCAG CCAAAACGACACCCCCATCTGTCTATCCACT GGCCCCTGGATCTGCTGCCCAAACTAACTCC ATGGTGACCCTGGGATGCCTGGTCAAGGGCT ATTTCCCTGAGCCAGTGACAGTGACCTGGAA CTCTGGATCCCTGTCCAGCGGTGTGCACACC TTCCCAGCTGTCCTGGAGTCTGACCTCTACA CTCTGAGCAGCTCAGTGACTGTCCCCTCCAG CCCTCGGCCCAGCGAGACCGTCACCTGCAAC GTTGCCCACCCGGCCAGCAGCACCAAGGTG GACAAGAAAATTGTGCCCAGGGATTGTGGT TGTAAGCCTTGCATATGTACAGTCCCAGAAG TATCATCTGTCTTCATCTTCCCCCCAAAGCCC AAGGATGTGCTCACCATTACTCTGACTCCTA AGGTCACGTGTGTTGTGGTAGACATCAGCAA GGATGATCCCGAGGTCCAGTTCAGCTGGTTT GTAGATGATGTGGAGGTGCACACAGCTCAG ACGCAACCCCGGGAGGAGCAGTTCAACAGC ACTTTCCGCTCAGTCAGTGAACTTCCCATCA TGCACCAGGACTGGCTCAATGGCAAGGAGT TCAAATGCAGGGTCAACAGTGCAGCTTTCCC TGCCCCCATCGAGAAAACCATCTCCAAAACC AAAGGCAGACCGAAGGCTCCACAGGTGTAC ACCATTCCACCTCCCAAGGAGCAGATGGCC AAGGATAAAGTCAGTCTGACCTGCATGATA ACAGACTTCTTCCCTGAAGACATTACTGTGG AGTGGCAGTGGAATGGGCAGCCAGCGGAGA ACTACAAGAACACTCAGCCCATCATGAACA CGAATGGCTCTTACTTCGTCTACAGCAAGCT CAATGTGCAGAAGAGCAACTGGGAGGCAGG	881

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		AAATACTTTCACCTGCTCTGTGTTACATGAG GGCCTGCACAACCACCATACTGAGAAGAGC CTCTCCCACTCTCCTGGTAAATGA	
SM1B112	pDR000023623	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCCAGG TGCAGCTGAAGGAGTCAGGACCTGAACTGA AGAAGCCTGGAGAGACAGTCAGGATCTCCT GCAAGGCTTCTGGGTATACTTTCACAAATTA TGGAATGAACTGGGTGAAGCAGACTCCAGG AAAGGGTTTAAAGTGGATAGACTGGTTAAA GTCCTACACTGGAGAGCCAACACATACTGGT GACTTCAAGGGACGGTTTGACCTCTCTTTGG AAACCTCTGCCAACACTGCCTATTTGCAGAT CAACAACCTCAAAAATGAGGACACGGCTAC ATATTTCTGTGCAAGAGGGTCCCTCTTTGGT TTGGACTACTGGGGTCAAGGAACCTCAGTCA CCGTCTCCTCAGCCAAAACGACACCCCCATC TGTCTATCCACTGGCCCCTGGATCTGCTGCC CAAACTAACTCCATGGTGACCCTGGGATGCC TGGTCAAGGGCTATTTCCCTGAGCCAGTGAC AGTGACCTGGAACTCTGGATCCCTGTCCAGC GGTGTGCACACCTTCCCAGCTGTCCTGGAGT CTGACCTCTACACTCTGAGCAGCTCAGTGAC TGTCCCCTCCAGCCCTCGGCCCAGCGAGACC GTCACCTGCAACGTTGCCCACCCGGCCAGCA GCACCAAGGTGGACAAGAAAATTGTGCCCA GGGATTGTGGTTGTAAGCCTTGCATATGTAC AGTCCCAGAAGTATCATCTGTCTTCATCTTC CCCCCAAAGCCCAAGGATGTGCTCACCATTA CTCTGACTCCTAAGGTCACGTGTGTTGTGGT AGACATCAGCAAGGATGATCCCGAGGTCCA GTTCAGCTGGTTTGTAGATGATGTGGAGGTG CACACAGCTCAGACGCAACCCCGGGAGGAG CAGTTCAACAGCACTTTCCGCTCAGTCAGTG AACTTCCCATCATGCACCAGGACTGGCTCAA TGGCAAGGAGTTCAAATGCAGGGTCAACAG TGCAGCTTTCCCTGCCCCCATCGAGAAAACC ATCTCCAAAACCAAAGGCAGACCGAAGGCT CCACAGGTGTACACCATTCCACCTCCCAAGG AGCAGATGGCCAAGGATAAAGTCAGTCTGA CCTGCATGATAACAGACTTCTTCCCTGAAGA CATTACTGTGGAGTGGCAGTGGAATGGGCA GCCAGCGGAGAACTACAAGAACACTCAGCC CATCATGAACACGAATGGCTCTTACTTCGTC TACAGCAAGCTCAATGTGCAGAAGAGCAAC TGGGAGGCAGGAAATACTTTCACCTGCTCTG TGTTACATGAGGGCCTGCACAACCACCATAC TGAGAAGAGCCTCTCCCACTCTCCTGGTAAA	882

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		TGA	
SM1B243	pDR000030109	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAAG TCCAGCTGCAGCAGAGCGGAGCCGAGCTGG TCAAAAGCGGAGCCAGCGTGAAGCTGAGCT GCACCGCCAGCGGCTTCAACATCAAGGACT ACTACATGCACTGGGTCAAGCAGCGGCCCG AGCAGGGCCTGGAATGGATCGGAAGAATCG ACCCCGCCAACGGCAACACCAAATACGACC CCAAGTTCCAGGACAAGGCCACCATCACCA GCGACACCAGCAGCAACACCGCCTACCTGC AGCTGAGCAGCCTGACCAGCGAGGACACCG CCGTGTACTACTGCGCCGAGGGCGATTACGT GCCCGGCTACTTTGATGTGTGGGGAGCCGGC ACCACCGTGACCGTGTCATCTGCCAAAACAA CAGCACCAAGTGTCTATCCACTGGCCCCTGT GTGTGGAGATACAACTGGCTCCTCGGTGACT CTAGGATGCCTGGTCAAGGGTTATTTCCCTG AGCCAGTGACCTTGACCTGGAACTCTGGATC CCTGTCCAGTGGTGTGCACACCTTCCCAGCT GTCCTGCAGTCTGACCTCTACACCCTCAGCA GCTCAGTGACTGTAACCTCGAGCACCTGGCC CAGCCAGTCCATCACCTGCAATGTGGCCCAC CCGGCAAGCAGCACCAAGGTGGACAAGAAA ATTGAGCCCAGAGGGCCCACAATCAAGCCC TGTCCTCCATGCAAATGCCCAGCACCTAACC TCTTGGGTGGACCATCCGTCTTCATCTTCCCT CCAAAGATCAAGGATGTACTCATGATCTCCC TGAGCCCCATAGTCACATGTGTGGTGGTGGA TGTGAGCGAGGATGACCCAGATGTCCAGAT CAGCTGGTTTGTGAACAACGTGGAAGTACA CACAGCTCAGACACAAACCCATAGAGAGGA TTACAACAGTACTCTCCGGGTGGTCAGTGCC CTCCCCATCCAGCACCAGGACTGGATGAGTG GCAAGGAGTTCAAATGCAAGGTCAACAACA AAGACCTCCCAGCGCCCATCGAGAGAACCA TCTCAAAACCCAAAGGGTCAGTAAGAGCTC CACAGGTATATGTCTTGCCTCCACCAGAAGA AGAGATGACTAAGAAACAGGTCACTCTGAC CTGCATGGTCACAGACTTCATGCCTGAAGAC ATTTACGTGGAGTGGACCAACAACGGGAAA ACAGAGCTAAACTACAAGAACACTGAACCA GTCCTGGACTCTGATGGTTCTTACTTCATGT ACAGCAAGCTGAGAGTGGAAAAGAAGAACT GGGTGGAAAGAAATAGCTACTCCTGTTCAGT GGTCCACGAGGGTCTGCACAATCACCACAC GACTAAGAGCTTCTCCCGGACTCCGGGTAAA TGA	883

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
SM1B244	pDR000030218	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAGG TCCAGCTGCAGGAATCTGGCCCTAGCCTGGT CAAGCCCAGCCAGACCCTGAGCCTGACCTGT AGCGTGACCGGCGACAGCATCACCAGCGAC TACTGGAACTGGATCCGGAAGTTCCCCGGCA ACAAGCTCGAGTACATGGGCTACATCAGCT ACAGCGGCAGCACCTACTACAACCCCAGCC TGAAGTCCCGGATCTCCATCACCCGGGACAC CAGCAAGAACCAGTACTATCTGCAGCTGAA CAGCGTGACCACCGAGGACACCGCCACCTA CTATTGTGCCGGCGACTACGGCAGCCCCTAC GCCATGGATTATTGGGGCCAGGGCACCTCCG TGACCGTGTCTAGTGCCAAAACAACAGCAC CAAGTGTCTATCCACTGGCCCCTGTGTGTGG AGATACAACTGGCTCCTCGGTGACTCTAGGA TGCCTGGTCAAGGGTTATTTCCCTGAGCCAG TGACCTTGACCTGGAACTCTGGATCCCTGTC CAGTGGTGTGCACACCTTCCCAGCTGTCCTG CAGTCTGACCTCTACACCCTCAGCAGCTCAG TGACTGTAACCTCGAGCACCTGGCCCAGCCA GTCCATCACCTGCAATGTGGCCCACCCGGCA AGCAGCACCAAGGTGGACAAGAAAATTGAG CCCAGAGGGCCCACAATCAAGCCCTGTCCTC CATGCAAATGCCCAGCACCTAACCTCTTGGG TGGACCATCCGTCTTCATCTTCCCTCCAAAG ATCAAGGATGTACTCATGATCTCCCTGAGCC CCATAGTCACATGTGTGGTGGTGGATGTGAG CGAGGATGACCCAGATGTCCAGATCAGCTG GTTTGTGAACAACGTGGAAGTACACACAGC TCAGACACAAACCCATAGAGAGGATTACAA CAGTACTCTCCGGGTGGTCAGTGCCCTCCCC ATCCAGCACCAGGACTGGATGAGTGGCAAG GAGTTCAAATGCAAGGTCAACAACAAAGAC CTCCCAGCGCCCATCGAGAGAACCATCTCAA AACCCAAAGGGTCAGTAAGAGCTCCACAGG TATATGTCTTGCCTCCACCAGAAGAAGAGAT GACTAAGAAACAGGTCACTCTGACCTGCAT GGTCACAGACTTCATGCCTGAAGACATTTAC GTGGAGTGGACCAACAACGGGAAAACAGAG CTAAACTACAAGAACACTGAACCAGTCCTG GACTCTGATGGTTCTTACTTCATGTACAGCA AGCTGAGAGTGGAAAAGAAGAACTGGGTGG AAAGAAATAGCTACTCCTGTTCAGTGGTCCA CGAGGGTCTGCACAATCACCACACGACTAA GAGCTTCTCCCGGACTCCGGGTAAATGA	884
SM1B245	pDR000030219	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCCAGG	885

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		TCCAGCTGCAGCAGTCTGGCGCTGAACTGGC CAAGCCTGGGGCCAGCGTGAAGATGAGCTG CAAGAGCAGCGGCTACACCTTCAGCACCTA CTGGATGCACTGGGTCAAGCAGAGGCCAGG CCAGGGCCTGGAATGGATCGGCTACATCAA CCCCAACACCGGCTACACAGAGTACAACCA GAAGTTCAAGGACACCGCCACCCTGACCGC CGACAAGTCTAGCAGCACCGCCTACATGCA GCTGAGCAGCCTGACCAGCGAGGACAGCGC CGTGTACTATTGTGCCAGAGGCGGCAGCAA GGCCTTCCCCTACTACGCCATGGACTATTGG GGCCAGGGCACCAGCGTGACCGTGTCTAGT GCCAAAACAACAGCACCAAGTGTCTATCCA CTGGCCCCTGTGTGTGGAGATACAACTGGCT CCTCGGTGACTCTAGGATGCCTGGTCAAGGG TTATTTCCCTGAGCCAGTGACCTTGACCTGG AACTCTGGATCCCTGTCCAGTGGTGTGCACA CCTTCCCAGCTGTCCTGCAGTCTGACCTCTA CACCCTCAGCAGCTCAGTGACTGTAACCTCG AGCACCTGGCCCAGCCAGTCCATCACCTGCA ATGTGGCCCACCCGGCAAGCAGCACCAAGG TGGACAAGAAAATTGAGCCCAGAGGGCCCA CAATCAAGCCCTGTCCTCCATGCAAATGCCC AGCACCTAACCTCTTGGGTGGACCATCCGTC TTCATCTTCCCTCCAAAGATCAAGGATGTAC TCATGATCTCCCTGAGCCCCATAGTCACATG TGTGGTGGTGGATGTGAGCGAGGATGACCC AGATGTCCAGATCAGCTGGTTTGTGAACAAC GTGGAAGTACACACAGCTCAGACACAAACC CATAGAGAGGATTACAACAGTACTCTCCGG GTGGTCAGTGCCCTCCCCATCCAGCACCAGG ACTGGATGAGTGGCAAGGAGTTCAAATGCA AGGTCAACAACAAAGACCTCCCAGCGCCCA TCGAGAGAACCATCTCAAAACCCAAAGGGT CAGTAAGAGCTCCACAGGTATATGTCTTGCC TCCACCAGAAGAAGAGATGACTAAGAAACA GGTCACTCTGACCTGCATGGTCACAGACTTC ATGCCTGAAGACATTTACGTGGAGTGGACC AACAACGGGAAAACAGAGCTAAACTACAAG AACACTGAACCAGTCCTGGACTCTGATGGTT CTTACTTCATGTACAGCAAGCTGAGAGTGGA AAAGAAGAACTGGGTGGAAAGAAATAGCTA CTCCTGTTCAGTGGTCCACGAGGGTCTGCAC AATCACCACACGACTAAGAGCTTCTCCCGGA CTCCGGGTAAATGA	
SM1B246	pDR000030220	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAGA TCCAGCTGCAGCAGTCTGGCCCTGAGCTGGT	886

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CAAGCCTGGGGCCAGCGTGAAGATGAGCTG CAAGGCCAGCGGCTACAGCTTCACCGGCTA CAACATGCACTGGGTCAAGCAGAGCCACGG CAAGAGCCTGGAATGGATCGGCTACATCGA CCCCTACAACGGGGCCACCAGCCACAACCA GAAGTTCAAGGGCAAGGCCACCCTGACCGT GGAAAAGAGCAGCAGCACCGCCTACATGCA GCTGAACAGCCTGACCAGCGAGGACAGCGC CGTGTACTACTGCGCCAGAGGCCTGTACGGC GACTATTGGTACGCCTATTGGGGCCAGGGCA CCCTGGTCACCGTGTCTAGTGCCAAAACAAC AGCACCAAGTGTCTATCCACTGGCCCCTGTG TGTGGAGATACAACTGGCTCCTCGGTGACTC TAGGATGCCTGGTCAAGGGTTATTTCCCTGA GCCAGTGACCTTGACCTGGAACTCTGGATCC CTGTCCAGTGGTGTGCACACCTTCCCAGCTG TCCTGCAGTCTGACCTCTACACCCTCAGCAG CTCAGTGACTGTAACCTCGAGCACCTGGCCC AGCCAGTCCATCACCTGCAATGTGGCCCACC CGGCAAGCAGCACCAAGGTGGACAAGAAAA TTGAGCCCAGAGGGCCCACAATCAAGCCCT GTCCTCCATGCAAATGCCCAGCACCTAACCT CTTGGGTGGACCATCCGTCTTCATCTTCCCTC CAAAGATCAAGGATGTACTCATGATCTCCCT GAGCCCCATAGTCACATGTGTGGTGGTGGAT GTGAGCGAGGATGACCCAGATGTCCAGATC AGCTGGTTTGTGAACAACGTGGAAGTACAC ACAGCTCAGACACAAACCCATAGAGAGGAT TACAACAGTACTCTCCGGGTGGTCAGTGCCC TCCCCATCCAGCACCAGGACTGGATGAGTG GCAAGGAGTTCAAATGCAAGGTCAACAACA AAGACCTCCCAGCGCCCATCGAGAGAACCA TCTCAAAACCCAAAGGGTCAGTAAGAGCTC CACAGGTATATGTCTTGCCTCCACCAGAAGA AGAGATGACTAAGAAACAGGTCACTCTGAC CTGCATGGTCACAGACTTCATGCCTGAAGAC ATTTACGTGGAGTGGACCAACAACGGGAAA ACAGAGCTAAACTACAAGAACACTGAACCA GTCCTGGACTCTGATGGTTCTTACTTCATGT ACAGCAAGCTGAGAGTGGAAAAGAAGAACT GGGTGGAAAGAAATAGCTACTCCTGTTCAGT GGTCCACGAGGGTCTGCACAATCACCACAC GACTAAGAGCTTCTCCCGGACTCCGGGTAAA TGA	
SM1B247	pDR000030221	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAGG TGCAGCTGGTGGAATCTGGCGGAGGACTGG TCAAGCCTGGCGGCAGCCTGAAACTGTCTTG	887

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CGCCGCCAGCGGCTTCACCTTCAGCGACTAC TACATGTACTGGGTCCGACAGACCCCTGAGA AGCGGCTGGAATGGGTGGCCACAATCAGCG ACGGCGGCAGCTACACCTTCTACCCCGACAG CGTGAAGGGCCGGTTCACCATCAGCCGGGA CAACGCCAAGAACAACCTGTACCTGCAGAT GTCCAGCCTGAAGTCCGAGGACACCGCCAT GTACTACTGCGCCAGAGGCCCCACCTACTAC GGCCTGGATTATTGGGGCCAGGGCACCACC CTGACCGTGTCTAGTGCCAAAACAACAGCA CCAAGTGTCTATCCACTGGCCCCTGTGTGTG GAGATACAACTGGCTCCTCGGTGACTCTAGG ATGCCTGGTCAAGGGTTATTTCCCTGAGCCA GTGACCTTGACCTGGAACTCTGGATCCCTGT CCAGTGGTGTGCACACCTTCCCAGCTGTCCT GCAGTCTGACCTCTACACCCTCAGCAGCTCA GTGACTGTAACCTCGAGCACCTGGCCCAGCC AGTCCATCACCTGCAATGTGGCCCACCCGGC AAGCAGCACCAAGGTGGACAAGAAAATTGA GCCCAGAGGGCCCACAATCAAGCCCTGTCCT CCATGCAAATGCCCAGCACCTAACCTCTTGG GTGGACCATCCGTCTTCATCTTCCCTCCAAA GATCAAGGATGTACTCATGATCTCCCTGAGC CCCATAGTCACATGTGTGGTGGTGGATGTGA GCGAGGATGACCCAGATGTCCAGATCAGCT GGTTTGTGAACAACGTGGAAGTACACACAG CTCAGACACAAACCCATAGAGAGGATTACA ACAGTACTCTCCGGGTGGTCAGTGCCCTCCC CATCCAGCACCAGGACTGGATGAGTGGCAA GGAGTTCAAATGCAAGGTCAACAACAAAGA CCTCCCAGCGCCCATCGAGAGAACCATCTCA AAACCCAAAGGGTCAGTAAGAGCTCCACAG GTATATGTCTTGCCTCCACCAGAAGAAGAGA TGACTAAGAAACAGGTCACTCTGACCTGCAT GGTCACAGACTTCATGCCTGAAGACATTTAC GTGGAGTGGACCAACAACGGGAAAACAGAG CTAAACTACAAGAACACTGAACCAGTCCTG GACTCTGATGGTTCTTACTTCATGTACAGCA AGCTGAGAGTGGAAAAGAAGAACTGGGTGG AAAGAAATAGCTACTCCTGTTCAGTGGTCCA CGAGGGTCTGCACAATCACCACACGACTAA GAGCTTCTCCCGGACTCCGGGTAAATGA	
SM1B248	pDR000030222	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCCAGG TCCAGCTGCAGCAGCCTGGCGCTGAACTCGT CAGACCTGGCGCTTCTGTGCGGCTGAGCTGC AAGGCCAGCGGCTACAGCTTCACCAGCTACT GGATGAGCTGGGTCAAAGTGCGGCCAGGCC	888

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		AGGGCCTGGAATGGATCGGAATGATCCACC CCAGCGACAGCGAGACACGGCTGAACCAGA AGTTCAAGGACAAGGCCACCCTGACCGTGG ACAAGAGCAGCAGCACCGCCTACATGCAGC TGTCCAGCCCCACAAGCGAGGACAGCGCCG TGTACTACTGCGCCAGACTGTACGTGGACTT CTTCGACTACTGGGGCCAGGGCACCACACTG ACAGTGTCCTCTGCCAAAACAACAGCACCA AGTGTCTATCCACTGGCCCCTGTGTGTGGAG ATACAACTGGCTCCTCGGTGACTCTAGGATG CCTGGTCAAGGGTTATTTCCCTGAGCCAGTG ACCTTGACCTGGAACTCTGGATCCCTGTCCA GTGGTGTGCACACCTTCCCAGCTGTCCTGCA GTCTGACCTCTACACCCTCAGCAGCTCAGTG ACTGTAACCTCGAGCACCTGGCCCAGCCAGT CCATCACCTGCAATGTGGCCCACCCGGCAAG CAGCACCAAGGTGGACAAGAAAATTGAGCC CAGAGGGCCCACAATCAAGCCCTGTCCTCCA TGCAAATGCCCAGCACCTAACCTCTTGGGTG GACCATCCGTCTTCATCTTCCCTCCAAAGAT CAAGGATGTACTCATGATCTCCCTGAGCCCC ATAGTCACATGTGTGGTGGTGGATGTGAGCG AGGATGACCCAGATGTCCAGATCAGCTGGTT TGTGAACAACGTGGAAGTACACACAGCTCA GACACAAACCCATAGAGAGGATTACAACAG TACTCTCCGGGTGGTCAGTGCCCTCCCCATC CAGCACCAGGACTGGATGAGTGGCAAGGAG TTCAAATGCAAGGTCAACAACAAAGACCTC CCAGCGCCCATCGAGAGAACCATCTCAAAA CCCAAAGGGTCAGTAAGAGCTCCACAGGTA TATGTCTTGCCTCCACCAGAAGAAGAGATGA CTAAGAAACAGGTCACTCTGACCTGCATGGT CACAGACTTCATGCCTGAAGACATTTACGTG GAGTGGACCAACAACGGGAAAACAGAGCTA AACTACAAGAACACTGAACCAGTCCTGGAC TCTGATGGTTCTTACTTCATGTACAGCAAGC TGAGAGTGGAAAAGAAGAACTGGGTGGAAA GAAATAGCTACTCCTGTTCAGTGGTCCACGA GGGTCTGCACAATCACCACACGACTAAGAG CTTCTCCCGGACTCCGGGTAAATGA	
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mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		ACCGTGAAGGGCCGGTTCACCATCTCCCGGG ACAACGCCAAGAACACCCTGTACCTGCAGA TGTCCAGCCTGAAGTCCGAGGACACCGCCCT GTACTACTGCGCCAGACCCGACTACCCCTAC GCCATGGATTACTGGGGCCAGGGCACCAGC GTGACCGTGTCATCTGCCAAAACAACAGCA CCAAGTGTCTATCCACTGGCCCCTGTGTGTG GAGATACAACTGGCTCCTCGGTGACTCTAGG ATGCCTGGTCAAGGGTTATTTCCCTGAGCCA GTGACCTTGACCTGGAACTCTGGATCCCTGT CCAGTGGTGTGCACACCTTCCCAGCTGTCCT GCAGTCTGACCTCTACACCCTCAGCAGCTCA GTGACTGTAACCTCGAGCACCTGGCCCAGCC AGTCCATCACCTGCAATGTGGCCCACCCGGC AAGCAGCACCAAGGTGGACAAGAAAATTGA GCCCAGAGGGCCCACAATCAAGCCCTGTCCT CCATGCAAATGCCCAGCACCTAACCTCTTGG GTGGACCATCCGTCTTCATCTTCCCTCCAAA GATCAAGGATGTACTCATGATCTCCCTGAGC CCCATAGTCACATGTGTGGTGGTGGATGTGA GCGAGGATGACCCAGATGTCCAGATCAGCT GGTTTGTGAACAACGTGGAAGTACACACAG CTCAGACACAAACCCATAGAGAGGATTACA ACAGTACTCTCCGGGTGGTCAGTGCCCTCCC CATCCAGCACCAGGACTGGATGAGTGGCAA GGAGTTCAAATGCAAGGTCAACAACAAAGA CCTCCCAGCGCCCATCGAGAGAACCATCTCA AAACCCAAAGGGTCAGTAAGAGCTCCACAG GTATATGTCTTGCCTCCACCAGAAGAAGAGA TGACTAAGAAACAGGTCACTCTGACCTGCAT GGTCACAGACTTCATGCCTGAAGACATTTAC GTGGAGTGGACCAACAACGGGAAAACAGAG CTAAACTACAAGAACACTGAACCAGTCCTG GACTCTGATGGTTCTTACTTCATGTACAGCA AGCTGAGAGTGGAAAAGAAGAACTGGGTGG AAAGAAATAGCTACTCCTGTTCAGTGGTCCA CGAGGGTCTGCACAATCACCACACGACTAA GAGCTTCTCCCGGACTCCGGGTAAATGA	
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mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GATCAACAACCTGAAGAACGAGGACACCGC CACCTACTTTTGCGCCAGAAGCCCCAGCTAC GGCAGCAGAGGCGCTTGGTTTGCCTATTGGA GCCAGGGCACCCTGGTCACCGTGTCTGCTGC CAAAACAACAGCACCAAGTGTCTATCCACT GGCCCCTGTGTGTGGAGATACAACTGGCTCC TCGGTGACTCTAGGATGCCTGGTCAAGGGTT ATTTCCCTGAGCCAGTGACCTTGACCTGGAA CTCTGGATCCCTGTCCAGTGGTGTGCACACC TTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAG CACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTG GACAAGAAAATTGAGCCCAGAGGGCCCACA ATCAAGCCCTGTCCTCCATGCAAATGCCCAG CACCTAACCTCTTGGGTGGACCATCCGTCTT CATCTTCCCTCCAAAGATCAAGGATGTACTC ATGATCTCCCTGAGCCCCATAGTCACATGTG TGGTGGTGGATGTGAGCGAGGATGACCCAG ATGTCCAGATCAGCTGGTTTGTGAACAACGT GGAAGTACACACAGCTCAGACACAAACCCA TAGAGAGGATTACAACAGTACTCTCCGGGT GGTCAGTGCCCTCCCCATCCAGCACCAGGAC TGGATGAGTGGCAAGGAGTTCAAATGCAAG GTCAACAACAAAGACCTCCCAGCGCCCATC GAGAGAACCATCTCAAAACCCAAAGGGTCA GTAAGAGCTCCACAGGTATATGTCTTGCCTC CACCAGAAGAAGAGATGACTAAGAAACAGG TCACTCTGACCTGCATGGTCACAGACTTCAT GCCTGAAGACATTTACGTGGAGTGGACCAA CAACGGGAAAACAGAGCTAAACTACAAGAA CACTGAACCAGTCCTGGACTCTGATGGTTCT TACTTCATGTACAGCAAGCTGAGAGTGGAA AAGAAGAACTGGGTGGAAAGAAATAGCTAC TCCTGTTCAGTGGTCCACGAGGGTCTGCACA ATCACCACACGACTAAGAGCTTCTCCCGGAC TCCGGGTAAATGA	
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mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CACCTACTTTTGCGCCAGAAGCCCCAGCTAC GGCAGCAGAGGCGCTTGGTTTGCCTACTGGG GCCAGGGCACCCTGGTCACAGTGTCTGCTGC CAAAACAACAGCACCAAGTGTCTATCCACT GGCCCCTGTGTGTGGAGATACAACTGGCTCC TCGGTGACTCTAGGATGCCTGGTCAAGGGTT ATTTCCCTGAGCCAGTGACCTTGACCTGGAA CTCTGGATCCCTGTCCAGTGGTGTGCACACC TTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAG CACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTG GACAAGAAAATTGAGCCCAGAGGGCCCACA ATCAAGCCCTGTCCTCCATGCAAATGCCCAG CACCTAACCTCTTGGGTGGACCATCCGTCTT CATCTTCCCTCCAAAGATCAAGGATGTACTC ATGATCTCCCTGAGCCCCATAGTCACATGTG TGGTGGTGGATGTGAGCGAGGATGACCCAG ATGTCCAGATCAGCTGGTTTGTGAACAACGT GGAAGTACACACAGCTCAGACACAAACCCA TAGAGAGGATTACAACAGTACTCTCCGGGT GGTCAGTGCCCTCCCCATCCAGCACCAGGAC TGGATGAGTGGCAAGGAGTTCAAATGCAAG GTCAACAACAAAGACCTCCCAGCGCCCATC GAGAGAACCATCTCAAAACCCAAAGGGTCA GTAAGAGCTCCACAGGTATATGTCTTGCCTC CACCAGAAGAAGAGATGACTAAGAAACAGG TCACTCTGACCTGCATGGTCACAGACTTCAT GCCTGAAGACATTTACGTGGAGTGGACCAA CAACGGGAAAACAGAGCTAAACTACAAGAA CACTGAACCAGTCCTGGACTCTGATGGTTCT TACTTCATGTACAGCAAGCTGAGAGTGGAA AAGAAGAACTGGGTGGAAAGAAATAGCTAC TCCTGTTCAGTGGTCCACGAGGGTCTGCACA ATCACCACACGACTAAGAGCTTCTCCCGGAC TCCGGGTAAATGA	
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mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CTACGTGAAGTGGGGACAGGGCACCCTGGT CACCGTGTCTGCTGCCAAAACAACAGCACC AAGTGTCTATCCACTGGCCCCTGTGTGTGGA GATACAACTGGCTCCTCGGTGACTCTAGGAT GCCTGGTCAAGGGTTATTTCCCTGAGCCAGT GACCTTGACCTGGAACTCTGGATCCCTGTCC AGTGGTGTGCACACCTTCCCAGCTGTCCTGC AGTCTGACCTCTACACCCTCAGCAGCTCAGT GACTGTAACCTCGAGCACCTGGCCCAGCCA GTCCATCACCTGCAATGTGGCCCACCCGGCA AGCAGCACCAAGGTGGACAAGAAAATTGAG CCCAGAGGGCCCACAATCAAGCCCTGTCCTC CATGCAAATGCCCAGCACCTAACCTCTTGGG TGGACCATCCGTCTTCATCTTCCCTCCAAAG ATCAAGGATGTACTCATGATCTCCCTGAGCC CCATAGTCACATGTGTGGTGGTGGATGTGAG CGAGGATGACCCAGATGTCCAGATCAGCTG GTTTGTGAACAACGTGGAAGTACACACAGC TCAGACACAAACCCATAGAGAGGATTACAA CAGTACTCTCCGGGTGGTCAGTGCCCTCCCC ATCCAGCACCAGGACTGGATGAGTGGCAAG GAGTTCAAATGCAAGGTCAACAACAAAGAC CTCCCAGCGCCCATCGAGAGAACCATCTCAA AACCCAAAGGGTCAGTAAGAGCTCCACAGG TATATGTCTTGCCTCCACCAGAAGAAGAGAT GACTAAGAAACAGGTCACTCTGACCTGCAT GGTCACAGACTTCATGCCTGAAGACATTTAC GTGGAGTGGACCAACAACGGGAAAACAGAG CTAAACTACAAGAACACTGAACCAGTCCTG GACTCTGATGGTTCTTACTTCATGTACAGCA AGCTGAGAGTGGAAAAGAAGAACTGGGTGG AAAGAAATAGCTACTCCTGTTCAGTGGTCCA CGAGGGTCTGCACAATCACCACACGACTAA GAGCTTCTCCCGGACTCCGGGTAAATGA	
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mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CTATCCACTGGCCCCTGTGTGTGGAGATACA ACTGGCTCCTCGGTGACTCTAGGATGCCTGG TCAAGGGTTATTTCCCTGAGCCAGTGACCTT GACCTGGAACTCTGGATCCCTGTCCAGTGGT GTGCACACCTTCCCAGCTGTCCTGCAGTCTG ACCTCTACACCCTCAGCAGCTCAGTGACTGT AACCTCGAGCACCTGGCCCAGCCAGTCCATC ACCTGCAATGTGGCCCACCCGGCAAGCAGC ACCAAGGTGGACAAGAAAATTGAGCCCAGA GGGCCCACAATCAAGCCCTGTCCTCCATGCA AATGCCCAGCACCTAACCTCTTGGGTGGACC ATCCGTCTTCATCTTCCCTCCAAAGATCAAG GATGTACTCATGATCTCCCTGAGCCCCATAG TCACATGTGTGGTGGTGGATGTGAGCGAGG ATGACCCAGATGTCCAGATCAGCTGGTTTGT GAACAACGTGGAAGTACACACAGCTCAGAC ACAAACCCATAGAGAGGATTACAACAGTAC TCTCCGGGTGGTCAGTGCCCTCCCCATCCAG CACCAGGACTGGATGAGTGGCAAGGAGTTC AAATGCAAGGTCAACAACAAAGACCTCCCA GCGCCCATCGAGAGAACCATCTCAAAACCC AAAGGGTCAGTAAGAGCTCCACAGGTATAT GTCTTGCCTCCACCAGAAGAAGAGATGACT AAGAAACAGGTCACTCTGACCTGCATGGTC ACAGACTTCATGCCTGAAGACATTTACGTGG AGTGGACCAACAACGGGAAAACAGAGCTAA ACTACAAGAACACTGAACCAGTCCTGGACT CTGATGGTTCTTACTTCATGTACAGCAAGCT GAGAGTGGAAAAGAAGAACTGGGTGGAAA GAAATAGCTACTCCTGTTCAGTGGTCCACGA GGGTCTGCACAATCACCACACGACTAAGAG CTTCTCCCGGACTCCGGGTAAATGA	
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mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		TCAAGGGTTATTTCCCTGAGCCAGTGACCTT GACCTGGAACTCTGGATCCCTGTCCAGTGGT GTGCACACCTTCCCAGCTGTCCTGCAGTCTG ACCTCTACACCCTCAGCAGCTCAGTGACTGT AACCTCGAGCACCTGGCCCAGCCAGTCCATC ACCTGCAATGTGGCCCACCCGGCAAGCAGC ACCAAGGTGGACAAGAAAATTGAGCCCAGA GGGCCCACAATCAAGCCCTGTCCTCCATGCA AATGCCCAGCACCTAACCTCTTGGGTGGACC ATCCGTCTTCATCTTCCCTCCAAAGATCAAG GATGTACTCATGATCTCCCTGAGCCCCATAG TCACATGTGTGGTGGTGGATGTGAGCGAGG ATGACCCAGATGTCCAGATCAGCTGGTTTGT GAACAACGTGGAAGTACACACAGCTCAGAC ACAAACCCATAGAGAGGATTACAACAGTAC TCTCCGGGTGGTCAGTGCCCTCCCCATCCAG CACCAGGACTGGATGAGTGGCAAGGAGTTC AAATGCAAGGTCAACAACAAAGACCTCCCA GCGCCCATCGAGAGAACCATCTCAAAACCC AAAGGGTCAGTAAGAGCTCCACAGGTATAT GTCTTGCCTCCACCAGAAGAAGAGATGACT AAGAAACAGGTCACTCTGACCTGCATGGTC ACAGACTTCATGCCTGAAGACATTTACGTGG AGTGGACCAACAACGGGAAAACAGAGCTAA ACTACAAGAACACTGAACCAGTCCTGGACT CTGATGGTTCTTACTTCATGTACAGCAAGCT GAGAGTGGAAAAGAAGAACTGGGTGGAAA GAAATAGCTACTCCTGTTCAGTGGTCCACGA GGGTCTGCACAATCACCACACGACTAAGAG CTTCTCCCGGACTCCGGGTAAATGA	
SM1B255	pDR000030229	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCCAGG TCCAGCTGCAGCAGCCTGGCGCTGAACTGGT CAAGCCAGGCGCTTCCGTGAAGCTGAGCTG CAAGGCCAGCGGCTACACCTTCACCCGGTAC TGGATGCACTGGGTCAAGCAGAGGCCAGGC CAGGGCCTGGAATGGATCGGCGAGATCAAC CCCAACAACGGCCACACCAACTACAACGAG AAGTTCGAGAGCCGGGCCACCCTGACCGTG GACAAGAGCAGCAGCACCGCCTACATGCAG TTCAACAGCCTGACCAGCGAGGACAGCGCC GTGTACTACTGCGGCAGACTGGATGGCCACC TGTACGCCGTGGATTACTGGGGCCAGGGCA CCAGCGTGACCGTGTCATCTGCCAAAACAAC AGCACCAAGTGTCTATCCACTGGCCCCTGTG TGTGGAGATACAACTGGCTCCTCGGTGACTC TAGGATGCCTGGTCAAGGGTTATTTCCCTGA GCCAGTGACCTTGACCTGGAACTCTGGATCC	895

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CTGTCCAGTGGTGTGCACACCTTCCCAGCTG TCCTGCAGTCTGACCTCTACACCCTCAGCAG CTCAGTGACTGTAACCTCGAGCACCTGGCCC AGCCAGTCCATCACCTGCAATGTGGCCCACC CGGCAAGCAGCACCAAGGTGGACAAGAAAA TTGAGCCCAGAGGGCCCACAATCAAGCCCT GTCCTCCATGCAAATGCCCAGCACCTAACCT CTTGGGTGGACCATCCGTCTTCATCTTCCCTC CAAAGATCAAGGATGTACTCATGATCTCCCT GAGCCCCATAGTCACATGTGTGGTGGTGGAT GTGAGCGAGGATGACCCAGATGTCCAGATC AGCTGGTTTGTGAACAACGTGGAAGTACAC ACAGCTCAGACACAAACCCATAGAGAGGAT TACAACAGTACTCTCCGGGTGGTCAGTGCCC TCCCCATCCAGCACCAGGACTGGATGAGTG GCAAGGAGTTCAAATGCAAGGTCAACAACA AAGACCTCCCAGCGCCCATCGAGAGAACCA TCTCAAAACCCAAAGGGTCAGTAAGAGCTC CACAGGTATATGTCTTGCCTCCACCAGAAGA AGAGATGACTAAGAAACAGGTCACTCTGAC CTGCATGGTCACAGACTTCATGCCTGAAGAC ATTTACGTGGAGTGGACCAACAACGGGAAA ACAGAGCTAAACTACAAGAACACTGAACCA GTCCTGGACTCTGATGGTTCTTACTTCATGT ACAGCAAGCTGAGAGTGGAAAAGAAGAACT GGGTGGAAAGAAATAGCTACTCCTGTTCAGT GGTCCACGAGGGTCTGCACAATCACCACAC GACTAAGAGCTTCTCCCGGACTCCGGGTAAA TGA	
SM1B256	pDR000030230	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCCAGG TCCAGCTGCAGCAGCCTGGCACAGAGCTGA AGATGCCCGGCACCAGCGTGAAGCTGAGCT GCAAGGCCAGCGGCTACACCTTCACCACCTA CTGGATGCACTGGGTCAAGCTGCGGCCAGG CCAGGGCTTTGAGTGGATCGGCGAGATCAA CCCCAGCAACGACGGCACCAACTACAACGA GAAGTTCAAGCGGAAGGCCACCCTGACCGT GGACAAGCCTAGCAGCACCGCCTACATGCA GCTGTCCAGCCTGACCAGCGAGGACAGCAC CATCTACTACTGCACCATCAGCTACTACGGC TACGGCGACTTCGACTACTGGGGCCAGGGC ACCACACTGACAGTGTCCTCTGCCAAAACAA CAGCACCAAGTGTCTATCCACTGGCCCCTGT GTGTGGAGATACAACTGGCTCCTCGGTGACT CTAGGATGCCTGGTCAAGGGTTATTTCCCTG AGCCAGTGACCTTGACCTGGAACTCTGGATC CCTGTCCAGTGGTGTGCACACCTTCCCAGCT	896

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GTCCTGCAGTCTGACCTCTACACCCTCAGCA GCTCAGTGACTGTAACCTCGAGCACCTGGCC CAGCCAGTCCATCACCTGCAATGTGGCCCAC CCGGCAAGCAGCACCAAGGTGGACAAGAAA ATTGAGCCCAGAGGGCCCACAATCAAGCCC TGTCCTCCATGCAAATGCCCAGCACCTAACC TCTTGGGTGGACCATCCGTCTTCATCTTCCCT CCAAAGATCAAGGATGTACTCATGATCTCCC TGAGCCCCATAGTCACATGTGTGGTGGTGGA TGTGAGCGAGGATGACCCAGATGTCCAGAT CAGCTGGTTTGTGAACAACGTGGAAGTACA CACAGCTCAGACACAAACCCATAGAGAGGA TTACAACAGTACTCTCCGGGTGGTCAGTGCC CTCCCCATCCAGCACCAGGACTGGATGAGTG GCAAGGAGTTCAAATGCAAGGTCAACAACA AAGACCTCCCAGCGCCCATCGAGAGAACCA TCTCAAAACCCAAAGGGTCAGTAAGAGCTC CACAGGTATATGTCTTGCCTCCACCAGAAGA AGAGATGACTAAGAAACAGGTCACTCTGAC CTGCATGGTCACAGACTTCATGCCTGAAGAC ATTTACGTGGAGTGGACCAACAACGGGAAA ACAGAGCTAAACTACAAGAACACTGAACCA GTCCTGGACTCTGATGGTTCTTACTTCATGT ACAGCAAGCTGAGAGTGGAAAAGAAGAACT GGGTGGAAAGAAATAGCTACTCCTGTTCAGT GGTCCACGAGGGTCTGCACAATCACCACAC GACTAAGAGCTTCTCCCGGACTCCGGGTAAA TGA	
SM1B257	pDR000030231	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCCAGG TGCAGCTGAAAGAGTCCGGCCCTGATCTGGT GCAGCCCAGCCAGACCCTGAGCCTGACCTGT ACCGTGTCCGGCTTCAGCCTGACCAGCTACG GCGTGCACTGGGTCCGACAGCCACCTGGCA AAGGCCTGGAATGGGTCGGAACCATGGGCT GGAACGACAAGAAGTACTACAACAGCGCCC TGAAGTCCCGGCTGAGCATCAGCAGAAACA CCAGCAAGAACCAGGTGTTCCTGAAGCTGA GCAGCCTGCAGACCGAGGACACCGCCATGT ACTACTGCACCAGGGACGGCGATAGCAGCG GCAGTTGGTTCGCCTATTGGGGCCAGGGCAC CCTGGTCACCGTGTCTAGTGCCAAAACAACA GCACCAAGTGTCTATCCACTGGCCCCTGTGT GTGGAGATACAACTGGCTCCTCGGTGACTCT AGGATGCCTGGTCAAGGGTTATTTCCCTGAG CCAGTGACCTTGACCTGGAACTCTGGATCCC TGTCCAGTGGTGTGCACACCTTCCCAGCTGT CCTGCAGTCTGACCTCTACACCCTCAGCAGC	897

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		TCAGTGACTGTAACCTCGAGCACCTGGCCCA GCCAGTCCATCACCTGCAATGTGGCCCACCC GGCAAGCAGCACCAAGGTGGACAAGAAAAT TGAGCCCAGAGGGCCCACAATCAAGCCCTG TCCTCCATGCAAATGCCCAGCACCTAACCTC TTGGGTGGACCATCCGTCTTCATCTTCCCTCC AAAGATCAAGGATGTACTCATGATCTCCCTG AGCCCCATAGTCACATGTGTGGTGGTGGATG TGAGCGAGGATGACCCAGATGTCCAGATCA GCTGGTTTGTGAACAACGTGGAAGTACACA CAGCTCAGACACAAACCCATAGAGAGGATT ACAACAGTACTCTCCGGGTGGTCAGTGCCCT CCCCATCCAGCACCAGGACTGGATGAGTGG CAAGGAGTTCAAATGCAAGGTCAACAACAA AGACCTCCCAGCGCCCATCGAGAGAACCAT CTCAAAACCCAAAGGGTCAGTAAGAGCTCC ACAGGTATATGTCTTGCCTCCACCAGAAGAA GAGATGACTAAGAAACAGGTCACTCTGACC TGCATGGTCACAGACTTCATGCCTGAAGACA TTTACGTGGAGTGGACCAACAACGGGAAAA CAGAGCTAAACTACAAGAACACTGAACCAG TCCTGGACTCTGATGGTTCTTACTTCATGTAC AGCAAGCTGAGAGTGGAAAAGAAGAACTGG GTGGAAAGAAATAGCTACTCCTGTTCAGTGG TCCACGAGGGTCTGCACAATCACCACACGA CTAAGAGCTTCTCCCGGACTCCGGGTAAATG A	
SM1B258	pDR000030232	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCCAGG TGCAGCTGAAAGAGTCCGGCCCTGATCTGGT GCAGCCCAGCCAGACCCTGAGCCTGACCTGT ACCGTGTCCGGCTTCAGCCTGACAGGCTACG CTGTGCATTGGGTCCGACAGCCTCCAGGCAA GGGCGTGGAATGGGTCGGAACCATGGGCTG GGACGACAAGAAGTTCTACAACAGCGCCCT GAAGTCCCGGCTGAGCATCTCCAGGGACCC CAGCAAGAACCAGGTGTTCTTCAAGCTGAG CAGCCTGCAGACCGAGGACACCGCCATGTA CTACTGCACCAGGGATCACGGCGACGGCGG CTTTGCCTATTGGGGCCAGGGAACCCTGGTC ACCGTGTCCTCTGCCAAAACAACAGCACCA AGTGTCTATCCACTGGCCCCTGTGTGTGGAG ATACAACTGGCTCCTCGGTGACTCTAGGATG CCTGGTCAAGGGTTATTTCCCTGAGCCAGTG ACCTTGACCTGGAACTCTGGATCCCTGTCCA GTGGTGTGCACACCTTCCCAGCTGTCCTGCA GTCTGACCTCTACACCCTCAGCAGCTCAGTG ACTGTAACCTCGAGCACCTGGCCCAGCCAGT	898

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CCATCACCTGCAATGTGGCCCACCCGGCAAG CAGCACCAAGGTGGACAAGAAAATTGAGCC CAGAGGGCCCACAATCAAGCCCTGTCCTCCA TGCAAATGCCCAGCACCTAACCTCTTGGGTG GACCATCCGTCTTCATCTTCCCTCCAAAGAT CAAGGATGTACTCATGATCTCCCTGAGCCCC ATAGTCACATGTGTGGTGGTGGATGTGAGCG AGGATGACCCAGATGTCCAGATCAGCTGGTT TGTGAACAACGTGGAAGTACACACAGCTCA GACACAAACCCATAGAGAGGATTACAACAG TACTCTCCGGGTGGTCAGTGCCCTCCCCATC CAGCACCAGGACTGGATGAGTGGCAAGGAG TTCAAATGCAAGGTCAACAACAAAGACCTC CCAGCGCCCATCGAGAGAACCATCTCAAAA CCCAAAGGGTCAGTAAGAGCTCCACAGGTA TATGTCTTGCCTCCACCAGAAGAAGAGATGA CTAAGAAACAGGTCACTCTGACCTGCATGGT CACAGACTTCATGCCTGAAGACATTTACGTG GAGTGGACCAACAACGGGAAAACAGAGCTA AACTACAAGAACACTGAACCAGTCCTGGAC TCTGATGGTTCTTACTTCATGTACAGCAAGC TGAGAGTGGAAAAGAAGAACTGGGTGGAAA GAAATAGCTACTCCTGTTCAGTGGTCCACGA GGGTCTGCACAATCACCACACGACTAAGAG CTTCTCCCGGACTCCGGGTAAATGA	
SM1B259	pDR000030233	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAAG TCCAGCTGCAGCAGTCTGGCCCTGAGCTGGT CAAGCCTGGGGCCAGCGTGAAGATCCCATG CAAGGCCAGCGGCTACACCTTCACCGACTAC AACATGGACTGGGTCAAGCAGAGCCACGGC AAGAGCCTGGAATGGATCGGCAACATCAAC CCCAACAACGGCGGCACCATCTACAACCAG AACTTCAAGGACCGGGCCACCCTGACCGTG GACAAGAGCAGCAGCACCGCCTACATGGAA CTGCGGAGCCTGACCAGCGAGGACACCGCC GTGTACTACTGCACCAGAGAGAACTCCGGCT ACGGCGGCAACTACTTCGCCTATTGGGGCCA GGGCACCACACTGACAGTGTCCTCTGCCAAA ACAACAGCACCAAGTGTCTATCCACTGGCCC CTGTGTGTGGAGATACAACTGGCTCCTCGGT GACTCTAGGATGCCTGGTCAAGGGTTATTTC CCTGAGCCAGTGACCTTGACCTGGAACTCTG GATCCCTGTCCAGTGGTGTGCACACCTTCCC AGCTGTCCTGCAGTCTGACCTCTACACCCTC AGCAGCTCAGTGACTGTAACCTCGAGCACCT GGCCCAGCCAGTCCATCACCTGCAATGTGGC CCACCCGGCAAGCAGCACCAAGGTGGACAA	899

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GAAAATTGAGCCCAGAGGGCCCACAATCAA GCCCTGTCCTCCATGCAAATGCCCAGCACCT AACCTCTTGGGTGGACCATCCGTCTTCATCT TCCCTCCAAAGATCAAGGATGTACTCATGAT CTCCCTGAGCCCCATAGTCACATGTGTGGTG GTGGATGTGAGCGAGGATGACCCAGATGTC CAGATCAGCTGGTTTGTGAACAACGTGGAA GTACACACAGCTCAGACACAAACCCATAGA GAGGATTACAACAGTACTCTCCGGGTGGTCA GTGCCCTCCCCATCCAGCACCAGGACTGGAT GAGTGGCAAGGAGTTCAAATGCAAGGTCAA CAACAAAGACCTCCCAGCGCCCATCGAGAG AACCATCTCAAAACCCAAAGGGTCAGTAAG AGCTCCACAGGTATATGTCTTGCCTCCACCA GAAGAAGAGATGACTAAGAAACAGGTCACT CTGACCTGCATGGTCACAGACTTCATGCCTG AAGACATTTACGTGGAGTGGACCAACAACG GGAAAACAGAGCTAAACTACAAGAACACTG AACCAGTCCTGGACTCTGATGGTTCTTACTT CATGTACAGCAAGCTGAGAGTGGAAAAGAA GAACTGGGTGGAAAGAAATAGCTACTCCTG TTCAGTGGTCCACGAGGGTCTGCACAATCAC CACACGACTAAGAGCTTCTCCCGGACTCCGG GTAAATGA	
SM1B260	pDR000030234	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAAG TCCAGCTGCAGCAGAGCGGAGCCGAACTCG TCAGACCTGGCGCTTCCGTGAAGCTGAGCTG CACCACCAGCGGCTTCAACATCAAGGACAG CCTGATCTACTGGGTCAAGCAGCGGCCCGA GCAGGGCCTGGAATGGATCGGCTGGATTGA CCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAG CGACACCAGCAGCAACACCGCCTACCTGAG ACTGAGCAGCCTGACCAGCGAGGACACCGC CATCTACTACTGCACCCGGTCCTTCGGCGTG TGTTGGGGCCAGGGAACCCTGGTCACAGTGT CTGCTGCCAAAACAACAGCACCAAGTGTCT ATCCACTGGCCCCTGTGTGTGGAGATACAAC TGGCTCCTCGGTGACTCTAGGATGCCTGGTC AAGGGTTATTTCCCTGAGCCAGTGACCTTGA CCTGGAACTCTGGATCCCTGTCCAGTGGTGT GCACACCTTCCCAGCTGTCCTGCAGTCTGAC CTCTACACCCTCAGCAGCTCAGTGACTGTAA CCTCGAGCACCTGGCCCAGCCAGTCCATCAC CTGCAATGTGGCCCACCCGGCAAGCAGCAC CAAGGTGGACAAGAAAATTGAGCCCAGAGG GCCCACAATCAAGCCCTGTCCTCCATGCAAA	900

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		TGCCCAGCACCTAACCTCTTGGGTGGACCAT CCGTCTTCATCTTCCCTCCAAAGATCAAGGA TGTACTCATGATCTCCCTGAGCCCCATAGTC ACATGTGTGGTGGTGGATGTGAGCGAGGAT GACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTC TCCGGGTGGTCAGTGCCCTCCCCATCCAGCA CCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAA AGGGTCAGTAAGAGCTCCACAGGTATATGT CTTGCCTCCACCAGAAGAAGAGATGACTAA GAAACAGGTCACTCTGACCTGCATGGTCACA GACTTCATGCCTGAAGACATTTACGTGGAGT GGACCAACAACGGGAAAACAGAGCTAAACT ACAAGAACACTGAACCAGTCCTGGACTCTG ATGGTTCTTACTTCATGTACAGCAAGCTGAG AGTGGAAAAGAAGAACTGGGTGGAAAGAA ATAGCTACTCCTGTTCAGTGGTCCACGAGGG TCTGCACAATCACCACACGACTAAGAGCTTC TCCCGGACTCCGGGTAAATGA	
SM1B261	pDR000030234	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAAG TCCAGCTGCAGCAGAGCGGAGCCGAACTCG TCAGACCTGGCGCTTCCGTGAAGCTGAGCTG CACCACCAGCGGCTTCAACATCAAGGACAG CCTGATCTACTGGGTCAAGCAGCGGCCCGA GCAGGGCCTGGAATGGATCGGCTGGATTGA CCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAG CGACACCAGCAGCAACACCGCCTACCTGAG ACTGAGCAGCCTGACCAGCGAGGACACCGC CATCTACTACTGCACCCGGTCCTTCGGCGTG TGTTGGGGCCAGGGAACCCTGGTCACAGTGT CTGCTGCCAAAACAACAGCACCAAGTGTCT ATCCACTGGCCCCTGTGTGTGGAGATACAAC TGGCTCCTCGGTGACTCTAGGATGCCTGGTC AAGGGTTATTTCCCTGAGCCAGTGACCTTGA CCTGGAACTCTGGATCCCTGTCCAGTGGTGT GCACACCTTCCCAGCTGTCCTGCAGTCTGAC CTCTACACCCTCAGCAGCTCAGTGACTGTAA CCTCGAGCACCTGGCCCAGCCAGTCCATCAC CTGCAATGTGGCCCACCCGGCAAGCAGCAC CAAGGTGGACAAGAAAATTGAGCCCAGAGG GCCCACAATCAAGCCCTGTCCTCCATGCAAA TGCCCAGCACCTAACCTCTTGGGTGGACCAT CCGTCTTCATCTTCCCTCCAAAGATCAAGGA	901

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		TGTACTCATGATCTCCCTGAGCCCCATAGTC ACATGTGTGGTGGTGGATGTGAGCGAGGAT GACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTC TCCGGGTGGTCAGTGCCCTCCCCATCCAGCA CCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAA AGGGTCAGTAAGAGCTCCACAGGTATATGT CTTGCCTCCACCAGAAGAAGAGATGACTAA GAAACAGGTCACTCTGACCTGCATGGTCACA GACTTCATGCCTGAAGACATTTACGTGGAGT GGACCAACAACGGGAAAACAGAGCTAAACT ACAAGAACACTGAACCAGTCCTGGACTCTG ATGGTTCTTACTTCATGTACAGCAAGCTGAG AGTGGAAAAGAAGAACTGGGTGGAAAGAA ATAGCTACTCCTGTTCAGTGGTCCACGAGGG TCTGCACAATCACCACACGACTAAGAGCTTC TCCCGGACTCCGGGTAAATGA	
SM1B262	pDR000030234	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAAG TCCAGCTGCAGCAGAGCGGAGCCGAACTCG TCAGACCTGGCGCTTCCGTGAAGCTGAGCTG CACCACCAGCGGCTTCAACATCAAGGACAG CCTGATCTACTGGGTCAAGCAGCGGCCCGA GCAGGGCCTGGAATGGATCGGCTGGATTGA CCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAG CGACACCAGCAGCAACACCGCCTACCTGAG ACTGAGCAGCCTGACCAGCGAGGACACCGC CATCTACTACTGCACCCGGTCCTTCGGCGTG TGTTGGGGCCAGGGAACCCTGGTCACAGTGT CTGCTGCCAAAACAACAGCACCAAGTGTCT ATCCACTGGCCCCTGTGTGTGGAGATACAAC TGGCTCCTCGGTGACTCTAGGATGCCTGGTC AAGGGTTATTTCCCTGAGCCAGTGACCTTGA CCTGGAACTCTGGATCCCTGTCCAGTGGTGT GCACACCTTCCCAGCTGTCCTGCAGTCTGAC CTCTACACCCTCAGCAGCTCAGTGACTGTAA CCTCGAGCACCTGGCCCAGCCAGTCCATCAC CTGCAATGTGGCCCACCCGGCAAGCAGCAC CAAGGTGGACAAGAAAATTGAGCCCAGAGG GCCCACAATCAAGCCCTGTCCTCCATGCAAA TGCCCAGCACCTAACCTCTTGGGTGGACCAT CCGTCTTCATCTTCCCTCCAAAGATCAAGGA TGTACTCATGATCTCCCTGAGCCCCATAGTC ACATGTGTGGTGGTGGATGTGAGCGAGGAT	902

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTC TCCGGGTGGTCAGTGCCCTCCCCATCCAGCA CCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAA AGGGTCAGTAAGAGCTCCACAGGTATATGT CTTGCCTCCACCAGAAGAAGAGATGACTAA GAAACAGGTCACTCTGACCTGCATGGTCACA GACTTCATGCCTGAAGACATTTACGTGGAGT GGACCAACAACGGGAAAACAGAGCTAAACT ACAAGAACACTGAACCAGTCCTGGACTCTG ATGGTTCTTACTTCATGTACAGCAAGCTGAG AGTGGAAAAGAAGAACTGGGTGGAAAGAA ATAGCTACTCCTGTTCAGTGGTCCACGAGGG TCTGCACAATCACCACACGACTAAGAGCTTC TCCCGGACTCCGGGTAAATGA	
SM1B263	pDR000030234	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAAG TCCAGCTGCAGCAGAGCGGAGCCGAACTCG TCAGACCTGGCGCTTCCGTGAAGCTGAGCTG CACCACCAGCGGCTTCAACATCAAGGACAG CCTGATCTACTGGGTCAAGCAGCGGCCCGA GCAGGGCCTGGAATGGATCGGCTGGATTGA CCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAG CGACACCAGCAGCAACACCGCCTACCTGAG ACTGAGCAGCCTGACCAGCGAGGACACCGC CATCTACTACTGCACCCGGTCCTTCGGCGTG TGTTGGGGCCAGGGAACCCTGGTCACAGTGT CTGCTGCCAAAACAACAGCACCAAGTGTCT ATCCACTGGCCCCTGTGTGTGGAGATACAAC TGGCTCCTCGGTGACTCTAGGATGCCTGGTC AAGGGTTATTTCCCTGAGCCAGTGACCTTGA CCTGGAACTCTGGATCCCTGTCCAGTGGTGT GCACACCTTCCCAGCTGTCCTGCAGTCTGAC CTCTACACCCTCAGCAGCTCAGTGACTGTAA CCTCGAGCACCTGGCCCAGCCAGTCCATCAC CTGCAATGTGGCCCACCCGGCAAGCAGCAC CAAGGTGGACAAGAAAATTGAGCCCAGAGG GCCCACAATCAAGCCCTGTCCTCCATGCAAA TGCCCAGCACCTAACCTCTTGGGTGGACCAT CCGTCTTCATCTTCCCTCCAAAGATCAAGGA TGTACTCATGATCTCCCTGAGCCCCATAGTC ACATGTGTGGTGGTGGATGTGAGCGAGGAT GACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACAC	903

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		AAACCCATAGAGAGGATTACAACAGTACTC TCCGGGTGGTCAGTGCCCTCCCCATCCAGCA CCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAA AGGGTCAGTAAGAGCTCCACAGGTATATGT CTTGCCTCCACCAGAAGAAGAGATGACTAA GAAACAGGTCACTCTGACCTGCATGGTCACA GACTTCATGCCTGAAGACATTTACGTGGAGT GGACCAACAACGGGAAAACAGAGCTAAACT ACAAGAACACTGAACCAGTCCTGGACTCTG ATGGTTCTTACTTCATGTACAGCAAGCTGAG AGTGGAAAAGAAGAACTGGGTGGAAAGAA ATAGCTACTCCTGTTCAGTGGTCCACGAGGG TCTGCACAATCACCACACGACTAAGAGCTTC TCCCGGACTCCGGGTAAATGA	
SM1B264	pDR000030234	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAAG TCCAGCTGCAGCAGAGCGGAGCCGAACTCG TCAGACCTGGCGCTTCCGTGAAGCTGAGCTG CACCACCAGCGGCTTCAACATCAAGGACAG CCTGATCTACTGGGTCAAGCAGCGGCCCGA GCAGGGCCTGGAATGGATCGGCTGGATTGA CCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAG CGACACCAGCAGCAACACCGCCTACCTGAG ACTGAGCAGCCTGACCAGCGAGGACACCGC CATCTACTACTGCACCCGGTCCTTCGGCGTG TGTTGGGGCCAGGGAACCCTGGTCACAGTGT CTGCTGCCAAAACAACAGCACCAAGTGTCT ATCCACTGGCCCCTGTGTGTGGAGATACAAC TGGCTCCTCGGTGACTCTAGGATGCCTGGTC AAGGGTTATTTCCCTGAGCCAGTGACCTTGA CCTGGAACTCTGGATCCCTGTCCAGTGGTGT GCACACCTTCCCAGCTGTCCTGCAGTCTGAC CTCTACACCCTCAGCAGCTCAGTGACTGTAA CCTCGAGCACCTGGCCCAGCCAGTCCATCAC CTGCAATGTGGCCCACCCGGCAAGCAGCAC CAAGGTGGACAAGAAAATTGAGCCCAGAGG GCCCACAATCAAGCCCTGTCCTCCATGCAAA TGCCCAGCACCTAACCTCTTGGGTGGACCAT CCGTCTTCATCTTCCCTCCAAAGATCAAGGA TGTACTCATGATCTCCCTGAGCCCCATAGTC ACATGTGTGGTGGTGGATGTGAGCGAGGAT GACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTC TCCGGGTGGTCAGTGCCCTCCCCATCCAGCA	904

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAA AGGGTCAGTAAGAGCTCCACAGGTATATGT CTTGCCTCCACCAGAAGAAGAGATGACTAA GAAACAGGTCACTCTGACCTGCATGGTCACA GACTTCATGCCTGAAGACATTTACGTGGAGT GGACCAACAACGGGAAAACAGAGCTAAACT ACAAGAACACTGAACCAGTCCTGGACTCTG ATGGTTCTTACTTCATGTACAGCAAGCTGAG AGTGGAAAAGAAGAACTGGGTGGAAAGAA ATAGCTACTCCTGTTCAGTGGTCCACGAGGG TCTGCACAATCACCACACGACTAAGAGCTTC TCCCGGACTCCGGGTAAATGA	
SM1B265	pDR000030234	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAAG TCCAGCTGCAGCAGAGCGGAGCCGAACTCG TCAGACCTGGCGCTTCCGTGAAGCTGAGCTG CACCACCAGCGGCTTCAACATCAAGGACAG CCTGATCTACTGGGTCAAGCAGCGGCCCGA GCAGGGCCTGGAATGGATCGGCTGGATTGA CCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAG CGACACCAGCAGCAACACCGCCTACCTGAG ACTGAGCAGCCTGACCAGCGAGGACACCGC CATCTACTACTGCACCCGGTCCTTCGGCGTG TGTTGGGGCCAGGGAACCCTGGTCACAGTGT CTGCTGCCAAAACAACAGCACCAAGTGTCT ATCCACTGGCCCCTGTGTGTGGAGATACAAC TGGCTCCTCGGTGACTCTAGGATGCCTGGTC AAGGGTTATTTCCCTGAGCCAGTGACCTTGA CCTGGAACTCTGGATCCCTGTCCAGTGGTGT GCACACCTTCCCAGCTGTCCTGCAGTCTGAC CTCTACACCCTCAGCAGCTCAGTGACTGTAA CCTCGAGCACCTGGCCCAGCCAGTCCATCAC CTGCAATGTGGCCCACCCGGCAAGCAGCAC CAAGGTGGACAAGAAAATTGAGCCCAGAGG GCCCACAATCAAGCCCTGTCCTCCATGCAAA TGCCCAGCACCTAACCTCTTGGGTGGACCAT CCGTCTTCATCTTCCCTCCAAAGATCAAGGA TGTACTCATGATCTCCCTGAGCCCCATAGTC ACATGTGTGGTGGTGGATGTGAGCGAGGAT GACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTC TCCGGGTGGTCAGTGCCCTCCCCATCCAGCA CCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGC	905

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GCCCATCGAGAGAACCATCTCAAAACCCAA AGGGTCAGTAAGAGCTCCACAGGTATATGT CTTGCCTCCACCAGAAGAAGAGATGACTAA GAAACAGGTCACTCTGACCTGCATGGTCACA GACTTCATGCCTGAAGACATTTACGTGGAGT GGACCAACAACGGGAAAACAGAGCTAAACT ACAAGAACACTGAACCAGTCCTGGACTCTG ATGGTTCTTACTTCATGTACAGCAAGCTGAG AGTGGAAAAGAAGAACTGGGTGGAAAGAA ATAGCTACTCCTGTTCAGTGGTCCACGAGGG TCTGCACAATCACCACACGACTAAGAGCTTC TCCCGGACTCCGGGTAAATGA	
SM1B266	pDR000030234	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAAG TCCAGCTGCAGCAGAGCGGAGCCGAACTCG TCAGACCTGGCGCTTCCGTGAAGCTGAGCTG CACCACCAGCGGCTTCAACATCAAGGACAG CCTGATCTACTGGGTCAAGCAGCGGCCCGA GCAGGGCCTGGAATGGATCGGCTGGATTGA CCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAG CGACACCAGCAGCAACACCGCCTACCTGAG ACTGAGCAGCCTGACCAGCGAGGACACCGC CATCTACTACTGCACCCGGTCCTTCGGCGTG TGTTGGGGCCAGGGAACCCTGGTCACAGTGT CTGCTGCCAAAACAACAGCACCAAGTGTCT ATCCACTGGCCCCTGTGTGTGGAGATACAAC TGGCTCCTCGGTGACTCTAGGATGCCTGGTC AAGGGTTATTTCCCTGAGCCAGTGACCTTGA CCTGGAACTCTGGATCCCTGTCCAGTGGTGT GCACACCTTCCCAGCTGTCCTGCAGTCTGAC CTCTACACCCTCAGCAGCTCAGTGACTGTAA CCTCGAGCACCTGGCCCAGCCAGTCCATCAC CTGCAATGTGGCCCACCCGGCAAGCAGCAC CAAGGTGGACAAGAAAATTGAGCCCAGAGG GCCCACAATCAAGCCCTGTCCTCCATGCAAA TGCCCAGCACCTAACCTCTTGGGTGGACCAT CCGTCTTCATCTTCCCTCCAAAGATCAAGGA TGTACTCATGATCTCCCTGAGCCCCATAGTC ACATGTGTGGTGGTGGATGTGAGCGAGGAT GACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTC TCCGGGTGGTCAGTGCCCTCCCCATCCAGCA CCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAA AGGGTCAGTAAGAGCTCCACAGGTATATGT	906

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CTTGCCTCCACCAGAAGAAGAGATGACTAA GAAACAGGTCACTCTGACCTGCATGGTCACA GACTTCATGCCTGAAGACATTTACGTGGAGT GGACCAACAACGGGAAAACAGAGCTAAACT ACAAGAACACTGAACCAGTCCTGGACTCTG ATGGTTCTTACTTCATGTACAGCAAGCTGAG AGTGGAAAAGAAGAACTGGGTGGAAAGAA ATAGCTACTCCTGTTCAGTGGTCCACGAGGG TCTGCACAATCACCACACGACTAAGAGCTTC TCCCGGACTCCGGGTAAATGA	
SM1B267	pDR000030234	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAAG TCCAGCTGCAGCAGAGCGGAGCCGAACTCG TCAGACCTGGCGCTTCCGTGAAGCTGAGCTG CACCACCAGCGGCTTCAACATCAAGGACAG CCTGATCTACTGGGTCAAGCAGCGGCCCGA GCAGGGCCTGGAATGGATCGGCTGGATTGA CCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAG CGACACCAGCAGCAACACCGCCTACCTGAG ACTGAGCAGCCTGACCAGCGAGGACACCGC CATCTACTACTGCACCCGGTCCTTCGGCGTG TGTTGGGGCCAGGGAACCCTGGTCACAGTGT CTGCTGCCAAAACAACAGCACCAAGTGTCT ATCCACTGGCCCCTGTGTGTGGAGATACAAC TGGCTCCTCGGTGACTCTAGGATGCCTGGTC AAGGGTTATTTCCCTGAGCCAGTGACCTTGA CCTGGAACTCTGGATCCCTGTCCAGTGGTGT GCACACCTTCCCAGCTGTCCTGCAGTCTGAC CTCTACACCCTCAGCAGCTCAGTGACTGTAA CCTCGAGCACCTGGCCCAGCCAGTCCATCAC CTGCAATGTGGCCCACCCGGCAAGCAGCAC CAAGGTGGACAAGAAAATTGAGCCCAGAGG GCCCACAATCAAGCCCTGTCCTCCATGCAAA TGCCCAGCACCTAACCTCTTGGGTGGACCAT CCGTCTTCATCTTCCCTCCAAAGATCAAGGA TGTACTCATGATCTCCCTGAGCCCCATAGTC ACATGTGTGGTGGTGGATGTGAGCGAGGAT GACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTC TCCGGGTGGTCAGTGCCCTCCCCATCCAGCA CCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAA AGGGTCAGTAAGAGCTCCACAGGTATATGT CTTGCCTCCACCAGAAGAAGAGATGACTAA GAAACAGGTCACTCTGACCTGCATGGTCACA	907

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GACTTCATGCCTGAAGACATTTACGTGGAGT GGACCAACAACGGGAAAACAGAGCTAAACT ACAAGAACACTGAACCAGTCCTGGACTCTG ATGGTTCTTACTTCATGTACAGCAAGCTGAG AGTGGAAAAGAAGAACTGGGTGGAAAGAA ATAGCTACTCCTGTTCAGTGGTCCACGAGGG TCTGCACAATCACCACACGACTAAGAGCTTC TCCCGGACTCCGGGTAAATGA	
SM1B268	pDR000030234	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAAG TCCAGCTGCAGCAGAGCGGAGCCGAACTCG TCAGACCTGGCGCTTCCGTGAAGCTGAGCTG CACCACCAGCGGCTTCAACATCAAGGACAG CCTGATCTACTGGGTCAAGCAGCGGCCCGA GCAGGGCCTGGAATGGATCGGCTGGATTGA CCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAG CGACACCAGCAGCAACACCGCCTACCTGAG ACTGAGCAGCCTGACCAGCGAGGACACCGC CATCTACTACTGCACCCGGTCCTTCGGCGTG TGTTGGGGCCAGGGAACCCTGGTCACAGTGT CTGCTGCCAAAACAACAGCACCAAGTGTCT ATCCACTGGCCCCTGTGTGTGGAGATACAAC TGGCTCCTCGGTGACTCTAGGATGCCTGGTC AAGGGTTATTTCCCTGAGCCAGTGACCTTGA CCTGGAACTCTGGATCCCTGTCCAGTGGTGT GCACACCTTCCCAGCTGTCCTGCAGTCTGAC CTCTACACCCTCAGCAGCTCAGTGACTGTAA CCTCGAGCACCTGGCCCAGCCAGTCCATCAC CTGCAATGTGGCCCACCCGGCAAGCAGCAC CAAGGTGGACAAGAAAATTGAGCCCAGAGG GCCCACAATCAAGCCCTGTCCTCCATGCAAA TGCCCAGCACCTAACCTCTTGGGTGGACCAT CCGTCTTCATCTTCCCTCCAAAGATCAAGGA TGTACTCATGATCTCCCTGAGCCCCATAGTC ACATGTGTGGTGGTGGATGTGAGCGAGGAT GACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTC TCCGGGTGGTCAGTGCCCTCCCCATCCAGCA CCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAA AGGGTCAGTAAGAGCTCCACAGGTATATGT CTTGCCTCCACCAGAAGAAGAGATGACTAA GAAACAGGTCACTCTGACCTGCATGGTCACA GACTTCATGCCTGAAGACATTTACGTGGAGT GGACCAACAACGGGAAAACAGAGCTAAACT	908

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		ACAAGAACACTGAACCAGTCCTGGACTCTG ATGGTTCTTACTTCATGTACAGCAAGCTGAG AGTGGAAAAGAAGAACTGGGTGGAAAGAA ATAGCTACTCCTGTTCAGTGGTCCACGAGGG TCTGCACAATCACCACACGACTAAGAGCTTC TCCCGGACTCCGGGTAAATGA	
SM1B269	pDR000030234	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAAG TCCAGCTGCAGCAGAGCGGAGCCGAACTCG TCAGACCTGGCGCTTCCGTGAAGCTGAGCTG CACCACCAGCGGCTTCAACATCAAGGACAG CCTGATCTACTGGGTCAAGCAGCGGCCCGA GCAGGGCCTGGAATGGATCGGCTGGATTGA CCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAG CGACACCAGCAGCAACACCGCCTACCTGAG ACTGAGCAGCCTGACCAGCGAGGACACCGC CATCTACTACTGCACCCGGTCCTTCGGCGTG TGTTGGGGCCAGGGAACCCTGGTCACAGTGT CTGCTGCCAAAACAACAGCACCAAGTGTCT ATCCACTGGCCCCTGTGTGTGGAGATACAAC TGGCTCCTCGGTGACTCTAGGATGCCTGGTC AAGGGTTATTTCCCTGAGCCAGTGACCTTGA CCTGGAACTCTGGATCCCTGTCCAGTGGTGT GCACACCTTCCCAGCTGTCCTGCAGTCTGAC CTCTACACCCTCAGCAGCTCAGTGACTGTAA CCTCGAGCACCTGGCCCAGCCAGTCCATCAC CTGCAATGTGGCCCACCCGGCAAGCAGCAC CAAGGTGGACAAGAAAATTGAGCCCAGAGG GCCCACAATCAAGCCCTGTCCTCCATGCAAA TGCCCAGCACCTAACCTCTTGGGTGGACCAT CCGTCTTCATCTTCCCTCCAAAGATCAAGGA TGTACTCATGATCTCCCTGAGCCCCATAGTC ACATGTGTGGTGGTGGATGTGAGCGAGGAT GACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTC TCCGGGTGGTCAGTGCCCTCCCCATCCAGCA CCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAA AGGGTCAGTAAGAGCTCCACAGGTATATGT CTTGCCTCCACCAGAAGAAGAGATGACTAA GAAACAGGTCACTCTGACCTGCATGGTCACA GACTTCATGCCTGAAGACATTTACGTGGAGT GGACCAACAACGGGAAAACAGAGCTAAACT ACAAGAACACTGAACCAGTCCTGGACTCTG ATGGTTCTTACTTCATGTACAGCAAGCTGAG	909

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		AGTGGAAAAGAAGAACTGGGTGGAAAGAA ATAGCTACTCCTGTTCAGTGGTCCACGAGGG TCTGCACAATCACCACACGACTAAGAGCTTC TCCCGGACTCCGGGTAAATGA	
SM1B270	pDR000030234	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAAG TCCAGCTGCAGCAGAGCGGAGCCGAACTCG TCAGACCTGGCGCTTCCGTGAAGCTGAGCTG CACCACCAGCGGCTTCAACATCAAGGACAG CCTGATCTACTGGGTCAAGCAGCGGCCCGA GCAGGGCCTGGAATGGATCGGCTGGATTGA CCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAG CGACACCAGCAGCAACACCGCCTACCTGAG ACTGAGCAGCCTGACCAGCGAGGACACCGC CATCTACTACTGCACCCGGTCCTTCGGCGTG TGTTGGGGCCAGGGAACCCTGGTCACAGTGT CTGCTGCCAAAACAACAGCACCAAGTGTCT ATCCACTGGCCCCTGTGTGTGGAGATACAAC TGGCTCCTCGGTGACTCTAGGATGCCTGGTC AAGGGTTATTTCCCTGAGCCAGTGACCTTGA CCTGGAACTCTGGATCCCTGTCCAGTGGTGT GCACACCTTCCCAGCTGTCCTGCAGTCTGAC CTCTACACCCTCAGCAGCTCAGTGACTGTAA CCTCGAGCACCTGGCCCAGCCAGTCCATCAC CTGCAATGTGGCCCACCCGGCAAGCAGCAC CAAGGTGGACAAGAAAATTGAGCCCAGAGG GCCCACAATCAAGCCCTGTCCTCCATGCAAA TGCCCAGCACCTAACCTCTTGGGTGGACCAT CCGTCTTCATCTTCCCTCCAAAGATCAAGGA TGTACTCATGATCTCCCTGAGCCCCATAGTC ACATGTGTGGTGGTGGATGTGAGCGAGGAT GACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTC TCCGGGTGGTCAGTGCCCTCCCCATCCAGCA CCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAA AGGGTCAGTAAGAGCTCCACAGGTATATGT CTTGCCTCCACCAGAAGAAGAGATGACTAA GAAACAGGTCACTCTGACCTGCATGGTCACA GACTTCATGCCTGAAGACATTTACGTGGAGT GGACCAACAACGGGAAAACAGAGCTAAACT ACAAGAACACTGAACCAGTCCTGGACTCTG ATGGTTCTTACTTCATGTACAGCAAGCTGAG AGTGGAAAAGAAGAACTGGGTGGAAAGAA ATAGCTACTCCTGTTCAGTGGTCCACGAGGG	910

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		TCTGCACAATCACCACACGACTAAGAGCTTC TCCCGGACTCCGGGTAAATGA	
SM1B271	pDR000030234	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAAG TCCAGCTGCAGCAGAGCGGAGCCGAACTCG TCAGACCTGGCGCTTCCGTGAAGCTGAGCTG CACCACCAGCGGCTTCAACATCAAGGACAG CCTGATCTACTGGGTCAAGCAGCGGCCCGA GCAGGGCCTGGAATGGATCGGCTGGATTGA CCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAG CGACACCAGCAGCAACACCGCCTACCTGAG ACTGAGCAGCCTGACCAGCGAGGACACCGC CATCTACTACTGCACCCGGTCCTTCGGCGTG TGTTGGGGCCAGGGAACCCTGGTCACAGTGT CTGCTGCCAAAACAACAGCACCAAGTGTCT ATCCACTGGCCCCTGTGTGTGGAGATACAAC TGGCTCCTCGGTGACTCTAGGATGCCTGGTC AAGGGTTATTTCCCTGAGCCAGTGACCTTGA CCTGGAACTCTGGATCCCTGTCCAGTGGTGT GCACACCTTCCCAGCTGTCCTGCAGTCTGAC CTCTACACCCTCAGCAGCTCAGTGACTGTAA CCTCGAGCACCTGGCCCAGCCAGTCCATCAC CTGCAATGTGGCCCACCCGGCAAGCAGCAC CAAGGTGGACAAGAAAATTGAGCCCAGAGG GCCCACAATCAAGCCCTGTCCTCCATGCAAA TGCCCAGCACCTAACCTCTTGGGTGGACCAT CCGTCTTCATCTTCCCTCCAAAGATCAAGGA TGTACTCATGATCTCCCTGAGCCCCATAGTC ACATGTGTGGTGGTGGATGTGAGCGAGGAT GACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTC TCCGGGTGGTCAGTGCCCTCCCCATCCAGCA CCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAA AGGGTCAGTAAGAGCTCCACAGGTATATGT CTTGCCTCCACCAGAAGAAGAGATGACTAA GAAACAGGTCACTCTGACCTGCATGGTCACA GACTTCATGCCTGAAGACATTTACGTGGAGT GGACCAACAACGGGAAAACAGAGCTAAACT ACAAGAACACTGAACCAGTCCTGGACTCTG ATGGTTCTTACTTCATGTACAGCAAGCTGAG AGTGGAAAAGAAGAACTGGGTGGAAAGAA ATAGCTACTCCTGTTCAGTGGTCCACGAGGG TCTGCACAATCACCACACGACTAAGAGCTTC TCCCGGACTCCGGGTAAATGA	911

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
SM1B272	pDR000030234	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAAG TCCAGCTGCAGCAGAGCGGAGCCGAACTCG TCAGACCTGGCGCTTCCGTGAAGCTGAGCTG CACCACCAGCGGCTTCAACATCAAGGACAG CCTGATCTACTGGGTCAAGCAGCGGCCCGA GCAGGGCCTGGAATGGATCGGCTGGATTGA CCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAG CGACACCAGCAGCAACACCGCCTACCTGAG ACTGAGCAGCCTGACCAGCGAGGACACCGC CATCTACTACTGCACCCGGTCCTTCGGCGTG TGTTGGGGCCAGGGAACCCTGGTCACAGTGT CTGCTGCCAAAACAACAGCACCAAGTGTCT ATCCACTGGCCCCTGTGTGTGGAGATACAAC TGGCTCCTCGGTGACTCTAGGATGCCTGGTC AAGGGTTATTTCCCTGAGCCAGTGACCTTGA CCTGGAACTCTGGATCCCTGTCCAGTGGTGT GCACACCTTCCCAGCTGTCCTGCAGTCTGAC CTCTACACCCTCAGCAGCTCAGTGACTGTAA CCTCGAGCACCTGGCCCAGCCAGTCCATCAC CTGCAATGTGGCCCACCCGGCAAGCAGCAC CAAGGTGGACAAGAAAATTGAGCCCAGAGG GCCCACAATCAAGCCCTGTCCTCCATGCAAA TGCCCAGCACCTAACCTCTTGGGTGGACCAT CCGTCTTCATCTTCCCTCCAAAGATCAAGGA TGTACTCATGATCTCCCTGAGCCCCATAGTC ACATGTGTGGTGGTGGATGTGAGCGAGGAT GACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTC TCCGGGTGGTCAGTGCCCTCCCCATCCAGCA CCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAA AGGGTCAGTAAGAGCTCCACAGGTATATGT CTTGCCTCCACCAGAAGAAGAGATGACTAA GAAACAGGTCACTCTGACCTGCATGGTCACA GACTTCATGCCTGAAGACATTTACGTGGAGT GGACCAACAACGGGAAAACAGAGCTAAACT ACAAGAACACTGAACCAGTCCTGGACTCTG ATGGTTCTTACTTCATGTACAGCAAGCTGAG AGTGGAAAAGAAGAACTGGGTGGAAAGAA ATAGCTACTCCTGTTCAGTGGTCCACGAGGG TCTGCACAATCACCACACGACTAAGAGCTTC TCCCGGACTCCGGGTAAATGA	912
SM1B273	pDR000030234	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAAG	913

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		TCCAGCTGCAGCAGAGCGGAGCCGAACTCG TCAGACCTGGCGCTTCCGTGAAGCTGAGCTG CACCACCAGCGGCTTCAACATCAAGGACAG CCTGATCTACTGGGTCAAGCAGCGGCCCGA GCAGGGCCTGGAATGGATCGGCTGGATTGA CCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAG CGACACCAGCAGCAACACCGCCTACCTGAG ACTGAGCAGCCTGACCAGCGAGGACACCGC CATCTACTACTGCACCCGGTCCTTCGGCGTG TGTTGGGGCCAGGGAACCCTGGTCACAGTGT CTGCTGCCAAAACAACAGCACCAAGTGTCT ATCCACTGGCCCCTGTGTGTGGAGATACAAC TGGCTCCTCGGTGACTCTAGGATGCCTGGTC AAGGGTTATTTCCCTGAGCCAGTGACCTTGA CCTGGAACTCTGGATCCCTGTCCAGTGGTGT GCACACCTTCCCAGCTGTCCTGCAGTCTGAC CTCTACACCCTCAGCAGCTCAGTGACTGTAA CCTCGAGCACCTGGCCCAGCCAGTCCATCAC CTGCAATGTGGCCCACCCGGCAAGCAGCAC CAAGGTGGACAAGAAAATTGAGCCCAGAGG GCCCACAATCAAGCCCTGTCCTCCATGCAAA TGCCCAGCACCTAACCTCTTGGGTGGACCAT CCGTCTTCATCTTCCCTCCAAAGATCAAGGA TGTACTCATGATCTCCCTGAGCCCCATAGTC ACATGTGTGGTGGTGGATGTGAGCGAGGAT GACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTC TCCGGGTGGTCAGTGCCCTCCCCATCCAGCA CCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAA AGGGTCAGTAAGAGCTCCACAGGTATATGT CTTGCCTCCACCAGAAGAAGAGATGACTAA GAAACAGGTCACTCTGACCTGCATGGTCACA GACTTCATGCCTGAAGACATTTACGTGGAGT GGACCAACAACGGGAAAACAGAGCTAAACT ACAAGAACACTGAACCAGTCCTGGACTCTG ATGGTTCTTACTTCATGTACAGCAAGCTGAG AGTGGAAAAGAAGAACTGGGTGGAAAGAA ATAGCTACTCCTGTTCAGTGGTCCACGAGGG TCTGCACAATCACCACACGACTAAGAGCTTC TCCCGGACTCCGGGTAAATGA	
SM1B274	pDR000030234	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAAG TCCAGCTGCAGCAGAGCGGAGCCGAACTCG TCAGACCTGGCGCTTCCGTGAAGCTGAGCTG	914

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CACCACCAGCGGCTTCAACATCAAGGACAG CCTGATCTACTGGGTCAAGCAGCGGCCCGA GCAGGGCCTGGAATGGATCGGCTGGATTGA CCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAG CGACACCAGCAGCAACACCGCCTACCTGAG ACTGAGCAGCCTGACCAGCGAGGACACCGC CATCTACTACTGCACCCGGTCCTTCGGCGTG TGTTGGGGCCAGGGAACCCTGGTCACAGTGT CTGCTGCCAAAACAACAGCACCAAGTGTCT ATCCACTGGCCCCTGTGTGTGGAGATACAAC TGGCTCCTCGGTGACTCTAGGATGCCTGGTC AAGGGTTATTTCCCTGAGCCAGTGACCTTGA CCTGGAACTCTGGATCCCTGTCCAGTGGTGT GCACACCTTCCCAGCTGTCCTGCAGTCTGAC CTCTACACCCTCAGCAGCTCAGTGACTGTAA CCTCGAGCACCTGGCCCAGCCAGTCCATCAC CTGCAATGTGGCCCACCCGGCAAGCAGCAC CAAGGTGGACAAGAAAATTGAGCCCAGAGG GCCCACAATCAAGCCCTGTCCTCCATGCAAA TGCCCAGCACCTAACCTCTTGGGTGGACCAT CCGTCTTCATCTTCCCTCCAAAGATCAAGGA TGTACTCATGATCTCCCTGAGCCCCATAGTC ACATGTGTGGTGGTGGATGTGAGCGAGGAT GACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTC TCCGGGTGGTCAGTGCCCTCCCCATCCAGCA CCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAA AGGGTCAGTAAGAGCTCCACAGGTATATGT CTTGCCTCCACCAGAAGAAGAGATGACTAA GAAACAGGTCACTCTGACCTGCATGGTCACA GACTTCATGCCTGAAGACATTTACGTGGAGT GGACCAACAACGGGAAAACAGAGCTAAACT ACAAGAACACTGAACCAGTCCTGGACTCTG ATGGTTCTTACTTCATGTACAGCAAGCTGAG AGTGGAAAAGAAGAACTGGGTGGAAAGAA ATAGCTACTCCTGTTCAGTGGTCCACGAGGG TCTGCACAATCACCACACGACTAAGAGCTTC TCCCGGACTCCGGGTAAATGA	
SM1B275	pDR000030234	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAAG TCCAGCTGCAGCAGAGCGGAGCCGAACTCG TCAGACCTGGCGCTTCCGTGAAGCTGAGCTG CACCACCAGCGGCTTCAACATCAAGGACAG CCTGATCTACTGGGTCAAGCAGCGGCCCGA	915

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GCAGGGCCTGGAATGGATCGGCTGGATTGA CCCCGAGGACGGCGAGACAAAGTTCGCCCC TAGATTCCAGGACAAGGCCACCATCACCAG CGACACCAGCAGCAACACCGCCTACCTGAG ACTGAGCAGCCTGACCAGCGAGGACACCGC CATCTACTACTGCACCCGGTCCTTCGGCGTG TGTTGGGGCCAGGGAACCCTGGTCACAGTGT CTGCTGCCAAAACAACAGCACCAAGTGTCT ATCCACTGGCCCCTGTGTGTGGAGATACAAC TGGCTCCTCGGTGACTCTAGGATGCCTGGTC AAGGGTTATTTCCCTGAGCCAGTGACCTTGA CCTGGAACTCTGGATCCCTGTCCAGTGGTGT GCACACCTTCCCAGCTGTCCTGCAGTCTGAC CTCTACACCCTCAGCAGCTCAGTGACTGTAA CCTCGAGCACCTGGCCCAGCCAGTCCATCAC CTGCAATGTGGCCCACCCGGCAAGCAGCAC CAAGGTGGACAAGAAAATTGAGCCCAGAGG GCCCACAATCAAGCCCTGTCCTCCATGCAAA TGCCCAGCACCTAACCTCTTGGGTGGACCAT CCGTCTTCATCTTCCCTCCAAAGATCAAGGA TGTACTCATGATCTCCCTGAGCCCCATAGTC ACATGTGTGGTGGTGGATGTGAGCGAGGAT GACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTC TCCGGGTGGTCAGTGCCCTCCCCATCCAGCA CCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAA AGGGTCAGTAAGAGCTCCACAGGTATATGT CTTGCCTCCACCAGAAGAAGAGATGACTAA GAAACAGGTCACTCTGACCTGCATGGTCACA GACTTCATGCCTGAAGACATTTACGTGGAGT GGACCAACAACGGGAAAACAGAGCTAAACT ACAAGAACACTGAACCAGTCCTGGACTCTG ATGGTTCTTACTTCATGTACAGCAAGCTGAG AGTGGAAAAGAAGAACTGGGTGGAAAGAA ATAGCTACTCCTGTTCAGTGGTCCACGAGGG TCTGCACAATCACCACACGACTAAGAGCTTC TCCCGGACTCCGGGTAAATGA	

Table 28. LukAB Antibody Light Chain CDSs

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
SM1B105	pDR000023603	GATATTGTGCTAACTCAGTCTCCAGCAATAA TGGCTGCCTCTCTGGGGCAGAAGGTCACCAT GACCTGCAGTGCCAGCTCAAGTGTAAGTTCC AGTTACTTGCACTGGTACCAGCAGAAGTCAG GCGCTTCCCCCAAACCCTTGATTCATAGGAC ATCCAACCTGGCTTCTGGAGTCCCAGCTCGCT TCAGTGGCAGTGGGTCTGGGACCTCTTACTCT CTCACAATCAGCAGCGTGGAGGCTGAAGATG ATGCAACTTATTACTGCCAGCAGTGGAGTGG TTACCCATTCACGTTCGGTGCTGGGACCAAG CTGGAGCTGAAACGGGCTGATGCTGCACCAA CTGTATCCATCTTCCCACCATCCAGTGAGCAG TTAACATCTGGAGGTGCCTCAGTCGTGTGCTT CTTGAACAACTTCTACCCCAAAGACATCAAT GTCAAGTGGAAGATTGATGGCAGTGAACGAC AAAATGGCGTCCTGAACAGTTGGACTGATCA GGACAGCAAAGACAGCACCTACAGCATGAG CAGCACCCTCACGTTGACCAAGGACGAGTAT GAACGACATAACAGCTATACCTGTGAGGCCA CTCACAAGACATCAACTTCACCCATTGTCAA GAGCTTCAACAGGAATGAGTGT	916
SM1B106	pDR000023628	GACATTGTGATGACCCAGTCTCCAGCTTCTTT GGCTGTGTCTCTAGGGCAGAGGGCCACCATC TCCTGCAGAGCCAGCGAAAGTGTTGATAATT CTGGCATTAGTTTTATGAACTGGTTCCAACAG AAACCAGGACAGCCACCCAAACTCCTCATCT ATGCTGCATCCAACCAAGGATCCGGGGTCCC TGCCAGGTTTAGTGGCAGTGGGTCTGGGACA GACTTCAGCCTCAACATCCATCCTATGGAGG AGGATGATACTGCAATGTATTTCTGTCAGCA AAGTAAGGAGGTTCCGTACACGTTCGGAGGG GGGACCAAGCTGGAAATAAAACGGGCTGAT GCTGCACCAACTGTATCCATCTTCCCACCATC CAGTGAGCAGTTAACATCTGGAGGTGCCTCA GTCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGGC AGTGAACGACAAAATGGCGTCCTGAACAGTT GGACTGATCAGGACAGCAAAGACAGCACCT ACAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATACC TGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTG T	917
SM1B107	pDR000023626	GATATTGTGCTAACTCAGTCTCCAGCTTCTTT GGCTGTGTCTCTAGGGCAGAGGGCCACCATC TCCTGCAGAGCCAGCGAAAGTGTTGATAATT	918

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		CTGGCATTAGTTTTATGAACTGGTTCCAACAG AAACCAGGACAGCCACCCAAACTCCTCATCT ATGCTGCATCCAACCAAGGATCCGGGGTCCC TGCCAGGTTTAGTGGCAGTGGGTCTGGGACA GACTTCAGCCTCAACATCCATCCTATGGAGG AGGATGATACTGCAATGTATTTCTGTCAGCA AAGTAAGGAGGTTCCGTACACGTTCGGAGGG GGGACCAAGCTGGAAATAAAACGGGCTGAT GCTGCACCAACTGTATCCATCTTCCCACCATC CAGTGAGCAGTTAACATCTGGAGGTGCCTCA GTCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGGC AGTGAACGACAAAATGGCGTCCTGAACAGTT GGACTGATCAGGACAGCAAAGACAGCACCT ACAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATACC TGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTG T	
SM1B108	pDR000023627	GATGTTGTGATGACCCAAACTCCCAAATTCC TGCTTGTATCAGCAGGAGACAGGGTTACCAT TACCTGCAAGGCCAGTCAGAGTGTGAGTGAT GATGTAACTTGGTACCAACAGAAGTCAGGAC AGTCTCCTAAACTGCTGATATACTATGCATCC AATCGCTACACTGGAGTCCCTGATCGCTTCA CTGGCAGTGGATATGGGACGGATTTCACTTT CACCATCAGCACTGTGCAGGCTGAAGACCTG GCAGTTTATTTCTGTCAGCAGGATTATAGCTC TCCGTGGACGTTCGGTGGAGGCACCAAGCTG GAAATCAAACGGGCTGATGCTGCACCAACTG TATCCATCTTCTCACCATCCAGTGAGCAGTTA ACATCTGGAGGTGCCTCAGTCGTGTGCTTCTT GAACAACTTCTACCCCAAAGACATCAATGTC AAGTGGAAGATTGATGGCAGTGAACGACAA AATGGCGTCCTGAACAGTTGGACTGATCAGG ACAGCAAAGACAGCACCTACAGCATGAGCA GCACCCTCACGTTGACCAAGGACGAGTATGA ACGACATAACAGCTATACCTGTGAGGCCACT CACAAGACATCAACTTCACCCATTGTCAAGA GCTTCAACAGGAATGAGTGT	919
SM1B109	pDR000023628	GACATTGTGATGACCCAGTCTCCAGCTTCTTT GGCTGTGTCTCTAGGGCAGAGGGCCACCATC TCCTGCAGAGCCAGCGAAAGTGTTGATAATT CTGGCATTAGTTTTATGAACTGGTTCCAACAG AAACCAGGACAGCCACCCAAACTCCTCATCT ATGCTGCATCCAACCAAGGATCCGGGGTCCC TGCCAGGTTTAGTGGCAGTGGGTCTGGGACA GACTTCAGCCTCAACATCCATCCTATGGAGG	920

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		AGGATGATACTGCAATGTATTTCTGTCAGCA AAGTAAGGAGGTTCCGTACACGTTCGGAGGG GGGACCAAGCTGGAAATAAAACGGGCTGAT GCTGCACCAACTGTATCCATCTTCCCACCATC CAGTGAGCAGTTAACATCTGGAGGTGCCTCA GTCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGGC AGTGAACGACAAAATGGCGTCCTGAACAGTT GGACTGATCAGGACAGCAAAGACAGCACCT ACAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATACC TGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTG T	
SM1B110	pDR000023629	GATATTGTGCTAACTCAGTCTCCAGCAATCAT GTCTGCATCTCCAGGGGAGAAGGTCACCATA ACCTGCAGTGCCAGCTCAAGTGTAAGTTACA TGCACTGGTTCCAGCAGAAGCCAGGCACTTC TCCCAAACTCTGGATTTATAGCACATCCAAC CTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGG CAGTGGATCTGGGACCTCTTACTCTCTCACAA TCAGCCGAATGGAGGCTGAAGATGCTGCCAC TTATTACTGCCAGCAAAGGAGTAGTTACCCA TTCACGTTCGGCTCGGGGACAAAGTTGGAAA TAAAACGGGCTGATGCTGCACCAACTGTATC CATCTTCCCACCATCCAGTGAGCAGTTAACA TCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAA CAACTTCTACCCCAAAGACATCAATGTCAAG TGGAAGATTGATGGCAGTGAACGACAAAATG GCGTCCTGAACAGTTGGACTGATCAGGACAG CAAAGACAGCACCTACAGCATGAGCAGCACC CTCACGTTGACCAAGGACGAGTATGAACGAC ATAACAGCTATACCTGTGAGGCCACTCACAA GACATCAACTTCACCCATTGTCAAGAGCTTC AACAGGAATGAGTGT	921
SM1B111	pDR000023631	GACATTGTGATGACCCAGTCTCCAACCACCA TGGCTGCATCTCCCGGGGAGAGGATCACTAT CACCTGCAGTGCCCACTCAAATTTAATTTCCA ATTACTTACATTGGTATCAGCAGAAGCCAGG ATTCTCCCCTAAACTCTTGATTTATAGGACAT CCAATCTGGCTTCTGGAGTCCCAGCTCGCTTC AGTGGCAGTGGGTCTGGGACCTCTTACTCTCT CACAATTGGCACCATGGAGGCTGAAGATGTT GCCACTTACTTCTGCCAACAGGGTAGTAGTA TACCATTCACGTTCGGCTCGGGGACAAAGTT GGAAATAAAACGGGCTGATGCTGCACCAACT GTATCCATCTTCCCACCATCCAGTGAGCAGTT AACATCTGGAGGTGCCTCAGTCGTGTGCTTCT	922

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		TGAACAACTTCTACCCCAAAGACATCAATGT CAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAG GACAGCAAAGACAGCACCTACAGCATGAGC AGCACCCTCACGTTGACCAAGGACGAGTATG AACGACATAACAGCTATACCTGTGAGGCCAC TCACAAGACATCAACTTCACCCATTGTCAAG AGCTTCAACAGGAATGAGTGT	
SM1B112	pDR000023630	CAAATTGTTCTCACCCAGTCTCCAACAATCAT GTCTGCATCTCCAGGGGAAAAGGTCACCATG ACCTGCAGTGCCAGCTCACATGTAAGTTACA TATACTGGTACCAGCAGAAGCCAGGCTCCTC CCCCAGACTCTGGATTTATGACACATCCAAC CTGGTTTCTGGAGTCCCTGCTCGCTTCAGTGG CAGTAGGTCTGGGACCTCTTATTCTCTCACAA TCAGCAGCATGGAGGCTGAAGATGCTGCCAC TTATTACTGCCAGCAGTACAGTGGTTACCCGT ACACGTTCGGAGGGGGGACCAAGCTGGAAA TAAAACGGGCTGATGCTGCACCAACTGTATC CATCTTCCCACCATCCAGTGAGCAGTTAACA TCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAA CAACTTCTACCCCAAAGACATCAATGTCAAG TGGAAGATTGATGGCAGTGAACGACAAAATG GCGTCCTGAACAGTTGGACTGATCAGGACAG CAAAGACAGCACCTACAGCATGAGCAGCACC CTCACGTTGACCAAGGACGAGTATGAACGAC ATAACAGCTATACCTGTGAGGCCACTCACAA GACATCAACTTCACCCATTGTCAAGAGCTTC AACAGGAATGAGTGT	923
SM1B243	pDR000030110	GACATCAAGATGACCCAGAGCCCCAGCTCTA TGTACGCCAGCCTGGGCGAGCGCGTGACCAT CACCTGTAAAGCCAGCCAGGACATCAACAGC TACCTGAGCTGGTTCCAGCAGAAGCCCGGCA AGAGCCCCAAGACCCTGATCTACCGGGCCAA CAGACTGGTGGACGGCGTGCCAAGCAGATTC AGCGGCTCTGGCAGCGGCCAGGACTACAGCC CTACCATCAGCAGCCTGGAATACGAGGACAT GGGCATCTACTACTGCCTGCAGTACGACGAG TTCCCCTACACCTTCGGCGGAGGCACCAAGC TGGAAATCAAGCGGGCTGATGCTGCACCGAC TGTGTCCATCTTCCCACCATCCAGTGAGCAGT TAACATCTGGAGGTGCCTCAGTCGTGTGCTTC TTGAACAACTTCTACCCCAAAGACATCAATG TCAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAG GACAGCAAAGACAGCACCTACAGCATGAGC AGCACCCTCACGTTGACCAAGGACGAGTATG AACGACATAACAGCTATACCTGTGAGGCCAC	924

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		TCACAAGACATCAACTTCACCCATTGTCAAG AGCTTCAACAGGAATGAGTGT	
SM1B244	pDR000030235	GACATCGTGATGACCCAGAGCCAGAAATTCA TGAGCACCAGCGTGGGCGACCGGGTGTCCGT GACATGCAAGGCCAGCCAGAACGTGGGCAC CAACGTGGCCTGGTATCAGCAGAAGCCCGGC CAGAGCCCCAAGACCCTGATCTACAGCGCCA GCTACAGATACAGCGGCGTGCCCGATAGCTT CACAGGCAGCGGCTCTGGCACCGACTTCACC CTGACCATCAGCAACGTGCAGAGCGAGGACT GGGCCGAGTACTTCTGCCAGCAGTACAACAG CTACCCCTTCACCTTCGGCAGCGGCACCAAG CTGGAAATCAAGCGGGCTGATGCTGCACCGA CTGTGTCCATCTTCCCACCATCCAGTGAGCAG TTAACATCTGGAGGTGCCTCAGTCGTGTGCTT CTTGAACAACTTCTACCCCAAAGACATCAAT GTCAAGTGGAAGATTGATGGCAGTGAACGAC AAAATGGCGTCCTGAACAGTTGGACTGATCA GGACAGCAAAGACAGCACCTACAGCATGAG CAGCACCCTCACGTTGACCAAGGACGAGTAT GAACGACATAACAGCTATACCTGTGAGGCCA CTCACAAGACATCAACTTCACCCATTGTCAA GAGCTTCAACAGGAATGAGTGT	925
SM1B245	pDR000030236	GACATCGTGCTGACACAGTCTCCAGCCAGCC TGGCCGTGTCTCTGGGACAGAGGGCCACCAT GAGCTGCAGAGCCAGCGAGTCTGTGGACGGC TACGGCAACAGCTTCCTGCACTGGTATCAGC AGAAGCCCGGCCAGCCTCCCAAGCTGCTGAT CTACAGGGCCAGCAACCTGGAAAGCGGCATC CCCGCCAGATTCAGCGGCACCGGCAGCAGAA CCGACTTCACCCTGACCATCACCCCTGTGGA AGCCGACGACGTGGCCACCTACTACTGCCAG CAGAGCAACGGCGACCCCTTCACCTTCGGCT CCGGCACCAAGCTGGAAATCAAGCGGGCTGA TGCTGCACCGACTGTGTCCATCTTCCCACCAT CCAGTGAGCAGTTAACATCTGGAGGTGCCTC AGTCGTGTGCTTCTTGAACAACTTCTACCCCA AAGACATCAATGTCAAGTGGAAGATTGATGG CAGTGAACGACAAAATGGCGTCCTGAACAGT TGGACTGATCAGGACAGCAAAGACAGCACCT ACAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATACC TGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTG T	926
SM1B246	pDR000030237	GACGTGCTGATGACCCAGACACCCCTGAGCC TGCCTGTGTCTCTGGGCGATCAGGCCAGCAT CAGCTGCCGGTCTAGCCAGAGCATCGTGCAC	927

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		AGCAACGGCAAGACCTACCTGGAATGGTATC TGCAGAAGCCCGGCCAGAGCCCCAAGCTGCT GATCTACAAGGTGTCCAACAGATTCAGCGGC GTGCCCGACAGATTCTCTGGCAGCGGCTCTG GCACCGACTTCACCCTGAAGATCAGCCGGGT GGAAGCCGAGGACCTGGGCGTGTACTACTGT CTGCAGGGCAGCCACGTGCCCTGGACCTTTG GCGGCGGAACAAAGCTGGAACTGAAGCGGG CTGATGCTGCACCGACTGTGTCCATCTTCCCA CCATCCAGTGAGCAGTTAACATCTGGAGGTG CCTCAGTCGTGTGCTTCTTGAACAACTTCTAC CCCAAAGACATCAATGTCAAGTGGAAGATTG ATGGCAGTGAACGACAAAATGGCGTCCTGAA CAGTTGGACTGATCAGGACAGCAAAGACAGC ACCTACAGCATGAGCAGCACCCTCACGTTGA CCAAGGACGAGTATGAACGACATAACAGCTA TACCTGTGAGGCCACTCACAAGACATCAACT TCACCCATTGTCAAGAGCTTCAACAGGAATG AGTGT	
SM1B247	pDR000030238	GACATCGTGCTGACACAGTCTCCAGCCAGCC TGGCCGTGTCTCTGGGACAGAGAGCCACCAT CAGCTGCCGGGCCAGCAAGAGCGTGTCCATC AGCGGCTACAGCTACATGCACTGGTATCAGC AGAAGCCCGGCCAGCCTCCCAAGCTGCTGAT CGACCTGGCCAGCAACCTGGAAAGCGGCGTG CCAGCCAGATTTTCTGGCAGCGGCTCCGGCA CCGACTTCACCCTGAACATCCACCCCGTGGA AGAAGAGGACGCCGCCACCTACTACTGCCAG CACAGCAGAGAGCTGCCCTTCACCTTCGGCA GCGGCACCAAGCTGGAAATCAAGCGGGCTG ATGCTGCACCGACTGTGTCCATCTTCCCACCA TCCAGTGAGCAGTTAACATCTGGAGGTGCCT CAGTCGTGTGCTTCTTGAACAACTTCTACCCC AAAGACATCAATGTCAAGTGGAAGATTGATG GCAGTGAACGACAAAATGGCGTCCTGAACAG TTGGACTGATCAGGACAGCAAAGACAGCACC TACAGCATGAGCAGCACCCTCACGTTGACCA AGGACGAGTATGAACGACATAACAGCTATAC CTGTGAGGCCACTCACAAGACATCAACTTCA CCCATTGTCAAGAGCTTCAACAGGAATGAGT GT	928
SM1B248	pDR000030236	GACATCGTGCTGACACAGTCTCCAGCCAGCC TGGCCGTGTCTCTGGGACAGAGGGCCACCAT GAGCTGCAGAGCCAGCGAGTCTGTGGACGGC TACGGCAACAGCTTCCTGCACTGGTATCAGC AGAAGCCCGGCCAGCCTCCCAAGCTGCTGAT CTACAGGGCCAGCAACCTGGAAAGCGGCATC CCCGCCAGATTCAGCGGCACCGGCAGCAGAA	929

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		CCGACTTCACCCTGACCATCACCCCTGTGGA AGCCGACGACGTGGCCACCTACTACTGCCAG CAGAGCAACGGCGACCCCTTCACCTTCGGCT CCGGCACCAAGCTGGAAATCAAGCGGGCTGA TGCTGCACCGACTGTGTCCATCTTCCCACCAT CCAGTGAGCAGTTAACATCTGGAGGTGCCTC AGTCGTGTGCTTCTTGAACAACTTCTACCCCA AAGACATCAATGTCAAGTGGAAGATTGATGG CAGTGAACGACAAAATGGCGTCCTGAACAGT TGGACTGATCAGGACAGCAAAGACAGCACCT ACAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATACC TGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTG T	
SM1B249	pDR000030239	CAGATCGTGCTGACCCAGAGCCCTGCCATCA TGTCTGCCAGCCCTGGCGAGAAAGTGACCAT GACCTGTAGCGCCAGCAGCAGCGTGTCCTAC ATGCACTGGTATCAGCAGAAGTCCGGCACCA GCCCCAAGCGGTGGATCTACGATACCAGCAA GCTGGCCTCCGGCGTGCCAGCCAGATTTTCT GGCTCTGGCAGCGGCACCTCCTACAGCCTGA CCATCAGCAGCATGGAAGCCGAGGACGCCGC CACCTACTACTGCCAGCAGTGGATCAGCAAC CCTCCCACCTTCGGCGGAGGCACCAAGCTGG AAATCAAGCGGGCTGATGCTGCACCGACTGT GTCCATCTTCCCACCATCCAGTGAGCAGTTA ACATCTGGAGGTGCCTCAGTCGTGTGCTTCTT GAACAACTTCTACCCCAAAGACATCAATGTC AAGTGGAAGATTGATGGCAGTGAACGACAA AATGGCGTCCTGAACAGTTGGACTGATCAGG ACAGCAAAGACAGCACCTACAGCATGAGCA GCACCCTCACGTTGACCAAGGACGAGTATGA ACGACATAACAGCTATACCTGTGAGGCCACT CACAAGACATCAACTTCACCCATTGTCAAGA GCTTCAACAGGAATGAGTGT	930
SM1B250	pDR000030240	GACATCGTGCTGACACAGTCTCCAGCCAGCC TGGCCGTGTCCCTGGAACAGAGAGCCACCAT CAGCTGCAAGGCCAGCCAGAGCGTGGACTAC GACGGCGACAGCTACATGAACTGGTATCAGC AGAAGCCCGGCCAGCCTCCCAAGCTGCTGAT CTACGCCGCCAGCAACCTGGAAAGCGGCATC CCTGCCAGATTCAGCGGCAGCGGCTCTGGCA CCGACTTCACCCTGAACATCCACCCCGTGGA AGAAGAGGACGCCGCCACCTACTACTGCCAG CAGAGCAACGAGGACCCTCTGACCTTCGGAG CCGGCACCAAGCTGGAACTGAAGCGGGCTGA TGCTGCACCGACTGTGTCCATCTTCCCACCAT	931

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		CCAGTGAGCAGTTAACATCTGGAGGTGCCTC AGTCGTGTGCTTCTTGAACAACTTCTACCCCA AAGACATCAATGTCAAGTGGAAGATTGATGG CAGTGAACGACAAAATGGCGTCCTGAACAGT TGGACTGATCAGGACAGCAAAGACAGCACCT ACAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATACC TGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTG T	
SM1B251	pDR000030241	GACATCCAGATGACCCAGAGCCCTGCCAGCC TGAGCGCCTCTGTGGGCGAGACAGTGACCAC CATCTGCCGGGCCAGCGAGAACATCTACAGC TACCTGGCCTGGTATCAGCAGAAGCAGGGCA AGAGCCCTCAGCTGCTGGTGTACAACGCCAA GACCCTGGTGGAAGGCGTGCCCAGCAGATTT TCTGGCTCTGGCAGCGGCACCCAGTTCAGCC TGAAGATCAACAGCCTGCAGCCCGAGGACTT CGGCAGCTACTACTGCCAGCACCACTACGGC AGCCCCTACACCTTTGGCGGAGGCACCAAGC TGGAACTGAAGCGGGCTGATGCTGCACCGAC TGTGTCCATCTTCCCACCATCCAGTGAGCAGT TAACATCTGGAGGTGCCTCAGTCGTGTGCTTC TTGAACAACTTCTACCCCAAAGACATCAATG TCAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAG GACAGCAAAGACAGCACCTACAGCATGAGC AGCACCCTCACGTTGACCAAGGACGAGTATG AACGACATAACAGCTATACCTGTGAGGCCAC TCACAAGACATCAACTTCACCCATTGTCAAG AGCTTCAACAGGAATGAGTGT	932
SM1B252	pDR000030242	GACGTGCTGATGACCCAGACACCCCTGAGCC TGCCTGTGTCTCTGGGCGATCAGGCCAGCAT CAGCTGCCGGTCTAGCCAGAGCATCGTGTAC AGCAACGGCAACACCTACCTGGAATGGTATC TGCAGAAGCCCGGCCAGAGCCCCAAGCTGCT GATCTACAAGGTGTCCAACAGATTCAGCGGC GTGCCCGACAGATTCTCTGGCAGCGGCTCTG GCACCGACTTCACCCTGAAGATCAGCCGGGT GGAAGCCGAGGACCTGGGCGTGTACTACTGT TTTCAGGGCAGCCACGTGCCCTTCACCTTCGG CAGCGGCACCAAGCTGGAAATCAAGCGGGCT GATGCTGCACCGACTGTGTCCATCTTCCCACC ATCCAGTGAGCAGTTAACATCTGGAGGTGCC TCAGTCGTGTGCTTCTTGAACAACTTCTACCC CAAAGACATCAATGTCAAGTGGAAGATTGAT GGCAGTGAACGACAAAATGGCGTCCTGAACA GTTGGACTGATCAGGACAGCAAAGACAGCAC	933

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		CTACAGCATGAGCAGCACCCTCACGTTGACC AAGGACGAGTATGAACGACATAACAGCTATA CCTGTGAGGCCACTCACAAGACATCAACTTC ACCCATTGTCAAGAGCTTCAACAGGAATGAG TGT	
SM1B253	pDR000030243	GACGTCGTGATGACCCAGACCCCTCTGACCC TGAGCGTGACAATCGGCCAGGCCGCCAGCAT CAGCTGCAAGAGCAGCCAGAGCCTGCTGCAC AGCGACGGCAAGACCTACCTGAACTGGCTGC TGCAGAGGCCTGGCCAGAGCCCCAAGAGACT GATCTACCTGGTGTCCAAGCTGGACAGCGGC GTGCCCGATAGATTCACAGGCAGCGGCTCCG GCACCGACTTCACCCTGAAGATCAGCCGGGT GGAAGCCGAGGACCTGGGCGTGTACTACTGC TGGCAGGGCACCCACTTCCCTTACACCTTCG GCGGAGGCACAAAGCTGGAAATCAAGCGGG CTGATGCTGCACCGACTGTGTCCATCTTCCCA CCATCCAGTGAGCAGTTAACATCTGGAGGTG CCTCAGTCGTGTGCTTCTTGAACAACTTCTAC CCCAAAGACATCAATGTCAAGTGGAAGATTG ATGGCAGTGAACGACAAAATGGCGTCCTGAA CAGTTGGACTGATCAGGACAGCAAAGACAGC ACCTACAGCATGAGCAGCACCCTCACGTTGA CCAAGGACGAGTATGAACGACATAACAGCTA TACCTGTGAGGCCACTCACAAGACATCAACT TCACCCATTGTCAAGAGCTTCAACAGGAATG AGTGT	934
SM1B254	pDR000030244	GACGTCGTGATGACCCAGACCCCTCTGACCC TGAGCGTGACAGTGGGCCAGCCTGCCAGCAT CAGCTGCAAGAGCAGCCAGAGCCTGCTGCAC AGCGACGGCAAGACCTACCTGAACTGGCTGC TGCAGAGGCCTGGCCAGAGCCCCAAGAGACT GATCTACCTGGTGTCCAAGCTGGACAGCGGC GTGCCCGATAGATTCACAGGCAGCGGCTCCG GCACCGACTTCACCCTGAAGATCAGCCGGGT GGAAGCCGAGGACCTGGGCGTGTACTACTGT TGGCAGGGCACCCACTTCCCTTACACCTTCG GCGGAGGCACAAAGCTGGAAATCAAGCGGG CTGATGCTGCACCGACTGTGTCCATCTTCCCA CCATCCAGTGAGCAGTTAACATCTGGAGGTG CCTCAGTCGTGTGCTTCTTGAACAACTTCTAC CCCAAAGACATCAATGTCAAGTGGAAGATTG ATGGCAGTGAACGACAAAATGGCGTCCTGAA CAGTTGGACTGATCAGGACAGCAAAGACAGC ACCTACAGCATGAGCAGCACCCTCACGTTGA CCAAGGACGAGTATGAACGACATAACAGCTA TACCTGTGAGGCCACTCACAAGACATCAACT TCACCCATTGTCAAGAGCTTCAACAGGAATG	935

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		AGTGT	
SM1B255	pDR000030245	GACGTCGTGATGACCCAGACCCCTCTGACCC TGAGCGTGACAATCGGCCAGCCTGCCAGCAT CAGCTGCAAGAGCAGCCAGAGCCTGCTGGAC AGCGACGGCGAGACATACCTGAACTGGCTGC TGCAGAGGCCTGGCCAGAGCCCCAAGCGGCT GATCTACATGGTGTCCAAGCTGGACTCCGGC GTGCCCGACAGATTCACAGGCAGCGGCAGCG GAACCGACTTCACCCTGAAGATCAGCAGAGT GGAAGCCGAGGACCTGGGCGTGTACTACTGT TGGCAGGGCACCCACTTCCCTCAGACCTTCG GCGGAGGCACAAAGCTGGAACTGAAGCGGG CTGATGCTGCACCGACTGTGTCCATCTTCCCA CCATCCAGTGAGCAGTTAACATCTGGAGGTG CCTCAGTCGTGTGCTTCTTGAACAACTTCTAC CCCAAAGACATCAATGTCAAGTGGAAGATTG ATGGCAGTGAACGACAAAATGGCGTCCTGAA CAGTTGGACTGATCAGGACAGCAAAGACAGC ACCTACAGCATGAGCAGCACCCTCACGTTGA CCAAGGACGAGTATGAACGACATAACAGCTA TACCTGTGAGGCCACTCACAAGACATCAACT TCACCCATTGTCAAGAGCTTCAACAGGAATG AGTGT	936
SM1B256	pDR000030246	GACGTCGTGATGACCCAGACCCCTCTGACCC TGAGCGTGACCAATGGCCAGCCTGCCAGCAT CAGCTGCAAGAGCAGCCAGAGCCTGCTGGAC AGCGACGGCGAGACATACCTGAACTGGCTGC TGCAGAGGCCTGGCCAGAGCCCCAAGAGACT GATCTACCTGGTGTCCAAGCTGGACTCCGGC GTGCCCGACAGATTCATCGGCTCTGGCAGCG GCACCGACTTCACCCTGAAGATCAGCCGGGT GGAAGCCGAGGACCTGGGCGTGTACTTCTGT TGGCAGGGCACCCACAGCCCCTACACCTTTG GCGGCGGAACAAAGCTGGAAATCAAGCGGG CTGATGCTGCACCGACTGTGTCCATCTTCCCA CCATCCAGTGAGCAGTTAACATCTGGAGGTG CCTCAGTCGTGTGCTTCTTGAACAACTTCTAC CCCAAAGACATCAATGTCAAGTGGAAGATTG ATGGCAGTGAACGACAAAATGGCGTCCTGAA CAGTTGGACTGATCAGGACAGCAAAGACAGC ACCTACAGCATGAGCAGCACCCTCACGTTGA CCAAGGACGAGTATGAACGACATAACAGCTA TACCTGTGAGGCCACTCACAAGACATCAACT TCACCCATTGTCAAGAGCTTCAACAGGAATG AGTGT	937
SM1B257	pDR000030247	GACATCCAGATGACCCAGAGCCCTAGCAGCC TGTCTGCCAGCCTGGGCGGCAAAGTGACCAT CACATGCAAGGCCAGCCAGGACATCAACAA	938

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		GTATATCGCCTGGTATCAGCACAAGCCCGGC AAGGGCCCCAGACTGCTGATCCACTACACCA GCACCCTGCAGCCCGGCATCCCTAGCAGATT TTCTGGCAGCGGCTCCGGCAGAGACTACAGC TTCAGCATCAGCAACCTGGAACCCGAGGATA TCGCCACCTACTACTGCCTGCAGTACGACAA CCTGCGGACCTTCGGCGGAGGCACCAAGGTG GAAATCAAGCGGGCTGATGCTGCACCGACTG TGTCCATCTTCCCACCATCCAGTGAGCAGTTA ACATCTGGAGGTGCCTCAGTCGTGTGCTTCTT GAACAACTTCTACCCCAAAGACATCAATGTC AAGTGGAAGATTGATGGCAGTGAACGACAA AATGGCGTCCTGAACAGTTGGACTGATCAGG ACAGCAAAGACAGCACCTACAGCATGAGCA GCACCCTCACGTTGACCAAGGACGAGTATGA ACGACATAACAGCTATACCTGTGAGGCCACT CACAAGACATCAACTTCACCCATTGTCAAGA GCTTCAACAGGAATGAGTGT	
SM1B258	pDR000030248	GACGTGCTGATGACCCAGACACCCCTGAGCC TGCCTGTGTCTCTGGGCGATCAGGCCAGCAT CAGCTGCCGGTCTAGCCAGAGCATCGTGCAC AGCAACGGCAACACCTACCTGGAATGGTATC TGCAGAAGCCCGGCCAGAGCCCCAAGCTGCT GATCTACAAGGTGTCCAACAGATTCAGCGGC GTGCCCGACAGATTCTCTGGCAGCGGCTCTG GCACCGACTTCACCCTGAAGATCAGCCGGGT GGAAGCCGAGGACCTGGGCGTGTACTACTGT TTTCAGGGCAGCCACGTGCCCTTCACCTTCGG CAGCGGCACCAAGCTGGAAATCAAGCGGGCT GATGCTGCACCGACTGTGTCCATCTTCCCACC ATCCAGTGAGCAGTTAACATCTGGAGGTGCC TCAGTCGTGTGCTTCTTGAACAACTTCTACCC CAAAGACATCAATGTCAAGTGGAAGATTGAT GGCAGTGAACGACAAAATGGCGTCCTGAACA GTTGGACTGATCAGGACAGCAAAGACAGCAC CTACAGCATGAGCAGCACCCTCACGTTGACC AAGGACGAGTATGAACGACATAACAGCTATA CCTGTGAGGCCACTCACAAGACATCAACTTC ACCCATTGTCAAGAGCTTCAACAGGAATGAG TGT	939
SM1B259	pDR000030249	CAGATCGTGCTGACCCAGAGCCCTGCCATCA TGTCTGCCAGCCCTGGCGAGAAAGTGACCAT GACCTGTAGCGCCAGCAGCAGCGTGTCCTAC ATGTACTGGTATCAGCAGAAGCCCGGCAGCA GCCCCAGACTGCTGATCTACGACACCAGCAA CCTGGCCAGCGGCGTGCCAGTGCGGTTTTCT GGCAGCGGCAGCGGAACCAGCTACAGCCTG ACCATCAGCCGGATGGAAGCCGAGGACGCC	940

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		GCCACCTACTACTGCCAGCAGTGGTCCAGCT ACCCTCCCACCTTTGGCGGAGGCACCAAGCT GGAAATCAAGCGGGCTGATGCTGCACCGACT GTGTCCATCTTCCCACCATCCAGTGAGCAGTT AACATCTGGAGGTGCCTCAGTCGTGTGCTTCT TGAACAACTTCTACCCCAAAGACATCAATGT CAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAG GACAGCAAAGACAGCACCTACAGCATGAGC AGCACCCTCACGTTGACCAAGGACGAGTATG AACGACATAACAGCTATACCTGTGAGGCCAC TCACAAGACATCAACTTCACCCATTGTCAAG AGCTTCAACAGGAATGAGTGT	
SM1B260	pDR000030236	GACATCGTGCTGACACAGTCTCCAGCCAGCC TGGCCGTGTCTCTGGGACAGAGGGCCACCAT GAGCTGCAGAGCCAGCGAGTCTGTGGACGGC TACGGCAACAGCTTCCTGCACTGGTATCAGC AGAAGCCCGGCCAGCCTCCCAAGCTGCTGAT CTACAGGGCCAGCAACCTGGAAAGCGGCATC CCCGCCAGATTCAGCGGCACCGGCAGCAGAA CCGACTTCACCCTGACCATCACCCCTGTGGA AGCCGACGACGTGGCCACCTACTACTGCCAG CAGAGCAACGGCGACCCCTTCACCTTCGGCT CCGGCACCAAGCTGGAAATCAAGCGGGCTGA TGCTGCACCGACTGTGTCCATCTTCCCACCAT CCAGTGAGCAGTTAACATCTGGAGGTGCCTC AGTCGTGTGCTTCTTGAACAACTTCTACCCCA AAGACATCAATGTCAAGTGGAAGATTGATGG CAGTGAACGACAAAATGGCGTCCTGAACAGT TGGACTGATCAGGACAGCAAAGACAGCACCT ACAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATACC TGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTG T	941
SM1B261	pDR000030250	AACATCGTGATGACCCAGAGCCCCAAGAGCA TGAGCATGTCCGTGGGCGAGAGAGTGACCCT GAGCTGCAAGGCCAGCGAGAACGTGGGCAC CTACGTGTCCTGGTATCAGCAGAAGCCCGAG CAGAGCCCTAAGCTGCTGATCTACGGGGCCA GCAACAGATACACCGGCGTGCCCGAGAGATT CACAGGCAGCGGCAGCGCCACCGACTTCACC CTGACAATCAGCAGCGTGCAGGCCGAGGACC TGGCCGATTACCACTGTGGCCAGAGCTACAG CTACCCTCTGACCTTCGGAGCCGGCACCAAG CTGGAACTGAAGCGGGCTGATGCTGCACCGA CTGTGTCCATCTTCCCACCATCCAGTGAGCAG TTAACATCTGGAGGTGCCTCAGTCGTGTGCTT	942

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		CTTGAACAACTTCTACCCCAAAGACATCAAT GTCAAGTGGAAGATTGATGGCAGTGAACGAC AAAATGGCGTCCTGAACAGTTGGACTGATCA GGACAGCAAAGACAGCACCTACAGCATGAG CAGCACCCTCACGTTGACCAAGGACGAGTAT GAACGACATAACAGCTATACCTGTGAGGCCA CTCACAAGACATCAACTTCACCCATTGTCAA GAGCTTCAACAGGAATGAGTGT	
SM1B262	pDR000030251	GACATCAAGATGACCCAGAGCCCCAGCTCTA TGTACGCCAGCCTGGGCGAGCGCGTGACCAT CACCTGTAAAGCCAGCCAGGACATCAACAGC TACCTGAGCTGGTTCCAGCAGAAGCCCGGCA AGAGCCCCAAGACCCTGATCTACCGGGCCAA CAGACTGGTGGACGGCGTGCCAAGCAGATTC AGCGGCTCTGGCAGCGGCCAGGACTACAGCC TGACCATCAGCAGCCTGGAATACGAGGACAT GGGCATCTACTACTGCCTGCAGTACGACGAG TTCCCTCTGACCTTCGGAGCCGGCACCAAGC TGGAACTGAAGCGGGCTGATGCTGCACCGAC TGTGTCCATCTTCCCACCATCCAGTGAGCAGT TAACATCTGGAGGTGCCTCAGTCGTGTGCTTC TTGAACAACTTCTACCCCAAAGACATCAATG TCAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAG GACAGCAAAGACAGCACCTACAGCATGAGC AGCACCCTCACGTTGACCAAGGACGAGTATG AACGACATAACAGCTATACCTGTGAGGCCAC TCACAAGACATCAACTTCACCCATTGTCAAG AGCTTCAACAGGAATGAGTGT	943
SM1B263	pDR000030252	GACATCCAGATGACCCAGAGCCCTAGCAGCC TGTCTGCCAGCCTGGGCGGCAAAGTGACCAT CACATGCAAGGCCAGCCAGGACATCAACAA GTATATCGCCTGGTATCAGCACAAGCCCGGC AAGGGCCCCAGACTGCTGATCCACTACACCA GCACCCTGCAGCCCGGCATCCCTAGCAGATT TTCTGGCAGCGGCTCCGGCAGAGACTACAGC TTCAGCATCAGCAACCTGGAACCCGAGGATA TCGCCACCTACTACTGCCTGCAGTACGACAA CCTGTGGACCTTCGGCGGAGGCACCAAGGTG GAAATCAAGCGGGCTGATGCTGCACCGACTG TGTCCATCTTCCCACCATCCAGTGAGCAGTTA ACATCTGGAGGTGCCTCAGTCGTGTGCTTCTT GAACAACTTCTACCCCAAAGACATCAATGTC AAGTGGAAGATTGATGGCAGTGAACGACAA AATGGCGTCCTGAACAGTTGGACTGATCAGG ACAGCAAAGACAGCACCTACAGCATGAGCA GCACCCTCACGTTGACCAAGGACGAGTATGA ACGACATAACAGCTATACCTGTGAGGCCACT	944

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		CACAAGACATCAACTTCACCCATTGTCAAGA GCTTCAACAGGAATGAGTGT	
SM1B264	pDR000030253	GACATCCAGATGACCCAGAGCCCTGCCAGCC TGAGCGCCTCTGTGGGCGAGACAGTGACCAT CATCTGCCGGGCCAGCGAGAACATCTACAGC AACCTGGCCTGGTATCAGCAGAAGCAGGGCA AGAGCCCTCAGCTGCTGGTGTACGCCGCCAC CAATCTGGCCGACGGCATGCCTAGCAGATTC AGCGGCTCTGGCAGCGGCACCCAGTACAGCC TGAAGATCAACAGCCTGCAGAGCGAGGACTT CGGCAGCTACTACTGCCAGCACTTCTGGGGC ACCCCTTGGACCTTTGGCGGAGGCACCAAGC TGGAAATCAAGCGGGCTGATGCTGCACCGAC TGTGTCCATCTTCCCACCATCCAGTGAGCAGT TAACATCTGGAGGTGCCTCAGTCGTGTGCTTC TTGAACAACTTCTACCCCAAAGACATCAATG TCAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAG GACAGCAAAGACAGCACCTACAGCATGAGC AGCACCCTCACGTTGACCAAGGACGAGTATG AACGACATAACAGCTATACCTGTGAGGCCAC TCACAAGACATCAACTTCACCCATTGTCAAG AGCTTCAACAGGAATGAGTGT	945
SM1B265	pDR000030254	GACATCCAGATGACCCAGAGCCCTGCCAGCC TGAGCGCCTCTGTGGGCGAGACAGTGACCAT CATCTGCCGGGCCAGCGAGAACATCTACAGC TACCTGGCCTGGTATCAGCAGAAGCAGGGCA AGAGCCCTCAGCTGCTGTTCTACAACGCCAA GACCCTGGTGGAAGGCGTGCCCAGCAGATTT TCTGGCTCTGGCAGCGGCACCCAGTTCAGCC TGAAGATCAACAGCCTGCAGCCCGAGGACTT CGGCAGCTACTACTGCCAGCACCACTACGGC AGCCCCTACACCTTTGGCGGAGGCACCAAGC TGGAACTGAAGCGGGCTGATGCTGCACCGAC TGTGTCCATCTTCCCACCATCCAGTGAGCAGT TAACATCTGGAGGTGCCTCAGTCGTGTGCTTC TTGAACAACTTCTACCCCAAAGACATCAATG TCAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAG GACAGCAAAGACAGCACCTACAGCATGAGC AGCACCCTCACGTTGACCAAGGACGAGTATG AACGACATAACAGCTATACCTGTGAGGCCAC TCACAAGACATCAACTTCACCCATTGTCAAG AGCTTCAACAGGAATGAGTGT	946
SM1B266	pDR000030255	GACATCCAGATGACCCAGAGCCCTAGCACAC TGAGCGCCAGCCTGGGCGACACCATCACCAT CACATGCCACGCCAGCCAGAACATCAACGTG TGGCTGAGCTGGTATCAGCAGAAGCCCGGCA	947

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		ACATCCCCAAGCTGCTGATCTACAAGGCCAG CAACCTGCACACCGGCGTGCCCAGCAGATTT TCTGGCAGCGGCTCTGGCACCGGCTTCACCC TGACAATCAGCAGCCTGCAGCCCGAGGATAT CGCCACCTACTACTGCCAGCAGGGCCAGAGC TACCCTCTGACCTTTGGCGCTGGCACCAAGG TGGAAATCAAGCGGGCTGATGCTGCACCGAC TGTGTCCATCTTCCCACCATCCAGTGAGCAGT TAACATCTGGAGGTGCCTCAGTCGTGTGCTTC TTGAACAACTTCTACCCCAAAGACATCAATG TCAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAG GACAGCAAAGACAGCACCTACAGCATGAGC AGCACCCTCACGTTGACCAAGGACGAGTATG AACGACATAACAGCTATACCTGTGAGGCCAC TCACAAGACATCAACTTCACCCATTGTCAAG AGCTTCAACAGGAATGAGTGT	
SM1B267	pDR000030256	GACATCCAGATGACCCAGAGCCCTAGCACAC TGAGCGCCAGCCTGGGCGACACCATCACCAT CACATGCCACGCCAGCCAGAACATCAACGTG TGGCTGAGCTGGTATCAGCAGAAGCCCGGCA ACATCCCCAAGCTGCTGATCTACAAGGCCAG CAACCTGCACACCGGCGTGCCCAGCAGATTT TCTGGCAGCGGCTCTGGCACCGGCTTCACCC TGACAATCAGCAGCCTGCAGCCCGAGGATAT CGCCACCTACTACTGCCAGCAGGGCCAGAGC TACCCCTACACCTTTGGCGGAGGCACCAAGC TGGAAATCAAGCGGGCTGATGCTGCACCGAC TGTGTCCATCTTCCCACCATCCAGTGAGCAGT TAACATCTGGAGGTGCCTCAGTCGTGTGCTTC TTGAACAACTTCTACCCCAAAGACATCAATG TCAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAG GACAGCAAAGACAGCACCTACAGCATGAGC AGCACCCTCACGTTGACCAAGGACGAGTATG AACGACATAACAGCTATACCTGTGAGGCCAC TCACAAGACATCAACTTCACCCATTGTCAAG AGCTTCAACAGGAATGAGTGT	948
SM1B268	pDR000030257	GAGATCGTGCTGACCCAGAGCCCTACCACAA TGGCCGCCAGCCCTGGCGAGAAGATCACCAT CACATGCAGCGCCAGCAGCAGCATCAGCAGC AACTACCTGCACTGGTATCAGCAGAAGCCCG GCTTCAGCCCCAAGCTGCTGATCTACAGAAC CAGCAACCTGGCCAGCGGCGTGCCAGCCAGA TTTTCTGGCAGCGGCTCTGGCACCAGCTACA GCCTGACCATCGGCACCATGGAAGCCGAGGA CGTGGCCACCTACTACTGCCAGCAGGGCAGC TCCATCCCCAGAACCTTTGGCGGAGGCACCA	949

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		AGCTGGAAATCAAGCGGGCTGATGCTGCACC GACTGTGTCCATCTTCCCACCATCCAGTGAGC AGTTAACATCTGGAGGTGCCTCAGTCGTGTG CTTCTTGAACAACTTCTACCCCAAAGACATC AATGTCAAGTGGAAGATTGATGGCAGTGAAC GACAAAATGGCGTCCTGAACAGTTGGACTGA TCAGGACAGCAAAGACAGCACCTACAGCATG AGCAGCACCCTCACGTTGACCAAGGACGAGT ATGAACGACATAACAGCTATACCTGTGAGGC CACTCACAAGACATCAACTTCACCCATTGTC AAGAGCTTCAACAGGAATGAGTGT	
SM1B269	pDR000030258	GACATCGTGCTGACACAGTCTCCAGCCAGCC TGGCCGTGTCTCTGGGACAGAGAGCCACCAT CAGCTGCAAGGCCAGCCAGAGCGTGGACTAC GACGGCGACAGCTACATGAACTGGTATCAGC AGAAGCCCGGCCAGCCTCCCAAGCTGCTGAT CTACGCCGCCAGCAACCTGGAAAGCGGCATC CCTGCCAGATTCAGCGGCAGCGGCTCTGGCA CCGACTTCACCCTGAACATCCACCCCGTGGA AGAAGAGGACGCCGCCACCTACTACTGCCAG CAGAGCAACGAGGACCCCTACACCTTCGGCG GAGGCACCAAGCTGGAAATCAAGCGGGCTG ATGCTGCACCGACTGTGTCCATCTTCCCACCA TCCAGTGAGCAGTTAACATCTGGAGGTGCCT CAGTCGTGTGCTTCTTGAACAACTTCTACCCC AAAGACATCAATGTCAAGTGGAAGATTGATG GCAGTGAACGACAAAATGGCGTCCTGAACAG TTGGACTGATCAGGACAGCAAAGACAGCACC TACAGCATGAGCAGCACCCTCACGTTGACCA AGGACGAGTATGAACGACATAACAGCTATAC CTGTGAGGCCACTCACAAGACATCAACTTCA CCCATTGTCAAGAGCTTCAACAGGAATGAGT GT	950
SM1B270	pDR000030259	GACATCGTGCTGACACAGTCTCCAGCCAGCC TGGCCGTGTCTCTGGGACAGAGAGCCAGCAT CAGCTGCAAGGCCAGCCAGAGCGTGGACTAC GACGGCGACAGCTACATGAACTGGTATCAGC AGAAGCCCGGCCAGCCTCCCAAGCTGCTGAT CTACGCCGCCAGCAACCTGGAAAGCGGCATC CCTGCCAGATTCAGCGGCAGCGGCTCTGGCA CCGACTTCACCCTGAACATCCACCCCGTGGA AGAAGAGGACGCCGCCACCTACTACTGCCAG CAGAGCTACGAGGACCCCTTCACCTTCGGCT CCGGCACCAAGCTGGAAATCAAGCGGGCTGA TGCTGCACCGACTGTGTCCATCTTCCCACCAT CCAGTGAGCAGTTAACATCTGGAGGTGCCTC AGTCGTGTGCTTCTTGAACAACTTCTACCCCA AAGACATCAATGTCAAGTGGAAGATTGATGG	951

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		CAGTGAACGACAAAATGGCGTCCTGAACAGT TGGACTGATCAGGACAGCAAAGACAGCACCT ACAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATACC TGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTG T	
SM1B271	pDR000030249	CAGATCGTGCTGACCCAGAGCCCTGCCATCA TGTCTGCCAGCCCTGGCGAGAAAGTGACCAT GACCTGTAGCGCCAGCAGCAGCGTGTCCTAC ATGTACTGGTATCAGCAGAAGCCCGGCAGCA GCCCCAGACTGCTGATCTACGACACCAGCAA CCTGGCCAGCGGCGTGCCAGTGCGGTTTTCT GGCAGCGGCAGCGGAACCAGCTACAGCCTG ACCATCAGCCGGATGGAAGCCGAGGACGCC GCCACCTACTACTGCCAGCAGTGGTCCAGCT ACCCTCCCACCTTTGGCGGAGGCACCAAGCT GGAAATCAAGCGGGCTGATGCTGCACCGACT GTGTCCATCTTCCCACCATCCAGTGAGCAGTT AACATCTGGAGGTGCCTCAGTCGTGTGCTTCT TGAACAACTTCTACCCCAAAGACATCAATGT CAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAG GACAGCAAAGACAGCACCTACAGCATGAGC AGCACCCTCACGTTGACCAAGGACGAGTATG AACGACATAACAGCTATACCTGTGAGGCCAC TCACAAGACATCAACTTCACCCATTGTCAAG AGCTTCAACAGGAATGAGTGT	952
SM1B272	pDR000030260	GACATCGTGATGACCCAGAGCCAGAAATTCA TGAGCACCAGCGTGGGCGACCGGGTGTCCGT GACATGCAAGGCCAGCCAGAACGTGGGCAC CAACGTGGCCTGGTATCAGCAGAAGCCCGGC CAGAGCCCCAAGGCCCTGATCTACAGCGCCA GCTACAGATACAGCGGCGTGCCCGACAGATT CACAGGCAGCGGCTCTGGCACCGACTTCACC CTGACCATCAGCAACGTGCAGAGCGAGGACC TGGCCGAGTACTTCTGCCAGCAGTACAACAG CTACCCCTTCACCTTCGGCAGCGGCACCAAG CTGGAAATCAAGCGGGCTGATGCTGCACCGA CTGTGTCCATCTTCCCACCATCCAGTGAGCAG TTAACATCTGGAGGTGCCTCAGTCGTGTGCTT CTTGAACAACTTCTACCCCAAAGACATCAAT GTCAAGTGGAAGATTGATGGCAGTGAACGAC AAAATGGCGTCCTGAACAGTTGGACTGATCA GGACAGCAAAGACAGCACCTACAGCATGAG CAGCACCCTCACGTTGACCAAGGACGAGTAT GAACGACATAACAGCTATACCTGTGAGGCCA CTCACAAGACATCAACTTCACCCATTGTCAA	953

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		GAGCTTCAACAGGAATGAGTGT	
SM1B273	pDR000030261	GACATCGTGATGAGCCAGAGCCCTAGCAGCC TGGCCGTGTCCGTGGGCGAGAAAGTGACCAT GAGCTGCAAGAGCAGCCAGTCCCTGCTGTAC TCCAGCAACCAGAAGAACTACCTGGCCTGGT ATCAGCAGAAGCCCGGCCAGTCCCCTAAGCT GCTGATCTACTGGGCCAGCACCAGAGAAAGC GGCGTGCCCGATAGATTCACAGGCAGCGGCT CCGGCACCGACTTCACCCTGACAATCAGCAG CGTGAAGGCCGAGGACCTGGCTGTGTACTAC TGCCAGCAGTACTACAGCTACCCCTACACCT TCGGCGGAGGCACCAAGCTGGAAATCAAGC GGGCTGATGCTGCACCGACTGTGTCCATCTTC CCACCATCCAGTGAGCAGTTAACATCTGGAG GTGCCTCAGTCGTGTGCTTCTTGAACAACTTC TACCCCAAAGACATCAATGTCAAGTGGAAGA TTGATGGCAGTGAACGACAAAATGGCGTCCT GAACAGTTGGACTGATCAGGACAGCAAAGA CAGCACCTACAGCATGAGCAGCACCCTCACG TTGACCAAGGACGAGTATGAACGACATAACA GCTATACCTGTGAGGCCACTCACAAGACATC AACTTCACCCATTGTCAAGAGCTTCAACAGG AATGAGTGT	954
SM1B274	pDR000030262	GACGTCGTGATGACCCAGACACCCCTGAGCC TGCCTGTGTCTCTGGGCGATCAGGCCAGCAT CAGCTGCAGATCCAGCCAGAGCCTGGTGCAC AGCAACGGCAACACCTACCTGCACTGGTATC TGCAGAAGCCCGGCCAGAGCCCCAAGCTGCT GATCTACAAGGTGTCCAACAGATTCAGCGGC GTGCCCGACAGATTCTCTGGCAGCGGCTCTG GCACCGACTTCACCCTGAAGATCAGCCGGGT GGAAGCCGAGGACCTGGGCGTGTACTTCTGC AGCCAGTCCACCCACGTGCCACCCTACACCT TTGGCGGAGGCACCAAGCTGGAACTGAAGCG GGCTGATGCTGCACCGACTGTGTCCATCTTCC CACCATCCAGTGAGCAGTTAACATCTGGAGG TGCCTCAGTCGTGTGCTTCTTGAACAACTTCT ACCCCAAAGACATCAATGTCAAGTGGAAGAT TGATGGCAGTGAACGACAAAATGGCGTCCTG AACAGTTGGACTGATCAGGACAGCAAAGAC AGCACCTACAGCATGAGCAGCACCCTCACGT TGACCAAGGACGAGTATGAACGACATAACA GCTATACCTGTGAGGCCACTCACAAGACATC AACTTCACCCATTGTCAAGAGCTTCAACAGG AATGAGTGT	955
SM1B275	pDR000030263	GACGTCGTGATGACCCAGACCCCTCTGACCC TGAGCGTGACAATCGGCCAGCCTGCCAGCAT CAGCTGCAAGAGCAGCCAGAGCCTGCTGTAC	956

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		TCCAACGGCAAGACCTACCTGAACTGGCTGC TGCAGAGGCCTGGCCAGAGCCCCAAGAGACT GATCTACCTGGTGTCCAAGCTGGACAGCGGC GTGCCCGATAGATTCACAGGCAGCGGCTCCG GCACCGACTTCACCCTGAAGATCAGCCGGGT GGAAGCCGAGGACCTGGGCGTGTTCTACTGT GTGCAGGGCACCCACTTCCCTCAGACCTTCG GCGGAGGCACAAAGCTGGAACTGAAGCGGG CTGATGCTGCACCGACTGTGTCCATCTTCCCA CCATCCAGTGAGCAGTTAACATCTGGAGGTG CCTCAGTCGTGTGCTTCTTGAACAACTTCTAC CCCAAAGACATCAATGTCAAGTGGAAGATTG ATGGCAGTGAACGACAAAATGGCGTCCTGAA CAGTTGGACTGATCAGGACAGCAAAGACAGC ACCTACAGCATGAGCAGCACCCTCACGTTGA CCAAGGACGAGTATGAACGACATAACAGCTA TACCTGTGAGGCCACTCACAAGACATCAACT TCACCCATTGTCAAGAGCTTCAACAGGAATG AGTGT	

Table 29. LukAB Antibody Light Chain Primary Transcripts

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
SM1B105	pDR000023603	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA TATTGTGCTAACTCAGTCTCCAGCAATAATG GCTGCCTCTCTGGGGCAGAAGGTCACCATG ACCTGCAGTGCCAGCTCAAGTGTAAGTTCC AGTTACTTGCACTGGTACCAGCAGAAGTCA GGCGCTTCCCCCAAACCCTTGATTCATAGGA CATCCAACCTGGCTTCTGGAGTCCCAGCTCG CTTCAGTGGCAGTGGGTCTGGGACCTCTTAC TCTCTCACAATCAGCAGCGTGGAGGCTGAA GATGATGCAACTTATTACTGCCAGCAGTGG AGTGGTTACCCATTCACGTTCGGTGCTGGGA CCAAGCTGGAGCTGAAACGGGCTGATGCTG CACCAACTGTATCCATCTTCCCACCATCCAG TGAGCAGTTAACATCTGGAGGTGCCTCAGT CGTGTGCTTCTTGAACAACTTCTACCCCAAA GACATCAATGTCAAGTGGAAGATTGATGGC AGTGAACGACAAAATGGCGTCCTGAACAGT TGGACTGATCAGGACAGCAAAGACAGCACC TACAGCATGAGCAGCACCCTCACGTTGACC AAGGACGAGTATGAACGACATAACAGCTAT ACCTGTGAGGCCACTCACAAGACATCAACT	957

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		TCACCCATTGTCAAGAGCTTCAACAGGAAT GAGTGTTAG	
SM1B106	pDR000023628	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CATTGTGATGACCCAGTCTCCAGCTTCTTTG GCTGTGTCTCTAGGGCAGAGGGCCACCATC TCCTGCAGAGCCAGCGAAAGTGTTGATAAT TCTGGCATTAGTTTTATGAACTGGTTCCAAC AGAAACCAGGACAGCCACCCAAACTCCTCA TCTATGCTGCATCCAACCAAGGATCCGGGG TCCCTGCCAGGTTTAGTGGCAGTGGGTCTGG GACAGACTTCAGCCTCAACATCCATCCTATG GAGGAGGATGATACTGCAATGTATTTCTGTC AGCAAAGTAAGGAGGTTCCGTACACGTTCG GAGGGGGGACCAAGCTGGAAATAAAACGG GCTGATGCTGCACCAACTGTATCCATCTTCC CACCATCCAGTGAGCAGTTAACATCTGGAG GTGCCTCAGTCGTGTGCTTCTTGAACAACTT CTACCCCAAAGACATCAATGTCAAGTGGAA GATTGATGGCAGTGAACGACAAAATGGCGT CCTGAACAGTTGGACTGATCAGGACAGCAA AGACAGCACCTACAGCATGAGCAGCACCCT CACGTTGACCAAGGACGAGTATGAACGACA TAACAGCTATACCTGTGAGGCCACTCACAA GACATCAACTTCACCCATTGTCAAGAGCTTC AACAGGAATGAGTGTTAG	958
SM1B107	pDR000023626	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA TATTGTGCTAACTCAGTCTCCAGCTTCTTTG GCTGTGTCTCTAGGGCAGAGGGCCACCATC TCCTGCAGAGCCAGCGAAAGTGTTGATAAT TCTGGCATTAGTTTTATGAACTGGTTCCAAC AGAAACCAGGACAGCCACCCAAACTCCTCA TCTATGCTGCATCCAACCAAGGATCCGGGG TCCCTGCCAGGTTTAGTGGCAGTGGGTCTGG GACAGACTTCAGCCTCAACATCCATCCTATG GAGGAGGATGATACTGCAATGTATTTCTGTC AGCAAAGTAAGGAGGTTCCGTACACGTTCG GAGGGGGGACCAAGCTGGAAATAAAACGG GCTGATGCTGCACCAACTGTATCCATCTTCC CACCATCCAGTGAGCAGTTAACATCTGGAG GTGCCTCAGTCGTGTGCTTCTTGAACAACTT CTACCCCAAAGACATCAATGTCAAGTGGAA GATTGATGGCAGTGAACGACAAAATGGCGT CCTGAACAGTTGGACTGATCAGGACAGCAA AGACAGCACCTACAGCATGAGCAGCACCCT CACGTTGACCAAGGACGAGTATGAACGACA TAACAGCTATACCTGTGAGGCCACTCACAA	959

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		GACATCAACTTCACCCATTGTCAAGAGCTTC AACAGGAATGAGTGTTAG	
SM1B108	pDR000023627	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA TGTTGTGATGACCCAAACTCCCAAATTCCTG CTTGTATCAGCAGGAGACAGGGTTACCATT ACCTGCAAGGCCAGTCAGAGTGTGAGTGAT GATGTAACTTGGTACCAACAGAAGTCAGGA CAGTCTCCTAAACTGCTGATATACTATGCAT CCAATCGCTACACTGGAGTCCCTGATCGCTT CACTGGCAGTGGATATGGGACGGATTTCAC TTTCACCATCAGCACTGTGCAGGCTGAAGA CCTGGCAGTTTATTTCTGTCAGCAGGATTAT AGCTCTCCGTGGACGTTCGGTGGAGGCACC AAGCTGGAAATCAAACGGGCTGATGCTGCA CCAACTGTATCCATCTTCTCACCATCCAGTG AGCAGTTAACATCTGGAGGTGCCTCAGTCG TGTGCTTCTTGAACAACTTCTACCCCAAAGA CATCAATGTCAAGTGGAAGATTGATGGCAG TGAACGACAAAATGGCGTCCTGAACAGTTG GACTGATCAGGACAGCAAAGACAGCACCTA CAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATAC CTGTGAGGCCACTCACAAGACATCAACTTC ACCCATTGTCAAGAGCTTCAACAGGAATGA GTGTTAG	960
SM1B109	pDR000023628	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CATTGTGATGACCCAGTCTCCAGCTTCTTTG GCTGTGTCTCTAGGGCAGAGGGCCACCATC TCCTGCAGAGCCAGCGAAAGTGTTGATAAT TCTGGCATTAGTTTTATGAACTGGTTCCAAC AGAAACCAGGACAGCCACCCAAACTCCTCA TCTATGCTGCATCCAACCAAGGATCCGGGG TCCCTGCCAGGTTTAGTGGCAGTGGGTCTGG GACAGACTTCAGCCTCAACATCCATCCTATG GAGGAGGATGATACTGCAATGTATTTCTGTC AGCAAAGTAAGGAGGTTCCGTACACGTTCG GAGGGGGGACCAAGCTGGAAATAAAACGG GCTGATGCTGCACCAACTGTATCCATCTTCC CACCATCCAGTGAGCAGTTAACATCTGGAG GTGCCTCAGTCGTGTGCTTCTTGAACAACTT CTACCCCAAAGACATCAATGTCAAGTGGAA GATTGATGGCAGTGAACGACAAAATGGCGT CCTGAACAGTTGGACTGATCAGGACAGCAA AGACAGCACCTACAGCATGAGCAGCACCCT CACGTTGACCAAGGACGAGTATGAACGACA TAACAGCTATACCTGTGAGGCCACTCACAA	961

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		GACATCAACTTCACCCATTGTCAAGAGCTTC AACAGGAATGAGTGTTAG	
SM1B110	pDR000023629	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA TATTGTGCTAACTCAGTCTCCAGCAATCATG TCTGCATCTCCAGGGGAGAAGGTCACCATA ACCTGCAGTGCCAGCTCAAGTGTAAGTTAC ATGCACTGGTTCCAGCAGAAGCCAGGCACT TCTCCCAAACTCTGGATTTATAGCACATCCA ACCTGGCTTCTGGAGTCCCTGCTCGCTTCAG TGGCAGTGGATCTGGGACCTCTTACTCTCTC ACAATCAGCCGAATGGAGGCTGAAGATGCT GCCACTTATTACTGCCAGCAAAGGAGTAGT TACCCATTCACGTTCGGCTCGGGGACAAAG TTGGAAATAAAACGGGCTGATGCTGCACCA ACTGTATCCATCTTCCCACCATCCAGTGAGC AGTTAACATCTGGAGGTGCCTCAGTCGTGTG CTTCTTGAACAACTTCTACCCCAAAGACATC AATGTCAAGTGGAAGATTGATGGCAGTGAA CGACAAAATGGCGTCCTGAACAGTTGGACT GATCAGGACAGCAAAGACAGCACCTACAGC ATGAGCAGCACCCTCACGTTGACCAAGGAC GAGTATGAACGACATAACAGCTATACCTGT GAGGCCACTCACAAGACATCAACTTCACCC ATTGTCAAGAGCTTCAACAGGAATGAGTGT TAG	962
SM1B111	pDR000023631	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CATTGTGATGACCCAGTCTCCAACCACCATG GCTGCATCTCCCGGGGAGAGGATCACTATC ACCTGCAGTGCCCACTCAAATTTAATTTCCA ATTACTTACATTGGTATCAGCAGAAGCCAG GATTCTCCCCTAAACTCTTGATTTATAGGAC ATCCAATCTGGCTTCTGGAGTCCCAGCTCGC TTCAGTGGCAGTGGGTCTGGGACCTCTTACT CTCTCACAATTGGCACCATGGAGGCTGAAG ATGTTGCCACTTACTTCTGCCAACAGGGTAG TAGTATACCATTCACGTTCGGCTCGGGGACA AAGTTGGAAATAAAACGGGCTGATGCTGCA CCAACTGTATCCATCTTCCCACCATCCAGTG AGCAGTTAACATCTGGAGGTGCCTCAGTCG TGTGCTTCTTGAACAACTTCTACCCCAAAGA CATCAATGTCAAGTGGAAGATTGATGGCAG TGAACGACAAAATGGCGTCCTGAACAGTTG GACTGATCAGGACAGCAAAGACAGCACCTA CAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATAC CTGTGAGGCCACTCACAAGACATCAACTTC	963

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		ACCCATTGTCAAGAGCTTCAACAGGAATGA GTGTTAG	
SM1B112	pDR000023630	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCCA AATTGTTCTCACCCAGTCTCCAACAATCATG TCTGCATCTCCAGGGGAAAAGGTCACCATG ACCTGCAGTGCCAGCTCACATGTAAGTTAC ATATACTGGTACCAGCAGAAGCCAGGCTCC TCCCCCAGACTCTGGATTTATGACACATCCA ACCTGGTTTCTGGAGTCCCTGCTCGCTTCAG TGGCAGTAGGTCTGGGACCTCTTATTCTCTC ACAATCAGCAGCATGGAGGCTGAAGATGCT GCCACTTATTACTGCCAGCAGTACAGTGGTT ACCCGTACACGTTCGGAGGGGGGACCAAGC TGGAAATAAAACGGGCTGATGCTGCACCAA CTGTATCCATCTTCCCACCATCCAGTGAGCA GTTAACATCTGGAGGTGCCTCAGTCGTGTGC TTCTTGAACAACTTCTACCCCAAAGACATCA ATGTCAAGTGGAAGATTGATGGCAGTGAAC GACAAAATGGCGTCCTGAACAGTTGGACTG ATCAGGACAGCAAAGACAGCACCTACAGCA TGAGCAGCACCCTCACGTTGACCAAGGACG AGTATGAACGACATAACAGCTATACCTGTG AGGCCACTCACAAGACATCAACTTCACCCA TTGTCAAGAGCTTCAACAGGAATGAGTGTT AG	964
SM1B243	pDR000030110	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CATCAAGATGACCCAGAGCCCCAGCTCTAT GTACGCCAGCCTGGGCGAGCGCGTGACCAT CACCTGTAAAGCCAGCCAGGACATCAACAG CTACCTGAGCTGGTTCCAGCAGAAGCCCGG CAAGAGCCCCAAGACCCTGATCTACCGGGC CAACAGACTGGTGGACGGCGTGCCAAGCAG ATTCAGCGGCTCTGGCAGCGGCCAGGACTA CAGCCCTACCATCAGCAGCCTGGAATACGA GGACATGGGCATCTACTACTGCCTGCAGTA CGACGAGTTCCCCTACACCTTCGGCGGAGG CACCAAGCTGGAAATCAAGCGGGCTGATGC TGCACCGACTGTGTCCATCTTCCCACCATCC AGTGAGCAGTTAACATCTGGAGGTGCCTCA GTCGTGTGCTTCTTGAACAACTTCTACCCCA AAGACATCAATGTCAAGTGGAAGATTGATG GCAGTGAACGACAAAATGGCGTCCTGAACA GTTGGACTGATCAGGACAGCAAAGACAGCA CCTACAGCATGAGCAGCACCCTCACGTTGA CCAAGGACGAGTATGAACGACATAACAGCT ATACCTGTGAGGCCACTCACAAGACATCAA	965

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		CTTCACCCATTGTCAAGAGCTTCAACAGGA ATGAGTGTTAG	
SM1B244	pDR000030235	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CATCGTGATGACCCAGAGCCAGAAATTCAT GAGCACCAGCGTGGGCGACCGGGTGTCCGT GACATGCAAGGCCAGCCAGAACGTGGGCAC CAACGTGGCCTGGTATCAGCAGAAGCCCGG CCAGAGCCCCAAGACCCTGATCTACAGCGC CAGCTACAGATACAGCGGCGTGCCCGATAG CTTCACAGGCAGCGGCTCTGGCACCGACTTC ACCCTGACCATCAGCAACGTGCAGAGCGAG GACTGGGCCGAGTACTTCTGCCAGCAGTAC AACAGCTACCCCTTCACCTTCGGCAGCGGC ACCAAGCTGGAAATCAAGCGGGCTGATGCT GCACCGACTGTGTCCATCTTCCCACCATCCA GTGAGCAGTTAACATCTGGAGGTGCCTCAG TCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGG CAGTGAACGACAAAATGGCGTCCTGAACAG TTGGACTGATCAGGACAGCAAAGACAGCAC CTACAGCATGAGCAGCACCCTCACGTTGAC CAAGGACGAGTATGAACGACATAACAGCTA TACCTGTGAGGCCACTCACAAGACATCAAC TTCACCCATTGTCAAGAGCTTCAACAGGAAT GAGTGTTAG	966
SM1B245	pDR000030236	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CATCGTGCTGACACAGTCTCCAGCCAGCCTG GCCGTGTCTCTGGGACAGAGGGCCACCATG AGCTGCAGAGCCAGCGAGTCTGTGGACGGC TACGGCAACAGCTTCCTGCACTGGTATCAGC AGAAGCCCGGCCAGCCTCCCAAGCTGCTGA TCTACAGGGCCAGCAACCTGGAAAGCGGCA TCCCCGCCAGATTCAGCGGCACCGGCAGCA GAACCGACTTCACCCTGACCATCACCCCTGT GGAAGCCGACGACGTGGCCACCTACTACTG CCAGCAGAGCAACGGCGACCCCTTCACCTT CGGCTCCGGCACCAAGCTGGAAATCAAGCG GGCTGATGCTGCACCGACTGTGTCCATCTTC CCACCATCCAGTGAGCAGTTAACATCTGGA GGTGCCTCAGTCGTGTGCTTCTTGAACAACT TCTACCCCAAAGACATCAATGTCAAGTGGA AGATTGATGGCAGTGAACGACAAAATGGCG TCCTGAACAGTTGGACTGATCAGGACAGCA AAGACAGCACCTACAGCATGAGCAGCACCC TCACGTTGACCAAGGACGAGTATGAACGAC ATAACAGCTATACCTGTGAGGCCACTCACA	967

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		AGACATCAACTTCACCCATTGTCAAGAGCTT CAACAGGAATGAGTGTTAG	
SM1B246	pDR000030237	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CGTGCTGATGACCCAGACACCCCTGAGCCT GCCTGTGTCTCTGGGCGATCAGGCCAGCATC AGCTGCCGGTCTAGCCAGAGCATCGTGCAC AGCAACGGCAAGACCTACCTGGAATGGTAT CTGCAGAAGCCCGGCCAGAGCCCCAAGCTG CTGATCTACAAGGTGTCCAACAGATTCAGC GGCGTGCCCGACAGATTCTCTGGCAGCGGC TCTGGCACCGACTTCACCCTGAAGATCAGCC GGGTGGAAGCCGAGGACCTGGGCGTGTACT ACTGTCTGCAGGGCAGCCACGTGCCCTGGA CCTTTGGCGGCGGAACAAAGCTGGAACTGA AGCGGGCTGATGCTGCACCGACTGTGTCCA TCTTCCCACCATCCAGTGAGCAGTTAACATC TGGAGGTGCCTCAGTCGTGTGCTTCTTGAAC AACTTCTACCCCAAAGACATCAATGTCAAG TGGAAGATTGATGGCAGTGAACGACAAAAT GGCGTCCTGAACAGTTGGACTGATCAGGAC AGCAAAGACAGCACCTACAGCATGAGCAGC ACCCTCACGTTGACCAAGGACGAGTATGAA CGACATAACAGCTATACCTGTGAGGCCACT CACAAGACATCAACTTCACCCATTGTCAAG AGCTTCAACAGGAATGAGTGTTAG	968
SM1B247	pDR000030238	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CATCGTGCTGACACAGTCTCCAGCCAGCCTG GCCGTGTCTCTGGGACAGAGAGCCACCATC AGCTGCCGGGCCAGCAAGAGCGTGTCCATC AGCGGCTACAGCTACATGCACTGGTATCAG CAGAAGCCCGGCCAGCCTCCCAAGCTGCTG ATCGACCTGGCCAGCAACCTGGAAAGCGGC GTGCCAGCCAGATTTTCTGGCAGCGGCTCCG GCACCGACTTCACCCTGAACATCCACCCCGT GGAAGAAGAGGACGCCGCCACCTACTACTG CCAGCACAGCAGAGAGCTGCCCTTCACCTT CGGCAGCGGCACCAAGCTGGAAATCAAGCG GGCTGATGCTGCACCGACTGTGTCCATCTTC CCACCATCCAGTGAGCAGTTAACATCTGGA GGTGCCTCAGTCGTGTGCTTCTTGAACAACT TCTACCCCAAAGACATCAATGTCAAGTGGA AGATTGATGGCAGTGAACGACAAAATGGCG TCCTGAACAGTTGGACTGATCAGGACAGCA AAGACAGCACCTACAGCATGAGCAGCACCC TCACGTTGACCAAGGACGAGTATGAACGAC ATAACAGCTATACCTGTGAGGCCACTCACA	969

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		AGACATCAACTTCACCCATTGTCAAGAGCTT CAACAGGAATGAGTGTTAG	
SM1B248	pDR000030236	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CATCGTGCTGACACAGTCTCCAGCCAGCCTG GCCGTGTCTCTGGGACAGAGGGCCACCATG AGCTGCAGAGCCAGCGAGTCTGTGGACGGC TACGGCAACAGCTTCCTGCACTGGTATCAGC AGAAGCCCGGCCAGCCTCCCAAGCTGCTGA TCTACAGGGCCAGCAACCTGGAAAGCGGCA TCCCCGCCAGATTCAGCGGCACCGGCAGCA GAACCGACTTCACCCTGACCATCACCCCTGT GGAAGCCGACGACGTGGCCACCTACTACTG CCAGCAGAGCAACGGCGACCCCTTCACCTT CGGCTCCGGCACCAAGCTGGAAATCAAGCG GGCTGATGCTGCACCGACTGTGTCCATCTTC CCACCATCCAGTGAGCAGTTAACATCTGGA GGTGCCTCAGTCGTGTGCTTCTTGAACAACT TCTACCCCAAAGACATCAATGTCAAGTGGA AGATTGATGGCAGTGAACGACAAAATGGCG TCCTGAACAGTTGGACTGATCAGGACAGCA AAGACAGCACCTACAGCATGAGCAGCACCC TCACGTTGACCAAGGACGAGTATGAACGAC ATAACAGCTATACCTGTGAGGCCACTCACA AGACATCAACTTCACCCATTGTCAAGAGCTT CAACAGGAATGAGTGTTAG	970
SM1B249	pDR000030239	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCCA GATCGTGCTGACCCAGAGCCCTGCCATCAT GTCTGCCAGCCCTGGCGAGAAAGTGACCAT GACCTGTAGCGCCAGCAGCAGCGTGTCCTA CATGCACTGGTATCAGCAGAAGTCCGGCAC CAGCCCCAAGCGGTGGATCTACGATACCAG CAAGCTGGCCTCCGGCGTGCCAGCCAGATT TTCTGGCTCTGGCAGCGGCACCTCCTACAGC CTGACCATCAGCAGCATGGAAGCCGAGGAC GCCGCCACCTACTACTGCCAGCAGTGGATC AGCAACCCTCCCACCTTCGGCGGAGGCACC AAGCTGGAAATCAAGCGGGCTGATGCTGCA CCGACTGTGTCCATCTTCCCACCATCCAGTG AGCAGTTAACATCTGGAGGTGCCTCAGTCG TGTGCTTCTTGAACAACTTCTACCCCAAAGA CATCAATGTCAAGTGGAAGATTGATGGCAG TGAACGACAAAATGGCGTCCTGAACAGTTG GACTGATCAGGACAGCAAAGACAGCACCTA CAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATAC CTGTGAGGCCACTCACAAGACATCAACTTC	971

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		ACCCATTGTCAAGAGCTTCAACAGGAATGA GTGTTAG	
SM1B250	pDR000030240	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CATCGTGCTGACACAGTCTCCAGCCAGCCTG GCCGTGTCCCTGGAACAGAGAGCCACCATC AGCTGCAAGGCCAGCCAGAGCGTGGACTAC GACGGCGACAGCTACATGAACTGGTATCAG CAGAAGCCCGGCCAGCCTCCCAAGCTGCTG ATCTACGCCGCCAGCAACCTGGAAAGCGGC ATCCCTGCCAGATTCAGCGGCAGCGGCTCT GGCACCGACTTCACCCTGAACATCCACCCC GTGGAAGAAGAGGACGCCGCCACCTACTAC TGCCAGCAGAGCAACGAGGACCCTCTGACC TTCGGAGCCGGCACCAAGCTGGAACTGAAG CGGGCTGATGCTGCACCGACTGTGTCCATCT TCCCACCATCCAGTGAGCAGTTAACATCTGG AGGTGCCTCAGTCGTGTGCTTCTTGAACAAC TTCTACCCCAAAGACATCAATGTCAAGTGG AAGATTGATGGCAGTGAACGACAAAATGGC GTCCTGAACAGTTGGACTGATCAGGACAGC AAAGACAGCACCTACAGCATGAGCAGCACC CTCACGTTGACCAAGGACGAGTATGAACGA CATAACAGCTATACCTGTGAGGCCACTCAC AAGACATCAACTTCACCCATTGTCAAGAGC TTCAACAGGAATGAGTGTTAG	972
SM1B251	pDR000030241	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CATCCAGATGACCCAGAGCCCTGCCAGCCT GAGCGCCTCTGTGGGCGAGACAGTGACCAC CATCTGCCGGGCCAGCGAGAACATCTACAG CTACCTGGCCTGGTATCAGCAGAAGCAGGG CAAGAGCCCTCAGCTGCTGGTGTACAACGC CAAGACCCTGGTGGAAGGCGTGCCCAGCAG ATTTTCTGGCTCTGGCAGCGGCACCCAGTTC AGCCTGAAGATCAACAGCCTGCAGCCCGAG GACTTCGGCAGCTACTACTGCCAGCACCACT ACGGCAGCCCCTACACCTTTGGCGGAGGCA CCAAGCTGGAACTGAAGCGGGCTGATGCTG CACCGACTGTGTCCATCTTCCCACCATCCAG TGAGCAGTTAACATCTGGAGGTGCCTCAGT CGTGTGCTTCTTGAACAACTTCTACCCCAAA GACATCAATGTCAAGTGGAAGATTGATGGC AGTGAACGACAAAATGGCGTCCTGAACAGT TGGACTGATCAGGACAGCAAAGACAGCACC TACAGCATGAGCAGCACCCTCACGTTGACC AAGGACGAGTATGAACGACATAACAGCTAT ACCTGTGAGGCCACTCACAAGACATCAACT	973

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		TCACCCATTGTCAAGAGCTTCAACAGGAAT GAGTGTTAG	
SM1B252	pDR000030242	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CGTGCTGATGACCCAGACACCCCTGAGCCT GCCTGTGTCTCTGGGCGATCAGGCCAGCATC AGCTGCCGGTCTAGCCAGAGCATCGTGTAC AGCAACGGCAACACCTACCTGGAATGGTAT CTGCAGAAGCCCGGCCAGAGCCCCAAGCTG CTGATCTACAAGGTGTCCAACAGATTCAGC GGCGTGCCCGACAGATTCTCTGGCAGCGGC TCTGGCACCGACTTCACCCTGAAGATCAGCC GGGTGGAAGCCGAGGACCTGGGCGTGTACT ACTGTTTTCAGGGCAGCCACGTGCCCTTCAC CTTCGGCAGCGGCACCAAGCTGGAAATCAA GCGGGCTGATGCTGCACCGACTGTGTCCATC TTCCCACCATCCAGTGAGCAGTTAACATCTG GAGGTGCCTCAGTCGTGTGCTTCTTGAACAA CTTCTACCCCAAAGACATCAATGTCAAGTG GAAGATTGATGGCAGTGAACGACAAAATGG CGTCCTGAACAGTTGGACTGATCAGGACAG CAAAGACAGCACCTACAGCATGAGCAGCAC CCTCACGTTGACCAAGGACGAGTATGAACG ACATAACAGCTATACCTGTGAGGCCACTCA CAAGACATCAACTTCACCCATTGTCAAGAG CTTCAACAGGAATGAGTGTTAG	974
SM1B253	pDR000030243	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CGTCGTGATGACCCAGACCCCTCTGACCCTG AGCGTGACAATCGGCCAGGCCGCCAGCATC AGCTGCAAGAGCAGCCAGAGCCTGCTGCAC AGCGACGGCAAGACCTACCTGAACTGGCTG CTGCAGAGGCCTGGCCAGAGCCCCAAGAGA CTGATCTACCTGGTGTCCAAGCTGGACAGC GGCGTGCCCGATAGATTCACAGGCAGCGGC TCCGGCACCGACTTCACCCTGAAGATCAGC CGGGTGGAAGCCGAGGACCTGGGCGTGTAC TACTGCTGGCAGGGCACCCACTTCCCTTACA CCTTCGGCGGAGGCACAAAGCTGGAAATCA AGCGGGCTGATGCTGCACCGACTGTGTCCA TCTTCCCACCATCCAGTGAGCAGTTAACATC TGGAGGTGCCTCAGTCGTGTGCTTCTTGAAC AACTTCTACCCCAAAGACATCAATGTCAAG TGGAAGATTGATGGCAGTGAACGACAAAAT GGCGTCCTGAACAGTTGGACTGATCAGGAC AGCAAAGACAGCACCTACAGCATGAGCAGC ACCCTCACGTTGACCAAGGACGAGTATGAA CGACATAACAGCTATACCTGTGAGGCCACT	975

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		CACAAGACATCAACTTCACCCATTGTCAAG AGCTTCAACAGGAATGAGTGTTAG	
SM1B254	pDR000030244	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CGTCGTGATGACCCAGACCCCTCTGACCCTG AGCGTGACAGTGGGCCAGCCTGCCAGCATC AGCTGCAAGAGCAGCCAGAGCCTGCTGCAC AGCGACGGCAAGACCTACCTGAACTGGCTG CTGCAGAGGCCTGGCCAGAGCCCCAAGAGA CTGATCTACCTGGTGTCCAAGCTGGACAGC GGCGTGCCCGATAGATTCACAGGCAGCGGC TCCGGCACCGACTTCACCCTGAAGATCAGC CGGGTGGAAGCCGAGGACCTGGGCGTGTAC TACTGTTGGCAGGGCACCCACTTCCCTTACA CCTTCGGCGGAGGCACAAAGCTGGAAATCA AGCGGGCTGATGCTGCACCGACTGTGTCCA TCTTCCCACCATCCAGTGAGCAGTTAACATC TGGAGGTGCCTCAGTCGTGTGCTTCTTGAAC AACTTCTACCCCAAAGACATCAATGTCAAG TGGAAGATTGATGGCAGTGAACGACAAAAT GGCGTCCTGAACAGTTGGACTGATCAGGAC AGCAAAGACAGCACCTACAGCATGAGCAGC ACCCTCACGTTGACCAAGGACGAGTATGAA CGACATAACAGCTATACCTGTGAGGCCACT CACAAGACATCAACTTCACCCATTGTCAAG AGCTTCAACAGGAATGAGTGTTAG	976
SM1B255	pDR000030245	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CGTCGTGATGACCCAGACCCCTCTGACCCTG AGCGTGACAATCGGCCAGCCTGCCAGCATC AGCTGCAAGAGCAGCCAGAGCCTGCTGGAC AGCGACGGCGAGACATACCTGAACTGGCTG CTGCAGAGGCCTGGCCAGAGCCCCAAGCGG CTGATCTACATGGTGTCCAAGCTGGACTCCG GCGTGCCCGACAGATTCACAGGCAGCGGCA GCGGAACCGACTTCACCCTGAAGATCAGCA GAGTGGAAGCCGAGGACCTGGGCGTGTACT ACTGTTGGCAGGGCACCCACTTCCCTCAGAC CTTCGGCGGAGGCACAAAGCTGGAACTGAA GCGGGCTGATGCTGCACCGACTGTGTCCATC TTCCCACCATCCAGTGAGCAGTTAACATCTG GAGGTGCCTCAGTCGTGTGCTTCTTGAACAA CTTCTACCCCAAAGACATCAATGTCAAGTG GAAGATTGATGGCAGTGAACGACAAAATGG CGTCCTGAACAGTTGGACTGATCAGGACAG CAAAGACAGCACCTACAGCATGAGCAGCAC CCTCACGTTGACCAAGGACGAGTATGAACG ACATAACAGCTATACCTGTGAGGCCACTCA	977

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		CAAGACATCAACTTCACCCATTGTCAAGAG CTTCAACAGGAATGAGTGTTAG	
SM1B256	pDR000030246	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CGTCGTGATGACCCAGACCCCTCTGACCCTG AGCGTGACCAATGGCCAGCCTGCCAGCATC AGCTGCAAGAGCAGCCAGAGCCTGCTGGAC AGCGACGGCGAGACATACCTGAACTGGCTG CTGCAGAGGCCTGGCCAGAGCCCCAAGAGA CTGATCTACCTGGTGTCCAAGCTGGACTCCG GCGTGCCCGACAGATTCATCGGCTCTGGCA GCGGCACCGACTTCACCCTGAAGATCAGCC GGGTGGAAGCCGAGGACCTGGGCGTGTACT TCTGTTGGCAGGGCACCCACAGCCCCTACA CCTTTGGCGGCGGAACAAAGCTGGAAATCA AGCGGGCTGATGCTGCACCGACTGTGTCCA TCTTCCCACCATCCAGTGAGCAGTTAACATC TGGAGGTGCCTCAGTCGTGTGCTTCTTGAAC AACTTCTACCCCAAAGACATCAATGTCAAG TGGAAGATTGATGGCAGTGAACGACAAAAT GGCGTCCTGAACAGTTGGACTGATCAGGAC AGCAAAGACAGCACCTACAGCATGAGCAGC ACCCTCACGTTGACCAAGGACGAGTATGAA CGACATAACAGCTATACCTGTGAGGCCACT CACAAGACATCAACTTCACCCATTGTCAAG AGCTTCAACAGGAATGAGTGTTAG	978
SM1B257	pDR000030247	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CATCCAGATGACCCAGAGCCCTAGCAGCCT GTCTGCCAGCCTGGGCGGCAAAGTGACCAT CACATGCAAGGCCAGCCAGGACATCAACAA GTATATCGCCTGGTATCAGCACAAGCCCGG CAAGGGCCCCAGACTGCTGATCCACTACAC CAGCACCCTGCAGCCCGGCATCCCTAGCAG ATTTTCTGGCAGCGGCTCCGGCAGAGACTA CAGCTTCAGCATCAGCAACCTGGAACCCGA GGATATCGCCACCTACTACTGCCTGCAGTAC GACAACCTGCGGACCTTCGGCGGAGGCACC AAGGTGGAAATCAAGCGGGCTGATGCTGCA CCGACTGTGTCCATCTTCCCACCATCCAGTG AGCAGTTAACATCTGGAGGTGCCTCAGTCG TGTGCTTCTTGAACAACTTCTACCCCAAAGA CATCAATGTCAAGTGGAAGATTGATGGCAG TGAACGACAAAATGGCGTCCTGAACAGTTG GACTGATCAGGACAGCAAAGACAGCACCTA CAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATAC CTGTGAGGCCACTCACAAGACATCAACTTC	979

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		ACCCATTGTCAAGAGCTTCAACAGGAATGA GTGTTAG	
SM1B258	pDR000030248	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CGTGCTGATGACCCAGACACCCCTGAGCCT GCCTGTGTCTCTGGGCGATCAGGCCAGCATC AGCTGCCGGTCTAGCCAGAGCATCGTGCAC AGCAACGGCAACACCTACCTGGAATGGTAT CTGCAGAAGCCCGGCCAGAGCCCCAAGCTG CTGATCTACAAGGTGTCCAACAGATTCAGC GGCGTGCCCGACAGATTCTCTGGCAGCGGC TCTGGCACCGACTTCACCCTGAAGATCAGCC GGGTGGAAGCCGAGGACCTGGGCGTGTACT ACTGTTTTCAGGGCAGCCACGTGCCCTTCAC CTTCGGCAGCGGCACCAAGCTGGAAATCAA GCGGGCTGATGCTGCACCGACTGTGTCCATC TTCCCACCATCCAGTGAGCAGTTAACATCTG GAGGTGCCTCAGTCGTGTGCTTCTTGAACAA CTTCTACCCCAAAGACATCAATGTCAAGTG GAAGATTGATGGCAGTGAACGACAAAATGG CGTCCTGAACAGTTGGACTGATCAGGACAG CAAAGACAGCACCTACAGCATGAGCAGCAC CCTCACGTTGACCAAGGACGAGTATGAACG ACATAACAGCTATACCTGTGAGGCCACTCA CAAGACATCAACTTCACCCATTGTCAAGAG CTTCAACAGGAATGAGTGTTAG	980
SM1B259	pDR000030249	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCCA GATCGTGCTGACCCAGAGCCCTGCCATCAT GTCTGCCAGCCCTGGCGAGAAAGTGACCAT GACCTGTAGCGCCAGCAGCAGCGTGTCCTA CATGTACTGGTATCAGCAGAAGCCCGGCAG CAGCCCCAGACTGCTGATCTACGACACCAG CAACCTGGCCAGCGGCGTGCCAGTGCGGTT TTCTGGCAGCGGCAGCGGAACCAGCTACAG CCTGACCATCAGCCGGATGGAAGCCGAGGA CGCCGCCACCTACTACTGCCAGCAGTGGTCC AGCTACCCTCCCACCTTTGGCGGAGGCACC AAGCTGGAAATCAAGCGGGCTGATGCTGCA CCGACTGTGTCCATCTTCCCACCATCCAGTG AGCAGTTAACATCTGGAGGTGCCTCAGTCG TGTGCTTCTTGAACAACTTCTACCCCAAAGA CATCAATGTCAAGTGGAAGATTGATGGCAG TGAACGACAAAATGGCGTCCTGAACAGTTG GACTGATCAGGACAGCAAAGACAGCACCTA CAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATAC CTGTGAGGCCACTCACAAGACATCAACTTC	981

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		ACCCATTGTCAAGAGCTTCAACAGGAATGA GTGTTAG	
SM1B260	pDR000030236	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CATCGTGCTGACACAGTCTCCAGCCAGCCTG GCCGTGTCTCTGGGACAGAGGGCCACCATG AGCTGCAGAGCCAGCGAGTCTGTGGACGGC TACGGCAACAGCTTCCTGCACTGGTATCAGC AGAAGCCCGGCCAGCCTCCCAAGCTGCTGA TCTACAGGGCCAGCAACCTGGAAAGCGGCA TCCCCGCCAGATTCAGCGGCACCGGCAGCA GAACCGACTTCACCCTGACCATCACCCCTGT GGAAGCCGACGACGTGGCCACCTACTACTG CCAGCAGAGCAACGGCGACCCCTTCACCTT CGGCTCCGGCACCAAGCTGGAAATCAAGCG GGCTGATGCTGCACCGACTGTGTCCATCTTC CCACCATCCAGTGAGCAGTTAACATCTGGA GGTGCCTCAGTCGTGTGCTTCTTGAACAACT TCTACCCCAAAGACATCAATGTCAAGTGGA AGATTGATGGCAGTGAACGACAAAATGGCG TCCTGAACAGTTGGACTGATCAGGACAGCA AAGACAGCACCTACAGCATGAGCAGCACCC TCACGTTGACCAAGGACGAGTATGAACGAC ATAACAGCTATACCTGTGAGGCCACTCACA AGACATCAACTTCACCCATTGTCAAGAGCTT CAACAGGAATGAGTGTTAG	982
SM1B261	pDR000030250	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCAA CATCGTGATGACCCAGAGCCCCAAGAGCAT GAGCATGTCCGTGGGCGAGAGAGTGACCCT GAGCTGCAAGGCCAGCGAGAACGTGGGCAC CTACGTGTCCTGGTATCAGCAGAAGCCCGA GCAGAGCCCTAAGCTGCTGATCTACGGGGC CAGCAACAGATACACCGGCGTGCCCGAGAG ATTCACAGGCAGCGGCAGCGCCACCGACTT CACCCTGACAATCAGCAGCGTGCAGGCCGA GGACCTGGCCGATTACCACTGTGGCCAGAG CTACAGCTACCCTCTGACCTTCGGAGCCGGC ACCAAGCTGGAACTGAAGCGGGCTGATGCT GCACCGACTGTGTCCATCTTCCCACCATCCA GTGAGCAGTTAACATCTGGAGGTGCCTCAG TCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGG CAGTGAACGACAAAATGGCGTCCTGAACAG TTGGACTGATCAGGACAGCAAAGACAGCAC CTACAGCATGAGCAGCACCCTCACGTTGAC CAAGGACGAGTATGAACGACATAACAGCTA TACCTGTGAGGCCACTCACAAGACATCAAC	983

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		TTCACCCATTGTCAAGAGCTTCAACAGGAAT GAGTGTTAG	
SM1B262	pDR000030251	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CATCAAGATGACCCAGAGCCCCAGCTCTAT GTACGCCAGCCTGGGCGAGCGCGTGACCAT CACCTGTAAAGCCAGCCAGGACATCAACAG CTACCTGAGCTGGTTCCAGCAGAAGCCCGG CAAGAGCCCCAAGACCCTGATCTACCGGGC CAACAGACTGGTGGACGGCGTGCCAAGCAG ATTCAGCGGCTCTGGCAGCGGCCAGGACTA CAGCCTGACCATCAGCAGCCTGGAATACGA GGACATGGGCATCTACTACTGCCTGCAGTA CGACGAGTTCCCTCTGACCTTCGGAGCCGGC ACCAAGCTGGAACTGAAGCGGGCTGATGCT GCACCGACTGTGTCCATCTTCCCACCATCCA GTGAGCAGTTAACATCTGGAGGTGCCTCAG TCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGG CAGTGAACGACAAAATGGCGTCCTGAACAG TTGGACTGATCAGGACAGCAAAGACAGCAC CTACAGCATGAGCAGCACCCTCACGTTGAC CAAGGACGAGTATGAACGACATAACAGCTA TACCTGTGAGGCCACTCACAAGACATCAAC TTCACCCATTGTCAAGAGCTTCAACAGGAAT GAGTGTTAG	984
SM1B263	pDR000030252	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CATCCAGATGACCCAGAGCCCTAGCAGCCT GTCTGCCAGCCTGGGCGGCAAAGTGACCAT CACATGCAAGGCCAGCCAGGACATCAACAA GTATATCGCCTGGTATCAGCACAAGCCCGG CAAGGGCCCCAGACTGCTGATCCACTACAC CAGCACCCTGCAGCCCGGCATCCCTAGCAG ATTTTCTGGCAGCGGCTCCGGCAGAGACTA CAGCTTCAGCATCAGCAACCTGGAACCCGA GGATATCGCCACCTACTACTGCCTGCAGTAC GACAACCTGTGGACCTTCGGCGGAGGCACC AAGGTGGAAATCAAGCGGGCTGATGCTGCA CCGACTGTGTCCATCTTCCCACCATCCAGTG AGCAGTTAACATCTGGAGGTGCCTCAGTCG TGTGCTTCTTGAACAACTTCTACCCCAAAGA CATCAATGTCAAGTGGAAGATTGATGGCAG TGAACGACAAAATGGCGTCCTGAACAGTTG GACTGATCAGGACAGCAAAGACAGCACCTA CAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATAC CTGTGAGGCCACTCACAAGACATCAACTTC	985

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		ACCCATTGTCAAGAGCTTCAACAGGAATGA GTGTTAG	
SM1B264	pDR000030253	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CATCCAGATGACCCAGAGCCCTGCCAGCCT GAGCGCCTCTGTGGGCGAGACAGTGACCAT CATCTGCCGGGCCAGCGAGAACATCTACAG CAACCTGGCCTGGTATCAGCAGAAGCAGGG CAAGAGCCCTCAGCTGCTGGTGTACGCCGC CACCAATCTGGCCGACGGCATGCCTAGCAG ATTCAGCGGCTCTGGCAGCGGCACCCAGTA CAGCCTGAAGATCAACAGCCTGCAGAGCGA GGACTTCGGCAGCTACTACTGCCAGCACTTC TGGGGCACCCCTTGGACCTTTGGCGGAGGC ACCAAGCTGGAAATCAAGCGGGCTGATGCT GCACCGACTGTGTCCATCTTCCCACCATCCA GTGAGCAGTTAACATCTGGAGGTGCCTCAG TCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGG CAGTGAACGACAAAATGGCGTCCTGAACAG TTGGACTGATCAGGACAGCAAAGACAGCAC CTACAGCATGAGCAGCACCCTCACGTTGAC CAAGGACGAGTATGAACGACATAACAGCTA TACCTGTGAGGCCACTCACAAGACATCAAC TTCACCCATTGTCAAGAGCTTCAACAGGAAT GAGTGTTAG	986
SM1B265	pDR000030254	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CATCCAGATGACCCAGAGCCCTGCCAGCCT GAGCGCCTCTGTGGGCGAGACAGTGACCAT CATCTGCCGGGCCAGCGAGAACATCTACAG CTACCTGGCCTGGTATCAGCAGAAGCAGGG CAAGAGCCCTCAGCTGCTGTTCTACAACGCC AAGACCCTGGTGGAAGGCGTGCCCAGCAGA TTTTCTGGCTCTGGCAGCGGCACCCAGTTCA GCCTGAAGATCAACAGCCTGCAGCCCGAGG ACTTCGGCAGCTACTACTGCCAGCACCACTA CGGCAGCCCCTACACCTTTGGCGGAGGCAC CAAGCTGGAACTGAAGCGGGCTGATGCTGC ACCGACTGTGTCCATCTTCCCACCATCCAGT GAGCAGTTAACATCTGGAGGTGCCTCAGTC GTGTGCTTCTTGAACAACTTCTACCCCAAAG ACATCAATGTCAAGTGGAAGATTGATGGCA GTGAACGACAAAATGGCGTCCTGAACAGTT GGACTGATCAGGACAGCAAAGACAGCACCT ACAGCATGAGCAGCACCCTCACGTTGACCA AGGACGAGTATGAACGACATAACAGCTATA CCTGTGAGGCCACTCACAAGACATCAACTT	987

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		CACCCATTGTCAAGAGCTTCAACAGGAATG AGTGTTAG	
SM1B266	pDR000030255	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CATCCAGATGACCCAGAGCCCTAGCACACT GAGCGCCAGCCTGGGCGACACCATCACCAT CACATGCCACGCCAGCCAGAACATCAACGT GTGGCTGAGCTGGTATCAGCAGAAGCCCGG CAACATCCCCAAGCTGCTGATCTACAAGGC CAGCAACCTGCACACCGGCGTGCCCAGCAG ATTTTCTGGCAGCGGCTCTGGCACCGGCTTC ACCCTGACAATCAGCAGCCTGCAGCCCGAG GATATCGCCACCTACTACTGCCAGCAGGGC CAGAGCTACCCTCTGACCTTTGGCGCTGGCA CCAAGGTGGAAATCAAGCGGGCTGATGCTG CACCGACTGTGTCCATCTTCCCACCATCCAG TGAGCAGTTAACATCTGGAGGTGCCTCAGT CGTGTGCTTCTTGAACAACTTCTACCCCAAA GACATCAATGTCAAGTGGAAGATTGATGGC AGTGAACGACAAAATGGCGTCCTGAACAGT TGGACTGATCAGGACAGCAAAGACAGCACC TACAGCATGAGCAGCACCCTCACGTTGACC AAGGACGAGTATGAACGACATAACAGCTAT ACCTGTGAGGCCACTCACAAGACATCAACT TCACCCATTGTCAAGAGCTTCAACAGGAAT GAGTGTTAG	988
SM1B267	pDR000030256	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CATCCAGATGACCCAGAGCCCTAGCACACT GAGCGCCAGCCTGGGCGACACCATCACCAT CACATGCCACGCCAGCCAGAACATCAACGT GTGGCTGAGCTGGTATCAGCAGAAGCCCGG CAACATCCCCAAGCTGCTGATCTACAAGGC CAGCAACCTGCACACCGGCGTGCCCAGCAG ATTTTCTGGCAGCGGCTCTGGCACCGGCTTC ACCCTGACAATCAGCAGCCTGCAGCCCGAG GATATCGCCACCTACTACTGCCAGCAGGGC CAGAGCTACCCCTACACCTTTGGCGGAGGC ACCAAGCTGGAAATCAAGCGGGCTGATGCT GCACCGACTGTGTCCATCTTCCCACCATCCA GTGAGCAGTTAACATCTGGAGGTGCCTCAG TCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGG CAGTGAACGACAAAATGGCGTCCTGAACAG TTGGACTGATCAGGACAGCAAAGACAGCAC CTACAGCATGAGCAGCACCCTCACGTTGAC CAAGGACGAGTATGAACGACATAACAGCTA TACCTGTGAGGCCACTCACAAGACATCAAC	989

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		TTCACCCATTGTCAAGAGCTTCAACAGGAAT GAGTGTTAG	
SM1B268	pDR000030257	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA GATCGTGCTGACCCAGAGCCCTACCACAAT GGCCGCCAGCCCTGGCGAGAAGATCACCAT CACATGCAGCGCCAGCAGCAGCATCAGCAG CAACTACCTGCACTGGTATCAGCAGAAGCC CGGCTTCAGCCCCAAGCTGCTGATCTACAG AACCAGCAACCTGGCCAGCGGCGTGCCAGC CAGATTTTCTGGCAGCGGCTCTGGCACCAGC TACAGCCTGACCATCGGCACCATGGAAGCC GAGGACGTGGCCACCTACTACTGCCAGCAG GGCAGCTCCATCCCCAGAACCTTTGGCGGA GGCACCAAGCTGGAAATCAAGCGGGCTGAT GCTGCACCGACTGTGTCCATCTTCCCACCAT CCAGTGAGCAGTTAACATCTGGAGGTGCCT CAGTCGTGTGCTTCTTGAACAACTTCTACCC CAAAGACATCAATGTCAAGTGGAAGATTGA TGGCAGTGAACGACAAAATGGCGTCCTGAA CAGTTGGACTGATCAGGACAGCAAAGACAG CACCTACAGCATGAGCAGCACCCTCACGTT GACCAAGGACGAGTATGAACGACATAACAG CTATACCTGTGAGGCCACTCACAAGACATC AACTTCACCCATTGTCAAGAGCTTCAACAG GAATGAGTGTTAG	990
SM1B269	pDR000030258	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CATCGTGCTGACACAGTCTCCAGCCAGCCTG GCCGTGTCTCTGGGACAGAGAGCCACCATC AGCTGCAAGGCCAGCCAGAGCGTGGACTAC GACGGCGACAGCTACATGAACTGGTATCAG CAGAAGCCCGGCCAGCCTCCCAAGCTGCTG ATCTACGCCGCCAGCAACCTGGAAAGCGGC ATCCCTGCCAGATTCAGCGGCAGCGGCTCT GGCACCGACTTCACCCTGAACATCCACCCC GTGGAAGAAGAGGACGCCGCCACCTACTAC TGCCAGCAGAGCAACGAGGACCCCTACACC TTCGGCGGAGGCACCAAGCTGGAAATCAAG CGGGCTGATGCTGCACCGACTGTGTCCATCT TCCCACCATCCAGTGAGCAGTTAACATCTGG AGGTGCCTCAGTCGTGTGCTTCTTGAACAAC TTCTACCCCAAAGACATCAATGTCAAGTGG AAGATTGATGGCAGTGAACGACAAAATGGC GTCCTGAACAGTTGGACTGATCAGGACAGC AAAGACAGCACCTACAGCATGAGCAGCACC CTCACGTTGACCAAGGACGAGTATGAACGA CATAACAGCTATACCTGTGAGGCCACTCAC	991

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		AAGACATCAACTTCACCCATTGTCAAGAGC TTCAACAGGAATGAGTGTTAG	
SM1B270	pDR000030259	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CATCGTGCTGACACAGTCTCCAGCCAGCCTG GCCGTGTCTCTGGGACAGAGAGCCAGCATC AGCTGCAAGGCCAGCCAGAGCGTGGACTAC GACGGCGACAGCTACATGAACTGGTATCAG CAGAAGCCCGGCCAGCCTCCCAAGCTGCTG ATCTACGCCGCCAGCAACCTGGAAAGCGGC ATCCCTGCCAGATTCAGCGGCAGCGGCTCT GGCACCGACTTCACCCTGAACATCCACCCC GTGGAAGAAGAGGACGCCGCCACCTACTAC TGCCAGCAGAGCTACGAGGACCCCTTCACC TTCGGCTCCGGCACCAAGCTGGAAATCAAG CGGGCTGATGCTGCACCGACTGTGTCCATCT TCCCACCATCCAGTGAGCAGTTAACATCTGG AGGTGCCTCAGTCGTGTGCTTCTTGAACAAC TTCTACCCCAAAGACATCAATGTCAAGTGG AAGATTGATGGCAGTGAACGACAAAATGGC GTCCTGAACAGTTGGACTGATCAGGACAGC AAAGACAGCACCTACAGCATGAGCAGCACC CTCACGTTGACCAAGGACGAGTATGAACGA CATAACAGCTATACCTGTGAGGCCACTCAC AAGACATCAACTTCACCCATTGTCAAGAGC TTCAACAGGAATGAGTGTTAG	992
SM1B271	pDR000030249	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCCA GATCGTGCTGACCCAGAGCCCTGCCATCAT GTCTGCCAGCCCTGGCGAGAAAGTGACCAT GACCTGTAGCGCCAGCAGCAGCGTGTCCTA CATGTACTGGTATCAGCAGAAGCCCGGCAG CAGCCCCAGACTGCTGATCTACGACACCAG CAACCTGGCCAGCGGCGTGCCAGTGCGGTT TTCTGGCAGCGGCAGCGGAACCAGCTACAG CCTGACCATCAGCCGGATGGAAGCCGAGGA CGCCGCCACCTACTACTGCCAGCAGTGGTCC AGCTACCCTCCCACCTTTGGCGGAGGCACC AAGCTGGAAATCAAGCGGGCTGATGCTGCA CCGACTGTGTCCATCTTCCCACCATCCAGTG AGCAGTTAACATCTGGAGGTGCCTCAGTCG TGTGCTTCTTGAACAACTTCTACCCCAAAGA CATCAATGTCAAGTGGAAGATTGATGGCAG TGAACGACAAAATGGCGTCCTGAACAGTTG GACTGATCAGGACAGCAAAGACAGCACCTA CAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATAC CTGTGAGGCCACTCACAAGACATCAACTTC	993

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		ACCCATTGTCAAGAGCTTCAACAGGAATGA GTGTTAG	
SM1B272	pDR000030260	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CATCGTGATGACCCAGAGCCAGAAATTCAT GAGCACCAGCGTGGGCGACCGGGTGTCCGT GACATGCAAGGCCAGCCAGAACGTGGGCAC CAACGTGGCCTGGTATCAGCAGAAGCCCGG CCAGAGCCCCAAGGCCCTGATCTACAGCGC CAGCTACAGATACAGCGGCGTGCCCGACAG ATTCACAGGCAGCGGCTCTGGCACCGACTT CACCCTGACCATCAGCAACGTGCAGAGCGA GGACCTGGCCGAGTACTTCTGCCAGCAGTA CAACAGCTACCCCTTCACCTTCGGCAGCGGC ACCAAGCTGGAAATCAAGCGGGCTGATGCT GCACCGACTGTGTCCATCTTCCCACCATCCA GTGAGCAGTTAACATCTGGAGGTGCCTCAG TCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGG CAGTGAACGACAAAATGGCGTCCTGAACAG TTGGACTGATCAGGACAGCAAAGACAGCAC CTACAGCATGAGCAGCACCCTCACGTTGAC CAAGGACGAGTATGAACGACATAACAGCTA TACCTGTGAGGCCACTCACAAGACATCAAC TTCACCCATTGTCAAGAGCTTCAACAGGAAT GAGTGTTAG	994
SM1B273	pDR000030261	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CATCGTGATGAGCCAGAGCCCTAGCAGCCT GGCCGTGTCCGTGGGCGAGAAAGTGACCAT GAGCTGCAAGAGCAGCCAGTCCCTGCTGTA CTCCAGCAACCAGAAGAACTACCTGGCCTG GTATCAGCAGAAGCCCGGCCAGTCCCCTAA GCTGCTGATCTACTGGGCCAGCACCAGAGA AAGCGGCGTGCCCGATAGATTCACAGGCAG CGGCTCCGGCACCGACTTCACCCTGACAATC AGCAGCGTGAAGGCCGAGGACCTGGCTGTG TACTACTGCCAGCAGTACTACAGCTACCCCT ACACCTTCGGCGGAGGCACCAAGCTGGAAA TCAAGCGGGCTGATGCTGCACCGACTGTGT CCATCTTCCCACCATCCAGTGAGCAGTTAAC ATCTGGAGGTGCCTCAGTCGTGTGCTTCTTG AACAACTTCTACCCCAAAGACATCAATGTC AAGTGGAAGATTGATGGCAGTGAACGACAA AATGGCGTCCTGAACAGTTGGACTGATCAG GACAGCAAAGACAGCACCTACAGCATGAGC AGCACCCTCACGTTGACCAAGGACGAGTAT GAACGACATAACAGCTATACCTGTGAGGCC	995

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		ACTCACAAGACATCAACTTCACCCATTGTCA AGAGCTTCAACAGGAATGAGTGTTAG	
SM1B274	pDR000030262	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CGTCGTGATGACCCAGACACCCCTGAGCCT GCCTGTGTCTCTGGGCGATCAGGCCAGCATC AGCTGCAGATCCAGCCAGAGCCTGGTGCAC AGCAACGGCAACACCTACCTGCACTGGTAT CTGCAGAAGCCCGGCCAGAGCCCCAAGCTG CTGATCTACAAGGTGTCCAACAGATTCAGC GGCGTGCCCGACAGATTCTCTGGCAGCGGC TCTGGCACCGACTTCACCCTGAAGATCAGCC GGGTGGAAGCCGAGGACCTGGGCGTGTACT TCTGCAGCCAGTCCACCCACGTGCCACCCTA CACCTTTGGCGGAGGCACCAAGCTGGAACT GAAGCGGGCTGATGCTGCACCGACTGTGTC CATCTTCCCACCATCCAGTGAGCAGTTAACA TCTGGAGGTGCCTCAGTCGTGTGCTTCTTGA ACAACTTCTACCCCAAAGACATCAATGTCA AGTGGAAGATTGATGGCAGTGAACGACAAA ATGGCGTCCTGAACAGTTGGACTGATCAGG ACAGCAAAGACAGCACCTACAGCATGAGCA GCACCCTCACGTTGACCAAGGACGAGTATG AACGACATAACAGCTATACCTGTGAGGCCA CTCACAAGACATCAACTTCACCCATTGTCAA GAGCTTCAACAGGAATGAGTGTTAG	996
SM1B275	pDR000030263	ATGGAGACACATTCTCAGGTCTTTGTATACA TGTTGCTGTGGTTGTCTGGTGTCGAGGGCGA CGTCGTGATGACCCAGACCCCTCTGACCCTG AGCGTGACAATCGGCCAGCCTGCCAGCATC AGCTGCAAGAGCAGCCAGAGCCTGCTGTAC TCCAACGGCAAGACCTACCTGAACTGGCTG CTGCAGAGGCCTGGCCAGAGCCCCAAGAGA CTGATCTACCTGGTGTCCAAGCTGGACAGC GGCGTGCCCGATAGATTCACAGGCAGCGGC TCCGGCACCGACTTCACCCTGAAGATCAGC CGGGTGGAAGCCGAGGACCTGGGCGTGTTC TACTGTGTGCAGGGCACCCACTTCCCTCAGA CCTTCGGCGGAGGCACAAAGCTGGAACTGA AGCGGGCTGATGCTGCACCGACTGTGTCCA TCTTCCCACCATCCAGTGAGCAGTTAACATC TGGAGGTGCCTCAGTCGTGTGCTTCTTGAAC AACTTCTACCCCAAAGACATCAATGTCAAG TGGAAGATTGATGGCAGTGAACGACAAAAT GGCGTCCTGAACAGTTGGACTGATCAGGAC AGCAAAGACAGCACCTACAGCATGAGCAGC ACCCTCACGTTGACCAAGGACGAGTATGAA CGACATAACAGCTATACCTGTGAGGCCACT	997

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		CACAAGACATCAACTTCACCCATTGTCAAG AGCTTCAACAGGAATGAGTGTTAG	

Table 30. LukE Antibody Heavy Chain CDSs

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
SM1B208	pDR000027280	GAGGTTCAGCTGCAGCAGTCTGGGGGAGGC TCAGTGCAGCCTGGAGGGTCCCGGAAACTC TCCTGTGCAGCCTCTGGATTCACCTTCAGTA GTTTTGGAATGCACTGGGTTCGTCAGGCTCC AGAGAAGGGGCTGGAGTGGGTCGCATACAT TAGTAGTGGCAGTAGTTTCATCTACTATGGA GACACAGTGAAGGGCCGATTCACCATCTCC AGAGACAATCCCAATAACACCCTGTTCCTG CAAATGACCAGTCTAAGGTCTGAGGACACG GCCATATATTACTGTGCAAGAGAAGGAATT TATTTCTACGATAGTAGGTACTTCGATGTCT GGGGCGCAGGGACCACGGTCACCGTCTCCT CAGCCAAAACGACACCCCCATCTGTCTATCC ACTGGCCCCTGGATCTGCTGCCCAAACTAAC TCCATGGTGACCCTGGGATGCCTGGTCAAG GGCTATTTCCCTGAGCCAGTGACAGTGACCT GGAACTCTGGATCCCTGTCCAGCGGTGTGC ACACCTTCCCAGCTGTCCTGGAGTCTGACCT CTACACTCTGAGCAGCTCAGTGACTGTCCCC TCCAGCCCTCGGCCCAGCGAGACCGTCACC TGCAACGTTGCCCACCCGGCCAGCAGCACC AAGGTGGACAAGAAAATTGTGCCCAGGGAT TGTGGTTGTAAGCCTTGCATATGTACAGTCC CAGAAGTATCATCTGTCTTCATCTTCCCCCC AAAGCCCAAGGATGTGCTCACCATTACTCT GACTCCTAAGGTCACGTGTGTTGTGGTAGAC ATCAGCAAGGATGATCCCGAGGTCCAGTTC AGCTGGTTTGTAGATGATGTGGAGGTGCAC ACAGCTCAGACGCAACCCCGGGAGGAGCAG TTCAACAGCACTTTCCGCTCAGTCAGTGAAC TTCCCATCATGCACCAGGACTGGCTCAATGG CAAGGAGTTCAAATGCAGGGTCAACAGTGC AGCTTTCCCTGCCCCCATCGAGAAAACCATC TCCAAAACCAAAGGCAGACCGAAGGCTCCA CAGGTGTACACCATTCCACCTCCCAAGGAG CAGATGGCCAAGGATAAAGTCAGTCTGACC TGCATGATAACAGACTTCTTCCCTGAAGACA TTACTGTGGAGTGGCAGTGGAATGGGCAGC CAGCGGAGAACTACAAGAACACTCAGCCCA	998

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		TCATGAACACGAATGGCTCTTACTTCGTCTA CAGCAAGCTCAATGTGCAGAAGAGCAACTG GGAGGCAGGAAATACTTTCACCTGCTCTGT GTTACATGAGGGCCTGCACAACCACCATAC TGAGAAGAGCCTCTCCCACTCTCCTGGTAAA	
SM1B209	pDR000027280	GAGGTTCAGCTGCAGCAGTCTGGGGGAGGC TCAGTGCAGCCTGGAGGGTCCCGGAAACTC TCCTGTGCAGCCTCTGGATTCACCTTCAGTA GTTTTGGAATGCACTGGGTTCGTCAGGCTCC AGAGAAGGGGCTGGAGTGGGTCGCATACAT TAGTAGTGGCAGTAGTTTCATCTACTATGGA GACACAGTGAAGGGCCGATTCACCATCTCC AGAGACAATCCCAATAACACCCTGTTCCTG CAAATGACCAGTCTAAGGTCTGAGGACACG GCCATATATTACTGTGCAAGAGAAGGAATT TATTTCTACGATAGTAGGTACTTCGATGTCT GGGGCGCAGGGACCACGGTCACCGTCTCCT CAGCCAAAACGACACCCCCATCTGTCTATCC ACTGGCCCCTGGATCTGCTGCCCAAACTAAC TCCATGGTGACCCTGGGATGCCTGGTCAAG GGCTATTTCCCTGAGCCAGTGACAGTGACCT GGAACTCTGGATCCCTGTCCAGCGGTGTGC ACACCTTCCCAGCTGTCCTGGAGTCTGACCT CTACACTCTGAGCAGCTCAGTGACTGTCCCC TCCAGCCCTCGGCCCAGCGAGACCGTCACC TGCAACGTTGCCCACCCGGCCAGCAGCACC AAGGTGGACAAGAAAATTGTGCCCAGGGAT TGTGGTTGTAAGCCTTGCATATGTACAGTCC CAGAAGTATCATCTGTCTTCATCTTCCCCCC AAAGCCCAAGGATGTGCTCACCATTACTCT GACTCCTAAGGTCACGTGTGTTGTGGTAGAC ATCAGCAAGGATGATCCCGAGGTCCAGTTC AGCTGGTTTGTAGATGATGTGGAGGTGCAC ACAGCTCAGACGCAACCCCGGGAGGAGCAG TTCAACAGCACTTTCCGCTCAGTCAGTGAAC TTCCCATCATGCACCAGGACTGGCTCAATGG CAAGGAGTTCAAATGCAGGGTCAACAGTGC AGCTTTCCCTGCCCCCATCGAGAAAACCATC TCCAAAACCAAAGGCAGACCGAAGGCTCCA CAGGTGTACACCATTCCACCTCCCAAGGAG CAGATGGCCAAGGATAAAGTCAGTCTGACC TGCATGATAACAGACTTCTTCCCTGAAGACA TTACTGTGGAGTGGCAGTGGAATGGGCAGC CAGCGGAGAACTACAAGAACACTCAGCCCA TCATGAACACGAATGGCTCTTACTTCGTCTA CAGCAAGCTCAATGTGCAGAAGAGCAACTG GGAGGCAGGAAATACTTTCACCTGCTCTGT GTTACATGAGGGCCTGCACAACCACCATAC	999

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		TGAGAAGAGCCTCTCCCACTCTCCTGGTAAA	
SM1B210	pDR000027281	GATGTACAGCTTCAGGAGTCAGGACCTGGG CACTCCATGGTGACCCTGGGATGCCTGGTTG GGCAAAGTATACAGGCCGAGTTCCAGCTGC AGCAGTCTGGACCTGAACTAGTGAAGACTG GGGCTTCAGTGAAGATATCCTGCAAGGCTT CTGGTTACTCTTTCACTGGTTACTACATGCA CTGGGTCAAGCAGAGCCATGGAAGGAGCCT TGAGTGGATTGGATATCTTAGTTGTTACAGT GGTGCTACTAGCTACAACCAGAAGTTCAAG GGCAAGGCCACATTTACTGTAGACACATCC TCCACCACAGCCTACATGCAGTTCAACAGC CTGACATCTGAAGACTCTGCGGTCTATTACT GTGCACGAGGGGAGAGCTACTATGTTATGG ACTATTGGGGTCAAGGAACCTCAGTCACCG TCTCCTCAGCCAAAACGACACCCCCATCTGT CTATCCACTGGCCCCTGGATCTGCTGCCCAA ACTAACTCCATGGTGACCCTGGGATGCCTG GTCAAGGGCTATTTCCCTGAGCCAGTGACA GTGACCTGGAACTCTGGATCCCTGTCCAGCG GTGTGCACACCTTCCCAGCTGTCCTGGAGTC TGACCTCTACACTCTGAGCAGCTCAGTGACT GTCCCCTCCAGCCCTCGGCCCAGCGAGACC GTCACCTGCAACGTTGCCCACCCGGCCAGC AGCACCAAGGTGGACAAGAAAATTGTGCCC AGGGATTGTGGTTGTAAGCCTTGCATATGTA CAGTCCCAGAAGTATCATCTGTCTTCATCTT CCCCCCAAAGCCCAAGGATGTGCTCACCAT TACTCTGACTCCTAAGGTCACGTGTGTTGTG GTAGACATCAGCAAGGATGATCCCGAGGTC CAGTTCAGCTGGTTTGTAGATGATGTGGAG GTGCACACAGCTCAGACGCAACCCCGGGAG GAGCAGTTCAACAGCACTTTCCGCTCAGTCA GTGAACTTCCCATCATGCACCAGGACTGGCT CAATGGCAAGGAGTTCAAATGCAGGGTCAA CAGTGCAGCTTTCCCTGCCCCCATCGAGAAA ACCATCTCCAAAACCAAAGGCAGACCGAAG GCTCCACAGGTGTACACCATTCCACCTCCCA AGGAGCAGATGGCCAAGGATAAAGTCAGTC TGACCTGCATGATAACAGACTTCTTCCCTGA AGACATTACTGTGGAGTGGCAGTGGAATGG GCAGCCAGCGGAGAACTACAAGAACACTCA GCCCATCATGAACACGAATGGCTCTTACTTC GTCTACAGCAAGCTCAATGTGCAGAAGAGC AACTGGGAGGCAGGAAATACTTTCACCTGC TCTGTGTTACATGAGGGCCTGCACAACCACC ATACTGAGAAGAGCCTCTCCCACTCTCCTGG TAAA	1000

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
SM1B211	pDR000027282	GAGGTTCAGCTGCAGCAGTCTGGACCTGGC CTGGTGAAGCCTTCTCAGACAGTGTCCCTCA CCTGCACTGTCACTGGCTACTCTATCACTAA TGGTAATCACTGGTGGAACTGGATCCGGCA GGTTTCAGGAAGCAAACTGGAGTGGATAGG GTACATAAGCTCCAGTGGTAGCACTGACAG CAATCCATCTCTCAAAAGTCGAATCTCCATC ACTAGAGACACTTCCAAGAACCAGTTATTC CTGCAGTTGAACTCTGTGACTACTGAAGATA TAGCCACATATTACTGTGCAAGAGGGCATT ACTACGATGGTAGCTCCTATGCTATGGACTA CTGGGGTCAAGGAACCTCAGTCACCGTCTC CTCAGCCAAAACAACAGCCCCATCGGTCTA TCCACTGGCCCCTGTGTGTGGAGATACAAGT GACTCCATGGTGACCCTGGGATGCCTGGTC AAGGGCTATTTCCCTGAGCCAGTGACAGTG ACCTGGAACTCTGGATCCCTGTCCAGCGGTG TGCACACCTTCCCAGCTGTCCTGGAGTCTGA CCTCTACACTCTGAGCAGCTCAGTGACTGTC CCCTCCAGCCCTCGGCCCAGCGAGACCGTC ACCTGCAACGTTGCCCACCCGGCCAGCAGC ACCAAGGTGGACAAGAAAATTGTGCCCAGG GATTGTGGTTGTAAGCCTTGCATATGTACAG TCCCAGAAGTATCATCTGTCTTCATCTTCCC CCCAAAGCCCAAGGATGTGCTCACCATTAC TCTGACTCCTAAGGTCACGTGTGTTGTGGTA GACATCAGCAAGGATGATCCCGAGGTCCAG TTCAGCTGGTTTGTAGATGATGTGGAGGTGC ACACAGCTCAGACGCAACCCCGGGAGGAGC AGTTCAACAGCACTTTCCGCTCAGTCAGTGA ACTTCCCATCATGCACCAGGACTGGCTCAAT GGCAAGGAGTTCAAATGCAGGGTCAACAGT GCAGCTTTCCCTGCCCCCATCGAGAAAACC ATCTCCAAAACCAAAGGCAGACCGAAGGCT CCACAGGTGTACACCATTCCACCTCCCAAG GAGCAGATGGCCAAGGATAAAGTCAGTCTG ACCTGCATGATAACAGACTTCTTCCCTGAAG ACATTACTGTGGAGTGGCAGTGGAATGGGC AGCCAGCGGAGAACTACAAGAACACTCAGC CCATCATGAACACGAATGGCTCTTACTTCGT CTACAGCAAGCTCAATGTGCAGAAGAGCAA CTGGGAGGCAGGAAATACTTTCACCTGCTCT GTGTTACATGAGGGCCTGCACAACCACCAT ACTGAGAAGAGCCTCTCCCACTCTCCTGGTA AA	1001
SM1B507	pDR000034825	GAGGTTCAGCTGCAGCAGTCTGGGGCTGAG CTGGTGAAGCCTGGGGCTTCAGTGAAGATG TCCTGTAAGGCTTCTGGATACACATTCACTG	1002

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		ACTACTACATGGACTGGGTGAAGCAGAGCC ATGGAAAAAGCTTTGAGTGGATTGGACATG TTAATCCTTACAATGGTGATACTAGGTACAA CCAGAAGTTCAAGGGCAAGGCCACATTGAC TGTTGACAAGTCCTCCACCACAGCCTACATG GAGCTCAACAGCCTGACATCTGAGGACTCT GCGGTCTATTACTGTGCAAGAGGGAACTTCT TTGACTACTGGGGCCAAGGCACCACTCTCTC AGTCTCCTCAGCCAAAACGACACCCCCATCT GTCTATCCACTGGCCCCTGGATCTGCTGCCC AAACTAACTCCATGGTGACCCTGGGATGCC TGGTCAAGGGCTATTTCCCTGAGCCAGTGAC AGTGACCTGGAACTCTGGATCCCTGTCCAGC GGTGTGCACACCTTCCCAGCTGTCCTGGAGT CTGACCTCTACACTCTGAGCAGCTCAGTGAC TGTCCCCTCCAGCCCTCGGCCCAGCGAGACC GTCACCTGCAACGTTGCCCACCCGGCCAGC AGCACCAAGGTGGACAAGAAAATTGTGCCC AGGGATTGTGGTTGTAAGCCTTGCATATGTA CAGTCCCAGAAGTATCATCTGTCTTCATCTT CCCCCCAAAGCCCAAGGATGTGCTCACCAT TACTCTGACTCCTAAGGTCACGTGTGTTGTG GTAGACATCAGCAAGGATGATCCCGAGGTC CAGTTCAGCTGGTTTGTAGATGATGTGGAG GTGCACACAGCTCAGACGCAACCCCGGGAG GAGCAGTTCAACAGCACTTTCCGCTCAGTCA GTGAACTTCCCATCATGCACCAGGACTGGCT CAATGGCAAGGAGTTCAAATGCAGGGTCAA CAGTGCAGCTTTCCCTGCCCCCATCGAGAAA ACCATCTCCAAAACCAAAGGCAGACCGAAG GCTCCACAGGTGTACACCATTCCACCTCCCA AGGAGCAGATGGCCAAGGATAAAGTCAGTC TGACCTGCATGATAACAGACTTCTTCCCTGA AGACATTACTGTGGAGTGGCAGTGGAATGG GCAGCCAGCGGAGAACTACAAGAACACTCA GCCCATCATGAACACGAATGGCTCTTACTTC GTCTACAGCAAGCTCAATGTGCAGAAGAGC AACTGGGAGGCAGGAAATACTTTCACCTGC TCTGTGTTACATGAGGGCCTGCACAACCACC ATACTGAGAAGAGCCTCTCCCACTCTCCTGG TAAA	
SM1B508	pDR000034826	GAGGTTCAGCTGCAGCAGTCTGGGGCTGAG CTGGTGAAGCCTGGGGCTTCAGTGAAGATA TCCTGCAAGACTTCTGGTTACTCATTTACTG GCTACTTTATGAATTGGGTGATGCAGAGCC ATGGAAAGAGCCTTGAGTGGATTGGACGTA TTAATCCTTACAATGGTGATACTTTCTACAA CCAGAAGTTCAAGGGCAAGGCCACATTGAC	1003

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		TGTAGACAAATCCTCTAGCACAGCCCACAT GGAGCTCCGGAGCCTGGCATCTGAGGACTC TGCAGTCTATTATTGTGCAAGAAGCTACGGC TATGCTATGGACTACTGGGGTCAAGGAACC TCAGTCACCGTCTCCTCAGCCAAAACGACA CCCCCATCTGTCTATCCACTGGCCCCTGGAT CTGCTGCCCAAACTAACTCCATGGTGACCCT GGGATGCCTGGTCAAGGGCTATTTCCCTGA GCCAGTGACAGTGACCTGGAACTCTGGATC CCTGTCCAGCGGTGTGCACACCTTCCCAGCT GTCCTGGAGTCTGACCTCTACACTCTGAGCA GCTCAGTGACTGTCCCCTCCAGCCCTCGGCC CAGCGAGACCGTCACCTGCAACGTTGCCCA CCCGGCCAGCAGCACCAAGGTGGACAAGAA AATTGTGCCCAGGGATTGTGGTTGTAAGCCT TGCATATGTACAGTCCCAGAAGTATCATCTG TCTTCATCTTCCCCCCAAAGCCCAAGGATGT GCTCACCATTACTCTGACTCCTAAGGTCACG TGTGTTGTGGTAGACATCAGCAAGGATGAT CCCGAGGTCCAGTTCAGCTGGTTTGTAGATG ATGTGGAGGTGCACACAGCTCAGACGCAAC CCCGGGAGGAGCAGTTCAACAGCACTTTCC GCTCAGTCAGTGAACTTCCCATCATGCACCA GGACTGGCTCAATGGCAAGGAGTTCAAATG CAGGGTCAACAGTGCAGCTTTCCCTGCCCCC ATCGAGAAAACCATCTCCAAAACCAAAGGC AGACCGAAGGCTCCACAGGTGTACACCATT CCACCTCCCAAGGAGCAGATGGCCAAGGAT AAAGTCAGTCTGACCTGCATGATAACAGAC TTCTTCCCTGAAGACATTACTGTGGAGTGGC AGTGGAATGGGCAGCCAGCGGAGAACTACA AGAACACTCAGCCCATCATGAACACGAATG GCTCTTACTTCGTCTACAGCAAGCTCAATGT GCAGAAGAGCAACTGGGAGGCAGGAAATA CTTTCACCTGCTCTGTGTTACATGAGGGCCT GCACAACCACCATACTGAGAAGAGCCTCTC CCACTCTCCTGGTAAA	
SM1B509	pDR000034827	CAGGTGCAGCTGAAGGAGTCAGGACCTGGC CTGGTGGCGCCCTCACAGAGCCTGTCCATCA CATGCACCGTCTCAGGGTTCTCATTAACCGG CTATGGTGTAAACTGGGTTCGCCAGCCTCCA GGAAAGGGTCTGGAGTGGCTGGGGTTGATG TGGGGTGATGGAAGCACAGACTATAATTCA GCTCTCAACTCCAGACTGCGCATCAACAAG GACAACTCCAAGAGTCAAGTTTTCTTAAAA ATGAGCAGTCTTCAAACTGATGACACAGCC ATTTACTACTGTGTCAGAAAGGGCGGTAAT AGCCCCTATGCTATGGACTACTGGGGTCAA	1004

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		GGAACCTCAGTCACCGTCTCCTCAGCCAAA ACGACACCCCCATCTGTCTATCCACTGGCCC CTGGATCTGCTGCCCAAACTAACTCCATGGT GACCCTGGGATGCCTGGTCAAGGGCTATTTC CCTGAGCCAGTGACAGTGACCTGGAACTCT GGATCCCTGTCCAGCGGTGTGCACACCTTCC CAGCTGTCCTGGAGTCTGACCTCTACACTCT GAGCAGCTCAGTGACTGTCCCCTCCAGCCCT CGGCCCAGCGAGACCGTCACCTGCAACGTT GCCCACCCGGCCAGCAGCACCAAGGTGGAC AAGAAAATTGTGCCCAGGGATTGTGGTTGT AAGCCTTGCATATGTACAGTCCCAGAAGTA TCATCTGTCTTCATCTTCCCCCCAAAGCCCA AGGATGTGCTCACCATTACTCTGACTCCTAA GGTCACGTGTGTTGTGGTAGACATCAGCAA GGATGATCCCGAGGTCCAGTTCAGCTGGTTT GTAGATGATGTGGAGGTGCACACAGCTCAG ACGCAACCCCGGGAGGAGCAGTTCAACAGC ACTTTCCGCTCAGTCAGTGAACTTCCCATCA TGCACCAGGACTGGCTCAATGGCAAGGAGT TCAAATGCAGGGTCAACAGTGCAGCTTTCC CTGCCCCCATCGAGAAAACCATCTCCAAAA CCAAAGGCAGACCGAAGGCTCCACAGGTGT ACACCATTCCACCTCCCAAGGAGCAGATGG CCAAGGATAAAGTCAGTCTGACCTGCATGA TAACAGACTTCTTCCCTGAAGACATTACTGT GGAGTGGCAGTGGAATGGGCAGCCAGCGGA GAACTACAAGAACACTCAGCCCATCATGAA CACGAATGGCTCTTACTTCGTCTACAGCAAG CTCAATGTGCAGAAGAGCAACTGGGAGGCA GGAAATACTTTCACCTGCTCTGTGTTACATG AGGGCCTGCACAACCACCATACTGAGAAGA GCCTCTCCCACTCTCCTGGTAAA	
SM1B510	pDR000034827	CAGGTGCAGCTGAAGGAGTCAGGACCTGGC CTGGTGGCGCCCTCACAGAGCCTGTCCATCA CATGCACCGTCTCAGGGTTCTCATTAACCGG CTATGGTGTAAACTGGGTTCGCCAGCCTCCA GGAAAGGGTCTGGAGTGGCTGGGGTTGATG TGGGGTGATGGAAGCACAGACTATAATTCA GCTCTCAACTCCAGACTGCGCATCAACAAG GACAACTCCAAGAGTCAAGTTTTCTTAAAA ATGAGCAGTCTTCAAACTGATGACACAGCC ATTTACTACTGTGTCAGAAAGGGCGGTAAT AGCCCCTATGCTATGGACTACTGGGGTCAA GGAACCTCAGTCACCGTCTCCTCAGCCAAA ACGACACCCCCATCTGTCTATCCACTGGCCC CTGGATCTGCTGCCCAAACTAACTCCATGGT GACCCTGGGATGCCTGGTCAAGGGCTATTTC	1005

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		CCTGAGCCAGTGACAGTGACCTGGAACTCT GGATCCCTGTCCAGCGGTGTGCACACCTTCC CAGCTGTCCTGGAGTCTGACCTCTACACTCT GAGCAGCTCAGTGACTGTCCCCTCCAGCCCT CGGCCCAGCGAGACCGTCACCTGCAACGTT GCCCACCCGGCCAGCAGCACCAAGGTGGAC AAGAAAATTGTGCCCAGGGATTGTGGTTGT AAGCCTTGCATATGTACAGTCCCAGAAGTA TCATCTGTCTTCATCTTCCCCCCAAAGCCCA AGGATGTGCTCACCATTACTCTGACTCCTAA GGTCACGTGTGTTGTGGTAGACATCAGCAA GGATGATCCCGAGGTCCAGTTCAGCTGGTTT GTAGATGATGTGGAGGTGCACACAGCTCAG ACGCAACCCCGGGAGGAGCAGTTCAACAGC ACTTTCCGCTCAGTCAGTGAACTTCCCATCA TGCACCAGGACTGGCTCAATGGCAAGGAGT TCAAATGCAGGGTCAACAGTGCAGCTTTCC CTGCCCCCATCGAGAAAACCATCTCCAAAA CCAAAGGCAGACCGAAGGCTCCACAGGTGT ACACCATTCCACCTCCCAAGGAGCAGATGG CCAAGGATAAAGTCAGTCTGACCTGCATGA TAACAGACTTCTTCCCTGAAGACATTACTGT GGAGTGGCAGTGGAATGGGCAGCCAGCGGA GAACTACAAGAACACTCAGCCCATCATGAA CACGAATGGCTCTTACTTCGTCTACAGCAAG CTCAATGTGCAGAAGAGCAACTGGGAGGCA GGAAATACTTTCACCTGCTCTGTGTTACATG AGGGCCTGCACAACCACCATACTGAGAAGA GCCTCTCCCACTCTCCTGGTAAA	
SM1B511	pDR000034830	GAAGTGAAGCTGGTGGAGTCTGGGCCTGAG CTGGTGAAGCCTGGGGCTTCAGTGAAGATA TCCTGCAAGACTTCTGGTTACTCATTTACTG GCTACTTTATGAATTGGGTGATGCAGAGCC ATGGAAAGAGCCTTGAGTGGATTGGACGTA TTAATCCTTACAATGGTGATACTTTCTACAA CCAGAAGTTCAAGGGCAAGGCCACATTGAC TGTAGACAAATCCTCTAGCACAGCCCACAT GGAGCTCCGGAGCCTGGCATCTGAGGACTC TGCAGTCTATTATTGTGCAAGAAGCTACGGC TATGCTATGGACTACTGGGGTCAAGGAACC TCAGTCACCGTCTCCTCAGCCAAAACGACA CCCCCATCTGTCTATCCACTGGCCCCTGGAT CTGCTGCCCAAACTAACTCCATGGTGACCCT GGGATGCCTGGTCAAGGGCTATTTCCCTGA GCCAGTGACAGTGACCTGGAACTCTGGATC CCTGTCCAGCGGTGTGCACACCTTCCCAGCT GTCCTGGAGTCTGACCTCTACACTCTGAGCA GCTCAGTGACTGTCCCCTCCAGCCCTCGGCC	1006

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		CAGCGAGACCGTCACCTGCAACGTTGCCCA CCCGGCCAGCAGCACCAAGGTGGACAAGAA AATTGTGCCCAGGGATTGTGGTTGTAAGCCT TGCATATGTACAGTCCCAGAAGTATCATCTG TCTTCATCTTCCCCCCAAAGCCCAAGGATGT GCTCACCATTACTCTGACTCCTAAGGTCACG TGTGTTGTGGTAGACATCAGCAAGGATGAT CCCGAGGTCCAGTTCAGCTGGTTTGTAGATG ATGTGGAGGTGCACACAGCTCAGACGCAAC CCCGGGAGGAGCAGTTCAACAGCACTTTCC GCTCAGTCAGTGAACTTCCCATCATGCACCA GGACTGGCTCAATGGCAAGGAGTTCAAATG CAGGGTCAACAGTGCAGCTTTCCCTGCCCCC ATCGAGAAAACCATCTCCAAAACCAAAGGC AGACCGAAGGCTCCACAGGTGTACACCATT CCACCTCCCAAGGAGCAGATGGCCAAGGAT AAAGTCAGTCTGACCTGCATGATAACAGAC TTCTTCCCTGAAGACATTACTGTGGAGTGGC AGTGGAATGGGCAGCCAGCGGAGAACTACA AGAACACTCAGCCCATCATGAACACGAATG GCTCTTACTTCGTCTACAGCAAGCTCAATGT GCAGAAGAGCAACTGGGAGGCAGGAAATA CTTTCACCTGCTCTGTGTTACATGAGGGCCT GCACAACCACCATACTGAGAAGAGCCTCTC CCACTCTCCTGGTAAA	
SM1B512	pDR000034830	GAAGTGAAGCTGGTGGAGTCTGGGCCTGAG CTGGTGAAGCCTGGGGCTTCAGTGAAGATA TCCTGCAAGACTTCTGGTTACTCATTTACTG GCTACTTTATGAATTGGGTGATGCAGAGCC ATGGAAAGAGCCTTGAGTGGATTGGACGTA TTAATCCTTACAATGGTGATACTTTCTACAA CCAGAAGTTCAAGGGCAAGGCCACATTGAC TGTAGACAAATCCTCTAGCACAGCCCACAT GGAGCTCCGGAGCCTGGCATCTGAGGACTC TGCAGTCTATTATTGTGCAAGAAGCTACGGC TATGCTATGGACTACTGGGGTCAAGGAACC TCAGTCACCGTCTCCTCAGCCAAAACGACA CCCCCATCTGTCTATCCACTGGCCCCTGGAT CTGCTGCCCAAACTAACTCCATGGTGACCCT GGGATGCCTGGTCAAGGGCTATTTCCCTGA GCCAGTGACAGTGACCTGGAACTCTGGATC CCTGTCCAGCGGTGTGCACACCTTCCCAGCT GTCCTGGAGTCTGACCTCTACACTCTGAGCA GCTCAGTGACTGTCCCCTCCAGCCCTCGGCC CAGCGAGACCGTCACCTGCAACGTTGCCCA CCCGGCCAGCAGCACCAAGGTGGACAAGAA AATTGTGCCCAGGGATTGTGGTTGTAAGCCT TGCATATGTACAGTCCCAGAAGTATCATCTG	1007

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		TCTTCATCTTCCCCCCAAAGCCCAAGGATGT GCTCACCATTACTCTGACTCCTAAGGTCACG TGTGTTGTGGTAGACATCAGCAAGGATGAT CCCGAGGTCCAGTTCAGCTGGTTTGTAGATG ATGTGGAGGTGCACACAGCTCAGACGCAAC CCCGGGAGGAGCAGTTCAACAGCACTTTCC GCTCAGTCAGTGAACTTCCCATCATGCACCA GGACTGGCTCAATGGCAAGGAGTTCAAATG CAGGGTCAACAGTGCAGCTTTCCCTGCCCCC ATCGAGAAAACCATCTCCAAAACCAAAGGC AGACCGAAGGCTCCACAGGTGTACACCATT CCACCTCCCAAGGAGCAGATGGCCAAGGAT AAAGTCAGTCTGACCTGCATGATAACAGAC TTCTTCCCTGAAGACATTACTGTGGAGTGGC AGTGGAATGGGCAGCCAGCGGAGAACTACA AGAACACTCAGCCCATCATGAACACGAATG GCTCTTACTTCGTCTACAGCAAGCTCAATGT GCAGAAGAGCAACTGGGAGGCAGGAAATA CTTTCACCTGCTCTGTGTTACATGAGGGCCT GCACAACCACCATACTGAGAAGAGCCTCTC CCACTCTCCTGGTAAA	
SM1B513	pDR000034831	GAGGTTCAGCTGCAGCAGTCTGGACCTGAG CTGGTGAAGCCTGGGGCTTCAGTGAAGATA TCCTGCAAGGCTTCTGGTTACTCATTTACTG GCTACTTTATGAATTGGGTGATGCAGAGCC ATGGAAAGAGCCTTGAGTGGATTGGACGTA TTAATCCTTACAATGGTGATACTTTCTACAA CCAGAAATTCAAGGCCAAGGCCACATTGAC TGTAGACAAATCCTCTAACACAGCCCACAT GGAGCTCCGGAGCCTGGCATCTGAGGACTC TGCAGTCTATTTTTGTGCAAGAAGTTACGGC TATGCTATGGACTACTGGGGTCTAGGAACCT CAGTCACCGTCTCCTCAGCCAAAACGACAC CCCCATCTGTCTATCCACTGGCCCCTGGATC TGCTGCCCAAACTAACTCCATGGTGACCCTG GGATGCCTGGTCAAGGGCTATTTCCCTGAGC CAGTGACAGTGACCTGGAACTCTGGATCCC TGTCCAGCGGTGTGCACACCTTCCCAGCTGT CCTGGAGTCTGACCTCTACACTCTGAGCAGC TCAGTGACTGTCCCCTCCAGCCCTCGGCCCA GCGAGACCGTCACCTGCAACGTTGCCCACC CGGCCAGCAGCACCAAGGTGGACAAGAAA ATTGTGCCCAGGGATTGTGGTTGTAAGCCTT GCATATGTACAGTCCCAGAAGTATCATCTGT CTTCATCTTCCCCCCAAAGCCCAAGGATGTG CTCACCATTACTCTGACTCCTAAGGTCACGT GTGTTGTGGTAGACATCAGCAAGGATGATC CCGAGGTCCAGTTCAGCTGGTTTGTAGATGA	1008

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		TGTGGAGGTGCACACAGCTCAGACGCAACC CCGGGAGGAGCAGTTCAACAGCACTTTCCG CTCAGTCAGTGAACTTCCCATCATGCACCAG GACTGGCTCAATGGCAAGGAGTTCAAATGC AGGGTCAACAGTGCAGCTTTCCCTGCCCCCA TCGAGAAAACCATCTCCAAAACCAAAGGCA GACCGAAGGCTCCACAGGTGTACACCATTC CACCTCCCAAGGAGCAGATGGCCAAGGATA AAGTCAGTCTGACCTGCATGATAACAGACT TCTTCCCTGAAGACATTACTGTGGAGTGGCA GTGGAATGGGCAGCCAGCGGAGAACTACAA GAACACTCAGCCCATCATGAACACGAATGG CTCTTACTTCGTCTACAGCAAGCTCAATGTG CAGAAGAGCAACTGGGAGGCAGGAAATACT TTCACCTGCTCTGTGTTACATGAGGGCCTGC ACAACCACCATACTGAGAAGAGCCTCTCCC ACTCTCCTGGTAAA	
SM1B514	pDR000034833	GAGGTTCAGCTGCAGCAGTCTGGGCCTGAA CTAGTGAAGACTGGGGCTTCAGTGAAGATA TCCTGCAAGGCTTCTGGTTACTCTTTCACTG GTTACTACATGCACTGGGTCAAGCAGAGCC ATGGAAAGAGCCTTGAGTGGATTGGATATC TTAGTTGTTACAGTGGTGCTACTAGCTACAA CCAGAAGTTCAAGGGCAAGGCCACATTTAC TGTAGACACATCCTCCACCACAGCCTACATG CAGTTCAACAGCCTGACATCTGAAGACTCT GCGGTCTATTACTGTGCACGAGGGGAGAGC TACTATGTTATGGACTATTGGGGTCAAGGA ACCTCAGTCACCGTCTCCTCAGCCAAAACG ACACCCCCATCTGTCTATCCACTGGCCCCTG GATCTGCTGCCCAAACTAACTCCATGGTGAC CCTGGGATGCCTGGTCAAGGGCTATTTCCCT GAGCCAGTGACAGTGACCTGGAACTCTGGA TCCCTGTCCAGCGGTGTGCACACCTTCCCAG CTGTCCTGGAGTCTGACCTCTACACTCTGAG CAGCTCAGTGACTGTCCCCTCCAGCCCTCGG CCCAGCGAGACCGTCACCTGCAACGTTGCC CACCCGGCCAGCAGCACCAAGGTGGACAAG AAAATTGTGCCCAGGGATTGTGGTTGTAAG CCTTGCATATGTACAGTCCCAGAAGTATCAT CTGTCTTCATCTTCCCCCCAAAGCCCAAGGA TGTGCTCACCATTACTCTGACTCCTAAGGTC ACGTGTGTTGTGGTAGACATCAGCAAGGAT GATCCCGAGGTCCAGTTCAGCTGGTTTGTAG ATGATGTGGAGGTGCACACAGCTCAGACGC AACCCCGGGAGGAGCAGTTCAACAGCACTT TCCGCTCAGTCAGTGAACTTCCCATCATGCA CCAGGACTGGCTCAATGGCAAGGAGTTCAA	1009

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		ATGCAGGGTCAACAGTGCAGCTTTCCCTGCC CCCATCGAGAAAACCATCTCCAAAACCAAA GGCAGACCGAAGGCTCCACAGGTGTACACC ATTCCACCTCCCAAGGAGCAGATGGCCAAG GATAAAGTCAGTCTGACCTGCATGATAACA GACTTCTTCCCTGAAGACATTACTGTGGAGT GGCAGTGGAATGGGCAGCCAGCGGAGAACT ACAAGAACACTCAGCCCATCATGAACACGA ATGGCTCTTACTTCGTCTACAGCAAGCTCAA TGTGCAGAAGAGCAACTGGGAGGCAGGAA ATACTTTCACCTGCTCTGTGTTACATGAGGG CCTGCACAACCACCATACTGAGAAGAGCCT CTCCCACTCTCCTGGTAAA	

Table 31. LukE Antibody Heavy Chain Primary Transcripts

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
SM1B208	pDR000027280	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAGG TTCAGCTGCAGCAGTCTGGGGGAGGCTCAGT GCAGCCTGGAGGGTCCCGGAAACTCTCCTGT GCAGCCTCTGGATTCACCTTCAGTAGTTTTG GAATGCACTGGGTTCGTCAGGCTCCAGAGA AGGGGCTGGAGTGGGTCGCATACATTAGTA GTGGCAGTAGTTTCATCTACTATGGAGACAC AGTGAAGGGCCGATTCACCATCTCCAGAGA CAATCCCAATAACACCCTGTTCCTGCAAATG ACCAGTCTAAGGTCTGAGGACACGGCCATA TATTACTGTGCAAGAGAAGGAATTTATTTCT ACGATAGTAGGTACTTCGATGTCTGGGGCGC AGGGACCACGGTCACCGTCTCCTCAGCCAA AACGACACCCCCATCTGTCTATCCACTGGCC CCTGGATCTGCTGCCCAAACTAACTCCATGG TGACCCTGGGATGCCTGGTCAAGGGCTATTT CCCTGAGCCAGTGACAGTGACCTGGAACTCT GGATCCCTGTCCAGCGGTGTGCACACCTTCC CAGCTGTCCTGGAGTCTGACCTCTACACTCT GAGCAGCTCAGTGACTGTCCCCTCCAGCCCT CGGCCCAGCGAGACCGTCACCTGCAACGTT GCCCACCCGGCCAGCAGCACCAAGGTGGAC AAGAAAATTGTGCCCAGGGATTGTGGTTGTA AGCCTTGCATATGTACAGTCCCAGAAGTATC ATCTGTCTTCATCTTCCCCCCAAAGCCCAAG	1010

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GATGTGCTCACCATTACTCTGACTCCTAAGG TCACGTGTGTTGTGGTAGACATCAGCAAGGA TGATCCCGAGGTCCAGTTCAGCTGGTTTGTA GATGATGTGGAGGTGCACACAGCTCAGACG CAACCCCGGGAGGAGCAGTTCAACAGCACT TTCCGCTCAGTCAGTGAACTTCCCATCATGC ACCAGGACTGGCTCAATGGCAAGGAGTTCA AATGCAGGGTCAACAGTGCAGCTTTCCCTGC CCCCATCGAGAAAACCATCTCCAAAACCAA AGGCAGACCGAAGGCTCCACAGGTGTACAC CATTCCACCTCCCAAGGAGCAGATGGCCAA GGATAAAGTCAGTCTGACCTGCATGATAAC AGACTTCTTCCCTGAAGACATTACTGTGGAG TGGCAGTGGAATGGGCAGCCAGCGGAGAAC TACAAGAACACTCAGCCCATCATGAACACG AATGGCTCTTACTTCGTCTACAGCAAGCTCA ATGTGCAGAAGAGCAACTGGGAGGCAGGAA ATACTTTCACCTGCTCTGTGTTACATGAGGG CCTGCACAACCACCATACTGAGAAGAGCCT CTCCCACTCTCCTGGTAAATGA	
SM1B209	pDR000027280	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAGG TTCAGCTGCAGCAGTCTGGGGGAGGCTCAGT GCAGCCTGGAGGGTCCCGGAAACTCTCCTGT GCAGCCTCTGGATTCACCTTCAGTAGTTTTG GAATGCACTGGGTTCGTCAGGCTCCAGAGA AGGGGCTGGAGTGGGTCGCATACATTAGTA GTGGCAGTAGTTTCATCTACTATGGAGACAC AGTGAAGGGCCGATTCACCATCTCCAGAGA CAATCCCAATAACACCCTGTTCCTGCAAATG ACCAGTCTAAGGTCTGAGGACACGGCCATA TATTACTGTGCAAGAGAAGGAATTTATTTCT ACGATAGTAGGTACTTCGATGTCTGGGGCGC AGGGACCACGGTCACCGTCTCCTCAGCCAA AACGACACCCCCATCTGTCTATCCACTGGCC CCTGGATCTGCTGCCCAAACTAACTCCATGG TGACCCTGGGATGCCTGGTCAAGGGCTATTT CCCTGAGCCAGTGACAGTGACCTGGAACTCT GGATCCCTGTCCAGCGGTGTGCACACCTTCC CAGCTGTCCTGGAGTCTGACCTCTACACTCT GAGCAGCTCAGTGACTGTCCCCTCCAGCCCT CGGCCCAGCGAGACCGTCACCTGCAACGTT GCCCACCCGGCCAGCAGCACCAAGGTGGAC AAGAAAATTGTGCCCAGGGATTGTGGTTGTA AGCCTTGCATATGTACAGTCCCAGAAGTATC ATCTGTCTTCATCTTCCCCCCAAAGCCCAAG GATGTGCTCACCATTACTCTGACTCCTAAGG TCACGTGTGTTGTGGTAGACATCAGCAAGGA	1011

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		TGATCCCGAGGTCCAGTTCAGCTGGTTTGTA GATGATGTGGAGGTGCACACAGCTCAGACG CAACCCCGGGAGGAGCAGTTCAACAGCACT TTCCGCTCAGTCAGTGAACTTCCCATCATGC ACCAGGACTGGCTCAATGGCAAGGAGTTCA AATGCAGGGTCAACAGTGCAGCTTTCCCTGC CCCCATCGAGAAAACCATCTCCAAAACCAA AGGCAGACCGAAGGCTCCACAGGTGTACAC CATTCCACCTCCCAAGGAGCAGATGGCCAA GGATAAAGTCAGTCTGACCTGCATGATAAC AGACTTCTTCCCTGAAGACATTACTGTGGAG TGGCAGTGGAATGGGCAGCCAGCGGAGAAC TACAAGAACACTCAGCCCATCATGAACACG AATGGCTCTTACTTCGTCTACAGCAAGCTCA ATGTGCAGAAGAGCAACTGGGAGGCAGGAA ATACTTTCACCTGCTCTGTGTTACATGAGGG CCTGCACAACCACCATACTGAGAAGAGCCT CTCCCACTCTCCTGGTAAATGA	
SM1B210	pDR000027281	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGATG TACAGCTTCAGGAGTCAGGACCTGGGCACTC CATGGTGACCCTGGGATGCCTGGTTGGGCAA AGTATACAGGCCGAGTTCCAGCTGCAGCAG TCTGGACCTGAACTAGTGAAGACTGGGGCTT CAGTGAAGATATCCTGCAAGGCTTCTGGTTA CTCTTTCACTGGTTACTACATGCACTGGGTC AAGCAGAGCCATGGAAGGAGCCTTGAGTGG ATTGGATATCTTAGTTGTTACAGTGGTGCTA CTAGCTACAACCAGAAGTTCAAGGGCAAGG CCACATTTACTGTAGACACATCCTCCACCAC AGCCTACATGCAGTTCAACAGCCTGACATCT GAAGACTCTGCGGTCTATTACTGTGCACGAG GGGAGAGCTACTATGTTATGGACTATTGGGG TCAAGGAACCTCAGTCACCGTCTCCTCAGCC AAAACGACACCCCCATCTGTCTATCCACTGG CCCCTGGATCTGCTGCCCAAACTAACTCCAT GGTGACCCTGGGATGCCTGGTCAAGGGCTAT TTCCCTGAGCCAGTGACAGTGACCTGGAACT CTGGATCCCTGTCCAGCGGTGTGCACACCTT CCCAGCTGTCCTGGAGTCTGACCTCTACACT CTGAGCAGCTCAGTGACTGTCCCCTCCAGCC CTCGGCCCAGCGAGACCGTCACCTGCAACGT TGCCCACCCGGCCAGCAGCACCAAGGTGGA CAAGAAAATTGTGCCCAGGGATTGTGGTTGT AAGCCTTGCATATGTACAGTCCCAGAAGTAT CATCTGTCTTCATCTTCCCCCCAAAGCCCAA GGATGTGCTCACCATTACTCTGACTCCTAAG GTCACGTGTGTTGTGGTAGACATCAGCAAGG	1012

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		ATGATCCCGAGGTCCAGTTCAGCTGGTTTGT AGATGATGTGGAGGTGCACACAGCTCAGAC GCAACCCCGGGAGGAGCAGTTCAACAGCAC TTTCCGCTCAGTCAGTGAACTTCCCATCATG CACCAGGACTGGCTCAATGGCAAGGAGTTC AAATGCAGGGTCAACAGTGCAGCTTTCCCTG CCCCCATCGAGAAAACCATCTCCAAAACCA AAGGCAGACCGAAGGCTCCACAGGTGTACA CCATTCCACCTCCCAAGGAGCAGATGGCCA AGGATAAAGTCAGTCTGACCTGCATGATAA CAGACTTCTTCCCTGAAGACATTACTGTGGA GTGGCAGTGGAATGGGCAGCCAGCGGAGAA CTACAAGAACACTCAGCCCATCATGAACAC GAATGGCTCTTACTTCGTCTACAGCAAGCTC AATGTGCAGAAGAGCAACTGGGAGGCAGGA AATACTTTCACCTGCTCTGTGTTACATGAGG GCCTGCACAACCACCATACTGAGAAGAGCC TCTCCCACTCTCCTGGTAAATGA	
SM1B211	pDR000027282	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAGG TTCAGCTGCAGCAGTCTGGACCTGGCCTGGT GAAGCCTTCTCAGACAGTGTCCCTCACCTGC ACTGTCACTGGCTACTCTATCACTAATGGTA ATCACTGGTGGAACTGGATCCGGCAGGTTTC AGGAAGCAAACTGGAGTGGATAGGGTACAT AAGCTCCAGTGGTAGCACTGACAGCAATCC ATCTCTCAAAAGTCGAATCTCCATCACTAGA GACACTTCCAAGAACCAGTTATTCCTGCAGT TGAACTCTGTGACTACTGAAGATATAGCCAC ATATTACTGTGCAAGAGGGCATTACTACGAT GGTAGCTCCTATGCTATGGACTACTGGGGTC AAGGAACCTCAGTCACCGTCTCCTCAGCCAA AACAACAGCCCCATCGGTCTATCCACTGGCC CCTGTGTGTGGAGATACAAGTGACTCCATGG TGACCCTGGGATGCCTGGTCAAGGGCTATTT CCCTGAGCCAGTGACAGTGACCTGGAACTCT GGATCCCTGTCCAGCGGTGTGCACACCTTCC CAGCTGTCCTGGAGTCTGACCTCTACACTCT GAGCAGCTCAGTGACTGTCCCCTCCAGCCCT CGGCCCAGCGAGACCGTCACCTGCAACGTT GCCCACCCGGCCAGCAGCACCAAGGTGGAC AAGAAAATTGTGCCCAGGGATTGTGGTTGTA AGCCTTGCATATGTACAGTCCCAGAAGTATC ATCTGTCTTCATCTTCCCCCCAAAGCCCAAG GATGTGCTCACCATTACTCTGACTCCTAAGG TCACGTGTGTTGTGGTAGACATCAGCAAGGA TGATCCCGAGGTCCAGTTCAGCTGGTTTGTA GATGATGTGGAGGTGCACACAGCTCAGACG	1013

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CAACCCCGGGAGGAGCAGTTCAACAGCACT TTCCGCTCAGTCAGTGAACTTCCCATCATGC ACCAGGACTGGCTCAATGGCAAGGAGTTCA AATGCAGGGTCAACAGTGCAGCTTTCCCTGC CCCCATCGAGAAAACCATCTCCAAAACCAA AGGCAGACCGAAGGCTCCACAGGTGTACAC CATTCCACCTCCCAAGGAGCAGATGGCCAA GGATAAAGTCAGTCTGACCTGCATGATAAC AGACTTCTTCCCTGAAGACATTACTGTGGAG TGGCAGTGGAATGGGCAGCCAGCGGAGAAC TACAAGAACACTCAGCCCATCATGAACACG AATGGCTCTTACTTCGTCTACAGCAAGCTCA ATGTGCAGAAGAGCAACTGGGAGGCAGGAA ATACTTTCACCTGCTCTGTGTTACATGAGGG CCTGCACAACCACCATACTGAGAAGAGCCT CTCCCACTCTCCTGGTAAATGA	
SM1B507	pDR000034825	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAGG TTCAGCTGCAGCAGTCTGGGGCTGAGCTGGT GAAGCCTGGGGCTTCAGTGAAGATGTCCTGT AAGGCTTCTGGATACACATTCACTGACTACT ACATGGACTGGGTGAAGCAGAGCCATGGAA AAAGCTTTGAGTGGATTGGACATGTTAATCC TTACAATGGTGATACTAGGTACAACCAGAA GTTCAAGGGCAAGGCCACATTGACTGTTGAC AAGTCCTCCACCACAGCCTACATGGAGCTCA ACAGCCTGACATCTGAGGACTCTGCGGTCTA TTACTGTGCAAGAGGGAACTTCTTTGACTAC TGGGGCCAAGGCACCACTCTCTCAGTCTCCT CAGCCAAAACGACACCCCCATCTGTCTATCC ACTGGCCCCTGGATCTGCTGCCCAAACTAAC TCCATGGTGACCCTGGGATGCCTGGTCAAGG GCTATTTCCCTGAGCCAGTGACAGTGACCTG GAACTCTGGATCCCTGTCCAGCGGTGTGCAC ACCTTCCCAGCTGTCCTGGAGTCTGACCTCT ACACTCTGAGCAGCTCAGTGACTGTCCCCTC CAGCCCTCGGCCCAGCGAGACCGTCACCTGC AACGTTGCCCACCCGGCCAGCAGCACCAAG GTGGACAAGAAAATTGTGCCCAGGGATTGT GGTTGTAAGCCTTGCATATGTACAGTCCCAG AAGTATCATCTGTCTTCATCTTCCCCCCAAA GCCCAAGGATGTGCTCACCATTACTCTGACT CCTAAGGTCACGTGTGTTGTGGTAGACATCA GCAAGGATGATCCCGAGGTCCAGTTCAGCT GGTTTGTAGATGATGTGGAGGTGCACACAG CTCAGACGCAACCCCGGGAGGAGCAGTTCA ACAGCACTTTCCGCTCAGTCAGTGAACTTCC CATCATGCACCAGGACTGGCTCAATGGCAA	1014

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GGAGTTCAAATGCAGGGTCAACAGTGCAGC TTTCCCTGCCCCCATCGAGAAAACCATCTCC AAAACCAAAGGCAGACCGAAGGCTCCACAG GTGTACACCATTCCACCTCCCAAGGAGCAGA TGGCCAAGGATAAAGTCAGTCTGACCTGCAT GATAACAGACTTCTTCCCTGAAGACATTACT GTGGAGTGGCAGTGGAATGGGCAGCCAGCG GAGAACTACAAGAACACTCAGCCCATCATG AACACGAATGGCTCTTACTTCGTCTACAGCA AGCTCAATGTGCAGAAGAGCAACTGGGAGG CAGGAAATACTTTCACCTGCTCTGTGTTACA TGAGGGCCTGCACAACCACCATACTGAGAA GAGCCTCTCCCACTCTCCTGGTAAATGA	
SM1B508	pDR000034826	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAGG TTCAGCTGCAGCAGTCTGGGGCTGAGCTGGT GAAGCCTGGGGCTTCAGTGAAGATATCCTGC AAGACTTCTGGTTACTCATTTACTGGCTACT TTATGAATTGGGTGATGCAGAGCCATGGAA AGAGCCTTGAGTGGATTGGACGTATTAATCC TTACAATGGTGATACTTTCTACAACCAGAAG TTCAAGGGCAAGGCCACATTGACTGTAGAC AAATCCTCTAGCACAGCCCACATGGAGCTCC GGAGCCTGGCATCTGAGGACTCTGCAGTCTA TTATTGTGCAAGAAGCTACGGCTATGCTATG GACTACTGGGGTCAAGGAACCTCAGTCACC GTCTCCTCAGCCAAAACGACACCCCCATCTG TCTATCCACTGGCCCCTGGATCTGCTGCCCA AACTAACTCCATGGTGACCCTGGGATGCCTG GTCAAGGGCTATTTCCCTGAGCCAGTGACAG TGACCTGGAACTCTGGATCCCTGTCCAGCGG TGTGCACACCTTCCCAGCTGTCCTGGAGTCT GACCTCTACACTCTGAGCAGCTCAGTGACTG TCCCCTCCAGCCCTCGGCCCAGCGAGACCGT CACCTGCAACGTTGCCCACCCGGCCAGCAGC ACCAAGGTGGACAAGAAAATTGTGCCCAGG GATTGTGGTTGTAAGCCTTGCATATGTACAG TCCCAGAAGTATCATCTGTCTTCATCTTCCCC CCAAAGCCCAAGGATGTGCTCACCATTACTC TGACTCCTAAGGTCACGTGTGTTGTGGTAGA CATCAGCAAGGATGATCCCGAGGTCCAGTTC AGCTGGTTTGTAGATGATGTGGAGGTGCACA CAGCTCAGACGCAACCCCGGGAGGAGCAGT TCAACAGCACTTTCCGCTCAGTCAGTGAACT TCCCATCATGCACCAGGACTGGCTCAATGGC AAGGAGTTCAAATGCAGGGTCAACAGTGCA GCTTTCCCTGCCCCCATCGAGAAAACCATCT CCAAAACCAAAGGCAGACCGAAGGCTCCAC	1015

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		AGGTGTACACCATTCCACCTCCCAAGGAGCA GATGGCCAAGGATAAAGTCAGTCTGACCTG CATGATAACAGACTTCTTCCCTGAAGACATT ACTGTGGAGTGGCAGTGGAATGGGCAGCCA GCGGAGAACTACAAGAACACTCAGCCCATC ATGAACACGAATGGCTCTTACTTCGTCTACA GCAAGCTCAATGTGCAGAAGAGCAACTGGG AGGCAGGAAATACTTTCACCTGCTCTGTGTT ACATGAGGGCCTGCACAACCACCATACTGA GAAGAGCCTCTCCCACTCTCCTGGTAAATGA	
SM1B509	pDR000034827	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCCAGG TGCAGCTGAAGGAGTCAGGACCTGGCCTGG TGGCGCCCTCACAGAGCCTGTCCATCACATG CACCGTCTCAGGGTTCTCATTAACCGGCTAT GGTGTAAACTGGGTTCGCCAGCCTCCAGGA AAGGGTCTGGAGTGGCTGGGGTTGATGTGG GGTGATGGAAGCACAGACTATAATTCAGCT CTCAACTCCAGACTGCGCATCAACAAGGAC AACTCCAAGAGTCAAGTTTTCTTAAAAATGA GCAGTCTTCAAACTGATGACACAGCCATTTA CTACTGTGTCAGAAAGGGCGGTAATAGCCC CTATGCTATGGACTACTGGGGTCAAGGAACC TCAGTCACCGTCTCCTCAGCCAAAACGACAC CCCCATCTGTCTATCCACTGGCCCCTGGATC TGCTGCCCAAACTAACTCCATGGTGACCCTG GGATGCCTGGTCAAGGGCTATTTCCCTGAGC CAGTGACAGTGACCTGGAACTCTGGATCCCT GTCCAGCGGTGTGCACACCTTCCCAGCTGTC CTGGAGTCTGACCTCTACACTCTGAGCAGCT CAGTGACTGTCCCCTCCAGCCCTCGGCCCAG CGAGACCGTCACCTGCAACGTTGCCCACCCG GCCAGCAGCACCAAGGTGGACAAGAAAATT GTGCCCAGGGATTGTGGTTGTAAGCCTTGCA TATGTACAGTCCCAGAAGTATCATCTGTCTT CATCTTCCCCCCAAAGCCCAAGGATGTGCTC ACCATTACTCTGACTCCTAAGGTCACGTGTG TTGTGGTAGACATCAGCAAGGATGATCCCG AGGTCCAGTTCAGCTGGTTTGTAGATGATGT GGAGGTGCACACAGCTCAGACGCAACCCCG GGAGGAGCAGTTCAACAGCACTTTCCGCTCA GTCAGTGAACTTCCCATCATGCACCAGGACT GGCTCAATGGCAAGGAGTTCAAATGCAGGG TCAACAGTGCAGCTTTCCCTGCCCCCATCGA GAAAACCATCTCCAAAACCAAAGGCAGACC GAAGGCTCCACAGGTGTACACCATTCCACCT CCCAAGGAGCAGATGGCCAAGGATAAAGTC AGTCTGACCTGCATGATAACAGACTTCTTCC	1016

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CTGAAGACATTACTGTGGAGTGGCAGTGGA ATGGGCAGCCAGCGGAGAACTACAAGAACA CTCAGCCCATCATGAACACGAATGGCTCTTA CTTCGTCTACAGCAAGCTCAATGTGCAGAAG AGCAACTGGGAGGCAGGAAATACTTTCACC TGCTCTGTGTTACATGAGGGCCTGCACAACC ACCATACTGAGAAGAGCCTCTCCCACTCTCC TGGTAAATGA	
SM1B510	pDR000034827	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCCAGG TGCAGCTGAAGGAGTCAGGACCTGGCCTGG TGGCGCCCTCACAGAGCCTGTCCATCACATG CACCGTCTCAGGGTTCTCATTAACCGGCTAT GGTGTAAACTGGGTTCGCCAGCCTCCAGGA AAGGGTCTGGAGTGGCTGGGGTTGATGTGG GGTGATGGAAGCACAGACTATAATTCAGCT CTCAACTCCAGACTGCGCATCAACAAGGAC AACTCCAAGAGTCAAGTTTTCTTAAAAATGA GCAGTCTTCAAACTGATGACACAGCCATTTA CTACTGTGTCAGAAAGGGCGGTAATAGCCC CTATGCTATGGACTACTGGGGTCAAGGAACC TCAGTCACCGTCTCCTCAGCCAAAACGACAC CCCCATCTGTCTATCCACTGGCCCCTGGATC TGCTGCCCAAACTAACTCCATGGTGACCCTG GGATGCCTGGTCAAGGGCTATTTCCCTGAGC CAGTGACAGTGACCTGGAACTCTGGATCCCT GTCCAGCGGTGTGCACACCTTCCCAGCTGTC CTGGAGTCTGACCTCTACACTCTGAGCAGCT CAGTGACTGTCCCCTCCAGCCCTCGGCCCAG CGAGACCGTCACCTGCAACGTTGCCCACCCG GCCAGCAGCACCAAGGTGGACAAGAAAATT GTGCCCAGGGATTGTGGTTGTAAGCCTTGCA TATGTACAGTCCCAGAAGTATCATCTGTCTT CATCTTCCCCCCAAAGCCCAAGGATGTGCTC ACCATTACTCTGACTCCTAAGGTCACGTGTG TTGTGGTAGACATCAGCAAGGATGATCCCG AGGTCCAGTTCAGCTGGTTTGTAGATGATGT GGAGGTGCACACAGCTCAGACGCAACCCCG GGAGGAGCAGTTCAACAGCACTTTCCGCTCA GTCAGTGAACTTCCCATCATGCACCAGGACT GGCTCAATGGCAAGGAGTTCAAATGCAGGG TCAACAGTGCAGCTTTCCCTGCCCCCATCGA GAAAACCATCTCCAAAACCAAAGGCAGACC GAAGGCTCCACAGGTGTACACCATTCCACCT CCCAAGGAGCAGATGGCCAAGGATAAAGTC AGTCTGACCTGCATGATAACAGACTTCTTCC CTGAAGACATTACTGTGGAGTGGCAGTGGA ATGGGCAGCCAGCGGAGAACTACAAGAACA	1017

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CTCAGCCCATCATGAACACGAATGGCTCTTA CTTCGTCTACAGCAAGCTCAATGTGCAGAAG AGCAACTGGGAGGCAGGAAATACTTTCACC TGCTCTGTGTTACATGAGGGCCTGCACAACC ACCATACTGAGAAGAGCCTCTCCCACTCTCC TGGTAAATGA	
SM1B511	pDR000034830	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAAG TGAAGCTGGTGGAGTCTGGGCCTGAGCTGGT GAAGCCTGGGGCTTCAGTGAAGATATCCTGC AAGACTTCTGGTTACTCATTTACTGGCTACT TTATGAATTGGGTGATGCAGAGCCATGGAA AGAGCCTTGAGTGGATTGGACGTATTAATCC TTACAATGGTGATACTTTCTACAACCAGAAG TTCAAGGGCAAGGCCACATTGACTGTAGAC AAATCCTCTAGCACAGCCCACATGGAGCTCC GGAGCCTGGCATCTGAGGACTCTGCAGTCTA TTATTGTGCAAGAAGCTACGGCTATGCTATG GACTACTGGGGTCAAGGAACCTCAGTCACC GTCTCCTCAGCCAAAACGACACCCCCATCTG TCTATCCACTGGCCCCTGGATCTGCTGCCCA AACTAACTCCATGGTGACCCTGGGATGCCTG GTCAAGGGCTATTTCCCTGAGCCAGTGACAG TGACCTGGAACTCTGGATCCCTGTCCAGCGG TGTGCACACCTTCCCAGCTGTCCTGGAGTCT GACCTCTACACTCTGAGCAGCTCAGTGACTG TCCCCTCCAGCCCTCGGCCCAGCGAGACCGT CACCTGCAACGTTGCCCACCCGGCCAGCAGC ACCAAGGTGGACAAGAAAATTGTGCCCAGG GATTGTGGTTGTAAGCCTTGCATATGTACAG TCCCAGAAGTATCATCTGTCTTCATCTTCCCC CCAAAGCCCAAGGATGTGCTCACCATTACTC TGACTCCTAAGGTCACGTGTGTTGTGGTAGA CATCAGCAAGGATGATCCCGAGGTCCAGTTC AGCTGGTTTGTAGATGATGTGGAGGTGCACA CAGCTCAGACGCAACCCCGGGAGGAGCAGT TCAACAGCACTTTCCGCTCAGTCAGTGAACT TCCCATCATGCACCAGGACTGGCTCAATGGC AAGGAGTTCAAATGCAGGGTCAACAGTGCA GCTTTCCCTGCCCCCATCGAGAAAACCATCT CCAAAACCAAAGGCAGACCGAAGGCTCCAC AGGTGTACACCATTCCACCTCCCAAGGAGCA GATGGCCAAGGATAAAGTCAGTCTGACCTG CATGATAACAGACTTCTTCCCTGAAGACATT ACTGTGGAGTGGCAGTGGAATGGGCAGCCA GCGGAGAACTACAAGAACACTCAGCCCATC ATGAACACGAATGGCTCTTACTTCGTCTACA GCAAGCTCAATGTGCAGAAGAGCAACTGGG	1018

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		AGGCAGGAAATACTTTCACCTGCTCTGTGTT ACATGAGGGCCTGCACAACCACCATACTGA GAAGAGCCTCTCCCACTCTCCTGGTAAATGA	
SM1B512	pDR000034830	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAAG TGAAGCTGGTGGAGTCTGGGCCTGAGCTGGT GAAGCCTGGGGCTTCAGTGAAGATATCCTGC AAGACTTCTGGTTACTCATTTACTGGCTACT TTATGAATTGGGTGATGCAGAGCCATGGAA AGAGCCTTGAGTGGATTGGACGTATTAATCC TTACAATGGTGATACTTTCTACAACCAGAAG TTCAAGGGCAAGGCCACATTGACTGTAGAC AAATCCTCTAGCACAGCCCACATGGAGCTCC GGAGCCTGGCATCTGAGGACTCTGCAGTCTA TTATTGTGCAAGAAGCTACGGCTATGCTATG GACTACTGGGGTCAAGGAACCTCAGTCACC GTCTCCTCAGCCAAAACGACACCCCCATCTG TCTATCCACTGGCCCCTGGATCTGCTGCCCA AACTAACTCCATGGTGACCCTGGGATGCCTG GTCAAGGGCTATTTCCCTGAGCCAGTGACAG TGACCTGGAACTCTGGATCCCTGTCCAGCGG TGTGCACACCTTCCCAGCTGTCCTGGAGTCT GACCTCTACACTCTGAGCAGCTCAGTGACTG TCCCCTCCAGCCCTCGGCCCAGCGAGACCGT CACCTGCAACGTTGCCCACCCGGCCAGCAGC ACCAAGGTGGACAAGAAAATTGTGCCCAGG GATTGTGGTTGTAAGCCTTGCATATGTACAG TCCCAGAAGTATCATCTGTCTTCATCTTCCCC CCAAAGCCCAAGGATGTGCTCACCATTACTC TGACTCCTAAGGTCACGTGTGTTGTGGTAGA CATCAGCAAGGATGATCCCGAGGTCCAGTTC AGCTGGTTTGTAGATGATGTGGAGGTGCACA CAGCTCAGACGCAACCCCGGGAGGAGCAGT TCAACAGCACTTTCCGCTCAGTCAGTGAACT TCCCATCATGCACCAGGACTGGCTCAATGGC AAGGAGTTCAAATGCAGGGTCAACAGTGCA GCTTTCCCTGCCCCCATCGAGAAAACCATCT CCAAAACCAAAGGCAGACCGAAGGCTCCAC AGGTGTACACCATTCCACCTCCCAAGGAGCA GATGGCCAAGGATAAAGTCAGTCTGACCTG CATGATAACAGACTTCTTCCCTGAAGACATT ACTGTGGAGTGGCAGTGGAATGGGCAGCCA GCGGAGAACTACAAGAACACTCAGCCCATC ATGAACACGAATGGCTCTTACTTCGTCTACA GCAAGCTCAATGTGCAGAAGAGCAACTGGG AGGCAGGAAATACTTTCACCTGCTCTGTGTT ACATGAGGGCCTGCACAACCACCATACTGA GAAGAGCCTCTCCCACTCTCCTGGTAAATGA	1019

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
SM1B513	pDR000034831	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAGG TTCAGCTGCAGCAGTCTGGACCTGAGCTGGT GAAGCCTGGGGCTTCAGTGAAGATATCCTGC AAGGCTTCTGGTTACTCATTTACTGGCTACT TTATGAATTGGGTGATGCAGAGCCATGGAA AGAGCCTTGAGTGGATTGGACGTATTAATCC TTACAATGGTGATACTTTCTACAACCAGAAA TTCAAGGCCAAGGCCACATTGACTGTAGAC AAATCCTCTAACACAGCCCACATGGAGCTCC GGAGCCTGGCATCTGAGGACTCTGCAGTCTA TTTTTGTGCAAGAAGTTACGGCTATGCTATG GACTACTGGGGTCTAGGAACCTCAGTCACCG TCTCCTCAGCCAAAACGACACCCCCATCTGT CTATCCACTGGCCCCTGGATCTGCTGCCCAA ACTAACTCCATGGTGACCCTGGGATGCCTGG TCAAGGGCTATTTCCCTGAGCCAGTGACAGT GACCTGGAACTCTGGATCCCTGTCCAGCGGT GTGCACACCTTCCCAGCTGTCCTGGAGTCTG ACCTCTACACTCTGAGCAGCTCAGTGACTGT CCCCTCCAGCCCTCGGCCCAGCGAGACCGTC ACCTGCAACGTTGCCCACCCGGCCAGCAGC ACCAAGGTGGACAAGAAAATTGTGCCCAGG GATTGTGGTTGTAAGCCTTGCATATGTACAG TCCCAGAAGTATCATCTGTCTTCATCTTCCCC CCAAAGCCCAAGGATGTGCTCACCATTACTC TGACTCCTAAGGTCACGTGTGTTGTGGTAGA CATCAGCAAGGATGATCCCGAGGTCCAGTTC AGCTGGTTTGTAGATGATGTGGAGGTGCACA CAGCTCAGACGCAACCCCGGGAGGAGCAGT TCAACAGCACTTTCCGCTCAGTCAGTGAACT TCCCATCATGCACCAGGACTGGCTCAATGGC AAGGAGTTCAAATGCAGGGTCAACAGTGCA GCTTTCCCTGCCCCCATCGAGAAAACCATCT CCAAAACCAAAGGCAGACCGAAGGCTCCAC AGGTGTACACCATTCCACCTCCCAAGGAGCA GATGGCCAAGGATAAAGTCAGTCTGACCTG CATGATAACAGACTTCTTCCCTGAAGACATT ACTGTGGAGTGGCAGTGGAATGGGCAGCCA GCGGAGAACTACAAGAACACTCAGCCCATC ATGAACACGAATGGCTCTTACTTCGTCTACA GCAAGCTCAATGTGCAGAAGAGCAACTGGG AGGCAGGAAATACTTTCACCTGCTCTGTGTT ACATGAGGGCCTGCACAACCACCATACTGA GAAGAGCCTCTCCCACTCTCCTGGTAAATGA	1020
SM1B514	pDR000034833	ATGGCTTGGGTGTGGACCTTGCTATTCCTGA TGGCAGCTGCCCAAAGTATACAGGCCGAGG TTCAGCTGCAGCAGTCTGGGCCTGAACTAGT	1021

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GAAGACTGGGGCTTCAGTGAAGATATCCTG CAAGGCTTCTGGTTACTCTTTCACTGGTTACT ACATGCACTGGGTCAAGCAGAGCCATGGAA AGAGCCTTGAGTGGATTGGATATCTTAGTTG TTACAGTGGTGCTACTAGCTACAACCAGAAG TTCAAGGGCAAGGCCACATTTACTGTAGACA CATCCTCCACCACAGCCTACATGCAGTTCAA CAGCCTGACATCTGAAGACTCTGCGGTCTAT TACTGTGCACGAGGGGAGAGCTACTATGTTA TGGACTATTGGGGTCAAGGAACCTCAGTCAC CGTCTCCTCAGCCAAAACGACACCCCCATCT GTCTATCCACTGGCCCCTGGATCTGCTGCCC AAACTAACTCCATGGTGACCCTGGGATGCCT GGTCAAGGGCTATTTCCCTGAGCCAGTGACA GTGACCTGGAACTCTGGATCCCTGTCCAGCG GTGTGCACACCTTCCCAGCTGTCCTGGAGTC TGACCTCTACACTCTGAGCAGCTCAGTGACT GTCCCCTCCAGCCCTCGGCCCAGCGAGACCG TCACCTGCAACGTTGCCCACCCGGCCAGCAG CACCAAGGTGGACAAGAAAATTGTGCCCAG GGATTGTGGTTGTAAGCCTTGCATATGTACA GTCCCAGAAGTATCATCTGTCTTCATCTTCC CCCCAAAGCCCAAGGATGTGCTCACCATTAC TCTGACTCCTAAGGTCACGTGTGTTGTGGTA GACATCAGCAAGGATGATCCCGAGGTCCAG TTCAGCTGGTTTGTAGATGATGTGGAGGTGC ACACAGCTCAGACGCAACCCCGGGAGGAGC AGTTCAACAGCACTTTCCGCTCAGTCAGTGA ACTTCCCATCATGCACCAGGACTGGCTCAAT GGCAAGGAGTTCAAATGCAGGGTCAACAGT GCAGCTTTCCCTGCCCCCATCGAGAAAACCA TCTCCAAAACCAAAGGCAGACCGAAGGCTC CACAGGTGTACACCATTCCACCTCCCAAGGA GCAGATGGCCAAGGATAAAGTCAGTCTGAC CTGCATGATAACAGACTTCTTCCCTGAAGAC ATTACTGTGGAGTGGCAGTGGAATGGGCAG CCAGCGGAGAACTACAAGAACACTCAGCCC ATCATGAACACGAATGGCTCTTACTTCGTCT ACAGCAAGCTCAATGTGCAGAAGAGCAACT GGGAGGCAGGAAATACTTTCACCTGCTCTGT GTTACATGAGGGCCTGCACAACCACCATACT GAGAAGAGCCTCTCCCACTCTCCTGGTAAAT GA	

Table 32. LukE Antibody Light Chain CDSs

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
SM1B208	pDR000027284	GACATTGTGATGACCCAGTCTCCGCTCTCCCT GCCTGTCAGTCTTGGAGATCAAGCCTCCATCT CTTGCAGATCTAGTCAGGACATTGTACATAG TAATGGAAACACCTATTTAGGGTGGTACCTG CAGAAACCAGGCCGGTCTCCGAAGCTCCTGA TCTACAAAGTTTCCAACCGATTTTCTGGGGTC CCAGACAGGTTCAGTGGCAGTGGATCAGGGA CAGATTTCACACTCAAGATCAGCAGAGTGGA GGCTGAGGATCTGGGAGTTTATTACTGCTTTC AAAGCTCACATTTTCCGTGGACGTTCGGTGG AGGCACCAGGCTGGAAATCAAACGGGCTGAT GCTGCACCAACTGTATCCATCTTCCCACCATC CAGTGAGCAGTTAACATCTGGAGGTGCCTCA GTCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGGC AGTGAACGACAAAATGGCGTCCTGAACAGTT GGACTGATCAGGACAGCAAAGACAGCACCT ACAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATACC TGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTG T	1022
SM1B209	pDR000027285	GATGTTGTGATGACCCAAACTCCACTCTCCCT GCCTGTCAGTCTTGGAGATCAAGCCTCCATCT CTTGCAGATCTAGTCAGGACATTGTACATAG TAATGGAAACACCTATTTAGGGTGGTACCTG CAGAAACCAGGCCGGTCTCCGAAGCTCCTGA TCTACAAAGTTTCCAACCGATTTTCTGGGGTC CCAGACAGGTTCAGTGGCAGTGGATCAGGGA CAGATTTCACACTCAAGATCAGCAGAGTGGA GGCTGAGGATCTGGGAGTTTATTACTGCTTTC AAAGCTCACATTTTCCGTGGACGTTCGGTGG AGGCACCAGGCTGGAAATCAAACGGGCTGAT GCTGCACCAACTGTATCCATCTTCCCACCATC CAGTGAGCAGTTAACATCTGGAGGTGCCTCA GTCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGGC AGTGAACGACAAAATGGCGTCCTGAACAGTT GGACTGATCAGGACAGCAAAGACAGCACCT ACAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATACC TGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTG T	1023
SM1B210	pDR000027283	GATATTGTGCTAACTCAGTCTCCACTCTCCCT GCCTGTCAGTCTTGGAGATCAAGCCTCCATCT	1024

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		CTTGCAGATCTAGTCAGAGCCTTGTACACAG TAATGGAAACACCTATTTACATTGGTACCTG CAGAAGCCAGGCCAGTCTCCAAAGCTCCTGA TCTACAAAGTTTCCAACCGATTTTCTGGGGTC CCAGACAGGTTCAGTGGCAGTGGATCAGGGA CAGATTTCACACTCAAGATCAGCAGAGTGGA GGCTGAGGATCTGGGAGTTTATTTCTGCTCTC AAAGTACACATGTTCCATTCACGTTCGGCTC GGGGACAAAGTTGGAAATAAAACGGGCTGA TGCTGCACCAACTGTATCCATCTTCCCACCAT CCAGTGAGCAGTTAACATCTGGAGGTGCCTC AGTCGTGTGCTTCTTGAACAACTTCTACCCCA AAGACATCAATGTCAAGTGGAAGATTGATGG CAGTGAACGACAAAATGGCGTCCTGAACAGT TGGACTGATCAGGACAGCAAAGACAGCACCT ACAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATACC TGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTG T	
SM1B211	pDR000027286	GATATTGTGCTAACTCAGTCTCCAGCTTCTTT GGCTGTGTCTCTAGGGCAGAGGGCCACCATA TCCTGCAGAGCCAGTGAAAGTGTTGATAGTT ATGGCAATAGTTTTATGCACTGGTACCAGCA GAAACCAGGACAGCCACCCAAACTCCTCATC TATCGTGCATCCAACCTAGAATCTGGGATCC CTGCCAGGTTCAGTGGCAGTGGGTCTAGGAC AGACTTCACCCTCACCATTAATCCTGTGGAG GCTGATGATGTTGCAACCTATTACTGTCAGC AAAGTAATGAGGATCCGCTCACGTTCGGTGC TGGGACCAAGCTGGAGCTGAAACGGGCTGAT GCTGCACCAACTGTATCCATCTTCCCACCATC CAGTGAGCAGTTAACATCTGGAGGTGCCTCA GTCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGGC AGTGAACGACAAAATGGCGTCCTGAACAGTT GGACTGATCAGGACAGCAAAGACAGCACCT ACAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATACC TGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTG T	1025
SM1B507	pDR000034834	GACATTGTGATGACCCAGTCTCCAGCAATCA TGTCTGCATCTCCAGGGGAGAAGGTCACCAT ACCCTGCAGTGCCAGTTCAAGTGTAAGTTAC ATGCACTGGTTCCAGCAGAAGCCAGGCACTT CCCCCAAACTCTGGATTTATAGCACATCCAA CCTGGCTTCTGGAGTCCCTGGTCGCTTCAGTG	1026

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		GCAGTGGATCTGGGACCTCTTACTCTCTCACA ATCAGCCGAATGGAGGCTGAAGATGCTGCCA CTTATTACTGCCAGCAAAGGAGTAATTACCC GCTCACGTTCGGTGCTGGGACCAAGCTGGAG CTGAAACGGGCTGATGCTGCACCAACTGTAT CCATCTTCCCACCATCCAGTGAGCAGTTAAC ATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGA ACAACTTCTACCCCAAAGACATCAATGTCAA GTGGAAGATTGATGGCAGTGAACGACAAAAT GGCGTCCTGAACAGTTGGACTGATCAGGACA GCAAAGACAGCACCTACAGCATGAGCAGCA CCCTCACGTTGACCAAGGACGAGTATGAACG ACATAACAGCTATACCTGTGAGGCCACTCAC AAGACATCAACTTCACCCATTGTCAAGAGCT TCAACAGGAATGAGTGT	
SM1B508	pDR000034835	GATGTTGTGATGACCCAAACTCCACTCTCCCT GCCTGTCAGTCTTGGAGATCAAGCCTCCATCT CTTGCAGATCTAGTCAGACCATTGTACATAG TAATGGAAACACCTATTTAGAATGGTACCTG CAGAAACCAGGCCAGTCTCCAAAGCTCCTGA TCTACAAAGTTTCCAACCGATTTTCTGGGGTC CCAGACAGGTTCAGTGGCAGTGGATCAGGGA CAGATTTCACACTCAAGATCAGCCGAGTGGA GGCTGAGGATCTGGGAGTTTATTACTGCTTTC AAGGTTCACATGTTCCGTTCACGTTCGGAGG GGGGACCAAGCTGGAAATAAGACGGGCTGA TGCTGCACCAACTGTATCCATCTTCCCACCAT CCAGTGAGCAGTTAACATCTGGAGGTGCCTC AGTCGTGTGCTTCTTGAACAACTTCTACCCCA AAGACATCAATGTCAAGTGGAAGATTGATGG CAGTGAACGACAAAATGGCGTCCTGAACAGT TGGACTGATCAGGACAGCAAAGACAGCACCT ACAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATACC TGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTG T	1027
SM1B509	pDR000034836	GATATTGTGATGACTCAGGCTGCAGCAATCA TGTCTGCATCTCCTGGGGAGAAGGTCACCTT GACCTGCAGTGCCAGTTCAAGTGTAAGTTCC AGCTACTTGTACTGGTACCAGCAGAAGCCAG GATCCTCCCCCAAACTCTGGATTTATAGCAC ATCCAACCTGGCTTCTGGAGTCCCTGCTCGCT TCAGTGGCAGTGGGTCTGGGACCTCTTACTCT CTCACAATCAGCAGCATGGAGGCTGAAGATG CTGCCTCTTATTTCTGCCATCAGTGGACTACT TTCCCACCCACGTTCGGAGGGGGGACCAAGC TGGAAATAAAACGGGCTGATGCTGCACCAAC	1028

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		TGTATCCATCTTCCCACCATCCAGTGAGCAGT TAACATCTGGAGGTGCCTCAGTCGTGTGCTTC TTGAACAACTTCTACCCCAAAGACATCAATG TCAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAG GACAGCAAAGACAGCACCTACAGCATGAGC AGCACCCTCACGTTGACCAAGGACGAGTATG AACGACATAACAGCTATACCTGTGAGGCCAC TCACAAGACATCAACTTCACCCATTGTCAAG AGCTTCAACAGGAATGAGTGT	
SM1B510	pDR000034838	GATGTTGTGATGACCCAAACTCCACTCTCCCT GCCTGTCAGTCTTGGAGATCAAGCCTCCATCT CTTGCAGATCTAGTCAGAGCCTTGTACACAG TAATGGAAACACCTATTTACATTGGTACCTG CAGAAGCCAGGCCAGTCTCCAAAGCTCCTGA TCTACAAAGTTTCCAACCGATTTTCTGGGGTC CCAGACAGGTTCAGTGGCAGTGGATCAGGGA CAGATTTCACACTCAAGATCAGCAGAGTGGA GGCTGAGGATCTGGGAGTTTATTTCTGCTCTC AAAGTACACATGTTCCTCCGACGTTCGGTGG AGGCACCAAGCTGGAAATCAAACGGGCTGAT GCTGCACCAACTGTATCCATCTTCCCACCATC CAGTGAGCAGTTAACATCTGGAGGTGCCTCA GTCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGGC AGTGAACGACAAAATGGCGTCCTGAACAGTT GGACTGATCAGGACAGCAAAGACAGCACCT ACAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATACC TGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTG T	1029
SM1B511	pDR000034839	GATGTTGTGATGACCCAAACTCCACTCTCCCT GCCTGTCAGTCTTGGAGATCAAGCCTCCATCT CTTGCAGATCTAGTCAGAGCCTTGTACACAG TAATGGAAACACCTATTTACATTGGTACCTG CAGAAGCCAGGCCAGTCTCCAAAGCTCCTGA TCTACAAAGTTTCCAACCGATTTTCTGGGGTC CCAGACAGGTTCAGTGGCAGTGGATCAGGGA CAGATTTCACACTCAAGATCAGCAGAGTGGA GGCTGAGGATCTGGGAGTTTATTTCTGCTCTC AAAGTACACATGTTCCTCTCACGTTCGGTGCT GGGACCAAGCTGGAGCTGAAACGGGCTGAT GCTGCACCAACTGTATCCATCTTCCCACCATC CAGTGAGCAGTTAACATCTGGAGGTGCCTCA GTCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGGC AGTGAACGACAAAATGGCGTCCTGAACAGTT	1030

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		GGACTGATCAGGACAGCAAAGACAGCACCT ACAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATACC TGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTG T	
SM1B512	pDR000034840	GACATCAAGATGACCCAGTCTCCACTCTCCC TGCCTGTCAGTCTTGGAGATCAAGCCTCCATC TCTTGCAGATCTAGTCAGACCATTGTACATA GTAATGGAAACACCTATTTAGAATGGTACCT GCAGAAACCAGGCCAGTCTCCAAAGCTCCTG ATCTACAAAGTTTCCAACCGATTTTCTGGGGT CCCAGACAGGTTCAGTGGCAGTGGATCAGGG ACAGATTTCACACTCAAGATCAGCCGAGTGG AGGCTGAGGATCTGGGAGTTTATTACTGCTTT CAAGGTTCACATGTTCCGTTCACGTTCGGAG GGGGGACCAAGCTGGAAATAAGACGGGCTG ATGCTGCACCAACTGTATCCATCTTCCCACCA TCCAGTGAGCAGTTAACATCTGGAGGTGCCT CAGTCGTGTGCTTCTTGAACAACTTCTACCCC AAAGACATCAATGTCAAGTGGAAGATTGATG GCAGTGAACGACAAAATGGCGTCCTGAACAG TTGGACTGATCAGGACAGCAAAGACAGCACC TACAGCATGAGCAGCACCCTCACGTTGACCA AGGACGAGTATGAACGACATAACAGCTATAC CTGTGAGGCCACTCACAAGACATCAACTTCA CCCATTGTCAAGAGCTTCAACAGGAATGAGT GT	1031
SM1B513	pDR000034841	GATATTGTGCTAACTCAGTCTCCAGCAATCAT GTCTGCATCTCCAGGGGAGAAGGTCACCATA ACCTGCAGTGCCAGCTCAAGTGTAAGTTACA TGCACTGGTTCCAGCAGAAGCCAGGCACTTC TCCCAAACTCTGGATTTATAGCACATCCAAC CTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGG CAGTGGATCTGGGACCTCTTACTCTCTCACAA TCAGCCGAATGGAGGCTGAAGATGCTGCCAC TTATTACTGCCAGCAAAGGAGTAGTTACCCG TGGACGTTCGGTGGAGGCACCAAGCTGGAAA TCAAACGGGCTGATGCTGCACCAACTGTATC CATCTTCCCACCATCCAGTGAGCAGTTAACA TCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAA CAACTTCTACCCCAAAGACATCAATGTCAAG TGGAAGATTGATGGCAGTGAACGACAAAATG GCGTCCTGAACAGTTGGACTGATCAGGACAG CAAAGACAGCACCTACAGCATGAGCAGCACC CTCACGTTGACCAAGGACGAGTATGAACGAC ATAACAGCTATACCTGTGAGGCCACTCACAA GACATCAACTTCACCCATTGTCAAGAGCTTC	1032

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		AACAGGAATGAGTGT	
SM1B514	pDR000034843	GACATTGTGATGACCCAGTCTCCATCTTCCAT GTATGCATCTCTAGGAGAGAGAGTCACTATC ACTTGCAAGGCGAGTCAGGACATTAATAGCT ATTTAAGCTGGTTCCAGCAGAAACCAGGAAA ATCTCCTAAGACCCTGATCTATCGTGCAAAC AGATTGGTAGATGGGGTCCCATCAAGGTTCA GTGGCAGTGGATCTGGGCAAGATTATTCTCT CACCATCAGCAGCCTGGAGTATGAAGATATG GGAATTTATTATTGTCTACAGTATGATGAGTT TCCGTACACGTTCGGAGGGGGGACCAAGCTG GAAATAAAACGGGCTGATGCTGCACCAACTG TATCCATCTTCCCACCATCCAGTGAGCAGTTA ACATCTGGAGGTGCCTCAGTCGTGTGCTTCTT GAACAACTTCTACCCCAAAGACATCAATGTC AAGTGGAAGATTGATGGCAGTGAACGACAA AATGGCGTCCTGAACAGTTGGACTGATCAGG ACAGCAAAGACAGCACCTACAGCATGAGCA GCACCCTCACGTTGACCAAGGACGAGTATGA ACGACATAACAGCTATACCTGTGAGGCCACT CACAAGACATCAACTTCACCCATTGTCAAGA GCTTCAACAGGAATGAGTGT	1033

Table 33. LukE Antibody Light Chain Primary Transcripts

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
SM1B208	pDR000027284	ATGGAGACACATTCTCAGGTCTTTGTATACAT GTTGCTGTGGTTGTCTGGTGTCGAGGGCGAC ATTGTGATGACCCAGTCTCCGCTCTCCCTGCC TGTCAGTCTTGGAGATCAAGCCTCCATCTCTT GCAGATCTAGTCAGGACATTGTACATAGTAA TGGAAACACCTATTTAGGGTGGTACCTGCAG AAACCAGGCCGGTCTCCGAAGCTCCTGATCT ACAAAGTTTCCAACCGATTTTCTGGGGTCCC AGACAGGTTCAGTGGCAGTGGATCAGGGACA GATTTCACACTCAAGATCAGCAGAGTGGAGG CTGAGGATCTGGGAGTTTATTACTGCTTTCAA AGCTCACATTTTCCGTGGACGTTCGGTGGAG GCACCAGGCTGGAAATCAAACGGGCTGATGC TGCACCAACTGTATCCATCTTCCCACCATCCA GTGAGCAGTTAACATCTGGAGGTGCCTCAGT CGTGTGCTTCTTGAACAACTTCTACCCCAAAG ACATCAATGTCAAGTGGAAGATTGATGGCAG TGAACGACAAAATGGCGTCCTGAACAGTTGG ACTGATCAGGACAGCAAAGACAGCACCTACA	1034

		GCATGAGCAGCACCCTCACGTTGACCAAGGA CGAGTATGAACGACATAACAGCTATACCTGT GAGGCCACTCACAAGACATCAACTTCACCCA TTGTCAAGAGCTTCAACAGGAATGAGTGTTA G	
SM1B209	pDR000027285	ATGGAGACACATTCTCAGGTCTTTGTATACAT GTTGCTGTGGTTGTCTGGTGTCGAGGGCGAT GTTGTGATGACCCAAACTCCACTCTCCCTGCC TGTCAGTCTTGGAGATCAAGCCTCCATCTCTT GCAGATCTAGTCAGGACATTGTACATAGTAA TGGAAACACCTATTTAGGGTGGTACCTGCAG AAACCAGGCCGGTCTCCGAAGCTCCTGATCT ACAAAGTTTCCAACCGATTTTCTGGGGTCCC AGACAGGTTCAGTGGCAGTGGATCAGGGACA GATTTCACACTCAAGATCAGCAGAGTGGAGG CTGAGGATCTGGGAGTTTATTACTGCTTTCAA AGCTCACATTTTCCGTGGACGTTCGGTGGAG GCACCAGGCTGGAAATCAAACGGGCTGATGC TGCACCAACTGTATCCATCTTCCCACCATCCA GTGAGCAGTTAACATCTGGAGGTGCCTCAGT CGTGTGCTTCTTGAACAACTTCTACCCCAAAG ACATCAATGTCAAGTGGAAGATTGATGGCAG TGAACGACAAAATGGCGTCCTGAACAGTTGG ACTGATCAGGACAGCAAAGACAGCACCTACA GCATGAGCAGCACCCTCACGTTGACCAAGGA CGAGTATGAACGACATAACAGCTATACCTGT GAGGCCACTCACAAGACATCAACTTCACCCA TTGTCAAGAGCTTCAACAGGAATGAGTGTTA G	1035
SM1B210	pDR000027283	ATGGAGACACATTCTCAGGTCTTTGTATACAT GTTGCTGTGGTTGTCTGGTGTCGAGGGCGAT ATTGTGCTAACTCAGTCTCCACTCTCCCTGCC TGTCAGTCTTGGAGATCAAGCCTCCATCTCTT GCAGATCTAGTCAGAGCCTTGTACACAGTAA TGGAAACACCTATTTACATTGGTACCTGCAG AAGCCAGGCCAGTCTCCAAAGCTCCTGATCT ACAAAGTTTCCAACCGATTTTCTGGGGTCCC AGACAGGTTCAGTGGCAGTGGATCAGGGACA GATTTCACACTCAAGATCAGCAGAGTGGAGG CTGAGGATCTGGGAGTTTATTTCTGCTCTCAA AGTACACATGTTCCATTCACGTTCGGCTCGG GGACAAAGTTGGAAATAAAACGGGCTGATG CTGCACCAACTGTATCCATCTTCCCACCATCC AGTGAGCAGTTAACATCTGGAGGTGCCTCAG TCGTGTGCTTCTTGAACAACTTCTACCCCAAA GACATCAATGTCAAGTGGAAGATTGATGGCA GTGAACGACAAAATGGCGTCCTGAACAGTTG GACTGATCAGGACAGCAAAGACAGCACCTAC AGCATGAGCAGCACCCTCACGTTGACCAAGG ACGAGTATGAACGACATAACAGCTATACCTG TGAGGCCACTCACAAGACATCAACTTCACCC	1036

		ATTGTCAAGAGCTTCAACAGGAATGAGTGTT AG	
SM1B211	pDR000027286	ATGGAGACACATTCTCAGGTCTTTGTATACAT GTTGCTGTGGTTGTCTGGTGTCGAGGGCGAT ATTGTGCTAACTCAGTCTCCAGCTTCTTTGGC TGTGTCTCTAGGGCAGAGGGCCACCATATCC TGCAGAGCCAGTGAAAGTGTTGATAGTTATG GCAATAGTTTTATGCACTGGTACCAGCAGAA ACCAGGACAGCCACCCAAACTCCTCATCTAT CGTGCATCCAACCTAGAATCTGGGATCCCTG CCAGGTTCAGTGGCAGTGGGTCTAGGACAGA CTTCACCCTCACCATTAATCCTGTGGAGGCTG ATGATGTTGCAACCTATTACTGTCAGCAAAG TAATGAGGATCCGCTCACGTTCGGTGCTGGG ACCAAGCTGGAGCTGAAACGGGCTGATGCTG CACCAACTGTATCCATCTTCCCACCATCCAGT GAGCAGTTAACATCTGGAGGTGCCTCAGTCG TGTGCTTCTTGAACAACTTCTACCCCAAAGAC ATCAATGTCAAGTGGAAGATTGATGGCAGTG AACGACAAAATGGCGTCCTGAACAGTTGGAC TGATCAGGACAGCAAAGACAGCACCTACAGC ATGAGCAGCACCCTCACGTTGACCAAGGACG AGTATGAACGACATAACAGCTATACCTGTGA GGCCACTCACAAGACATCAACTTCACCCATT GTCAAGAGCTTCAACAGGAATGAGTGTTAG	1037
SM1B507	pDR000034834	ATGGAGACACATTCTCAGGTCTTTGTATACAT GTTGCTGTGGTTGTCTGGTGTCGAGGGCGAC ATTGTGATGACCCAGTCTCCAGCAATCATGT CTGCATCTCCAGGGGAGAAGGTCACCATACC CTGCAGTGCCAGTTCAAGTGTAAGTTACATG CACTGGTTCCAGCAGAAGCCAGGCACTTCCC CCAAACTCTGGATTTATAGCACATCCAACCT GGCTTCTGGAGTCCCTGGTCGCTTCAGTGGC AGTGGATCTGGGACCTCTTACTCTCTCACAAT CAGCCGAATGGAGGCTGAAGATGCTGCCACT TATTACTGCCAGCAAAGGAGTAATTACCCGC TCACGTTCGGTGCTGGGACCAAGCTGGAGCT GAAACGGGCTGATGCTGCACCAACTGTATCC ATCTTCCCACCATCCAGTGAGCAGTTAACAT CTGGAGGTGCCTCAGTCGTGTGCTTCTTGAAC AACTTCTACCCCAAAGACATCAATGTCAAGT GGAAGATTGATGGCAGTGAACGACAAAATG GCGTCCTGAACAGTTGGACTGATCAGGACAG CAAAGACAGCACCTACAGCATGAGCAGCACC CTCACGTTGACCAAGGACGAGTATGAACGAC ATAACAGCTATACCTGTGAGGCCACTCACAA GACATCAACTTCACCCATTGTCAAGAGCTTC AACAGGAATGAGTGTTAG	1038
SM1B508	pDR000034835	ATGGAGACACATTCTCAGGTCTTTGTATACAT GTTGCTGTGGTTGTCTGGTGTCGAGGGCGAT GTTGTGATGACCCAAACTCCACTCTCCCTGCC	1039

		TGTCAGTCTTGGAGATCAAGCCTCCATCTCTT GCAGATCTAGTCAGACCATTGTACATAGTAA TGGAAACACCTATTTAGAATGGTACCTGCAG AAACCAGGCCAGTCTCCAAAGCTCCTGATCT ACAAAGTTTCCAACCGATTTTCTGGGGTCCC AGACAGGTTCAGTGGCAGTGGATCAGGGACA GATTTCACACTCAAGATCAGCCGAGTGGAGG CTGAGGATCTGGGAGTTTATTACTGCTTTCAA GGTTCACATGTTCCGTTCACGTTCGGAGGGG GGACCAAGCTGGAAATAAGACGGGCTGATG CTGCACCAACTGTATCCATCTTCCCACCATCC AGTGAGCAGTTAACATCTGGAGGTGCCTCAG TCGTGTGCTTCTTGAACAACTTCTACCCCAAA GACATCAATGTCAAGTGGAAGATTGATGGCA GTGAACGACAAAATGGCGTCCTGAACAGTTG GACTGATCAGGACAGCAAAGACAGCACCTAC AGCATGAGCAGCACCCTCACGTTGACCAAGG ACGAGTATGAACGACATAACAGCTATACCTG TGAGGCCACTCACAAGACATCAACTTCACCC ATTGTCAAGAGCTTCAACAGGAATGAGTGTT AG	
SM1B509	pDR000034836	ATGGAGACACATTCTCAGGTCTTTGTATACAT GTTGCTGTGGTTGTCTGGTGTCGAGGGCGAT ATTGTGATGACTCAGGCTGCAGCAATCATGT CTGCATCTCCTGGGGAGAAGGTCACCTTGAC CTGCAGTGCCAGTTCAAGTGTAAGTTCCAGC TACTTGTACTGGTACCAGCAGAAGCCAGGAT CCTCCCCCAAACTCTGGATTTATAGCACATCC AACCTGGCTTCTGGAGTCCCTGCTCGCTTCAG TGGCAGTGGGTCTGGGACCTCTTACTCTCTCA CAATCAGCAGCATGGAGGCTGAAGATGCTGC CTCTTATTTCTGCCATCAGTGGACTACTTTCC CACCCACGTTCGGAGGGGGGACCAAGCTGGA AATAAAACGGGCTGATGCTGCACCAACTGTA TCCATCTTCCCACCATCCAGTGAGCAGTTAAC ATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGA ACAACTTCTACCCCAAAGACATCAATGTCAA GTGGAAGATTGATGGCAGTGAACGACAAAAT GGCGTCCTGAACAGTTGGACTGATCAGGACA GCAAAGACAGCACCTACAGCATGAGCAGCA CCCTCACGTTGACCAAGGACGAGTATGAACG ACATAACAGCTATACCTGTGAGGCCACTCAC AAGACATCAACTTCACCCATTGTCAAGAGCT TCAACAGGAATGAGTGTTAG	1040
SM1B510	pDR000034838	ATGGAGACACATTCTCAGGTCTTTGTATACAT GTTGCTGTGGTTGTCTGGTGTCGAGGGCGAT GTTGTGATGACCCAAACTCCACTCTCCCTGCC TGTCAGTCTTGGAGATCAAGCCTCCATCTCTT GCAGATCTAGTCAGAGCCTTGTACACAGTAA TGGAAACACCTATTTACATTGGTACCTGCAG AAGCCAGGCCAGTCTCCAAAGCTCCTGATCT	1041

		ACAAAGTTTCCAACCGATTTTCTGGGGTCCC AGACAGGTTCAGTGGCAGTGGATCAGGGACA GATTTCACACTCAAGATCAGCAGAGTGGAGG CTGAGGATCTGGGAGTTTATTTCTGCTCTCAA AGTACACATGTTCCTCCGACGTTCGGTGGAG GCACCAAGCTGGAAATCAAACGGGCTGATGC TGCACCAACTGTATCCATCTTCCCACCATCCA GTGAGCAGTTAACATCTGGAGGTGCCTCAGT CGTGTGCTTCTTGAACAACTTCTACCCCAAAG ACATCAATGTCAAGTGGAAGATTGATGGCAG TGAACGACAAAATGGCGTCCTGAACAGTTGG ACTGATCAGGACAGCAAAGACAGCACCTACA GCATGAGCAGCACCCTCACGTTGACCAAGGA CGAGTATGAACGACATAACAGCTATACCTGT GAGGCCACTCACAAGACATCAACTTCACCCA TTGTCAAGAGCTTCAACAGGAATGAGTGTTA G	
SM1B511	pDR000034839	ATGGAGACACATTCTCAGGTCTTTGTATACAT GTTGCTGTGGTTGTCTGGTGTCGAGGGCGAT GTTGTGATGACCCAAACTCCACTCTCCCTGCC TGTCAGTCTTGGAGATCAAGCCTCCATCTCTT GCAGATCTAGTCAGAGCCTTGTACACAGTAA TGGAAACACCTATTTACATTGGTACCTGCAG AAGCCAGGCCAGTCTCCAAAGCTCCTGATCT ACAAAGTTTCCAACCGATTTTCTGGGGTCCC AGACAGGTTCAGTGGCAGTGGATCAGGGACA GATTTCACACTCAAGATCAGCAGAGTGGAGG CTGAGGATCTGGGAGTTTATTTCTGCTCTCAA AGTACACATGTTCCTCTCACGTTCGGTGCTGG GACCAAGCTGGAGCTGAAACGGGCTGATGCT GCACCAACTGTATCCATCTTCCCACCATCCAG TGAGCAGTTAACATCTGGAGGTGCCTCAGTC GTGTGCTTCTTGAACAACTTCTACCCCAAAG ACATCAATGTCAAGTGGAAGATTGATGGCAG TGAACGACAAAATGGCGTCCTGAACAGTTGG ACTGATCAGGACAGCAAAGACAGCACCTACA GCATGAGCAGCACCCTCACGTTGACCAAGGA CGAGTATGAACGACATAACAGCTATACCTGT GAGGCCACTCACAAGACATCAACTTCACCCA TTGTCAAGAGCTTCAACAGGAATGAGTGTTA G	1042
SM1B512	pDR000034840	ATGGAGACACATTCTCAGGTCTTTGTATACAT GTTGCTGTGGTTGTCTGGTGTCGAGGGCGAC ATCAAGATGACCCAGTCTCCACTCTCCCTGCC TGTCAGTCTTGGAGATCAAGCCTCCATCTCTT GCAGATCTAGTCAGACCATTGTACATAGTAA TGGAAACACCTATTTAGAATGGTACCTGCAG AAACCAGGCCAGTCTCCAAAGCTCCTGATCT ACAAAGTTTCCAACCGATTTTCTGGGGTCCC AGACAGGTTCAGTGGCAGTGGATCAGGGACA GATTTCACACTCAAGATCAGCCGAGTGGAGG	1043

		CTGAGGATCTGGGAGTTTATTACTGCTTTCAA GGTTCACATGTTCCGTTCACGTTCGGAGGGG GGACCAAGCTGGAAATAAGACGGGCTGATG CTGCACCAACTGTATCCATCTTCCCACCATCC AGTGAGCAGTTAACATCTGGAGGTGCCTCAG TCGTGTGCTTCTTGAACAACTTCTACCCCAAA GACATCAATGTCAAGTGGAAGATTGATGGCA GTGAACGACAAAATGGCGTCCTGAACAGTTG GACTGATCAGGACAGCAAAGACAGCACCTAC AGCATGAGCAGCACCCTCACGTTGACCAAGG ACGAGTATGAACGACATAACAGCTATACCTG TGAGGCCACTCACAAGACATCAACTTCACCC ATTGTCAAGAGCTTCAACAGGAATGAGTGTT AG	
SM1B513	pDR000034841	ATGGAGACACATTCTCAGGTCTTTGTATACAT GTTGCTGTGGTTGTCTGGTGTCGAGGGCGAT ATTGTGCTAACTCAGTCTCCAGCAATCATGTC TGCATCTCCAGGGGAGAAGGTCACCATAACC TGCAGTGCCAGCTCAAGTGTAAGTTACATGC ACTGGTTCCAGCAGAAGCCAGGCACTTCTCC CAAACTCTGGATTTATAGCACATCCAACCTG GCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAG TGGATCTGGGACCTCTTACTCTCTCACAATCA GCCGAATGGAGGCTGAAGATGCTGCCACTTA TTACTGCCAGCAAAGGAGTAGTTACCCGTGG ACGTTCGGTGGAGGCACCAAGCTGGAAATCA AACGGGCTGATGCTGCACCAACTGTATCCAT CTTCCCACCATCCAGTGAGCAGTTAACATCT GGAGGTGCCTCAGTCGTGTGCTTCTTGAACA ACTTCTACCCCAAAGACATCAATGTCAAGTG GAAGATTGATGGCAGTGAACGACAAAATGG CGTCCTGAACAGTTGGACTGATCAGGACAGC AAAGACAGCACCTACAGCATGAGCAGCACCC TCACGTTGACCAAGGACGAGTATGAACGACA TAACAGCTATACCTGTGAGGCCACTCACAAG ACATCAACTTCACCCATTGTCAAGAGCTTCA ACAGGAATGAGTGTTAG	1044
SM1B514	pDR000034843	ATGGAGACACATTCTCAGGTCTTTGTATACAT GTTGCTGTGGTTGTCTGGTGTCGAGGGCGAC ATTGTGATGACCCAGTCTCCATCTTCCATGTA TGCATCTCTAGGAGAGAGAGTCACTATCACT TGCAAGGCGAGTCAGGACATTAATAGCTATT TAAGCTGGTTCCAGCAGAAACCAGGAAAATC TCCTAAGACCCTGATCTATCGTGCAAACAGA TTGGTAGATGGGGTCCCATCAAGGTTCAGTG GCAGTGGATCTGGGCAAGATTATTCTCTCAC CATCAGCAGCCTGGAGTATGAAGATATGGGA ATTTATTATTGTCTACAGTATGATGAGTTTCC GTACACGTTCGGAGGGGGGACCAAGCTGGA AATAAAACGGGCTGATGCTGCACCAACTGTA TCCATCTTCCCACCATCCAGTGAGCAGTTAAC	1045

		ATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGA ACAACTTCTACCCCAAAGACATCAATGTCAA GTGGAAGATTGATGGCAGTGAACGACAAAAT GGCGTCCTGAACAGTTGGACTGATCAGGACA GCAAAGACAGCACCTACAGCATGAGCAGCA CCCTCACGTTGACCAAGGACGAGTATGAACG ACATAACAGCTATACCTGTGAGGCCACTCAC AAGACATCAACTTCACCCATTGTCAAGAGCT TCAACAGGAATGAGTGTTAG	

Table 34. LukD Antibody Heavy Chain CDSs

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
SM1B221	pDR000028067	CAGGTTCAGCTGCAGCAGTCTGGGGCTGAGC TTGTGATGCCTGGGGCTTCAGTGAAGATGTC CTGCAAGGCTTCTGGCTACACATTCACTGACT ACTGGATGCACTGGGTGAAGCAGAGGCCTGG ACAAGGCCTTGAGTGGATCGGAGCGATTGAT ACTTCTGATAGTTATACTAGCTACAATCAAA AGTTCAAGGGCAAGGCCACATTGACTGTAGA CGAATCCTCCAGCACAGCCTACATGCAGCTC AGCAGCCTGACATCTGAGGACTCTGCGGTCT ATTACTGTGCAAGGGACTACGGCTACGCTAT GGACTACTGGGGTCAAGGAACCTCAGTCACC GTCTCCTCAGCCAAAACGACACCCCCATCTG TCTATCCACTGGCCCCTGGATCTGCTGCCCAA ACTAACTCCATGGTGACCCTGGGATGCCTGG TCAAGGGCTATTTCCCTGAGCCAGTGACAGT GACCTGGAACTCTGGATCCCTGTCCAGCGGT GTGCACACCTTCCCAGCTGTCCTGGAGTCTG ACCTCTACACTCTGAGCAGCTCAGTGACTGT CCCCTCCAGCCCTCGGCCCAGCGAGACCGTC ACCTGCAACGTTGCCCACCCGGCCAGCAGCA CCAAGGTGGACAAGAAAATTGTGCCCAGGG ATTGTGGTTGTAAGCCTTGCATATGTACAGTC CCAGAAGTATCATCTGTCTTCATCTTCCCCCC AAAGCCCAAGGATGTGCTCACCATTACTCTG ACTCCTAAGGTCACGTGTGTTGTGGTAGACA TCAGCAAGGATGATCCCGAGGTCCAGTTCAG CTGGTTTGTAGATGATGTGGAGGTGCACACA GCTCAGACGCAACCCCGGGAGGAGCAGTTCA ACAGCACTTTCCGCTCAGTCAGTGAACTTCCC ATCATGCACCAGGACTGGCTCAATGGCAAGG AGTTCAAATGCAGGGTCAACAGTGCAGCTTT CCCTGCCCCCATCGAGAAAACCATCTCCAAA ACCAAAGGCAGACCGAAGGCTCCACAGGTGT ACACCATTCCACCTCCCAAGGAGCAGATGGC CAAGGATAAAGTCAGTCTGACCTGCATGATA	1046

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		ACAGACTTCTTCCCTGAAGACATTACTGTGG AGTGGCAGTGGAATGGGCAGCCAGCGGAGA ACTACAAGAACACTCAGCCCATCATGAACAC GAATGGCTCTTACTTCGTCTACAGCAAGCTC AATGTGCAGAAGAGCAACTGGGAGGCAGGA AATACTTTCACCTGCTCTGTGTTACATGAGGG CCTGCACAACCACCATACTGAGAAGAGCCTC TCCCACTCTCCTGGTAAA	
SM1B222	pDR000028068	GAGGTTCAGCTGCAGCAGTCTGGGGCTATGC TGGCAAGGCCTGGGGCTTCAGTGACGATGTC CTGCAAGGCTTCTGGCTACACCTTTACCGATT ACTGGATGCACTGGGTAAGACAGGGGCCTGG ACAGGGTCTGGAATGGATTGGCGCTATTTTT CCTGGAAATAGTGATACTACCTACAATCAGA AATTCAGGGGCAAGGCCAAACTGACTGCAGT CACATCTGCCATCACTGCCTACATGGAGGTC AGCAGCCTGACAAATATTGACTCTGCGGTCT ATTACTGTACGGTAACTGAACTTGACTACTG GGGCCAAGGCACCACTCTCACAGTCTCCTCA GCCAAAACGACACCCCCATCTGTCTATCCAC TGGCCCCTGGATCTGCTGCCCAAACTAACTC CATGGTGACCCTGGGATGCCTGGTCAAGGGC TATTTCCCTGAGCCAGTGACAGTGACCTGGA ACTCTGGATCCCTGTCCAGCGGTGTGCACAC CTTCCCAGCTGTCCTGGAGTCTGACCTCTACA CTCTGAGCAGCTCAGTGACTGTCCCCTCCAG CCCTCGGCCCAGCGAGACCGTCACCTGCAAC GTTGCCCACCCGGCCAGCAGCACCAAGGTGG ACAAGAAAATTGTGCCCAGGGATTGTGGTTG TAAGCCTTGCATATGTACAGTCCCAGAAGTA TCATCTGTCTTCATCTTCCCCCCAAAGCCCAA GGATGTGCTCACCATTACTCTGACTCCTAAG GTCACGTGTGTTGTGGTAGACATCAGCAAGG ATGATCCCGAGGTCCAGTTCAGCTGGTTTGT AGATGATGTGGAGGTGCACACAGCTCAGACG CAACCCCGGGAGGAGCAGTTCAACAGCACTT TCCGCTCAGTCAGTGAACTTCCCATCATGCAC CAGGACTGGCTCAATGGCAAGGAGTTCAAAT GCAGGGTCAACAGTGCAGCTTTCCCTGCCCC CATCGAGAAAACCATCTCCAAAACCAAAGGC AGACCGAAGGCTCCACAGGTGTACACCATTC CACCTCCCAAGGAGCAGATGGCCAAGGATAA AGTCAGTCTGACCTGCATGATAACAGACTTC TTCCCTGAAGACATTACTGTGGAGTGGCAGT GGAATGGGCAGCCAGCGGAGAACTACAAGA ACACTCAGCCCATCATGAACACGAATGGCTC TTACTTCGTCTACAGCAAGCTCAATGTGCAG AAGAGCAACTGGGAGGCAGGAAATACTTTCA	1047

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		CCTGCTCTGTGTTACATGAGGGCCTGCACAA CCACCATACTGAGAAGAGCCTCTCCCACTCT CCTGGTAAA	
SM1B223	pDR000028069	GAGGTTCAGCTGCAGCAGTCTGGGGCTGACC TTGTGATGCCTGGGACTTCAATGAAGCTGTC CTGCAAGGCTTCTGGCTACACATTCACTGACT ACTGGATTCACTGGGTGAAGCAGGGGCCTGG ACAAGGCCTTGAGTGGATCGGAGCGATTGAT ACTTCGGATAGTTATATTAATTACAATCAAA AGTTCACGGACAAGGCCACATTGACCGTTGA CGAATCCTCCAGCACAGCCTACATGCACCTC AGCAGCCTGACATCTGAGGACTCTGCGGTCT ATTATTGTGCAAGGGACTACGGCTACGCTAT GGACTACTGGGGTCAAGGAACCTCAGTCACC GTCTCCTCAGCCAAAACGACACCCCCATCTG TCTATCCACTGGCCCCTGGATCTGCTGCCCAA ACTAACTCCATGGTGACCCTGGGATGCCTGG TCAAGGGCTATTTCCCTGAGCCAGTGACAGT GACCTGGAACTCTGGATCCCTGTCCAGCGGT GTGCACACCTTCCCAGCTGTCCTGGAGTCTG ACCTCTACACTCTGAGCAGCTCAGTGACTGT CCCCTCCAGCCCTCGGCCCAGCGAGACCGTC ACCTGCAACGTTGCCCACCCGGCCAGCAGCA CCAAGGTGGACAAGAAAATTGTGCCCAGGG ATTGTGGTTGTAAGCCTTGCATATGTACAGTC CCAGAAGTATCATCTGTCTTCATCTTCCCCCC AAAGCCCAAGGATGTGCTCACCATTACTCTG ACTCCTAAGGTCACGTGTGTTGTGGTAGACA TCAGCAAGGATGATCCCGAGGTCCAGTTCAG CTGGTTTGTAGATGATGTGGAGGTGCACACA GCTCAGACGCAACCCCGGGAGGAGCAGTTCA ACAGCACTTTCCGCTCAGTCAGTGAACTTCCC ATCATGCACCAGGACTGGCTCAATGGCAAGG AGTTCAAATGCAGGGTCAACAGTGCAGCTTT CCCTGCCCCCATCGAGAAAACCATCTCCAAA ACCAAAGGCAGACCGAAGGCTCCACAGGTGT ACACCATTCCACCTCCCAAGGAGCAGATGGC CAAGGATAAAGTCAGTCTGACCTGCATGATA ACAGACTTCTTCCCTGAAGACATTACTGTGG AGTGGCAGTGGAATGGGCAGCCAGCGGAGA ACTACAAGAACACTCAGCCCATCATGAACAC GAATGGCTCTTACTTCGTCTACAGCAAGCTC AATGTGCAGAAGAGCAACTGGGAGGCAGGA AATACTTTCACCTGCTCTGTGTTACATGAGGG CCTGCACAACCACCATACTGAGAAGAGCCTC TCCCACTCTCCTGGTAAA	1048
SM1B224	pDR000028070	CAGGTCCAACTGCAGCAGCCTGGGGCTGAGC TTGTGATGCCTGGGTCTTCAGTGAAGATGTCC	1049

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		TGCAAGGCTTCTGGCTACACATTCACTGATTA CTGGATGCACTGGGTGAAGCAGAGGCCGGG ACAAGGCCTTGAGTGGATCGGAGCGATTGAT GCTTCTGATAGTTATACTAGCTACGATCAAA AGTTCAAGGGCAAGGCCACATTGACTGTTGA CGATTCCTCCAGCACAGCCTACATTCACCTCA ACAGCCTGACATCTGAGGACTCTGCGGTCTA TTACTGTGCAAGAGACTTCGGCTATGCTATG GACTACTGGGGTCAAGGAACCTCAGTCACCG TCTCCTCAGCCAAAACGACACCCCCATCTGT CTATCCACTGGCCCCTGGATCTGCTGCCCAA ACTAACTCCATGGTGACCCTGGGATGCCTGG TCAAGGGCTATTTCCCTGAGCCAGTGACAGT GACCTGGAACTCTGGATCCCTGTCCAGCGGT GTGCACACCTTCCCAGCTGTCCTGGAGTCTG ACCTCTACACTCTGAGCAGCTCAGTGACTGT CCCCTCCAGCCCTCGGCCCAGCGAGACCGTC ACCTGCAACGTTGCCCACCCGGCCAGCAGCA CCAAGGTGGACAAGAAAATTGTGCCCAGGG ATTGTGGTTGTAAGCCTTGCATATGTACAGTC CCAGAAGTATCATCTGTCTTCATCTTCCCCCC AAAGCCCAAGGATGTGCTCACCATTACTCTG ACTCCTAAGGTCACGTGTGTTGTGGTAGACA TCAGCAAGGATGATCCCGAGGTCCAGTTCAG CTGGTTTGTAGATGATGTGGAGGTGCACACA GCTCAGACGCAACCCCGGGAGGAGCAGTTCA ACAGCACTTTCCGCTCAGTCAGTGAACTTCCC ATCATGCACCAGGACTGGCTCAATGGCAAGG AGTTCAAATGCAGGGTCAACAGTGCAGCTTT CCCTGCCCCCATCGAGAAAACCATCTCCAAA ACCAAAGGCAGACCGAAGGCTCCACAGGTGT ACACCATTCCACCTCCCAAGGAGCAGATGGC CAAGGATAAAGTCAGTCTGACCTGCATGATA ACAGACTTCTTCCCTGAAGACATTACTGTGG AGTGGCAGTGGAATGGGCAGCCAGCGGAGA ACTACAAGAACACTCAGCCCATCATGAACAC GAATGGCTCTTACTTCGTCTACAGCAAGCTC AATGTGCAGAAGAGCAACTGGGAGGCAGGA AATACTTTCACCTGCTCTGTGTTACATGAGGG CCTGCACAACCACCATACTGAGAAGAGCCTC TCCCACTCTCCTGGTAAA	
SM1B225	pDR000028071	GAGGTTCAGCTGCAGCAGTCTGGGGGAGGCT TAGTGAAGCCTGGAGGGTCCCTGAAACTCTC CTGTGCAGCCTCTGGATTCACTTTCAGTAGCT ATGCCATGTCTTGGGTTCGCCAGACTCCGGA GAAGAGGCTGGAGTGGGTCGCAACCATTACT GGTGGTGGTACTTACACCTACTATCTAGACA GTGTGAAGGGTCGATTCACCATCTCCAGAGA	1050

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		CAATGCCAAGACCTCCCTGTACCTGCAAATG AGCAGTCTGAGGTCGGAGGACACGGCCATGT ATTACTGTGCAAGACATCGGGATGGTAACTA CGGGTGCTTCGATGTCTGGGGCGCAGGGACC ACGGTCACCGTCTCCTCAGCCAAAACGACAC CCCCATCTGTCTATCCACTGGCCCCTGGATCT GCTGCCCAAACTAACCCCATGGTGACCCTGG GATGCCTGGTCAAGGGCTATTTCCCTGAGCC AGTGACAGTGACCTGGAACTCTGGATCCCTG TCCAGCGGTGTGCACACCTTCCCAGCTGTCCT GGAGTCTGACCTCTACACTCTGAGCAGCTCA GTGACTGTCCCCTCCAGCCCTCGGCCCAGCG AGACCGTCACCTGCAACGTTGCCCACCCGGC CAGCAGCACCAAGGTGGACAAGAAAATTGT GCCCAGGGATTGTGGTTGTAAGCCTTGCATA TGTACAGTCCCAGAAGTATCATCTGTCTTCAT CTTCCCCCCAAAGCCCAAGGATGTGCTCACC ATTACTCTGACTCCTAAGGTCACGTGTGTTGT GGTAGACATCAGCAAGGATGATCCCGAGGTC CAGTTCAGCTGGTTTGTAGATGATGTGGAGG TGCACACAGCTCAGACGCAACCCCGGGAGGA GCAGTTCAACAGCACTTTCCGCTCAGTCAGT GAACTTCCCATCATGCACCAGGACTGGCTCA ATGGCAAGGAGTTCAAATGCAGGGTCAACAG TGCAGCTTTCCCTGCCCCCATCGAGAAAACC ATCTCCAAAACCAAAGGCAGACCGAAGGCTC CACAGGTGTACACCATTCCACCTCCCAAGGA GCAGATGGCCAAGGATAAAGTCAGTCTGACC TGCATGATAACAGACTTCTTCCCTGAAGACA TTACTGTGGAGTGGCAGTGGAATGGGCAGCC AGCGGAGAACTACAAGAACACTCAGCCCATC ATGAACACGAATGGCTCTTACTTCGTCTACA GCAAGCTCAATGTGCAGAAGAGCAACTGGG AGGCAGGAAATACTTTCACCTGCTCTGTGTT ACATGAGGGCCTGCACAACCACCATACTGAG AAGAGCCTCTCCCACTCTCCTGGTAAA	
SM1B226	pDR000028072	GAGGTTCAGCTGCAGCAGTCTGGGGCTGAGC TTGTGATGCCTGGGGCTTCAGTGAAGATGTC CTGCAAGGCTTCTGGTTACACATTCACTGACT ACTGGATGCACTGGGTGCTGCAGAGGCCTGG ACAAGGCCTTGAGTGGATCGGAGCGATTGAT ACTTCTGATAGTTATACTACCTACAATCAAA AATTCAAGGGCAAGGCCACATTGACTGTAGA CGAATCCTCCAGCACGGCCTACATGCTGCTC AGCAGCCTGACATCTGAGGACTCTGCGGTCT ATTACTGTGCAAGAGACTACGGCTATGCTAT GGACTACTGGGGTCAAGGATCCTCAGTCACC GTCTCCTCAGCCAAAACGACACCCCCATCTG	1051

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		TCTATCCACTGGCCCCTGGATCTGCTGCCCAA ACTAACTCCATGGTGACCCTGGGATGCCTGG TCAAGGGCTATTTCCCTGAGCCAGTGACAGT GACCTGGAACTCTGGATCCCTGTCCAGCGGT GTGCACACCTTCCCAGCTGTCCTGGAGTCTG ACCTCTACACTCTGAGCAGCTCAGTGACTGT CCCCTCCAGCCCTCGGCCCAGCGAGACCGTC ACCTGCAACGTTGCCCACCCGGCCAGCAGCA CCAAGGTGGACAAGAAAATTGTGCCCAGGG ATTGTGGTTGTAAGCCTTGCATATGTACAGTC CCAGAAGTATCATCTGTCTTCATCTTCCCCCC AAAGCCCAAGGATGTGCTCACCATTACTCTG ACTCCTAAGGTCACGTGTGTTGTGGTAGACA TCAGCAAGGATGATCCCGAGGTCCAGTTCAG CTGGTTTGTAGATGATGTGGAGGTGCACACA GCTCAGACGCAACCCCGGGAGGAGCAGTTCA ACAGCACTTTCCGCTCAGTCAGTGAACTTCCC ATCATGCACCAGGACTGGCTCAATGGCAAGG AGTTCAAATGCAGGGTCAACAGTGCAGCTTT CCCTGCCCCCATCGAGAAAACCATCTCCAAA ACCAAAGGCAGACCGAAGGCTCCACAGGTGT ACACCATTCCACCTCCCAAGGAGCAGATGGC CAAGGATAAAGTCAGTCTGACCTGCATGATA ACAGACTTCTTCCCTGAAGACATTACTGTGG AGTGGCAGTGGAATGGGCAGCCAGCGGAGA ACTACAAGAACACTCAGCCCATCATGAACAC GAATGGCTCTTACTTCGTCTACAGCAAGCTC AATGTGCAGAAGAGCAACTGGGAGGCAGGA AATACTTTCACCTGCTCTGTGTTACATGAGGG CCTGCACAACCACCATACTGAGAAGAGCCTC TCCCACTCTCCTGGTAAA	
SM1B227	pDR000028073	GAGTTCCAGCTGCAGCAGTCTGGACCTGAGC TGGTAAAGCCTGGGGCTTCAGTGAAGATGTC CTGCAAGGCTTCTGGATACACATTCACTAGC TATTTTATACACTGGGTGAAGCAGAAGCCTG GACAGGGCCTTGAGTGGATTGGATTTATTAA TCCTTACAATGCTGATACTAACTACAATGAG AAATTCAAAGGCAAGGCCACACTGACTTCAG ACAAATCCTCCAGCACAGCCTACATGGAGCT CAGCAGCCTGACCTCTGAGGACTCTGCGGTC TATTACTGTACTCCGAGTGCTATGGACTACTG GGGTCAAGGAACCTCAGTCACCGTCTCCTCA GCCAAAACGACACCCCCATCTGTCTATCCAC TGGCCCCTGGATCTGCTGCCCAAACTAACTC CATGGTGACCCTGGGATGCCTGGTCAAGGGC TATTTCCCTGAGCCAGTGACAGTGACCTGGA ACTCTGGATCCCTGTCCAGCGGTGTGCACAC CTTCCCAGCTGTCCTGGAGTCTGACCTCTACA	1052

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		CTCTGAGCAGCTCAGTGACTGTCCCCTCCAG CCCTCGGCCCAGCGAGACCGTCACCTGCAAC GTTGCCCACCCGGCCAGCAGCACCAAGGTGG ACAAGAAAATTGTGCCCAGGGATTGTGGTTG TAAGCCTTGCATATGTACAGTCCCAGAAGTA TCATCTGTCTTCATCTTCCCCCCAAAGCCCAA GGATGTGCTCACCATTACTCTGACTCCTAAG GTCACGTGTGTTGTGGTAGACATCAGCAAGG ATGATCCCGAGGTCCAGTTCAGCTGGTTTGT AGATGATGTGGAGGTGCACACAGCTCAGACG CAACCCCGGGAGGAGCAGTTCAACAGCACTT TCCGCTCAGTCAGTGAACTTCCCATCATGCAC CAGGACTGGCTCAATGGCAAGGAGTTCAAAT GCAGGGTCAACAGTGCAGCTTTCCCTGCCCC CATCGAGAAAACCATCTCCAAAACCAAAGGC AGACCGAAGGCTCCACAGGTGTACACCATTC CACCTCCCAAGGAGCAGATGGCCAAGGATAA AGTCAGTCTGACCTGCATGATAACAGACTTC TTCCCTGAAGACATTACTGTGGAGTGGCAGT GGAATGGGCAGCCAGCGGAGAACTACAAGA ACACTCAGCCCATCATGAACACGAATGGCTC TTACTTCGTCTACAGCAAGCTCAATGTGCAG AAGAGCAACTGGGAGGCAGGAAATACTTTCA CCTGCTCTGTGTTACATGAGGGCCTGCACAA CCACCATACTGAGAAGAGCCTCTCCCACTCT CCTGGTAAA	
SM1B228	pDR000028074	CAGGTTCAGCTGCAGCAGTCTGGGGCTGAGC TTGTGATGCCTGGGGCTTCAGTGAAGATGTC CTGCAAGGCTTCTGGCTACACATTCACTGACT ACTGGATGCACTGGGTGAAGCAGAGGCCTGG ACAAGGCCTTGAGTGGATCGGAGCGATTGAT ACTTCTGATAGTTATACTACCTACAATCAAA AGTTCAAGGGCAAGGCCACATTGACTGTAGA CGAATCCTCCAGCACAGCCTACATGCAGCTC AGCAGCCTGACATCTGAGGACTCTGCGGTCT ATTACTGTGCAAGGGACTACGGCTACGCTAT GGACTACTGGGGTCAAGGAACCTCAGTCACC GTCTCCTCAGCCAAAACGACACCCCCATCTG TCTATCCACTGGCCCCTGGATCTGCTGCCCAA ACTAACTCCATGGTGACCCTGGGATGCCTGG TCAAGGGCTATTTCCCTGAGCCAGTGACAGT GACCTGGAACTCTGGATCCCTGTCCAGCGGT GTGCACACCTTCCCAGCTGTCCTGGAGTCTG ACCTCTACACTCTGAGCAGCTCAGTGACTGT CCCCTCCAGCCCTCGGCCCAGCGAGACCGTC ACCTGCAACGTTGCCCACCCGGCCAGCAGCA CCAAGGTGGACAAGAAAATTGTGCCCAGGG ATTGTGGTTGTAAGCCTTGCATATGTACAGTC	1053

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		CCAGAAGTATCATCTGTCTTCATCTTCCCCCC AAAGCCCAAGGATGTGCTCACCATTACTCTG ACTCCTAAGGTCACGTGTGTTGTGGTAGACA TCAGCAAGGATGATCCCGAGGTCCAGTTCAG CTGGTTTGTAGATGATGTGGAGGTGCACACA GCTCAGACGCAACCCCGGGAGGAGCAGTTCA ACAGCACTTTCCGCTCAGTCAGTGAACTTCCC ATCATGCACCAGGACTGGCTCAATGGCAAGG AGTTCAAATGCAGGGTCAACAGTGCAGCTTT CCCTGCCCCCATCGAGAAAACCATCTCCAAA ACCAAAGGCAGACCGAAGGCTCCACAGGTGT ACACCATTCCACCTCCCAAGGAGCAGATGGC CAAGGATAAAGTCAGTCTGACCTGCATGATA ACAGACTTCTTCCCTGAAGACATTACTGTGG AGTGGCAGTGGAATGGGCAGCCAGCGGAGA ACTACAAGAACACTCAGCCCATCATGAACAC GAATGGCTCTTACTTCGTCTACAGCAAGCTC AATGTGCAGAAGAGCAACTGGGAGGCAGGA AATACTTTCACCTGCTCTGTGTTACATGAGGG CCTGCACAACCACCATACTGAGAAGAGCCTC TCCCACTCTCCTGGTAAA	

Table 35. LukD Antibody Heavy Chain Primary Transcripts

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
SM1B221	pDR000028067	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGGTTCA GCTGCAGCAGTCTGGGGCTGAGCTTGTGATGC CTGGGGCTTCAGTGAAGATGTCCTGCAAGGCT TCTGGCTACACATTCACTGACTACTGGATGCAC TGGGTGAAGCAGAGGCCTGGACAAGGCCTTGA GTGGATCGGAGCGATTGATACTTCTGATAGTT ATACTAGCTACAATCAAAAGTTCAAGGGCAAG GCCACATTGACTGTAGACGAATCCTCCAGCAC AGCCTACATGCAGCTCAGCAGCCTGACATCTG AGGACTCTGCGGTCTATTACTGTGCAAGGGAC TACGGCTACGCTATGGACTACTGGGGTCAAGG AACCTCAGTCACCGTCTCCTCAGCCAAAACGA CACCCCCATCTGTCTATCCACTGGCCCCTGGAT CTGCTGCCCAAACTAACTCCATGGTGACCCTG GGATGCCTGGTCAAGGGCTATTTCCCTGAGCC AGTGACAGTGACCTGGAACTCTGGATCCCTGT CCAGCGGTGTGCACACCTTCCCAGCTGTCCTGG AGTCTGACCTCTACACTCTGAGCAGCTCAGTG ACTGTCCCCTCCAGCCCTCGGCCCAGCGAGAC	1054

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CGTCACCTGCAACGTTGCCCACCCGGCCAGCA GCACCAAGGTGGACAAGAAAATTGTGCCCAGG GATTGTGGTTGTAAGCCTTGCATATGTACAGTC CCAGAAGTATCATCTGTCTTCATCTTCCCCCCA AAGCCCAAGGATGTGCTCACCATTACTCTGAC TCCTAAGGTCACGTGTGTTGTGGTAGACATCA GCAAGGATGATCCCGAGGTCCAGTTCAGCTGG TTTGTAGATGATGTGGAGGTGCACACAGCTCA GACGCAACCCCGGGAGGAGCAGTTCAACAGCA CTTTCCGCTCAGTCAGTGAACTTCCCATCATGC ACCAGGACTGGCTCAATGGCAAGGAGTTCAAA TGCAGGGTCAACAGTGCAGCTTTCCCTGCCCCC ATCGAGAAAACCATCTCCAAAACCAAAGGCAG ACCGAAGGCTCCACAGGTGTACACCATTCCAC CTCCCAAGGAGCAGATGGCCAAGGATAAAGTC AGTCTGACCTGCATGATAACAGACTTCTTCCCT GAAGACATTACTGTGGAGTGGCAGTGGAATGG GCAGCCAGCGGAGAACTACAAGAACACTCAGC CCATCATGAACACGAATGGCTCTTACTTCGTCT ACAGCAAGCTCAATGTGCAGAAGAGCAACTGG GAGGCAGGAAATACTTTCACCTGCTCTGTGTTA CATGAGGGCCTGCACAACCACCATACTGAGAA GAGCCTCTCCCACTCTCCTGGTAAATGA	
SM1B222	pDR000028068	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAGGTTCA GCTGCAGCAGTCTGGGGCTATGCTGGCAAGGC CTGGGGCTTCAGTGACGATGTCCTGCAAGGCT TCTGGCTACACCTTTACCGATTACTGGATGCAC TGGGTAAGACAGGGGCCTGGACAGGGTCTGGA ATGGATTGGCGCTATTTTTCCTGGAAATAGTGA TACTACCTACAATCAGAAATTCAGGGGCAAGG CCAAACTGACTGCAGTCACATCTGCCATCACT GCCTACATGGAGGTCAGCAGCCTGACAAATAT TGACTCTGCGGTCTATTACTGTACGGTAACTGA ACTTGACTACTGGGGCCAAGGCACCACTCTCA CAGTCTCCTCAGCCAAAACGACACCCCCATCT GTCTATCCACTGGCCCCTGGATCTGCTGCCCAA ACTAACTCCATGGTGACCCTGGGATGCCTGGT CAAGGGCTATTTCCCTGAGCCAGTGACAGTGA CCTGGAACTCTGGATCCCTGTCCAGCGGTGTGC ACACCTTCCCAGCTGTCCTGGAGTCTGACCTCT ACACTCTGAGCAGCTCAGTGACTGTCCCCTCCA GCCCTCGGCCCAGCGAGACCGTCACCTGCAAC GTTGCCCACCCGGCCAGCAGCACCAAGGTGGA CAAGAAAATTGTGCCCAGGGATTGTGGTTGTA AGCCTTGCATATGTACAGTCCCAGAAGTATCA TCTGTCTTCATCTTCCCCCCAAAGCCCAAGGAT GTGCTCACCATTACTCTGACTCCTAAGGTCACG	1055

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		TGTGTTGTGGTAGACATCAGCAAGGATGATCC CGAGGTCCAGTTCAGCTGGTTTGTAGATGATGT GGAGGTGCACACAGCTCAGACGCAACCCCGGG AGGAGCAGTTCAACAGCACTTTCCGCTCAGTC AGTGAACTTCCCATCATGCACCAGGACTGGCT CAATGGCAAGGAGTTCAAATGCAGGGTCAACA GTGCAGCTTTCCCTGCCCCCATCGAGAAAACC ATCTCCAAAACCAAAGGCAGACCGAAGGCTCC ACAGGTGTACACCATTCCACCTCCCAAGGAGC AGATGGCCAAGGATAAAGTCAGTCTGACCTGC ATGATAACAGACTTCTTCCCTGAAGACATTACT GTGGAGTGGCAGTGGAATGGGCAGCCAGCGG AGAACTACAAGAACACTCAGCCCATCATGAAC ACGAATGGCTCTTACTTCGTCTACAGCAAGCTC AATGTGCAGAAGAGCAACTGGGAGGCAGGAA ATACTTTCACCTGCTCTGTGTTACATGAGGGCC TGCACAACCACCATACTGAGAAGAGCCTCTCC CACTCTCCTGGTAAATGA	
SM1B223	pDR000028069	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAGGTTCA GCTGCAGCAGTCTGGGGCTGACCTTGTGATGC CTGGGACTTCAATGAAGCTGTCCTGCAAGGCT TCTGGCTACACATTCACTGACTACTGGATTCAC TGGGTGAAGCAGGGGCCTGGACAAGGCCTTGA GTGGATCGGAGCGATTGATACTTCGGATAGTT ATATTAATTACAATCAAAAGTTCACGGACAAG GCCACATTGACCGTTGACGAATCCTCCAGCAC AGCCTACATGCACCTCAGCAGCCTGACATCTG AGGACTCTGCGGTCTATTATTGTGCAAGGGAC TACGGCTACGCTATGGACTACTGGGGTCAAGG AACCTCAGTCACCGTCTCCTCAGCCAAAACGA CACCCCCATCTGTCTATCCACTGGCCCCTGGAT CTGCTGCCCAAACTAACTCCATGGTGACCCTG GGATGCCTGGTCAAGGGCTATTTCCCTGAGCC AGTGACAGTGACCTGGAACTCTGGATCCCTGT CCAGCGGTGTGCACACCTTCCCAGCTGTCCTGG AGTCTGACCTCTACACTCTGAGCAGCTCAGTG ACTGTCCCCTCCAGCCCTCGGCCCAGCGAGAC CGTCACCTGCAACGTTGCCCACCCGGCCAGCA GCACCAAGGTGGACAAGAAAATTGTGCCCAGG GATTGTGGTTGTAAGCCTTGCATATGTACAGTC CCAGAAGTATCATCTGTCTTCATCTTCCCCCCA AAGCCCAAGGATGTGCTCACCATTACTCTGAC TCCTAAGGTCACGTGTGTTGTGGTAGACATCA GCAAGGATGATCCCGAGGTCCAGTTCAGCTGG TTTGTAGATGATGTGGAGGTGCACACAGCTCA GACGCAACCCCGGGAGGAGCAGTTCAACAGCA CTTTCCGCTCAGTCAGTGAACTTCCCATCATGC	1056

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		ACCAGGACTGGCTCAATGGCAAGGAGTTCAAA TGCAGGGTCAACAGTGCAGCTTTCCCTGCCCCC ATCGAGAAAACCATCTCCAAAACCAAAGGCAG ACCGAAGGCTCCACAGGTGTACACCATTCCAC CTCCCAAGGAGCAGATGGCCAAGGATAAAGTC AGTCTGACCTGCATGATAACAGACTTCTTCCCT GAAGACATTACTGTGGAGTGGCAGTGGAATGG GCAGCCAGCGGAGAACTACAAGAACACTCAGC CCATCATGAACACGAATGGCTCTTACTTCGTCT ACAGCAAGCTCAATGTGCAGAAGAGCAACTGG GAGGCAGGAAATACTTTCACCTGCTCTGTGTTA CATGAGGGCCTGCACAACCACCATACTGAGAA GAGCCTCTCCCACTCTCCTGGTAAATGA	
SM1B224	pDR000028070	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGGTCCA ACTGCAGCAGCCTGGGGCTGAGCTTGTGATGC CTGGGTCTTCAGTGAAGATGTCCTGCAAGGCTT CTGGCTACACATTCACTGATTACTGGATGCACT GGGTGAAGCAGAGGCCGGGACAAGGCCTTGA GTGGATCGGAGCGATTGATGCTTCTGATAGTT ATACTAGCTACGATCAAAAGTTCAAGGGCAAG GCCACATTGACTGTTGACGATTCCTCCAGCACA GCCTACATTCACCTCAACAGCCTGACATCTGA GGACTCTGCGGTCTATTACTGTGCAAGAGACTT CGGCTATGCTATGGACTACTGGGGTCAAGGAA CCTCAGTCACCGTCTCCTCAGCCAAAACGACA CCCCCATCTGTCTATCCACTGGCCCCTGGATCT GCTGCCCAAACTAACTCCATGGTGACCCTGGG ATGCCTGGTCAAGGGCTATTTCCCTGAGCCAGT GACAGTGACCTGGAACTCTGGATCCCTGTCCA GCGGTGTGCACACCTTCCCAGCTGTCCTGGAGT CTGACCTCTACACTCTGAGCAGCTCAGTGACTG TCCCCTCCAGCCCTCGGCCCAGCGAGACCGTC ACCTGCAACGTTGCCCACCCGGCCAGCAGCAC CAAGGTGGACAAGAAAATTGTGCCCAGGGATT GTGGTTGTAAGCCTTGCATATGTACAGTCCCAG AAGTATCATCTGTCTTCATCTTCCCCCCAAAGC CCAAGGATGTGCTCACCATTACTCTGACTCCTA AGGTCACGTGTGTTGTGGTAGACATCAGCAAG GATGATCCCGAGGTCCAGTTCAGCTGGTTTGTA GATGATGTGGAGGTGCACACAGCTCAGACGCA ACCCCGGGAGGAGCAGTTCAACAGCACTTTCC GCTCAGTCAGTGAACTTCCCATCATGCACCAG GACTGGCTCAATGGCAAGGAGTTCAAATGCAG GGTCAACAGTGCAGCTTTCCCTGCCCCCATCGA GAAAACCATCTCCAAAACCAAAGGCAGACCGA AGGCTCCACAGGTGTACACCATTCCACCTCCC AAGGAGCAGATGGCCAAGGATAAAGTCAGTCT	1057

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GACCTGCATGATAACAGACTTCTTCCCTGAAG ACATTACTGTGGAGTGGCAGTGGAATGGGCAG CCAGCGGAGAACTACAAGAACACTCAGCCCAT CATGAACACGAATGGCTCTTACTTCGTCTACAG CAAGCTCAATGTGCAGAAGAGCAACTGGGAGG CAGGAAATACTTTCACCTGCTCTGTGTTACATG AGGGCCTGCACAACCACCATACTGAGAAGAGC CTCTCCCACTCTCCTGGTAAATGA	
SM1B225	pDR000028071	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAGGTTCA GCTGCAGCAGTCTGGGGGAGGCTTAGTGAAGC CTGGAGGGTCCCTGAAACTCTCCTGTGCAGCCT CTGGATTCACTTTCAGTAGCTATGCCATGTCTT GGGTTCGCCAGACTCCGGAGAAGAGGCTGGAG TGGGTCGCAACCATTACTGGTGGTGGTACTTAC ACCTACTATCTAGACAGTGTGAAGGGTCGATT CACCATCTCCAGAGACAATGCCAAGACCTCCC TGTACCTGCAAATGAGCAGTCTGAGGTCGGAG GACACGGCCATGTATTACTGTGCAAGACATCG GGATGGTAACTACGGGTGCTTCGATGTCTGGG GCGCAGGGACCACGGTCACCGTCTCCTCAGCC AAAACGACACCCCCATCTGTCTATCCACTGGC CCCTGGATCTGCTGCCCAAACTAACCCCATGGT GACCCTGGGATGCCTGGTCAAGGGCTATTTCC CTGAGCCAGTGACAGTGACCTGGAACTCTGGA TCCCTGTCCAGCGGTGTGCACACCTTCCCAGCT GTCCTGGAGTCTGACCTCTACACTCTGAGCAGC TCAGTGACTGTCCCCTCCAGCCCTCGGCCCAGC GAGACCGTCACCTGCAACGTTGCCCACCCGGC CAGCAGCACCAAGGTGGACAAGAAAATTGTGC CCAGGGATTGTGGTTGTAAGCCTTGCATATGTA CAGTCCCAGAAGTATCATCTGTCTTCATCTTCC CCCCAAAGCCCAAGGATGTGCTCACCATTACT CTGACTCCTAAGGTCACGTGTGTTGTGGTAGAC ATCAGCAAGGATGATCCCGAGGTCCAGTTCAG CTGGTTTGTAGATGATGTGGAGGTGCACACAG CTCAGACGCAACCCCGGGAGGAGCAGTTCAAC AGCACTTTCCGCTCAGTCAGTGAACTTCCCATC ATGCACCAGGACTGGCTCAATGGCAAGGAGTT CAAATGCAGGGTCAACAGTGCAGCTTTCCCTG CCCCCATCGAGAAAACCATCTCCAAAACCAAA GGCAGACCGAAGGCTCCACAGGTGTACACCAT TCCACCTCCCAAGGAGCAGATGGCCAAGGATA AAGTCAGTCTGACCTGCATGATAACAGACTTC TTCCCTGAAGACATTACTGTGGAGTGGCAGTG GAATGGGCAGCCAGCGGAGAACTACAAGAAC ACTCAGCCCATCATGAACACGAATGGCTCTTA CTTCGTCTACAGCAAGCTCAATGTGCAGAAGA	1058

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GCAACTGGGAGGCAGGAAATACTTTCACCTGC TCTGTGTTACATGAGGGCCTGCACAACCACCA TACTGAGAAGAGCCTCTCCCACTCTCCTGGTAA ATGA	
SM1B226	pDR000028072	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAGGTTCA GCTGCAGCAGTCTGGGGCTGAGCTTGTGATGC CTGGGGCTTCAGTGAAGATGTCCTGCAAGGCT TCTGGTTACACATTCACTGACTACTGGATGCAC TGGGTGCTGCAGAGGCCTGGACAAGGCCTTGA GTGGATCGGAGCGATTGATACTTCTGATAGTT ATACTACCTACAATCAAAAATTCAAGGGCAAG GCCACATTGACTGTAGACGAATCCTCCAGCAC GGCCTACATGCTGCTCAGCAGCCTGACATCTG AGGACTCTGCGGTCTATTACTGTGCAAGAGAC TACGGCTATGCTATGGACTACTGGGGTCAAGG ATCCTCAGTCACCGTCTCCTCAGCCAAAACGA CACCCCCATCTGTCTATCCACTGGCCCCTGGAT CTGCTGCCCAAACTAACTCCATGGTGACCCTG GGATGCCTGGTCAAGGGCTATTTCCCTGAGCC AGTGACAGTGACCTGGAACTCTGGATCCCTGT CCAGCGGTGTGCACACCTTCCCAGCTGTCCTGG AGTCTGACCTCTACACTCTGAGCAGCTCAGTG ACTGTCCCCTCCAGCCCTCGGCCCAGCGAGAC CGTCACCTGCAACGTTGCCCACCCGGCCAGCA GCACCAAGGTGGACAAGAAAATTGTGCCCAGG GATTGTGGTTGTAAGCCTTGCATATGTACAGTC CCAGAAGTATCATCTGTCTTCATCTTCCCCCCA AAGCCCAAGGATGTGCTCACCATTACTCTGAC TCCTAAGGTCACGTGTGTTGTGGTAGACATCA GCAAGGATGATCCCGAGGTCCAGTTCAGCTGG TTTGTAGATGATGTGGAGGTGCACACAGCTCA GACGCAACCCCGGGAGGAGCAGTTCAACAGCA CTTTCCGCTCAGTCAGTGAACTTCCCATCATGC ACCAGGACTGGCTCAATGGCAAGGAGTTCAAA TGCAGGGTCAACAGTGCAGCTTTCCCTGCCCCC ATCGAGAAAACCATCTCCAAAACCAAAGGCAG ACCGAAGGCTCCACAGGTGTACACCATTCCAC CTCCCAAGGAGCAGATGGCCAAGGATAAAGTC AGTCTGACCTGCATGATAACAGACTTCTTCCCT GAAGACATTACTGTGGAGTGGCAGTGGAATGG GCAGCCAGCGGAGAACTACAAGAACACTCAGC CCATCATGAACACGAATGGCTCTTACTTCGTCT ACAGCAAGCTCAATGTGCAGAAGAGCAACTGG GAGGCAGGAAATACTTTCACCTGCTCTGTGTTA CATGAGGGCCTGCACAACCACCATACTGAGAA GAGCCTCTCCCACTCTCCTGGTAAATGA	1059
SM1B227	pDR000028073	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG	1060

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GCAGCTGCCCAAAGTATACAGGCCGAGTTCCA GCTGCAGCAGTCTGGACCTGAGCTGGTAAAGC CTGGGGCTTCAGTGAAGATGTCCTGCAAGGCT TCTGGATACACATTCACTAGCTATTTTATACAC TGGGTGAAGCAGAAGCCTGGACAGGGCCTTGA GTGGATTGGATTTATTAATCCTTACAATGCTGA TACTAACTACAATGAGAAATTCAAAGGCAAGG CCACACTGACTTCAGACAAATCCTCCAGCACA GCCTACATGGAGCTCAGCAGCCTGACCTCTGA GGACTCTGCGGTCTATTACTGTACTCCGAGTGC TATGGACTACTGGGGTCAAGGAACCTCAGTCA CCGTCTCCTCAGCCAAAACGACACCCCCATCT GTCTATCCACTGGCCCCTGGATCTGCTGCCCAA ACTAACTCCATGGTGACCCTGGGATGCCTGGT CAAGGGCTATTTCCCTGAGCCAGTGACAGTGA CCTGGAACTCTGGATCCCTGTCCAGCGGTGTGC ACACCTTCCCAGCTGTCCTGGAGTCTGACCTCT ACACTCTGAGCAGCTCAGTGACTGTCCCCTCCA GCCCTCGGCCCAGCGAGACCGTCACCTGCAAC GTTGCCCACCCGGCCAGCAGCACCAAGGTGGA CAAGAAAATTGTGCCCAGGGATTGTGGTTGTA AGCCTTGCATATGTACAGTCCCAGAAGTATCA TCTGTCTTCATCTTCCCCCCAAAGCCCAAGGAT GTGCTCACCATTACTCTGACTCCTAAGGTCACG TGTGTTGTGGTAGACATCAGCAAGGATGATCC CGAGGTCCAGTTCAGCTGGTTTGTAGATGATGT GGAGGTGCACACAGCTCAGACGCAACCCCGGG AGGAGCAGTTCAACAGCACTTTCCGCTCAGTC AGTGAACTTCCCATCATGCACCAGGACTGGCT CAATGGCAAGGAGTTCAAATGCAGGGTCAACA GTGCAGCTTTCCCTGCCCCCATCGAGAAAACC ATCTCCAAAACCAAAGGCAGACCGAAGGCTCC ACAGGTGTACACCATTCCACCTCCCAAGGAGC AGATGGCCAAGGATAAAGTCAGTCTGACCTGC ATGATAACAGACTTCTTCCCTGAAGACATTACT GTGGAGTGGCAGTGGAATGGGCAGCCAGCGG AGAACTACAAGAACACTCAGCCCATCATGAAC ACGAATGGCTCTTACTTCGTCTACAGCAAGCTC AATGTGCAGAAGAGCAACTGGGAGGCAGGAA ATACTTTCACCTGCTCTGTGTTACATGAGGGCC TGCACAACCACCATACTGAGAAGAGCCTCTCC CACTCTCCTGGTAAATGA	
SM1B228	pDR000028074	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGGTTCA GCTGCAGCAGTCTGGGGCTGAGCTTGTGATGC CTGGGGCTTCAGTGAAGATGTCCTGCAAGGCT TCTGGCTACACATTCACTGACTACTGGATGCAC TGGGTGAAGCAGAGGCCTGGACAAGGCCTTGA	1061

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GTGGATCGGAGCGATTGATACTTCTGATAGTT ATACTACCTACAATCAAAAGTTCAAGGGCAAG GCCACATTGACTGTAGACGAATCCTCCAGCAC AGCCTACATGCAGCTCAGCAGCCTGACATCTG AGGACTCTGCGGTCTATTACTGTGCAAGGGAC TACGGCTACGCTATGGACTACTGGGGTCAAGG AACCTCAGTCACCGTCTCCTCAGCCAAAACGA CACCCCCATCTGTCTATCCACTGGCCCCTGGAT CTGCTGCCCAAACTAACTCCATGGTGACCCTG GGATGCCTGGTCAAGGGCTATTTCCCTGAGCC AGTGACAGTGACCTGGAACTCTGGATCCCTGT CCAGCGGTGTGCACACCTTCCCAGCTGTCCTGG AGTCTGACCTCTACACTCTGAGCAGCTCAGTG ACTGTCCCCTCCAGCCCTCGGCCCAGCGAGAC CGTCACCTGCAACGTTGCCCACCCGGCCAGCA GCACCAAGGTGGACAAGAAAATTGTGCCCAGG GATTGTGGTTGTAAGCCTTGCATATGTACAGTC CCAGAAGTATCATCTGTCTTCATCTTCCCCCCA AAGCCCAAGGATGTGCTCACCATTACTCTGAC TCCTAAGGTCACGTGTGTTGTGGTAGACATCA GCAAGGATGATCCCGAGGTCCAGTTCAGCTGG TTTGTAGATGATGTGGAGGTGCACACAGCTCA GACGCAACCCCGGGAGGAGCAGTTCAACAGCA CTTTCCGCTCAGTCAGTGAACTTCCCATCATGC ACCAGGACTGGCTCAATGGCAAGGAGTTCAAA TGCAGGGTCAACAGTGCAGCTTTCCCTGCCCCC ATCGAGAAAACCATCTCCAAAACCAAAGGCAG ACCGAAGGCTCCACAGGTGTACACCATTCCAC CTCCCAAGGAGCAGATGGCCAAGGATAAAGTC AGTCTGACCTGCATGATAACAGACTTCTTCCCT GAAGACATTACTGTGGAGTGGCAGTGGAATGG GCAGCCAGCGGAGAACTACAAGAACACTCAGC CCATCATGAACACGAATGGCTCTTACTTCGTCT ACAGCAAGCTCAATGTGCAGAAGAGCAACTGG GAGGCAGGAAATACTTTCACCTGCTCTGTGTTA CATGAGGGCCTGCACAACCACCATACTGAGAA GAGCCTCTCCCACTCTCCTGGTAAATGA	

Table 36. LukD Antibody Light Chain CDSs

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
SM1B221	pDR000028075	CAAATTGTTCTCACCCAGTCTCCAGCAATCATG TCTGCATCTCCAGGGGAGAAGGTCACCATAAC CTGCAGTGCCAGCTTAAGTGTCAGTTACATGCA CTGGTTCCAGCAGAAGCCAGGCACTTCTCCCA	1062

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		AACTCTGGATTTATAGCGCTTCCAACCTGGCTT CTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGAT CTGGGACCTCTTACTCTCTCACAATCAGCCGAA TGGAGGCTGAAGATGCTGCCACTTATTACTGCC AGCAAAGGAGTAGTTACCCATTCACGTTCGGC TCGGGGACAAAGTTGGAAATAAAACGGGCTGA TGCTGCACCAACTGTATCCATCTTCCCACCATC CAGTGAGCAGTTAACATCTGGAGGTGCCTCAG TCGTGTGCTTCTTGAACAACTTCTACCCCAAAG ACATCAATGTCAAGTGGAAGATTGATGGCAGT GAACGACAAAATGGCGTCCTGAACAGTTGGAC TGATCAGGACAGCAAAGACAGCACCTACAGCA TGAGCAGCACCCTCACGTTGACCAAGGACGAG TATGAACGACATAACAGCTATACCTGTGAGGC CACTCACAAGACATCAACTTCACCCATTGTCAA GAGCTTCAACAGGAATGAGTGT	
SM1B222	pDR000028076	GATGTTGTGATGACCCAAACTCCACTCTCCCTG CCTGTCAGTCTTGGAGATCAAGCCTCCATCTCT TGCAGATCTAGTCAGAGCCTTATACACAATGA TGGAAACACCTATTTACATTGGTACCTCCAGAA GCCAGGCCAGTCTCCAAAGCTCCTGATCTACA AAGTTTCCAACCGATTTTCTGGGGTCCCAGACA GGTTCAGTGGCAGTGGATCAGGGACAGATTTC ACAGTCAAGATCAGCAGAGTGGAGGCTGAGGA TCTGGGAGTTTATTTCTGCTCTCAAAGTACACA TGTTCCGTTCACGTTCGGTGCTGGGACCAAGCT GGAGCTGAAACGGGCTGATGCTGCACCAACTG TATCCATCTTCCCACCATCCAGTGAGCAGTTAA CATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGA ACAACTTCTACCCCAAAGACATCAATGTCAAG TGGAAGATTGATGGCAGTGAACGACAAAATGG CGTCCTGAACAGTTGGACTGATCAGGACAGCA AAGACAGCACCTACAGCATGAGCAGCACCCTC ACGTTGACCAAGGACGAGTATGAACGACATAA CAGCTATACCTGTGAGGCCACTCACAAGACAT CAACTTCACCCATTGTCAAGAGCTTCAACAGG AATGAGTGT	1063
SM1B223	pDR000028077	CAAATTGTTCTCTCCCAGTCTCCAGCAATCATG TCTGCATCTCCAGGGGAGAAGGTCACCATAAC CTGCAGTGCCAGCTTAAGTGTCAGTTTCATGCA CTGGTTCCAGCAGAAGCCAGGCACTTCTCCCA AACTCTGGATTTATAGCGCTTCCAACCTGGCTT CTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGAT CTGGGACCTCTTACTCTCTCACAATCAGCCGAA TGGAGGCTGAAGATGCTGCCACTTATTACTGCC AGCAAAGGAGTAGCTACCCATTCACGTTCGGC TCGGGGACAAAGTTGGAAATAAAACGGGCTGA TGCTGCACCAACTGTATCCATCTTCCCACCATC	1064

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		CAGTGAGCAGTTAACATCTGGAGGTGCCTCAG TCGTGTGCTTCTTGAACAACTTCTACCCCAAAG ACATCAATGTCAAGTGGAAGATTGATGGCAGT GAACGACAAAATGGCGTCCTGAACAGTTGGAC TGATCAGGACAGCAAAGACAGCACCTACAGCA TGAGCAGCACCCTCACGTTGACCAAGGACGAG TATGAACGACATAACAGCTATACCTGTGAGGC CACTCACAAGACATCAACTTCACCCATTGTCAA GAGCTTCAACAGGAATGAGTGT	
SM1B224	pDR000028078	CAAATTGTTCTCACCCAGTCTCCAGCAATCATG TCTGCATCTCCAGGGGAGAAGGTCACCATAAC CTGCAGTGCCAGCTCAAGTGTAAGTTTCATGCA CTGGTTCCAGCAGAAGCCAGGCACTTCTCCCA AACTCTGGATTTATAGCACATCCAACCTGGCTT CTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGAT CTGGGACCTCTTACTCTCTCACAATCAGCCGAA TGGAGGCTGAAGATGCTGCCACTTATTACTGCC AGCAAAGGAGTACTTACCCATACACGTTCGGA GGGGGGACCAAGATGGAAATAAAACGGGCTG ATGCTGCACCAACTGTATCCATCTTCCCACCAT CCAGTGAGCAGTTAACATCTGGAGGTGCCTCA GTCGTGTGCTTCTTGAACAACTTCTACCCCAAA GACATCAATGTCAAGTGGAAGATTGATGGCAG TGAACGACAAAATGGCGTCCTGAACAGTTGGA CTGATCAGGACAGCAAAGACAGCACCTACAGC ATGAGCAGCACCCTCACGTTGACCAAGGACGA GTATGAACGACATAACAGCTATACCTGTGAGG CCACTCACAAGACATCAACTTCACCCATTGTCA AGAGCTTCAACAGGAATGAGTGT	1065
SM1B225	pDR000028079	GATATTGTGCTAACTCAGTCTCCAGCAATCATG TCTGCATCTCTAGGGGAACGGGTCACCATGAC CTGCACTGCCAGCTCAAGTGTAAGTTCCAGTTA CTTGCACTGGTACCAGCAGAAGCCAGGATCCT CCCCCAAACTCTGGGTTTATAGCACATCCAACC TGGCTTCTGGAGTCCCAGCTCGCTTCAGTGGCA GTGGGTCTGGGTCCTCTTACTCTCTCACAATCA GCAGCATGGAGCCTGAAGATACTGCCACTTAT TACTGCCACCAGTATCATCGTTCCCCACAGACG TTCGGTGGAGGCACCAAGCTGGAAATCAAACG GGCTGATGCTGCACCAACTGTATCCATCTTCCC ACCATCCAGTGAGCAGTTAACATCTGGAGGTG CCTCAGTCGTGTGCTTCTTGAACAACTTCTACC CCAAAGACATCAATGTCAAGTGGAAGATTGAT GGCAGTGAACGACAAAATGGCGTCCTGAACAG TTGGACTGATCAGGACAGCAAAGACAGCACCT ACAGCATGAGCAGCACCCTCACGTTGACCAAG GACGAGTATGAACGACATAACAGCTATACCTG TGAGGCCACTCACAAGACATCAACTTCACCCA	1066

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		TTGTCAAGAGCTTCAACAGGAATGAGTGT	
SM1B226	pDR000028080	CAAATTGTTCTCACCCAGTCTCCAGCAATCATG TCTGCATCTCCAGGGGAGAAGGTCACCATTAC CTGCAGTGCCAGCTCAAGTGTCAGTTTCATGCA CTGGTTCCAGCAGAAGCCAGGCACTTCTCCCA AACTCTGGATTTATAGCGCATCCAACCTGGCTT CTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGAT CTGGGACCTCTTACTCTCTCACAATCAGCCGAA TGGAGGCTGAAGATGCTGCCACTTATTACTGCC AGCAAAGGAGTAGTTACCCATACACGTTCGGA GGGGGGACCAAGCTGGAAATAAAGCGGGCTG ATGCTGCACCAACTGTATCCATCTTCCCACCAT CCAGTGAGCAGTTAACATCTGGAGGTGCCTCA GTCGTGTGCTTCTTGAACAACTTCTACCCCAAA GACATCAATGTCAAGTGGAAGATTGATGGCAG TGAACGACAAAATGGCGTCCTGAACAGTTGGA CTGATCAGGACAGCAAAGACAGCACCTACAGC ATGAGCAGCACCCTCACGTTGACCAAGGACGA GTATGAACGACATAACAGCTATACCTGTGAGG CCACTCACAAGACATCAACTTCACCCATTGTCA AGAGCTTCAACAGGAATGAGTGT	1067
SM1B227	pDR000028081	GATATTGTGCTAACTCAGTCTCCAGCAATCATG TCTGCATCTCCAGGGGAAAAGGTCACCATGAC CTGCAGTGCCAGCTCAAGTGTAAGTTACATGC ACTGGTACCAGCAGAAGTCAAGCACCTCCCCC AAACTCTGGATTTATGACACATCCAAACTGGCT TCTGGAGTCCCAGGTCGCTTCAGTGGCAGTGG GTCTGGAAACTCTTACTCTCTCACGATCAGCAG CATGGAGGCTGAAGATGTTGCCACTTATTACTG TTTTCAGGGGAGTGGGTACCCACTCACGTTCGG CTCGGGGACAAAGTTGGAAATAAAACGGGCTG ATGCTGCACCAACTGTATCCATCTTCCCACCAT CCAGTGAGCAGTTAACATCTGGAGGTGCCTCA GTCGTGTGCTTCTTGAACAACTTCTACCCCAAA GACATCAATGTCAAGTGGAAGATTGATGGCAG TGAACGACAAAATGGCGTCCTGAACAGTTGGA CTGATCAGGACAGCAAAGACAGCACCTACAGC ATGAGCAGCACCCTCACGTTGACCAAGGACGA GTATGAACGACATAACAGCTATACCTGTGAGG CCACTCACAAGACATCAACTTCACCCATTGTCA AGAGCTTCAACAGGAATGAGTGT	1068
SM1B228	pDR000028082	CAAATTGTTCTCACCCAGTCTCCAGCAATCATG TCTGCATCTCCAGGGGAGAAGGTCACCATAAC CTGCAGTGCCAGCTCAAGTGTCAGTTACATGC ACTGGTTCCAGCAGAAGCCAGGCACTTCTCCC AAACTCTGGATTTATAGCGCATCCAACCTGGCT TCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGA TCTGGGACCTCTTACTCTCTCACAATCAGCCGA	1069

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		ATGGAGGCTGAAGATGCTGCCACTTATTACTG CCAGCAAAGGAGTAGTTACCCATTCACGTTCG GCTCGGGGACAAAGTTGGAAATAAAACGGGCT GATGCTGCACCAACTGTATCCATCTTCCCACCA TCCAGTGAGCAGTTAACATCTGGAGGTGCCTC AGTCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGGCA GTGAACGACAAAATGGCGTCCTGAACAGTTGG ACTGATCAGGACAGCAAAGACAGCACCTACAG CATGAGCAGCACCCTCACGTTGACCAAGGACG AGTATGAACGACATAACAGCTATACCTGTGAG GCCACTCACAAGACATCAACTTCACCCATTGTC AAGAGCTTCAACAGGAATGAGTGT	

Table 37. LukD Antibody Light Chain Primary Transcripts

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
SM1B221	pDR000028075	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCCAAATT GTTCTCACCCAGTCTCCAGCAATCATGTCTGCA TCTCCAGGGGAGAAGGTCACCATAACCTGCAG TGCCAGCTTAAGTGTCAGTTACATGCACTGGTT CCAGCAGAAGCCAGGCACTTCTCCCAAACTCT GGATTTATAGCGCTTCCAACCTGGCTTCTGGAG TCCCTGCTCGCTTCAGTGGCAGTGGATCTGGGA CCTCTTACTCTCTCACAATCAGCCGAATGGAGG CTGAAGATGCTGCCACTTATTACTGCCAGCAA AGGAGTAGTTACCCATTCACGTTCGGCTCGGG GACAAAGTTGGAAATAAAACGGGCTGATGCTG CACCAACTGTATCCATCTTCCCACCATCCAGTG AGCAGTTAACATCTGGAGGTGCCTCAGTCGTG TGCTTCTTGAACAACTTCTACCCCAAAGACATC AATGTCAAGTGGAAGATTGATGGCAGTGAACG ACAAAATGGCGTCCTGAACAGTTGGACTGATC AGGACAGCAAAGACAGCACCTACAGCATGAGC AGCACCCTCACGTTGACCAAGGACGAGTATGA ACGACATAACAGCTATACCTGTGAGGCCACTC ACAAGACATCAACTTCACCCATTGTCAAGAGC TTCAACAGGAATGAGTGTTAG	1070
SM1B222	pDR000028076	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGATGTT GTGATGACCCAAACTCCACTCTCCCTGCCTGTC AGTCTTGGAGATCAAGCCTCCATCTCTTGCAGA TCTAGTCAGAGCCTTATACACAATGATGGAAA CACCTATTTACATTGGTACCTCCAGAAGCCAGG	1071

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		CCAGTCTCCAAAGCTCCTGATCTACAAAGTTTC CAACCGATTTTCTGGGGTCCCAGACAGGTTCA GTGGCAGTGGATCAGGGACAGATTTCACAGTC AAGATCAGCAGAGTGGAGGCTGAGGATCTGGG AGTTTATTTCTGCTCTCAAAGTACACATGTTCC GTTCACGTTCGGTGCTGGGACCAAGCTGGAGC TGAAACGGGCTGATGCTGCACCAACTGTATCC ATCTTCCCACCATCCAGTGAGCAGTTAACATCT GGAGGTGCCTCAGTCGTGTGCTTCTTGAACAAC TTCTACCCCAAAGACATCAATGTCAAGTGGAA GATTGATGGCAGTGAACGACAAAATGGCGTCC TGAACAGTTGGACTGATCAGGACAGCAAAGAC AGCACCTACAGCATGAGCAGCACCCTCACGTT GACCAAGGACGAGTATGAACGACATAACAGCT ATACCTGTGAGGCCACTCACAAGACATCAACT TCACCCATTGTCAAGAGCTTCAACAGGAATGA GTGTTAG	
SM1B223	pDR000028077	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCCAAATT GTTCTCTCCCAGTCTCCAGCAATCATGTCTGCA TCTCCAGGGGAGAAGGTCACCATAACCTGCAG TGCCAGCTTAAGTGTCAGTTTCATGCACTGGTT CCAGCAGAAGCCAGGCACTTCTCCCAAACTCT GGATTTATAGCGCTTCCAACCTGGCTTCTGGAG TCCCTGCTCGCTTCAGTGGCAGTGGATCTGGGA CCTCTTACTCTCTCACAATCAGCCGAATGGAGG CTGAAGATGCTGCCACTTATTACTGCCAGCAA AGGAGTAGCTACCCATTCACGTTCGGCTCGGG GACAAAGTTGGAAATAAAACGGGCTGATGCTG CACCAACTGTATCCATCTTCCCACCATCCAGTG AGCAGTTAACATCTGGAGGTGCCTCAGTCGTG TGCTTCTTGAACAACTTCTACCCCAAAGACATC AATGTCAAGTGGAAGATTGATGGCAGTGAACG ACAAAATGGCGTCCTGAACAGTTGGACTGATC AGGACAGCAAAGACAGCACCTACAGCATGAGC AGCACCCTCACGTTGACCAAGGACGAGTATGA ACGACATAACAGCTATACCTGTGAGGCCACTC ACAAGACATCAACTTCACCCATTGTCAAGAGC TTCAACAGGAATGAGTGTTAG	1072
SM1B224	pDR000028078	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCCAAATT GTTCTCACCCAGTCTCCAGCAATCATGTCTGCA TCTCCAGGGGAGAAGGTCACCATAACCTGCAG TGCCAGCTCAAGTGTAAGTTTCATGCACTGGTT CCAGCAGAAGCCAGGCACTTCTCCCAAACTCT GGATTTATAGCACATCCAACCTGGCTTCTGGAG TCCCTGCTCGCTTCAGTGGCAGTGGATCTGGGA CCTCTTACTCTCTCACAATCAGCCGAATGGAGG	1073

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		CTGAAGATGCTGCCACTTATTACTGCCAGCAA AGGAGTACTTACCCATACACGTTCGGAGGGGG GACCAAGATGGAAATAAAACGGGCTGATGCTG CACCAACTGTATCCATCTTCCCACCATCCAGTG AGCAGTTAACATCTGGAGGTGCCTCAGTCGTG TGCTTCTTGAACAACTTCTACCCCAAAGACATC AATGTCAAGTGGAAGATTGATGGCAGTGAACG ACAAAATGGCGTCCTGAACAGTTGGACTGATC AGGACAGCAAAGACAGCACCTACAGCATGAGC AGCACCCTCACGTTGACCAAGGACGAGTATGA ACGACATAACAGCTATACCTGTGAGGCCACTC ACAAGACATCAACTTCACCCATTGTCAAGAGC TTCAACAGGAATGAGTGTTAG	
SM1B225	pDR000028079	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGATATT GTGCTAACTCAGTCTCCAGCAATCATGTCTGCA TCTCTAGGGGAACGGGTCACCATGACCTGCAC TGCCAGCTCAAGTGTAAGTTCCAGTTACTTGCA CTGGTACCAGCAGAAGCCAGGATCCTCCCCCA AACTCTGGGTTTATAGCACATCCAACCTGGCTT CTGGAGTCCCAGCTCGCTTCAGTGGCAGTGGG TCTGGGTCCTCTTACTCTCTCACAATCAGCAGC ATGGAGCCTGAAGATACTGCCACTTATTACTGC CACCAGTATCATCGTTCCCCACAGACGTTCGGT GGAGGCACCAAGCTGGAAATCAAACGGGCTGA TGCTGCACCAACTGTATCCATCTTCCCACCATC CAGTGAGCAGTTAACATCTGGAGGTGCCTCAG TCGTGTGCTTCTTGAACAACTTCTACCCCAAAG ACATCAATGTCAAGTGGAAGATTGATGGCAGT GAACGACAAAATGGCGTCCTGAACAGTTGGAC TGATCAGGACAGCAAAGACAGCACCTACAGCA TGAGCAGCACCCTCACGTTGACCAAGGACGAG TATGAACGACATAACAGCTATACCTGTGAGGC CACTCACAAGACATCAACTTCACCCATTGTCAA GAGCTTCAACAGGAATGAGTGTTAG	1074
SM1B226	pDR000028080	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCCAAATT GTTCTCACCCAGTCTCCAGCAATCATGTCTGCA TCTCCAGGGGAGAAGGTCACCATTACCTGCAG TGCCAGCTCAAGTGTCAGTTTCATGCACTGGTT CCAGCAGAAGCCAGGCACTTCTCCCAAACTCT GGATTTATAGCGCATCCAACCTGGCTTCTGGAG TCCCTGCTCGCTTCAGTGGCAGTGGATCTGGGA CCTCTTACTCTCTCACAATCAGCCGAATGGAGG CTGAAGATGCTGCCACTTATTACTGCCAGCAA AGGAGTAGTTACCCATACACGTTCGGAGGGGG GACCAAGCTGGAAATAAAGCGGGCTGATGCTG CACCAACTGTATCCATCTTCCCACCATCCAGTG	1075

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		AGCAGTTAACATCTGGAGGTGCCTCAGTCGTG TGCTTCTTGAACAACTTCTACCCCAAAGACATC AATGTCAAGTGGAAGATTGATGGCAGTGAACG ACAAAATGGCGTCCTGAACAGTTGGACTGATC AGGACAGCAAAGACAGCACCTACAGCATGAGC AGCACCCTCACGTTGACCAAGGACGAGTATGA ACGACATAACAGCTATACCTGTGAGGCCACTC ACAAGACATCAACTTCACCCATTGTCAAGAGC TTCAACAGGAATGAGTGTTAG	
SM1B227	pDR000028081	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGATATT GTGCTAACTCAGTCTCCAGCAATCATGTCTGCA TCTCCAGGGGAAAAGGTCACCATGACCTGCAG TGCCAGCTCAAGTGTAAGTTACATGCACTGGT ACCAGCAGAAGTCAAGCACCTCCCCCAAACTC TGGATTTATGACACATCCAAACTGGCTTCTGGA GTCCCAGGTCGCTTCAGTGGCAGTGGGTCTGG AAACTCTTACTCTCTCACGATCAGCAGCATGGA GGCTGAAGATGTTGCCACTTATTACTGTTTTCA GGGGAGTGGGTACCCACTCACGTTCGGCTCGG GGACAAAGTTGGAAATAAAACGGGCTGATGCT GCACCAACTGTATCCATCTTCCCACCATCCAGT GAGCAGTTAACATCTGGAGGTGCCTCAGTCGT GTGCTTCTTGAACAACTTCTACCCCAAAGACAT CAATGTCAAGTGGAAGATTGATGGCAGTGAAC GACAAAATGGCGTCCTGAACAGTTGGACTGAT CAGGACAGCAAAGACAGCACCTACAGCATGAG CAGCACCCTCACGTTGACCAAGGACGAGTATG AACGACATAACAGCTATACCTGTGAGGCCACT CACAAGACATCAACTTCACCCATTGTCAAGAG CTTCAACAGGAATGAGTGTTAG	1076
SM1B228	pDR000028082	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCCAAATT GTTCTCACCCAGTCTCCAGCAATCATGTCTGCA TCTCCAGGGGAGAAGGTCACCATAACCTGCAG TGCCAGCTCAAGTGTCAGTTACATGCACTGGTT CCAGCAGAAGCCAGGCACTTCTCCCAAACTCT GGATTTATAGCGCATCCAACCTGGCTTCTGGAG TCCCTGCTCGCTTCAGTGGCAGTGGATCTGGGA CCTCTTACTCTCTCACAATCAGCCGAATGGAGG CTGAAGATGCTGCCACTTATTACTGCCAGCAA AGGAGTAGTTACCCATTCACGTTCGGCTCGGG GACAAAGTTGGAAATAAAACGGGCTGATGCTG CACCAACTGTATCCATCTTCCCACCATCCAGTG AGCAGTTAACATCTGGAGGTGCCTCAGTCGTG TGCTTCTTGAACAACTTCTACCCCAAAGACATC AATGTCAAGTGGAAGATTGATGGCAGTGAACG ACAAAATGGCGTCCTGAACAGTTGGACTGATC	1077

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		AGGACAGCAAAGACAGCACCTACAGCATGAGC AGCACCCTCACGTTGACCAAGGACGAGTATGA ACGACATAACAGCTATACCTGTGAGGCCACTC ACAAGACATCAACTTCACCCATTGTCAAGAGC TTCAACAGGAATGAGTGTTAG	

Table 38. HlgA Antibody Heavy Chain CDSs

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
SM1B215	pDR000027230	GAGGTTCAGCTGCAGCAGTCTGGGCCTGAGCT GAAGAAGCCTGGAGAGACAGTCAAGATCTCCT GCAAGACTTCTGGATATACCTTCACAATTTATG GAATGAACTGGATGAAGCAGGCTCCAGGAAAG GGTTTAAAGTGGATGGGCTGGATAAACACCTA CACTGGAGAGCCAACATATGCTGATGACTTCA AGGGACGGTTTGCCTTCTCTTTGGAAACCTCTG CCAGCACTGCCTATTTGCAGATCAACAACCTCA AAAATGAGGACACGGCTACATATTTCTGTGCA AGATGCTACTATAAATACGAGGACTATGCTAT GGACTACTGGGGTCAAGGAACCTCAGTCACCG TCTCCTCAGCCAAAACGACACCCCCATCTGTCT ATCCACTGGCCCCTGGATCTGCTGCCCAAACTA ACTCCATGGTGACCCTGGGATGCCTGGTCAAG GGCTATTTCCCTGAGCCAGTGACAGTGACCTG GAACTCTGGATCCCTGTCCAGCGGTGTGCACA CCTTCCCAGCTGTCCTGGAGTCTGACCTCTACA CTCTGAGCAGCTCAGTGACTGTCCCCTCCAGCC CTCGGCCCAGCGAGACCGTCACCTGCAACGTT GCCCACCCGGCCAGCAGCACCAAGGTGGACAA GAAAATTGTGCCCAGGGATTGTGGTTGTAAGC CTTGCATATGTACAGTCCCAGAAGTATCATCTG TCTTCATCTTCCCCCCAAAGCCCAAGGATGTGC TCACCATTACTCTGACTCCTAAGGTCACGTGTG TTGTGGTAGACATCAGCAAGGATGATCCCGAG GTCCAGTTCAGCTGGTTTGTAGATGATGTGGAG GTGCACACAGCTCAGACGCAACCCCGGGAGGA GCAGTTCAACAGCACTTTCCGCTCAGTCAGTGA ACTTCCCATCATGCACCAGGACTGGCTCAATG GCAAGGAGTTCAAATGCAGGGTCAACAGTGCA GCTTTCCCTGCCCCCATCGAGAAAACCATCTCC AAAACCAAAGGCAGACCGAAGGCTCCACAGGT GTACACCATTCCACCTCCCAAGGAGCAGATGG CCAAGGATAAAGTCAGTCTGACCTGCATGATA ACAGACTTCTTCCCTGAAGACATTACTGTGGAG TGGCAGTGGAATGGGCAGCCAGCGGAGAACTA	1078

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		CAAGAACACTCAGCCCATCATGAACACGAATG GCTCTTACTTCGTCTACAGCAAGCTCAATGTGC AGAAGAGCAACTGGGAGGCAGGAAATACTTTC ACCTGCTCTGTGTTACATGAGGGCCTGCACAAC CACCATACTGAGAAGAGCCTCTCCCACTCTCCT GGTAAA	
SM1B216	pDR000027231	GAAGTGAAGCTGGTGGAGTCTGGGGGAGGTTT AGTGAAGCCTGGAGGGTCCCTGAAACTCTCCT GTGCAGCCTCTGGATTCACTTTCAGTAGCTATG CCATGTCTTGGGTTCGCCAGACTCCAGAAAAG AGGCTGGAGTGGGTCGCAGCCATTAATGGTAA TGGTGGTAGCACCTACTATCCAGACACTGTGA AGGACCGATTCACCATCTCCAGAGACAATGCC AAGAACACCCTTTACCTACAAATGAGCAGTCT GAGGTCTGAGGACACAGCCTTGTATTACTGTG CAAGACATAGGGCTGATGGTCCCTGGTTTACTT ACTGGGGCCAAGGGACTCTGGTCACTGTCTCT GCAGCCAAAACGACACCCCCATCTGTCTATCC ACTGGCCCCTGGATCTGCTGCCCAAACTAACCC CATGGTGACCCTGGGATGCCTGGTCAAGGGCT ATTTCCCTGAGCCAGTGACAGTGACCTGGAAC TCTGGATCCCTGTCCAGCGGTGTGCACACCTTC CCAGCTGTCCTGGAGTCTGACCTCTACACTCTG AGCAGCTCAGTGACTGTCCCCTCCAGCCCTCGG CCCAGCGAGACCGTCACCTGCAACGTTGCCCA CCCGGCCAGCAGCACCAAGGTGGACAAGAAA ATTGTGCCCAGGGATTGTGGTTGTAAGCCTTGC ATATGTACAGTCCCAGAAGTATCATCTGTCTTC ATCTTCCCCCCAAAGCCCAAGGATGTGCTCACC ATTACTCTGACTCCTAAGGTCACGTGTGTTGTG GTAGACATCAGCAAGGATGATCCCGAGGTCCA GTTCAGCTGGTTTGTAGATGATGTGGAGGTGC ACACAGCTCAGACGCAACCCCGGGAGGAGCAG TTCAACAGCACTTTCCGCTCAGTCAGTGAACTT CCCATCATGCACCAGGACTGGCTCAATGGCAA GGAGTTCAAATGCAGGGTCAACAGTGCAGCTT TCCCTGCCCCCATCGAGAAAACCATCTCCAAA ACCAAAGGCAGACCGAAGGCTCCACAGGTGTA CACCATTCCACCTCCCAAGGAGCAGATGGCCA AGGATAAAGTCAGTCTGACCTGCATGATAACA GACTTCTTCCCTGAAGACATTACTGTGGAGTGG CAGTGGAATGGGCAGCCAGCGGAGAACTACAA GAACACTCAGCCCATCATGAACACGAATGGCT CTTACTTCGTCTACAGCAAGCTCAATGTGCAGA AGAGCAACTGGGAGGCAGGAAATACTTTCACC TGCTCTGTGTTACATGAGGGCCTGCACAACCAC CATACTGAGAAGAGCCTCTCCCACTCTCCTGGT AAA	1079

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
SM1B217	pDR000027921	GAAGTGAAGCTGGTGGAAAGCGGCGGAGGCCT GGTGAAACCTGGCGGCAGCCTGAAGCTGAGCT GCGCCGCCAGCGGCTTCACCTTCAGCAACTAC GCCATGAGCTGGGTGCGCCAGACCCCCGAGAA GCGGCTGGAATGGGTGGCCAGCATCAGCAGAC GGGGCAGCACCTACTACCCCGACAGCGTGAAG GGCCGGTTCACCATCAGCCGGGACAACGCCCG GAACATCCTGTACCTGCAGATGAGCAGCCTGC GGAGCGAGGACACCGCCCTGTACTACTGCGCC ACCGTGTACTACGACAACCCTTGGTTTGTGTAC TGGGGCCAGGGCACCCTGGTGACAGTGTCCGC TGCCAAAACGACACCACCAAGTGTCTATCCAC TGGCCCCTGGATCTGCTGCCCAAACTAACTCCA TGGTGACCCTGGGATGCCTGGTCAAGGGCTAT TTCCCTGAGCCAGTGACAGTGACCTGGAACTCT GGATCCCTGTCCAGCGGTGTGCACACCTTCCCA GCTGTCCTGGAGTCTGACCTCTACACTCTGAGC AGCTCAGTGACTGTCCCCTCCAGCCCTCGGCCC AGCGAGACCGTCACCTGCAACGTTGCCCACCC GGCCAGCAGCACCAAGGTGGACAAGAAAATTG TGCCCAGGGATTGTGGTTGTAAGCCTTGCATAT GTACAGTCCCAGAAGTATCATCTGTCTTCATCT TCCCCCCAAAGCCCAAGGATGTGCTCACCATT ACTCTGACTCCTAAGGTCACGTGTGTTGTGGTA GACATCAGCAAGGATGATCCCGAGGTCCAGTT CAGCTGGTTTGTAGATGATGTGGAGGTGCACA CAGCTCAGACGCAACCCCGGGAGGAGCAGTTC AACAGCACTTTCCGCTCAGTCAGTGAACTTCCC ATCATGCACCAGGACTGGCTCAATGGCAAGGA GTTCAAATGCAGGGTCAACAGTGCAGCTTTCC CTGCCCCCATCGAGAAAACCATCTCCAAAACC AAAGGCAGACCGAAGGCTCCACAGGTGTACAC CATTCCACCTCCCAAGGAGCAGATGGCCAAGG ATAAAGTCAGTCTGACCTGCATGATAACAGAC TTCTTCCCTGAAGACATTACTGTGGAGTGGCAG TGGAATGGGCAGCCAGCGGAGAACTACAAGA ACACTCAGCCCATCATGAACACGAATGGCTCT TACTTCGTCTACAGCAAGCTCAATGTGCAGAA GAGCAACTGGGAGGCAGGAAATACTTTCACCT GCTCTGTGTTACATGAGGGCCTGCACAACCAC CATACTGAGAAGAGCCTCTCCCACTCTCCTGGT AAA	1080
SM1B218	pDR000027922	CAGATCCAGCTGGTGCAGAGCGGCCCTGAGCT GAAGAAACCCGGCGAGACAGTGAAGATCAGCT GCAAGACCAGCGGCTACACCTTCACCATCTAC GGCATGAACTGGACCAAGCAGGCCCCTGGCAA GGGCCTGAAGTGGATGGGCTGGATCAACACCT ACACCGGCGAGCCCACCTACGCCGACGACTTC	1081

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		AAGGGCAGATTCGCCTTCAGCCTGGAAACCAG CGCCAGCACCGCCTACCTGCAGATCAACAACC TGAAGAACGAGGACACCGCCACCTACTTTTGC GCCCGGTGCTACTATAAGTACGAGGACTACGC CATGGACTACTGGGGCCAGGGCACCAGCGTGA CCGTGTCCTCTGCCAAAACGACACCACCAAGT GTCTATCCACTGGCCCCTGGATCTGCTGCCCAA ACTAACTCCATGGTGACCCTGGGATGCCTGGTC AAGGGCTATTTCCCTGAGCCAGTGACAGTGAC CTGGAACTCTGGATCCCTGTCCAGCGGTGTGCA CACCTTCCCAGCTGTCCTGGAGTCTGACCTCTA CACTCTGAGCAGCTCAGTGACTGTCCCCTCCAG CCCTCGGCCCAGCGAGACCGTCACCTGCAACG TTGCCCACCCGGCCAGCAGCACCAAGGTGGAC AAGAAAATTGTGCCCAGGGATTGTGGTTGTAA GCCTTGCATATGTACAGTCCCAGAAGTATCATC TGTCTTCATCTTCCCCCCAAAGCCCAAGGATGT GCTCACCATTACTCTGACTCCTAAGGTCACGTG TGTTGTGGTAGACATCAGCAAGGATGATCCCG AGGTCCAGTTCAGCTGGTTTGTAGATGATGTGG AGGTGCACACAGCTCAGACGCAACCCCGGGAG GAGCAGTTCAACAGCACTTTCCGCTCAGTCAGT GAACTTCCCATCATGCACCAGGACTGGCTCAA TGGCAAGGAGTTCAAATGCAGGGTCAACAGTG CAGCTTTCCCTGCCCCCATCGAGAAAACCATCT CCAAAACCAAAGGCAGACCGAAGGCTCCACAG GTGTACACCATTCCACCTCCCAAGGAGCAGAT GGCCAAGGATAAAGTCAGTCTGACCTGCATGA TAACAGACTTCTTCCCTGAAGACATTACTGTGG AGTGGCAGTGGAATGGGCAGCCAGCGGAGAA CTACAAGAACACTCAGCCCATCATGAACACGA ATGGCTCTTACTTCGTCTACAGCAAGCTCAATG TGCAGAAGAGCAACTGGGAGGCAGGAAATACT TTCACCTGCTCTGTGTTACATGAGGGCCTGCAC AACCACCATACTGAGAAGAGCCTCTCCCACTC TCCTGGTAAA	
SM1B219	pDR000027923	GACGTGAAGCTGGTGGAAAGCGGCGGAGGCCT GGTGAAACCTGGCGGCAGCCTGAAGCTGAGCT GCGCCGCCAGCGGCTTCACCTTCAGCAGCTAC GCCATGAGCTGGGTGCGCCAGACCCCCGAGAA GCGGCTGGAATGGGTGGCCGCCATCAACGGCA ACGGCGGCAGCACCTACTACCCCGACACCGTG AAGGACCGGTTCACCATCAGCCGGGACAACGC CAAGAACACCCTGTACCTGCAGATGAGCAGCC TGCGGAGCGAGGACACCGCCCTGTACTACTGC GCCAGACACAGAGCCGACGGCCCCTGGTTCAC ATACTGGGGCCAGGGCACCCTGGTGACAGTGT CCGCTGCCAAAACGACACCACCAAGTGTCTAT	1082

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		CCACTGGCCCCTGGATCTGCTGCCCAAACTAAC TCCATGGTGACCCTGGGATGCCTGGTCAAGGG CTATTTCCCTGAGCCAGTGACAGTGACCTGGA ACTCTGGATCCCTGTCCAGCGGTGTGCACACCT TCCCAGCTGTCCTGGAGTCTGACCTCTACACTC TGAGCAGCTCAGTGACTGTCCCCTCCAGCCCTC GGCCCAGCGAGACCGTCACCTGCAACGTTGCC CACCCGGCCAGCAGCACCAAGGTGGACAAGAA AATTGTGCCCAGGGATTGTGGTTGTAAGCCTTG CATATGTACAGTCCCAGAAGTATCATCTGTCTT CATCTTCCCCCCAAAGCCCAAGGATGTGCTCAC CATTACTCTGACTCCTAAGGTCACGTGTGTTGT GGTAGACATCAGCAAGGATGATCCCGAGGTCC AGTTCAGCTGGTTTGTAGATGATGTGGAGGTG CACACAGCTCAGACGCAACCCCGGGAGGAGCA GTTCAACAGCACTTTCCGCTCAGTCAGTGAACT TCCCATCATGCACCAGGACTGGCTCAATGGCA AGGAGTTCAAATGCAGGGTCAACAGTGCAGCT TTCCCTGCCCCCATCGAGAAAACCATCTCCAAA ACCAAAGGCAGACCGAAGGCTCCACAGGTGTA CACCATTCCACCTCCCAAGGAGCAGATGGCCA AGGATAAAGTCAGTCTGACCTGCATGATAACA GACTTCTTCCCTGAAGACATTACTGTGGAGTGG CAGTGGAATGGGCAGCCAGCGGAGAACTACAA GAACACTCAGCCCATCATGAACACGAATGGCT CTTACTTCGTCTACAGCAAGCTCAATGTGCAGA AGAGCAACTGGGAGGCAGGAAATACTTTCACC TGCTCTGTGTTACATGAGGGCCTGCACAACCAC CATACTGAGAAGAGCCTCTCCCACTCTCCTGGT AAA	
SM1B220	pDR000027921	GAAGTGAAGCTGGTGGAAAGCGGCGGAGGCCT GGTGAAACCTGGCGGCAGCCTGAAGCTGAGCT GCGCCGCCAGCGGCTTCACCTTCAGCAACTAC GCCATGAGCTGGGTGCGCCAGACCCCCGAGAA GCGGCTGGAATGGGTGGCCAGCATCAGCAGAC GGGGCAGCACCTACTACCCCGACAGCGTGAAG GGCCGGTTCACCATCAGCCGGGACAACGCCCG GAACATCCTGTACCTGCAGATGAGCAGCCTGC GGAGCGAGGACACCGCCCTGTACTACTGCGCC ACCGTGTACTACGACAACCCTTGGTTTGTGTAC TGGGGCCAGGGCACCCTGGTGACAGTGTCCGC TGCCAAAACGACACCACCAAGTGTCTATCCAC TGGCCCCTGGATCTGCTGCCCAAACTAACTCCA TGGTGACCCTGGGATGCCTGGTCAAGGGCTAT TTCCCTGAGCCAGTGACAGTGACCTGGAACTCT GGATCCCTGTCCAGCGGTGTGCACACCTTCCCA GCTGTCCTGGAGTCTGACCTCTACACTCTGAGC AGCTCAGTGACTGTCCCCTCCAGCCCTCGGCCC	1083

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		AGCGAGACCGTCACCTGCAACGTTGCCCACCC GGCCAGCAGCACCAAGGTGGACAAGAAAATTG TGCCCAGGGATTGTGGTTGTAAGCCTTGCATAT GTACAGTCCCAGAAGTATCATCTGTCTTCATCT TCCCCCCAAAGCCCAAGGATGTGCTCACCATT ACTCTGACTCCTAAGGTCACGTGTGTTGTGGTA GACATCAGCAAGGATGATCCCGAGGTCCAGTT CAGCTGGTTTGTAGATGATGTGGAGGTGCACA CAGCTCAGACGCAACCCCGGGAGGAGCAGTTC AACAGCACTTTCCGCTCAGTCAGTGAACTTCCC ATCATGCACCAGGACTGGCTCAATGGCAAGGA GTTCAAATGCAGGGTCAACAGTGCAGCTTTCC CTGCCCCCATCGAGAAAACCATCTCCAAAACC AAAGGCAGACCGAAGGCTCCACAGGTGTACAC CATTCCACCTCCCAAGGAGCAGATGGCCAAGG ATAAAGTCAGTCTGACCTGCATGATAACAGAC TTCTTCCCTGAAGACATTACTGTGGAGTGGCAG TGGAATGGGCAGCCAGCGGAGAACTACAAGA ACACTCAGCCCATCATGAACACGAATGGCTCT TACTTCGTCTACAGCAAGCTCAATGTGCAGAA GAGCAACTGGGAGGCAGGAAATACTTTCACCT GCTCTGTGTTACATGAGGGCCTGCACAACCAC CATACTGAGAAGAGCCTCTCCCACTCTCCTGGT AAA	

Table 39. HlgA Antibody Heavy Chain Primary Transcripts

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
SM1B215	pDR000027230	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAGGTTCA GCTGCAGCAGTCTGGGCCTGAGCTGAAGAAGC CTGGAGAGACAGTCAAGATCTCCTGCAAGACT TCTGGATATACCTTCACAATTTATGGAATGAAC TGGATGAAGCAGGCTCCAGGAAAGGGTTTAAA GTGGATGGGCTGGATAAACACCTACACTGGAG AGCCAACATATGCTGATGACTTCAAGGGACGG TTTGCCTTCTCTTTGGAAACCTCTGCCAGCACT GCCTATTTGCAGATCAACAACCTCAAAAATGA GGACACGGCTACATATTTCTGTGCAAGATGCT ACTATAAATACGAGGACTATGCTATGGACTAC TGGGGTCAAGGAACCTCAGTCACCGTCTCCTC AGCCAAAACGACACCCCCATCTGTCTATCCAC TGGCCCCTGGATCTGCTGCCCAAACTAACTCCA TGGTGACCCTGGGATGCCTGGTCAAGGGCTAT TTCCCTGAGCCAGTGACAGTGACCTGGAACTC	1084

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		TGGATCCCTGTCCAGCGGTGTGCACACCTTCCC AGCTGTCCTGGAGTCTGACCTCTACACTCTGAG CAGCTCAGTGACTGTCCCCTCCAGCCCTCGGCC CAGCGAGACCGTCACCTGCAACGTTGCCCACC CGGCCAGCAGCACCAAGGTGGACAAGAAAATT GTGCCCAGGGATTGTGGTTGTAAGCCTTGCAT ATGTACAGTCCCAGAAGTATCATCTGTCTTCAT CTTCCCCCCAAAGCCCAAGGATGTGCTCACCA TTACTCTGACTCCTAAGGTCACGTGTGTTGTGG TAGACATCAGCAAGGATGATCCCGAGGTCCAG TTCAGCTGGTTTGTAGATGATGTGGAGGTGCA CACAGCTCAGACGCAACCCCGGGAGGAGCAGT TCAACAGCACTTTCCGCTCAGTCAGTGAACTTC CCATCATGCACCAGGACTGGCTCAATGGCAAG GAGTTCAAATGCAGGGTCAACAGTGCAGCTTT CCCTGCCCCCATCGAGAAAACCATCTCCAAAA CCAAAGGCAGACCGAAGGCTCCACAGGTGTAC ACCATTCCACCTCCCAAGGAGCAGATGGCCAA GGATAAAGTCAGTCTGACCTGCATGATAACAG ACTTCTTCCCTGAAGACATTACTGTGGAGTGGC AGTGGAATGGGCAGCCAGCGGAGAACTACAA GAACACTCAGCCCATCATGAACACGAATGGCT CTTACTTCGTCTACAGCAAGCTCAATGTGCAGA AGAGCAACTGGGAGGCAGGAAATACTTTCACC TGCTCTGTGTTACATGAGGGCCTGCACAACCA CCATACTGAGAAGAGCCTCTCCCACTCTCCTGG TAAATGA	
SM1B216	pDR000027231	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAAGTGAA GCTGGTGGAGTCTGGGGGAGGTTTAGTGAAGC CTGGAGGGTCCCTGAAACTCTCCTGTGCAGCCT CTGGATTCACTTTCAGTAGCTATGCCATGTCTT GGGTTCGCCAGACTCCAGAAAAGAGGCTGGAG TGGGTCGCAGCCATTAATGGTAATGGTGGTAG CACCTACTATCCAGACACTGTGAAGGACCGAT TCACCATCTCCAGAGACAATGCCAAGAACACC CTTTACCTACAAATGAGCAGTCTGAGGTCTGA GGACACAGCCTTGTATTACTGTGCAAGACATA GGGCTGATGGTCCCTGGTTTACTTACTGGGGCC AAGGGACTCTGGTCACTGTCTCTGCAGCCAAA ACGACACCCCCATCTGTCTATCCACTGGCCCCT GGATCTGCTGCCCAAACTAACCCCATGGTGAC CCTGGGATGCCTGGTCAAGGGCTATTTCCCTGA GCCAGTGACAGTGACCTGGAACTCTGGATCCC TGTCCAGCGGTGTGCACACCTTCCCAGCTGTCC TGGAGTCTGACCTCTACACTCTGAGCAGCTCA GTGACTGTCCCCTCCAGCCCTCGGCCCAGCGA GACCGTCACCTGCAACGTTGCCCACCCGGCCA	1085

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GCAGCACCAAGGTGGACAAGAAAATTGTGCCC AGGGATTGTGGTTGTAAGCCTTGCATATGTAC AGTCCCAGAAGTATCATCTGTCTTCATCTTCCC CCCAAAGCCCAAGGATGTGCTCACCATTACTC TGACTCCTAAGGTCACGTGTGTTGTGGTAGAC ATCAGCAAGGATGATCCCGAGGTCCAGTTCAG CTGGTTTGTAGATGATGTGGAGGTGCACACAG CTCAGACGCAACCCCGGGAGGAGCAGTTCAAC AGCACTTTCCGCTCAGTCAGTGAACTTCCCATC ATGCACCAGGACTGGCTCAATGGCAAGGAGTT CAAATGCAGGGTCAACAGTGCAGCTTTCCCTG CCCCCATCGAGAAAACCATCTCCAAAACCAAA GGCAGACCGAAGGCTCCACAGGTGTACACCAT TCCACCTCCCAAGGAGCAGATGGCCAAGGATA AAGTCAGTCTGACCTGCATGATAACAGACTTC TTCCCTGAAGACATTACTGTGGAGTGGCAGTG GAATGGGCAGCCAGCGGAGAACTACAAGAAC ACTCAGCCCATCATGAACACGAATGGCTCTTA CTTCGTCTACAGCAAGCTCAATGTGCAGAAGA GCAACTGGGAGGCAGGAAATACTTTCACCTGC TCTGTGTTACATGAGGGCCTGCACAACCACCA TACTGAGAAGAGCCTCTCCCACTCTCCTGGTAA ATGA	
SM1B217	pDR000027921	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAAGTGAA GCTGGTGGAAAGCGGCGGAGGCCTGGTGAAAC CTGGCGGCAGCCTGAAGCTGAGCTGCGCCGCC AGCGGCTTCACCTTCAGCAACTACGCCATGAG CTGGGTGCGCCAGACCCCCGAGAAGCGGCTGG AATGGGTGGCCAGCATCAGCAGACGGGGCAGC ACCTACTACCCCGACAGCGTGAAGGGCCGGTT CACCATCAGCCGGGACAACGCCCGGAACATCC TGTACCTGCAGATGAGCAGCCTGCGGAGCGAG GACACCGCCCTGTACTACTGCGCCACCGTGTA CTACGACAACCCTTGGTTTGTGTACTGGGGCCA GGGCACCCTGGTGACAGTGTCCGCTGCCAAAA CGACACCACCAAGTGTCTATCCACTGGCCCCT GGATCTGCTGCCCAAACTAACTCCATGGTGAC CCTGGGATGCCTGGTCAAGGGCTATTTCCCTGA GCCAGTGACAGTGACCTGGAACTCTGGATCCC TGTCCAGCGGTGTGCACACCTTCCCAGCTGTCC TGGAGTCTGACCTCTACACTCTGAGCAGCTCA GTGACTGTCCCCTCCAGCCCTCGGCCCAGCGA GACCGTCACCTGCAACGTTGCCCACCCGGCCA GCAGCACCAAGGTGGACAAGAAAATTGTGCCC AGGGATTGTGGTTGTAAGCCTTGCATATGTAC AGTCCCAGAAGTATCATCTGTCTTCATCTTCCC CCCAAAGCCCAAGGATGTGCTCACCATTACTC	1086

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		TGACTCCTAAGGTCACGTGTGTTGTGGTAGAC ATCAGCAAGGATGATCCCGAGGTCCAGTTCAG CTGGTTTGTAGATGATGTGGAGGTGCACACAG CTCAGACGCAACCCCGGGAGGAGCAGTTCAAC AGCACTTTCCGCTCAGTCAGTGAACTTCCCATC ATGCACCAGGACTGGCTCAATGGCAAGGAGTT CAAATGCAGGGTCAACAGTGCAGCTTTCCCTG CCCCCATCGAGAAAACCATCTCCAAAACCAAA GGCAGACCGAAGGCTCCACAGGTGTACACCAT TCCACCTCCCAAGGAGCAGATGGCCAAGGATA AAGTCAGTCTGACCTGCATGATAACAGACTTC TTCCCTGAAGACATTACTGTGGAGTGGCAGTG GAATGGGCAGCCAGCGGAGAACTACAAGAAC ACTCAGCCCATCATGAACACGAATGGCTCTTA CTTCGTCTACAGCAAGCTCAATGTGCAGAAGA GCAACTGGGAGGCAGGAAATACTTTCACCTGC TCTGTGTTACATGAGGGCCTGCACAACCACCA TACTGAGAAGAGCCTCTCCCACTCTCCTGGTAA ATGA	
SM1B218	pDR000027922	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGATCCA GCTGGTGCAGAGCGGCCCTGAGCTGAAGAAAC CCGGCGAGACAGTGAAGATCAGCTGCAAGACC AGCGGCTACACCTTCACCATCTACGGCATGAA CTGGACCAAGCAGGCCCCTGGCAAGGGCCTGA AGTGGATGGGCTGGATCAACACCTACACCGGC GAGCCCACCTACGCCGACGACTTCAAGGGCAG ATTCGCCTTCAGCCTGGAAACCAGCGCCAGCA CCGCCTACCTGCAGATCAACAACCTGAAGAAC GAGGACACCGCCACCTACTTTTGCGCCCGGTG CTACTATAAGTACGAGGACTACGCCATGGACT ACTGGGGCCAGGGCACCAGCGTGACCGTGTCC TCTGCCAAAACGACACCACCAAGTGTCTATCC ACTGGCCCCTGGATCTGCTGCCCAAACTAACTC CATGGTGACCCTGGGATGCCTGGTCAAGGGCT ATTTCCCTGAGCCAGTGACAGTGACCTGGAAC TCTGGATCCCTGTCCAGCGGTGTGCACACCTTC CCAGCTGTCCTGGAGTCTGACCTCTACACTCTG AGCAGCTCAGTGACTGTCCCCTCCAGCCCTCG GCCCAGCGAGACCGTCACCTGCAACGTTGCCC ACCCGGCCAGCAGCACCAAGGTGGACAAGAA AATTGTGCCCAGGGATTGTGGTTGTAAGCCTTG CATATGTACAGTCCCAGAAGTATCATCTGTCTT CATCTTCCCCCCAAAGCCCAAGGATGTGCTCA CCATTACTCTGACTCCTAAGGTCACGTGTGTTG TGGTAGACATCAGCAAGGATGATCCCGAGGTC CAGTTCAGCTGGTTTGTAGATGATGTGGAGGT GCACACAGCTCAGACGCAACCCCGGGAGGAGC	1087

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		AGTTCAACAGCACTTTCCGCTCAGTCAGTGAA CTTCCCATCATGCACCAGGACTGGCTCAATGG CAAGGAGTTCAAATGCAGGGTCAACAGTGCAG CTTTCCCTGCCCCCATCGAGAAAACCATCTCCA AAACCAAAGGCAGACCGAAGGCTCCACAGGT GTACACCATTCCACCTCCCAAGGAGCAGATGG CCAAGGATAAAGTCAGTCTGACCTGCATGATA ACAGACTTCTTCCCTGAAGACATTACTGTGGA GTGGCAGTGGAATGGGCAGCCAGCGGAGAACT ACAAGAACACTCAGCCCATCATGAACACGAAT GGCTCTTACTTCGTCTACAGCAAGCTCAATGTG CAGAAGAGCAACTGGGAGGCAGGAAATACTTT CACCTGCTCTGTGTTACATGAGGGCCTGCACA ACCACCATACTGAGAAGAGCCTCTCCCACTCT CCTGGTAAATGA	
SM1B219	pDR000027923	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGACGTGAA GCTGGTGGAAAGCGGCGGAGGCCTGGTGAAAC CTGGCGGCAGCCTGAAGCTGAGCTGCGCCGCC AGCGGCTTCACCTTCAGCAGCTACGCCATGAG CTGGGTGCGCCAGACCCCCGAGAAGCGGCTGG AATGGGTGGCCGCCATCAACGGCAACGGCGGC AGCACCTACTACCCCGACACCGTGAAGGACCG GTTCACCATCAGCCGGGACAACGCCAAGAACA CCCTGTACCTGCAGATGAGCAGCCTGCGGAGC GAGGACACCGCCCTGTACTACTGCGCCAGACA CAGAGCCGACGGCCCCTGGTTCACATACTGGG GCCAGGGCACCCTGGTGACAGTGTCCGCTGCC AAAACGACACCACCAAGTGTCTATCCACTGGC CCCTGGATCTGCTGCCCAAACTAACTCCATGGT GACCCTGGGATGCCTGGTCAAGGGCTATTTCC CTGAGCCAGTGACAGTGACCTGGAACTCTGGA TCCCTGTCCAGCGGTGTGCACACCTTCCCAGCT GTCCTGGAGTCTGACCTCTACACTCTGAGCAGC TCAGTGACTGTCCCCTCCAGCCCTCGGCCCAGC GAGACCGTCACCTGCAACGTTGCCCACCCGGC CAGCAGCACCAAGGTGGACAAGAAAATTGTGC CCAGGGATTGTGGTTGTAAGCCTTGCATATGTA CAGTCCCAGAAGTATCATCTGTCTTCATCTTCC CCCCAAAGCCCAAGGATGTGCTCACCATTACT CTGACTCCTAAGGTCACGTGTGTTGTGGTAGAC ATCAGCAAGGATGATCCCGAGGTCCAGTTCAG CTGGTTTGTAGATGATGTGGAGGTGCACACAG CTCAGACGCAACCCCGGGAGGAGCAGTTCAAC AGCACTTTCCGCTCAGTCAGTGAACTTCCCATC ATGCACCAGGACTGGCTCAATGGCAAGGAGTT CAAATGCAGGGTCAACAGTGCAGCTTTCCCTG CCCCCATCGAGAAAACCATCTCCAAAACCAAA	1088

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GGCAGACCGAAGGCTCCACAGGTGTACACCAT TCCACCTCCCAAGGAGCAGATGGCCAAGGATA AAGTCAGTCTGACCTGCATGATAACAGACTTC TTCCCTGAAGACATTACTGTGGAGTGGCAGTG GAATGGGCAGCCAGCGGAGAACTACAAGAAC ACTCAGCCCATCATGAACACGAATGGCTCTTA CTTCGTCTACAGCAAGCTCAATGTGCAGAAGA GCAACTGGGAGGCAGGAAATACTTTCACCTGC TCTGTGTTACATGAGGGCCTGCACAACCACCA TACTGAGAAGAGCCTCTCCCACTCTCCTGGTAA ATGA	
SM1B220	pDR000027921	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAAGTGAA GCTGGTGGAAAGCGGCGGAGGCCTGGTGAAAC CTGGCGGCAGCCTGAAGCTGAGCTGCGCCGCC AGCGGCTTCACCTTCAGCAACTACGCCATGAG CTGGGTGCGCCAGACCCCCGAGAAGCGGCTGG AATGGGTGGCCAGCATCAGCAGACGGGGCAGC ACCTACTACCCCGACAGCGTGAAGGGCCGGTT CACCATCAGCCGGGACAACGCCCGGAACATCC TGTACCTGCAGATGAGCAGCCTGCGGAGCGAG GACACCGCCCTGTACTACTGCGCCACCGTGTA CTACGACAACCCTTGGTTTGTGTACTGGGGCCA GGGCACCCTGGTGACAGTGTCCGCTGCCAAAA CGACACCACCAAGTGTCTATCCACTGGCCCCT GGATCTGCTGCCCAAACTAACTCCATGGTGAC CCTGGGATGCCTGGTCAAGGGCTATTTCCCTGA GCCAGTGACAGTGACCTGGAACTCTGGATCCC TGTCCAGCGGTGTGCACACCTTCCCAGCTGTCC TGGAGTCTGACCTCTACACTCTGAGCAGCTCA GTGACTGTCCCCTCCAGCCCTCGGCCCAGCGA GACCGTCACCTGCAACGTTGCCCACCCGGCCA GCAGCACCAAGGTGGACAAGAAAATTGTGCCC AGGGATTGTGGTTGTAAGCCTTGCATATGTAC AGTCCCAGAAGTATCATCTGTCTTCATCTTCCC CCCAAAGCCCAAGGATGTGCTCACCATTACTC TGACTCCTAAGGTCACGTGTGTTGTGGTAGAC ATCAGCAAGGATGATCCCGAGGTCCAGTTCAG CTGGTTTGTAGATGATGTGGAGGTGCACACAG CTCAGACGCAACCCCGGGAGGAGCAGTTCAAC AGCACTTTCCGCTCAGTCAGTGAACTTCCCATC ATGCACCAGGACTGGCTCAATGGCAAGGAGTT CAAATGCAGGGTCAACAGTGCAGCTTTCCCTG CCCCCATCGAGAAAACCATCTCCAAAACCAAA GGCAGACCGAAGGCTCCACAGGTGTACACCAT TCCACCTCCCAAGGAGCAGATGGCCAAGGATA AAGTCAGTCTGACCTGCATGATAACAGACTTC TTCCCTGAAGACATTACTGTGGAGTGGCAGTG	1089

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GAATGGGCAGCCAGCGGAGAACTACAAGAAC ACTCAGCCCATCATGAACACGAATGGCTCTTA CTTCGTCTACAGCAAGCTCAATGTGCAGAAGA GCAACTGGGAGGCAGGAAATACTTTCACCTGC TCTGTGTTACATGAGGGCCTGCACAACCACCA TACTGAGAAGAGCCTCTCCCACTCTCCTGGTAA ATGA	

Table 40. HlgA Antibody Light Chain CDSs

mAB/Fab name	Construct ID	Light_Chain.CDS	SEQ ID NO:
SM1B215	pDR000027233	GATGTTGTGATGACCCAAACTCCACTCACTTTG TCGGTTACCATTGGACAACCCGCCTCCATCTCT TGCAAGTCAAGTCAGAGCCTCTTAGATAGTGA TGGAAAGACATATTTGAATTGGTTGTTACAGA GGCCAGGCCAGTCTCCGAAGCGCCTAATCTAT GTGGTGTCTAAATTGGACTCTGGAGTCCCTGAC AGGTTCACTGGCAGTGGATCAGGGACAGATTT CACACTGAAAATCAGCAGAGTGGAGGCTGAGG ATTTGGGAGTTTATTATTGCTGGCAAGGTACAC ATTTTCCGCTCACGTTCGGTGCTGGGACCAAGC TGGAGCTGAAACGGGCTGATGCTGCACCAACT GTATCCATCTTCCCACCATCCAGTGAGCAGTTA ACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTG AACAACTTCTACCCCAAAGACATCAATGTCAA GTGGAAGATTGATGGCAGTGAACGACAAAATG GCGTCCTGAACAGTTGGACTGATCAGGACAGC AAAGACAGCACCTACAGCATGAGCAGCACCCT CACGTTGACCAAGGACGAGTATGAACGACATA ACAGCTATACCTGTGAGGCCACTCACAAGACA TCAACTTCACCCATTGTCAAGAGCTTCAACAG GAATGAGTGT	1090
SM1B216	pDR000027232	GATGTTGTGATGACCCAAACTCCATCCTCCTTT TCTGTATCTCTAGGAGACGGAGTCACCATTACT TGCAAGGCAAGTGAGGACATATATATTCGGTT AGCCTGGTATCAGCAGAAACCAGGAAATGCTC CTAGGCTCCTAATATTTGGTGCAACCAGTTTGG AAACTGGGGTTCCTTCAAGATTCAGTGGCAGT GGATCTGGAAAGGATTACACTCTCAGCATTAC CAGTCTTCAGACTGAAGATGTTGCTACTTATTA CTGTCAACAGTATTGGAGAACTCCGCTCACGTT CGGTGCTGGGACCAAGCTGGAGCTGAAACGGG CTGATGCTGCACCAACTGTATCCATCTTCCCAC CATCCAGTGAGCAGTTAACATCTGGAGGTGCC TCAGTCGTGTGCTTCTTGAACAACTTCTACCCC	1091

mAB/Fab name	Construct ID	Light_Chain.CDS	SEQ ID NO:
		AAAGACATCAATGTCAAGTGGAAGATTGATGG CAGTGAACGACAAAATGGCGTCCTGAACAGTT GGACTGATCAGGACAGCAAAGACAGCACCTAC AGCATGAGCAGCACCCTCACGTTGACCAAGGA CGAGTATGAACGACATAACAGCTATACCTGTG AGGCCACTCACAAGACATCAACTTCACCCATT GTCAAGAGCTTCAACAGGAATGAGTGT	
SM1B217	pDR000027924	GACGTGGTGATGACCCAGACCCCCCTGACCCT GAGCGTGACCATCGGCCAGCCTGCCAGCATCA GCTGCAAGAGCAGCCAGAGCCTGCTGGACAGC GACGGCAAGACCTACCTGAACTGGCTGCTGCA GCGGCCTGGCCAGAGCCCCAAGCGGCTGATCT ACCTGGTGTCCAAGCTGGACTCCGGCGTGCCC GACAGATTCACAGGCAGCGGCAGCGGCACCGA CTTCACCCTGAAGATCAGCCGGGTGGAAGCCG AGGACCTGGGCGTGTACTACTGCTGGCAGGGC ACCCACTTCCCACTGACCTTCGGAGCCGGCAC CAAGCTGGAACTGAAGCGGGCTGATGCTGCAC CGACTGTGTCCATCTTCCCACCATCCAGTGAGC AGTTAACATCTGGAGGTGCCTCAGTCGTGTGCT TCTTGAACAACTTCTACCCCAAAGACATCAAT GTCAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAGG ACAGCAAAGACAGCACCTACAGCATGAGCAGC ACCCTCACGTTGACCAAGGACGAGTATGAACG ACATAACAGCTATACCTGTGAGGCCACTCACA AGACATCAACTTCACCCATTGTCAAGAGCTTC AACAGGAATGAGTGT	1092
SM1B218	pDR000027924	GACGTGGTGATGACCCAGACCCCCCTGACCCT GAGCGTGACCATCGGCCAGCCTGCCAGCATCA GCTGCAAGAGCAGCCAGAGCCTGCTGGACAGC GACGGCAAGACCTACCTGAACTGGCTGCTGCA GCGGCCTGGCCAGAGCCCCAAGCGGCTGATCT ACCTGGTGTCCAAGCTGGACTCCGGCGTGCCC GACAGATTCACAGGCAGCGGCAGCGGCACCGA CTTCACCCTGAAGATCAGCCGGGTGGAAGCCG AGGACCTGGGCGTGTACTACTGCTGGCAGGGC ACCCACTTCCCACTGACCTTCGGAGCCGGCAC CAAGCTGGAACTGAAGCGGGCTGATGCTGCAC CGACTGTGTCCATCTTCCCACCATCCAGTGAGC AGTTAACATCTGGAGGTGCCTCAGTCGTGTGCT TCTTGAACAACTTCTACCCCAAAGACATCAAT GTCAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAGG ACAGCAAAGACAGCACCTACAGCATGAGCAGC ACCCTCACGTTGACCAAGGACGAGTATGAACG ACATAACAGCTATACCTGTGAGGCCACTCACA AGACATCAACTTCACCCATTGTCAAGAGCTTC	1093

mAB/Fab name	Construct ID	Light_Chain.CDS	SEQ ID NO:
		AACAGGAATGAGTGT	
SM1B219	pDR000027233	GATGTTGTGATGACCCAAACTCCACTCACTTTG TCGGTTACCATTGGACAACCCGCCTCCATCTCT TGCAAGTCAAGTCAGAGCCTCTTAGATAGTGA TGGAAAGACATATTTGAATTGGTTGTTACAGA GGCCAGGCCAGTCTCCGAAGCGCCTAATCTAT GTGGTGTCTAAATTGGACTCTGGAGTCCCTGAC AGGTTCACTGGCAGTGGATCAGGGACAGATTT CACACTGAAAATCAGCAGAGTGGAGGCTGAGG ATTTGGGAGTTTATTATTGCTGGCAAGGTACAC ATTTTCCGCTCACGTTCGGTGCTGGGACCAAGC TGGAGCTGAAACGGGCTGATGCTGCACCAACT GTATCCATCTTCCCACCATCCAGTGAGCAGTTA ACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTG AACAACTTCTACCCCAAAGACATCAATGTCAA GTGGAAGATTGATGGCAGTGAACGACAAAATG GCGTCCTGAACAGTTGGACTGATCAGGACAGC AAAGACAGCACCTACAGCATGAGCAGCACCCT CACGTTGACCAAGGACGAGTATGAACGACATA ACAGCTATACCTGTGAGGCCACTCACAAGACA TCAACTTCACCCATTGTCAAGAGCTTCAACAG GAATGAGTGT	1094
SM1B220	pDR000027233	GATGTTGTGATGACCCAAACTCCACTCACTTTG TCGGTTACCATTGGACAACCCGCCTCCATCTCT TGCAAGTCAAGTCAGAGCCTCTTAGATAGTGA TGGAAAGACATATTTGAATTGGTTGTTACAGA GGCCAGGCCAGTCTCCGAAGCGCCTAATCTAT GTGGTGTCTAAATTGGACTCTGGAGTCCCTGAC AGGTTCACTGGCAGTGGATCAGGGACAGATTT CACACTGAAAATCAGCAGAGTGGAGGCTGAGG ATTTGGGAGTTTATTATTGCTGGCAAGGTACAC ATTTTCCGCTCACGTTCGGTGCTGGGACCAAGC TGGAGCTGAAACGGGCTGATGCTGCACCAACT GTATCCATCTTCCCACCATCCAGTGAGCAGTTA ACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTG AACAACTTCTACCCCAAAGACATCAATGTCAA GTGGAAGATTGATGGCAGTGAACGACAAAATG GCGTCCTGAACAGTTGGACTGATCAGGACAGC AAAGACAGCACCTACAGCATGAGCAGCACCCT CACGTTGACCAAGGACGAGTATGAACGACATA ACAGCTATACCTGTGAGGCCACTCACAAGACA TCAACTTCACCCATTGTCAAGAGCTTCAACAG GAATGAGTGT	1095

Table 41. HlgA Antibody Light Chain Primary Transcripts

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
SM1B215	pDR000027233	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGATGTT GTGATGACCCAAACTCCACTCACTTTGTCGGTT ACCATTGGACAACCCGCCTCCATCTCTTGCAAG TCAAGTCAGAGCCTCTTAGATAGTGATGGAAA GACATATTTGAATTGGTTGTTACAGAGGCCAG GCCAGTCTCCGAAGCGCCTAATCTATGTGGTGT CTAAATTGGACTCTGGAGTCCCTGACAGGTTC ACTGGCAGTGGATCAGGGACAGATTTCACACT GAAAATCAGCAGAGTGGAGGCTGAGGATTTGG GAGTTTATTATTGCTGGCAAGGTACACATTTTC CGCTCACGTTCGGTGCTGGGACCAAGCTGGAG CTGAAACGGGCTGATGCTGCACCAACTGTATC CATCTTCCCACCATCCAGTGAGCAGTTAACATC TGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAA CTTCTACCCCAAAGACATCAATGTCAAGTGGA AGATTGATGGCAGTGAACGACAAAATGGCGTC CTGAACAGTTGGACTGATCAGGACAGCAAAGA CAGCACCTACAGCATGAGCAGCACCCTCACGT TGACCAAGGACGAGTATGAACGACATAACAGC TATACCTGTGAGGCCACTCACAAGACATCAAC TTCACCCATTGTCAAGAGCTTCAACAGGAATG AGTGTTAG	1096
SM1B216	pDR000027232	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGATGTT GTGATGACCCAAACTCCATCCTCCTTTTCTGTA TCTCTAGGAGACGGAGTCACCATTACTTGCAA GGCAAGTGAGGACATATATATTCGGTTAGCCT GGTATCAGCAGAAACCAGGAAATGCTCCTAGG CTCCTAATATTTGGTGCAACCAGTTTGGAAACT GGGGTTCCTTCAAGATTCAGTGGCAGTGGATC TGGAAAGGATTACACTCTCAGCATTACCAGTC TTCAGACTGAAGATGTTGCTACTTATTACTGTC AACAGTATTGGAGAACTCCGCTCACGTTCGGT GCTGGGACCAAGCTGGAGCTGAAACGGGCTGA TGCTGCACCAACTGTATCCATCTTCCCACCATC CAGTGAGCAGTTAACATCTGGAGGTGCCTCAG TCGTGTGCTTCTTGAACAACTTCTACCCCAAAG ACATCAATGTCAAGTGGAAGATTGATGGCAGT GAACGACAAAATGGCGTCCTGAACAGTTGGAC TGATCAGGACAGCAAAGACAGCACCTACAGCA TGAGCAGCACCCTCACGTTGACCAAGGACGAG TATGAACGACATAACAGCTATACCTGTGAGGC CACTCACAAGACATCAACTTCACCCATTGTCA AGAGCTTCAACAGGAATGAGTGTTAG	1097
SM1B217	pDR000027924	ATGGAGACACATTCTCAGGTCTTTGTATACATG	1098

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		TTGCTGTGGTTGTCTGGTGTCGAGGGCGACGTG GTGATGACCCAGACCCCCCTGACCCTGAGCGT GACCATCGGCCAGCCTGCCAGCATCAGCTGCA AGAGCAGCCAGAGCCTGCTGGACAGCGACGGC AAGACCTACCTGAACTGGCTGCTGCAGCGGCC TGGCCAGAGCCCCAAGCGGCTGATCTACCTGG TGTCCAAGCTGGACTCCGGCGTGCCCGACAGA TTCACAGGCAGCGGCAGCGGCACCGACTTCAC CCTGAAGATCAGCCGGGTGGAAGCCGAGGACC TGGGCGTGTACTACTGCTGGCAGGGCACCCAC TTCCCACTGACCTTCGGAGCCGGCACCAAGCT GGAACTGAAGCGGGCTGATGCTGCACCGACTG TGTCCATCTTCCCACCATCCAGTGAGCAGTTAA CATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGA ACAACTTCTACCCCAAAGACATCAATGTCAAG TGGAAGATTGATGGCAGTGAACGACAAAATGG CGTCCTGAACAGTTGGACTGATCAGGACAGCA AAGACAGCACCTACAGCATGAGCAGCACCCTC ACGTTGACCAAGGACGAGTATGAACGACATAA CAGCTATACCTGTGAGGCCACTCACAAGACAT CAACTTCACCCATTGTCAAGAGCTTCAACAGG AATGAGTGTTAG	
SM1B218	pDR000027924	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACGTG GTGATGACCCAGACCCCCCTGACCCTGAGCGT GACCATCGGCCAGCCTGCCAGCATCAGCTGCA AGAGCAGCCAGAGCCTGCTGGACAGCGACGGC AAGACCTACCTGAACTGGCTGCTGCAGCGGCC TGGCCAGAGCCCCAAGCGGCTGATCTACCTGG TGTCCAAGCTGGACTCCGGCGTGCCCGACAGA TTCACAGGCAGCGGCAGCGGCACCGACTTCAC CCTGAAGATCAGCCGGGTGGAAGCCGAGGACC TGGGCGTGTACTACTGCTGGCAGGGCACCCAC TTCCCACTGACCTTCGGAGCCGGCACCAAGCT GGAACTGAAGCGGGCTGATGCTGCACCGACTG TGTCCATCTTCCCACCATCCAGTGAGCAGTTAA CATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGA ACAACTTCTACCCCAAAGACATCAATGTCAAG TGGAAGATTGATGGCAGTGAACGACAAAATGG CGTCCTGAACAGTTGGACTGATCAGGACAGCA AAGACAGCACCTACAGCATGAGCAGCACCCTC ACGTTGACCAAGGACGAGTATGAACGACATAA CAGCTATACCTGTGAGGCCACTCACAAGACAT CAACTTCACCCATTGTCAAGAGCTTCAACAGG AATGAGTGTTAG	1099
SM1B219	pDR000027233	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGATGTT GTGATGACCCAAACTCCACTCACTTTGTCGGTT	1100

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		ACCATTGGACAACCCGCCTCCATCTCTTGCAAG TCAAGTCAGAGCCTCTTAGATAGTGATGGAAA GACATATTTGAATTGGTTGTTACAGAGGCCAG GCCAGTCTCCGAAGCGCCTAATCTATGTGGTGT CTAAATTGGACTCTGGAGTCCCTGACAGGTTC ACTGGCAGTGGATCAGGGACAGATTTCACACT GAAAATCAGCAGAGTGGAGGCTGAGGATTTGG GAGTTTATTATTGCTGGCAAGGTACACATTTTC CGCTCACGTTCGGTGCTGGGACCAAGCTGGAG CTGAAACGGGCTGATGCTGCACCAACTGTATC CATCTTCCCACCATCCAGTGAGCAGTTAACATC TGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAA CTTCTACCCCAAAGACATCAATGTCAAGTGGA AGATTGATGGCAGTGAACGACAAAATGGCGTC CTGAACAGTTGGACTGATCAGGACAGCAAAGA CAGCACCTACAGCATGAGCAGCACCCTCACGT TGACCAAGGACGAGTATGAACGACATAACAGC TATACCTGTGAGGCCACTCACAAGACATCAAC TTCACCCATTGTCAAGAGCTTCAACAGGAATG AGTGTTAG	
SM1B220	pDR000027233	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGATGTT GTGATGACCCAAACTCCACTCACTTTGTCGGTT ACCATTGGACAACCCGCCTCCATCTCTTGCAAG TCAAGTCAGAGCCTCTTAGATAGTGATGGAAA GACATATTTGAATTGGTTGTTACAGAGGCCAG GCCAGTCTCCGAAGCGCCTAATCTATGTGGTGT CTAAATTGGACTCTGGAGTCCCTGACAGGTTC ACTGGCAGTGGATCAGGGACAGATTTCACACT GAAAATCAGCAGAGTGGAGGCTGAGGATTTGG GAGTTTATTATTGCTGGCAAGGTACACATTTTC CGCTCACGTTCGGTGCTGGGACCAAGCTGGAG CTGAAACGGGCTGATGCTGCACCAACTGTATC CATCTTCCCACCATCCAGTGAGCAGTTAACATC TGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAA CTTCTACCCCAAAGACATCAATGTCAAGTGGA AGATTGATGGCAGTGAACGACAAAATGGCGTC CTGAACAGTTGGACTGATCAGGACAGCAAAGA CAGCACCTACAGCATGAGCAGCACCCTCACGT TGACCAAGGACGAGTATGAACGACATAACAGC TATACCTGTGAGGCCACTCACAAGACATCAAC TTCACCCATTGTCAAGAGCTTCAACAGGAATG AGTGTTAG	1101

Table 42. HlgC Antibody Heavy Chain CDSs

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
SM1B202	pDR000027136	GAAGTGATGCTGGTGGAAAGCGGCGGAGGCCT GGTGAAACCTGGCGGCAGCCTGAAGCTGAGCT GCGCCGCCAGCGGCTTCACCTTCAGCAACTAC GCCATGAGCTGGGTCCGCCAGACCCCCGAGAA GCGGCTGGAATGGGTGGCCAGCATCAGCAGAC GGGGCAGCACCTACTACCCCGACAGCGGCAAG GGCCGGTTCACCATCAGCCGGGACAACGCCCG GAACATCCCCTACCTGCAGATGAGCAGCCTGC GGAGCGAGGACACCGCCCTGTACTACTGCGCC ACCGTGTACTACGACAACCCTTGGTTTGTGTAC TGGGGCCAGGGCACCCTGGTGACAGTGTCCGC TGCCAAAACAACAGCACCAAGTGTCTATCCAC TGGCCCCTGTGTGTGGAGATACAACTGGCTCCT CGGTGACTCTAGGATGCCTGGTCAAGGGTTATT TCCCTGAGCCAGTGACCTTGACCTGGAACTCTG GATCCCTGTCCAGTGGTGTGCACACCTTCCCAG CTGTCCTGCAGTCTGACCTCTACACCCTCAGCA GCTCAGTGACTGTAACCTCGAGCACCTGGCCC AGCCAGTCCATCACCTGCAATGTGGCCCACCC GGCAAGCAGCACCAAGGTGGACAAGAAAATT GAGCCCAGAGGGCCCACAATCAAGCCCTGTCC TCCATGCAAATGCCCAGCACCTAACCTCTTGGG TGGACCATCCGTCTTCATCTTCCCTCCAAAGAT CAAGGATGTACTCATGATCTCCCTGAGCCCCAT AGTCACATGTGTGGTGGTGGATGTGAGCGAGG ATGACCCAGATGTCCAGATCAGCTGGTTTGTG AACAACGTGGAAGTACACACAGCTCAGACACA AACCCATAGAGAGGATTACAACAGTACTCTCC GGGTGGTCAGTGCCCTCCCCATCCAGCACCAG GACTGGATGAGTGGCAAGGAGTTCAAATGCAA GGTCAACAACAAAGACCTCCCAGCGCCCATCG AGAGAACCATCTCAAAACCCAAAGGGTCAGTA AGAGCTCCACAGGTATATGTCTTGCCTCCACCA GAAGAAGAGATGACTAAGAAACAGGTCACTCT GACCTGCATGGTCACAGACTTCATGCCTGAAG ACATTTACGTGGAGTGGACCAACAACGGGAAA ACAGAGCTAAACTACAAGAACACTGAACCAGT CCTGGACTCTGATGGTTCTTACTTCATGTACAG CAAGCTGAGAGTGGAAAAGAAGAACTGGGTG GAAAGAAATAGCTACTCCTGTTCAGTGGTCCA CGAGGGTCTGCACAATCACCACACGACTAAGA GCTTCTCCCGGACTCCGGGTAAA	1102
SM1B203	pDR000027135	GAAGTGATGCTGGTGGAAAGCGGCGGAGGCCT GGTGAAACCTGGCGGCAGCCTGAAGCTGAGCT GCGCCGCCAGCGGCTTCACCTTCAGCAACTAC GCCATGAGCTGGGTCCGCCAGACCCCCGAGAA	1103

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		GCGGCTGGAATGGGTGGCCAGCATCAGCAGAC GGGGCAGCACCTACTACCCCGACAGCGTGAAG GGCCGGTTCACCATCAGCCGGGACAACGCCCG GAACATCCTGTACCTGCAGATGAGCAGCCTGC GGAGCGAGGACACCGCCCTGTACTACTGCGCC ACCGTGTACTACGACAACCCTTGGTTTGTGTAC TGGGGCCAGGGCACCCTGGTGACAGTGTCCGC TGCCAAAACAACAGCACCAAGTGTCTATCCAC TGGCCCCTGTGTGTGGAGATACAACTGGCTCCT CGGTGACTCTAGGATGCCTGGTCAAGGGTTATT TCCCTGAGCCAGTGACCTTGACCTGGAACTCTG GATCCCTGTCCAGTGGTGTGCACACCTTCCCAG CTGTCCTGCAGTCTGACCTCTACACCCTCAGCA GCTCAGTGACTGTAACCTCGAGCACCTGGCCC AGCCAGTCCATCACCTGCAATGTGGCCCACCC GGCAAGCAGCACCAAGGTGGACAAGAAAATT GAGCCCAGAGGGCCCACAATCAAGCCCTGTCC TCCATGCAAATGCCCAGCACCTAACCTCTTGGG TGGACCATCCGTCTTCATCTTCCCTCCAAAGAT CAAGGATGTACTCATGATCTCCCTGAGCCCCAT AGTCACATGTGTGGTGGTGGATGTGAGCGAGG ATGACCCAGATGTCCAGATCAGCTGGTTTGTG AACAACGTGGAAGTACACACAGCTCAGACACA AACCCATAGAGAGGATTACAACAGTACTCTCC GGGTGGTCAGTGCCCTCCCCATCCAGCACCAG GACTGGATGAGTGGCAAGGAGTTCAAATGCAA GGTCAACAACAAAGACCTCCCAGCGCCCATCG AGAGAACCATCTCAAAACCCAAAGGGTCAGTA AGAGCTCCACAGGTATATGTCTTGCCTCCACCA GAAGAAGAGATGACTAAGAAACAGGTCACTCT GACCTGCATGGTCACAGACTTCATGCCTGAAG ACATTTACGTGGAGTGGACCAACAACGGGAAA ACAGAGCTAAACTACAAGAACACTGAACCAGT CCTGGACTCTGATGGTTCTTACTTCATGTACAG CAAGCTGAGAGTGGAAAAGAAGAACTGGGTG GAAAGAAATAGCTACTCCTGTTCAGTGGTCCA CGAGGGTCTGCACAATCACCACACGACTAAGA GCTTCTCCCGGACTCCGGGTAAA	
SM1B204	pDR000027134	GAAGTGAAGCTGGTGGAAAGCGGCGGAGGCCT GGTGAAACCTGGCGGCAGCCTGAAGCTGAGCT GCGCCGCCAGCGGCTTCACCTTCAGCAACTAC GCCATGAGCTGGGTCCGCCAGACCCCCGAGAA GCGGCTGGAATGGGTGGCCAGCATCAGCAGAC GGGGCAGCACCTACTACCCCGACAGCGTGAAG GGCCGGTTCACCATCAGCCGGGACAACGCCCG GAACATCCTGTACCTGCAGATGAGCAGCCTGC GGAGCGAGGACACCGCCCTGTACTACTGCGCC ACCGTGTACTACGACAACCCTTGGTTTGTGTAC	1104

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		TGGGGCCAGGGCACCCTGGTGACAGTGTCCGC TGCCAAAACAACAGCACCAAGTGTCTATCCAC TGGCCCCTGTGTGTGGAGATACAACTGGCTCCT CGGTGACTCTAGGATGCCTGGTCAAGGGTTATT TCCCTGAGCCAGTGACCTTGACCTGGAACTCTG GATCCCTGTCCAGTGGTGTGCACACCTTCCCAG CTGTCCTGCAGTCTGACCTCTACACCCTCAGCA GCTCAGTGACTGTAACCTCGAGCACCTGGCCC AGCCAGTCCATCACCTGCAATGTGGCCCACCC GGCAAGCAGCACCAAGGTGGACAAGAAAATT GAGCCCAGAGGGCCCACAATCAAGCCCTGTCC TCCATGCAAATGCCCAGCACCTAACCTCTTGGG TGGACCATCCGTCTTCATCTTCCCTCCAAAGAT CAAGGATGTACTCATGATCTCCCTGAGCCCCAT AGTCACATGTGTGGTGGTGGATGTGAGCGAGG ATGACCCAGATGTCCAGATCAGCTGGTTTGTG AACAACGTGGAAGTACACACAGCTCAGACACA AACCCATAGAGAGGATTACAACAGTACTCTCC GGGTGGTCAGTGCCCTCCCCATCCAGCACCAG GACTGGATGAGTGGCAAGGAGTTCAAATGCAA GGTCAACAACAAAGACCTCCCAGCGCCCATCG AGAGAACCATCTCAAAACCCAAAGGGTCAGTA AGAGCTCCACAGGTATATGTCTTGCCTCCACCA GAAGAAGAGATGACTAAGAAACAGGTCACTCT GACCTGCATGGTCACAGACTTCATGCCTGAAG ACATTTACGTGGAGTGGACCAACAACGGGAAA ACAGAGCTAAACTACAAGAACACTGAACCAGT CCTGGACTCTGATGGTTCTTACTTCATGTACAG CAAGCTGAGAGTGGAAAAGAAGAACTGGGTG GAAAGAAATAGCTACTCCTGTTCAGTGGTCCA CGAGGGTCTGCACAATCACCACACGACTAAGA GCTTCTCCCGGACTCCGGGTAAA	
SM1B205	pDR000027134	GAAGTGAAGCTGGTGGAAAGCGGCGGAGGCCT GGTGAAACCTGGCGGCAGCCTGAAGCTGAGCT GCGCCGCCAGCGGCTTCACCTTCAGCAACTAC GCCATGAGCTGGGTCCGCCAGACCCCCGAGAA GCGGCTGGAATGGGTGGCCAGCATCAGCAGAC GGGGCAGCACCTACTACCCCGACAGCGTGAAG GGCCGGTTCACCATCAGCCGGGACAACGCCCG GAACATCCTGTACCTGCAGATGAGCAGCCTGC GGAGCGAGGACACCGCCCTGTACTACTGCGCC ACCGTGTACTACGACAACCCTTGGTTTGTGTAC TGGGGCCAGGGCACCCTGGTGACAGTGTCCGC TGCCAAAACAACAGCACCAAGTGTCTATCCAC TGGCCCCTGTGTGTGGAGATACAACTGGCTCCT CGGTGACTCTAGGATGCCTGGTCAAGGGTTATT TCCCTGAGCCAGTGACCTTGACCTGGAACTCTG GATCCCTGTCCAGTGGTGTGCACACCTTCCCAG	1105

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		CTGTCCTGCAGTCTGACCTCTACACCCTCAGCA GCTCAGTGACTGTAACCTCGAGCACCTGGCCC AGCCAGTCCATCACCTGCAATGTGGCCCACCC GGCAAGCAGCACCAAGGTGGACAAGAAAATT GAGCCCAGAGGGCCCACAATCAAGCCCTGTCC TCCATGCAAATGCCCAGCACCTAACCTCTTGGG TGGACCATCCGTCTTCATCTTCCCTCCAAAGAT CAAGGATGTACTCATGATCTCCCTGAGCCCCAT AGTCACATGTGTGGTGGTGGATGTGAGCGAGG ATGACCCAGATGTCCAGATCAGCTGGTTTGTG AACAACGTGGAAGTACACACAGCTCAGACACA AACCCATAGAGAGGATTACAACAGTACTCTCC GGGTGGTCAGTGCCCTCCCCATCCAGCACCAG GACTGGATGAGTGGCAAGGAGTTCAAATGCAA GGTCAACAACAAAGACCTCCCAGCGCCCATCG AGAGAACCATCTCAAAACCCAAAGGGTCAGTA AGAGCTCCACAGGTATATGTCTTGCCTCCACCA GAAGAAGAGATGACTAAGAAACAGGTCACTCT GACCTGCATGGTCACAGACTTCATGCCTGAAG ACATTTACGTGGAGTGGACCAACAACGGGAAA ACAGAGCTAAACTACAAGAACACTGAACCAGT CCTGGACTCTGATGGTTCTTACTTCATGTACAG CAAGCTGAGAGTGGAAAAGAAGAACTGGGTG GAAAGAAATAGCTACTCCTGTTCAGTGGTCCA CGAGGGTCTGCACAATCACCACACGACTAAGA GCTTCTCCCGGACTCCGGGTAAA	
SM1B206	pDR000027134	GAAGTGAAGCTGGTGGAAAGCGGCGGAGGCCT GGTGAAACCTGGCGGCAGCCTGAAGCTGAGCT GCGCCGCCAGCGGCTTCACCTTCAGCAACTAC GCCATGAGCTGGGTCCGCCAGACCCCCGAGAA GCGGCTGGAATGGGTGGCCAGCATCAGCAGAC GGGGCAGCACCTACTACCCCGACAGCGTGAAG GGCCGGTTCACCATCAGCCGGGACAACGCCCG GAACATCCTGTACCTGCAGATGAGCAGCCTGC GGAGCGAGGACACCGCCCTGTACTACTGCGCC ACCGTGTACTACGACAACCCTTGGTTTGTGTAC TGGGGCCAGGGCACCCTGGTGACAGTGTCCGC TGCCAAAACAACAGCACCAAGTGTCTATCCAC TGGCCCCTGTGTGTGGAGATACAACTGGCTCCT CGGTGACTCTAGGATGCCTGGTCAAGGGTTATT TCCCTGAGCCAGTGACCTTGACCTGGAACTCTG GATCCCTGTCCAGTGGTGTGCACACCTTCCCAG CTGTCCTGCAGTCTGACCTCTACACCCTCAGCA GCTCAGTGACTGTAACCTCGAGCACCTGGCCC AGCCAGTCCATCACCTGCAATGTGGCCCACCC GGCAAGCAGCACCAAGGTGGACAAGAAAATT GAGCCCAGAGGGCCCACAATCAAGCCCTGTCC TCCATGCAAATGCCCAGCACCTAACCTCTTGGG	1106

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		TGGACCATCCGTCTTCATCTTCCCTCCAAAGAT CAAGGATGTACTCATGATCTCCCTGAGCCCCAT AGTCACATGTGTGGTGGTGGATGTGAGCGAGG ATGACCCAGATGTCCAGATCAGCTGGTTTGTG AACAACGTGGAAGTACACACAGCTCAGACACA AACCCATAGAGAGGATTACAACAGTACTCTCC GGGTGGTCAGTGCCCTCCCCATCCAGCACCAG GACTGGATGAGTGGCAAGGAGTTCAAATGCAA GGTCAACAACAAAGACCTCCCAGCGCCCATCG AGAGAACCATCTCAAAACCCAAAGGGTCAGTA AGAGCTCCACAGGTATATGTCTTGCCTCCACCA GAAGAAGAGATGACTAAGAAACAGGTCACTCT GACCTGCATGGTCACAGACTTCATGCCTGAAG ACATTTACGTGGAGTGGACCAACAACGGGAAA ACAGAGCTAAACTACAAGAACACTGAACCAGT CCTGGACTCTGATGGTTCTTACTTCATGTACAG CAAGCTGAGAGTGGAAAAGAAGAACTGGGTG GAAAGAAATAGCTACTCCTGTTCAGTGGTCCA CGAGGGTCTGCACAATCACCACACGACTAAGA GCTTCTCCCGGACTCCGGGTAAA	
SM1B207	pDR000027135	GAAGTGATGCTGGTGGAAAGCGGCGGAGGCCT GGTGAAACCTGGCGGCAGCCTGAAGCTGAGCT GCGCCGCCAGCGGCTTCACCTTCAGCAACTAC GCCATGAGCTGGGTCCGCCAGACCCCCGAGAA GCGGCTGGAATGGGTGGCCAGCATCAGCAGAC GGGGCAGCACCTACTACCCCGACAGCGTGAAG GGCCGGTTCACCATCAGCCGGGACAACGCCCG GAACATCCTGTACCTGCAGATGAGCAGCCTGC GGAGCGAGGACACCGCCCTGTACTACTGCGCC ACCGTGTACTACGACAACCCTTGGTTTGTGTAC TGGGGCCAGGGCACCCTGGTGACAGTGTCCGC TGCCAAAACAACAGCACCAAGTGTCTATCCAC TGGCCCCTGTGTGTGGAGATACAACTGGCTCCT CGGTGACTCTAGGATGCCTGGTCAAGGGTTATT TCCCTGAGCCAGTGACCTTGACCTGGAACTCTG GATCCCTGTCCAGTGGTGTGCACACCTTCCCAG CTGTCCTGCAGTCTGACCTCTACACCCTCAGCA GCTCAGTGACTGTAACCTCGAGCACCTGGCCC AGCCAGTCCATCACCTGCAATGTGGCCCACCC GGCAAGCAGCACCAAGGTGGACAAGAAAATT GAGCCCAGAGGGCCCACAATCAAGCCCTGTCC TCCATGCAAATGCCCAGCACCTAACCTCTTGGG TGGACCATCCGTCTTCATCTTCCCTCCAAAGAT CAAGGATGTACTCATGATCTCCCTGAGCCCCAT AGTCACATGTGTGGTGGTGGATGTGAGCGAGG ATGACCCAGATGTCCAGATCAGCTGGTTTGTG AACAACGTGGAAGTACACACAGCTCAGACACA AACCCATAGAGAGGATTACAACAGTACTCTCC	1107

mAB/Fab name	Construct ID	Heavy Chain CDS	SEQ ID NO:
		GGGTGGTCAGTGCCCTCCCCATCCAGCACCAG GACTGGATGAGTGGCAAGGAGTTCAAATGCAA GGTCAACAACAAAGACCTCCCAGCGCCCATCG AGAGAACCATCTCAAAACCCAAAGGGTCAGTA AGAGCTCCACAGGTATATGTCTTGCCTCCACCA GAAGAAGAGATGACTAAGAAACAGGTCACTCT GACCTGCATGGTCACAGACTTCATGCCTGAAG ACATTTACGTGGAGTGGACCAACAACGGGAAA ACAGAGCTAAACTACAAGAACACTGAACCAGT CCTGGACTCTGATGGTTCTTACTTCATGTACAG CAAGCTGAGAGTGGAAAAGAAGAACTGGGTG GAAAGAAATAGCTACTCCTGTTCAGTGGTCCA CGAGGGTCTGCACAATCACCACACGACTAAGA GCTTCTCCCGGACTCCGGGTAAA	

Table 43. HlgC Antibody Heavy Chain Primary Transcripts

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
SM1B202	pDR000027136	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAAGTGAT GCTGGTGGAAAGCGGCGGAGGCCTGGTGAAAC CTGGCGGCAGCCTGAAGCTGAGCTGCGCCGCC AGCGGCTTCACCTTCAGCAACTACGCCATGAG CTGGGTCCGCCAGACCCCCGAGAAGCGGCTGG AATGGGTGGCCAGCATCAGCAGACGGGGCAGC ACCTACTACCCCGACAGCGGCAAGGGCCGGTT CACCATCAGCCGGGACAACGCCCGGAACATCC CCTACCTGCAGATGAGCAGCCTGCGGAGCGAG GACACCGCCCTGTACTACTGCGCCACCGTGTAC TACGACAACCCTTGGTTTGTGTACTGGGGCCAG GGCACCCTGGTGACAGTGTCCGCTGCCAAAAC AACAGCACCAAGTGTCTATCCACTGGCCCCTGT GTGTGGAGATACAACTGGCTCCTCGGTGACTCT AGGATGCCTGGTCAAGGGTTATTTCCCTGAGCC AGTGACCTTGACCTGGAACTCTGGATCCCTGTC CAGTGGTGTGCACACCTTCCCAGCTGTCCTGCA GTCTGACCTCTACACCCTCAGCAGCTCAGTGAC TGTAACCTCGAGCACCTGGCCCAGCCAGTCCA TCACCTGCAATGTGGCCCACCCGGCAAGCAGC ACCAAGGTGGACAAGAAAATTGAGCCCAGAG GGCCCACAATCAAGCCCTGTCCTCCATGCAAA TGCCCAGCACCTAACCTCTTGGGTGGACCATCC GTCTTCATCTTCCCTCCAAAGATCAAGGATGTA CTCATGATCTCCCTGAGCCCCATAGTCACATGT GTGGTGGTGGATGTGAGCGAGGATGACCCAGA	1108

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		TGTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAGA GAGGATTACAACAGTACTCTCCGGGTGGTCAG TGCCCTCCCCATCCAGCACCAGGACTGGATGA GTGGCAAGGAGTTCAAATGCAAGGTCAACAAC AAAGACCTCCCAGCGCCCATCGAGAGAACCAT CTCAAAACCCAAAGGGTCAGTAAGAGCTCCAC AGGTATATGTCTTGCCTCCACCAGAAGAAGAG ATGACTAAGAAACAGGTCACTCTGACCTGCAT GGTCACAGACTTCATGCCTGAAGACATTTACGT GGAGTGGACCAACAACGGGAAAACAGAGCTA AACTACAAGAACACTGAACCAGTCCTGGACTC TGATGGTTCTTACTTCATGTACAGCAAGCTGAG AGTGGAAAAGAAGAACTGGGTGGAAAGAAAT AGCTACTCCTGTTCAGTGGTCCACGAGGGTCTG CACAATCACCACACGACTAAGAGCTTCTCCCG GACTCCGGGTAAATGA	
SM1B203	pDR000027135	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAAGTGAT GCTGGTGGAAAGCGGCGGAGGCCTGGTGAAAC CTGGCGGCAGCCTGAAGCTGAGCTGCGCCGCC AGCGGCTTCACCTTCAGCAACTACGCCATGAG CTGGGTCCGCCAGACCCCCGAGAAGCGGCTGG AATGGGTGGCCAGCATCAGCAGACGGGGCAGC ACCTACTACCCCGACAGCGTGAAGGGCCGGTT CACCATCAGCCGGGACAACGCCCGGAACATCC TGTACCTGCAGATGAGCAGCCTGCGGAGCGAG GACACCGCCCTGTACTACTGCGCCACCGTGTAC TACGACAACCCTTGGTTTGTGTACTGGGGCCAG GGCACCCTGGTGACAGTGTCCGCTGCCAAAAC AACAGCACCAAGTGTCTATCCACTGGCCCCTGT GTGTGGAGATACAACTGGCTCCTCGGTGACTCT AGGATGCCTGGTCAAGGGTTATTTCCCTGAGCC AGTGACCTTGACCTGGAACTCTGGATCCCTGTC CAGTGGTGTGCACACCTTCCCAGCTGTCCTGCA GTCTGACCTCTACACCCTCAGCAGCTCAGTGAC TGTAACCTCGAGCACCTGGCCCAGCCAGTCCA TCACCTGCAATGTGGCCCACCCGGCAAGCAGC ACCAAGGTGGACAAGAAAATTGAGCCCAGAG GGCCCACAATCAAGCCCTGTCCTCCATGCAAA TGCCCAGCACCTAACCTCTTGGGTGGACCATCC GTCTTCATCTTCCCTCCAAAGATCAAGGATGTA CTCATGATCTCCCTGAGCCCCATAGTCACATGT GTGGTGGTGGATGTGAGCGAGGATGACCCAGA TGTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAGA GAGGATTACAACAGTACTCTCCGGGTGGTCAG TGCCCTCCCCATCCAGCACCAGGACTGGATGA	1109

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GTGGCAAGGAGTTCAAATGCAAGGTCAACAAC AAAGACCTCCCAGCGCCCATCGAGAGAACCAT CTCAAAACCCAAAGGGTCAGTAAGAGCTCCAC AGGTATATGTCTTGCCTCCACCAGAAGAAGAG ATGACTAAGAAACAGGTCACTCTGACCTGCAT GGTCACAGACTTCATGCCTGAAGACATTTACGT GGAGTGGACCAACAACGGGAAAACAGAGCTA AACTACAAGAACACTGAACCAGTCCTGGACTC TGATGGTTCTTACTTCATGTACAGCAAGCTGAG AGTGGAAAAGAAGAACTGGGTGGAAAGAAAT AGCTACTCCTGTTCAGTGGTCCACGAGGGTCTG CACAATCACCACACGACTAAGAGCTTCTCCCG GACTCCGGGTAAATGA	
SM1B204	pDR000027134	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAAGTGAA GCTGGTGGAAAGCGGCGGAGGCCTGGTGAAAC CTGGCGGCAGCCTGAAGCTGAGCTGCGCCGCC AGCGGCTTCACCTTCAGCAACTACGCCATGAG CTGGGTCCGCCAGACCCCCGAGAAGCGGCTGG AATGGGTGGCCAGCATCAGCAGACGGGGCAGC ACCTACTACCCCGACAGCGTGAAGGGCCGGTT CACCATCAGCCGGGACAACGCCCGGAACATCC TGTACCTGCAGATGAGCAGCCTGCGGAGCGAG GACACCGCCCTGTACTACTGCGCCACCGTGTAC TACGACAACCCTTGGTTTGTGTACTGGGGCCAG GGCACCCTGGTGACAGTGTCCGCTGCCAAAAC AACAGCACCAAGTGTCTATCCACTGGCCCCTGT GTGTGGAGATACAACTGGCTCCTCGGTGACTCT AGGATGCCTGGTCAAGGGTTATTTCCCTGAGCC AGTGACCTTGACCTGGAACTCTGGATCCCTGTC CAGTGGTGTGCACACCTTCCCAGCTGTCCTGCA GTCTGACCTCTACACCCTCAGCAGCTCAGTGAC TGTAACCTCGAGCACCTGGCCCAGCCAGTCCA TCACCTGCAATGTGGCCCACCCGGCAAGCAGC ACCAAGGTGGACAAGAAAATTGAGCCCAGAG GGCCCACAATCAAGCCCTGTCCTCCATGCAAA TGCCCAGCACCTAACCTCTTGGGTGGACCATCC GTCTTCATCTTCCCTCCAAAGATCAAGGATGTA CTCATGATCTCCCTGAGCCCCATAGTCACATGT GTGGTGGTGGATGTGAGCGAGGATGACCCAGA TGTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAGA GAGGATTACAACAGTACTCTCCGGGTGGTCAG TGCCCTCCCCATCCAGCACCAGGACTGGATGA GTGGCAAGGAGTTCAAATGCAAGGTCAACAAC AAAGACCTCCCAGCGCCCATCGAGAGAACCAT CTCAAAACCCAAAGGGTCAGTAAGAGCTCCAC AGGTATATGTCTTGCCTCCACCAGAAGAAGAG	1110

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		ATGACTAAGAAACAGGTCACTCTGACCTGCAT GGTCACAGACTTCATGCCTGAAGACATTTACGT GGAGTGGACCAACAACGGGAAAACAGAGCTA AACTACAAGAACACTGAACCAGTCCTGGACTC TGATGGTTCTTACTTCATGTACAGCAAGCTGAG AGTGGAAAAGAAGAACTGGGTGGAAAGAAAT AGCTACTCCTGTTCAGTGGTCCACGAGGGTCTG CACAATCACCACACGACTAAGAGCTTCTCCCG GACTCCGGGTAAATGA	
SM1B205	pDR000027134	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAAGTGAA GCTGGTGGAAAGCGGCGGAGGCCTGGTGAAAC CTGGCGGCAGCCTGAAGCTGAGCTGCGCCGCC AGCGGCTTCACCTTCAGCAACTACGCCATGAG CTGGGTCCGCCAGACCCCCGAGAAGCGGCTGG AATGGGTGGCCAGCATCAGCAGACGGGGCAGC ACCTACTACCCCGACAGCGTGAAGGGCCGGTT CACCATCAGCCGGGACAACGCCCGGAACATCC TGTACCTGCAGATGAGCAGCCTGCGGAGCGAG GACACCGCCCTGTACTACTGCGCCACCGTGTAC TACGACAACCCTTGGTTTGTGTACTGGGGCCAG GGCACCCTGGTGACAGTGTCCGCTGCCAAAAC AACAGCACCAAGTGTCTATCCACTGGCCCCTGT GTGTGGAGATACAACTGGCTCCTCGGTGACTCT AGGATGCCTGGTCAAGGGTTATTTCCCTGAGCC AGTGACCTTGACCTGGAACTCTGGATCCCTGTC CAGTGGTGTGCACACCTTCCCAGCTGTCCTGCA GTCTGACCTCTACACCCTCAGCAGCTCAGTGAC TGTAACCTCGAGCACCTGGCCCAGCCAGTCCA TCACCTGCAATGTGGCCCACCCGGCAAGCAGC ACCAAGGTGGACAAGAAAATTGAGCCCAGAG GGCCCACAATCAAGCCCTGTCCTCCATGCAAA TGCCCAGCACCTAACCTCTTGGGTGGACCATCC GTCTTCATCTTCCCTCCAAAGATCAAGGATGTA CTCATGATCTCCCTGAGCCCCATAGTCACATGT GTGGTGGTGGATGTGAGCGAGGATGACCCAGA TGTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAGA GAGGATTACAACAGTACTCTCCGGGTGGTCAG TGCCCTCCCCATCCAGCACCAGGACTGGATGA GTGGCAAGGAGTTCAAATGCAAGGTCAACAAC AAAGACCTCCCAGCGCCCATCGAGAGAACCAT CTCAAAACCCAAAGGGTCAGTAAGAGCTCCAC AGGTATATGTCTTGCCTCCACCAGAAGAAGAG ATGACTAAGAAACAGGTCACTCTGACCTGCAT GGTCACAGACTTCATGCCTGAAGACATTTACGT GGAGTGGACCAACAACGGGAAAACAGAGCTA AACTACAAGAACACTGAACCAGTCCTGGACTC	1111

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		TGATGGTTCTTACTTCATGTACAGCAAGCTGAG AGTGGAAAAGAAGAACTGGGTGGAAAGAAAT AGCTACTCCTGTTCAGTGGTCCACGAGGGTCTG CACAATCACCACACGACTAAGAGCTTCTCCCG GACTCCGGGTAAATGA	
SM1B206	pDR000027134	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAAGTGAA GCTGGTGGAAAGCGGCGGAGGCCTGGTGAAAC CTGGCGGCAGCCTGAAGCTGAGCTGCGCCGCC AGCGGCTTCACCTTCAGCAACTACGCCATGAG CTGGGTCCGCCAGACCCCCGAGAAGCGGCTGG AATGGGTGGCCAGCATCAGCAGACGGGGCAGC ACCTACTACCCCGACAGCGTGAAGGGCCGGTT CACCATCAGCCGGGACAACGCCCGGAACATCC TGTACCTGCAGATGAGCAGCCTGCGGAGCGAG GACACCGCCCTGTACTACTGCGCCACCGTGTAC TACGACAACCCTTGGTTTGTGTACTGGGGCCAG GGCACCCTGGTGACAGTGTCCGCTGCCAAAAC AACAGCACCAAGTGTCTATCCACTGGCCCCTGT GTGTGGAGATACAACTGGCTCCTCGGTGACTCT AGGATGCCTGGTCAAGGGTTATTTCCCTGAGCC AGTGACCTTGACCTGGAACTCTGGATCCCTGTC CAGTGGTGTGCACACCTTCCCAGCTGTCCTGCA GTCTGACCTCTACACCCTCAGCAGCTCAGTGAC TGTAACCTCGAGCACCTGGCCCAGCCAGTCCA TCACCTGCAATGTGGCCCACCCGGCAAGCAGC ACCAAGGTGGACAAGAAAATTGAGCCCAGAG GGCCCACAATCAAGCCCTGTCCTCCATGCAAA TGCCCAGCACCTAACCTCTTGGGTGGACCATCC GTCTTCATCTTCCCTCCAAAGATCAAGGATGTA CTCATGATCTCCCTGAGCCCCATAGTCACATGT GTGGTGGTGGATGTGAGCGAGGATGACCCAGA TGTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAGA GAGGATTACAACAGTACTCTCCGGGTGGTCAG TGCCCTCCCCATCCAGCACCAGGACTGGATGA GTGGCAAGGAGTTCAAATGCAAGGTCAACAAC AAAGACCTCCCAGCGCCCATCGAGAGAACCAT CTCAAAACCCAAAGGGTCAGTAAGAGCTCCAC AGGTATATGTCTTGCCTCCACCAGAAGAAGAG ATGACTAAGAAACAGGTCACTCTGACCTGCAT GGTCACAGACTTCATGCCTGAAGACATTTACGT GGAGTGGACCAACAACGGGAAAACAGAGCTA AACTACAAGAACACTGAACCAGTCCTGGACTC TGATGGTTCTTACTTCATGTACAGCAAGCTGAG AGTGGAAAAGAAGAACTGGGTGGAAAGAAAT AGCTACTCCTGTTCAGTGGTCCACGAGGGTCTG CACAATCACCACACGACTAAGAGCTTCTCCCG	1112

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GACTCCGGGTAAATGA	
SM1B207	pDR000027135	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAAGTGAT GCTGGTGGAAAGCGGCGGAGGCCTGGTGAAAC CTGGCGGCAGCCTGAAGCTGAGCTGCGCCGCC AGCGGCTTCACCTTCAGCAACTACGCCATGAG CTGGGTCCGCCAGACCCCCGAGAAGCGGCTGG AATGGGTGGCCAGCATCAGCAGACGGGGCAGC ACCTACTACCCCGACAGCGTGAAGGGCCGGTT CACCATCAGCCGGGACAACGCCCGGAACATCC TGTACCTGCAGATGAGCAGCCTGCGGAGCGAG GACACCGCCCTGTACTACTGCGCCACCGTGTAC TACGACAACCCTTGGTTTGTGTACTGGGGCCAG GGCACCCTGGTGACAGTGTCCGCTGCCAAAAC AACAGCACCAAGTGTCTATCCACTGGCCCCTGT GTGTGGAGATACAACTGGCTCCTCGGTGACTCT AGGATGCCTGGTCAAGGGTTATTTCCCTGAGCC AGTGACCTTGACCTGGAACTCTGGATCCCTGTC CAGTGGTGTGCACACCTTCCCAGCTGTCCTGCA GTCTGACCTCTACACCCTCAGCAGCTCAGTGAC TGTAACCTCGAGCACCTGGCCCAGCCAGTCCA TCACCTGCAATGTGGCCCACCCGGCAAGCAGC ACCAAGGTGGACAAGAAAATTGAGCCCAGAG GGCCCACAATCAAGCCCTGTCCTCCATGCAAA TGCCCAGCACCTAACCTCTTGGGTGGACCATCC GTCTTCATCTTCCCTCCAAAGATCAAGGATGTA CTCATGATCTCCCTGAGCCCCATAGTCACATGT GTGGTGGTGGATGTGAGCGAGGATGACCCAGA TGTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAGA GAGGATTACAACAGTACTCTCCGGGTGGTCAG TGCCCTCCCCATCCAGCACCAGGACTGGATGA GTGGCAAGGAGTTCAAATGCAAGGTCAACAAC AAAGACCTCCCAGCGCCCATCGAGAGAACCAT CTCAAAACCCAAAGGGTCAGTAAGAGCTCCAC AGGTATATGTCTTGCCTCCACCAGAAGAAGAG ATGACTAAGAAACAGGTCACTCTGACCTGCAT GGTCACAGACTTCATGCCTGAAGACATTTACGT GGAGTGGACCAACAACGGGAAAACAGAGCTA AACTACAAGAACACTGAACCAGTCCTGGACTC TGATGGTTCTTACTTCATGTACAGCAAGCTGAG AGTGGAAAAGAAGAACTGGGTGGAAAGAAAT AGCTACTCCTGTTCAGTGGTCCACGAGGGTCTG CACAATCACCACACGACTAAGAGCTTCTCCCG GACTCCGGGTAAATGA	1113

Table 44. HlgC Antibody Light Chain CDSs

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
SM1B202	pDR000027142	GAGACAACCGTGACCCAGAGCCCCGCCAGCCT GAGCGTGGCCACCGGCGAGAAAGTGACCATCC GGTGCATCACCAGCACCGACATCGACGACGAC ATGAGCTGGTATCAGCAGAAGCCCGGCGAGCC CCCCAAGCTGCTGATCAGCGAGGGCAACACCC TGCGGCCTGGCGTGCCCAGCAGATTCAGCAGC AGCGGCTGCGGCACCGACTTCGTGTTCACCATC GAGAACACCCTGAGCGAGGACGTGGCCGACTA CTACTGCCTGCAGAGCGACAACATGCCCTACA CCTTCGGCGGAGGCACCAAGCTGGAAATCAAG CGGGCTGATGCTGCACCGACTGTGTCCATCTTC CCACCATCCAGTGAGCAGTTAACATCTGGAGG TGCCTCAGTCGTGTGCTTCTTGAACAACTTCTA CCCCAAAGACATCAATGTCAAGTGGAAGATTG ATGGCAGTGAACGACAAAATGGCGTCCTGAAC AGTTGGACTGATCAGGACAGCAAAGACAGCAC CTACAGCATGAGCAGCACCCTCACGTTGACCA AGGACGAGTATGAACGACATAACAGCTATACC TGTGAGGCCACTCACAAGACATCAACTTCACC CATTGTCAAGAGCTTCAACAGGAATGAGTGT	1114
SM1B203	pDR000027141	GACATCGTGATGACCCAGAGCCCCGCCACCCT GAGCGTGACCCCTGGCGATAGAGTGTCCCTGA GCTGCCGGGCCAGCCAGAGCATCAGCGACTAC CTGCACTGGTATCAGCAGAAGTCCCACGAGAG CCCCAGACTGCTGATTAAGTACGACAGCCAGT CCATCAGCGGCATCCCCAGCAGATTCAGCGGC AGCGGCTCCGGCTCCGACTTCACCCTGAGCATC AACAGCGTGGAACCCGAGGACGTGGGCGTGTA CTACTGCCAGAACGGCCACCGGTTCCCTTTCAC CTTCGGCGGAGGCACCAAGCTGGAAATCAAGC GGGCTGATGCTGCACCGACTGTGTCCATCTTCC CACCATCCAGTGAGCAGTTAACATCTGGAGGT GCCTCAGTCGTGTGCTTCTTGAACAACTTCTAC CCCAAAGACATCAATGTCAAGTGGAAGATTGA TGGCAGTGAACGACAAAATGGCGTCCTGAACA GTTGGACTGATCAGGACAGCAAAGACAGCACC TACAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATACCT GTGAGGCCACTCACAAGACATCAACTTCACCC ATTGTCAAGAGCTTCAACAGGAATGAGTGT	1115

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
SM1B204	pDR000027140	AACATCATGATGACCCAGAGCCCCAGCAGCCT GACCGTGTCTGCCGGCGAGAAAGTGACCATGA GCTGCAAGAGCAGCCAGAGCGTGCTGTACAGC TCCAACCAGAAGAACTACCTGGCCTGGTATCA GCAGAAGCCCGGCCAGTCCCCCAAGCTGCTGA TCTACTGGGCCAGCACCCGCGAGAGCGGCGTG CCCGATAGATTTGCCGGCTCCGGCTCCGGCACC GACTTCACCCTGAGCATCAGCAGCGTGCAGGC CGAGGACCTGGCCGTGTACTACTGCCACCAGT ACCTGAGCAGCTACACCTTCGGCGGAGGCACC AAGCTGGAAATCAAGCGGGCTGATGCTGCACC GACTGTGTCCATCTTCCCACCATCCAGTGAGCA GTTAACATCTGGAGGTGCCTCAGTCGTGTGCTT CTTGAACAACTTCTACCCCAAAGACATCAATGT CAAGTGGAAGATTGATGGCAGTGAACGACAAA ATGGCGTCCTGAACAGTTGGACTGATCAGGAC AGCAAAGACAGCACCTACAGCATGAGCAGCAC CCTCACGTTGACCAAGGACGAGTATGAACGAC ATAACAGCTATACCTGTGAGGCCACTCACAAG ACATCAACTTCACCCATTGTCAAGAGCTTCAAC AGGAATGAGTGT	1116
SM1B205	pDR000027139	GACATCGTGCTGACCCAGAGCCCTGCCAGCCT GGCCGTGTCTCTGGGCCAGAGAGCCACCATCA GCTACCGGGCCAGCAAGAGCGTGTCCACCAGC GGCTACAGCTACATGCACTGGAACCAGCAGAA GCCCGGCCAGCCCCCCAGACTGCTGATCTACCT GGTGTCCAACCTGGAAAGCGGCGTGCCCGCCA GATTCTCCGGCAGCGGCTCTGGCACCGACTTCA CCCTGAACATCCACCCCGTGGAAGAAGAGGAC GCCGCCACCTACTACTGCCAGCACATCAGAGA GCTGACCAGAAGCGAGGGCGGCACCAAGCTGG AAATCAAGCGGGCTGATGCTGCACCGACTGTG TCCATCTTCCCACCATCCAGTGAGCAGTTAACA TCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAAC AACTTCTACCCCAAAGACATCAATGTCAAGTG GAAGATTGATGGCAGTGAACGACAAAATGGCG TCCTGAACAGTTGGACTGATCAGGACAGCAAA GACAGCACCTACAGCATGAGCAGCACCCTCAC GTTGACCAAGGACGAGTATGAACGACATAACA GCTATACCTGTGAGGCCACTCACAAGACATCA ACTTCACCCATTGTCAAGAGCTTCAACAGGAA TGAGTGT	1117

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
SM1B206	pDR000027138	GACATCGTGATGACCCAGAGCCCCGCCACCCT GAGCGTGACCCCTGGCGATAGAGTGTCCCTGA GCTGCCGGGCCAGCCAGAGCATCAGCGACTAC CTGCACTGGTATCAGCAGAAGTCCCACGAGAG CCCCAGACTGCTGATTAAGTACGCCAGCCAGT CCATCTCCGGCATCCCCAGCAGATTCAGCGGC AGCGGCTCCGGCAGCGACTTCACCCTGTCCATC AACAGCGTGGAACCCGAGGACGTGGGCGTGTA CTACTGCCAGAACGGCCACAGCTTCCCCCTGA CCTTCGGCGCTGGCACCAAGCTGGAACTGAAG CGGGCTGATGCTGCACCGACTGTGTCCATCTTC CCACCATCCAGTGAGCAGTTAACATCTGGAGG TGCCTCAGTCGTGTGCTTCTTGAACAACTTCTA CCCCAAAGACATCAATGTCAAGTGGAAGATTG ATGGCAGTGAACGACAAAATGGCGTCCTGAAC AGTTGGACTGATCAGGACAGCAAAGACAGCAC CTACAGCATGAGCAGCACCCTCACGTTGACCA AGGACGAGTATGAACGACATAACAGCTATACC TGTGAGGCCACTCACAAGACATCAACTTCACC CATTGTCAAGAGCTTCAACAGGAATGAGTGT	1118
SM1B207	pDR000027137	GACATCGTGCTGACCCAGAGCCCTGCCAGCCT GGCCGTGTCTCTGGGCCAGAGAGCCACCATCA GCTGCCAGGCCAGCGAGAGCGTGTCCTTCGCC GGCACCAGCCTGATGCACTGGTATCAGCAGAA GCCCGGCCAGAGCCCCAAGCTGCTGATCTACT GGGCCAGCACCCGCGAGAGCGGCGTGCCCGAT AGATTTGCCGGCTCCGGCTCCGGCACCGACTTC ACCCTGAGCATCAGCAGCGTGCAGGCCGAGGA TCTGGCCGTGTACTACTGCCACCAGTACCTGAG CAGCTACACCTTCGGCGGAGGCACCAAGCTGG AAATCAAGCGGGCTGATGCTGCACCGACTGTG TCCATCTTCCCACCATCCAGTGAGCAGTTAACA TCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAAC AACTTCTACCCCAAAGACATCAATGTCAAGTG GAAGATTGATGGCAGTGAACGACAAAATGGCG TCCTGAACAGTTGGACTGATCAGGACAGCAAA GACAGCACCTACAGCATGAGCAGCACCCTCAC GTTGACCAAGGACGAGTATGAACGACATAACA GCTATACCTGTGAGGCCACTCACAAGACATCA ACTTCACCCATTGTCAAGAGCTTCAACAGGAA TGAGTGT	1119

Table 45. HlgC Antibody Light Chain Primary Transcripts

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
SM1B202	pDR000027142	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGAGAC AACCGTGACCCAGAGCCCCGCCAGCCTGAGCG TGGCCACCGGCGAGAAAGTGACCATCCGGTGC ATCACCAGCACCGACATCGACGACGACATGAG CTGGTATCAGCAGAAGCCCGGCGAGCCCCCCA AGCTGCTGATCAGCGAGGGCAACACCCTGCGG CCTGGCGTGCCCAGCAGATTCAGCAGCAGCGG CTGCGGCACCGACTTCGTGTTCACCATCGAGA ACACCCTGAGCGAGGACGTGGCCGACTACTAC TGCCTGCAGAGCGACAACATGCCCTACACCTT CGGCGGAGGCACCAAGCTGGAAATCAAGCGG GCTGATGCTGCACCGACTGTGTCCATCTTCCCA CCATCCAGTGAGCAGTTAACATCTGGAGGTGC CTCAGTCGTGTGCTTCTTGAACAACTTCTACCC CAAAGACATCAATGTCAAGTGGAAGATTGATG GCAGTGAACGACAAAATGGCGTCCTGAACAGT TGGACTGATCAGGACAGCAAAGACAGCACCTA CAGCATGAGCAGCACCCTCACGTTGACCAAGG ACGAGTATGAACGACATAACAGCTATACCTGT GAGGCCACTCACAAGACATCAACTTCACCCAT TGTCAAGAGCTTCAACAGGAATGAGTGTTAG	1120
SM1B203	pDR000027141	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC GTGATGACCCAGAGCCCCGCCACCCTGAGCGT GACCCCTGGCGATAGAGTGTCCCTGAGCTGCC GGGCCAGCCAGAGCATCAGCGACTACCTGCAC TGGTATCAGCAGAAGTCCCACGAGAGCCCCAG ACTGCTGATTAAGTACGACAGCCAGTCCATCA GCGGCATCCCCAGCAGATTCAGCGGCAGCGGC TCCGGCTCCGACTTCACCCTGAGCATCAACAG CGTGGAACCCGAGGACGTGGGCGTGTACTACT GCCAGAACGGCCACCGGTTCCCTTTCACCTTCG GCGGAGGCACCAAGCTGGAAATCAAGCGGGCT GATGCTGCACCGACTGTGTCCATCTTCCCACCA TCCAGTGAGCAGTTAACATCTGGAGGTGCCTC AGTCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGGCA GTGAACGACAAAATGGCGTCCTGAACAGTTGG ACTGATCAGGACAGCAAAGACAGCACCTACAG CATGAGCAGCACCCTCACGTTGACCAAGGACG AGTATGAACGACATAACAGCTATACCTGTGAG GCCACTCACAAGACATCAACTTCACCCATTGTC AAGAGCTTCAACAGGAATGAGTGTTAG	1121
SM1B204	pDR000027140	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCAACATC	1122

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		ATGATGACCCAGAGCCCCAGCAGCCTGACCGT GTCTGCCGGCGAGAAAGTGACCATGAGCTGCA AGAGCAGCCAGAGCGTGCTGTACAGCTCCAAC CAGAAGAACTACCTGGCCTGGTATCAGCAGAA GCCCGGCCAGTCCCCCAAGCTGCTGATCTACT GGGCCAGCACCCGCGAGAGCGGCGTGCCCGAT AGATTTGCCGGCTCCGGCTCCGGCACCGACTTC ACCCTGAGCATCAGCAGCGTGCAGGCCGAGGA CCTGGCCGTGTACTACTGCCACCAGTACCTGA GCAGCTACACCTTCGGCGGAGGCACCAAGCTG GAAATCAAGCGGGCTGATGCTGCACCGACTGT GTCCATCTTCCCACCATCCAGTGAGCAGTTAAC ATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAA CAACTTCTACCCCAAAGACATCAATGTCAAGT GGAAGATTGATGGCAGTGAACGACAAAATGGC GTCCTGAACAGTTGGACTGATCAGGACAGCAA AGACAGCACCTACAGCATGAGCAGCACCCTCA CGTTGACCAAGGACGAGTATGAACGACATAAC AGCTATACCTGTGAGGCCACTCACAAGACATC AACTTCACCCATTGTCAAGAGCTTCAACAGGA ATGAGTGTTAG	
SM1B205	pDR000027139	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC GTGCTGACCCAGAGCCCTGCCAGCCTGGCCGT GTCTCTGGGCCAGAGAGCCACCATCAGCTACC GGGCCAGCAAGAGCGTGTCCACCAGCGGCTAC AGCTACATGCACTGGAACCAGCAGAAGCCCGG CCAGCCCCCCAGACTGCTGATCTACCTGGTGTC CAACCTGGAAAGCGGCGTGCCCGCCAGATTCT CCGGCAGCGGCTCTGGCACCGACTTCACCCTG AACATCCACCCCGTGGAAGAAGAGGACGCCGC CACCTACTACTGCCAGCACATCAGAGAGCTGA CCAGAAGCGAGGGCGGCACCAAGCTGGAAAT CAAGCGGGCTGATGCTGCACCGACTGTGTCCA TCTTCCCACCATCCAGTGAGCAGTTAACATCTG GAGGTGCCTCAGTCGTGTGCTTCTTGAACAACT TCTACCCCAAAGACATCAATGTCAAGTGGAAG ATTGATGGCAGTGAACGACAAAATGGCGTCCT GAACAGTTGGACTGATCAGGACAGCAAAGACA GCACCTACAGCATGAGCAGCACCCTCACGTTG ACCAAGGACGAGTATGAACGACATAACAGCTA TACCTGTGAGGCCACTCACAAGACATCAACTT CACCCATTGTCAAGAGCTTCAACAGGAATGAG TGTTAG	1123
SM1B206	pDR000027138	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC GTGATGACCCAGAGCCCCGCCACCCTGAGCGT GACCCCTGGCGATAGAGTGTCCCTGAGCTGCC	1124

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		GGGCCAGCCAGAGCATCAGCGACTACCTGCAC TGGTATCAGCAGAAGTCCCACGAGAGCCCCAG ACTGCTGATTAAGTACGCCAGCCAGTCCATCTC CGGCATCCCCAGCAGATTCAGCGGCAGCGGCT CCGGCAGCGACTTCACCCTGTCCATCAACAGC GTGGAACCCGAGGACGTGGGCGTGTACTACTG CCAGAACGGCCACAGCTTCCCCCTGACCTTCG GCGCTGGCACCAAGCTGGAACTGAAGCGGGCT GATGCTGCACCGACTGTGTCCATCTTCCCACCA TCCAGTGAGCAGTTAACATCTGGAGGTGCCTC AGTCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGGCA GTGAACGACAAAATGGCGTCCTGAACAGTTGG ACTGATCAGGACAGCAAAGACAGCACCTACAG CATGAGCAGCACCCTCACGTTGACCAAGGACG AGTATGAACGACATAACAGCTATACCTGTGAG GCCACTCACAAGACATCAACTTCACCCATTGTC AAGAGCTTCAACAGGAATGAGTGTTAG	
SM1B207	pDR000027137	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC GTGCTGACCCAGAGCCCTGCCAGCCTGGCCGT GTCTCTGGGCCAGAGAGCCACCATCAGCTGCC AGGCCAGCGAGAGCGTGTCCTTCGCCGGCACC AGCCTGATGCACTGGTATCAGCAGAAGCCCGG CCAGAGCCCCAAGCTGCTGATCTACTGGGCCA GCACCCGCGAGAGCGGCGTGCCCGATAGATTT GCCGGCTCCGGCTCCGGCACCGACTTCACCCT GAGCATCAGCAGCGTGCAGGCCGAGGATCTGG CCGTGTACTACTGCCACCAGTACCTGAGCAGC TACACCTTCGGCGGAGGCACCAAGCTGGAAAT CAAGCGGGCTGATGCTGCACCGACTGTGTCCA TCTTCCCACCATCCAGTGAGCAGTTAACATCTG GAGGTGCCTCAGTCGTGTGCTTCTTGAACAACT TCTACCCCAAAGACATCAATGTCAAGTGGAAG ATTGATGGCAGTGAACGACAAAATGGCGTCCT GAACAGTTGGACTGATCAGGACAGCAAAGACA GCACCTACAGCATGAGCAGCACCCTCACGTTG ACCAAGGACGAGTATGAACGACATAACAGCTA TACCTGTGAGGCCACTCACAAGACATCAACTT CACCCATTGTCAAGAGCTTCAACAGGAATGAG TGTTAG	1125

Table 46. HlgA/LukE Antibody Heavy Chain CDSs

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
SM1B302	pDR000029296	GAAGTGAAGCTGGTGGAATCTGGCGGCGACCT GGTCAAGCCTGGCGGCAGCCTGAAGCTGAGCT GCGCCGCCAGCGGCTTCACCTTCAGCAGCTTC GCCATGAGCTGGGTCCGACAGACCCCCGAGAA GCGGCTGGAATGGGTGGCCAGCATCAGCCGGA CCGACAACACCTACTACCCCGACAGCATGAAG GGCCAGTTCACCATCAGCCGGGACAACGCCCG GAACATCCTGTACCTGCAGATGAGCAGCCTGC GGAGCGAGAACACCGCCATCTACTACTGCGCC AGAGCCGACTACGACGGCCCTTGGTTTGCCTA CTGGGGCCAGGGCACCCTGGTCACCGTGTCTG CTGCCAAAACAACAGCACCAAGTGTCTATCCA CTGGCCCCTGTGTGTGGAGATACAACTGGCTC CTCGGTGACTCTAGGATGCCTGGTCAAGGGTT ATTTCCCTGAGCCAGTGACCTTGACCTGGAACT CTGGATCCCTGTCCAGTGGTGTGCACACCTTCC CAGCTGTCCTGCAGTCTGACCTCTACACCCTCA GCAGCTCAGTGACTGTAACCTCGAGCACCTGG CCCAGCCAGTCCATCACCTGCAATGTGGCCCA CCCGGCAAGCAGCACCAAGGTGGACAAGAAA ATTGAGCCCAGAGGGCCCACAATCAAGCCCTG TCCTCCATGCAAATGCCCAGCACCTAACCTCTT GGGTGGACCATCCGTCTTCATCTTCCCTCCAAA GATCAAGGATGTACTCATGATCTCCCTGAGCC CCATAGTCACATGTGTGGTGGTGGATGTGAGC GAGGATGACCCAGATGTCCAGATCAGCTGGTT TGTGAACAACGTGGAAGTACACACAGCTCAGA CACAAACCCATAGAGAGGATTACAACAGTACT CTCCGGGTGGTCAGTGCCCTCCCCATCCAGCAC CAGGACTGGATGAGTGGCAAGGAGTTCAAATG CAAGGTCAACAACAAAGACCTCCCAGCGCCCA TCGAGAGAACCATCTCAAAACCCAAAGGGTCA GTAAGAGCTCCACAGGTATATGTCTTGCCTCCA CCAGAAGAAGAGATGACTAAGAAACAGGTCA CTCTGACCTGCATGGTCACAGACTTCATGCCTG AAGACATTTACGTGGAGTGGACCAACAACGGG AAAACAGAGCTAAACTACAAGAACACTGAACC AGTCCTGGACTCTGATGGTTCTTACTTCATGTA CAGCAAGCTGAGAGTGGAAAAGAAGAACTGG GTGGAAAGAAATAGCTACTCCTGTTCAGTGGT CCACGAGGGTCTGCACAATCACCACACGACTA AGAGCTTCTCCCGGACTCCGGGTAAA	1126
SM1B303	pDR000029295	GAGGTGCAGCTGCAGCAGAGCGGCCCTGATCT GGTCAAGCCCGGCACCAGCGTGAAGATGAGCT GCAAGGCCAGCGGCTACAGCTTCACCGGCTAC TACATGCACTGGGTCAAGCAGAGCCACGGCAA	1127

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		GAGCCTGGAATGGATCGGCAGAGTGAACCCCA ACAACGGCGGCACCAGCTACAACCAGAAGTTC AAGGGCAAGGCCATCCTGACCGTGGACAAGAG CAGCAGCACCGCCTACATGGAACTGCGGAGCC TGACCAGCGAGGACAGCGCCGTGTACTACTGC GCCAGGGACGACTACAGCTTCGCCTACTGGGG CCAGGGCACCCTGGTCACCGTGTCTGCTGCCA AAACAACAGCACCAAGTGTCTATCCACTGGCC CCTGTGTGTGGAGATACAACTGGCTCCTCGGT GACTCTAGGATGCCTGGTCAAGGGTTATTTCCC TGAGCCAGTGACCTTGACCTGGAACTCTGGAT CCCTGTCCAGTGGTGTGCACACCTTCCCAGCTG TCCTGCAGTCTGACCTCTACACCCTCAGCAGCT CAGTGACTGTAACCTCGAGCACCTGGCCCAGC CAGTCCATCACCTGCAATGTGGCCCACCCGGC AAGCAGCACCAAGGTGGACAAGAAAATTGAG CCCAGAGGGCCCACAATCAAGCCCTGTCCTCC ATGCAAATGCCCAGCACCTAACCTCTTGGGTG GACCATCCGTCTTCATCTTCCCTCCAAAGATCA AGGATGTACTCATGATCTCCCTGAGCCCCATA GTCACATGTGTGGTGGTGGATGTGAGCGAGGA TGACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACACAA ACCCATAGAGAGGATTACAACAGTACTCTCCG GGTGGTCAGTGCCCTCCCCATCCAGCACCAGG ACTGGATGAGTGGCAAGGAGTTCAAATGCAAG GTCAACAACAAAGACCTCCCAGCGCCCATCGA GAGAACCATCTCAAAACCCAAAGGGTCAGTAA GAGCTCCACAGGTATATGTCTTGCCTCCACCAG AAGAAGAGATGACTAAGAAACAGGTCACTCTG ACCTGCATGGTCACAGACTTCATGCCTGAAGA CATTTACGTGGAGTGGACCAACAACGGGAAAA CAGAGCTAAACTACAAGAACACTGAACCAGTC CTGGACTCTGATGGTTCTTACTTCATGTACAGC AAGCTGAGAGTGGAAAAGAAGAACTGGGTGG AAAGAAATAGCTACTCCTGTTCAGTGGTCCAC GAGGGTCTGCACAATCACCACACGACTAAGAG CTTCTCCCGGACTCCGGGTAAA	
SM1B304	pDR000029294	GAAGTGAAGCTGGTGGAAAGCGGCGGAGGCC TGGTGCAGCCTGGCGGCAGCCTGAGACTGAGC TGCGCCACCAGCGGCTTCACCTTCACCGACTTC TACATGAGCTGGGTCCGACAGCCCCCTGGCAA GGCCCTGGAATGGCTGGCCTTCATCCGGAACA AGGCCAACGGCTACACCACCGAGTACAGCAGC AGCGTGCGGGGCAGATTCACCATCAGCCGGGA CAACAGCCAGAGCATCCTGTACCTGCAGATGA ACACCCTGCGGGCCGAGGACAGCGGCACCTAC TACTGCGCCAGGGACGTGGGCGACTACGACTA	1128

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		CTGGGGCCAGGGCAGCACCCTGACCGTGTCCT CTGCCAAAACAACAGCACCAAGTGTCTATCCA CTGGCCCCTGTGTGTGGAGATACAACTGGCTC CTCGGTGACTCTAGGATGCCTGGTCAAGGGTT ATTTCCCTGAGCCAGTGACCTTGACCTGGAACT CTGGATCCCTGTCCAGTGGTGTGCACACCTTCC CAGCTGTCCTGCAGTCTGACCTCTACACCCTCA GCAGCTCAGTGACTGTAACCTCGAGCACCTGG CCCAGCCAGTCCATCACCTGCAATGTGGCCCA CCCGGCAAGCAGCACCAAGGTGGACAAGAAA ATTGAGCCCAGAGGGCCCACAATCAAGCCCTG TCCTCCATGCAAATGCCCAGCACCTAACCTCTT GGGTGGACCATCCGTCTTCATCTTCCCTCCAAA GATCAAGGATGTACTCATGATCTCCCTGAGCC CCATAGTCACATGTGTGGTGGTGGATGTGAGC GAGGATGACCCAGATGTCCAGATCAGCTGGTT TGTGAACAACGTGGAAGTACACACAGCTCAGA CACAAACCCATAGAGAGGATTACAACAGTACT CTCCGGGTGGTCAGTGCCCTCCCCATCCAGCAC CAGGACTGGATGAGTGGCAAGGAGTTCAAATG CAAGGTCAACAACAAAGACCTCCCAGCGCCCA TCGAGAGAACCATCTCAAAACCCAAAGGGTCA GTAAGAGCTCCACAGGTATATGTCTTGCCTCCA CCAGAAGAAGAGATGACTAAGAAACAGGTCA CTCTGACCTGCATGGTCACAGACTTCATGCCTG AAGACATTTACGTGGAGTGGACCAACAACGGG AAAACAGAGCTAAACTACAAGAACACTGAACC AGTCCTGGACTCTGATGGTTCTTACTTCATGTA CAGCAAGCTGAGAGTGGAAAAGAAGAACTGG GTGGAAAGAAATAGCTACTCCTGTTCAGTGGT CCACGAGGGTCTGCACAATCACCACACGACTA AGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B305	pDR000029293	CAGATCCAGCTGGTGCAGAGCGGCCCTGAGCT GAAGAAACCCGGCGAGACAGTGAAGATCAGC TGCAAGGCCAGCGGCTTCACCTTCACCAACTA CGGCATGAACTGGGTCAAGCAGGCCCCTGGCA AGGACCTGAAGTGGATGGGCTGGATCAACACC TACACCGGCGAGCCCACCTACGCCGACGACTT CAAGGGCAGATTCGCCTTCAGCCTGGAAACCA GCGCCAGCACCGCCTACCTGCAGATCAACAAC CTGAAGGACGAGGATACCGCCAGCTACTTCTG CGCCAGAGACTACCGGGACGGCGACGCCCTGG ATTACTGGGGCCAGGGCACCAGCGTGACCGTG TCCTCTGCCAAAACAACAGCACCAAGTGTCTA TCCACTGGCCCCTGTGTGTGGAGATACAACTG GCTCCTCGGTGACTCTAGGATGCCTGGTCAAG GGTTATTTCCCTGAGCCAGTGACCTTGACCTGG AACTCTGGATCCCTGTCCAGTGGTGTGCACACC	1129

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		TTCCCAGCTGTCCTGCAGTCTGACCTCTACACC CTCAGCAGCTCAGTGACTGTAACCTCGAGCAC CTGGCCCAGCCAGTCCATCACCTGCAATGTGG CCCACCCGGCAAGCAGCACCAAGGTGGACAAG AAAATTGAGCCCAGAGGGCCCACAATCAAGCC CTGTCCTCCATGCAAATGCCCAGCACCTAACCT CTTGGGTGGACCATCCGTCTTCATCTTCCCTCC AAAGATCAAGGATGTACTCATGATCTCCCTGA GCCCCATAGTCACATGTGTGGTGGTGGATGTG AGCGAGGATGACCCAGATGTCCAGATCAGCTG GTTTGTGAACAACGTGGAAGTACACACAGCTC AGACACAAACCCATAGAGAGGATTACAACAGT ACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAG CACCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGCGC CCATCGAGAGAACCATCTCAAAACCCAAAGGG TCAGTAAGAGCTCCACAGGTATATGTCTTGCCT CCACCAGAAGAAGAGATGACTAAGAAACAGG TCACTCTGACCTGCATGGTCACAGACTTCATGC CTGAAGACATTTACGTGGAGTGGACCAACAAC GGGAAAACAGAGCTAAACTACAAGAACACTG AACCAGTCCTGGACTCTGATGGTTCTTACTTCA TGTACAGCAAGCTGAGAGTGGAAAAGAAGAA CTGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACACG ACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B306	pDR000029292	CAGGTGCAGCTGCAGCAGCCTGGCGCCGAACT CGTCAGACCTGGCGCCAGCGTGAAGCTGAGCT GCAAGGCCAGCGGCTACAGCTTCACCAGCAAC TGGATGAATTGGATGAAGCAGCGGCCTGGCCA GGGCCTGGAATGGATCGGCATGATCCACCCCA GCGACAGCGAGAGCCGGCTGAACCAGAAGTTC AAGGACAAGGCCACCCTGACCGTGGACAAGA GCAGCAGCACCGCCTACATGCAGCTGTCCAGC CCCACCAGCGAGGACAGCGCCGTGTACTACTG TGCCAGAGGCGACGGCGGCTTCGCCTACTGGG GACAGGGCACCCTGGTCACCGTGTCCGCTGCC AAAACAACAGCACCAAGTGTCTATCCACTGGC CCCTGTGTGTGGAGATACAACTGGCTCCTCGGT GACTCTAGGATGCCTGGTCAAGGGTTATTTCCC TGAGCCAGTGACCTTGACCTGGAACTCTGGAT CCCTGTCCAGTGGTGTGCACACCTTCCCAGCTG TCCTGCAGTCTGACCTCTACACCCTCAGCAGCT CAGTGACTGTAACCTCGAGCACCTGGCCCAGC CAGTCCATCACCTGCAATGTGGCCCACCCGGC AAGCAGCACCAAGGTGGACAAGAAAATTGAG CCCAGAGGGCCCACAATCAAGCCCTGTCCTCC ATGCAAATGCCCAGCACCTAACCTCTTGGGTG	1130

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		GACCATCCGTCTTCATCTTCCCTCCAAAGATCA AGGATGTACTCATGATCTCCCTGAGCCCCATA GTCACATGTGTGGTGGTGGATGTGAGCGAGGA TGACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACACAA ACCCATAGAGAGGATTACAACAGTACTCTCCG GGTGGTCAGTGCCCTCCCCATCCAGCACCAGG ACTGGATGAGTGGCAAGGAGTTCAAATGCAAG GTCAACAACAAAGACCTCCCAGCGCCCATCGA GAGAACCATCTCAAAACCCAAAGGGTCAGTAA GAGCTCCACAGGTATATGTCTTGCCTCCACCAG AAGAAGAGATGACTAAGAAACAGGTCACTCTG ACCTGCATGGTCACAGACTTCATGCCTGAAGA CATTTACGTGGAGTGGACCAACAACGGGAAAA CAGAGCTAAACTACAAGAACACTGAACCAGTC CTGGACTCTGATGGTTCTTACTTCATGTACAGC AAGCTGAGAGTGGAAAAGAAGAACTGGGTGG AAAGAAATAGCTACTCCTGTTCAGTGGTCCAC GAGGGTCTGCACAATCACCACACGACTAAGAG CTTCTCCCGGACTCCGGGTAAA	
SM1B307	pDR000029291	GAAGTGAAGCTGCAGCAGAGCGGCCCTGAGCT GGTCAAGCCTGGCGCCAGCATGAAGATCAGCT GCAAGGCCAGCGGCTACAGCTTCACCGGCTAC ACCATGAACTGGGCCAAGCAGAGCCACGGCAA GAACCTGGAATGGATCGGCCTGATCAACCCCT ACAACGGCGGCACCAGCTACAACCAGAAGTTC AAGGGCAAGGCCACCCTGACCGTGGACAAGA GCAGCAGCACCGCCTACATGGAACTGCTGAGC CTGACCAGCGAGGACAGCGCCGTGTACTACTG CGCCAGAGGCTACCCCAGAGGATGGTTCGCCT ACTGGGGCCAGGGCACCCTGGTCACCGTGTCT GCTGCCAAAACAACAGCACCAAGTGTCTATCC ACTGGCCCCTGTGTGTGGAGATACAACTGGCT CCTCGGTGACTCTAGGATGCCTGGTCAAGGGT TATTTCCCTGAGCCAGTGACCTTGACCTGGAAC TCTGGATCCCTGTCCAGTGGTGTGCACACCTTC CCAGCTGTCCTGCAGTCTGACCTCTACACCCTC AGCAGCTCAGTGACTGTAACCTCGAGCACCTG GCCCAGCCAGTCCATCACCTGCAATGTGGCCC ACCCGGCAAGCAGCACCAAGGTGGACAAGAA AATTGAGCCCAGAGGGCCCACAATCAAGCCCT GTCCTCCATGCAAATGCCCAGCACCTAACCTCT TGGGTGGACCATCCGTCTTCATCTTCCCTCCAA AGATCAAGGATGTACTCATGATCTCCCTGAGC CCCATAGTCACATGTGTGGTGGTGGATGTGAG CGAGGATGACCCAGATGTCCAGATCAGCTGGT TTGTGAACAACGTGGAAGTACACACAGCTCAG ACACAAACCCATAGAGAGGATTACAACAGTAC	1131

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		TCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCA CCAGGACTGGATGAGTGGCAAGGAGTTCAAAT GCAAGGTCAACAACAAAGACCTCCCAGCGCCC ATCGAGAGAACCATCTCAAAACCCAAAGGGTC AGTAAGAGCTCCACAGGTATATGTCTTGCCTCC ACCAGAAGAAGAGATGACTAAGAAACAGGTC ACTCTGACCTGCATGGTCACAGACTTCATGCCT GAAGACATTTACGTGGAGTGGACCAACAACGG GAAAACAGAGCTAAACTACAAGAACACTGAA CCAGTCCTGGACTCTGATGGTTCTTACTTCATG TACAGCAAGCTGAGAGTGGAAAAGAAGAACT GGGTGGAAAGAAATAGCTACTCCTGTTCAGTG GTCCACGAGGGTCTGCACAATCACCACACGAC TAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B308	pDR000029290	GACGTGAAGCTGGTGGAAAGCGGCGGAGGCCT GGTCAAGCCTGGCGGCAGCCTGAAGCTGAGCT GCGCCGCCAGCGGCTTCACCTTCCGGAACCAC GCCATGAGCTGGGTCCGACAGACCCCCGAGAA GCGGCTGGAATGGGTGGCCGCCATCAACGTGA ACGCCGGCAGCACCTACTACCCCGACACCGTG AAGGACCGGTTCACCATCAGCCGGGACAACGC CAAGAACACCCTGTACCTGCAGATGAGCAGCC TGCGGAGCGAGGACACCGCCCTGTACTACTGC GCCAGACACCGGGCCTACTACAACTACGACGA GAACGCCATGGACTACTGGGGCCAGGGCACCA GCGTGACCGTGTCCTCTGCCAAAACAACAGCA CCAAGTGTCTATCCACTGGCCCCTGTGTGTGGA GATACAACTGGCTCCTCGGTGACTCTAGGATG CCTGGTCAAGGGTTATTTCCCTGAGCCAGTGAC CTTGACCTGGAACTCTGGATCCCTGTCCAGTGG TGTGCACACCTTCCCAGCTGTCCTGCAGTCTGA CCTCTACACCCTCAGCAGCTCAGTGACTGTAAC CTCGAGCACCTGGCCCAGCCAGTCCATCACCT GCAATGTGGCCCACCCGGCAAGCAGCACCAAG GTGGACAAGAAAATTGAGCCCAGAGGGCCCAC AATCAAGCCCTGTCCTCCATGCAAATGCCCAG CACCTAACCTCTTGGGTGGACCATCCGTCTTCA TCTTCCCTCCAAAGATCAAGGATGTACTCATGA TCTCCCTGAGCCCCATAGTCACATGTGTGGTGG TGGATGTGAGCGAGGATGACCCAGATGTCCAG ATCAGCTGGTTTGTGAACAACGTGGAAGTACA CACAGCTCAGACACAAACCCATAGAGAGGATT ACAACAGTACTCTCCGGGTGGTCAGTGCCCTC CCCATCCAGCACCAGGACTGGATGAGTGGCAA GGAGTTCAAATGCAAGGTCAACAACAAAGACC TCCCAGCGCCCATCGAGAGAACCATCTCAAAA CCCAAAGGGTCAGTAAGAGCTCCACAGGTATA TGTCTTGCCTCCACCAGAAGAAGAGATGACTA	1132

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		AGAAACAGGTCACTCTGACCTGCATGGTCACA GACTTCATGCCTGAAGACATTTACGTGGAGTG GACCAACAACGGGAAAACAGAGCTAAACTAC AAGAACACTGAACCAGTCCTGGACTCTGATGG TTCTTACTTCATGTACAGCAAGCTGAGAGTGG AAAAGAAGAACTGGGTGGAAAGAAATAGCTA CTCCTGTTCAGTGGTCCACGAGGGTCTGCACA ATCACCACACGACTAAGAGCTTCTCCCGGACT CCGGGTAAA	
SM1B309	pDR000029289	GAGGTGCAGCTGCAGCAGAGCGGCCCTGAGCT GGTCAAGCCCGGCGACAGCGTGAAGATGAGCT GCAAGGCCAGCGGCTACACCTTCACCGACTAC TACATCGACTGGATGAAGCAGAGCCACGGCAA GAGCCTGGAATGGATCGGCTACATCTACCCCA ACAACGGCGGCACCAGCTACAACCAGAACTTC AAGGACAAGGCCACCCTGACCGTGGACAAGA GCAGCAGCACCGCCTACATGGAACTGCACAGC CTGACCAGCGAGGACAGCGCCGTGTACTACTG CGCCAGACTGACCTACTACGCCAAGGTGGACA GCTGGGGCCAGGGCACCAGCGTGACCGTGTCT AGCGCCAAAACAACAGCACCAAGTGTCTATCC ACTGGCCCCTGTGTGTGGAGATACAACTGGCT CCTCGGTGACTCTAGGATGCCTGGTCAAGGGT TATTTCCCTGAGCCAGTGACCTTGACCTGGAAC TCTGGATCCCTGTCCAGTGGTGTGCACACCTTC CCAGCTGTCCTGCAGTCTGACCTCTACACCCTC AGCAGCTCAGTGACTGTAACCTCGAGCACCTG GCCCAGCCAGTCCATCACCTGCAATGTGGCCC ACCCGGCAAGCAGCACCAAGGTGGACAAGAA AATTGAGCCCAGAGGGCCCACAATCAAGCCCT GTCCTCCATGCAAATGCCCAGCACCTAACCTCT TGGGTGGACCATCCGTCTTCATCTTCCCTCCAA AGATCAAGGATGTACTCATGATCTCCCTGAGC CCCATAGTCACATGTGTGGTGGTGGATGTGAG CGAGGATGACCCAGATGTCCAGATCAGCTGGT TTGTGAACAACGTGGAAGTACACACAGCTCAG ACACAAACCCATAGAGAGGATTACAACAGTAC TCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCA CCAGGACTGGATGAGTGGCAAGGAGTTCAAAT GCAAGGTCAACAACAAAGACCTCCCAGCGCCC ATCGAGAGAACCATCTCAAAACCCAAAGGGTC AGTAAGAGCTCCACAGGTATATGTCTTGCCTCC ACCAGAAGAAGAGATGACTAAGAAACAGGTC ACTCTGACCTGCATGGTCACAGACTTCATGCCT GAAGACATTTACGTGGAGTGGACCAACAACGG GAAAACAGAGCTAAACTACAAGAACACTGAA CCAGTCCTGGACTCTGATGGTTCTTACTTCATG TACAGCAAGCTGAGAGTGGAAAAGAAGAACT	1133

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		GGGTGGAAAGAAATAGCTACTCCTGTTCAGTG GTCCACGAGGGTCTGCACAATCACCACACGAC TAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B310	pDR000029288	GACGTGAAGCTGGTGGAAAGCGGCGGAGGCCT GGTGGAATGGGAGGGCGTGCTGAAGCTGAGCT GCGCCGCCAGCGGCTTCACCTTCAGCAGCTAC GCCATGAGCTGGGTCCGACAGACCCCCGAGAA GCGGCTGGAATGGGTGGCCGCCATCAACAGCA ACGGCGGCAGCACCTACTACCCCGACACCGTG AAGGACCGGTTCACCATCAGCCGGGACAACGC CAAGAACACCCTGTACCTGCAGATGAGCAGCC TGCGGAGCGAGGACACCGCCCTGTACTACTGC GCCAGACTGTACTACGGCGACTACTGGGGCCA GGGCACCACCCTGACCGTGTCCTCTGCCAAAA CAACAGCACCAAGTGTCTATCCACTGGCCCCT GTGTGTGGAGATACAACTGGCTCCTCGGTGAC TCTAGGATGCCTGGTCAAGGGTTATTTCCCTGA GCCAGTGACCTTGACCTGGAACTCTGGATCCCT GTCCAGTGGTGTGCACACCTTCCCAGCTGTCCT GCAGTCTGACCTCTACACCCTCAGCAGCTCAGT GACTGTAACCTCGAGCACCTGGCCCAGCCAGT CCATCACCTGCAATGTGGCCCACCCGGCAAGC AGCACCAAGGTGGACAAGAAAATTGAGCCCA GAGGGCCCACAATCAAGCCCTGTCCTCCATGC AAATGCCCAGCACCTAACCTCTTGGGTGGACC ATCCGTCTTCATCTTCCCTCCAAAGATCAAGGA TGTACTCATGATCTCCCTGAGCCCCATAGTCAC ATGTGTGGTGGTGGATGTGAGCGAGGATGACC CAGATGTCCAGATCAGCTGGTTTGTGAACAAC GTGGAAGTACACACAGCTCAGACACAAACCCA TAGAGAGGATTACAACAGTACTCTCCGGGTGG TCAGTGCCCTCCCCATCCAGCACCAGGACTGG ATGAGTGGCAAGGAGTTCAAATGCAAGGTCAA CAACAAAGACCTCCCAGCGCCCATCGAGAGAA CCATCTCAAAACCCAAAGGGTCAGTAAGAGCT CCACAGGTATATGTCTTGCCTCCACCAGAAGA AGAGATGACTAAGAAACAGGTCACTCTGACCT GCATGGTCACAGACTTCATGCCTGAAGACATT TACGTGGAGTGGACCAACAACGGGAAAACAG AGCTAAACTACAAGAACACTGAACCAGTCCTG GACTCTGATGGTTCTTACTTCATGTACAGCAAG CTGAGAGTGGAAAAGAAGAACTGGGTGGAAA GAAATAGCTACTCCTGTTCAGTGGTCCACGAG GGTCTGCACAATCACCACACGACTAAGAGCTT CTCCCGGACTCCGGGTAAA	1134
SM1B311	pDR000029287	CAGGTGCAGCTGAAGCAGAGCGGCCCTAGCCT GGTGCAGCCCAGCCAGAGCCTGAGCATCACCT GTACCGTGTCCGGCTTCAGCCTGACCACCTACG	1135

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		GCCTGCACTGGATCCGGCAGAGCCCCGGCAAG GGCCTGGAATGGCTGGGAGTGATTTGGAGAGG CGGCACCACCGACTACAACGCCGCCTTCATGA GCCGGCTGACCATCACCAAGGACAACAGCAAG AGCCAGGTGTTCTTCAAGATGAACAGCCTGCA GGCCGACGACACCGCCATCTACTACTGCGCCC GGACCGACATCTGGGGCGCTGGCACCACCGTG ACCGTGTCCTCTGCCAAAACAACAGCACCAAG TGTCTATCCACTGGCCCCTGTGTGTGGAGATAC AACTGGCTCCTCGGTGACTCTAGGATGCCTGGT CAAGGGTTATTTCCCTGAGCCAGTGACCTTGAC CTGGAACTCTGGATCCCTGTCCAGTGGTGTGCA CACCTTCCCAGCTGTCCTGCAGTCTGACCTCTA CACCCTCAGCAGCTCAGTGACTGTAACCTCGA GCACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTGGA CAAGAAAATTGAGCCCAGAGGGCCCACAATCA AGCCCTGTCCTCCATGCAAATGCCCAGCACCT AACCTCTTGGGTGGACCATCCGTCTTCATCTTC CCTCCAAAGATCAAGGATGTACTCATGATCTC CCTGAGCCCCATAGTCACATGTGTGGTGGTGG ATGTGAGCGAGGATGACCCAGATGTCCAGATC AGCTGGTTTGTGAACAACGTGGAAGTACACAC AGCTCAGACACAAACCCATAGAGAGGATTACA ACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCA TCCAGCACCAGGACTGGATGAGTGGCAAGGAG TTCAAATGCAAGGTCAACAACAAAGACCTCCC AGCGCCCATCGAGAGAACCATCTCAAAACCCA AAGGGTCAGTAAGAGCTCCACAGGTATATGTC TTGCCTCCACCAGAAGAAGAGATGACTAAGAA ACAGGTCACTCTGACCTGCATGGTCACAGACT TCATGCCTGAAGACATTTACGTGGAGTGGACC AACAACGGGAAAACAGAGCTAAACTACAAGA ACACTGAACCAGTCCTGGACTCTGATGGTTCTT ACTTCATGTACAGCAAGCTGAGAGTGGAAAAG AAGAACTGGGTGGAAAGAAATAGCTACTCCTG TTCAGTGGTCCACGAGGGTCTGCACAATCACC ACACGACTAAGAGCTTCTCCCGGACTCCGGGT AAA	
SM1B312	pDR000029287	CAGGTGCAGCTGAAGCAGAGCGGCCCTAGCCT GGTGCAGCCCAGCCAGAGCCTGAGCATCACCT GTACCGTGTCCGGCTTCAGCCTGACCACCTACG GCCTGCACTGGATCCGGCAGAGCCCCGGCAAG GGCCTGGAATGGCTGGGAGTGATTTGGAGAGG CGGCACCACCGACTACAACGCCGCCTTCATGA GCCGGCTGACCATCACCAAGGACAACAGCAAG AGCCAGGTGTTCTTCAAGATGAACAGCCTGCA GGCCGACGACACCGCCATCTACTACTGCGCCC	1136

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		GGACCGACATCTGGGGCGCTGGCACCACCGTG ACCGTGTCCTCTGCCAAAACAACAGCACCAAG TGTCTATCCACTGGCCCCTGTGTGTGGAGATAC AACTGGCTCCTCGGTGACTCTAGGATGCCTGGT CAAGGGTTATTTCCCTGAGCCAGTGACCTTGAC CTGGAACTCTGGATCCCTGTCCAGTGGTGTGCA CACCTTCCCAGCTGTCCTGCAGTCTGACCTCTA CACCCTCAGCAGCTCAGTGACTGTAACCTCGA GCACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTGGA CAAGAAAATTGAGCCCAGAGGGCCCACAATCA AGCCCTGTCCTCCATGCAAATGCCCAGCACCT AACCTCTTGGGTGGACCATCCGTCTTCATCTTC CCTCCAAAGATCAAGGATGTACTCATGATCTC CCTGAGCCCCATAGTCACATGTGTGGTGGTGG ATGTGAGCGAGGATGACCCAGATGTCCAGATC AGCTGGTTTGTGAACAACGTGGAAGTACACAC AGCTCAGACACAAACCCATAGAGAGGATTACA ACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCA TCCAGCACCAGGACTGGATGAGTGGCAAGGAG TTCAAATGCAAGGTCAACAACAAAGACCTCCC AGCGCCCATCGAGAGAACCATCTCAAAACCCA AAGGGTCAGTAAGAGCTCCACAGGTATATGTC TTGCCTCCACCAGAAGAAGAGATGACTAAGAA ACAGGTCACTCTGACCTGCATGGTCACAGACT TCATGCCTGAAGACATTTACGTGGAGTGGACC AACAACGGGAAAACAGAGCTAAACTACAAGA ACACTGAACCAGTCCTGGACTCTGATGGTTCTT ACTTCATGTACAGCAAGCTGAGAGTGGAAAAG AAGAACTGGGTGGAAAGAAATAGCTACTCCTG TTCAGTGGTCCACGAGGGTCTGCACAATCACC ACACGACTAAGAGCTTCTCCCGGACTCCGGGT AAA	
SM1B313	pDR000029287	CAGGTGCAGCTGAAGCAGAGCGGCCCTAGCCT GGTGCAGCCCAGCCAGAGCCTGAGCATCACCT GTACCGTGTCCGGCTTCAGCCTGACCACCTACG GCCTGCACTGGATCCGGCAGAGCCCCGGCAAG GGCCTGGAATGGCTGGGAGTGATTTGGAGAGG CGGCACCACCGACTACAACGCCGCCTTCATGA GCCGGCTGACCATCACCAAGGACAACAGCAAG AGCCAGGTGTTCTTCAAGATGAACAGCCTGCA GGCCGACGACACCGCCATCTACTACTGCGCCC GGACCGACATCTGGGGCGCTGGCACCACCGTG ACCGTGTCCTCTGCCAAAACAACAGCACCAAG TGTCTATCCACTGGCCCCTGTGTGTGGAGATAC AACTGGCTCCTCGGTGACTCTAGGATGCCTGGT CAAGGGTTATTTCCCTGAGCCAGTGACCTTGAC CTGGAACTCTGGATCCCTGTCCAGTGGTGTGCA	1137

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		CACCTTCCCAGCTGTCCTGCAGTCTGACCTCTA CACCCTCAGCAGCTCAGTGACTGTAACCTCGA GCACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTGGA CAAGAAAATTGAGCCCAGAGGGCCCACAATCA AGCCCTGTCCTCCATGCAAATGCCCAGCACCT AACCTCTTGGGTGGACCATCCGTCTTCATCTTC CCTCCAAAGATCAAGGATGTACTCATGATCTC CCTGAGCCCCATAGTCACATGTGTGGTGGTGG ATGTGAGCGAGGATGACCCAGATGTCCAGATC AGCTGGTTTGTGAACAACGTGGAAGTACACAC AGCTCAGACACAAACCCATAGAGAGGATTACA ACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCA TCCAGCACCAGGACTGGATGAGTGGCAAGGAG TTCAAATGCAAGGTCAACAACAAAGACCTCCC AGCGCCCATCGAGAGAACCATCTCAAAACCCA AAGGGTCAGTAAGAGCTCCACAGGTATATGTC TTGCCTCCACCAGAAGAAGAGATGACTAAGAA ACAGGTCACTCTGACCTGCATGGTCACAGACT TCATGCCTGAAGACATTTACGTGGAGTGGACC AACAACGGGAAAACAGAGCTAAACTACAAGA ACACTGAACCAGTCCTGGACTCTGATGGTTCTT ACTTCATGTACAGCAAGCTGAGAGTGGAAAAG AAGAACTGGGTGGAAAGAAATAGCTACTCCTG TTCAGTGGTCCACGAGGGTCTGCACAATCACC ACACGACTAAGAGCTTCTCCCGGACTCCGGGT AAA	
SM1B314	pDR000029286	CAGGTGCAGCTGAAGCAGAGCGGCCCTGGCCT GGTGCAGCCTAGCCAGAGCCTGCCCATCACCT GTACCGTGTCCGGCTTCAGCCTGACCACCTACG GCCTGCACTGGATCCGGCAGAGCCCCGGCAAG GGCCTGGAATGGCTGGGAGTGATTTGGAGAGG CGGCACCACCGACTACAACGCCGCCTTCATGA GCCGGCTGACCATCACCAAGGACAACAGCAAG AGCCAGGTGTTCTTCAAGATGAACAGCCTGCA GGCCGACGACACCGCCATCTACTACTGCGCCC GGACCGACATCTGGGGCGCTGGCACCACCGTG ACCGTGTCCTCTGCCAAAACAACAGCACCAAG TGTCTATCCACTGGCCCCTGTGTGTGGAGATAC AACTGGCTCCTCGGTGACTCTAGGATGCCTGGT CAAGGGTTATTTCCCTGAGCCAGTGACCTTGAC CTGGAACTCTGGATCCCTGTCCAGTGGTGTGCA CACCTTCCCAGCTGTCCTGCAGTCTGACCTCTA CACCCTCAGCAGCTCAGTGACTGTAACCTCGA GCACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTGGA CAAGAAAATTGAGCCCAGAGGGCCCACAATCA AGCCCTGTCCTCCATGCAAATGCCCAGCACCT	1138

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		AACCTCTTGGGTGGACCATCCGTCTTCATCTTC CCTCCAAAGATCAAGGATGTACTCATGATCTC CCTGAGCCCCATAGTCACATGTGTGGTGGTGG ATGTGAGCGAGGATGACCCAGATGTCCAGATC AGCTGGTTTGTGAACAACGTGGAAGTACACAC AGCTCAGACACAAACCCATAGAGAGGATTACA ACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCA TCCAGCACCAGGACTGGATGAGTGGCAAGGAG TTCAAATGCAAGGTCAACAACAAAGACCTCCC AGCGCCCATCGAGAGAACCATCTCAAAACCCA AAGGGTCAGTAAGAGCTCCACAGGTATATGTC TTGCCTCCACCAGAAGAAGAGATGACTAAGAA ACAGGTCACTCTGACCTGCATGGTCACAGACT TCATGCCTGAAGACATTTACGTGGAGTGGACC AACAACGGGAAAACAGAGCTAAACTACAAGA ACACTGAACCAGTCCTGGACTCTGATGGTTCTT ACTTCATGTACAGCAAGCTGAGAGTGGAAAAG AAGAACTGGGTGGAAAGAAATAGCTACTCCTG TTCAGTGGTCCACGAGGGTCTGCACAATCACC ACACGACTAAGAGCTTCTCCCGGACTCCGGGT AAA	
SM1B315	pDR000029285	CAGGTGCAGCTGAAGCAGAGCGGCCCTGGCCT GGTGCAGCCTAGCCAGAGCCTGAGCATCACCT GTACCGTGTCCGGCTTCAGCCTGACCACCTACG GCCTGCACTGGATCCGGCAGAGCCCCGGCAAG GGCCTGGAATGGCTGGGAGTGATTTGGAGAGG CGGCACCACCGACTACAACGCCGCCTTCATGA GCCGGCTGACCATCACCAAGGACAACAGCAAG AGCCAGGTGTTCTTCAAGATGAACAGCCTGCA GGCCGACGACACCGCCATCTACTACTGCGCCC GGACCGACATCTGGGGCGCTGGCACCACCGTG ACCGTGTCCTCTGCCAAAACAACAGCACCAAG TGTCTATCCACTGGCCCCTGTGTGTGGAGATAC AACTGGCTCCTCGGTGACTCTAGGATGCCTGGT CAAGGGTTATTTCCCTGAGCCAGTGACCTTGAC CTGGAACTCTGGATCCCTGTCCAGTGGTGTGCA CACCTTCCCAGCTGTCCTGCAGTCTGACCTCTA CACCCTCAGCAGCTCAGTGACTGTAACCTCGA GCACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTGGA CAAGAAAATTGAGCCCAGAGGGCCCACAATCA AGCCCTGTCCTCCATGCAAATGCCCAGCACCT AACCTCTTGGGTGGACCATCCGTCTTCATCTTC CCTCCAAAGATCAAGGATGTACTCATGATCTC CCTGAGCCCCATAGTCACATGTGTGGTGGTGG ATGTGAGCGAGGATGACCCAGATGTCCAGATC AGCTGGTTTGTGAACAACGTGGAAGTACACAC AGCTCAGACACAAACCCATAGAGAGGATTACA	1139

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		ACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCA TCCAGCACCAGGACTGGATGAGTGGCAAGGAG TTCAAATGCAAGGTCAACAACAAAGACCTCCC AGCGCCCATCGAGAGAACCATCTCAAAACCCA AAGGGTCAGTAAGAGCTCCACAGGTATATGTC TTGCCTCCACCAGAAGAAGAGATGACTAAGAA ACAGGTCACTCTGACCTGCATGGTCACAGACT TCATGCCTGAAGACATTTACGTGGAGTGGACC AACAACGGGAAAACAGAGCTAAACTACAAGA ACACTGAACCAGTCCTGGACTCTGATGGTTCTT ACTTCATGTACAGCAAGCTGAGAGTGGAAAAG AAGAACTGGGTGGAAAGAAATAGCTACTCCTG TTCAGTGGTCCACGAGGGTCTGCACAATCACC ACACGACTAAGAGCTTCTCCCGGACTCCGGGT AAA	
SM1B316	pDR000029287	CAGGTGCAGCTGAAGCAGAGCGGCCCTAGCCT GGTGCAGCCCAGCCAGAGCCTGAGCATCACCT GTACCGTGTCCGGCTTCAGCCTGACCACCTACG GCCTGCACTGGATCCGGCAGAGCCCCGGCAAG GGCCTGGAATGGCTGGGAGTGATTTGGAGAGG CGGCACCACCGACTACAACGCCGCCTTCATGA GCCGGCTGACCATCACCAAGGACAACAGCAAG AGCCAGGTGTTCTTCAAGATGAACAGCCTGCA GGCCGACGACACCGCCATCTACTACTGCGCCC GGACCGACATCTGGGGCGCTGGCACCACCGTG ACCGTGTCCTCTGCCAAAACAACAGCACCAAG TGTCTATCCACTGGCCCCTGTGTGTGGAGATAC AACTGGCTCCTCGGTGACTCTAGGATGCCTGGT CAAGGGTTATTTCCCTGAGCCAGTGACCTTGAC CTGGAACTCTGGATCCCTGTCCAGTGGTGTGCA CACCTTCCCAGCTGTCCTGCAGTCTGACCTCTA CACCCTCAGCAGCTCAGTGACTGTAACCTCGA GCACCTGGCCCAGCCAGTCCATCACCTGCAAT GTGGCCCACCCGGCAAGCAGCACCAAGGTGGA CAAGAAAATTGAGCCCAGAGGGCCCACAATCA AGCCCTGTCCTCCATGCAAATGCCCAGCACCT AACCTCTTGGGTGGACCATCCGTCTTCATCTTC CCTCCAAAGATCAAGGATGTACTCATGATCTC CCTGAGCCCCATAGTCACATGTGTGGTGGTGG ATGTGAGCGAGGATGACCCAGATGTCCAGATC AGCTGGTTTGTGAACAACGTGGAAGTACACAC AGCTCAGACACAAACCCATAGAGAGGATTACA ACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCA TCCAGCACCAGGACTGGATGAGTGGCAAGGAG TTCAAATGCAAGGTCAACAACAAAGACCTCCC AGCGCCCATCGAGAGAACCATCTCAAAACCCA AAGGGTCAGTAAGAGCTCCACAGGTATATGTC TTGCCTCCACCAGAAGAAGAGATGACTAAGAA	1140

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		ACAGGTCACTCTGACCTGCATGGTCACAGACT TCATGCCTGAAGACATTTACGTGGAGTGGACC AACAACGGGAAAACAGAGCTAAACTACAAGA ACACTGAACCAGTCCTGGACTCTGATGGTTCTT ACTTCATGTACAGCAAGCTGAGAGTGGAAAAG AAGAACTGGGTGGAAAGAAATAGCTACTCCTG TTCAGTGGTCCACGAGGGTCTGCACAATCACC ACACGACTAAGAGCTTCTCCCGGACTCCGGGT AAA	
SM1B317	pDR000029284	CAGGTGCAGCTGAAGCAGAGCGGCCCTGGCCT GGTGCAGCCTAGCCAGAGCCTGAGCATCACCT GTACCGTGTCCGGCTTCAGCCTGACCAGCTAC GGCGTGCACTGGGTCCGACAGCCTCCCGGCAA GGGCCTGGAATGGCTGGGAGTGATTTGGAGCG GCGGCATCACCGACTACAACGCCGCCTTCATC AGCAGACTGAGCATCAGCAAGGACAACAGCA AGAGCCAGGTGTTCTTCAAGATGAACAGCCTG CAGGCCGACGACACCGCCATCTACTACTGCGC CAGAACCGACCTGTGGGGCCAGGGCACCCTGG TCACAGTGTCTGCCGCCAAAACAACAGCACCA AGTGTCTATCCACTGGCCCCTGTGTGTGGAGAT ACAACTGGCTCCTCGGTGACTCTAGGATGCCT GGTCAAGGGTTATTTCCCTGAGCCAGTGACCTT GACCTGGAACTCTGGATCCCTGTCCAGTGGTGT GCACACCTTCCCAGCTGTCCTGCAGTCTGACCT CTACACCCTCAGCAGCTCAGTGACTGTAACCTC GAGCACCTGGCCCAGCCAGTCCATCACCTGCA ATGTGGCCCACCCGGCAAGCAGCACCAAGGTG GACAAGAAAATTGAGCCCAGAGGGCCCACAAT CAAGCCCTGTCCTCCATGCAAATGCCCAGCAC CTAACCTCTTGGGTGGACCATCCGTCTTCATCT TCCCTCCAAAGATCAAGGATGTACTCATGATCT CCCTGAGCCCCATAGTCACATGTGTGGTGGTG GATGTGAGCGAGGATGACCCAGATGTCCAGAT CAGCTGGTTTGTGAACAACGTGGAAGTACACA CAGCTCAGACACAAACCCATAGAGAGGATTAC AACAGTACTCTCCGGGTGGTCAGTGCCCTCCCC ATCCAGCACCAGGACTGGATGAGTGGCAAGGA GTTCAAATGCAAGGTCAACAACAAAGACCTCC CAGCGCCCATCGAGAGAACCATCTCAAAACCC AAAGGGTCAGTAAGAGCTCCACAGGTATATGT CTTGCCTCCACCAGAAGAAGAGATGACTAAGA AACAGGTCACTCTGACCTGCATGGTCACAGAC TTCATGCCTGAAGACATTTACGTGGAGTGGAC CAACAACGGGAAAACAGAGCTAAACTACAAG AACACTGAACCAGTCCTGGACTCTGATGGTTCT TACTTCATGTACAGCAAGCTGAGAGTGGAAAA GAAGAACTGGGTGGAAAGAAATAGCTACTCCT	1141

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		GTTCAGTGGTCCACGAGGGTCTGCACAATCAC CACACGACTAAGAGCTTCTCCCGGACTCCGGG TAAA	
SM1B318	pDR000029283	CAGGTGCAGCTGCAGCAGTCTGGCGCCGAGCT GATGAACCCTGGCGCCAGCGTGAAGATCAGCT GCAAGAGCACCGGCTACAAGTTCAGCAGCTAC TGGATCGAGTGGGTCAAGCAGCGGCCTGGCCA CGGCCTGGAATGGATGGGCGAGATCCTGCCTG GCAGCGGCAGCACCAACCACAACGAGAAGTTC AAGGGCAAGGCCATCTTCACCGCCGACGCCAG CAGCAACACCGCCTACATGGAACTGAGCAGCC TGACCAGCGAGGACAGCGCCGTGTACTACTGC GCCCGGACCATCAGCACCGCCACCGATTGGTT CGCCTACTGGGGCCAGGGCACCCTGGTCACCG TGTCTGCTGCCAAAACAACAGCACCAAGTGTC TATCCACTGGCCCCTGTGTGTGGAGATACAACT GGCTCCTCGGTGACTCTAGGATGCCTGGTCAA GGGTTATTTCCCTGAGCCAGTGACCTTGACCTG GAACTCTGGATCCCTGTCCAGTGGTGTGCACA CCTTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAGC ACCTGGCCCAGCCAGTCCATCACCTGCAATGT GGCCCACCCGGCAAGCAGCACCAAGGTGGACA AGAAAATTGAGCCCAGAGGGCCCACAATCAAG CCCTGTCCTCCATGCAAATGCCCAGCACCTAAC CTCTTGGGTGGACCATCCGTCTTCATCTTCCCT CCAAAGATCAAGGATGTACTCATGATCTCCCT GAGCCCCATAGTCACATGTGTGGTGGTGGATG TGAGCGAGGATGACCCAGATGTCCAGATCAGC TGGTTTGTGAACAACGTGGAAGTACACACAGC TCAGACACAAACCCATAGAGAGGATTACAACA GTACTCTCCGGGTGGTCAGTGCCCTCCCCATCC AGCACCAGGACTGGATGAGTGGCAAGGAGTTC AAATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAAAG GGTCAGTAAGAGCTCCACAGGTATATGTCTTG CCTCCACCAGAAGAAGAGATGACTAAGAAACA GGTCACTCTGACCTGCATGGTCACAGACTTCAT GCCTGAAGACATTTACGTGGAGTGGACCAACA ACGGGAAAACAGAGCTAAACTACAAGAACAC TGAACCAGTCCTGGACTCTGATGGTTCTTACTT CATGTACAGCAAGCTGAGAGTGGAAAAGAAG AACTGGGTGGAAAGAAATAGCTACTCCTGTTC AGTGGTCCACGAGGGTCTGCACAATCACCACA CGACTAAGAGCTTCTCCCGGACTCCGGGTAAA	1142
SM1B319	pDR000029283	CAGGTGCAGCTGCAGCAGTCTGGCGCCGAGCT GATGAACCCTGGCGCCAGCGTGAAGATCAGCT GCAAGAGCACCGGCTACAAGTTCAGCAGCTAC	1143

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		TGGATCGAGTGGGTCAAGCAGCGGCCTGGCCA CGGCCTGGAATGGATGGGCGAGATCCTGCCTG GCAGCGGCAGCACCAACCACAACGAGAAGTTC AAGGGCAAGGCCATCTTCACCGCCGACGCCAG CAGCAACACCGCCTACATGGAACTGAGCAGCC TGACCAGCGAGGACAGCGCCGTGTACTACTGC GCCCGGACCATCAGCACCGCCACCGATTGGTT CGCCTACTGGGGCCAGGGCACCCTGGTCACCG TGTCTGCTGCCAAAACAACAGCACCAAGTGTC TATCCACTGGCCCCTGTGTGTGGAGATACAACT GGCTCCTCGGTGACTCTAGGATGCCTGGTCAA GGGTTATTTCCCTGAGCCAGTGACCTTGACCTG GAACTCTGGATCCCTGTCCAGTGGTGTGCACA CCTTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAGC ACCTGGCCCAGCCAGTCCATCACCTGCAATGT GGCCCACCCGGCAAGCAGCACCAAGGTGGACA AGAAAATTGAGCCCAGAGGGCCCACAATCAAG CCCTGTCCTCCATGCAAATGCCCAGCACCTAAC CTCTTGGGTGGACCATCCGTCTTCATCTTCCCT CCAAAGATCAAGGATGTACTCATGATCTCCCT GAGCCCCATAGTCACATGTGTGGTGGTGGATG TGAGCGAGGATGACCCAGATGTCCAGATCAGC TGGTTTGTGAACAACGTGGAAGTACACACAGC TCAGACACAAACCCATAGAGAGGATTACAACA GTACTCTCCGGGTGGTCAGTGCCCTCCCCATCC AGCACCAGGACTGGATGAGTGGCAAGGAGTTC AAATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAAAG GGTCAGTAAGAGCTCCACAGGTATATGTCTTG CCTCCACCAGAAGAAGAGATGACTAAGAAACA GGTCACTCTGACCTGCATGGTCACAGACTTCAT GCCTGAAGACATTTACGTGGAGTGGACCAACA ACGGGAAAACAGAGCTAAACTACAAGAACAC TGAACCAGTCCTGGACTCTGATGGTTCTTACTT CATGTACAGCAAGCTGAGAGTGGAAAAGAAG AACTGGGTGGAAAGAAATAGCTACTCCTGTTC AGTGGTCCACGAGGGTCTGCACAATCACCACA CGACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B320	pDR000029282	CAGGTGCAGCTGCAGCAGTCTGGCGCCGAGCT GATGAAGCCTGGCGCCAGCGTGAAGATGAGCT GCAAGGCCACCGGCTACAAGTTCAGCAGCTAC TGGATCGAGTGGGTCAAGCAGCGGCCTGGCCA CGGCCTGGAATGGATGGGCGAGATCCTGCCTG GCAGCGGCAGCACCAACCACAACGAGAAGTTC AAGGGCAAGGCCATCTTCACCGCCGACGCCAG CAGCAACACCGCCTACATGGAACTGAGCAGCC TGACCAGCGAGGACAGCGCCGTGTACTACTGC	1144

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		GCCCGGACCATCAGCACCGCCACCGATTGGTT CGCCTACTGGGGCCAGGGCACCCTGGTCACCG TGTCTGCTGCCAAAACAACAGCACCAAGTGTC TATCCACTGGCCCCTGTGTGTGGAGATACAACT GGCTCCTCGGTGACTCTAGGATGCCTGGTCAA GGGTTATTTCCCTGAGCCAGTGACCTTGACCTG GAACTCTGGATCCCTGTCCAGTGGTGTGCACA CCTTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAGC ACCTGGCCCAGCCAGTCCATCACCTGCAATGT GGCCCACCCGGCAAGCAGCACCAAGGTGGACA AGAAAATTGAGCCCAGAGGGCCCACAATCAAG CCCTGTCCTCCATGCAAATGCCCAGCACCTAAC CTCTTGGGTGGACCATCCGTCTTCATCTTCCCT CCAAAGATCAAGGATGTACTCATGATCTCCCT GAGCCCCATAGTCACATGTGTGGTGGTGGATG TGAGCGAGGATGACCCAGATGTCCAGATCAGC TGGTTTGTGAACAACGTGGAAGTACACACAGC TCAGACACAAACCCATAGAGAGGATTACAACA GTACTCTCCGGGTGGTCAGTGCCCTCCCCATCC AGCACCAGGACTGGATGAGTGGCAAGGAGTTC AAATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAAAG GGTCAGTAAGAGCTCCACAGGTATATGTCTTG CCTCCACCAGAAGAAGAGATGACTAAGAAACA GGTCACTCTGACCTGCATGGTCACAGACTTCAT GCCTGAAGACATTTACGTGGAGTGGACCAACA ACGGGAAAACAGAGCTAAACTACAAGAACAC TGAACCAGTCCTGGACTCTGATGGTTCTTACTT CATGTACAGCAAGCTGAGAGTGGAAAAGAAG AACTGGGTGGAAAGAAATAGCTACTCCTGTTC AGTGGTCCACGAGGGTCTGCACAATCACCACA CGACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B321	pDR000029281	CAGGTGCAGCTGCAGCAGTCTGGCGCCGAGCT GATGAAGCCTGGCGCCAGCGTGAAGATGAGCT GCAAGGCCACCGGCTACAAGTTCAGCAGCTAC TGGATCGAGTGGGTCAAGCAGCGGCCTGGCCA CGGCCTGGAATGGATGGGCGAGATCCTGCCTG GCAGCGGCAGCACCAACCACAACGAGAAGTTC ACCGGCAGAGCCATCTTCACCGCCGACGCCAG CAGCAACACCGCCTACATGGAACTGAGCAGCC TGACCAGCGAGGACAGCGCCGTGTACTACTGC GCCCGGACCATCAGCACCGCCACCGATTGGTT CGCCTACTGGGGCCAGGGCACCCTGGTCACCG TGTCTGCTGCCAAAACAACAGCACCAAGTGTC TATCCACTGGCCCCTGTGTGTGGAGATACAACT GGCTCCTCGGTGACTCTAGGATGCCTGGTCAA GGGTTATTTCCCTGAGCCAGTGACCTTGACCTG	1145

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		GAACTCTGGATCCCTGTCCAGTGGTGTGCACA CCTTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAGC ACCTGGCCCAGCCAGTCCATCACCTGCAATGT GGCCCACCCGGCAAGCAGCACCAAGGTGGACA AGAAAATTGAGCCCAGAGGGCCCACAATCAAG CCCTGTCCTCCATGCAAATGCCCAGCACCTAAC CTCTTGGGTGGACCATCCGTCTTCATCTTCCCT CCAAAGATCAAGGATGTACTCATGATCTCCCT GAGCCCCATAGTCACATGTGTGGTGGTGGATG TGAGCGAGGATGACCCAGATGTCCAGATCAGC TGGTTTGTGAACAACGTGGAAGTACACACAGC TCAGACACAAACCCATAGAGAGGATTACAACA GTACTCTCCGGGTGGTCAGTGCCCTCCCCATCC AGCACCAGGACTGGATGAGTGGCAAGGAGTTC AAATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAAAG GGTCAGTAAGAGCTCCACAGGTATATGTCTTG CCTCCACCAGAAGAAGAGATGACTAAGAAACA GGTCACTCTGACCTGCATGGTCACAGACTTCAT GCCTGAAGACATTTACGTGGAGTGGACCAACA ACGGGAAAACAGAGCTAAACTACAAGAACAC TGAACCAGTCCTGGACTCTGATGGTTCTTACTT CATGTACAGCAAGCTGAGAGTGGAAAAGAAG AACTGGGTGGAAAGAAATAGCTACTCCTGTTC AGTGGTCCACGAGGGTCTGCACAATCACCACA CGACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B322	pDR000029282	CAGGTGCAGCTGCAGCAGTCTGGCGCCGAGCT GATGAAGCCTGGCGCCAGCGTGAAGATGAGCT GCAAGGCCACCGGCTACAAGTTCAGCAGCTAC TGGATCGAGTGGGTCAAGCAGCGGCCTGGCCA CGGCCTGGAATGGATGGGCGAGATCCTGCCTG GCAGCGGCAGCACCAACCACAACGAGAAGTTC AAGGGCAAGGCCATCTTCACCGCCGACGCCAG CAGCAACACCGCCTACATGGAACTGAGCAGCC TGACCAGCGAGGACAGCGCCGTGTACTACTGC GCCCGGACCATCAGCACCGCCACCGATTGGTT CGCCTACTGGGGCCAGGGCACCCTGGTCACCG TGTCTGCTGCCAAAACAACAGCACCAAGTGTC TATCCACTGGCCCCTGTGTGTGGAGATACAACT GGCTCCTCGGTGACTCTAGGATGCCTGGTCAA GGGTTATTTCCCTGAGCCAGTGACCTTGACCTG GAACTCTGGATCCCTGTCCAGTGGTGTGCACA CCTTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAGC ACCTGGCCCAGCCAGTCCATCACCTGCAATGT GGCCCACCCGGCAAGCAGCACCAAGGTGGACA AGAAAATTGAGCCCAGAGGGCCCACAATCAAG	1146

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		CCCTGTCCTCCATGCAAATGCCCAGCACCTAAC CTCTTGGGTGGACCATCCGTCTTCATCTTCCCT CCAAAGATCAAGGATGTACTCATGATCTCCCT GAGCCCCATAGTCACATGTGTGGTGGTGGATG TGAGCGAGGATGACCCAGATGTCCAGATCAGC TGGTTTGTGAACAACGTGGAAGTACACACAGC TCAGACACAAACCCATAGAGAGGATTACAACA GTACTCTCCGGGTGGTCAGTGCCCTCCCCATCC AGCACCAGGACTGGATGAGTGGCAAGGAGTTC AAATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAAAG GGTCAGTAAGAGCTCCACAGGTATATGTCTTG CCTCCACCAGAAGAAGAGATGACTAAGAAACA GGTCACTCTGACCTGCATGGTCACAGACTTCAT GCCTGAAGACATTTACGTGGAGTGGACCAACA ACGGGAAAACAGAGCTAAACTACAAGAACAC TGAACCAGTCCTGGACTCTGATGGTTCTTACTT CATGTACAGCAAGCTGAGAGTGGAAAAGAAG AACTGGGTGGAAAGAAATAGCTACTCCTGTTC AGTGGTCCACGAGGGTCTGCACAATCACCACA CGACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B323	pDR000029280	CAGGTGCAGCTGCAGCAGTCTGGCGCCGAGCT GATGAAGCCTGGCGCCAGCGTGAAGATGCCCT GCAAGGCCACCGGCTACAAGTTCAGCAGCTAC TGGATCGAGTGGGTCAAGCAGCGGCCTGGCCA CGGCCTGGAATGGATGGGCGAGATCCTGCCTG GCAGCGGCAGCACCAACCACAACGAGAAGTTC AAGGGCAAGGCCATCTTCACCGCCGACGCCAG CAGCAACACCGCCTACATGGAACTGAGCAGCC TGACCAGCGAGGACAGCGCCGTGTACTACTGC GCCCGGACCATCAGCACCGCCACCGATTGGTT CGCCTACTGGGGCCAGGGCACCCTGGTCACCG TGTCTGCTGCCAAAACAACAGCACCAAGTGTC TATCCACTGGCCCCTGTGTGTGGAGATACAACT GGCTCCTCGGTGACTCTAGGATGCCTGGTCAA GGGTTATTTCCCTGAGCCAGTGACCTTGACCTG GAACTCTGGATCCCTGTCCAGTGGTGTGCACA CCTTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAGC ACCTGGCCCAGCCAGTCCATCACCTGCAATGT GGCCCACCCGGCAAGCAGCACCAAGGTGGACA AGAAAATTGAGCCCAGAGGGCCCACAATCAAG CCCTGTCCTCCATGCAAATGCCCAGCACCTAAC CTCTTGGGTGGACCATCCGTCTTCATCTTCCCT CCAAAGATCAAGGATGTACTCATGATCTCCCT GAGCCCCATAGTCACATGTGTGGTGGTGGATG TGAGCGAGGATGACCCAGATGTCCAGATCAGC TGGTTTGTGAACAACGTGGAAGTACACACAGC	1147

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		TCAGACACAAACCCATAGAGAGGATTACAACA GTACTCTCCGGGTGGTCAGTGCCCTCCCCATCC AGCACCAGGACTGGATGAGTGGCAAGGAGTTC AAATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAAAG GGTCAGTAAGAGCTCCACAGGTATATGTCTTG CCTCCACCAGAAGAAGAGATGACTAAGAAACA GGTCACTCTGACCTGCATGGTCACAGACTTCAT GCCTGAAGACATTTACGTGGAGTGGACCAACA ACGGGAAAACAGAGCTAAACTACAAGAACAC TGAACCAGTCCTGGACTCTGATGGTTCTTACTT CATGTACAGCAAGCTGAGAGTGGAAAAGAAG AACTGGGTGGAAAGAAATAGCTACTCCTGTTC AGTGGTCCACGAGGGTCTGCACAATCACCACA CGACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B324	pDR000029279	GAGGTGCAGCTGCAGCAGTCTGGCGCTGAACT CGTGCGGCCTGGCGCCCTGGTCAAGCTGAGCT GCAAGGCCAGCGGCTTCAACATCAAGGACTAC TACATGCACTGGGTCAAGCAGCGGCCCGAGCA GGGCCTGGAATGGATCGGCTGGATCGACCCCG AGAACGGCAACACCATCTACGACCCCAAGTTC CAGGGCAAGGCCTCCATCACCGCCGACACCAG CAGCAACACCGCCTACCTGCAGCTGAGCAGCC TGACCAGCGAGGACACCGCCGTGTACTACTGC GCCAGATACGACGGCTACGCCATGGACTACTG GGGCCAGGGCACCAGCGTGACCGTGTCCTCTG CCAAAACAACAGCACCAAGTGTCTATCCACTG GCCCCTGTGTGTGGAGATACAACTGGCTCCTC GGTGACTCTAGGATGCCTGGTCAAGGGTTATTT CCCTGAGCCAGTGACCTTGACCTGGAACTCTG GATCCCTGTCCAGTGGTGTGCACACCTTCCCAG CTGTCCTGCAGTCTGACCTCTACACCCTCAGCA GCTCAGTGACTGTAACCTCGAGCACCTGGCCC AGCCAGTCCATCACCTGCAATGTGGCCCACCC GGCAAGCAGCACCAAGGTGGACAAGAAAATT GAGCCCAGAGGGCCCACAATCAAGCCCTGTCC TCCATGCAAATGCCCAGCACCTAACCTCTTGG GTGGACCATCCGTCTTCATCTTCCCTCCAAAGA TCAAGGATGTACTCATGATCTCCCTGAGCCCCA TAGTCACATGTGTGGTGGTGGATGTGAGCGAG GATGACCCAGATGTCCAGATCAGCTGGTTTGT GAACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTCTC CGGGTGGTCAGTGCCCTCCCCATCCAGCACCA GGACTGGATGAGTGGCAAGGAGTTCAAATGCA AGGTCAACAACAAAGACCTCCCAGCGCCCATC GAGAGAACCATCTCAAAACCCAAAGGGTCAGT AAGAGCTCCACAGGTATATGTCTTGCCTCCACC	1148

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		AGAAGAAGAGATGACTAAGAAACAGGTCACT CTGACCTGCATGGTCACAGACTTCATGCCTGA AGACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAACCA GTCCTGGACTCTGATGGTTCTTACTTCATGTAC AGCAAGCTGAGAGTGGAAAAGAAGAACTGGG TGGAAAGAAATAGCTACTCCTGTTCAGTGGTC CACGAGGGTCTGCACAATCACCACACGACTAA GAGCTTCTCCCGGACTCCGGGTAAA	
SM1B325	pDR000029278	CAGGTGCAGCTGCAGCAGTCTGGCGCTGAACT CGTGCGGCCTGGCACCAGCGTGAAGATGAGCT GCAAGGCCGCTGGCTACACCTTCACCAACTAC TGGATCGGCTGGGTCAAGCAGCGGCCTGGCCA CGGCCTGGAATGGATCGGCGACATCTACCCTG GCGGCGGATACACCAACTACAACGAGAAGTTC AAGGACAAGACCACCCTGACCGCCGACACCAG CAGCAACACCGCCTACATGCAGCTGAGCAGCC TGACCAGCGAGGACAGCGCCATCTACTACTGC GCCAGCAACGACTGCTGGGGCCAGGGCACCAC ACTGACCGTGTCCAGCGCCAAAACAACAGCAC CAAGTGTCTATCCACTGGCCCCTGTGTGTGGAG ATACAACTGGCTCCTCGGTGACTCTAGGATGC CTGGTCAAGGGTTATTTCCCTGAGCCAGTGACC TTGACCTGGAACTCTGGATCCCTGTCCAGTGGT GTGCACACCTTCCCAGCTGTCCTGCAGTCTGAC CTCTACACCCTCAGCAGCTCAGTGACTGTAACC TCGAGCACCTGGCCCAGCCAGTCCATCACCTG CAATGTGGCCCACCCGGCAAGCAGCACCAAGG TGGACAAGAAAATTGAGCCCAGAGGGCCCACA ATCAAGCCCTGTCCTCCATGCAAATGCCCAGC ACCTAACCTCTTGGGTGGACCATCCGTCTTCAT CTTCCCTCCAAAGATCAAGGATGTACTCATGAT CTCCCTGAGCCCCATAGTCACATGTGTGGTGGT GGATGTGAGCGAGGATGACCCAGATGTCCAGA TCAGCTGGTTTGTGAACAACGTGGAAGTACAC ACAGCTCAGACACAAACCCATAGAGAGGATTA CAACAGTACTCTCCGGGTGGTCAGTGCCCTCCC CATCCAGCACCAGGACTGGATGAGTGGCAAGG AGTTCAAATGCAAGGTCAACAACAAAGACCTC CCAGCGCCCATCGAGAGAACCATCTCAAAACC CAAAGGGTCAGTAAGAGCTCCACAGGTATATG TCTTGCCTCCACCAGAAGAAGAGATGACTAAG AAACAGGTCACTCTGACCTGCATGGTCACAGA CTTCATGCCTGAAGACATTTACGTGGAGTGGA CCAACAACGGGAAAACAGAGCTAAACTACAA GAACACTGAACCAGTCCTGGACTCTGATGGTT CTTACTTCATGTACAGCAAGCTGAGAGTGGAA AAGAAGAACTGGGTGGAAAGAAATAGCTACTC	1149

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		CTGTTCAGTGGTCCACGAGGGTCTGCACAATC ACCACACGACTAAGAGCTTCTCCCGGACTCCG GGTAAA	
SM1B326	pDR000029277	CAGGTGCAGCTGAAGCAGAGCGGCCCTGGCCT GGTGCAGCCTAGCCAGAGCCTGAGCATCACCT GTACCGTGTCCGGCTTCAGCATCACCAGCTAC GGCGTGCACTGGATCCGGCAGAGCCCCGGCAA GGGCCTGGAATGGCTGGGAGTGATTTGGAGCG GCGGCAGCACCGACTACAACGCCGCCTTCATC AGCAGACTGAGCATCAGCGAGGACAACAGCA AGAGCCAGGTGTTCTTCAAGATGAACAGCCTG CAGGCCAACGACACCGCCATCTACTACTGCGC CACCTTCTACTACGACTACGACGAGGGCTTCG ACTACTGGGGCCAGGGCACCACCCTGACCGTG TCCTCTGCCAAAACAACAGCACCAAGTGTCTA TCCACTGGCCCCTGTGTGTGGAGATACAACTG GCTCCTCGGTGACTCTAGGATGCCTGGTCAAG GGTTATTTCCCTGAGCCAGTGACCTTGACCTGG AACTCTGGATCCCTGTCCAGTGGTGTGCACACC TTCCCAGCTGTCCTGCAGTCTGACCTCTACACC CTCAGCAGCTCAGTGACTGTAACCTCGAGCAC CTGGCCCAGCCAGTCCATCACCTGCAATGTGG CCCACCCGGCAAGCAGCACCAAGGTGGACAAG AAAATTGAGCCCAGAGGGCCCACAATCAAGCC CTGTCCTCCATGCAAATGCCCAGCACCTAACCT CTTGGGTGGACCATCCGTCTTCATCTTCCCTCC AAAGATCAAGGATGTACTCATGATCTCCCTGA GCCCCATAGTCACATGTGTGGTGGTGGATGTG AGCGAGGATGACCCAGATGTCCAGATCAGCTG GTTTGTGAACAACGTGGAAGTACACACAGCTC AGACACAAACCCATAGAGAGGATTACAACAGT ACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAG CACCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGCGC CCATCGAGAGAACCATCTCAAAACCCAAAGGG TCAGTAAGAGCTCCACAGGTATATGTCTTGCCT CCACCAGAAGAAGAGATGACTAAGAAACAGG TCACTCTGACCTGCATGGTCACAGACTTCATGC CTGAAGACATTTACGTGGAGTGGACCAACAAC GGGAAAACAGAGCTAAACTACAAGAACACTG AACCAGTCCTGGACTCTGATGGTTCTTACTTCA TGTACAGCAAGCTGAGAGTGGAAAAGAAGAA CTGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACACG ACTAAGAGCTTCTCCCGGACTCCGGGTAAA	1150
SM1B327	pDR000029276	CAGGTGCAGCTGAAGCAGAGCGGCCCTGGCCT GGTGCAGCCTAGCCAGAGCCTGAGCATCACCT GTACCGTGTCCGGCTTCAGCATCACCAGCTAC	1151

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		GGCGTGCACTGGATCCGGCAGAGCCCCGGCAA GGGCCTGGAATGGCTGGGAGTGATTTGGAGCG GCGGCAGCACCGACTACAACGCCGCCTTCATC AGCAGACTGAGCATCAGCAAGGACAACAGCA AGAGCCAGGTGTTCTTCAAGATGAACAGCCTG CAGGCCAACGACACCGCCATCTACTACTGCGC CACCTTCTACTACGACTACGACGAGGGCTTCG ACTACTGGGGCCAGGGCACCACCCTGACCGTG TCCTCTGCCAAAACAACAGCACCAAGTGTCTA TCCACTGGCCCCTGTGTGTGGAGATACAACTG GCTCCTCGGTGACTCTAGGATGCCTGGTCAAG GGTTATTTCCCTGAGCCAGTGACCTTGACCTGG AACTCTGGATCCCTGTCCAGTGGTGTGCACACC TTCCCAGCTGTCCTGCAGTCTGACCTCTACACC CTCAGCAGCTCAGTGACTGTAACCTCGAGCAC CTGGCCCAGCCAGTCCATCACCTGCAATGTGG CCCACCCGGCAAGCAGCACCAAGGTGGACAAG AAAATTGAGCCCAGAGGGCCCACAATCAAGCC CTGTCCTCCATGCAAATGCCCAGCACCTAACCT CTTGGGTGGACCATCCGTCTTCATCTTCCCTCC AAAGATCAAGGATGTACTCATGATCTCCCTGA GCCCCATAGTCACATGTGTGGTGGTGGATGTG AGCGAGGATGACCCAGATGTCCAGATCAGCTG GTTTGTGAACAACGTGGAAGTACACACAGCTC AGACACAAACCCATAGAGAGGATTACAACAGT ACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAG CACCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGCGC CCATCGAGAGAACCATCTCAAAACCCAAAGGG TCAGTAAGAGCTCCACAGGTATATGTCTTGCCT CCACCAGAAGAAGAGATGACTAAGAAACAGG TCACTCTGACCTGCATGGTCACAGACTTCATGC CTGAAGACATTTACGTGGAGTGGACCAACAAC GGGAAAACAGAGCTAAACTACAAGAACACTG AACCAGTCCTGGACTCTGATGGTTCTTACTTCA TGTACAGCAAGCTGAGAGTGGAAAAGAAGAA CTGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACACG ACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B328	pDR000029276	CAGGTGCAGCTGAAGCAGAGCGGCCCTGGCCT GGTGCAGCCTAGCCAGAGCCTGAGCATCACCT GTACCGTGTCCGGCTTCAGCATCACCAGCTAC GGCGTGCACTGGATCCGGCAGAGCCCCGGCAA GGGCCTGGAATGGCTGGGAGTGATTTGGAGCG GCGGCAGCACCGACTACAACGCCGCCTTCATC AGCAGACTGAGCATCAGCAAGGACAACAGCA AGAGCCAGGTGTTCTTCAAGATGAACAGCCTG CAGGCCAACGACACCGCCATCTACTACTGCGC	1152

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		CACCTTCTACTACGACTACGACGAGGGCTTCG ACTACTGGGGCCAGGGCACCACCCTGACCGTG TCCTCTGCCAAAACAACAGCACCAAGTGTCTA TCCACTGGCCCCTGTGTGTGGAGATACAACTG GCTCCTCGGTGACTCTAGGATGCCTGGTCAAG GGTTATTTCCCTGAGCCAGTGACCTTGACCTGG AACTCTGGATCCCTGTCCAGTGGTGTGCACACC TTCCCAGCTGTCCTGCAGTCTGACCTCTACACC CTCAGCAGCTCAGTGACTGTAACCTCGAGCAC CTGGCCCAGCCAGTCCATCACCTGCAATGTGG CCCACCCGGCAAGCAGCACCAAGGTGGACAAG AAAATTGAGCCCAGAGGGCCCACAATCAAGCC CTGTCCTCCATGCAAATGCCCAGCACCTAACCT CTTGGGTGGACCATCCGTCTTCATCTTCCCTCC AAAGATCAAGGATGTACTCATGATCTCCCTGA GCCCCATAGTCACATGTGTGGTGGTGGATGTG AGCGAGGATGACCCAGATGTCCAGATCAGCTG GTTTGTGAACAACGTGGAAGTACACACAGCTC AGACACAAACCCATAGAGAGGATTACAACAGT ACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAG CACCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGCGC CCATCGAGAGAACCATCTCAAAACCCAAAGGG TCAGTAAGAGCTCCACAGGTATATGTCTTGCCT CCACCAGAAGAAGAGATGACTAAGAAACAGG TCACTCTGACCTGCATGGTCACAGACTTCATGC CTGAAGACATTTACGTGGAGTGGACCAACAAC GGGAAAACAGAGCTAAACTACAAGAACACTG AACCAGTCCTGGACTCTGATGGTTCTTACTTCA TGTACAGCAAGCTGAGAGTGGAAAAGAAGAA CTGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACACG ACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B329	pDR000029276	CAGGTGCAGCTGAAGCAGAGCGGCCCTGGCCT GGTGCAGCCTAGCCAGAGCCTGAGCATCACCT GTACCGTGTCCGGCTTCAGCATCACCAGCTAC GGCGTGCACTGGATCCGGCAGAGCCCCGGCAA GGGCCTGGAATGGCTGGGAGTGATTTGGAGCG GCGGCAGCACCGACTACAACGCCGCCTTCATC AGCAGACTGAGCATCAGCAAGGACAACAGCA AGAGCCAGGTGTTCTTCAAGATGAACAGCCTG CAGGCCAACGACACCGCCATCTACTACTGCGC CACCTTCTACTACGACTACGACGAGGGCTTCG ACTACTGGGGCCAGGGCACCACCCTGACCGTG TCCTCTGCCAAAACAACAGCACCAAGTGTCTA TCCACTGGCCCCTGTGTGTGGAGATACAACTG GCTCCTCGGTGACTCTAGGATGCCTGGTCAAG GGTTATTTCCCTGAGCCAGTGACCTTGACCTGG	1153

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		AACTCTGGATCCCTGTCCAGTGGTGTGCACACC TTCCCAGCTGTCCTGCAGTCTGACCTCTACACC CTCAGCAGCTCAGTGACTGTAACCTCGAGCAC CTGGCCCAGCCAGTCCATCACCTGCAATGTGG CCCACCCGGCAAGCAGCACCAAGGTGGACAAG AAAATTGAGCCCAGAGGGCCCACAATCAAGCC CTGTCCTCCATGCAAATGCCCAGCACCTAACCT CTTGGGTGGACCATCCGTCTTCATCTTCCCTCC AAAGATCAAGGATGTACTCATGATCTCCCTGA GCCCCATAGTCACATGTGTGGTGGTGGATGTG AGCGAGGATGACCCAGATGTCCAGATCAGCTG GTTTGTGAACAACGTGGAAGTACACACAGCTC AGACACAAACCCATAGAGAGGATTACAACAGT ACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAG CACCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGCGC CCATCGAGAGAACCATCTCAAAACCCAAAGGG TCAGTAAGAGCTCCACAGGTATATGTCTTGCCT CCACCAGAAGAAGAGATGACTAAGAAACAGG TCACTCTGACCTGCATGGTCACAGACTTCATGC CTGAAGACATTTACGTGGAGTGGACCAACAAC GGGAAAACAGAGCTAAACTACAAGAACACTG AACCAGTCCTGGACTCTGATGGTTCTTACTTCA TGTACAGCAAGCTGAGAGTGGAAAAGAAGAA CTGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACACG ACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B330	pDR000029276	CAGGTGCAGCTGAAGCAGAGCGGCCCTGGCCT GGTGCAGCCTAGCCAGAGCCTGAGCATCACCT GTACCGTGTCCGGCTTCAGCATCACCAGCTAC GGCGTGCACTGGATCCGGCAGAGCCCCGGCAA GGGCCTGGAATGGCTGGGAGTGATTTGGAGCG GCGGCAGCACCGACTACAACGCCGCCTTCATC AGCAGACTGAGCATCAGCAAGGACAACAGCA AGAGCCAGGTGTTCTTCAAGATGAACAGCCTG CAGGCCAACGACACCGCCATCTACTACTGCGC CACCTTCTACTACGACTACGACGAGGGCTTCG ACTACTGGGGCCAGGGCACCACCCTGACCGTG TCCTCTGCCAAAACAACAGCACCAAGTGTCTA TCCACTGGCCCCTGTGTGTGGAGATACAACTG GCTCCTCGGTGACTCTAGGATGCCTGGTCAAG GGTTATTTCCCTGAGCCAGTGACCTTGACCTGG AACTCTGGATCCCTGTCCAGTGGTGTGCACACC TTCCCAGCTGTCCTGCAGTCTGACCTCTACACC CTCAGCAGCTCAGTGACTGTAACCTCGAGCAC CTGGCCCAGCCAGTCCATCACCTGCAATGTGG CCCACCCGGCAAGCAGCACCAAGGTGGACAAG AAAATTGAGCCCAGAGGGCCCACAATCAAGCC	1154

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		CTGTCCTCCATGCAAATGCCCAGCACCTAACCT CTTGGGTGGACCATCCGTCTTCATCTTCCCTCC AAAGATCAAGGATGTACTCATGATCTCCCTGA GCCCCATAGTCACATGTGTGGTGGTGGATGTG AGCGAGGATGACCCAGATGTCCAGATCAGCTG GTTTGTGAACAACGTGGAAGTACACACAGCTC AGACACAAACCCATAGAGAGGATTACAACAGT ACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAG CACCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGCGC CCATCGAGAGAACCATCTCAAAACCCAAAGGG TCAGTAAGAGCTCCACAGGTATATGTCTTGCCT CCACCAGAAGAAGAGATGACTAAGAAACAGG TCACTCTGACCTGCATGGTCACAGACTTCATGC CTGAAGACATTTACGTGGAGTGGACCAACAAC GGGAAAACAGAGCTAAACTACAAGAACACTG AACCAGTCCTGGACTCTGATGGTTCTTACTTCA TGTACAGCAAGCTGAGAGTGGAAAAGAAGAA CTGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACACG ACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B331	pDR000029276	CAGGTGCAGCTGAAGCAGAGCGGCCCTGGCCT GGTGCAGCCTAGCCAGAGCCTGAGCATCACCT GTACCGTGTCCGGCTTCAGCATCACCAGCTAC GGCGTGCACTGGATCCGGCAGAGCCCCGGCAA GGGCCTGGAATGGCTGGGAGTGATTTGGAGCG GCGGCAGCACCGACTACAACGCCGCCTTCATC AGCAGACTGAGCATCAGCAAGGACAACAGCA AGAGCCAGGTGTTCTTCAAGATGAACAGCCTG CAGGCCAACGACACCGCCATCTACTACTGCGC CACCTTCTACTACGACTACGACGAGGGCTTCG ACTACTGGGGCCAGGGCACCACCCTGACCGTG TCCTCTGCCAAAACAACAGCACCAAGTGTCTA TCCACTGGCCCCTGTGTGTGGAGATACAACTG GCTCCTCGGTGACTCTAGGATGCCTGGTCAAG GGTTATTTCCCTGAGCCAGTGACCTTGACCTGG AACTCTGGATCCCTGTCCAGTGGTGTGCACACC TTCCCAGCTGTCCTGCAGTCTGACCTCTACACC CTCAGCAGCTCAGTGACTGTAACCTCGAGCAC CTGGCCCAGCCAGTCCATCACCTGCAATGTGG CCCACCCGGCAAGCAGCACCAAGGTGGACAAG AAAATTGAGCCCAGAGGGCCCACAATCAAGCC CTGTCCTCCATGCAAATGCCCAGCACCTAACCT CTTGGGTGGACCATCCGTCTTCATCTTCCCTCC AAAGATCAAGGATGTACTCATGATCTCCCTGA GCCCCATAGTCACATGTGTGGTGGTGGATGTG AGCGAGGATGACCCAGATGTCCAGATCAGCTG GTTTGTGAACAACGTGGAAGTACACACAGCTC	1155

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		AGACACAAACCCATAGAGAGGATTACAACAGT ACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAG CACCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGCGC CCATCGAGAGAACCATCTCAAAACCCAAAGGG TCAGTAAGAGCTCCACAGGTATATGTCTTGCCT CCACCAGAAGAAGAGATGACTAAGAAACAGG TCACTCTGACCTGCATGGTCACAGACTTCATGC CTGAAGACATTTACGTGGAGTGGACCAACAAC GGGAAAACAGAGCTAAACTACAAGAACACTG AACCAGTCCTGGACTCTGATGGTTCTTACTTCA TGTACAGCAAGCTGAGAGTGGAAAAGAAGAA CTGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACACG ACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B332	pDR000029275	CAGGTGCAGCTGAAAGAGTCCGGCCCTGGACT GGTGGCCCCCAGCCAGAGCCTGAGCATCACCT GTACCGTGTCCGGCCTGAGCCTGACCAGCTAC GGCCTGTCTTGGGTCCGACAGCCCCCTGGCAA GGGCCTGGAATGGCTGGGAGTGATCTGGGGCG ACGGCAGCACCAACTACCACAGCGCCCTGATC AGCAGACTGAGCATCAGCAAGGACAACAGCA AGAGCCAGGTGTTCCTGAAGCTGAACAGCCTG CAGAGCGACGACACCGCCACCTACTACTGCGC CACCAGAGGCGACTACGGCAGCTACGCCATGG ACTACTGGGGCCAGGGCACCAGCGTGACCGTG TCCTCTGCCAAAACAACAGCACCAAGTGTCTA TCCACTGGCCCCTGTGTGTGGAGATACAACTG GCTCCTCGGTGACTCTAGGATGCCTGGTCAAG GGTTATTTCCCTGAGCCAGTGACCTTGACCTGG AACTCTGGATCCCTGTCCAGTGGTGTGCACACC TTCCCAGCTGTCCTGCAGTCTGACCTCTACACC CTCAGCAGCTCAGTGACTGTAACCTCGAGCAC CTGGCCCAGCCAGTCCATCACCTGCAATGTGG CCCACCCGGCAAGCAGCACCAAGGTGGACAAG AAAATTGAGCCCAGAGGGCCCACAATCAAGCC CTGTCCTCCATGCAAATGCCCAGCACCTAACCT CTTGGGTGGACCATCCGTCTTCATCTTCCCTCC AAAGATCAAGGATGTACTCATGATCTCCCTGA GCCCCATAGTCACATGTGTGGTGGTGGATGTG AGCGAGGATGACCCAGATGTCCAGATCAGCTG GTTTGTGAACAACGTGGAAGTACACACAGCTC AGACACAAACCCATAGAGAGGATTACAACAGT ACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAG CACCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGCGC CCATCGAGAGAACCATCTCAAAACCCAAAGGG TCAGTAAGAGCTCCACAGGTATATGTCTTGCCT	1156

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		CCACCAGAAGAAGAGATGACTAAGAAACAGG TCACTCTGACCTGCATGGTCACAGACTTCATGC CTGAAGACATTTACGTGGAGTGGACCAACAAC GGGAAAACAGAGCTAAACTACAAGAACACTG AACCAGTCCTGGACTCTGATGGTTCTTACTTCA TGTACAGCAAGCTGAGAGTGGAAAAGAAGAA CTGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACACG ACTAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B333	pDR000029274	GAGGTGCAGCTGCAGCAGTCTGGCGCTGAACT CGTGCGGCCTGGCGCCAGCGTGAAGCTGAGCT GTACCGCCAGCGGCTTCAACATCAAGGACAGC CTGATCCACTGGGTCAAGCAGCGGCCCGAGCA GGGCCTGGAATGGATCGGCTGGATCGACCCCG AGGACGGCGAGACTAAGTACGCCCCCAAGTTC CAGGACAAGGCCGCCCTGACCACCGACACCAG CAGCAACACCGCCTACCTGCACCTGAACAGCC TGACCAGCGAGGACACCGCCATCTACTACTGC GGCAGAGGCGGCCTGATCCTGGACTACTGGGG CCAGGGCACCACCCTGACCGTGTCCTCTGCCA AAACAACAGCACCAAGTGTCTATCCACTGGCC CCTGTGTGTGGAGATACAACTGGCTCCTCGGT GACTCTAGGATGCCTGGTCAAGGGTTATTTCCC TGAGCCAGTGACCTTGACCTGGAACTCTGGAT CCCTGTCCAGTGGTGTGCACACCTTCCCAGCTG TCCTGCAGTCTGACCTCTACACCCTCAGCAGCT CAGTGACTGTAACCTCGAGCACCTGGCCCAGC CAGTCCATCACCTGCAATGTGGCCCACCCGGC AAGCAGCACCAAGGTGGACAAGAAAATTGAG CCCAGAGGGCCCACAATCAAGCCCTGTCCTCC ATGCAAATGCCCAGCACCTAACCTCTTGGGTG GACCATCCGTCTTCATCTTCCCTCCAAAGATCA AGGATGTACTCATGATCTCCCTGAGCCCCATA GTCACATGTGTGGTGGTGGATGTGAGCGAGGA TGACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACACAA ACCCATAGAGAGGATTACAACAGTACTCTCCG GGTGGTCAGTGCCCTCCCCATCCAGCACCAGG ACTGGATGAGTGGCAAGGAGTTCAAATGCAAG GTCAACAACAAAGACCTCCCAGCGCCCATCGA GAGAACCATCTCAAAACCCAAAGGGTCAGTAA GAGCTCCACAGGTATATGTCTTGCCTCCACCAG AAGAAGAGATGACTAAGAAACAGGTCACTCTG ACCTGCATGGTCACAGACTTCATGCCTGAAGA CATTTACGTGGAGTGGACCAACAACGGGAAAA CAGAGCTAAACTACAAGAACACTGAACCAGTC CTGGACTCTGATGGTTCTTACTTCATGTACAGC AAGCTGAGAGTGGAAAAGAAGAACTGGGTGG	1157

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		AAAGAAATAGCTACTCCTGTTCAGTGGTCCAC GAGGGTCTGCACAATCACCACACGACTAAGAG CTTCTCCCGGACTCCGGGTAAA	
SM1B334	pDR000029273	CAGATCCAGCTGGTGCAGAGCGGCCCTGAGCT GAAGAAACCCGGCGAGACAGTGAAGATCAGC TGCAGAAGCAGCGGCTACACCTTCACCAACTA CGGCCTGAACTGGGTCAAGCAGGCCCCTGGCA AGGACCTGAAGTGGATGGGCTGGCTGAACACC TACACCGGCGAGCCCACCTACGCCGACGACTT CAAGGGCAGATTCGCCTTCAGCCTGGAAACCA GCGCCGGCACCGCCTACCTGCAGATCAACAAC CTGAAGAACGAGGACACCGCCACCTACTTTTG CTCCCGGGACTACCGCGAGGGCGACGCCATGG ATTACTGGTCCCAGGGCACCAGCGTGACCGTG TCCAGCGCCAAAACAACAGCACCAAGTGTCTA TCCACTGGCCCCTGTGTGTGGAGATACAACTG GCTCCTCGGTGACTCTAGGATGCCTGGTCAAG GGTTATTTCCCTGAGCCAGTGACCTTGACCTGG AACTCTGGATCCCTGTCCAGTGGTGTGCACACC TTCCCAGCTGTCCTGCAGTCTGACCTCTACACC CTCAGCAGCTCAGTGACTGTAACCTCGAGCAC CTGGCCCAGCCAGTCCATCACCTGCAATGTGG CCCACCCGGCAAGCAGCACCAAGGTGGACAAG AAAATTGAGCCCAGAGGGCCCACAATCAAGCC CTGTCCTCCATGCAAATGCCCAGCACCTAACCT CTTGGGTGGACCATCCGTCTTCATCTTCCCTCC AAAGATCAAGGATGTACTCATGATCTCCCTGA GCCCCATAGTCACATGTGTGGTGGTGGATGTG AGCGAGGATGACCCAGATGTCCAGATCAGCTG GTTTGTGAACAACGTGGAAGTACACACAGCTC AGACACAAACCCATAGAGAGGATTACAACAGT ACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAG CACCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGCGC CCATCGAGAGAACCATCTCAAAACCCAAAGGG TCAGTAAGAGCTCCACAGGTATATGTCTTGCCT CCACCAGAAGAAGAGATGACTAAGAAACAGG TCACTCTGACCTGCATGGTCACAGACTTCATGC CTGAAGACATTTACGTGGAGTGGACCAACAAC GGGAAAACAGAGCTAAACTACAAGAACACTG AACCAGTCCTGGACTCTGATGGTTCTTACTTCA TGTACAGCAAGCTGAGAGTGGAAAAGAAGAA CTGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACACG ACTAAGAGCTTCTCCCGGACTCCGGGTAAA	1158
SM1B335	pDR000029272	GAGGTGCAGCTGGTGGAAAGCGGCGGAGGAC TGGTCAAGCCTGGCGGCAGCCTGAAGCTGAGC TGCGCCGCCAGCGGCTTCACCTTCAGCAGCTA	1159

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		CGCCATGAGCTGGGTCCGACAGACCCCCGAGA AGCGGCTGGAATGGGTGGCCACCATCAGCACC AGCGGCAGCTACACCTACTACCGGGACAGCGT GAAGGGCCGGCTGACCATCAGCCGGGACAACG CCAAGAACACCCTGTACCTGCAGATGACCAGC CTGCGGAGCGAGGACACCGCCATGTACTACTG CACCCGGCACGGCGACCACGACGGCTTCGATT ACTGGGGCCAGGGCACCACCCTGACCGTGTCC TCTGCCAAAACAACAGCACCAAGTGTCTATCC ACTGGCCCCTGTGTGTGGAGATACAACTGGCT CCTCGGTGACTCTAGGATGCCTGGTCAAGGGT TATTTCCCTGAGCCAGTGACCTTGACCTGGAAC TCTGGATCCCTGTCCAGTGGTGTGCACACCTTC CCAGCTGTCCTGCAGTCTGACCTCTACACCCTC AGCAGCTCAGTGACTGTAACCTCGAGCACCTG GCCCAGCCAGTCCATCACCTGCAATGTGGCCC ACCCGGCAAGCAGCACCAAGGTGGACAAGAA AATTGAGCCCAGAGGGCCCACAATCAAGCCCT GTCCTCCATGCAAATGCCCAGCACCTAACCTCT TGGGTGGACCATCCGTCTTCATCTTCCCTCCAA AGATCAAGGATGTACTCATGATCTCCCTGAGC CCCATAGTCACATGTGTGGTGGTGGATGTGAG CGAGGATGACCCAGATGTCCAGATCAGCTGGT TTGTGAACAACGTGGAAGTACACACAGCTCAG ACACAAACCCATAGAGAGGATTACAACAGTAC TCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCA CCAGGACTGGATGAGTGGCAAGGAGTTCAAAT GCAAGGTCAACAACAAAGACCTCCCAGCGCCC ATCGAGAGAACCATCTCAAAACCCAAAGGGTC AGTAAGAGCTCCACAGGTATATGTCTTGCCTCC ACCAGAAGAAGAGATGACTAAGAAACAGGTC ACTCTGACCTGCATGGTCACAGACTTCATGCCT GAAGACATTTACGTGGAGTGGACCAACAACGG GAAAACAGAGCTAAACTACAAGAACACTGAA CCAGTCCTGGACTCTGATGGTTCTTACTTCATG TACAGCAAGCTGAGAGTGGAAAAGAAGAACT GGGTGGAAAGAAATAGCTACTCCTGTTCAGTG GTCCACGAGGGTCTGCACAATCACCACACGAC TAAGAGCTTCTCCCGGACTCCGGGTAAA	
SM1B336	pDR000029271	GAGGTGCAGCTGGTGGAAAGCGGCGGAGGAC TGGTCAAGCCTGGCGGCAGCCTGAAGCTGAGC TGCGTGGCCTCCGGCTTCAGCTTCAGCAACTAC GCCATGAGCTGGGTCCGACAGACCCCCGAGCG GAGACTGGAATGGGTGGCCACCATCAACAGCG GCGGCAGCTTCAGCTTTTTCCCAGACTCCGTGA AGGGCCGGTTCACCATCAGCCGGGACAGCGCC AAGAACACCCTGTACCTGCAGATGAGCAGCCT GCGGAGCGACGACACCGCCATGTACTACTGCA	1160

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		CCCGGCACTGGGACCACCCTTGGTTTGCCTACT GGGGCCAGGGCACCCTGGTCACCGTGTCTGCT GCCAAAACAACAGCACCAAGTGTCTATCCACT GGCCCCTGTGTGTGGAGATACAACTGGCTCCT CGGTGACTCTAGGATGCCTGGTCAAGGGTTAT TTCCCTGAGCCAGTGACCTTGACCTGGAACTCT GGATCCCTGTCCAGTGGTGTGCACACCTTCCCA GCTGTCCTGCAGTCTGACCTCTACACCCTCAGC AGCTCAGTGACTGTAACCTCGAGCACCTGGCC CAGCCAGTCCATCACCTGCAATGTGGCCCACC CGGCAAGCAGCACCAAGGTGGACAAGAAAAT TGAGCCCAGAGGGCCCACAATCAAGCCCTGTC CTCCATGCAAATGCCCAGCACCTAACCTCTTGG GTGGACCATCCGTCTTCATCTTCCCTCCAAAGA TCAAGGATGTACTCATGATCTCCCTGAGCCCCA TAGTCACATGTGTGGTGGTGGATGTGAGCGAG GATGACCCAGATGTCCAGATCAGCTGGTTTGT GAACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTCTC CGGGTGGTCAGTGCCCTCCCCATCCAGCACCA GGACTGGATGAGTGGCAAGGAGTTCAAATGCA AGGTCAACAACAAAGACCTCCCAGCGCCCATC GAGAGAACCATCTCAAAACCCAAAGGGTCAGT AAGAGCTCCACAGGTATATGTCTTGCCTCCACC AGAAGAAGAGATGACTAAGAAACAGGTCACT CTGACCTGCATGGTCACAGACTTCATGCCTGA AGACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAACCA GTCCTGGACTCTGATGGTTCTTACTTCATGTAC AGCAAGCTGAGAGTGGAAAAGAAGAACTGGG TGGAAAGAAATAGCTACTCCTGTTCAGTGGTC CACGAGGGTCTGCACAATCACCACACGACTAA GAGCTTCTCCCGGACTCCGGGTAAA	
SM1B337	pDR000029271	GAGGTGCAGCTGGTGGAAAGCGGCGGAGGAC TGGTCAAGCCTGGCGGCAGCCTGAAGCTGAGC TGCGTGGCCTCCGGCTTCAGCTTCAGCAACTAC GCCATGAGCTGGGTCCGACAGACCCCCGAGCG GAGACTGGAATGGGTGGCCACCATCAACAGCG GCGGCAGCTTCAGCTTTTTCCCAGACTCCGTGA AGGGCCGGTTCACCATCAGCCGGGACAGCGCC AAGAACACCCTGTACCTGCAGATGAGCAGCCT GCGGAGCGACGACACCGCCATGTACTACTGCA CCCGGCACTGGGACCACCCTTGGTTTGCCTACT GGGGCCAGGGCACCCTGGTCACCGTGTCTGCT GCCAAAACAACAGCACCAAGTGTCTATCCACT GGCCCCTGTGTGTGGAGATACAACTGGCTCCT CGGTGACTCTAGGATGCCTGGTCAAGGGTTAT TTCCCTGAGCCAGTGACCTTGACCTGGAACTCT	1161

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		GGATCCCTGTCCAGTGGTGTGCACACCTTCCCA GCTGTCCTGCAGTCTGACCTCTACACCCTCAGC AGCTCAGTGACTGTAACCTCGAGCACCTGGCC CAGCCAGTCCATCACCTGCAATGTGGCCCACC CGGCAAGCAGCACCAAGGTGGACAAGAAAAT TGAGCCCAGAGGGCCCACAATCAAGCCCTGTC CTCCATGCAAATGCCCAGCACCTAACCTCTTGG GTGGACCATCCGTCTTCATCTTCCCTCCAAAGA TCAAGGATGTACTCATGATCTCCCTGAGCCCCA TAGTCACATGTGTGGTGGTGGATGTGAGCGAG GATGACCCAGATGTCCAGATCAGCTGGTTTGT GAACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTCTC CGGGTGGTCAGTGCCCTCCCCATCCAGCACCA GGACTGGATGAGTGGCAAGGAGTTCAAATGCA AGGTCAACAACAAAGACCTCCCAGCGCCCATC GAGAGAACCATCTCAAAACCCAAAGGGTCAGT AAGAGCTCCACAGGTATATGTCTTGCCTCCACC AGAAGAAGAGATGACTAAGAAACAGGTCACT CTGACCTGCATGGTCACAGACTTCATGCCTGA AGACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAACCA GTCCTGGACTCTGATGGTTCTTACTTCATGTAC AGCAAGCTGAGAGTGGAAAAGAAGAACTGGG TGGAAAGAAATAGCTACTCCTGTTCAGTGGTC CACGAGGGTCTGCACAATCACCACACGACTAA GAGCTTCTCCCGGACTCCGGGTAAA	
SM1B338	pDR000029271	GAGGTGCAGCTGGTGGAAAGCGGCGGAGGAC TGGTCAAGCCTGGCGGCAGCCTGAAGCTGAGC TGCGTGGCCTCCGGCTTCAGCTTCAGCAACTAC GCCATGAGCTGGGTCCGACAGACCCCCGAGCG GAGACTGGAATGGGTGGCCACCATCAACAGCG GCGGCAGCTTCAGCTTTTTCCCAGACTCCGTGA AGGGCCGGTTCACCATCAGCCGGGACAGCGCC AAGAACACCCTGTACCTGCAGATGAGCAGCCT GCGGAGCGACGACACCGCCATGTACTACTGCA CCCGGCACTGGGACCACCCTTGGTTTGCCTACT GGGGCCAGGGCACCCTGGTCACCGTGTCTGCT GCCAAAACAACAGCACCAAGTGTCTATCCACT GGCCCCTGTGTGTGGAGATACAACTGGCTCCT CGGTGACTCTAGGATGCCTGGTCAAGGGTTAT TTCCCTGAGCCAGTGACCTTGACCTGGAACTCT GGATCCCTGTCCAGTGGTGTGCACACCTTCCCA GCTGTCCTGCAGTCTGACCTCTACACCCTCAGC AGCTCAGTGACTGTAACCTCGAGCACCTGGCC CAGCCAGTCCATCACCTGCAATGTGGCCCACC CGGCAAGCAGCACCAAGGTGGACAAGAAAAT TGAGCCCAGAGGGCCCACAATCAAGCCCTGTC	1162

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		CTCCATGCAAATGCCCAGCACCTAACCTCTTGG GTGGACCATCCGTCTTCATCTTCCCTCCAAAGA TCAAGGATGTACTCATGATCTCCCTGAGCCCCA TAGTCACATGTGTGGTGGTGGATGTGAGCGAG GATGACCCAGATGTCCAGATCAGCTGGTTTGT GAACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTCTC CGGGTGGTCAGTGCCCTCCCCATCCAGCACCA GGACTGGATGAGTGGCAAGGAGTTCAAATGCA AGGTCAACAACAAAGACCTCCCAGCGCCCATC GAGAGAACCATCTCAAAACCCAAAGGGTCAGT AAGAGCTCCACAGGTATATGTCTTGCCTCCACC AGAAGAAGAGATGACTAAGAAACAGGTCACT CTGACCTGCATGGTCACAGACTTCATGCCTGA AGACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAACCA GTCCTGGACTCTGATGGTTCTTACTTCATGTAC AGCAAGCTGAGAGTGGAAAAGAAGAACTGGG TGGAAAGAAATAGCTACTCCTGTTCAGTGGTC CACGAGGGTCTGCACAATCACCACACGACTAA GAGCTTCTCCCGGACTCCGGGTAAA	
SM1B339	pDR000029270	GAGGTGCAGCTGCAGCAGTCTGGCGCTGAACT CGTGCGGCCTGGCGCCAGCGTGAAGCTGAGCT GCACCACCAGCGGCTTCAACATCAAGGACAGC CTGATCTACTGGGTCAAGCAGCGGCCCGAGCA GGGCCTGGAATGGATCGGCTGGATCGACCCCG AGGACGGCGAGACAAAGTTCGCCCCCAGATTC CAGGACAAGGCCACCATCACCAGCGACACCAG CAGCAACACCGCCTACCTGCGGCTGAGCAGCC TGACCAGCAAGGACACCGCCATCTACTACTGC ACCCGGTCCTTCGGCGTGTGCTGGGGCCAGGG CACCCTGGTCACAGTGTCTGCCGCCAAAACAA CAGCACCAAGTGTCTATCCACTGGCCCCTGTGT GTGGAGATACAACTGGCTCCTCGGTGACTCTA GGATGCCTGGTCAAGGGTTATTTCCCTGAGCC AGTGACCTTGACCTGGAACTCTGGATCCCTGTC CAGTGGTGTGCACACCTTCCCAGCTGTCCTGCA GTCTGACCTCTACACCCTCAGCAGCTCAGTGAC TGTAACCTCGAGCACCTGGCCCAGCCAGTCCA TCACCTGCAATGTGGCCCACCCGGCAAGCAGC ACCAAGGTGGACAAGAAAATTGAGCCCAGAG GGCCCACAATCAAGCCCTGTCCTCCATGCAAA TGCCCAGCACCTAACCTCTTGGGTGGACCATCC GTCTTCATCTTCCCTCCAAAGATCAAGGATGTA CTCATGATCTCCCTGAGCCCCATAGTCACATGT GTGGTGGTGGATGTGAGCGAGGATGACCCAGA TGTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAGA	1163

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		GAGGATTACAACAGTACTCTCCGGGTGGTCAG TGCCCTCCCCATCCAGCACCAGGACTGGATGA GTGGCAAGGAGTTCAAATGCAAGGTCAACAAC AAAGACCTCCCAGCGCCCATCGAGAGAACCAT CTCAAAACCCAAAGGGTCAGTAAGAGCTCCAC AGGTATATGTCTTGCCTCCACCAGAAGAAGAG ATGACTAAGAAACAGGTCACTCTGACCTGCAT GGTCACAGACTTCATGCCTGAAGACATTTACG TGGAGTGGACCAACAACGGGAAAACAGAGCT AAACTACAAGAACACTGAACCAGTCCTGGACT CTGATGGTTCTTACTTCATGTACAGCAAGCTGA GAGTGGAAAAGAAGAACTGGGTGGAAAGAAA TAGCTACTCCTGTTCAGTGGTCCACGAGGGTCT GCACAATCACCACACGACTAAGAGCTTCTCCC GGACTCCGGGTAAA	
SM1B340	pDR000029269	GAGGTGCAGCTGCAGCAGTCTGGCGCTGAACT CGTGCGGCCTGGCGCCAGCGTGAAGCTGAGCT GCACCACCAGCGGCTTCAACATCAAGGACAGC CTGATCTACTGGGTCAAGCAGCGGCCCGAGCA GGGCCTGGAATGGATCGGCTGGATCGACCCCG AGGACGGCGAGACAAAGTTCGCCCCCAGATTC CAGGACAAGGCCACCATCACCAGCGACACCAG CAGCAACACCGCCTACCTGCGGCTGAGCAGCC TGACCAGCGAGGACACCGCCATCTACTACTGC ACCCGGTCCTTCGGCGTGTGCTGGGGCCAGGG CACCCTGGTCACAGTGTCTGCCGCCAAAACAA CAGCACCAAGTGTCTATCCACTGGCCCCTGTGT GTGGAGATACAACTGGCTCCTCGGTGACTCTA GGATGCCTGGTCAAGGGTTATTTCCCTGAGCC AGTGACCTTGACCTGGAACTCTGGATCCCTGTC CAGTGGTGTGCACACCTTCCCAGCTGTCCTGCA GTCTGACCTCTACACCCTCAGCAGCTCAGTGAC TGTAACCTCGAGCACCTGGCCCAGCCAGTCCA TCACCTGCAATGTGGCCCACCCGGCAAGCAGC ACCAAGGTGGACAAGAAAATTGAGCCCAGAG GGCCCACAATCAAGCCCTGTCCTCCATGCAAA TGCCCAGCACCTAACCTCTTGGGTGGACCATCC GTCTTCATCTTCCCTCCAAAGATCAAGGATGTA CTCATGATCTCCCTGAGCCCCATAGTCACATGT GTGGTGGTGGATGTGAGCGAGGATGACCCAGA TGTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAGA GAGGATTACAACAGTACTCTCCGGGTGGTCAG TGCCCTCCCCATCCAGCACCAGGACTGGATGA GTGGCAAGGAGTTCAAATGCAAGGTCAACAAC AAAGACCTCCCAGCGCCCATCGAGAGAACCAT CTCAAAACCCAAAGGGTCAGTAAGAGCTCCAC AGGTATATGTCTTGCCTCCACCAGAAGAAGAG	1164

Protein AA ID	Construct ID	Heavy_Chain.CDS	SEQ ID NO:
		ATGACTAAGAAACAGGTCACTCTGACCTGCAT GGTCACAGACTTCATGCCTGAAGACATTTACG TGGAGTGGACCAACAACGGGAAAACAGAGCT AAACTACAAGAACACTGAACCAGTCCTGGACT CTGATGGTTCTTACTTCATGTACAGCAAGCTGA GAGTGGAAAAGAAGAACTGGGTGGAAAGAAA TAGCTACTCCTGTTCAGTGGTCCACGAGGGTCT GCACAATCACCACACGACTAAGAGCTTCTCCC GGACTCCGGGTAAA	

Table 47. HlgA/LukE Antibody Heavy Chain Primary Transcripts

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
SM1B302	pDR000029296	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAAGTGAA GCTGGTGGAATCTGGCGGCGACCTGGTCAAGC CTGGCGGCAGCCTGAAGCTGAGCTGCGCCGCC AGCGGCTTCACCTTCAGCAGCTTCGCCATGAG CTGGGTCCGACAGACCCCCGAGAAGCGGCTGG AATGGGTGGCCAGCATCAGCCGGACCGACAAC ACCTACTACCCCGACAGCATGAAGGGCCAGTT CACCATCAGCCGGGACAACGCCCGGAACATCC TGTACCTGCAGATGAGCAGCCTGCGGAGCGAG AACACCGCCATCTACTACTGCGCCAGAGCCGA CTACGACGGCCCTTGGTTTGCCTACTGGGGCCA GGGCACCCTGGTCACCGTGTCTGCTGCCAAAA CAACAGCACCAAGTGTCTATCCACTGGCCCCT GTGTGTGGAGATACAACTGGCTCCTCGGTGAC TCTAGGATGCCTGGTCAAGGGTTATTTCCCTGA GCCAGTGACCTTGACCTGGAACTCTGGATCCCT GTCCAGTGGTGTGCACACCTTCCCAGCTGTCCT GCAGTCTGACCTCTACACCCTCAGCAGCTCAGT GACTGTAACCTCGAGCACCTGGCCCAGCCAGT CCATCACCTGCAATGTGGCCCACCCGGCAAGC AGCACCAAGGTGGACAAGAAAATTGAGCCCA GAGGGCCCACAATCAAGCCCTGTCCTCCATGC AAATGCCCAGCACCTAACCTCTTGGGTGGACC ATCCGTCTTCATCTTCCCTCCAAAGATCAAGGA TGTACTCATGATCTCCCTGAGCCCCATAGTCAC ATGTGTGGTGGTGGATGTGAGCGAGGATGACC CAGATGTCCAGATCAGCTGGTTTGTGAACAAC GTGGAAGTACACACAGCTCAGACACAAACCCA TAGAGAGGATTACAACAGTACTCTCCGGGTGG TCAGTGCCCTCCCCATCCAGCACCAGGACTGG ATGAGTGGCAAGGAGTTCAAATGCAAGGTCAA	1165

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CAACAAAGACCTCCCAGCGCCCATCGAGAGAA CCATCTCAAAACCCAAAGGGTCAGTAAGAGCT CCACAGGTATATGTCTTGCCTCCACCAGAAGA AGAGATGACTAAGAAACAGGTCACTCTGACCT GCATGGTCACAGACTTCATGCCTGAAGACATT TACGTGGAGTGGACCAACAACGGGAAAACAG AGCTAAACTACAAGAACACTGAACCAGTCCTG GACTCTGATGGTTCTTACTTCATGTACAGCAAG CTGAGAGTGGAAAAGAAGAACTGGGTGGAAA GAAATAGCTACTCCTGTTCAGTGGTCCACGAG GGTCTGCACAATCACCACACGACTAAGAGCTT CTCCCGGACTCCGGGTAAATGA	
SM1B303	pDR000029295	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAGGTGCA GCTGCAGCAGAGCGGCCCTGATCTGGTCAAGC CCGGCACCAGCGTGAAGATGAGCTGCAAGGCC AGCGGCTACAGCTTCACCGGCTACTACATGCA CTGGGTCAAGCAGAGCCACGGCAAGAGCCTGG AATGGATCGGCAGAGTGAACCCCAACAACGGC GGCACCAGCTACAACCAGAAGTTCAAGGGCAA GGCCATCCTGACCGTGGACAAGAGCAGCAGCA CCGCCTACATGGAACTGCGGAGCCTGACCAGC GAGGACAGCGCCGTGTACTACTGCGCCAGGGA CGACTACAGCTTCGCCTACTGGGGCCAGGGCA CCCTGGTCACCGTGTCTGCTGCCAAAACAACA GCACCAAGTGTCTATCCACTGGCCCCTGTGTGT GGAGATACAACTGGCTCCTCGGTGACTCTAGG ATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGT GACCTTGACCTGGAACTCTGGATCCCTGTCCAG TGGTGTGCACACCTTCCCAGCTGTCCTGCAGTC TGACCTCTACACCCTCAGCAGCTCAGTGACTGT AACCTCGAGCACCTGGCCCAGCCAGTCCATCA CCTGCAATGTGGCCCACCCGGCAAGCAGCACC AAGGTGGACAAGAAAATTGAGCCCAGAGGGC CCACAATCAAGCCCTGTCCTCCATGCAAATGC CCAGCACCTAACCTCTTGGGTGGACCATCCGTC TTCATCTTCCCTCCAAAGATCAAGGATGTACTC ATGATCTCCCTGAGCCCCATAGTCACATGTGTG GTGGTGGATGTGAGCGAGGATGACCCAGATGT CCAGATCAGCTGGTTTGTGAACAACGTGGAAG TACACACAGCTCAGACACAAACCCATAGAGAG GATTACAACAGTACTCTCCGGGTGGTCAGTGC CCTCCCCATCCAGCACCAGGACTGGATGAGTG GCAAGGAGTTCAAATGCAAGGTCAACAACAAA GACCTCCCAGCGCCCATCGAGAGAACCATCTC AAAACCCAAAGGGTCAGTAAGAGCTCCACAGG TATATGTCTTGCCTCCACCAGAAGAAGAGATG ACTAAGAAACAGGTCACTCTGACCTGCATGGT	1166

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CACAGACTTCATGCCTGAAGACATTTACGTGG AGTGGACCAACAACGGGAAAACAGAGCTAAA CTACAAGAACACTGAACCAGTCCTGGACTCTG ATGGTTCTTACTTCATGTACAGCAAGCTGAGA GTGGAAAAGAAGAACTGGGTGGAAAGAAATA GCTACTCCTGTTCAGTGGTCCACGAGGGTCTGC ACAATCACCACACGACTAAGAGCTTCTCCCGG ACTCCGGGTAAATGA	
SM1B304	pDR000029294	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAAGTGAA GCTGGTGGAAAGCGGCGGAGGCCTGGTGCAGC CTGGCGGCAGCCTGAGACTGAGCTGCGCCACC AGCGGCTTCACCTTCACCGACTTCTACATGAGC TGGGTCCGACAGCCCCCTGGCAAGGCCCTGGA ATGGCTGGCCTTCATCCGGAACAAGGCCAACG GCTACACCACCGAGTACAGCAGCAGCGTGCGG GGCAGATTCACCATCAGCCGGGACAACAGCCA GAGCATCCTGTACCTGCAGATGAACACCCTGC GGGCCGAGGACAGCGGCACCTACTACTGCGCC AGGGACGTGGGCGACTACGACTACTGGGGCCA GGGCAGCACCCTGACCGTGTCCTCTGCCAAAA CAACAGCACCAAGTGTCTATCCACTGGCCCCT GTGTGTGGAGATACAACTGGCTCCTCGGTGAC TCTAGGATGCCTGGTCAAGGGTTATTTCCCTGA GCCAGTGACCTTGACCTGGAACTCTGGATCCCT GTCCAGTGGTGTGCACACCTTCCCAGCTGTCCT GCAGTCTGACCTCTACACCCTCAGCAGCTCAGT GACTGTAACCTCGAGCACCTGGCCCAGCCAGT CCATCACCTGCAATGTGGCCCACCCGGCAAGC AGCACCAAGGTGGACAAGAAAATTGAGCCCA GAGGGCCCACAATCAAGCCCTGTCCTCCATGC AAATGCCCAGCACCTAACCTCTTGGGTGGACC ATCCGTCTTCATCTTCCCTCCAAAGATCAAGGA TGTACTCATGATCTCCCTGAGCCCCATAGTCAC ATGTGTGGTGGTGGATGTGAGCGAGGATGACC CAGATGTCCAGATCAGCTGGTTTGTGAACAAC GTGGAAGTACACACAGCTCAGACACAAACCCA TAGAGAGGATTACAACAGTACTCTCCGGGTGG TCAGTGCCCTCCCCATCCAGCACCAGGACTGG ATGAGTGGCAAGGAGTTCAAATGCAAGGTCAA CAACAAAGACCTCCCAGCGCCCATCGAGAGAA CCATCTCAAAACCCAAAGGGTCAGTAAGAGCT CCACAGGTATATGTCTTGCCTCCACCAGAAGA AGAGATGACTAAGAAACAGGTCACTCTGACCT GCATGGTCACAGACTTCATGCCTGAAGACATT TACGTGGAGTGGACCAACAACGGGAAAACAG AGCTAAACTACAAGAACACTGAACCAGTCCTG GACTCTGATGGTTCTTACTTCATGTACAGCAAG	1167

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CTGAGAGTGGAAAAGAAGAACTGGGTGGAAA GAAATAGCTACTCCTGTTCAGTGGTCCACGAG GGTCTGCACAATCACCACACGACTAAGAGCTT CTCCCGGACTCCGGGTAAATGA	
SM1B305	pDR000029293	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGATCCA GCTGGTGCAGAGCGGCCCTGAGCTGAAGAAAC CCGGCGAGACAGTGAAGATCAGCTGCAAGGCC AGCGGCTTCACCTTCACCAACTACGGCATGAA CTGGGTCAAGCAGGCCCCTGGCAAGGACCTGA AGTGGATGGGCTGGATCAACACCTACACCGGC GAGCCCACCTACGCCGACGACTTCAAGGGCAG ATTCGCCTTCAGCCTGGAAACCAGCGCCAGCA CCGCCTACCTGCAGATCAACAACCTGAAGGAC GAGGATACCGCCAGCTACTTCTGCGCCAGAGA CTACCGGGACGGCGACGCCCTGGATTACTGGG GCCAGGGCACCAGCGTGACCGTGTCCTCTGCC AAAACAACAGCACCAAGTGTCTATCCACTGGC CCCTGTGTGTGGAGATACAACTGGCTCCTCGGT GACTCTAGGATGCCTGGTCAAGGGTTATTTCCC TGAGCCAGTGACCTTGACCTGGAACTCTGGAT CCCTGTCCAGTGGTGTGCACACCTTCCCAGCTG TCCTGCAGTCTGACCTCTACACCCTCAGCAGCT CAGTGACTGTAACCTCGAGCACCTGGCCCAGC CAGTCCATCACCTGCAATGTGGCCCACCCGGC AAGCAGCACCAAGGTGGACAAGAAAATTGAG CCCAGAGGGCCCACAATCAAGCCCTGTCCTCC ATGCAAATGCCCAGCACCTAACCTCTTGGGTG GACCATCCGTCTTCATCTTCCCTCCAAAGATCA AGGATGTACTCATGATCTCCCTGAGCCCCATA GTCACATGTGTGGTGGTGGATGTGAGCGAGGA TGACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACACAA ACCCATAGAGAGGATTACAACAGTACTCTCCG GGTGGTCAGTGCCCTCCCCATCCAGCACCAGG ACTGGATGAGTGGCAAGGAGTTCAAATGCAAG GTCAACAACAAAGACCTCCCAGCGCCCATCGA GAGAACCATCTCAAAACCCAAAGGGTCAGTAA GAGCTCCACAGGTATATGTCTTGCCTCCACCAG AAGAAGAGATGACTAAGAAACAGGTCACTCTG ACCTGCATGGTCACAGACTTCATGCCTGAAGA CATTTACGTGGAGTGGACCAACAACGGGAAAA CAGAGCTAAACTACAAGAACACTGAACCAGTC CTGGACTCTGATGGTTCTTACTTCATGTACAGC AAGCTGAGAGTGGAAAAGAAGAACTGGGTGG AAAGAAATAGCTACTCCTGTTCAGTGGTCCAC GAGGGTCTGCACAATCACCACACGACTAAGAG CTTCTCCCGGACTCCGGGTAAATGA	1168

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
SM1B306	pDR000029292	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGGTGCA GCTGCAGCAGCCTGGCGCCGAACTCGTCAGAC CTGGCGCCAGCGTGAAGCTGAGCTGCAAGGCC AGCGGCTACAGCTTCACCAGCAACTGGATGAA TTGGATGAAGCAGCGGCCTGGCCAGGGCCTGG AATGGATCGGCATGATCCACCCCAGCGACAGC GAGAGCCGGCTGAACCAGAAGTTCAAGGACA AGGCCACCCTGACCGTGGACAAGAGCAGCAGC ACCGCCTACATGCAGCTGTCCAGCCCCACCAG CGAGGACAGCGCCGTGTACTACTGTGCCAGAG GCGACGGCGGCTTCGCCTACTGGGGACAGGGC ACCCTGGTCACCGTGTCCGCTGCCAAAACAAC AGCACCAAGTGTCTATCCACTGGCCCCTGTGTG TGGAGATACAACTGGCTCCTCGGTGACTCTAG GATGCCTGGTCAAGGGTTATTTCCCTGAGCCA GTGACCTTGACCTGGAACTCTGGATCCCTGTCC AGTGGTGTGCACACCTTCCCAGCTGTCCTGCAG TCTGACCTCTACACCCTCAGCAGCTCAGTGACT GTAACCTCGAGCACCTGGCCCAGCCAGTCCAT CACCTGCAATGTGGCCCACCCGGCAAGCAGCA CCAAGGTGGACAAGAAAATTGAGCCCAGAGG GCCCACAATCAAGCCCTGTCCTCCATGCAAAT GCCCAGCACCTAACCTCTTGGGTGGACCATCC GTCTTCATCTTCCCTCCAAAGATCAAGGATGTA CTCATGATCTCCCTGAGCCCCATAGTCACATGT GTGGTGGTGGATGTGAGCGAGGATGACCCAGA TGTCCAGATCAGCTGGTTTGTGAACAACGTGG AAGTACACACAGCTCAGACACAAACCCATAGA GAGGATTACAACAGTACTCTCCGGGTGGTCAG TGCCCTCCCCATCCAGCACCAGGACTGGATGA GTGGCAAGGAGTTCAAATGCAAGGTCAACAAC AAAGACCTCCCAGCGCCCATCGAGAGAACCAT CTCAAAACCCAAAGGGTCAGTAAGAGCTCCAC AGGTATATGTCTTGCCTCCACCAGAAGAAGAG ATGACTAAGAAACAGGTCACTCTGACCTGCAT GGTCACAGACTTCATGCCTGAAGACATTTACG TGGAGTGGACCAACAACGGGAAAACAGAGCT AAACTACAAGAACACTGAACCAGTCCTGGACT CTGATGGTTCTTACTTCATGTACAGCAAGCTGA GAGTGGAAAAGAAGAACTGGGTGGAAAGAAA TAGCTACTCCTGTTCAGTGGTCCACGAGGGTCT GCACAATCACCACACGACTAAGAGCTTCTCCC GGACTCCGGGTAAATGA	1169
SM1B307	pDR000029291	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAAGTGAA GCTGCAGCAGAGCGGCCCTGAGCTGGTCAAGC CTGGCGCCAGCATGAAGATCAGCTGCAAGGCC	1170

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		AGCGGCTACAGCTTCACCGGCTACACCATGAA CTGGGCCAAGCAGAGCCACGGCAAGAACCTGG AATGGATCGGCCTGATCAACCCCTACAACGGC GGCACCAGCTACAACCAGAAGTTCAAGGGCAA GGCCACCCTGACCGTGGACAAGAGCAGCAGCA CCGCCTACATGGAACTGCTGAGCCTGACCAGC GAGGACAGCGCCGTGTACTACTGCGCCAGAGG CTACCCCAGAGGATGGTTCGCCTACTGGGGCC AGGGCACCCTGGTCACCGTGTCTGCTGCCAAA ACAACAGCACCAAGTGTCTATCCACTGGCCCC TGTGTGTGGAGATACAACTGGCTCCTCGGTGA CTCTAGGATGCCTGGTCAAGGGTTATTTCCCTG AGCCAGTGACCTTGACCTGGAACTCTGGATCC CTGTCCAGTGGTGTGCACACCTTCCCAGCTGTC CTGCAGTCTGACCTCTACACCCTCAGCAGCTCA GTGACTGTAACCTCGAGCACCTGGCCCAGCCA GTCCATCACCTGCAATGTGGCCCACCCGGCAA GCAGCACCAAGGTGGACAAGAAAATTGAGCCC AGAGGGCCCACAATCAAGCCCTGTCCTCCATG CAAATGCCCAGCACCTAACCTCTTGGGTGGAC CATCCGTCTTCATCTTCCCTCCAAAGATCAAGG ATGTACTCATGATCTCCCTGAGCCCCATAGTCA CATGTGTGGTGGTGGATGTGAGCGAGGATGAC CCAGATGTCCAGATCAGCTGGTTTGTGAACAA CGTGGAAGTACACACAGCTCAGACACAAACCC ATAGAGAGGATTACAACAGTACTCTCCGGGTG GTCAGTGCCCTCCCCATCCAGCACCAGGACTG GATGAGTGGCAAGGAGTTCAAATGCAAGGTCA ACAACAAAGACCTCCCAGCGCCCATCGAGAGA ACCATCTCAAAACCCAAAGGGTCAGTAAGAGC TCCACAGGTATATGTCTTGCCTCCACCAGAAG AAGAGATGACTAAGAAACAGGTCACTCTGACC TGCATGGTCACAGACTTCATGCCTGAAGACAT TTACGTGGAGTGGACCAACAACGGGAAAACAG AGCTAAACTACAAGAACACTGAACCAGTCCTG GACTCTGATGGTTCTTACTTCATGTACAGCAAG CTGAGAGTGGAAAAGAAGAACTGGGTGGAAA GAAATAGCTACTCCTGTTCAGTGGTCCACGAG GGTCTGCACAATCACCACACGACTAAGAGCTT CTCCCGGACTCCGGGTAAATGA	
SM1B308	pDR000029290	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGACGTGAA GCTGGTGGAAAGCGGCGGAGGCCTGGTCAAGC CTGGCGGCAGCCTGAAGCTGAGCTGCGCCGCC AGCGGCTTCACCTTCCGGAACCACGCCATGAG CTGGGTCCGACAGACCCCCGAGAAGCGGCTGG AATGGGTGGCCGCCATCAACGTGAACGCCGGC AGCACCTACTACCCCGACACCGTGAAGGACCG	1171

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GTTCACCATCAGCCGGGACAACGCCAAGAACA CCCTGTACCTGCAGATGAGCAGCCTGCGGAGC GAGGACACCGCCCTGTACTACTGCGCCAGACA CCGGGCCTACTACAACTACGACGAGAACGCCA TGGACTACTGGGGCCAGGGCACCAGCGTGACC GTGTCCTCTGCCAAAACAACAGCACCAAGTGT CTATCCACTGGCCCCTGTGTGTGGAGATACAA CTGGCTCCTCGGTGACTCTAGGATGCCTGGTCA AGGGTTATTTCCCTGAGCCAGTGACCTTGACCT GGAACTCTGGATCCCTGTCCAGTGGTGTGCAC ACCTTCCCAGCTGTCCTGCAGTCTGACCTCTAC ACCCTCAGCAGCTCAGTGACTGTAACCTCGAG CACCTGGCCCAGCCAGTCCATCACCTGCAATG TGGCCCACCCGGCAAGCAGCACCAAGGTGGAC AAGAAAATTGAGCCCAGAGGGCCCACAATCAA GCCCTGTCCTCCATGCAAATGCCCAGCACCTA ACCTCTTGGGTGGACCATCCGTCTTCATCTTCC CTCCAAAGATCAAGGATGTACTCATGATCTCC CTGAGCCCCATAGTCACATGTGTGGTGGTGGA TGTGAGCGAGGATGACCCAGATGTCCAGATCA GCTGGTTTGTGAACAACGTGGAAGTACACACA GCTCAGACACAAACCCATAGAGAGGATTACAA CAGTACTCTCCGGGTGGTCAGTGCCCTCCCCAT CCAGCACCAGGACTGGATGAGTGGCAAGGAGT TCAAATGCAAGGTCAACAACAAAGACCTCCCA GCGCCCATCGAGAGAACCATCTCAAAACCCAA AGGGTCAGTAAGAGCTCCACAGGTATATGTCT TGCCTCCACCAGAAGAAGAGATGACTAAGAAA CAGGTCACTCTGACCTGCATGGTCACAGACTTC ATGCCTGAAGACATTTACGTGGAGTGGACCAA CAACGGGAAAACAGAGCTAAACTACAAGAAC ACTGAACCAGTCCTGGACTCTGATGGTTCTTAC TTCATGTACAGCAAGCTGAGAGTGGAAAAGAA GAACTGGGTGGAAAGAAATAGCTACTCCTGTT CAGTGGTCCACGAGGGTCTGCACAATCACCAC ACGACTAAGAGCTTCTCCCGGACTCCGGGTAA ATGA	
SM1B309	pDR000029289	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAGGTGCA GCTGCAGCAGAGCGGCCCTGAGCTGGTCAAGC CCGGCGACAGCGTGAAGATGAGCTGCAAGGCC AGCGGCTACACCTTCACCGACTACTACATCGA CTGGATGAAGCAGAGCCACGGCAAGAGCCTGG AATGGATCGGCTACATCTACCCCAACAACGGC GGCACCAGCTACAACCAGAACTTCAAGGACAA GGCCACCCTGACCGTGGACAAGAGCAGCAGCA CCGCCTACATGGAACTGCACAGCCTGACCAGC GAGGACAGCGCCGTGTACTACTGCGCCAGACT	1172

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GACCTACTACGCCAAGGTGGACAGCTGGGGCC AGGGCACCAGCGTGACCGTGTCTAGCGCCAAA ACAACAGCACCAAGTGTCTATCCACTGGCCCC TGTGTGTGGAGATACAACTGGCTCCTCGGTGA CTCTAGGATGCCTGGTCAAGGGTTATTTCCCTG AGCCAGTGACCTTGACCTGGAACTCTGGATCC CTGTCCAGTGGTGTGCACACCTTCCCAGCTGTC CTGCAGTCTGACCTCTACACCCTCAGCAGCTCA GTGACTGTAACCTCGAGCACCTGGCCCAGCCA GTCCATCACCTGCAATGTGGCCCACCCGGCAA GCAGCACCAAGGTGGACAAGAAAATTGAGCCC AGAGGGCCCACAATCAAGCCCTGTCCTCCATG CAAATGCCCAGCACCTAACCTCTTGGGTGGAC CATCCGTCTTCATCTTCCCTCCAAAGATCAAGG ATGTACTCATGATCTCCCTGAGCCCCATAGTCA CATGTGTGGTGGTGGATGTGAGCGAGGATGAC CCAGATGTCCAGATCAGCTGGTTTGTGAACAA CGTGGAAGTACACACAGCTCAGACACAAACCC ATAGAGAGGATTACAACAGTACTCTCCGGGTG GTCAGTGCCCTCCCCATCCAGCACCAGGACTG GATGAGTGGCAAGGAGTTCAAATGCAAGGTCA ACAACAAAGACCTCCCAGCGCCCATCGAGAGA ACCATCTCAAAACCCAAAGGGTCAGTAAGAGC TCCACAGGTATATGTCTTGCCTCCACCAGAAG AAGAGATGACTAAGAAACAGGTCACTCTGACC TGCATGGTCACAGACTTCATGCCTGAAGACAT TTACGTGGAGTGGACCAACAACGGGAAAACAG AGCTAAACTACAAGAACACTGAACCAGTCCTG GACTCTGATGGTTCTTACTTCATGTACAGCAAG CTGAGAGTGGAAAAGAAGAACTGGGTGGAAA GAAATAGCTACTCCTGTTCAGTGGTCCACGAG GGTCTGCACAATCACCACACGACTAAGAGCTT CTCCCGGACTCCGGGTAAATGA	
SM1B310	pDR000029288	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGACGTGAA GCTGGTGGAAAGCGGCGGAGGCCTGGTGGAAT GGGAGGGCGTGCTGAAGCTGAGCTGCGCCGCC AGCGGCTTCACCTTCAGCAGCTACGCCATGAG CTGGGTCCGACAGACCCCCGAGAAGCGGCTGG AATGGGTGGCCGCCATCAACAGCAACGGCGGC AGCACCTACTACCCCGACACCGTGAAGGACCG GTTCACCATCAGCCGGGACAACGCCAAGAACA CCCTGTACCTGCAGATGAGCAGCCTGCGGAGC GAGGACACCGCCCTGTACTACTGCGCCAGACT GTACTACGGCGACTACTGGGGCCAGGGCACCA CCCTGACCGTGTCCTCTGCCAAAACAACAGCA CCAAGTGTCTATCCACTGGCCCCTGTGTGTGGA GATACAACTGGCTCCTCGGTGACTCTAGGATG	1173

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CCTGGTCAAGGGTTATTTCCCTGAGCCAGTGAC CTTGACCTGGAACTCTGGATCCCTGTCCAGTGG TGTGCACACCTTCCCAGCTGTCCTGCAGTCTGA CCTCTACACCCTCAGCAGCTCAGTGACTGTAAC CTCGAGCACCTGGCCCAGCCAGTCCATCACCT GCAATGTGGCCCACCCGGCAAGCAGCACCAAG GTGGACAAGAAAATTGAGCCCAGAGGGCCCAC AATCAAGCCCTGTCCTCCATGCAAATGCCCAG CACCTAACCTCTTGGGTGGACCATCCGTCTTCA TCTTCCCTCCAAAGATCAAGGATGTACTCATGA TCTCCCTGAGCCCCATAGTCACATGTGTGGTGG TGGATGTGAGCGAGGATGACCCAGATGTCCAG ATCAGCTGGTTTGTGAACAACGTGGAAGTACA CACAGCTCAGACACAAACCCATAGAGAGGATT ACAACAGTACTCTCCGGGTGGTCAGTGCCCTC CCCATCCAGCACCAGGACTGGATGAGTGGCAA GGAGTTCAAATGCAAGGTCAACAACAAAGACC TCCCAGCGCCCATCGAGAGAACCATCTCAAAA CCCAAAGGGTCAGTAAGAGCTCCACAGGTATA TGTCTTGCCTCCACCAGAAGAAGAGATGACTA AGAAACAGGTCACTCTGACCTGCATGGTCACA GACTTCATGCCTGAAGACATTTACGTGGAGTG GACCAACAACGGGAAAACAGAGCTAAACTAC AAGAACACTGAACCAGTCCTGGACTCTGATGG TTCTTACTTCATGTACAGCAAGCTGAGAGTGG AAAAGAAGAACTGGGTGGAAAGAAATAGCTA CTCCTGTTCAGTGGTCCACGAGGGTCTGCACA ATCACCACACGACTAAGAGCTTCTCCCGGACT CCGGGTAAATGA	
SM1B311	pDR000029287	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGGTGCA GCTGAAGCAGAGCGGCCCTAGCCTGGTGCAGC CCAGCCAGAGCCTGAGCATCACCTGTACCGTG TCCGGCTTCAGCCTGACCACCTACGGCCTGCAC TGGATCCGGCAGAGCCCCGGCAAGGGCCTGGA ATGGCTGGGAGTGATTTGGAGAGGCGGCACCA CCGACTACAACGCCGCCTTCATGAGCCGGCTG ACCATCACCAAGGACAACAGCAAGAGCCAGGT GTTCTTCAAGATGAACAGCCTGCAGGCCGACG ACACCGCCATCTACTACTGCGCCCGGACCGAC ATCTGGGGCGCTGGCACCACCGTGACCGTGTC CTCTGCCAAAACAACAGCACCAAGTGTCTATC CACTGGCCCCTGTGTGTGGAGATACAACTGGC TCCTCGGTGACTCTAGGATGCCTGGTCAAGGG TTATTTCCCTGAGCCAGTGACCTTGACCTGGAA CTCTGGATCCCTGTCCAGTGGTGTGCACACCTT CCCAGCTGTCCTGCAGTCTGACCTCTACACCCT CAGCAGCTCAGTGACTGTAACCTCGAGCACCT	1174

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GGCCCAGCCAGTCCATCACCTGCAATGTGGCC CACCCGGCAAGCAGCACCAAGGTGGACAAGA AAATTGAGCCCAGAGGGCCCACAATCAAGCCC TGTCCTCCATGCAAATGCCCAGCACCTAACCTC TTGGGTGGACCATCCGTCTTCATCTTCCCTCCA AAGATCAAGGATGTACTCATGATCTCCCTGAG CCCCATAGTCACATGTGTGGTGGTGGATGTGA GCGAGGATGACCCAGATGTCCAGATCAGCTGG TTTGTGAACAACGTGGAAGTACACACAGCTCA GACACAAACCCATAGAGAGGATTACAACAGTA CTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGC ACCAGGACTGGATGAGTGGCAAGGAGTTCAAA TGCAAGGTCAACAACAAAGACCTCCCAGCGCC CATCGAGAGAACCATCTCAAAACCCAAAGGGT CAGTAAGAGCTCCACAGGTATATGTCTTGCCTC CACCAGAAGAAGAGATGACTAAGAAACAGGT CACTCTGACCTGCATGGTCACAGACTTCATGCC TGAAGACATTTACGTGGAGTGGACCAACAACG GGAAAACAGAGCTAAACTACAAGAACACTGA ACCAGTCCTGGACTCTGATGGTTCTTACTTCAT GTACAGCAAGCTGAGAGTGGAAAAGAAGAAC TGGGTGGAAAGAAATAGCTACTCCTGTTCAGT GGTCCACGAGGGTCTGCACAATCACCACACGA CTAAGAGCTTCTCCCGGACTCCGGGTAAATGA	
SM1B312	pDR000029287	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGGTGCA GCTGAAGCAGAGCGGCCCTAGCCTGGTGCAGC CCAGCCAGAGCCTGAGCATCACCTGTACCGTG TCCGGCTTCAGCCTGACCACCTACGGCCTGCAC TGGATCCGGCAGAGCCCCGGCAAGGGCCTGGA ATGGCTGGGAGTGATTTGGAGAGGCGGCACCA CCGACTACAACGCCGCCTTCATGAGCCGGCTG ACCATCACCAAGGACAACAGCAAGAGCCAGGT GTTCTTCAAGATGAACAGCCTGCAGGCCGACG ACACCGCCATCTACTACTGCGCCCGGACCGAC ATCTGGGGCGCTGGCACCACCGTGACCGTGTC CTCTGCCAAAACAACAGCACCAAGTGTCTATC CACTGGCCCCTGTGTGTGGAGATACAACTGGC TCCTCGGTGACTCTAGGATGCCTGGTCAAGGG TTATTTCCCTGAGCCAGTGACCTTGACCTGGAA CTCTGGATCCCTGTCCAGTGGTGTGCACACCTT CCCAGCTGTCCTGCAGTCTGACCTCTACACCCT CAGCAGCTCAGTGACTGTAACCTCGAGCACCT GGCCCAGCCAGTCCATCACCTGCAATGTGGCC CACCCGGCAAGCAGCACCAAGGTGGACAAGA AAATTGAGCCCAGAGGGCCCACAATCAAGCCC TGTCCTCCATGCAAATGCCCAGCACCTAACCTC TTGGGTGGACCATCCGTCTTCATCTTCCCTCCA	1175

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		AAGATCAAGGATGTACTCATGATCTCCCTGAG CCCCATAGTCACATGTGTGGTGGTGGATGTGA GCGAGGATGACCCAGATGTCCAGATCAGCTGG TTTGTGAACAACGTGGAAGTACACACAGCTCA GACACAAACCCATAGAGAGGATTACAACAGTA CTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGC ACCAGGACTGGATGAGTGGCAAGGAGTTCAAA TGCAAGGTCAACAACAAAGACCTCCCAGCGCC CATCGAGAGAACCATCTCAAAACCCAAAGGGT CAGTAAGAGCTCCACAGGTATATGTCTTGCCTC CACCAGAAGAAGAGATGACTAAGAAACAGGT CACTCTGACCTGCATGGTCACAGACTTCATGCC TGAAGACATTTACGTGGAGTGGACCAACAACG GGAAAACAGAGCTAAACTACAAGAACACTGA ACCAGTCCTGGACTCTGATGGTTCTTACTTCAT GTACAGCAAGCTGAGAGTGGAAAAGAAGAAC TGGGTGGAAAGAAATAGCTACTCCTGTTCAGT GGTCCACGAGGGTCTGCACAATCACCACACGA CTAAGAGCTTCTCCCGGACTCCGGGTAAATGA	
SM1B313	pDR000029287	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGGTGCA GCTGAAGCAGAGCGGCCCTAGCCTGGTGCAGC CCAGCCAGAGCCTGAGCATCACCTGTACCGTG TCCGGCTTCAGCCTGACCACCTACGGCCTGCAC TGGATCCGGCAGAGCCCCGGCAAGGGCCTGGA ATGGCTGGGAGTGATTTGGAGAGGCGGCACCA CCGACTACAACGCCGCCTTCATGAGCCGGCTG ACCATCACCAAGGACAACAGCAAGAGCCAGGT GTTCTTCAAGATGAACAGCCTGCAGGCCGACG ACACCGCCATCTACTACTGCGCCCGGACCGAC ATCTGGGGCGCTGGCACCACCGTGACCGTGTC CTCTGCCAAAACAACAGCACCAAGTGTCTATC CACTGGCCCCTGTGTGTGGAGATACAACTGGC TCCTCGGTGACTCTAGGATGCCTGGTCAAGGG TTATTTCCCTGAGCCAGTGACCTTGACCTGGAA CTCTGGATCCCTGTCCAGTGGTGTGCACACCTT CCCAGCTGTCCTGCAGTCTGACCTCTACACCCT CAGCAGCTCAGTGACTGTAACCTCGAGCACCT GGCCCAGCCAGTCCATCACCTGCAATGTGGCC CACCCGGCAAGCAGCACCAAGGTGGACAAGA AAATTGAGCCCAGAGGGCCCACAATCAAGCCC TGTCCTCCATGCAAATGCCCAGCACCTAACCTC TTGGGTGGACCATCCGTCTTCATCTTCCCTCCA AAGATCAAGGATGTACTCATGATCTCCCTGAG CCCCATAGTCACATGTGTGGTGGTGGATGTGA GCGAGGATGACCCAGATGTCCAGATCAGCTGG TTTGTGAACAACGTGGAAGTACACACAGCTCA GACACAAACCCATAGAGAGGATTACAACAGTA	1176

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGC ACCAGGACTGGATGAGTGGCAAGGAGTTCAAA TGCAAGGTCAACAACAAAGACCTCCCAGCGCC CATCGAGAGAACCATCTCAAAACCCAAAGGGT CAGTAAGAGCTCCACAGGTATATGTCTTGCCTC CACCAGAAGAAGAGATGACTAAGAAACAGGT CACTCTGACCTGCATGGTCACAGACTTCATGCC TGAAGACATTTACGTGGAGTGGACCAACAACG GGAAAACAGAGCTAAACTACAAGAACACTGA ACCAGTCCTGGACTCTGATGGTTCTTACTTCAT GTACAGCAAGCTGAGAGTGGAAAAGAAGAAC TGGGTGGAAAGAAATAGCTACTCCTGTTCAGT GGTCCACGAGGGTCTGCACAATCACCACACGA CTAAGAGCTTCTCCCGGACTCCGGGTAAATGA	
SM1B314	pDR000029286	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGGTGCA GCTGAAGCAGAGCGGCCCTGGCCTGGTGCAGC CTAGCCAGAGCCTGCCCATCACCTGTACCGTGT CCGGCTTCAGCCTGACCACCTACGGCCTGCACT GGATCCGGCAGAGCCCCGGCAAGGGCCTGGAA TGGCTGGGAGTGATTTGGAGAGGCGGCACCAC CGACTACAACGCCGCCTTCATGAGCCGGCTGA CCATCACCAAGGACAACAGCAAGAGCCAGGTG TTCTTCAAGATGAACAGCCTGCAGGCCGACGA CACCGCCATCTACTACTGCGCCCGGACCGACA TCTGGGGCGCTGGCACCACCGTGACCGTGTCC TCTGCCAAAACAACAGCACCAAGTGTCTATCC ACTGGCCCCTGTGTGTGGAGATACAACTGGCT CCTCGGTGACTCTAGGATGCCTGGTCAAGGGT TATTTCCCTGAGCCAGTGACCTTGACCTGGAAC TCTGGATCCCTGTCCAGTGGTGTGCACACCTTC CCAGCTGTCCTGCAGTCTGACCTCTACACCCTC AGCAGCTCAGTGACTGTAACCTCGAGCACCTG GCCCAGCCAGTCCATCACCTGCAATGTGGCCC ACCCGGCAAGCAGCACCAAGGTGGACAAGAA AATTGAGCCCAGAGGGCCCACAATCAAGCCCT GTCCTCCATGCAAATGCCCAGCACCTAACCTCT TGGGTGGACCATCCGTCTTCATCTTCCCTCCAA AGATCAAGGATGTACTCATGATCTCCCTGAGC CCCATAGTCACATGTGTGGTGGTGGATGTGAG CGAGGATGACCCAGATGTCCAGATCAGCTGGT TTGTGAACAACGTGGAAGTACACACAGCTCAG ACACAAACCCATAGAGAGGATTACAACAGTAC TCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCA CCAGGACTGGATGAGTGGCAAGGAGTTCAAAT GCAAGGTCAACAACAAAGACCTCCCAGCGCCC ATCGAGAGAACCATCTCAAAACCCAAAGGGTC AGTAAGAGCTCCACAGGTATATGTCTTGCCTCC	1177

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		ACCAGAAGAAGAGATGACTAAGAAACAGGTC ACTCTGACCTGCATGGTCACAGACTTCATGCCT GAAGACATTTACGTGGAGTGGACCAACAACGG GAAAACAGAGCTAAACTACAAGAACACTGAA CCAGTCCTGGACTCTGATGGTTCTTACTTCATG TACAGCAAGCTGAGAGTGGAAAAGAAGAACT GGGTGGAAAGAAATAGCTACTCCTGTTCAGTG GTCCACGAGGGTCTGCACAATCACCACACGAC TAAGAGCTTCTCCCGGACTCCGGGTAAATGA	
SM1B315	pDR000029285	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGGTGCA GCTGAAGCAGAGCGGCCCTGGCCTGGTGCAGC CTAGCCAGAGCCTGAGCATCACCTGTACCGTG TCCGGCTTCAGCCTGACCACCTACGGCCTGCAC TGGATCCGGCAGAGCCCCGGCAAGGGCCTGGA ATGGCTGGGAGTGATTTGGAGAGGCGGCACCA CCGACTACAACGCCGCCTTCATGAGCCGGCTG ACCATCACCAAGGACAACAGCAAGAGCCAGGT GTTCTTCAAGATGAACAGCCTGCAGGCCGACG ACACCGCCATCTACTACTGCGCCCGGACCGAC ATCTGGGGCGCTGGCACCACCGTGACCGTGTC CTCTGCCAAAACAACAGCACCAAGTGTCTATC CACTGGCCCCTGTGTGTGGAGATACAACTGGC TCCTCGGTGACTCTAGGATGCCTGGTCAAGGG TTATTTCCCTGAGCCAGTGACCTTGACCTGGAA CTCTGGATCCCTGTCCAGTGGTGTGCACACCTT CCCAGCTGTCCTGCAGTCTGACCTCTACACCCT CAGCAGCTCAGTGACTGTAACCTCGAGCACCT GGCCCAGCCAGTCCATCACCTGCAATGTGGCC CACCCGGCAAGCAGCACCAAGGTGGACAAGA AAATTGAGCCCAGAGGGCCCACAATCAAGCCC TGTCCTCCATGCAAATGCCCAGCACCTAACCTC TTGGGTGGACCATCCGTCTTCATCTTCCCTCCA AAGATCAAGGATGTACTCATGATCTCCCTGAG CCCCATAGTCACATGTGTGGTGGTGGATGTGA GCGAGGATGACCCAGATGTCCAGATCAGCTGG TTTGTGAACAACGTGGAAGTACACACAGCTCA GACACAAACCCATAGAGAGGATTACAACAGTA CTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGC ACCAGGACTGGATGAGTGGCAAGGAGTTCAAA TGCAAGGTCAACAACAAAGACCTCCCAGCGCC CATCGAGAGAACCATCTCAAAACCCAAAGGGT CAGTAAGAGCTCCACAGGTATATGTCTTGCCTC CACCAGAAGAAGAGATGACTAAGAAACAGGT CACTCTGACCTGCATGGTCACAGACTTCATGCC TGAAGACATTTACGTGGAGTGGACCAACAACG GGAAAACAGAGCTAAACTACAAGAACACTGA ACCAGTCCTGGACTCTGATGGTTCTTACTTCAT	1178

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GTACAGCAAGCTGAGAGTGGAAAAGAAGAAC TGGGTGGAAAGAAATAGCTACTCCTGTTCAGT GGTCCACGAGGGTCTGCACAATCACCACACGA CTAAGAGCTTCTCCCGGACTCCGGGTAAATGA	
SM1B316	pDR000029287	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGGTGCA GCTGAAGCAGAGCGGCCCTAGCCTGGTGCAGC CCAGCCAGAGCCTGAGCATCACCTGTACCGTG TCCGGCTTCAGCCTGACCACCTACGGCCTGCAC TGGATCCGGCAGAGCCCCGGCAAGGGCCTGGA ATGGCTGGGAGTGATTTGGAGAGGCGGCACCA CCGACTACAACGCCGCCTTCATGAGCCGGCTG ACCATCACCAAGGACAACAGCAAGAGCCAGGT GTTCTTCAAGATGAACAGCCTGCAGGCCGACG ACACCGCCATCTACTACTGCGCCCGGACCGAC ATCTGGGGCGCTGGCACCACCGTGACCGTGTC CTCTGCCAAAACAACAGCACCAAGTGTCTATC CACTGGCCCCTGTGTGTGGAGATACAACTGGC TCCTCGGTGACTCTAGGATGCCTGGTCAAGGG TTATTTCCCTGAGCCAGTGACCTTGACCTGGAA CTCTGGATCCCTGTCCAGTGGTGTGCACACCTT CCCAGCTGTCCTGCAGTCTGACCTCTACACCCT CAGCAGCTCAGTGACTGTAACCTCGAGCACCT GGCCCAGCCAGTCCATCACCTGCAATGTGGCC CACCCGGCAAGCAGCACCAAGGTGGACAAGA AAATTGAGCCCAGAGGGCCCACAATCAAGCCC TGTCCTCCATGCAAATGCCCAGCACCTAACCTC TTGGGTGGACCATCCGTCTTCATCTTCCCTCCA AAGATCAAGGATGTACTCATGATCTCCCTGAG CCCCATAGTCACATGTGTGGTGGTGGATGTGA GCGAGGATGACCCAGATGTCCAGATCAGCTGG TTTGTGAACAACGTGGAAGTACACACAGCTCA GACACAAACCCATAGAGAGGATTACAACAGTA CTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGC ACCAGGACTGGATGAGTGGCAAGGAGTTCAAA TGCAAGGTCAACAACAAAGACCTCCCAGCGCC CATCGAGAGAACCATCTCAAAACCCAAAGGGT CAGTAAGAGCTCCACAGGTATATGTCTTGCCTC CACCAGAAGAAGAGATGACTAAGAAACAGGT CACTCTGACCTGCATGGTCACAGACTTCATGCC TGAAGACATTTACGTGGAGTGGACCAACAACG GGAAAACAGAGCTAAACTACAAGAACACTGA ACCAGTCCTGGACTCTGATGGTTCTTACTTCAT GTACAGCAAGCTGAGAGTGGAAAAGAAGAAC TGGGTGGAAAGAAATAGCTACTCCTGTTCAGT GGTCCACGAGGGTCTGCACAATCACCACACGA CTAAGAGCTTCTCCCGGACTCCGGGTAAATGA	1179
SM1B317	pDR000029284	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG	1180

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GCAGCTGCCCAAAGTATACAGGCCCAGGTGCA GCTGAAGCAGAGCGGCCCTGGCCTGGTGCAGC CTAGCCAGAGCCTGAGCATCACCTGTACCGTG TCCGGCTTCAGCCTGACCAGCTACGGCGTGCA CTGGGTCCGACAGCCTCCCGGCAAGGGCCTGG AATGGCTGGGAGTGATTTGGAGCGGCGGCATC ACCGACTACAACGCCGCCTTCATCAGCAGACT GAGCATCAGCAAGGACAACAGCAAGAGCCAG GTGTTCTTCAAGATGAACAGCCTGCAGGCCGA CGACACCGCCATCTACTACTGCGCCAGAACCG ACCTGTGGGGCCAGGGCACCCTGGTCACAGTG TCTGCCGCCAAAACAACAGCACCAAGTGTCTA TCCACTGGCCCCTGTGTGTGGAGATACAACTG GCTCCTCGGTGACTCTAGGATGCCTGGTCAAG GGTTATTTCCCTGAGCCAGTGACCTTGACCTGG AACTCTGGATCCCTGTCCAGTGGTGTGCACACC TTCCCAGCTGTCCTGCAGTCTGACCTCTACACC CTCAGCAGCTCAGTGACTGTAACCTCGAGCAC CTGGCCCAGCCAGTCCATCACCTGCAATGTGG CCCACCCGGCAAGCAGCACCAAGGTGGACAAG AAAATTGAGCCCAGAGGGCCCACAATCAAGCC CTGTCCTCCATGCAAATGCCCAGCACCTAACCT CTTGGGTGGACCATCCGTCTTCATCTTCCCTCC AAAGATCAAGGATGTACTCATGATCTCCCTGA GCCCCATAGTCACATGTGTGGTGGTGGATGTG AGCGAGGATGACCCAGATGTCCAGATCAGCTG GTTTGTGAACAACGTGGAAGTACACACAGCTC AGACACAAACCCATAGAGAGGATTACAACAGT ACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAG CACCAGGACTGGATGAGTGGCAAGGAGTTCAA ATGCAAGGTCAACAACAAAGACCTCCCAGCGC CCATCGAGAGAACCATCTCAAAACCCAAAGGG TCAGTAAGAGCTCCACAGGTATATGTCTTGCCT CCACCAGAAGAAGAGATGACTAAGAAACAGG TCACTCTGACCTGCATGGTCACAGACTTCATGC CTGAAGACATTTACGTGGAGTGGACCAACAAC GGGAAAACAGAGCTAAACTACAAGAACACTG AACCAGTCCTGGACTCTGATGGTTCTTACTTCA TGTACAGCAAGCTGAGAGTGGAAAAGAAGAA CTGGGTGGAAAGAAATAGCTACTCCTGTTCAG TGGTCCACGAGGGTCTGCACAATCACCACACG ACTAAGAGCTTCTCCCGGACTCCGGGTAAATG A	
SM1B318	pDR000029283	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGGTGCA GCTGCAGCAGTCTGGCGCCGAGCTGATGAACC CTGGCGCCAGCGTGAAGATCAGCTGCAAGAGC ACCGGCTACAAGTTCAGCAGCTACTGGATCGA	1181

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GTGGGTCAAGCAGCGGCCTGGCCACGGCCTGG AATGGATGGGCGAGATCCTGCCTGGCAGCGGC AGCACCAACCACAACGAGAAGTTCAAGGGCA AGGCCATCTTCACCGCCGACGCCAGCAGCAAC ACCGCCTACATGGAACTGAGCAGCCTGACCAG CGAGGACAGCGCCGTGTACTACTGCGCCCGGA CCATCAGCACCGCCACCGATTGGTTCGCCTACT GGGGCCAGGGCACCCTGGTCACCGTGTCTGCT GCCAAAACAACAGCACCAAGTGTCTATCCACT GGCCCCTGTGTGTGGAGATACAACTGGCTCCT CGGTGACTCTAGGATGCCTGGTCAAGGGTTAT TTCCCTGAGCCAGTGACCTTGACCTGGAACTCT GGATCCCTGTCCAGTGGTGTGCACACCTTCCCA GCTGTCCTGCAGTCTGACCTCTACACCCTCAGC AGCTCAGTGACTGTAACCTCGAGCACCTGGCC CAGCCAGTCCATCACCTGCAATGTGGCCCACC CGGCAAGCAGCACCAAGGTGGACAAGAAAAT TGAGCCCAGAGGGCCCACAATCAAGCCCTGTC CTCCATGCAAATGCCCAGCACCTAACCTCTTGG GTGGACCATCCGTCTTCATCTTCCCTCCAAAGA TCAAGGATGTACTCATGATCTCCCTGAGCCCCA TAGTCACATGTGTGGTGGTGGATGTGAGCGAG GATGACCCAGATGTCCAGATCAGCTGGTTTGT GAACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTCTC CGGGTGGTCAGTGCCCTCCCCATCCAGCACCA GGACTGGATGAGTGGCAAGGAGTTCAAATGCA AGGTCAACAACAAAGACCTCCCAGCGCCCATC GAGAGAACCATCTCAAAACCCAAAGGGTCAGT AAGAGCTCCACAGGTATATGTCTTGCCTCCACC AGAAGAAGAGATGACTAAGAAACAGGTCACT CTGACCTGCATGGTCACAGACTTCATGCCTGA AGACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAACCA GTCCTGGACTCTGATGGTTCTTACTTCATGTAC AGCAAGCTGAGAGTGGAAAAGAAGAACTGGG TGGAAAGAAATAGCTACTCCTGTTCAGTGGTC CACGAGGGTCTGCACAATCACCACACGACTAA GAGCTTCTCCCGGACTCCGGGTAAATGA	
SM1B319	pDR000029283	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGGTGCA GCTGCAGCAGTCTGGCGCCGAGCTGATGAACC CTGGCGCCAGCGTGAAGATCAGCTGCAAGAGC ACCGGCTACAAGTTCAGCAGCTACTGGATCGA GTGGGTCAAGCAGCGGCCTGGCCACGGCCTGG AATGGATGGGCGAGATCCTGCCTGGCAGCGGC AGCACCAACCACAACGAGAAGTTCAAGGGCA AGGCCATCTTCACCGCCGACGCCAGCAGCAAC	1182

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		ACCGCCTACATGGAACTGAGCAGCCTGACCAG CGAGGACAGCGCCGTGTACTACTGCGCCCGGA CCATCAGCACCGCCACCGATTGGTTCGCCTACT GGGGCCAGGGCACCCTGGTCACCGTGTCTGCT GCCAAAACAACAGCACCAAGTGTCTATCCACT GGCCCCTGTGTGTGGAGATACAACTGGCTCCT CGGTGACTCTAGGATGCCTGGTCAAGGGTTAT TTCCCTGAGCCAGTGACCTTGACCTGGAACTCT GGATCCCTGTCCAGTGGTGTGCACACCTTCCCA GCTGTCCTGCAGTCTGACCTCTACACCCTCAGC AGCTCAGTGACTGTAACCTCGAGCACCTGGCC CAGCCAGTCCATCACCTGCAATGTGGCCCACC CGGCAAGCAGCACCAAGGTGGACAAGAAAAT TGAGCCCAGAGGGCCCACAATCAAGCCCTGTC CTCCATGCAAATGCCCAGCACCTAACCTCTTGG GTGGACCATCCGTCTTCATCTTCCCTCCAAAGA TCAAGGATGTACTCATGATCTCCCTGAGCCCCA TAGTCACATGTGTGGTGGTGGATGTGAGCGAG GATGACCCAGATGTCCAGATCAGCTGGTTTGT GAACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTCTC CGGGTGGTCAGTGCCCTCCCCATCCAGCACCA GGACTGGATGAGTGGCAAGGAGTTCAAATGCA AGGTCAACAACAAAGACCTCCCAGCGCCCATC GAGAGAACCATCTCAAAACCCAAAGGGTCAGT AAGAGCTCCACAGGTATATGTCTTGCCTCCACC AGAAGAAGAGATGACTAAGAAACAGGTCACT CTGACCTGCATGGTCACAGACTTCATGCCTGA AGACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAACCA GTCCTGGACTCTGATGGTTCTTACTTCATGTAC AGCAAGCTGAGAGTGGAAAAGAAGAACTGGG TGGAAAGAAATAGCTACTCCTGTTCAGTGGTC CACGAGGGTCTGCACAATCACCACACGACTAA GAGCTTCTCCCGGACTCCGGGTAAATGA	
SM1B320	pDR000029282	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGGTGCA GCTGCAGCAGTCTGGCGCCGAGCTGATGAAGC CTGGCGCCAGCGTGAAGATGAGCTGCAAGGCC ACCGGCTACAAGTTCAGCAGCTACTGGATCGA GTGGGTCAAGCAGCGGCCTGGCCACGGCCTGG AATGGATGGGCGAGATCCTGCCTGGCAGCGGC AGCACCAACCACAACGAGAAGTTCAAGGGCA AGGCCATCTTCACCGCCGACGCCAGCAGCAAC ACCGCCTACATGGAACTGAGCAGCCTGACCAG CGAGGACAGCGCCGTGTACTACTGCGCCCGGA CCATCAGCACCGCCACCGATTGGTTCGCCTACT GGGGCCAGGGCACCCTGGTCACCGTGTCTGCT	1183

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GCCAAAACAACAGCACCAAGTGTCTATCCACT GGCCCCTGTGTGTGGAGATACAACTGGCTCCT CGGTGACTCTAGGATGCCTGGTCAAGGGTTAT TTCCCTGAGCCAGTGACCTTGACCTGGAACTCT GGATCCCTGTCCAGTGGTGTGCACACCTTCCCA GCTGTCCTGCAGTCTGACCTCTACACCCTCAGC AGCTCAGTGACTGTAACCTCGAGCACCTGGCC CAGCCAGTCCATCACCTGCAATGTGGCCCACC CGGCAAGCAGCACCAAGGTGGACAAGAAAAT TGAGCCCAGAGGGCCCACAATCAAGCCCTGTC CTCCATGCAAATGCCCAGCACCTAACCTCTTGG GTGGACCATCCGTCTTCATCTTCCCTCCAAAGA TCAAGGATGTACTCATGATCTCCCTGAGCCCCA TAGTCACATGTGTGGTGGTGGATGTGAGCGAG GATGACCCAGATGTCCAGATCAGCTGGTTTGT GAACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTCTC CGGGTGGTCAGTGCCCTCCCCATCCAGCACCA GGACTGGATGAGTGGCAAGGAGTTCAAATGCA AGGTCAACAACAAAGACCTCCCAGCGCCCATC GAGAGAACCATCTCAAAACCCAAAGGGTCAGT AAGAGCTCCACAGGTATATGTCTTGCCTCCACC AGAAGAAGAGATGACTAAGAAACAGGTCACT CTGACCTGCATGGTCACAGACTTCATGCCTGA AGACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAACCA GTCCTGGACTCTGATGGTTCTTACTTCATGTAC AGCAAGCTGAGAGTGGAAAAGAAGAACTGGG TGGAAAGAAATAGCTACTCCTGTTCAGTGGTC CACGAGGGTCTGCACAATCACCACACGACTAA GAGCTTCTCCCGGACTCCGGGTAAATGA	
SM1B321	pDR000029281	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGGTGCA GCTGCAGCAGTCTGGCGCCGAGCTGATGAAGC CTGGCGCCAGCGTGAAGATGAGCTGCAAGGCC ACCGGCTACAAGTTCAGCAGCTACTGGATCGA GTGGGTCAAGCAGCGGCCTGGCCACGGCCTGG AATGGATGGGCGAGATCCTGCCTGGCAGCGGC AGCACCAACCACAACGAGAAGTTCACCGGCAG AGCCATCTTCACCGCCGACGCCAGCAGCAACA CCGCCTACATGGAACTGAGCAGCCTGACCAGC GAGGACAGCGCCGTGTACTACTGCGCCCGGAC CATCAGCACCGCCACCGATTGGTTCGCCTACTG GGGCCAGGGCACCCTGGTCACCGTGTCTGCTG CCAAAACAACAGCACCAAGTGTCTATCCACTG GCCCCTGTGTGTGGAGATACAACTGGCTCCTC GGTGACTCTAGGATGCCTGGTCAAGGGTTATTT CCCTGAGCCAGTGACCTTGACCTGGAACTCTG	1184

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GATCCCTGTCCAGTGGTGTGCACACCTTCCCAG CTGTCCTGCAGTCTGACCTCTACACCCTCAGCA GCTCAGTGACTGTAACCTCGAGCACCTGGCCC AGCCAGTCCATCACCTGCAATGTGGCCCACCC GGCAAGCAGCACCAAGGTGGACAAGAAAATT GAGCCCAGAGGGCCCACAATCAAGCCCTGTCC TCCATGCAAATGCCCAGCACCTAACCTCTTGG GTGGACCATCCGTCTTCATCTTCCCTCCAAAGA TCAAGGATGTACTCATGATCTCCCTGAGCCCCA TAGTCACATGTGTGGTGGTGGATGTGAGCGAG GATGACCCAGATGTCCAGATCAGCTGGTTTGT GAACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTCTC CGGGTGGTCAGTGCCCTCCCCATCCAGCACCA GGACTGGATGAGTGGCAAGGAGTTCAAATGCA AGGTCAACAACAAAGACCTCCCAGCGCCCATC GAGAGAACCATCTCAAAACCCAAAGGGTCAGT AAGAGCTCCACAGGTATATGTCTTGCCTCCACC AGAAGAAGAGATGACTAAGAAACAGGTCACT CTGACCTGCATGGTCACAGACTTCATGCCTGA AGACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAACCA GTCCTGGACTCTGATGGTTCTTACTTCATGTAC AGCAAGCTGAGAGTGGAAAAGAAGAACTGGG TGGAAAGAAATAGCTACTCCTGTTCAGTGGTC CACGAGGGTCTGCACAATCACCACACGACTAA GAGCTTCTCCCGGACTCCGGGTAAATGA	
SM1B322	pDR000029282	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGGTGCA GCTGCAGCAGTCTGGCGCCGAGCTGATGAAGC CTGGCGCCAGCGTGAAGATGAGCTGCAAGGCC ACCGGCTACAAGTTCAGCAGCTACTGGATCGA GTGGGTCAAGCAGCGGCCTGGCCACGGCCTGG AATGGATGGGCGAGATCCTGCCTGGCAGCGGC AGCACCAACCACAACGAGAAGTTCAAGGGCA AGGCCATCTTCACCGCCGACGCCAGCAGCAAC ACCGCCTACATGGAACTGAGCAGCCTGACCAG CGAGGACAGCGCCGTGTACTACTGCGCCCGGA CCATCAGCACCGCCACCGATTGGTTCGCCTACT GGGGCCAGGGCACCCTGGTCACCGTGTCTGCT GCCAAAACAACAGCACCAAGTGTCTATCCACT GGCCCCTGTGTGTGGAGATACAACTGGCTCCT CGGTGACTCTAGGATGCCTGGTCAAGGGTTAT TTCCCTGAGCCAGTGACCTTGACCTGGAACTCT GGATCCCTGTCCAGTGGTGTGCACACCTTCCCA GCTGTCCTGCAGTCTGACCTCTACACCCTCAGC AGCTCAGTGACTGTAACCTCGAGCACCTGGCC CAGCCAGTCCATCACCTGCAATGTGGCCCACC	1185

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CGGCAAGCAGCACCAAGGTGGACAAGAAAAT TGAGCCCAGAGGGCCCACAATCAAGCCCTGTC CTCCATGCAAATGCCCAGCACCTAACCTCTTGG GTGGACCATCCGTCTTCATCTTCCCTCCAAAGA TCAAGGATGTACTCATGATCTCCCTGAGCCCCA TAGTCACATGTGTGGTGGTGGATGTGAGCGAG GATGACCCAGATGTCCAGATCAGCTGGTTTGT GAACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTCTC CGGGTGGTCAGTGCCCTCCCCATCCAGCACCA GGACTGGATGAGTGGCAAGGAGTTCAAATGCA AGGTCAACAACAAAGACCTCCCAGCGCCCATC GAGAGAACCATCTCAAAACCCAAAGGGTCAGT AAGAGCTCCACAGGTATATGTCTTGCCTCCACC AGAAGAAGAGATGACTAAGAAACAGGTCACT CTGACCTGCATGGTCACAGACTTCATGCCTGA AGACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAACCA GTCCTGGACTCTGATGGTTCTTACTTCATGTAC AGCAAGCTGAGAGTGGAAAAGAAGAACTGGG TGGAAAGAAATAGCTACTCCTGTTCAGTGGTC CACGAGGGTCTGCACAATCACCACACGACTAA GAGCTTCTCCCGGACTCCGGGTAAATGA	
SM1B323	pDR000029280	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGGTGCA GCTGCAGCAGTCTGGCGCCGAGCTGATGAAGC CTGGCGCCAGCGTGAAGATGCCCTGCAAGGCC ACCGGCTACAAGTTCAGCAGCTACTGGATCGA GTGGGTCAAGCAGCGGCCTGGCCACGGCCTGG AATGGATGGGCGAGATCCTGCCTGGCAGCGGC AGCACCAACCACAACGAGAAGTTCAAGGGCA AGGCCATCTTCACCGCCGACGCCAGCAGCAAC ACCGCCTACATGGAACTGAGCAGCCTGACCAG CGAGGACAGCGCCGTGTACTACTGCGCCCGGA CCATCAGCACCGCCACCGATTGGTTCGCCTACT GGGGCCAGGGCACCCTGGTCACCGTGTCTGCT GCCAAAACAACAGCACCAAGTGTCTATCCACT GGCCCCTGTGTGTGGAGATACAACTGGCTCCT CGGTGACTCTAGGATGCCTGGTCAAGGGTTAT TTCCCTGAGCCAGTGACCTTGACCTGGAACTCT GGATCCCTGTCCAGTGGTGTGCACACCTTCCCA GCTGTCCTGCAGTCTGACCTCTACACCCTCAGC AGCTCAGTGACTGTAACCTCGAGCACCTGGCC CAGCCAGTCCATCACCTGCAATGTGGCCCACC CGGCAAGCAGCACCAAGGTGGACAAGAAAAT TGAGCCCAGAGGGCCCACAATCAAGCCCTGTC CTCCATGCAAATGCCCAGCACCTAACCTCTTGG GTGGACCATCCGTCTTCATCTTCCCTCCAAAGA	1186

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		TCAAGGATGTACTCATGATCTCCCTGAGCCCCA TAGTCACATGTGTGGTGGTGGATGTGAGCGAG GATGACCCAGATGTCCAGATCAGCTGGTTTGT GAACAACGTGGAAGTACACACAGCTCAGACAC AAACCCATAGAGAGGATTACAACAGTACTCTC CGGGTGGTCAGTGCCCTCCCCATCCAGCACCA GGACTGGATGAGTGGCAAGGAGTTCAAATGCA AGGTCAACAACAAAGACCTCCCAGCGCCCATC GAGAGAACCATCTCAAAACCCAAAGGGTCAGT AAGAGCTCCACAGGTATATGTCTTGCCTCCACC AGAAGAAGAGATGACTAAGAAACAGGTCACT CTGACCTGCATGGTCACAGACTTCATGCCTGA AGACATTTACGTGGAGTGGACCAACAACGGGA AAACAGAGCTAAACTACAAGAACACTGAACCA GTCCTGGACTCTGATGGTTCTTACTTCATGTAC AGCAAGCTGAGAGTGGAAAAGAAGAACTGGG TGGAAAGAAATAGCTACTCCTGTTCAGTGGTC CACGAGGGTCTGCACAATCACCACACGACTAA GAGCTTCTCCCGGACTCCGGGTAAATGA	
SM1B324	pDR000029279	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAGGTGCA GCTGCAGCAGTCTGGCGCTGAACTCGTGCGGC CTGGCGCCCTGGTCAAGCTGAGCTGCAAGGCC AGCGGCTTCAACATCAAGGACTACTACATGCA CTGGGTCAAGCAGCGGCCCGAGCAGGGCCTGG AATGGATCGGCTGGATCGACCCCGAGAACGGC AACACCATCTACGACCCCAAGTTCCAGGGCAA GGCCTCCATCACCGCCGACACCAGCAGCAACA CCGCCTACCTGCAGCTGAGCAGCCTGACCAGC GAGGACACCGCCGTGTACTACTGCGCCAGATA CGACGGCTACGCCATGGACTACTGGGGCCAGG GCACCAGCGTGACCGTGTCCTCTGCCAAAACA ACAGCACCAAGTGTCTATCCACTGGCCCCTGT GTGTGGAGATACAACTGGCTCCTCGGTGACTC TAGGATGCCTGGTCAAGGGTTATTTCCCTGAGC CAGTGACCTTGACCTGGAACTCTGGATCCCTGT CCAGTGGTGTGCACACCTTCCCAGCTGTCCTGC AGTCTGACCTCTACACCCTCAGCAGCTCAGTG ACTGTAACCTCGAGCACCTGGCCCAGCCAGTC CATCACCTGCAATGTGGCCCACCCGGCAAGCA GCACCAAGGTGGACAAGAAAATTGAGCCCAG AGGGCCCACAATCAAGCCCTGTCCTCCATGCA AATGCCCAGCACCTAACCTCTTGGGTGGACCA TCCGTCTTCATCTTCCCTCCAAAGATCAAGGAT GTACTCATGATCTCCCTGAGCCCCATAGTCACA TGTGTGGTGGTGGATGTGAGCGAGGATGACCC AGATGTCCAGATCAGCTGGTTTGTGAACAACG TGGAAGTACACACAGCTCAGACACAAACCCAT	1187

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		AGAGAGGATTACAACAGTACTCTCCGGGTGGT CAGTGCCCTCCCCATCCAGCACCAGGACTGGA TGAGTGGCAAGGAGTTCAAATGCAAGGTCAAC AACAAAGACCTCCCAGCGCCCATCGAGAGAAC CATCTCAAAACCCAAAGGGTCAGTAAGAGCTC CACAGGTATATGTCTTGCCTCCACCAGAAGAA GAGATGACTAAGAAACAGGTCACTCTGACCTG CATGGTCACAGACTTCATGCCTGAAGACATTT ACGTGGAGTGGACCAACAACGGGAAAACAGA GCTAAACTACAAGAACACTGAACCAGTCCTGG ACTCTGATGGTTCTTACTTCATGTACAGCAAGC TGAGAGTGGAAAAGAAGAACTGGGTGGAAAG AAATAGCTACTCCTGTTCAGTGGTCCACGAGG GTCTGCACAATCACCACACGACTAAGAGCTTC TCCCGGACTCCGGGTAAATGA	
SM1B325	pDR000029278	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGGTGCA GCTGCAGCAGTCTGGCGCTGAACTCGTGCGGC CTGGCACCAGCGTGAAGATGAGCTGCAAGGCC GCTGGCTACACCTTCACCAACTACTGGATCGG CTGGGTCAAGCAGCGGCCTGGCCACGGCCTGG AATGGATCGGCGACATCTACCCTGGCGGCGGA TACACCAACTACAACGAGAAGTTCAAGGACAA GACCACCCTGACCGCCGACACCAGCAGCAACA CCGCCTACATGCAGCTGAGCAGCCTGACCAGC GAGGACAGCGCCATCTACTACTGCGCCAGCAA CGACTGCTGGGGCCAGGGCACCACACTGACCG TGTCCAGCGCCAAAACAACAGCACCAAGTGTC TATCCACTGGCCCCTGTGTGTGGAGATACAACT GGCTCCTCGGTGACTCTAGGATGCCTGGTCAA GGGTTATTTCCCTGAGCCAGTGACCTTGACCTG GAACTCTGGATCCCTGTCCAGTGGTGTGCACA CCTTCCCAGCTGTCCTGCAGTCTGACCTCTACA CCCTCAGCAGCTCAGTGACTGTAACCTCGAGC ACCTGGCCCAGCCAGTCCATCACCTGCAATGT GGCCCACCCGGCAAGCAGCACCAAGGTGGACA AGAAAATTGAGCCCAGAGGGCCCACAATCAAG CCCTGTCCTCCATGCAAATGCCCAGCACCTAAC CTCTTGGGTGGACCATCCGTCTTCATCTTCCCT CCAAAGATCAAGGATGTACTCATGATCTCCCT GAGCCCCATAGTCACATGTGTGGTGGTGGATG TGAGCGAGGATGACCCAGATGTCCAGATCAGC TGGTTTGTGAACAACGTGGAAGTACACACAGC TCAGACACAAACCCATAGAGAGGATTACAACA GTACTCTCCGGGTGGTCAGTGCCCTCCCCATCC AGCACCAGGACTGGATGAGTGGCAAGGAGTTC AAATGCAAGGTCAACAACAAAGACCTCCCAGC GCCCATCGAGAGAACCATCTCAAAACCCAAAG	1188

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GGTCAGTAAGAGCTCCACAGGTATATGTCTTG CCTCCACCAGAAGAAGAGATGACTAAGAAACA GGTCACTCTGACCTGCATGGTCACAGACTTCAT GCCTGAAGACATTTACGTGGAGTGGACCAACA ACGGGAAAACAGAGCTAAACTACAAGAACAC TGAACCAGTCCTGGACTCTGATGGTTCTTACTT CATGTACAGCAAGCTGAGAGTGGAAAAGAAG AACTGGGTGGAAAGAAATAGCTACTCCTGTTC AGTGGTCCACGAGGGTCTGCACAATCACCACA CGACTAAGAGCTTCTCCCGGACTCCGGGTAAA TGA	
SM1B326	pDR000029277	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGGTGCA GCTGAAGCAGAGCGGCCCTGGCCTGGTGCAGC CTAGCCAGAGCCTGAGCATCACCTGTACCGTG TCCGGCTTCAGCATCACCAGCTACGGCGTGCA CTGGATCCGGCAGAGCCCCGGCAAGGGCCTGG AATGGCTGGGAGTGATTTGGAGCGGCGGCAGC ACCGACTACAACGCCGCCTTCATCAGCAGACT GAGCATCAGCGAGGACAACAGCAAGAGCCAG GTGTTCTTCAAGATGAACAGCCTGCAGGCCAA CGACACCGCCATCTACTACTGCGCCACCTTCTA CTACGACTACGACGAGGGCTTCGACTACTGGG GCCAGGGCACCACCCTGACCGTGTCCTCTGCC AAAACAACAGCACCAAGTGTCTATCCACTGGC CCCTGTGTGTGGAGATACAACTGGCTCCTCGGT GACTCTAGGATGCCTGGTCAAGGGTTATTTCCC TGAGCCAGTGACCTTGACCTGGAACTCTGGAT CCCTGTCCAGTGGTGTGCACACCTTCCCAGCTG TCCTGCAGTCTGACCTCTACACCCTCAGCAGCT CAGTGACTGTAACCTCGAGCACCTGGCCCAGC CAGTCCATCACCTGCAATGTGGCCCACCCGGC AAGCAGCACCAAGGTGGACAAGAAAATTGAG CCCAGAGGGCCCACAATCAAGCCCTGTCCTCC ATGCAAATGCCCAGCACCTAACCTCTTGGGTG GACCATCCGTCTTCATCTTCCCTCCAAAGATCA AGGATGTACTCATGATCTCCCTGAGCCCCATA GTCACATGTGTGGTGGTGGATGTGAGCGAGGA TGACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACACAA ACCCATAGAGAGGATTACAACAGTACTCTCCG GGTGGTCAGTGCCCTCCCCATCCAGCACCAGG ACTGGATGAGTGGCAAGGAGTTCAAATGCAAG GTCAACAACAAAGACCTCCCAGCGCCCATCGA GAGAACCATCTCAAAACCCAAAGGGTCAGTAA GAGCTCCACAGGTATATGTCTTGCCTCCACCAG AAGAAGAGATGACTAAGAAACAGGTCACTCTG ACCTGCATGGTCACAGACTTCATGCCTGAAGA	1189

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CATTTACGTGGAGTGGACCAACAACGGGAAAA CAGAGCTAAACTACAAGAACACTGAACCAGTC CTGGACTCTGATGGTTCTTACTTCATGTACAGC AAGCTGAGAGTGGAAAAGAAGAACTGGGTGG AAAGAAATAGCTACTCCTGTTCAGTGGTCCAC GAGGGTCTGCACAATCACCACACGACTAAGAG CTTCTCCCGGACTCCGGGTAAATGA	
SM1B327	pDR000029276	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGGTGCA GCTGAAGCAGAGCGGCCCTGGCCTGGTGCAGC CTAGCCAGAGCCTGAGCATCACCTGTACCGTG TCCGGCTTCAGCATCACCAGCTACGGCGTGCA CTGGATCCGGCAGAGCCCCGGCAAGGGCCTGG AATGGCTGGGAGTGATTTGGAGCGGCGGCAGC ACCGACTACAACGCCGCCTTCATCAGCAGACT GAGCATCAGCAAGGACAACAGCAAGAGCCAG GTGTTCTTCAAGATGAACAGCCTGCAGGCCAA CGACACCGCCATCTACTACTGCGCCACCTTCTA CTACGACTACGACGAGGGCTTCGACTACTGGG GCCAGGGCACCACCCTGACCGTGTCCTCTGCC AAAACAACAGCACCAAGTGTCTATCCACTGGC CCCTGTGTGTGGAGATACAACTGGCTCCTCGGT GACTCTAGGATGCCTGGTCAAGGGTTATTTCCC TGAGCCAGTGACCTTGACCTGGAACTCTGGAT CCCTGTCCAGTGGTGTGCACACCTTCCCAGCTG TCCTGCAGTCTGACCTCTACACCCTCAGCAGCT CAGTGACTGTAACCTCGAGCACCTGGCCCAGC CAGTCCATCACCTGCAATGTGGCCCACCCGGC AAGCAGCACCAAGGTGGACAAGAAAATTGAG CCCAGAGGGCCCACAATCAAGCCCTGTCCTCC ATGCAAATGCCCAGCACCTAACCTCTTGGGTG GACCATCCGTCTTCATCTTCCCTCCAAAGATCA AGGATGTACTCATGATCTCCCTGAGCCCCATA GTCACATGTGTGGTGGTGGATGTGAGCGAGGA TGACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACACAA ACCCATAGAGAGGATTACAACAGTACTCTCCG GGTGGTCAGTGCCCTCCCCATCCAGCACCAGG ACTGGATGAGTGGCAAGGAGTTCAAATGCAAG GTCAACAACAAAGACCTCCCAGCGCCCATCGA GAGAACCATCTCAAAACCCAAAGGGTCAGTAA GAGCTCCACAGGTATATGTCTTGCCTCCACCAG AAGAAGAGATGACTAAGAAACAGGTCACTCTG ACCTGCATGGTCACAGACTTCATGCCTGAAGA CATTTACGTGGAGTGGACCAACAACGGGAAAA CAGAGCTAAACTACAAGAACACTGAACCAGTC CTGGACTCTGATGGTTCTTACTTCATGTACAGC AAGCTGAGAGTGGAAAAGAAGAACTGGGTGG	1190

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		AAAGAAATAGCTACTCCTGTTCAGTGGTCCAC GAGGGTCTGCACAATCACCACACGACTAAGAG CTTCTCCCGGACTCCGGGTAAATGA	
SM1B328	pDR000029276	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGGTGCA GCTGAAGCAGAGCGGCCCTGGCCTGGTGCAGC CTAGCCAGAGCCTGAGCATCACCTGTACCGTG TCCGGCTTCAGCATCACCAGCTACGGCGTGCA CTGGATCCGGCAGAGCCCCGGCAAGGGCCTGG AATGGCTGGGAGTGATTTGGAGCGGCGGCAGC ACCGACTACAACGCCGCCTTCATCAGCAGACT GAGCATCAGCAAGGACAACAGCAAGAGCCAG GTGTTCTTCAAGATGAACAGCCTGCAGGCCAA CGACACCGCCATCTACTACTGCGCCACCTTCTA CTACGACTACGACGAGGGCTTCGACTACTGGG GCCAGGGCACCACCCTGACCGTGTCCTCTGCC AAAACAACAGCACCAAGTGTCTATCCACTGGC CCCTGTGTGTGGAGATACAACTGGCTCCTCGGT GACTCTAGGATGCCTGGTCAAGGGTTATTTCCC TGAGCCAGTGACCTTGACCTGGAACTCTGGAT CCCTGTCCAGTGGTGTGCACACCTTCCCAGCTG TCCTGCAGTCTGACCTCTACACCCTCAGCAGCT CAGTGACTGTAACCTCGAGCACCTGGCCCAGC CAGTCCATCACCTGCAATGTGGCCCACCCGGC AAGCAGCACCAAGGTGGACAAGAAAATTGAG CCCAGAGGGCCCACAATCAAGCCCTGTCCTCC ATGCAAATGCCCAGCACCTAACCTCTTGGGTG GACCATCCGTCTTCATCTTCCCTCCAAAGATCA AGGATGTACTCATGATCTCCCTGAGCCCCATA GTCACATGTGTGGTGGTGGATGTGAGCGAGGA TGACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACACAA ACCCATAGAGAGGATTACAACAGTACTCTCCG GGTGGTCAGTGCCCTCCCCATCCAGCACCAGG ACTGGATGAGTGGCAAGGAGTTCAAATGCAAG GTCAACAACAAAGACCTCCCAGCGCCCATCGA GAGAACCATCTCAAAACCCAAAGGGTCAGTAA GAGCTCCACAGGTATATGTCTTGCCTCCACCAG AAGAAGAGATGACTAAGAAACAGGTCACTCTG ACCTGCATGGTCACAGACTTCATGCCTGAAGA CATTTACGTGGAGTGGACCAACAACGGGAAAA CAGAGCTAAACTACAAGAACACTGAACCAGTC CTGGACTCTGATGGTTCTTACTTCATGTACAGC AAGCTGAGAGTGGAAAAGAAGAACTGGGTGG AAAGAAATAGCTACTCCTGTTCAGTGGTCCAC GAGGGTCTGCACAATCACCACACGACTAAGAG CTTCTCCCGGACTCCGGGTAAATGA	1191
SM1B329	pDR000029276	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG	1192

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GCAGCTGCCCAAAGTATACAGGCCCAGGTGCA GCTGAAGCAGAGCGGCCCTGGCCTGGTGCAGC CTAGCCAGAGCCTGAGCATCACCTGTACCGTG TCCGGCTTCAGCATCACCAGCTACGGCGTGCA CTGGATCCGGCAGAGCCCCGGCAAGGGCCTGG AATGGCTGGGAGTGATTTGGAGCGGCGGCAGC ACCGACTACAACGCCGCCTTCATCAGCAGACT GAGCATCAGCAAGGACAACAGCAAGAGCCAG GTGTTCTTCAAGATGAACAGCCTGCAGGCCAA CGACACCGCCATCTACTACTGCGCCACCTTCTA CTACGACTACGACGAGGGCTTCGACTACTGGG GCCAGGGCACCACCCTGACCGTGTCCTCTGCC AAAACAACAGCACCAAGTGTCTATCCACTGGC CCCTGTGTGTGGAGATACAACTGGCTCCTCGGT GACTCTAGGATGCCTGGTCAAGGGTTATTTCCC TGAGCCAGTGACCTTGACCTGGAACTCTGGAT CCCTGTCCAGTGGTGTGCACACCTTCCCAGCTG TCCTGCAGTCTGACCTCTACACCCTCAGCAGCT CAGTGACTGTAACCTCGAGCACCTGGCCCAGC CAGTCCATCACCTGCAATGTGGCCCACCCGGC AAGCAGCACCAAGGTGGACAAGAAAATTGAG CCCAGAGGGCCCACAATCAAGCCCTGTCCTCC ATGCAAATGCCCAGCACCTAACCTCTTGGGTG GACCATCCGTCTTCATCTTCCCTCCAAAGATCA AGGATGTACTCATGATCTCCCTGAGCCCCATA GTCACATGTGTGGTGGTGGATGTGAGCGAGGA TGACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACACAA ACCCATAGAGAGGATTACAACAGTACTCTCCG GGTGGTCAGTGCCCTCCCCATCCAGCACCAGG ACTGGATGAGTGGCAAGGAGTTCAAATGCAAG GTCAACAACAAAGACCTCCCAGCGCCCATCGA GAGAACCATCTCAAAACCCAAAGGGTCAGTAA GAGCTCCACAGGTATATGTCTTGCCTCCACCAG AAGAAGAGATGACTAAGAAACAGGTCACTCTG ACCTGCATGGTCACAGACTTCATGCCTGAAGA CATTTACGTGGAGTGGACCAACAACGGGAAAA CAGAGCTAAACTACAAGAACACTGAACCAGTC CTGGACTCTGATGGTTCTTACTTCATGTACAGC AAGCTGAGAGTGGAAAAGAAGAACTGGGTGG AAAGAAATAGCTACTCCTGTTCAGTGGTCCAC GAGGGTCTGCACAATCACCACACGACTAAGAG CTTCTCCCGGACTCCGGGTAAATGA	
SM1B330	pDR000029276	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGGTGCA GCTGAAGCAGAGCGGCCCTGGCCTGGTGCAGC CTAGCCAGAGCCTGAGCATCACCTGTACCGTG TCCGGCTTCAGCATCACCAGCTACGGCGTGCA	1193

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CTGGATCCGGCAGAGCCCCGGCAAGGGCCTGG AATGGCTGGGAGTGATTTGGAGCGGCGGCAGC ACCGACTACAACGCCGCCTTCATCAGCAGACT GAGCATCAGCAAGGACAACAGCAAGAGCCAG GTGTTCTTCAAGATGAACAGCCTGCAGGCCAA CGACACCGCCATCTACTACTGCGCCACCTTCTA CTACGACTACGACGAGGGCTTCGACTACTGGG GCCAGGGCACCACCCTGACCGTGTCCTCTGCC AAAACAACAGCACCAAGTGTCTATCCACTGGC CCCTGTGTGTGGAGATACAACTGGCTCCTCGGT GACTCTAGGATGCCTGGTCAAGGGTTATTTCCC TGAGCCAGTGACCTTGACCTGGAACTCTGGAT CCCTGTCCAGTGGTGTGCACACCTTCCCAGCTG TCCTGCAGTCTGACCTCTACACCCTCAGCAGCT CAGTGACTGTAACCTCGAGCACCTGGCCCAGC CAGTCCATCACCTGCAATGTGGCCCACCCGGC AAGCAGCACCAAGGTGGACAAGAAAATTGAG CCCAGAGGGCCCACAATCAAGCCCTGTCCTCC ATGCAAATGCCCAGCACCTAACCTCTTGGGTG GACCATCCGTCTTCATCTTCCCTCCAAAGATCA AGGATGTACTCATGATCTCCCTGAGCCCCATA GTCACATGTGTGGTGGTGGATGTGAGCGAGGA TGACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACACAA ACCCATAGAGAGGATTACAACAGTACTCTCCG GGTGGTCAGTGCCCTCCCCATCCAGCACCAGG ACTGGATGAGTGGCAAGGAGTTCAAATGCAAG GTCAACAACAAAGACCTCCCAGCGCCCATCGA GAGAACCATCTCAAAACCCAAAGGGTCAGTAA GAGCTCCACAGGTATATGTCTTGCCTCCACCAG AAGAAGAGATGACTAAGAAACAGGTCACTCTG ACCTGCATGGTCACAGACTTCATGCCTGAAGA CATTTACGTGGAGTGGACCAACAACGGGAAAA CAGAGCTAAACTACAAGAACACTGAACCAGTC CTGGACTCTGATGGTTCTTACTTCATGTACAGC AAGCTGAGAGTGGAAAAGAAGAACTGGGTGG AAAGAAATAGCTACTCCTGTTCAGTGGTCCAC GAGGGTCTGCACAATCACCACACGACTAAGAG CTTCTCCCGGACTCCGGGTAAATGA	
SM1B331	pDR000029276	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGGTGCA GCTGAAGCAGAGCGGCCCTGGCCTGGTGCAGC CTAGCCAGAGCCTGAGCATCACCTGTACCGTG TCCGGCTTCAGCATCACCAGCTACGGCGTGCA CTGGATCCGGCAGAGCCCCGGCAAGGGCCTGG AATGGCTGGGAGTGATTTGGAGCGGCGGCAGC ACCGACTACAACGCCGCCTTCATCAGCAGACT GAGCATCAGCAAGGACAACAGCAAGAGCCAG	1194

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GTGTTCTTCAAGATGAACAGCCTGCAGGCCAA CGACACCGCCATCTACTACTGCGCCACCTTCTA CTACGACTACGACGAGGGCTTCGACTACTGGG GCCAGGGCACCACCCTGACCGTGTCCTCTGCC AAAACAACAGCACCAAGTGTCTATCCACTGGC CCCTGTGTGTGGAGATACAACTGGCTCCTCGGT GACTCTAGGATGCCTGGTCAAGGGTTATTTCCC TGAGCCAGTGACCTTGACCTGGAACTCTGGAT CCCTGTCCAGTGGTGTGCACACCTTCCCAGCTG TCCTGCAGTCTGACCTCTACACCCTCAGCAGCT CAGTGACTGTAACCTCGAGCACCTGGCCCAGC CAGTCCATCACCTGCAATGTGGCCCACCCGGC AAGCAGCACCAAGGTGGACAAGAAAATTGAG CCCAGAGGGCCCACAATCAAGCCCTGTCCTCC ATGCAAATGCCCAGCACCTAACCTCTTGGGTG GACCATCCGTCTTCATCTTCCCTCCAAAGATCA AGGATGTACTCATGATCTCCCTGAGCCCCATA GTCACATGTGTGGTGGTGGATGTGAGCGAGGA TGACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACACAA ACCCATAGAGAGGATTACAACAGTACTCTCCG GGTGGTCAGTGCCCTCCCCATCCAGCACCAGG ACTGGATGAGTGGCAAGGAGTTCAAATGCAAG GTCAACAACAAAGACCTCCCAGCGCCCATCGA GAGAACCATCTCAAAACCCAAAGGGTCAGTAA GAGCTCCACAGGTATATGTCTTGCCTCCACCAG AAGAAGAGATGACTAAGAAACAGGTCACTCTG ACCTGCATGGTCACAGACTTCATGCCTGAAGA CATTTACGTGGAGTGGACCAACAACGGGAAAA CAGAGCTAAACTACAAGAACACTGAACCAGTC CTGGACTCTGATGGTTCTTACTTCATGTACAGC AAGCTGAGAGTGGAAAAGAAGAACTGGGTGG AAAGAAATAGCTACTCCTGTTCAGTGGTCCAC GAGGGTCTGCACAATCACCACACGACTAAGAG CTTCTCCCGGACTCCGGGTAAATGA	
SM1B332	pDR000029275	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGGTGCA GCTGAAAGAGTCCGGCCCTGGACTGGTGGCCC CCAGCCAGAGCCTGAGCATCACCTGTACCGTG TCCGGCCTGAGCCTGACCAGCTACGGCCTGTCT TGGGTCCGACAGCCCCCTGGCAAGGGCCTGGA ATGGCTGGGAGTGATCTGGGGCGACGGCAGCA CCAACTACCACAGCGCCCTGATCAGCAGACTG AGCATCAGCAAGGACAACAGCAAGAGCCAGG TGTTCCTGAAGCTGAACAGCCTGCAGAGCGAC GACACCGCCACCTACTACTGCGCCACCAGAGG CGACTACGGCAGCTACGCCATGGACTACTGGG GCCAGGGCACCAGCGTGACCGTGTCCTCTGCC	1195

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		AAAACAACAGCACCAAGTGTCTATCCACTGGC CCCTGTGTGTGGAGATACAACTGGCTCCTCGGT GACTCTAGGATGCCTGGTCAAGGGTTATTTCCC TGAGCCAGTGACCTTGACCTGGAACTCTGGAT CCCTGTCCAGTGGTGTGCACACCTTCCCAGCTG TCCTGCAGTCTGACCTCTACACCCTCAGCAGCT CAGTGACTGTAACCTCGAGCACCTGGCCCAGC CAGTCCATCACCTGCAATGTGGCCCACCCGGC AAGCAGCACCAAGGTGGACAAGAAAATTGAG CCCAGAGGGCCCACAATCAAGCCCTGTCCTCC ATGCAAATGCCCAGCACCTAACCTCTTGGGTG GACCATCCGTCTTCATCTTCCCTCCAAAGATCA AGGATGTACTCATGATCTCCCTGAGCCCCATA GTCACATGTGTGGTGGTGGATGTGAGCGAGGA TGACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACACAA ACCCATAGAGAGGATTACAACAGTACTCTCCG GGTGGTCAGTGCCCTCCCCATCCAGCACCAGG ACTGGATGAGTGGCAAGGAGTTCAAATGCAAG GTCAACAACAAAGACCTCCCAGCGCCCATCGA GAGAACCATCTCAAAACCCAAAGGGTCAGTAA GAGCTCCACAGGTATATGTCTTGCCTCCACCAG AAGAAGAGATGACTAAGAAACAGGTCACTCTG ACCTGCATGGTCACAGACTTCATGCCTGAAGA CATTTACGTGGAGTGGACCAACAACGGGAAAA CAGAGCTAAACTACAAGAACACTGAACCAGTC CTGGACTCTGATGGTTCTTACTTCATGTACAGC AAGCTGAGAGTGGAAAAGAAGAACTGGGTGG AAAGAAATAGCTACTCCTGTTCAGTGGTCCAC GAGGGTCTGCACAATCACCACACGACTAAGAG CTTCTCCCGGACTCCGGGTAAATGA	
SM1B333	pDR000029274	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAGGTGCA GCTGCAGCAGTCTGGCGCTGAACTCGTGCGGC CTGGCGCCAGCGTGAAGCTGAGCTGTACCGCC AGCGGCTTCAACATCAAGGACAGCCTGATCCA CTGGGTCAAGCAGCGGCCCGAGCAGGGCCTGG AATGGATCGGCTGGATCGACCCCGAGGACGGC GAGACTAAGTACGCCCCCAAGTTCCAGGACAA GGCCGCCCTGACCACCGACACCAGCAGCAACA CCGCCTACCTGCACCTGAACAGCCTGACCAGC GAGGACACCGCCATCTACTACTGCGGCAGAGG CGGCCTGATCCTGGACTACTGGGGCCAGGGCA CCACCCTGACCGTGTCCTCTGCCAAAACAACA GCACCAAGTGTCTATCCACTGGCCCCTGTGTGT GGAGATACAACTGGCTCCTCGGTGACTCTAGG ATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGT GACCTTGACCTGGAACTCTGGATCCCTGTCCAG	1196

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		TGGTGTGCACACCTTCCCAGCTGTCCTGCAGTC TGACCTCTACACCCTCAGCAGCTCAGTGACTGT AACCTCGAGCACCTGGCCCAGCCAGTCCATCA CCTGCAATGTGGCCCACCCGGCAAGCAGCACC AAGGTGGACAAGAAAATTGAGCCCAGAGGGC CCACAATCAAGCCCTGTCCTCCATGCAAATGC CCAGCACCTAACCTCTTGGGTGGACCATCCGTC TTCATCTTCCCTCCAAAGATCAAGGATGTACTC ATGATCTCCCTGAGCCCCATAGTCACATGTGTG GTGGTGGATGTGAGCGAGGATGACCCAGATGT CCAGATCAGCTGGTTTGTGAACAACGTGGAAG TACACACAGCTCAGACACAAACCCATAGAGAG GATTACAACAGTACTCTCCGGGTGGTCAGTGC CCTCCCCATCCAGCACCAGGACTGGATGAGTG GCAAGGAGTTCAAATGCAAGGTCAACAACAAA GACCTCCCAGCGCCCATCGAGAGAACCATCTC AAAACCCAAAGGGTCAGTAAGAGCTCCACAGG TATATGTCTTGCCTCCACCAGAAGAAGAGATG ACTAAGAAACAGGTCACTCTGACCTGCATGGT CACAGACTTCATGCCTGAAGACATTTACGTGG AGTGGACCAACAACGGGAAAACAGAGCTAAA CTACAAGAACACTGAACCAGTCCTGGACTCTG ATGGTTCTTACTTCATGTACAGCAAGCTGAGA GTGGAAAAGAAGAACTGGGTGGAAAGAAATA GCTACTCCTGTTCAGTGGTCCACGAGGGTCTGC ACAATCACCACACGACTAAGAGCTTCTCCCGG ACTCCGGGTAAATGA	
SM1B334	pDR000029273	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCCAGATCCA GCTGGTGCAGAGCGGCCCTGAGCTGAAGAAAC CCGGCGAGACAGTGAAGATCAGCTGCAGAAGC AGCGGCTACACCTTCACCAACTACGGCCTGAA CTGGGTCAAGCAGGCCCCTGGCAAGGACCTGA AGTGGATGGGCTGGCTGAACACCTACACCGGC GAGCCCACCTACGCCGACGACTTCAAGGGCAG ATTCGCCTTCAGCCTGGAAACCAGCGCCGGCA CCGCCTACCTGCAGATCAACAACCTGAAGAAC GAGGACACCGCCACCTACTTTTGCTCCCGGGA CTACCGCGAGGGCGACGCCATGGATTACTGGT CCCAGGGCACCAGCGTGACCGTGTCCAGCGCC AAAACAACAGCACCAAGTGTCTATCCACTGGC CCCTGTGTGTGGAGATACAACTGGCTCCTCGGT GACTCTAGGATGCCTGGTCAAGGGTTATTTCCC TGAGCCAGTGACCTTGACCTGGAACTCTGGAT CCCTGTCCAGTGGTGTGCACACCTTCCCAGCTG TCCTGCAGTCTGACCTCTACACCCTCAGCAGCT CAGTGACTGTAACCTCGAGCACCTGGCCCAGC CAGTCCATCACCTGCAATGTGGCCCACCCGGC	1197

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		AAGCAGCACCAAGGTGGACAAGAAAATTGAG CCCAGAGGGCCCACAATCAAGCCCTGTCCTCC ATGCAAATGCCCAGCACCTAACCTCTTGGGTG GACCATCCGTCTTCATCTTCCCTCCAAAGATCA AGGATGTACTCATGATCTCCCTGAGCCCCATA GTCACATGTGTGGTGGTGGATGTGAGCGAGGA TGACCCAGATGTCCAGATCAGCTGGTTTGTGA ACAACGTGGAAGTACACACAGCTCAGACACAA ACCCATAGAGAGGATTACAACAGTACTCTCCG GGTGGTCAGTGCCCTCCCCATCCAGCACCAGG ACTGGATGAGTGGCAAGGAGTTCAAATGCAAG GTCAACAACAAAGACCTCCCAGCGCCCATCGA GAGAACCATCTCAAAACCCAAAGGGTCAGTAA GAGCTCCACAGGTATATGTCTTGCCTCCACCAG AAGAAGAGATGACTAAGAAACAGGTCACTCTG ACCTGCATGGTCACAGACTTCATGCCTGAAGA CATTTACGTGGAGTGGACCAACAACGGGAAAA CAGAGCTAAACTACAAGAACACTGAACCAGTC CTGGACTCTGATGGTTCTTACTTCATGTACAGC AAGCTGAGAGTGGAAAAGAAGAACTGGGTGG AAAGAAATAGCTACTCCTGTTCAGTGGTCCAC GAGGGTCTGCACAATCACCACACGACTAAGAG CTTCTCCCGGACTCCGGGTAAATGA	
SM1B335	pDR000029272	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAGGTGCA GCTGGTGGAAAGCGGCGGAGGACTGGTCAAGC CTGGCGGCAGCCTGAAGCTGAGCTGCGCCGCC AGCGGCTTCACCTTCAGCAGCTACGCCATGAG CTGGGTCCGACAGACCCCCGAGAAGCGGCTGG AATGGGTGGCCACCATCAGCACCAGCGGCAGC TACACCTACTACCGGGACAGCGTGAAGGGCCG GCTGACCATCAGCCGGGACAACGCCAAGAACA CCCTGTACCTGCAGATGACCAGCCTGCGGAGC GAGGACACCGCCATGTACTACTGCACCCGGCA CGGCGACCACGACGGCTTCGATTACTGGGGCC AGGGCACCACCCTGACCGTGTCCTCTGCCAAA ACAACAGCACCAAGTGTCTATCCACTGGCCCC TGTGTGTGGAGATACAACTGGCTCCTCGGTGA CTCTAGGATGCCTGGTCAAGGGTTATTTCCCTG AGCCAGTGACCTTGACCTGGAACTCTGGATCC CTGTCCAGTGGTGTGCACACCTTCCCAGCTGTC CTGCAGTCTGACCTCTACACCCTCAGCAGCTCA GTGACTGTAACCTCGAGCACCTGGCCCAGCCA GTCCATCACCTGCAATGTGGCCCACCCGGCAA GCAGCACCAAGGTGGACAAGAAAATTGAGCCC AGAGGGCCCACAATCAAGCCCTGTCCTCCATG CAAATGCCCAGCACCTAACCTCTTGGGTGGAC CATCCGTCTTCATCTTCCCTCCAAAGATCAAGG	1198

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		ATGTACTCATGATCTCCCTGAGCCCCATAGTCA CATGTGTGGTGGTGGATGTGAGCGAGGATGAC CCAGATGTCCAGATCAGCTGGTTTGTGAACAA CGTGGAAGTACACACAGCTCAGACACAAACCC ATAGAGAGGATTACAACAGTACTCTCCGGGTG GTCAGTGCCCTCCCCATCCAGCACCAGGACTG GATGAGTGGCAAGGAGTTCAAATGCAAGGTCA ACAACAAAGACCTCCCAGCGCCCATCGAGAGA ACCATCTCAAAACCCAAAGGGTCAGTAAGAGC TCCACAGGTATATGTCTTGCCTCCACCAGAAG AAGAGATGACTAAGAAACAGGTCACTCTGACC TGCATGGTCACAGACTTCATGCCTGAAGACAT TTACGTGGAGTGGACCAACAACGGGAAAACAG AGCTAAACTACAAGAACACTGAACCAGTCCTG GACTCTGATGGTTCTTACTTCATGTACAGCAAG CTGAGAGTGGAAAAGAAGAACTGGGTGGAAA GAAATAGCTACTCCTGTTCAGTGGTCCACGAG GGTCTGCACAATCACCACACGACTAAGAGCTT CTCCCGGACTCCGGGTAAATGA	
SM1B336	pDR000029271	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAGGTGCA GCTGGTGGAAAGCGGCGGAGGACTGGTCAAGC CTGGCGGCAGCCTGAAGCTGAGCTGCGTGGCC TCCGGCTTCAGCTTCAGCAACTACGCCATGAG CTGGGTCCGACAGACCCCCGAGCGGAGACTGG AATGGGTGGCCACCATCAACAGCGGCGGCAGC TTCAGCTTTTTCCCAGACTCCGTGAAGGGCCGG TTCACCATCAGCCGGGACAGCGCCAAGAACAC CCTGTACCTGCAGATGAGCAGCCTGCGGAGCG ACGACACCGCCATGTACTACTGCACCCGGCAC TGGGACCACCCTTGGTTTGCCTACTGGGGCCA GGGCACCCTGGTCACCGTGTCTGCTGCCAAAA CAACAGCACCAAGTGTCTATCCACTGGCCCCT GTGTGTGGAGATACAACTGGCTCCTCGGTGAC TCTAGGATGCCTGGTCAAGGGTTATTTCCCTGA GCCAGTGACCTTGACCTGGAACTCTGGATCCCT GTCCAGTGGTGTGCACACCTTCCCAGCTGTCCT GCAGTCTGACCTCTACACCCTCAGCAGCTCAGT GACTGTAACCTCGAGCACCTGGCCCAGCCAGT CCATCACCTGCAATGTGGCCCACCCGGCAAGC AGCACCAAGGTGGACAAGAAAATTGAGCCCA GAGGGCCCACAATCAAGCCCTGTCCTCCATGC AAATGCCCAGCACCTAACCTCTTGGGTGGACC ATCCGTCTTCATCTTCCCTCCAAAGATCAAGGA TGTACTCATGATCTCCCTGAGCCCCATAGTCAC ATGTGTGGTGGTGGATGTGAGCGAGGATGACC CAGATGTCCAGATCAGCTGGTTTGTGAACAAC GTGGAAGTACACACAGCTCAGACACAAACCCA	1199

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		TAGAGAGGATTACAACAGTACTCTCCGGGTGG TCAGTGCCCTCCCCATCCAGCACCAGGACTGG ATGAGTGGCAAGGAGTTCAAATGCAAGGTCAA CAACAAAGACCTCCCAGCGCCCATCGAGAGAA CCATCTCAAAACCCAAAGGGTCAGTAAGAGCT CCACAGGTATATGTCTTGCCTCCACCAGAAGA AGAGATGACTAAGAAACAGGTCACTCTGACCT GCATGGTCACAGACTTCATGCCTGAAGACATT TACGTGGAGTGGACCAACAACGGGAAAACAG AGCTAAACTACAAGAACACTGAACCAGTCCTG GACTCTGATGGTTCTTACTTCATGTACAGCAAG CTGAGAGTGGAAAAGAAGAACTGGGTGGAAA GAAATAGCTACTCCTGTTCAGTGGTCCACGAG GGTCTGCACAATCACCACACGACTAAGAGCTT CTCCCGGACTCCGGGTAAATGA	
SM1B337	pDR000029271	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAGGTGCA GCTGGTGGAAAGCGGCGGAGGACTGGTCAAGC CTGGCGGCAGCCTGAAGCTGAGCTGCGTGGCC TCCGGCTTCAGCTTCAGCAACTACGCCATGAG CTGGGTCCGACAGACCCCCGAGCGGAGACTGG AATGGGTGGCCACCATCAACAGCGGCGGCAGC TTCAGCTTTTTCCCAGACTCCGTGAAGGGCCGG TTCACCATCAGCCGGGACAGCGCCAAGAACAC CCTGTACCTGCAGATGAGCAGCCTGCGGAGCG ACGACACCGCCATGTACTACTGCACCCGGCAC TGGGACCACCCTTGGTTTGCCTACTGGGGCCA GGGCACCCTGGTCACCGTGTCTGCTGCCAAAA CAACAGCACCAAGTGTCTATCCACTGGCCCCT GTGTGTGGAGATACAACTGGCTCCTCGGTGAC TCTAGGATGCCTGGTCAAGGGTTATTTCCCTGA GCCAGTGACCTTGACCTGGAACTCTGGATCCCT GTCCAGTGGTGTGCACACCTTCCCAGCTGTCCT GCAGTCTGACCTCTACACCCTCAGCAGCTCAGT GACTGTAACCTCGAGCACCTGGCCCAGCCAGT CCATCACCTGCAATGTGGCCCACCCGGCAAGC AGCACCAAGGTGGACAAGAAAATTGAGCCCA GAGGGCCCACAATCAAGCCCTGTCCTCCATGC AAATGCCCAGCACCTAACCTCTTGGGTGGACC ATCCGTCTTCATCTTCCCTCCAAAGATCAAGGA TGTACTCATGATCTCCCTGAGCCCCATAGTCAC ATGTGTGGTGGTGGATGTGAGCGAGGATGACC CAGATGTCCAGATCAGCTGGTTTGTGAACAAC GTGGAAGTACACACAGCTCAGACACAAACCCA TAGAGAGGATTACAACAGTACTCTCCGGGTGG TCAGTGCCCTCCCCATCCAGCACCAGGACTGG ATGAGTGGCAAGGAGTTCAAATGCAAGGTCAA CAACAAAGACCTCCCAGCGCCCATCGAGAGAA	1200

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		CCATCTCAAAACCCAAAGGGTCAGTAAGAGCT CCACAGGTATATGTCTTGCCTCCACCAGAAGA AGAGATGACTAAGAAACAGGTCACTCTGACCT GCATGGTCACAGACTTCATGCCTGAAGACATT TACGTGGAGTGGACCAACAACGGGAAAACAG AGCTAAACTACAAGAACACTGAACCAGTCCTG GACTCTGATGGTTCTTACTTCATGTACAGCAAG CTGAGAGTGGAAAAGAAGAACTGGGTGGAAA GAAATAGCTACTCCTGTTCAGTGGTCCACGAG GGTCTGCACAATCACCACACGACTAAGAGCTT CTCCCGGACTCCGGGTAAATGA	
SM1B338	pDR000029271	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAGGTGCA GCTGGTGGAAAGCGGCGGAGGACTGGTCAAGC CTGGCGGCAGCCTGAAGCTGAGCTGCGTGGCC TCCGGCTTCAGCTTCAGCAACTACGCCATGAG CTGGGTCCGACAGACCCCCGAGCGGAGACTGG AATGGGTGGCCACCATCAACAGCGGCGGCAGC TTCAGCTTTTTCCCAGACTCCGTGAAGGGCCGG TTCACCATCAGCCGGGACAGCGCCAAGAACAC CCTGTACCTGCAGATGAGCAGCCTGCGGAGCG ACGACACCGCCATGTACTACTGCACCCGGCAC TGGGACCACCCTTGGTTTGCCTACTGGGGCCA GGGCACCCTGGTCACCGTGTCTGCTGCCAAAA CAACAGCACCAAGTGTCTATCCACTGGCCCCT GTGTGTGGAGATACAACTGGCTCCTCGGTGAC TCTAGGATGCCTGGTCAAGGGTTATTTCCCTGA GCCAGTGACCTTGACCTGGAACTCTGGATCCCT GTCCAGTGGTGTGCACACCTTCCCAGCTGTCCT GCAGTCTGACCTCTACACCCTCAGCAGCTCAGT GACTGTAACCTCGAGCACCTGGCCCAGCCAGT CCATCACCTGCAATGTGGCCCACCCGGCAAGC AGCACCAAGGTGGACAAGAAAATTGAGCCCA GAGGGCCCACAATCAAGCCCTGTCCTCCATGC AAATGCCCAGCACCTAACCTCTTGGGTGGACC ATCCGTCTTCATCTTCCCTCCAAAGATCAAGGA TGTACTCATGATCTCCCTGAGCCCCATAGTCAC ATGTGTGGTGGTGGATGTGAGCGAGGATGACC CAGATGTCCAGATCAGCTGGTTTGTGAACAAC GTGGAAGTACACACAGCTCAGACACAAACCCA TAGAGAGGATTACAACAGTACTCTCCGGGTGG TCAGTGCCCTCCCCATCCAGCACCAGGACTGG ATGAGTGGCAAGGAGTTCAAATGCAAGGTCAA CAACAAAGACCTCCCAGCGCCCATCGAGAGAA CCATCTCAAAACCCAAAGGGTCAGTAAGAGCT CCACAGGTATATGTCTTGCCTCCACCAGAAGA AGAGATGACTAAGAAACAGGTCACTCTGACCT GCATGGTCACAGACTTCATGCCTGAAGACATT	1201

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		TACGTGGAGTGGACCAACAACGGGAAAACAG AGCTAAACTACAAGAACACTGAACCAGTCCTG GACTCTGATGGTTCTTACTTCATGTACAGCAAG CTGAGAGTGGAAAAGAAGAACTGGGTGGAAA GAAATAGCTACTCCTGTTCAGTGGTCCACGAG GGTCTGCACAATCACCACACGACTAAGAGCTT CTCCCGGACTCCGGGTAAATGA	
SM1B339	pDR000029270	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAGGTGCA GCTGCAGCAGTCTGGCGCTGAACTCGTGCGGC CTGGCGCCAGCGTGAAGCTGAGCTGCACCACC AGCGGCTTCAACATCAAGGACAGCCTGATCTA CTGGGTCAAGCAGCGGCCCGAGCAGGGCCTGG AATGGATCGGCTGGATCGACCCCGAGGACGGC GAGACAAAGTTCGCCCCCAGATTCCAGGACAA GGCCACCATCACCAGCGACACCAGCAGCAACA CCGCCTACCTGCGGCTGAGCAGCCTGACCAGC AAGGACACCGCCATCTACTACTGCACCCGGTC CTTCGGCGTGTGCTGGGGCCAGGGCACCCTGG TCACAGTGTCTGCCGCCAAAACAACAGCACCA AGTGTCTATCCACTGGCCCCTGTGTGTGGAGAT ACAACTGGCTCCTCGGTGACTCTAGGATGCCT GGTCAAGGGTTATTTCCCTGAGCCAGTGACCTT GACCTGGAACTCTGGATCCCTGTCCAGTGGTGT GCACACCTTCCCAGCTGTCCTGCAGTCTGACCT CTACACCCTCAGCAGCTCAGTGACTGTAACCTC GAGCACCTGGCCCAGCCAGTCCATCACCTGCA ATGTGGCCCACCCGGCAAGCAGCACCAAGGTG GACAAGAAAATTGAGCCCAGAGGGCCCACAAT CAAGCCCTGTCCTCCATGCAAATGCCCAGCAC CTAACCTCTTGGGTGGACCATCCGTCTTCATCT TCCCTCCAAAGATCAAGGATGTACTCATGATCT CCCTGAGCCCCATAGTCACATGTGTGGTGGTG GATGTGAGCGAGGATGACCCAGATGTCCAGAT CAGCTGGTTTGTGAACAACGTGGAAGTACACA CAGCTCAGACACAAACCCATAGAGAGGATTAC AACAGTACTCTCCGGGTGGTCAGTGCCCTCCCC ATCCAGCACCAGGACTGGATGAGTGGCAAGGA GTTCAAATGCAAGGTCAACAACAAAGACCTCC CAGCGCCCATCGAGAGAACCATCTCAAAACCC AAAGGGTCAGTAAGAGCTCCACAGGTATATGT CTTGCCTCCACCAGAAGAAGAGATGACTAAGA AACAGGTCACTCTGACCTGCATGGTCACAGAC TTCATGCCTGAAGACATTTACGTGGAGTGGAC CAACAACGGGAAAACAGAGCTAAACTACAAG AACACTGAACCAGTCCTGGACTCTGATGGTTCT TACTTCATGTACAGCAAGCTGAGAGTGGAAAA GAAGAACTGGGTGGAAAGAAATAGCTACTCCT	1202

mAB/Fab name	Construct ID	Heavy Chain Primary Transcript	SEQ ID NO:
		GTTCAGTGGTCCACGAGGGTCTGCACAATCAC CACACGACTAAGAGCTTCTCCCGGACTCCGGG TAAATGA	
SM1B340	pDR000029269	ATGGCTTGGGTGTGGACCTTGCTATTCCTGATG GCAGCTGCCCAAAGTATACAGGCCGAGGTGCA GCTGCAGCAGTCTGGCGCTGAACTCGTGCGGC CTGGCGCCAGCGTGAAGCTGAGCTGCACCACC AGCGGCTTCAACATCAAGGACAGCCTGATCTA CTGGGTCAAGCAGCGGCCCGAGCAGGGCCTGG AATGGATCGGCTGGATCGACCCCGAGGACGGC GAGACAAAGTTCGCCCCCAGATTCCAGGACAA GGCCACCATCACCAGCGACACCAGCAGCAACA CCGCCTACCTGCGGCTGAGCAGCCTGACCAGC GAGGACACCGCCATCTACTACTGCACCCGGTC CTTCGGCGTGTGCTGGGGCCAGGGCACCCTGG TCACAGTGTCTGCCGCCAAAACAACAGCACCA AGTGTCTATCCACTGGCCCCTGTGTGTGGAGAT ACAACTGGCTCCTCGGTGACTCTAGGATGCCT GGTCAAGGGTTATTTCCCTGAGCCAGTGACCTT GACCTGGAACTCTGGATCCCTGTCCAGTGGTGT GCACACCTTCCCAGCTGTCCTGCAGTCTGACCT CTACACCCTCAGCAGCTCAGTGACTGTAACCTC GAGCACCTGGCCCAGCCAGTCCATCACCTGCA ATGTGGCCCACCCGGCAAGCAGCACCAAGGTG GACAAGAAAATTGAGCCCAGAGGGCCCACAAT CAAGCCCTGTCCTCCATGCAAATGCCCAGCAC CTAACCTCTTGGGTGGACCATCCGTCTTCATCT TCCCTCCAAAGATCAAGGATGTACTCATGATCT CCCTGAGCCCCATAGTCACATGTGTGGTGGTG GATGTGAGCGAGGATGACCCAGATGTCCAGAT CAGCTGGTTTGTGAACAACGTGGAAGTACACA CAGCTCAGACACAAACCCATAGAGAGGATTAC AACAGTACTCTCCGGGTGGTCAGTGCCCTCCCC ATCCAGCACCAGGACTGGATGAGTGGCAAGGA GTTCAAATGCAAGGTCAACAACAAAGACCTCC CAGCGCCCATCGAGAGAACCATCTCAAAACCC AAAGGGTCAGTAAGAGCTCCACAGGTATATGT CTTGCCTCCACCAGAAGAAGAGATGACTAAGA AACAGGTCACTCTGACCTGCATGGTCACAGAC TTCATGCCTGAAGACATTTACGTGGAGTGGAC CAACAACGGGAAAACAGAGCTAAACTACAAG AACACTGAACCAGTCCTGGACTCTGATGGTTCT TACTTCATGTACAGCAAGCTGAGAGTGGAAAA GAAGAACTGGGTGGAAAGAAATAGCTACTCCT GTTCAGTGGTCCACGAGGGTCTGCACAATCAC CACACGACTAAGAGCTTCTCCCGGACTCCGGG TAAATGA	1203

Table 48. HlgA/LukE Antibody Light Chain CDSs

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
SM1B302	pDR000027850	GACATCCAGATGACCCAGAGCCCTAGCAGCCT GAGCGCCTCTCTGGGCGAGAGAGTGTCCCTGA CCTGCAGAGCCAGCCAGGACATCGGCAGCTCC CTGAACTGGCTGCAGCAGGAACCCGACGGCAC CATCAAGCGGCTGATCTACGCCACCAGCAGCC TGGATAGCGGCGTGCCCAAGAGATTCAGCGGC AGCAGAAGCGGCAGCGACTACAGCCTGACCAT CTCCAGCCTGGAATCCGAGGACTTCGTGGACT ACTACTGCCTGCAGTACGCCAGCAGCCCCTGG ACCTTTGGCGGAGGCACCAAGCTGGAAATCAA GCGGGCTGATGCTGCACCGACTGTGTCCATCTT CCCACCATCCAGTGAGCAGTTAACATCTGGAG GTGCCTCAGTCGTGTGCTTCTTGAACAACTTCT ACCCCAAAGACATCAATGTCAAGTGGAAGATT GATGGCAGTGAACGACAAAATGGCGTCCTGAA CAGTTGGACTGATCAGGACAGCAAAGACAGCA CCTACAGCATGAGCAGCACCCTCACGTTGACC AAGGACGAGTATGAACGACATAACAGCTATAC CTGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTGT	1204
SM1B303	pDR000029323	GACATCCAGATGACCCAGACCACCAGCAGCCT GAGCGCCAGCCTGGGCGACAGAGTGACCATCA GCTGCTGGGCCAGCCAGGACATCAGAAGCTAC CTGAACTGGTATCAGCAGAAACCCGACGGCAC CGTGAAGCTGCTGATCTACTACACCAGCCGGC TGCACAGCGGCGTGCCCAGCAGATTTTCTGGC AGCGGCAGCGGCACCGACTTCAGCCTGACCAT CTCCAACCTGGAACAGGAAGATATCGCTACCT ACTTCTGTCAGCAGGGCAACACCCTGCCCTAC ACCTTCGGCGGAGGCACCAAGCTGGAAATCAA GCGGGCTGATGCTGCACCGACTGTGTCCATCTT CCCACCATCCAGTGAGCAGTTAACATCTGGAG GTGCCTCAGTCGTGTGCTTCTTGAACAACTTCT ACCCCAAAGACATCAATGTCAAGTGGAAGATT GATGGCAGTGAACGACAAAATGGCGTCCTGAA CAGTTGGACTGATCAGGACAGCAAAGACAGCA CCTACAGCATGAGCAGCACCCTCACGTTGACC AAGGACGAGTATGAACGACATAACAGCTATAC CTGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTGT	1205
SM1B304	pDR000029322	GACATCCAGATGACCCAGAGCCCCAGCAGCCT GAGCGCCAGCCTGGGCGAGAGAGTGTCCCTGA CCTGCCGGGCCAGCCAGGAAATCAGCGGCTAC CTGAGCTGGCTGCAGCAGAAGCCCGACGGCAC CATCAAGCGGCTGATCTACGCCGCCAGCACCC TGGACAGCGGCGTGCCCAAGAGATTCAGCGGC	1206

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		AGCCGCAGCGGCAGCGACTACAGCCTGACCAT CAGCAGCCTGGAAAGCGAGGACTTCGCCGACT ACTACTGCCTGCAGTACGCCAGCTACCCCCGG ACCTTCGGCGGAGGCACCAAGCTGGAAATCAA GCGGGCTGATGCTGCACCGACTGTGTCCATCTT CCCACCATCCAGTGAGCAGTTAACATCTGGAG GTGCCTCAGTCGTGTGCTTCTTGAACAACTTCT ACCCCAAAGACATCAATGTCAAGTGGAAGATT GATGGCAGTGAACGACAAAATGGCGTCCTGAA CAGTTGGACTGATCAGGACAGCAAAGACAGCA CCTACAGCATGAGCAGCACCCTCACGTTGACC AAGGACGAGTATGAACGACATAACAGCTATAC CTGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTGT	
SM1B305	pDR000029321	GACGTGCTGATGACCCAGACCCCCCTGAGCCT GCCCGTGTCTCTGGGCGATCAGGCCAGCATCA GCTGCCGGTCCAGCCAGATCATCGTGCACAGC AACGGCAACACCTACCTGGACTGGTATCTGCA GAAGCCCGGCCAGAGCCCCAAGCTGCTGATCT ACAAGATCAGCAACCGGTTCAGCGGCGTGCCC GACAGATTCAGCGGCAGCGGCTCCGGCACCGA CTTCACCCTGAAGATCAGCCGGGTGGAAGCCG AGGACCTGGGCGTGTACTACTGTTTTCAGGGC AGCCACGTGCCCTGGACCTTCGGCGGAGGCAC CAAGCTGGAAATCAAGCGGGCTGATGCTGCAC CGACTGTGTCCATCTTCCCACCATCCAGTGAGC AGTTAACATCTGGAGGTGCCTCAGTCGTGTGCT TCTTGAACAACTTCTACCCCAAAGACATCAAT GTCAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAGG ACAGCAAAGACAGCACCTACAGCATGAGCAGC ACCCTCACGTTGACCAAGGACGAGTATGAACG ACATAACAGCTATACCTGTGAGGCCACTCACA AGACATCAACTTCACCCATTGTCAAGAGCTTC AACAGGAATGAGTGT	1207
SM1B306	pDR000029320	GACGTGGTGGTCACCCAGACCCCCCTGAGCCT GCCCGTGTCCTTCGGCGACCAGGTGTCCATCA GCTGCAGAAGCAGCCAGAGCCTGGCCAACAGC TACGGCAACACCTACCTGAGCTGGTATCTGCA CAAGCCCGGCCAGAGCCCCCAGCTGCTGATCT ACGGCATCAGCAACCGGTTCAGCGGCGTGCCC GACAGATTCAGCGGCAGCGGCTCCGGCACCGA CTTCACCCTGAAGATCAGCACCATCAAGCCCG AGGGCCTGGGCATGTACTACTGTCTGCAGGGC ACCCACCAGCCCCCCACCTTTGGCGCTGGCAC CAAGCTGGAACTGAAGCGGGCTGATGCTGCAC CGACTGTGTCCATCTTCCCACCATCCAGTGAGC AGTTAACATCTGGAGGTGCCTCAGTCGTGTGCT	1208

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		TCTTGAACAACTTCTACCCCAAAGACATCAAT GTCAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAGG ACAGCAAAGACAGCACCTACAGCATGAGCAGC ACCCTCACGTTGACCAAGGACGAGTATGAACG ACATAACAGCTATACCTGTGAGGCCACTCACA AGACATCAACTTCACCCATTGTCAAGAGCTTC AACAGGAATGAGTGT	
SM1B307	pDR000029319	GACATCGTGCTGACCCAGAGCCCTGCCAGCCT GGCCGTGTCTCTGGGCCAGAGAGCCACCATCA GCTGCCGGGCCAGCGAGAGCGTGGACAGCTAC GGCAACAGCTTCATGCACTGGTATCAGCAGAA GCCCGGCCAGCCCCCCAAGCTGCTGATCTACC GGGCCAGCAACCTGGAAAGCGGCATCCCCGCC AGATTCAGCGGCAGCGGCAGCCGGACCGACTT CACCCTGACCATCAACCCCGTGGAAGCCGACG ACGTGGCCACCTACTACTGCCAGCAGAGCAAC GAGGACCCCCCCTGGACCTTCGGCGGAGGCAC CAAGCTGGAAATCAAGCGGGCTGATGCTGCAC CGACTGTGTCCATCTTCCCACCATCCAGTGAGC AGTTAACATCTGGAGGTGCCTCAGTCGTGTGCT TCTTGAACAACTTCTACCCCAAAGACATCAAT GTCAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAGG ACAGCAAAGACAGCACCTACAGCATGAGCAGC ACCCTCACGTTGACCAAGGACGAGTATGAACG ACATAACAGCTATACCTGTGAGGCCACTCACA AGACATCAACTTCACCCATTGTCAAGAGCTTC AACAGGAATGAGTGT	1209
SM1B308	pDR000029318	GACATCGTGATGAGCCAGAGCCCCAGCAGCCT GGCCGTGTCTGCCGGCGAGAAAGTGACCATGA GCTGCAAGAGCAGCCAGAGCCTGCTGAACAGC CGGACCCGGAAGAACTACCTGGCCTGGTATCA GCAGAAGCCCGGCCAGTCCCCCAAGCTGCTGA TCTACTGGGCCAGCACCCGCGAGAGCGGCGTG CCCGATAGATTCACAGGCAGCGGCAGCGGCAC CGACTTCACCCTGACCATCAGCAGCGTGCAGG CCGAGGATCTGGCCGTGTACTACTGCAAGCAG AGCTACAACCTGTGGACCTTCGGCGGAGGCAC CAAGCTGGAAATCAAGCGGGCTGATGCTGCAC CGACTGTGTCCATCTTCCCACCATCCAGTGAGC AGTTAACATCTGGAGGTGCCTCAGTCGTGTGCT TCTTGAACAACTTCTACCCCAAAGACATCAAT GTCAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAGG ACAGCAAAGACAGCACCTACAGCATGAGCAGC ACCCTCACGTTGACCAAGGACGAGTATGAACG ACATAACAGCTATACCTGTGAGGCCACTCACA	1210

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		AGACATCAACTTCACCCATTGTCAAGAGCTTC AACAGGAATGAGTGT	
SM1B309	pDR000029317	GACGTGGTCATGACCCAGACCCCCCTGAGCCT GCCCGTGTCTCTGGGCGATCAGGCCAGCATCA GCTGCAGAAGCAGCCAGAGCCTGCTGCACAGC AACGGCAAGACCTACCTGCACTGGTATCTGCA GAAGCCCGGCCAGAGCCCCAAGCTGCTGATCT ACAAGGTGTCCAACCGGTTCAGCGGCGTGCCC GACAGATTCAGCGGCAGCGGCTCCGGCACCGA CTTCACCCTGAAGATCAGCCGGGTGGAAGCCG AGGACCTGGGCGTGTACTTCTGCAGCCAGTCC ACCCACGTGCCCCTGACCTTCGGAGCCGGCAC CAAGCTGGAACTGAAGCGGGCTGATGCTGCAC CGACTGTGTCCATCTTCCCACCATCCAGTGAGC AGTTAACATCTGGAGGTGCCTCAGTCGTGTGCT TCTTGAACAACTTCTACCCCAAAGACATCAAT GTCAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAGG ACAGCAAAGACAGCACCTACAGCATGAGCAGC ACCCTCACGTTGACCAAGGACGAGTATGAACG ACATAACAGCTATACCTGTGAGGCCACTCACA AGACATCAACTTCACCCATTGTCAAGAGCTTC AACAGGAATGAGTGT	1211
SM1B310	pDR000029316	GACATCGTGATGACCCAGAGCCACAAGTTCAT GAGCACCAGCGTGGGCGACCGGGTGTCCATCA CATGCAAGGCCAGCCAGGATGTGTCTGCCGCC GTGGCCTGGTATCAGCAGAAGCCCGGCCAGAG CCCCAAGCTGCTGATCTACTGGGCCAGCACCA GACACACCGGCGTGCCCGACAGATTCACAGGC AGCGGCAGCGGCACCGACTACACCCTGACCAT CAGCAGCGTGCAGGCCGAGGACCTGGCCCTGT ACTACTGCCAGCAGCACTACAGCACCCCCGGC ACCTTCGGCGGAGGCACCAAGCTGGAAATCAA GCGGGCTGATGCTGCACCGACTGTGTCCATCTT CCCACCATCCAGTGAGCAGTTAACATCTGGAG GTGCCTCAGTCGTGTGCTTCTTGAACAACTTCT ACCCCAAAGACATCAATGTCAAGTGGAAGATT GATGGCAGTGAACGACAAAATGGCGTCCTGAA CAGTTGGACTGATCAGGACAGCAAAGACAGCA CCTACAGCATGAGCAGCACCCTCACGTTGACC AAGGACGAGTATGAACGACATAACAGCTATAC CTGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTGT	1212
SM1B311	pDR000029315	GACGTGCTGATGACCCAGACCCCCCTGAGCCT GCCCGTGTCTCTGGGCGATCAGGCCAGCATCA GCTGCCGGTCCAGCCAGACCATCGTGCACAGC AGCGGCAACACCTACCTGGAATGGTATCTGCA GCGGCCTGGCCAGAGCCCCAAGCTGCTGATCT	1213

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		ACAAGGTGTCCAACCGGTTCAGCGGCGTGCCC GACAGATTCAGCGGCAGCGGCTCCGGCACCGA CTTCACCCTGAAGATCAGCCGGGTGGAAGCCG AGGACCTGGGCGTGTACTACTGTTTTCAGGGC AGCCACGTGCCCTACACCTTCGGCGGAGGCAC CAAGCTGGAAATCAAGCGGGCTGATGCTGCAC CGACTGTGTCCATCTTCCCACCATCCAGTGAGC AGTTAACATCTGGAGGTGCCTCAGTCGTGTGCT TCTTGAACAACTTCTACCCCAAAGACATCAAT GTCAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAGG ACAGCAAAGACAGCACCTACAGCATGAGCAGC ACCCTCACGTTGACCAAGGACGAGTATGAACG ACATAACAGCTATACCTGTGAGGCCACTCACA AGACATCAACTTCACCCATTGTCAAGAGCTTC AACAGGAATGAGTGT	
SM1B312	pDR000029297	GACATCCAGATGACCCAGACCACCAGCAGCCT GAGCGCCAGCCTGGGCGACAGAGTGACCATCA GCTGTAGCGCCTCCCAGGGCATCAGCAACTAC CTGAACTGGTATCAGCAGAAACCCGACGGCAC CGTGAAGCTGCTGATCTACTACACCAGCTCCCT GCACAGCGGCGTGCCCAGCAGATTTTCTGGCA GCGGCAGCGGCACCGACTACAGCCTGACCATC TCCAACCTGGAACCCGAGGATATCGCCACCTA CTACTGCCAGCAGTACAGCAAGCTGCCCTTCA CCTTCGGCTCCGGCACCAAGCTGGAAATCAAG CGGGCTGATGCTGCACCGACTGTGTCCATCTTC CCACCATCCAGTGAGCAGTTAACATCTGGAGG TGCCTCAGTCGTGTGCTTCTTGAACAACTTCTA CCCCAAAGACATCAATGTCAAGTGGAAGATTG ATGGCAGTGAACGACAAAATGGCGTCCTGAAC AGTTGGACTGATCAGGACAGCAAAGACAGCAC CTACAGCATGAGCAGCACCCTCACGTTGACCA AGGACGAGTATGAACGACATAACAGCTATACC TGTGAGGCCACTCACAAGACATCAACTTCACC CATTGTCAAGAGCTTCAACAGGAATGAGTGT	1214
SM1B313	pDR000029314	GACATCGTGATGAGCCAGAGCCCCAGCAGCCT GGCCGTGTCCGTGGGCGAGAAAGTGACCATGA GCTGCAAGAGCAGCCAGAGCCTGCTGTACAGC TCCAACCAGAAGAACTACCTGGCCTGGTATCA GCAGAAGCCCGGCCAGTCCCCCAAGCTGCTGA TCTACTGGGCCAGCACCCGCGAGAGCGGCGTG CCAGATAGACTGACAGGCAGCGGCAGCGGCAC CGACTTCACCCTGACCATCAGCAGCGTGAAGG CCGAGGATCTGGCCGTGTACTACTGCCAGCAG TACTACAGCTACCCCTACACCTTCGGCGGAGG CACCAAGCTGGAAATCAAGCGGGCTGATGCTG CACCGACTGTGTCCATCTTCCCACCATCCAGTG	1215

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		AGCAGTTAACATCTGGAGGTGCCTCAGTCGTG TGCTTCTTGAACAACTTCTACCCCAAAGACATC AATGTCAAGTGGAAGATTGATGGCAGTGAACG ACAAAATGGCGTCCTGAACAGTTGGACTGATC AGGACAGCAAAGACAGCACCTACAGCATGAG CAGCACCCTCACGTTGACCAAGGACGAGTATG AACGACATAACAGCTATACCTGTGAGGCCACT CACAAGACATCAACTTCACCCATTGTCAAGAG CTTCAACAGGAATGAGTGT	
SM1B314	pDR000007289	GACATTCAGATGACTCAGTCTCCAGCCTCCCTA TCTGTATCTGTGGGAGAAACTGTCACCATCAC ATGTCGAGCAAGTGAAAATATTTACAGTAATT TAGCATGGTATCAGCAGAAACAGGGAAAATCT CCTCAGCTCCTGGTCTATGCTGCAACAAACTTA GCAGATGGTGTGCCATCAAGGTTCAGTGGCAG TGGATCAGGCACACAGTATTCCCTCAAGATCA ACAGCCTGCAGTCTGAAGATTTTGGGAGTTATT ACTGTCAACATTTTTGGGGTACTCCGTACACGT TCGGAGGGGGGACCAAGCTGGAAATAAAACG GGCTGATGCTGCACCGACTGTGTCCATCTTCCC ACCATCCAGTGAGCAGTTAACATCTGGAGGTG CCTCAGTCGTGTGCTTCTTGAACAACTTCTACC CCAAAGACATCAATGTCAAGTGGAAGATTGAT GGCAGTGAACGACAAAATGGCGTCCTGAACAG TTGGACTGATCAGGACAGCAAAGACAGCACCT ACAGCATGAGCAGCACCCTCACGTTGACCAAG GACGAGTATGAACGACATAACAGCTATACCTG TGAGGCCACTCACAAGACATCAACTTCACCCA TTGTCAAGAGCTTCAACAGGAATGAGTGT	1216
SM1B315	pDR000026238	GACATCAAGATGACCCAGAGCCCCAGCTCTAT GTACGCCAGCCTGGGCGAGCGCGTGACCATCA CATGCAAGGCCAGCCAGGACATCAACAGCTAC CTGAGCTGGTTCCAGCAGAAGCCCGGCAAGAG CCCCAAGACCCTGATCTACCGGGCCAACAGAC TGGTGGACGGCGTGCCAAGCAGATTCAGCGGC AGCGGCTCTGGCCAGGACTACAGCCTGACCAT CAGCAGCCTGGAATACGAGGACATGGGCATCT ACTACTGCCTGCAGTACGACGAGTTCCCCTAC ACCTTCGGCGGAGGCACCAAGCTGGAAATCAA GCGGGCTGATGCTGCACCGACTGTGTCCATCTT CCCACCATCCAGTGAGCAGTTAACATCTGGAG GTGCCTCAGTCGTGTGCTTCTTGAACAACTTCT ACCCCAAAGACATCAATGTCAAGTGGAAGATT GATGGCAGTGAACGACAAAATGGCGTCCTGAA CAGTTGGACTGATCAGGACAGCAAAGACAGCA CCTACAGCATGAGCAGCACCCTCACGTTGACC AAGGACGAGTATGAACGACATAACAGCTATAC CTGTGAGGCCACTCACAAGACATCAACTTCAC	1217

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		CCATTGTCAAGAGCTTCAACAGGAATGAGTGT	
SM1B316	pDR000029313	GACATCCAGATGACCCAGACCACCAGCAGCCT GAGCGCCAGCCTGGGCGACAGAGTGACCATCA GCTGTAGCGCCTCCCAGGGCATCAGCAACTAC CTGAACTGGTATCAGCAGAAACCCGACGGCAC CGTGAAGCTGCTGATCCACTACACCAGCTCCCT GCACAGCGGCGTGCCCAGCAGATTTTCTGGCA GCGGCAGCGGCACCGACTACAGCCTGACCATC TCCAACCTGGAACCCGAGGATATCGCCACCTA CTACTGCCAGCAGTACAGCAAGCTGCCCTGGA CCTTCGGCGGAGGCACCAAGCTGGAAATCAAG CGGGCTGATGCTGCACCGACTGTGTCCATCTTC CCACCATCCAGTGAGCAGTTAACATCTGGAGG TGCCTCAGTCGTGTGCTTCTTGAACAACTTCTA CCCCAAAGACATCAATGTCAAGTGGAAGATTG ATGGCAGTGAACGACAAAATGGCGTCCTGAAC AGTTGGACTGATCAGGACAGCAAAGACAGCAC CTACAGCATGAGCAGCACCCTCACGTTGACCA AGGACGAGTATGAACGACATAACAGCTATACC TGTGAGGCCACTCACAAGACATCAACTTCACC CATTGTCAAGAGCTTCAACAGGAATGAGTGT	1218
SM1B317	pDR000029312	GACGTGCTGATGACCCAGACCCCCCTGAGCCT GCCCGTGTCTCTGGGCGATCAGGCCAGCATCA GCTGCCGGTCCAGCCAGACCATCGTGTACAGC GACGGCAACACCTACCTGGAATGGTATCTGCA GAAGCCCGGCCAGAGCCCCAAGCTGCTGATCT ACAAGGTGTCCAACCGGTTCAGCGGCGTGCCC GACAGAGTGTCTGGCAGCGGCAGCGGCACCGA CTTCACCCTGAAGATCAGCCGGGTGGAAGCCG AGGACCTGGGCGTGTACTACTGTTTTCAGGGC AGCCACGTGCCCTACACCTTCGGCGGAGGCAC CAAGCTGGAAATCAAGCGGGCTGATGCTGCAC CGACTGTGTCCATCTTCCCACCATCCAGTGAGC AGTTAACATCTGGAGGTGCCTCAGTCGTGTGCT TCTTGAACAACTTCTACCCCAAAGACATCAAT GTCAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAGG ACAGCAAAGACAGCACCTACAGCATGAGCAGC ACCCTCACGTTGACCAAGGACGAGTATGAACG ACATAACAGCTATACCTGTGAGGCCACTCACA AGACATCAACTTCACCCATTGTCAAGAGCTTC AACAGGAATGAGTGT	1219
SM1B318	pDR000029312	GACGTGCTGATGACCCAGACCCCCCTGAGCCT GCCCGTGTCTCTGGGCGATCAGGCCAGCATCA GCTGCCGGTCCAGCCAGACCATCGTGTACAGC GACGGCAACACCTACCTGGAATGGTATCTGCA GAAGCCCGGCCAGAGCCCCAAGCTGCTGATCT ACAAGGTGTCCAACCGGTTCAGCGGCGTGCCC	1220

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		GACAGAGTGTCTGGCAGCGGCAGCGGCACCGA CTTCACCCTGAAGATCAGCCGGGTGGAAGCCG AGGACCTGGGCGTGTACTACTGTTTTCAGGGC AGCCACGTGCCCTACACCTTCGGCGGAGGCAC CAAGCTGGAAATCAAGCGGGCTGATGCTGCAC CGACTGTGTCCATCTTCCCACCATCCAGTGAGC AGTTAACATCTGGAGGTGCCTCAGTCGTGTGCT TCTTGAACAACTTCTACCCCAAAGACATCAAT GTCAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAGG ACAGCAAAGACAGCACCTACAGCATGAGCAGC ACCCTCACGTTGACCAAGGACGAGTATGAACG ACATAACAGCTATACCTGTGAGGCCACTCACA AGACATCAACTTCACCCATTGTCAAGAGCTTC AACAGGAATGAGTGT	
SM1B319	pDR000029311	GACATCGTGATGACCCAGGCCGCTCCCAGCGT GCCAGTGACACCTGGCGAGAGCGTGTCCATCA GCTGCAGAAGCAGCAAGAGCCTGCTGCACAGC AACGGCAATACCTACCTGTACTGGTTCCTGCA GCGGCCTGGCCAGAGCCCCCAGCTGCTGATCT ACCGGATGAGCAACCTGGCCAGCGGCGTGCCC GACAGATTTTCTGGCAGCGGCAGCGGCACCGC CTTCACCCTGCGGATCAGCAGAGTGGAAGCCG AGGACGTGGGCGTGTACTACTGCATGCAGCAC CTGGAATACCCCTTCACCTTCGGCTCCGGCACC AAGCTGGAAATCAAGCGGGCTGATGCTGCACC GACTGTGTCCATCTTCCCACCATCCAGTGAGCA GTTAACATCTGGAGGTGCCTCAGTCGTGTGCTT CTTGAACAACTTCTACCCCAAAGACATCAATG TCAAGTGGAAGATTGATGGCAGTGAACGACAA AATGGCGTCCTGAACAGTTGGACTGATCAGGA CAGCAAAGACAGCACCTACAGCATGAGCAGCA CCCTCACGTTGACCAAGGACGAGTATGAACGA CATAACAGCTATACCTGTGAGGCCACTCACAA GACATCAACTTCACCCATTGTCAAGAGCTTCA ACAGGAATGAGTGT	1221
SM1B320	pDR000007336	GATATCCAGATGACACAGACTACATCCTCCCT GTCTGCCTCTCTGGGAGACAGAGTCACCATCA GTTGCAGTGCAAGTCAGGGCATTAGCAATTAT TTAAACTGGTATCAGCAGAAACCAGATGGAAC TGTTAAACTCCTGATCTATTACACATCAAGTTT ACACTCAGGAGTCCCATCAAGGTTCAGTGGCA GTGGGTCTGGGACAGATTATTCTCTCACCATCA GCAACCTGGAACCTGAAGATATTGCCACTTAC TATTGTCAGCAGTATAGTAAGCTTCCGTACACG TTCGGAGGGGGGACCAAGCTGGAAATAAAAC GGGCTGATGCTGCACCGACTGTGTCCATCTTCC CACCATCCAGTGAGCAGTTAACATCTGGAGGT	1222

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		GCCTCAGTCGTGTGCTTCTTGAACAACTTCTAC CCCAAAGACATCAATGTCAAGTGGAAGATTGA TGGCAGTGAACGACAAAATGGCGTCCTGAACA GTTGGACTGATCAGGACAGCAAAGACAGCACC TACAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATACCT GTGAGGCCACTCACAAGACATCAACTTCACCC ATTGTCAAGAGCTTCAACAGGAATGAGTGT	
SM1B321	pDR000027048	GACATCCAGATGACCCAGAGCCCCGCCAGCCT GAGCGCCTCTGTGGGCGAGACAGTGACCATCA TCTGCCGGGCCAGCGAGAACATCTACAGCTAC CTGGCCTGGTATCAGCAGAAGCAGGGCAAGAG CCCCCAGCTGCTGGTGTACAACGCCAAGACCC TGGTGGAAGGCGTGCCCAGCAGATTCAGCGGC AGCGGCTCCGGCACCCAGTTCAGCCTGAAGAT CAACAGCCTGCAGCCCGAGGACTTCGGCAGCT ACTACTGCCAGCACCACTACGGCAGCCCCTAC ACCTTCGGCGGAGGCACCAAGCTGGAAATCAA GCGGGCTGATGCTGCACCGACTGTGTCCATCTT CCCACCATCCAGTGAGCAGTTAACATCTGGAG GTGCCTCAGTCGTGTGCTTCTTGAACAACTTCT ACCCCAAAGACATCAATGTCAAGTGGAAGATT GATGGCAGTGAACGACAAAATGGCGTCCTGAA CAGTTGGACTGATCAGGACAGCAAAGACAGCA CCTACAGCATGAGCAGCACCCTCACGTTGACC AAGGACGAGTATGAACGACATAACAGCTATAC CTGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTGT	1223
SM1B322	pDR000007338	GACATTGTGATGACCCAGTCTCACAAATTCAT GTCCACATCAGTAGGAGACAGGGTCAGCATCA CCTGCAAGGCCAGTCAGGATGTGAGTACTGCT GTAGCCTGGTATCAACAGAAACCAGGACAATC TCCTAAACTACTGATTTACTCGGCATCCTACCG GTACACTGGAGTCCCTGATCGCTTCACTGGCA GTGGATCTGGGACGGATTTCACTTTCACCATCA GCAGTGTGCAGGCTGAAGACCTGGCAGTTTAT TACTGTCAGCAACATTATAGTACTCCGTGGAC GTTCGGTGGAGGCACCAAGCTGGAAATCAAAC GGGCTGATGCTGCACCGACTGTGTCCATCTTCC CACCATCCAGTGAGCAGTTAACATCTGGAGGT GCCTCAGTCGTGTGCTTCTTGAACAACTTCTAC CCCAAAGACATCAATGTCAAGTGGAAGATTGA TGGCAGTGAACGACAAAATGGCGTCCTGAACA GTTGGACTGATCAGGACAGCAAAGACAGCACC TACAGCATGAGCAGCACCCTCACGTTGACCAA GGACGAGTATGAACGACATAACAGCTATACCT GTGAGGCCACTCACAAGACATCAACTTCACCC ATTGTCAAGAGCTTCAACAGGAATGAGTGT	1224

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
SM1B323	pDR000029310	GAGACAACCGTGACCCAGAGCCCCGCCAGCCT GAGCATGGCCATCGGCGAGAAAGTGACCATCC GGTGCATCACCAGCACCGACATCGACGACGAC ATGAACTGGTATCAGCAGAAGCCCGGCGAGCC CCCCAAGCTGCTGATCAGCGAGGGCAACACCC TGCGGCCTGGCGTGCCCAGCAGATTCAGCAGC AGCGGCTACGGCACCGACTTCGTGTTCACCAT CGAGAACATGCTGAGCGAGGACGTGGCCGACT ACTACTGCCTGCAGAGCGACAACCTGCCCTAC ACCTTCGGCGGAGGCACCAAGCTGGAAATCAA GCGGGCTGATGCTGCACCGACTGTGTCCATCTT CCCACCATCCAGTGAGCAGTTAACATCTGGAG GTGCCTCAGTCGTGTGCTTCTTGAACAACTTCT ACCCCAAAGACATCAATGTCAAGTGGAAGATT GATGGCAGTGAACGACAAAATGGCGTCCTGAA CAGTTGGACTGATCAGGACAGCAAAGACAGCA CCTACAGCATGAGCAGCACCCTCACGTTGACC AAGGACGAGTATGAACGACATAACAGCTATAC CTGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTGT	1225
SM1B324	pDR000029309	GACATCGTGATGACCCAGAGCCCCAGCAGCCT GTCCGTGTCTGCCGGCGAGAAAGTGACCATGA GCTGCAAGAGCAGCCAGAGCCTGCTGAACAGC GGCAACCAGAAGAACTACCTGGCCTGGTATCA GCAGAAGCCCGGCCAGCCCCCCAAGCTGCTGA TCTACGGCGCCAGCACCAGAGAAAGCGGCGTG CCCGACAGATTCACCGGCAGCGGCTCCGGCAC CGACTTCACCCTGACCATCAGCAGCGTGCAGG CCGAGGACCTGGCCGTGTACTACTGCCAGAAC GACCACAGCTACCCCCCCACCTTCGGCGGAGG CACCAAGCTGGAAATCAAGCGGGCTGATGCTG CACCGACTGTGTCCATCTTCCCACCATCCAGTG AGCAGTTAACATCTGGAGGTGCCTCAGTCGTG TGCTTCTTGAACAACTTCTACCCCAAAGACATC AATGTCAAGTGGAAGATTGATGGCAGTGAACG ACAAAATGGCGTCCTGAACAGTTGGACTGATC AGGACAGCAAAGACAGCACCTACAGCATGAG CAGCACCCTCACGTTGACCAAGGACGAGTATG AACGACATAACAGCTATACCTGTGAGGCCACT CACAAGACATCAACTTCACCCATTGTCAAGAG CTTCAACAGGAATGAGTGT	1226
SM1B325	pDR000029308	GACATCCAGATGACCCAGAGCCCCAGCAGCCT GAGCGCCAGCCTGGGCGAGAGAGTGTCCCTGA CCTGCCGGGCCAGCCAGGACATCGGCAACAGC CTGAACTGGCTGCAGCAGAAGCCCGACGGCAC CATCAAGCGGCTGATCTACGCCACCAGCAACC TGGACAGCGGCGTGCCCAAGCGGTTCAGCGGC AGCAGATCCGGCAGCGACTACAGCCTGACCAT	1227

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		CAGCAGCCTGGAAAGCGAGGACTTCGTGAACT ACTACTGCCTGCAGTTCGCCAGCAGCCCCCTG ACCTTCGGCACCGGCACCAAGCTGGAAATCAA GCGGGCTGATGCTGCACCGACTGTGTCCATCTT CCCACCATCCAGTGAGCAGTTAACATCTGGAG GTGCCTCAGTCGTGTGCTTCTTGAACAACTTCT ACCCCAAAGACATCAATGTCAAGTGGAAGATT GATGGCAGTGAACGACAAAATGGCGTCCTGAA CAGTTGGACTGATCAGGACAGCAAAGACAGCA CCTACAGCATGAGCAGCACCCTCACGTTGACC AAGGACGAGTATGAACGACATAACAGCTATAC CTGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTGT	
SM1B326	pDR000007289	GACATTCAGATGACTCAGTCTCCAGCCTCCCTA TCTGTATCTGTGGGAGAAACTGTCACCATCAC ATGTCGAGCAAGTGAAAATATTTACAGTAATT TAGCATGGTATCAGCAGAAACAGGGAAAATCT CCTCAGCTCCTGGTCTATGCTGCAACAAACTTA GCAGATGGTGTGCCATCAAGGTTCAGTGGCAG TGGATCAGGCACACAGTATTCCCTCAAGATCA ACAGCCTGCAGTCTGAAGATTTTGGGAGTTATT ACTGTCAACATTTTTGGGGTACTCCGTACACGT TCGGAGGGGGGACCAAGCTGGAAATAAAACG GGCTGATGCTGCACCGACTGTGTCCATCTTCCC ACCATCCAGTGAGCAGTTAACATCTGGAGGTG CCTCAGTCGTGTGCTTCTTGAACAACTTCTACC CCAAAGACATCAATGTCAAGTGGAAGATTGAT GGCAGTGAACGACAAAATGGCGTCCTGAACAG TTGGACTGATCAGGACAGCAAAGACAGCACCT ACAGCATGAGCAGCACCCTCACGTTGACCAAG GACGAGTATGAACGACATAACAGCTATACCTG TGAGGCCACTCACAAGACATCAACTTCACCCA TTGTCAAGAGCTTCAACAGGAATGAGTGT	1228
SM1B327	pDR000029307	CAGATCGTGCTGACCCAGAGCCCCGCCATCAT GAGCGCCAGCCCTGGCGAGAAAGTGACCATGA CCTGCAGCGCCAGCAGCAACGTGTCCTACATG CACTGGTTCCAGCAGAAGTCCGGCACCAGCCC CAAGCGGTGGATCTACGACACCAGCAAGCTGG CCAGCGGCGTGCCCGCCAGATTTTCTGGCAGC GGCAGCGGCACCAGCTACAGCCTGACCGTGTC CAGCATGGAAGCCGAGGACGCCGCCACCTACT ACTGCCAGCAGTGGTCCAGCAACCCCCGGACC TTCGGCGGAGGCACCAAGCTGGAAATCAAGCG GGCTGATGCTGCACCGACTGTGTCCATCTTCCC ACCATCCAGTGAGCAGTTAACATCTGGAGGTG CCTCAGTCGTGTGCTTCTTGAACAACTTCTACC CCAAAGACATCAATGTCAAGTGGAAGATTGAT GGCAGTGAACGACAAAATGGCGTCCTGAACAG	1229

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		TTGGACTGATCAGGACAGCAAAGACAGCACCT ACAGCATGAGCAGCACCCTCACGTTGACCAAG GACGAGTATGAACGACATAACAGCTATACCTG TGAGGCCACTCACAAGACATCAACTTCACCCA TTGTCAAGAGCTTCAACAGGAATGAGTGT	
SM1B328	pDR000027029	GACATCCAGATGACCCAGAGCCCCAGCAGCCT GAGCGCCAGCCTGGGCGAGAGAGTGTCCCTGA CCTGCCGGGCCAGCCAGGACATCGGCAGCTAC CTGAACTGGCTGCAGCAGGAACCCGACGGCAC CATCAAGCGGCTGATCTACGCCACCAGCTCCC TGGACAGCGGCGTGCCCAAGCGGTTCAGCGGC AGCAGATCTGGCGCCGACTACAGCCTGACCAT CAGCAGCCTGGAAAGCGAGGACTTCGTGGACT ACTACTGCCTGCAGTACGCCACCTCCCCCTGGA CCTTCGGCGGAGGCACCAAGCTGGAAATCAAG CGGGCTGATGCTGCACCGACTGTGTCCATCTTC CCACCATCCAGTGAGCAGTTAACATCTGGAGG TGCCTCAGTCGTGTGCTTCTTGAACAACTTCTA CCCCAAAGACATCAATGTCAAGTGGAAGATTG ATGGCAGTGAACGACAAAATGGCGTCCTGAAC AGTTGGACTGATCAGGACAGCAAAGACAGCAC CTACAGCATGAGCAGCACCCTCACGTTGACCA AGGACGAGTATGAACGACATAACAGCTATACC TGTGAGGCCACTCACAAGACATCAACTTCACC CATTGTCAAGAGCTTCAACAGGAATGAGTGT	1230
SM1B329	pDR000029306	GACATCCAGATGACCCAGAGCAGCAGCTACCT GAGCGTGTCCCTGGGCGGCAGAGTGACCATCA CATGCAAGGCCAGCGACCACATCAACAACTGG CTGGCCTGGTATCAGCAGAAGCCCGGCAACGC CCCCAGACTGCTGATCAGCGGCGCCACCAGCC TGGAAACCGGCGTGCCAAGCAGATTCAGCGGC AGCGGCTCCGGCAAGGACTACACCCTGAGCAT CACCAGCCTGCAGACCGAGGACGTGGCCACCT ACTACTGCCAGCAGTACTGGTCCACCCCCTAC ACCTTCGGCGGAGGCACCAAGCTGGAAATCAA GCGGGCTGATGCTGCACCGACTGTGTCCATCTT CCCACCATCCAGTGAGCAGTTAACATCTGGAG GTGCCTCAGTCGTGTGCTTCTTGAACAACTTCT ACCCCAAAGACATCAATGTCAAGTGGAAGATT GATGGCAGTGAACGACAAAATGGCGTCCTGAA CAGTTGGACTGATCAGGACAGCAAAGACAGCA CCTACAGCATGAGCAGCACCCTCACGTTGACC AAGGACGAGTATGAACGACATAACAGCTATAC CTGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTGT	1231
SM1B330	pDR000029305	CAGATCGTGCTGACCCAGAGCCCTGCCCTGAT GAGCGCCAGCCCTGGCGAGAAAGTGACCATGA CCTGCAGCGCCAGCAGCAGCGTGTCCTACATG	1232

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		TACTGGTATCAGCAGAAGCCCAGAAGCAGCCC CAAGCTGAAGTACGCCAGCAACCTGGCCAGCG GCGTGCCCGCCAGATTTTCTGGCAGCGGCAGC GGCACCAGCTACAGCCTGACCATCAGCAGCAT GGAAGCCGAGGACGCCGCCACCTACTACTGCC AGCAGTGGTCCAGCAACCCCCCCATCACCTTC GGAGCCGGCACCAAGCTGGAACTGAAGCGGG CTGATGCTGCACCGACTGTGTCCATCTTCCCAC CATCCAGTGAGCAGTTAACATCTGGAGGTGCC TCAGTCGTGTGCTTCTTGAACAACTTCTACCCC AAAGACATCAATGTCAAGTGGAAGATTGATGG CAGTGAACGACAAAATGGCGTCCTGAACAGTT GGACTGATCAGGACAGCAAAGACAGCACCTAC AGCATGAGCAGCACCCTCACGTTGACCAAGGA CGAGTATGAACGACATAACAGCTATACCTGTG AGGCCACTCACAAGACATCAACTTCACCCATT GTCAAGAGCTTCAACAGGAATGAGTGT	
SM1B331	pDR000027141	GACATCGTGATGACCCAGAGCCCCGCCACCCT GAGCGTGACCCCTGGCGATAGAGTGTCCCTGA GCTGCCGGGCCAGCCAGAGCATCAGCGACTAC CTGCACTGGTATCAGCAGAAGTCCCACGAGAG CCCCAGACTGCTGATTAAGTACGACAGCCAGT CCATCAGCGGCATCCCCAGCAGATTCAGCGGC AGCGGCTCCGGCTCCGACTTCACCCTGAGCAT CAACAGCGTGGAACCCGAGGACGTGGGCGTGT ACTACTGCCAGAACGGCCACCGGTTCCCTTTCA CCTTCGGCGGAGGCACCAAGCTGGAAATCAAG CGGGCTGATGCTGCACCGACTGTGTCCATCTTC CCACCATCCAGTGAGCAGTTAACATCTGGAGG TGCCTCAGTCGTGTGCTTCTTGAACAACTTCTA CCCCAAAGACATCAATGTCAAGTGGAAGATTG ATGGCAGTGAACGACAAAATGGCGTCCTGAAC AGTTGGACTGATCAGGACAGCAAAGACAGCAC CTACAGCATGAGCAGCACCCTCACGTTGACCA AGGACGAGTATGAACGACATAACAGCTATACC TGTGAGGCCACTCACAAGACATCAACTTCACC CATTGTCAAGAGCTTCAACAGGAATGAGTGT	1233
SM1B332	pDR000029304	CAGATCGTGCTGACCCAGAGCCCCGCCATCAT GAGCGCCAGCCCTGGCGAGAAAGTGACCCTGA CCTGCAGCGCCAGCAGCAGCGTGTCCAGCAGC TACCTGTTCTGGTATCAGCAGAAGCCCGGCAG CAGCCCCAAGCTGTGGATCTACAGCACCAGCA ACCTGGCCAGCGGCGTGCCCGTGCGGTTTAGC GGCAGCGGCTTTGGCACCAGCTACAGCCTGAC CATCAGCCGGATGGAAGCCGAGGACGCCGCCA GCTACTTCTGCCACCAGTGGTCCAGCTACCCCC CCACCTTCGGAGCCGGCACCAAGCTGGAACTG AAGCGGGCTGATGCTGCACCGACTGTGTCCAT	1234

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		CTTCCCACCATCCAGTGAGCAGTTAACATCTGG AGGTGCCTCAGTCGTGTGCTTCTTGAACAACTT CTACCCCAAAGACATCAATGTCAAGTGGAAGA TTGATGGCAGTGAACGACAAAATGGCGTCCTG AACAGTTGGACTGATCAGGACAGCAAAGACAG CACCTACAGCATGAGCAGCACCCTCACGTTGA CCAAGGACGAGTATGAACGACATAACAGCTAT ACCTGTGAGGCCACTCACAAGACATCAACTTC ACCCATTGTCAAGAGCTTCAACAGGAATGAGT GT	
SM1B333	pDR000029303	GACATCGTGCTGACCCAGAGCCCTGCCAGCCT GGCCGTGTCTCTGGGCCAGAGAGCCACCATCA GCTGCCGGGCCAGCGAGAGCGTGGACAGCTAC GGCAACAGCTTCATGCACTGGTATCAGCAGAA GCCCGGCCAGCCCCCCAAGCTGCTGATCTACC TGGCCAGCAACCTGGAAAGCGGCGTGCCCGCC AGATTCAGCGGCAGCGGCAGCAGAACCGACTT CACCCTGACCATCGACCCCGTGGAAGCCGACG ACGCCGCCACCTACTACTGCCAGCAGAACAAC GAGGACCCCTACACCTTCGGCGGAGGCACCAA GCTGGAAATCAAGCGGGCTGATGCTGCACCGA CTGTGTCCATCTTCCCACCATCCAGTGAGCAGT TAACATCTGGAGGTGCCTCAGTCGTGTGCTTCT TGAACAACTTCTACCCCAAAGACATCAATGTC AAGTGGAAGATTGATGGCAGTGAACGACAAA ATGGCGTCCTGAACAGTTGGACTGATCAGGAC AGCAAAGACAGCACCTACAGCATGAGCAGCAC CCTCACGTTGACCAAGGACGAGTATGAACGAC ATAACAGCTATACCTGTGAGGCCACTCACAAG ACATCAACTTCACCCATTGTCAAGAGCTTCAAC AGGAATGAGTGT	1235
SM1B334	pDR000029302	GACGTGCTGATGACCCAGACCCCCCTGAGCCT GCCCGTGTCTCTGGGCGATCAGGCCAGCATCA GCTGCCGGTCCAGCCAGAGCATCGTGTACAGC AACGGCAACACCTACCTGGACTGGTATCTGCA GAAGCCCGGCCAGCCCCCCAAGCTGCTGATCT ACAAGGTGTCCAACCGGTTCAGCGGCGTGCCC GACAGATTCAGCGGCAGCGGCTCCGGCACCGA CTTCATCCTGAAGATCAGCCGGGTGGAAGCCG AGGACCTGGGCGTGTACTACTGTTTTCAGGGC AGCCACGTGCCCTGGACCTTCGGCGGAGGCAC CAAGCTGGAAATCAAGCGGGCTGATGCTGCAC CGACTGTGTCCATCTTCCCACCATCCAGTGAGC AGTTAACATCTGGAGGTGCCTCAGTCGTGTGCT TCTTGAACAACTTCTACCCCAAAGACATCAAT GTCAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAGG ACAGCAAAGACAGCACCTACAGCATGAGCAGC	1236

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		ACCCTCACGTTGACCAAGGACGAGTATGAACG ACATAACAGCTATACCTGTGAGGCCACTCACA AGACATCAACTTCACCCATTGTCAAGAGCTTC AACAGGAATGAGTGT	
SM1B335	pDR000029301	GACGTGGTGGTCACCCAGACCCCCCTGAGCCT GCCCGTGTCCTTCGGCGACCAGGTGTCCATCA GCTGCAGAAGCAGCCAGAGCCTGGCCAACAGC TACGGCAACACCTACCTGAGCTGGTATCTGCA CAAGCCCGGCCAGAGCCCCCAGCTGCTGATCT ACGGCATCAGCAACCGGTTCAGCGGCGTGCCC GACAGATTCAGCGGCAGCGGCTCCGGCACCGA CTTCACCCTGAAGATCAGCACCATCAAGCCCG AGGACCTGGGCATGTACTACTGTCTGCAGGGC ACCCACCAGCCCTACACCTTCGGCGGAGGCAC CAAGCTGGAAATCAAGCGGGCTGATGCTGCAC CGACTGTGTCCATCTTCCCACCATCCAGTGAGC AGTTAACATCTGGAGGTGCCTCAGTCGTGTGCT TCTTGAACAACTTCTACCCCAAAGACATCAAT GTCAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAGG ACAGCAAAGACAGCACCTACAGCATGAGCAGC ACCCTCACGTTGACCAAGGACGAGTATGAACG ACATAACAGCTATACCTGTGAGGCCACTCACA AGACATCAACTTCACCCATTGTCAAGAGCTTC AACAGGAATGAGTGT	1237
SM1B336	pDR000029300	GACATCGTGATGAGCCAGAGCCCCAGCAGCCT GGCCGTGTCCGTGGGCGAGAAAGTGACCATGA GCTGCAAGAGCAGCCAGAGCGTGCTGTACAAC AGCAACCAGCGGAACTACCTGGCCTGGTATCA GCAGAAGCCCGGCCAGTCCCCCAAGCTGCTGA TCTACTGGGCCAGCACCCGCGAGAGCGGCGTG CCAGATAGAAGCACAGGCAGCGGCAGCGGCA CCGACTTCACCCTGACCATCAGCAGCGTGCAG GCCGAGGATCTGGCCGTGTACTACTGCCACCA GTACCTGAGCAGCTACACCTTCGGCGGAGGCA CCAAGCTGGAAATCAAGCGGGCTGATGCTGCA CCGACTGTGTCCATCTTCCCACCATCCAGTGAG CAGTTAACATCTGGAGGTGCCTCAGTCGTGTG CTTCTTGAACAACTTCTACCCCAAAGACATCAA TGTCAAGTGGAAGATTGATGGCAGTGAACGAC AAAATGGCGTCCTGAACAGTTGGACTGATCAG GACAGCAAAGACAGCACCTACAGCATGAGCA GCACCCTCACGTTGACCAAGGACGAGTATGAA CGACATAACAGCTATACCTGTGAGGCCACTCA CAAGACATCAACTTCACCCATTGTCAAGAGCT TCAACAGGAATGAGTGT	1238
SM1B337	pDR000029299	GACATCGTGATGACCCAGAGCCACAAGTTCAT GAGCACCAGCGTGGGCGACCGGGTGTCCATCA	1239

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		CATGCAAGGCCAGCCAGGACGTGGGCACCGCC GTGGCCTGGTATCAGCAGAAGCCCGGCCAGAG CCCCAAGCTGCTGATCTACTGGGCCAGCACCA GACACACCGGCGTGCCCGACAGATTCACAGGC AGCGGCAGCGGCACCGACTTCACCCTGACCAT CAGCAACGTGCAGAGCGAGGACCTGGCCGACT ACTTCTGCCAGCAGTACAGCAGCTACCCCCTG ACCTTCGGAGCCGGCACCAAGCTGGAACTGAA GCGGGCTGATGCTGCACCGACTGTGTCCATCTT CCCACCATCCAGTGAGCAGTTAACATCTGGAG GTGCCTCAGTCGTGTGCTTCTTGAACAACTTCT ACCCCAAAGACATCAATGTCAAGTGGAAGATT GATGGCAGTGAACGACAAAATGGCGTCCTGAA CAGTTGGACTGATCAGGACAGCAAAGACAGCA CCTACAGCATGAGCAGCACCCTCACGTTGACC AAGGACGAGTATGAACGACATAACAGCTATAC CTGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTGT	
SM1B338	pDR000029319	GACATCGTGCTGACCCAGAGCCCTGCCAGCCT GGCCGTGTCTCTGGGCCAGAGAGCCACCATCA GCTGCCGGGCCAGCGAGAGCGTGGACAGCTAC GGCAACAGCTTCATGCACTGGTATCAGCAGAA GCCCGGCCAGCCCCCCAAGCTGCTGATCTACC GGGCCAGCAACCTGGAAAGCGGCATCCCCGCC AGATTCAGCGGCAGCGGCAGCCGGACCGACTT CACCCTGACCATCAACCCCGTGGAAGCCGACG ACGTGGCCACCTACTACTGCCAGCAGAGCAAC GAGGACCCCCCCTGGACCTTCGGCGGAGGCAC CAAGCTGGAAATCAAGCGGGCTGATGCTGCAC CGACTGTGTCCATCTTCCCACCATCCAGTGAGC AGTTAACATCTGGAGGTGCCTCAGTCGTGTGCT TCTTGAACAACTTCTACCCCAAAGACATCAAT GTCAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAGG ACAGCAAAGACAGCACCTACAGCATGAGCAGC ACCCTCACGTTGACCAAGGACGAGTATGAACG ACATAACAGCTATACCTGTGAGGCCACTCACA AGACATCAACTTCACCCATTGTCAAGAGCTTC AACAGGAATGAGTGT	1240
SM1B339	pDR000029319	GACATCGTGCTGACCCAGAGCCCTGCCAGCCT GGCCGTGTCTCTGGGCCAGAGAGCCACCATCA GCTGCCGGGCCAGCGAGAGCGTGGACAGCTAC GGCAACAGCTTCATGCACTGGTATCAGCAGAA GCCCGGCCAGCCCCCCAAGCTGCTGATCTACC GGGCCAGCAACCTGGAAAGCGGCATCCCCGCC AGATTCAGCGGCAGCGGCAGCCGGACCGACTT CACCCTGACCATCAACCCCGTGGAAGCCGACG ACGTGGCCACCTACTACTGCCAGCAGAGCAAC	1241

mAB/Fab name	Construct ID	Light Chain CDS	SEQ ID NO:
		GAGGACCCCCCCTGGACCTTCGGCGGAGGCAC CAAGCTGGAAATCAAGCGGGCTGATGCTGCAC CGACTGTGTCCATCTTCCCACCATCCAGTGAGC AGTTAACATCTGGAGGTGCCTCAGTCGTGTGCT TCTTGAACAACTTCTACCCCAAAGACATCAAT GTCAAGTGGAAGATTGATGGCAGTGAACGACA AAATGGCGTCCTGAACAGTTGGACTGATCAGG ACAGCAAAGACAGCACCTACAGCATGAGCAGC ACCCTCACGTTGACCAAGGACGAGTATGAACG ACATAACAGCTATACCTGTGAGGCCACTCACA AGACATCAACTTCACCCATTGTCAAGAGCTTC AACAGGAATGAGTGT	
SM1B340	pDR000029298	GACATCCAGATGACCCAGACCACCAGCAGCCT GAGCGCCAGCCTGGGCGACAGAGTGACCATCA GCTGCCGGGCCAGCCAGGACATCGACAACTAC CTGAACTGGTATCAGCAGAAACCCGACGGCAC CGTGAAGCTGCTGATCAGCTACACCAGCCGGC TGCACAGCGGCGTGCCCAGCAGATTTTCTGGC AGCGGCAGCGGCACCGACTACAGCCTGACCAT CTCCAACCTGGAACAGGAAGATTTCGCTACCT ACTTCTGTCAGCAGGGCTACACCCTGCCCTGG ACCTTCGGCGGAGGCACCAAGCTGGAAATCAA GCGGGCTGATGCTGCACCGACTGTGTCCATCTT CCCACCATCCAGTGAGCAGTTAACATCTGGAG GTGCCTCAGTCGTGTGCTTCTTGAACAACTTCT ACCCCAAAGACATCAATGTCAAGTGGAAGATT GATGGCAGTGAACGACAAAATGGCGTCCTGAA CAGTTGGACTGATCAGGACAGCAAAGACAGCA CCTACAGCATGAGCAGCACCCTCACGTTGACC AAGGACGAGTATGAACGACATAACAGCTATAC CTGTGAGGCCACTCACAAGACATCAACTTCAC CCATTGTCAAGAGCTTCAACAGGAATGAGTGT	1242

Table 49. HlgA/LukE Antibody Light Chain Primary Transcripts

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
SM1B302	pDR000027850	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC CAGATGACCCAGAGCCCTAGCAGCCTGAGCGC CTCTCTGGGCGAGAGAGTGTCCCTGACCTGCA GAGCCAGCCAGGACATCGGCAGCTCCCTGAAC TGGCTGCAGCAGGAACCCGACGGCACCATCAA GCGGCTGATCTACGCCACCAGCAGCCTGGATA GCGGCGTGCCCAAGAGATTCAGCGGCAGCAGA AGCGGCAGCGACTACAGCCTGACCATCTCCAG	1243

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		CCTGGAATCCGAGGACTTCGTGGACTACTACT GCCTGCAGTACGCCAGCAGCCCCTGGACCTTT GGCGGAGGCACCAAGCTGGAAATCAAGCGGG CTGATGCTGCACCGACTGTGTCCATCTTCCCAC CATCCAGTGAGCAGTTAACATCTGGAGGTGCC TCAGTCGTGTGCTTCTTGAACAACTTCTACCCC AAAGACATCAATGTCAAGTGGAAGATTGATGG CAGTGAACGACAAAATGGCGTCCTGAACAGTT GGACTGATCAGGACAGCAAAGACAGCACCTAC AGCATGAGCAGCACCCTCACGTTGACCAAGGA CGAGTATGAACGACATAACAGCTATACCTGTG AGGCCACTCACAAGACATCAACTTCACCCATT GTCAAGAGCTTCAACAGGAATGAGTGTTAG	
SM1B303	pDR000029323	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC CAGATGACCCAGACCACCAGCAGCCTGAGCGC CAGCCTGGGCGACAGAGTGACCATCAGCTGCT GGGCCAGCCAGGACATCAGAAGCTACCTGAAC TGGTATCAGCAGAAACCCGACGGCACCGTGAA GCTGCTGATCTACTACACCAGCCGGCTGCACA GCGGCGTGCCCAGCAGATTTTCTGGCAGCGGC AGCGGCACCGACTTCAGCCTGACCATCTCCAA CCTGGAACAGGAAGATATCGCTACCTACTTCT GTCAGCAGGGCAACACCCTGCCCTACACCTTC GGCGGAGGCACCAAGCTGGAAATCAAGCGGG CTGATGCTGCACCGACTGTGTCCATCTTCCCAC CATCCAGTGAGCAGTTAACATCTGGAGGTGCC TCAGTCGTGTGCTTCTTGAACAACTTCTACCCC AAAGACATCAATGTCAAGTGGAAGATTGATGG CAGTGAACGACAAAATGGCGTCCTGAACAGTT GGACTGATCAGGACAGCAAAGACAGCACCTAC AGCATGAGCAGCACCCTCACGTTGACCAAGGA CGAGTATGAACGACATAACAGCTATACCTGTG AGGCCACTCACAAGACATCAACTTCACCCATT GTCAAGAGCTTCAACAGGAATGAGTGTTAG	1244
SM1B304	pDR000029322	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC CAGATGACCCAGAGCCCCAGCAGCCTGAGCGC CAGCCTGGGCGAGAGAGTGTCCCTGACCTGCC GGGCCAGCCAGGAAATCAGCGGCTACCTGAGC TGGCTGCAGCAGAAGCCCGACGGCACCATCAA GCGGCTGATCTACGCCGCCAGCACCCTGGACA GCGGCGTGCCCAAGAGATTCAGCGGCAGCCGC AGCGGCAGCGACTACAGCCTGACCATCAGCAG CCTGGAAAGCGAGGACTTCGCCGACTACTACT GCCTGCAGTACGCCAGCTACCCCCGGACCTTC GGCGGAGGCACCAAGCTGGAAATCAAGCGGG CTGATGCTGCACCGACTGTGTCCATCTTCCCAC	1245

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		CATCCAGTGAGCAGTTAACATCTGGAGGTGCC TCAGTCGTGTGCTTCTTGAACAACTTCTACCCC AAAGACATCAATGTCAAGTGGAAGATTGATGG CAGTGAACGACAAAATGGCGTCCTGAACAGTT GGACTGATCAGGACAGCAAAGACAGCACCTAC AGCATGAGCAGCACCCTCACGTTGACCAAGGA CGAGTATGAACGACATAACAGCTATACCTGTG AGGCCACTCACAAGACATCAACTTCACCCATT GTCAAGAGCTTCAACAGGAATGAGTGTTAG	
SM1B305	pDR000029321	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACGTG CTGATGACCCAGACCCCCCTGAGCCTGCCCGT GTCTCTGGGCGATCAGGCCAGCATCAGCTGCC GGTCCAGCCAGATCATCGTGCACAGCAACGGC AACACCTACCTGGACTGGTATCTGCAGAAGCC CGGCCAGAGCCCCAAGCTGCTGATCTACAAGA TCAGCAACCGGTTCAGCGGCGTGCCCGACAGA TTCAGCGGCAGCGGCTCCGGCACCGACTTCAC CCTGAAGATCAGCCGGGTGGAAGCCGAGGACC TGGGCGTGTACTACTGTTTTCAGGGCAGCCAC GTGCCCTGGACCTTCGGCGGAGGCACCAAGCT GGAAATCAAGCGGGCTGATGCTGCACCGACTG TGTCCATCTTCCCACCATCCAGTGAGCAGTTAA CATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGA ACAACTTCTACCCCAAAGACATCAATGTCAAG TGGAAGATTGATGGCAGTGAACGACAAAATGG CGTCCTGAACAGTTGGACTGATCAGGACAGCA AAGACAGCACCTACAGCATGAGCAGCACCCTC ACGTTGACCAAGGACGAGTATGAACGACATAA CAGCTATACCTGTGAGGCCACTCACAAGACAT CAACTTCACCCATTGTCAAGAGCTTCAACAGG AATGAGTGTTAG	1246
SM1B306	pDR000029320	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACGTG GTGGTCACCCAGACCCCCCTGAGCCTGCCCGT GTCCTTCGGCGACCAGGTGTCCATCAGCTGCA GAAGCAGCCAGAGCCTGGCCAACAGCTACGGC AACACCTACCTGAGCTGGTATCTGCACAAGCC CGGCCAGAGCCCCCAGCTGCTGATCTACGGCA TCAGCAACCGGTTCAGCGGCGTGCCCGACAGA TTCAGCGGCAGCGGCTCCGGCACCGACTTCAC CCTGAAGATCAGCACCATCAAGCCCGAGGGCC TGGGCATGTACTACTGTCTGCAGGGCACCCAC CAGCCCCCCACCTTTGGCGCTGGCACCAAGCT GGAACTGAAGCGGGCTGATGCTGCACCGACTG TGTCCATCTTCCCACCATCCAGTGAGCAGTTAA CATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGA ACAACTTCTACCCCAAAGACATCAATGTCAAG	1247

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		TGGAAGATTGATGGCAGTGAACGACAAAATGG CGTCCTGAACAGTTGGACTGATCAGGACAGCA AAGACAGCACCTACAGCATGAGCAGCACCCTC ACGTTGACCAAGGACGAGTATGAACGACATAA CAGCTATACCTGTGAGGCCACTCACAAGACAT CAACTTCACCCATTGTCAAGAGCTTCAACAGG AATGAGTGTTAG	
SM1B307	pDR000029319	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC GTGCTGACCCAGAGCCCTGCCAGCCTGGCCGT GTCTCTGGGCCAGAGAGCCACCATCAGCTGCC GGGCCAGCGAGAGCGTGGACAGCTACGGCAA CAGCTTCATGCACTGGTATCAGCAGAAGCCCG GCCAGCCCCCCAAGCTGCTGATCTACCGGGCC AGCAACCTGGAAAGCGGCATCCCCGCCAGATT CAGCGGCAGCGGCAGCCGGACCGACTTCACCC TGACCATCAACCCCGTGGAAGCCGACGACGTG GCCACCTACTACTGCCAGCAGAGCAACGAGGA CCCCCCCTGGACCTTCGGCGGAGGCACCAAGC TGGAAATCAAGCGGGCTGATGCTGCACCGACT GTGTCCATCTTCCCACCATCCAGTGAGCAGTTA ACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTG AACAACTTCTACCCCAAAGACATCAATGTCAA GTGGAAGATTGATGGCAGTGAACGACAAAATG GCGTCCTGAACAGTTGGACTGATCAGGACAGC AAAGACAGCACCTACAGCATGAGCAGCACCCT CACGTTGACCAAGGACGAGTATGAACGACATA ACAGCTATACCTGTGAGGCCACTCACAAGACA TCAACTTCACCCATTGTCAAGAGCTTCAACAG GAATGAGTGTTAG	1248
SM1B308	pDR000029318	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC GTGATGAGCCAGAGCCCCAGCAGCCTGGCCGT GTCTGCCGGCGAGAAAGTGACCATGAGCTGCA AGAGCAGCCAGAGCCTGCTGAACAGCCGGACC CGGAAGAACTACCTGGCCTGGTATCAGCAGAA GCCCGGCCAGTCCCCCAAGCTGCTGATCTACT GGGCCAGCACCCGCGAGAGCGGCGTGCCCGAT AGATTCACAGGCAGCGGCAGCGGCACCGACTT CACCCTGACCATCAGCAGCGTGCAGGCCGAGG ATCTGGCCGTGTACTACTGCAAGCAGAGCTAC AACCTGTGGACCTTCGGCGGAGGCACCAAGCT GGAAATCAAGCGGGCTGATGCTGCACCGACTG TGTCCATCTTCCCACCATCCAGTGAGCAGTTAA CATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGA ACAACTTCTACCCCAAAGACATCAATGTCAAG TGGAAGATTGATGGCAGTGAACGACAAAATGG CGTCCTGAACAGTTGGACTGATCAGGACAGCA	1249

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		AAGACAGCACCTACAGCATGAGCAGCACCCTC ACGTTGACCAAGGACGAGTATGAACGACATAA CAGCTATACCTGTGAGGCCACTCACAAGACAT CAACTTCACCCATTGTCAAGAGCTTCAACAGG AATGAGTGTTAG	
SM1B309	pDR000029317	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACGTG GTCATGACCCAGACCCCCCTGAGCCTGCCCGT GTCTCTGGGCGATCAGGCCAGCATCAGCTGCA GAAGCAGCCAGAGCCTGCTGCACAGCAACGGC AAGACCTACCTGCACTGGTATCTGCAGAAGCC CGGCCAGAGCCCCAAGCTGCTGATCTACAAGG TGTCCAACCGGTTCAGCGGCGTGCCCGACAGA TTCAGCGGCAGCGGCTCCGGCACCGACTTCAC CCTGAAGATCAGCCGGGTGGAAGCCGAGGACC TGGGCGTGTACTTCTGCAGCCAGTCCACCCAC GTGCCCCTGACCTTCGGAGCCGGCACCAAGCT GGAACTGAAGCGGGCTGATGCTGCACCGACTG TGTCCATCTTCCCACCATCCAGTGAGCAGTTAA CATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGA ACAACTTCTACCCCAAAGACATCAATGTCAAG TGGAAGATTGATGGCAGTGAACGACAAAATGG CGTCCTGAACAGTTGGACTGATCAGGACAGCA AAGACAGCACCTACAGCATGAGCAGCACCCTC ACGTTGACCAAGGACGAGTATGAACGACATAA CAGCTATACCTGTGAGGCCACTCACAAGACAT CAACTTCACCCATTGTCAAGAGCTTCAACAGG AATGAGTGTTAG	1250
SM1B310	pDR000029316	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC GTGATGACCCAGAGCCACAAGTTCATGAGCAC CAGCGTGGGCGACCGGGTGTCCATCACATGCA AGGCCAGCCAGGATGTGTCTGCCGCCGTGGCC TGGTATCAGCAGAAGCCCGGCCAGAGCCCCAA GCTGCTGATCTACTGGGCCAGCACCAGACACA CCGGCGTGCCCGACAGATTCACAGGCAGCGGC AGCGGCACCGACTACACCCTGACCATCAGCAG CGTGCAGGCCGAGGACCTGGCCCTGTACTACT GCCAGCAGCACTACAGCACCCCCGGCACCTTC GGCGGAGGCACCAAGCTGGAAATCAAGCGGG CTGATGCTGCACCGACTGTGTCCATCTTCCCAC CATCCAGTGAGCAGTTAACATCTGGAGGTGCC TCAGTCGTGTGCTTCTTGAACAACTTCTACCCC AAAGACATCAATGTCAAGTGGAAGATTGATGG CAGTGAACGACAAAATGGCGTCCTGAACAGTT GGACTGATCAGGACAGCAAAGACAGCACCTAC AGCATGAGCAGCACCCTCACGTTGACCAAGGA CGAGTATGAACGACATAACAGCTATACCTGTG	1251

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		AGGCCACTCACAAGACATCAACTTCACCCATT GTCAAGAGCTTCAACAGGAATGAGTGTTAG	
SM1B311	pDR000029315	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACGTG CTGATGACCCAGACCCCCCTGAGCCTGCCCGT GTCTCTGGGCGATCAGGCCAGCATCAGCTGCC GGTCCAGCCAGACCATCGTGCACAGCAGCGGC AACACCTACCTGGAATGGTATCTGCAGCGGCC TGGCCAGAGCCCCAAGCTGCTGATCTACAAGG TGTCCAACCGGTTCAGCGGCGTGCCCGACAGA TTCAGCGGCAGCGGCTCCGGCACCGACTTCAC CCTGAAGATCAGCCGGGTGGAAGCCGAGGACC TGGGCGTGTACTACTGTTTTCAGGGCAGCCAC GTGCCCTACACCTTCGGCGGAGGCACCAAGCT GGAAATCAAGCGGGCTGATGCTGCACCGACTG TGTCCATCTTCCCACCATCCAGTGAGCAGTTAA CATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGA ACAACTTCTACCCCAAAGACATCAATGTCAAG TGGAAGATTGATGGCAGTGAACGACAAAATGG CGTCCTGAACAGTTGGACTGATCAGGACAGCA AAGACAGCACCTACAGCATGAGCAGCACCCTC ACGTTGACCAAGGACGAGTATGAACGACATAA CAGCTATACCTGTGAGGCCACTCACAAGACAT CAACTTCACCCATTGTCAAGAGCTTCAACAGG AATGAGTGTTAG	1252
SM1B312	pDR000029297	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC CAGATGACCCAGACCACCAGCAGCCTGAGCGC CAGCCTGGGCGACAGAGTGACCATCAGCTGTA GCGCCTCCCAGGGCATCAGCAACTACCTGAAC TGGTATCAGCAGAAACCCGACGGCACCGTGAA GCTGCTGATCTACTACACCAGCTCCCTGCACAG CGGCGTGCCCAGCAGATTTTCTGGCAGCGGCA GCGGCACCGACTACAGCCTGACCATCTCCAAC CTGGAACCCGAGGATATCGCCACCTACTACTG CCAGCAGTACAGCAAGCTGCCCTTCACCTTCG GCTCCGGCACCAAGCTGGAAATCAAGCGGGCT GATGCTGCACCGACTGTGTCCATCTTCCCACCA TCCAGTGAGCAGTTAACATCTGGAGGTGCCTC AGTCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGGCA GTGAACGACAAAATGGCGTCCTGAACAGTTGG ACTGATCAGGACAGCAAAGACAGCACCTACAG CATGAGCAGCACCCTCACGTTGACCAAGGACG AGTATGAACGACATAACAGCTATACCTGTGAG GCCACTCACAAGACATCAACTTCACCCATTGTC AAGAGCTTCAACAGGAATGAGTGTTAG	1253
SM1B313	pDR000029314	ATGGAGACACATTCTCAGGTCTTTGTATACATG	1254

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC GTGATGAGCCAGAGCCCCAGCAGCCTGGCCGT GTCCGTGGGCGAGAAAGTGACCATGAGCTGCA AGAGCAGCCAGAGCCTGCTGTACAGCTCCAAC CAGAAGAACTACCTGGCCTGGTATCAGCAGAA GCCCGGCCAGTCCCCCAAGCTGCTGATCTACT GGGCCAGCACCCGCGAGAGCGGCGTGCCAGAT AGACTGACAGGCAGCGGCAGCGGCACCGACTT CACCCTGACCATCAGCAGCGTGAAGGCCGAGG ATCTGGCCGTGTACTACTGCCAGCAGTACTAC AGCTACCCCTACACCTTCGGCGGAGGCACCAA GCTGGAAATCAAGCGGGCTGATGCTGCACCGA CTGTGTCCATCTTCCCACCATCCAGTGAGCAGT TAACATCTGGAGGTGCCTCAGTCGTGTGCTTCT TGAACAACTTCTACCCCAAAGACATCAATGTC AAGTGGAAGATTGATGGCAGTGAACGACAAA ATGGCGTCCTGAACAGTTGGACTGATCAGGAC AGCAAAGACAGCACCTACAGCATGAGCAGCAC CCTCACGTTGACCAAGGACGAGTATGAACGAC ATAACAGCTATACCTGTGAGGCCACTCACAAG ACATCAACTTCACCCATTGTCAAGAGCTTCAAC AGGAATGAGTGTTAG	
SM1B314	pDR000007289	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATT CAGATGACTCAGTCTCCAGCCTCCCTATCTGTA TCTGTGGGAGAAACTGTCACCATCACATGTCG AGCAAGTGAAAATATTTACAGTAATTTAGCAT GGTATCAGCAGAAACAGGGAAAATCTCCTCAG CTCCTGGTCTATGCTGCAACAAACTTAGCAGAT GGTGTGCCATCAAGGTTCAGTGGCAGTGGATC AGGCACACAGTATTCCCTCAAGATCAACAGCC TGCAGTCTGAAGATTTTGGGAGTTATTACTGTC AACATTTTTGGGGTACTCCGTACACGTTCGGAG GGGGGACCAAGCTGGAAATAAAACGGGCTGA TGCTGCACCGACTGTGTCCATCTTCCCACCATC CAGTGAGCAGTTAACATCTGGAGGTGCCTCAG TCGTGTGCTTCTTGAACAACTTCTACCCCAAAG ACATCAATGTCAAGTGGAAGATTGATGGCAGT GAACGACAAAATGGCGTCCTGAACAGTTGGAC TGATCAGGACAGCAAAGACAGCACCTACAGCA TGAGCAGCACCCTCACGTTGACCAAGGACGAG TATGAACGACATAACAGCTATACCTGTGAGGC CACTCACAAGACATCAACTTCACCCATTGTCA AGAGCTTCAACAGGAATGAGTGTTAG	1255
SM1B315	pDR000026238	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC AAGATGACCCAGAGCCCCAGCTCTATGTACGC CAGCCTGGGCGAGCGCGTGACCATCACATGCA	1256

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		AGGCCAGCCAGGACATCAACAGCTACCTGAGC TGGTTCCAGCAGAAGCCCGGCAAGAGCCCCAA GACCCTGATCTACCGGGCCAACAGACTGGTGG ACGGCGTGCCAAGCAGATTCAGCGGCAGCGGC TCTGGCCAGGACTACAGCCTGACCATCAGCAG CCTGGAATACGAGGACATGGGCATCTACTACT GCCTGCAGTACGACGAGTTCCCCTACACCTTCG GCGGAGGCACCAAGCTGGAAATCAAGCGGGCT GATGCTGCACCGACTGTGTCCATCTTCCCACCA TCCAGTGAGCAGTTAACATCTGGAGGTGCCTC AGTCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGGCA GTGAACGACAAAATGGCGTCCTGAACAGTTGG ACTGATCAGGACAGCAAAGACAGCACCTACAG CATGAGCAGCACCCTCACGTTGACCAAGGACG AGTATGAACGACATAACAGCTATACCTGTGAG GCCACTCACAAGACATCAACTTCACCCATTGTC AAGAGCTTCAACAGGAATGAGTGTTAG	
SM1B316	pDR000029313	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC CAGATGACCCAGACCACCAGCAGCCTGAGCGC CAGCCTGGGCGACAGAGTGACCATCAGCTGTA GCGCCTCCCAGGGCATCAGCAACTACCTGAAC TGGTATCAGCAGAAACCCGACGGCACCGTGAA GCTGCTGATCCACTACACCAGCTCCCTGCACA GCGGCGTGCCCAGCAGATTTTCTGGCAGCGGC AGCGGCACCGACTACAGCCTGACCATCTCCAA CCTGGAACCCGAGGATATCGCCACCTACTACT GCCAGCAGTACAGCAAGCTGCCCTGGACCTTC GGCGGAGGCACCAAGCTGGAAATCAAGCGGG CTGATGCTGCACCGACTGTGTCCATCTTCCCAC CATCCAGTGAGCAGTTAACATCTGGAGGTGCC TCAGTCGTGTGCTTCTTGAACAACTTCTACCCC AAAGACATCAATGTCAAGTGGAAGATTGATGG CAGTGAACGACAAAATGGCGTCCTGAACAGTT GGACTGATCAGGACAGCAAAGACAGCACCTAC AGCATGAGCAGCACCCTCACGTTGACCAAGGA CGAGTATGAACGACATAACAGCTATACCTGTG AGGCCACTCACAAGACATCAACTTCACCCATT GTCAAGAGCTTCAACAGGAATGAGTGTTAG	1257
SM1B317	pDR000029312	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACGTG CTGATGACCCAGACCCCCCTGAGCCTGCCCGT GTCTCTGGGCGATCAGGCCAGCATCAGCTGCC GGTCCAGCCAGACCATCGTGTACAGCGACGGC AACACCTACCTGGAATGGTATCTGCAGAAGCC CGGCCAGAGCCCCAAGCTGCTGATCTACAAGG TGTCCAACCGGTTCAGCGGCGTGCCCGACAGA	1258

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		GTGTCTGGCAGCGGCAGCGGCACCGACTTCAC CCTGAAGATCAGCCGGGTGGAAGCCGAGGACC TGGGCGTGTACTACTGTTTTCAGGGCAGCCAC GTGCCCTACACCTTCGGCGGAGGCACCAAGCT GGAAATCAAGCGGGCTGATGCTGCACCGACTG TGTCCATCTTCCCACCATCCAGTGAGCAGTTAA CATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGA ACAACTTCTACCCCAAAGACATCAATGTCAAG TGGAAGATTGATGGCAGTGAACGACAAAATGG CGTCCTGAACAGTTGGACTGATCAGGACAGCA AAGACAGCACCTACAGCATGAGCAGCACCCTC ACGTTGACCAAGGACGAGTATGAACGACATAA CAGCTATACCTGTGAGGCCACTCACAAGACAT CAACTTCACCCATTGTCAAGAGCTTCAACAGG AATGAGTGTTAG	
SM1B318	pDR000029312	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACGTG CTGATGACCCAGACCCCCCTGAGCCTGCCCGT GTCTCTGGGCGATCAGGCCAGCATCAGCTGCC GGTCCAGCCAGACCATCGTGTACAGCGACGGC AACACCTACCTGGAATGGTATCTGCAGAAGCC CGGCCAGAGCCCCAAGCTGCTGATCTACAAGG TGTCCAACCGGTTCAGCGGCGTGCCCGACAGA GTGTCTGGCAGCGGCAGCGGCACCGACTTCAC CCTGAAGATCAGCCGGGTGGAAGCCGAGGACC TGGGCGTGTACTACTGTTTTCAGGGCAGCCAC GTGCCCTACACCTTCGGCGGAGGCACCAAGCT GGAAATCAAGCGGGCTGATGCTGCACCGACTG TGTCCATCTTCCCACCATCCAGTGAGCAGTTAA CATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGA ACAACTTCTACCCCAAAGACATCAATGTCAAG TGGAAGATTGATGGCAGTGAACGACAAAATGG CGTCCTGAACAGTTGGACTGATCAGGACAGCA AAGACAGCACCTACAGCATGAGCAGCACCCTC ACGTTGACCAAGGACGAGTATGAACGACATAA CAGCTATACCTGTGAGGCCACTCACAAGACAT CAACTTCACCCATTGTCAAGAGCTTCAACAGG AATGAGTGTTAG	1259
SM1B319	pDR000029311	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC GTGATGACCCAGGCCGCTCCCAGCGTGCCAGT GACACCTGGCGAGAGCGTGTCCATCAGCTGCA GAAGCAGCAAGAGCCTGCTGCACAGCAACGGC AATACCTACCTGTACTGGTTCCTGCAGCGGCCT GGCCAGAGCCCCCAGCTGCTGATCTACCGGAT GAGCAACCTGGCCAGCGGCGTGCCCGACAGAT TTTCTGGCAGCGGCAGCGGCACCGCCTTCACC CTGCGGATCAGCAGAGTGGAAGCCGAGGACGT	1260

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		GGGCGTGTACTACTGCATGCAGCACCTGGAAT ACCCCTTCACCTTCGGCTCCGGCACCAAGCTGG AAATCAAGCGGGCTGATGCTGCACCGACTGTG TCCATCTTCCCACCATCCAGTGAGCAGTTAACA TCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAAC AACTTCTACCCCAAAGACATCAATGTCAAGTG GAAGATTGATGGCAGTGAACGACAAAATGGCG TCCTGAACAGTTGGACTGATCAGGACAGCAAA GACAGCACCTACAGCATGAGCAGCACCCTCAC GTTGACCAAGGACGAGTATGAACGACATAACA GCTATACCTGTGAGGCCACTCACAAGACATCA ACTTCACCCATTGTCAAGAGCTTCAACAGGAA TGAGTGTTAG	
SM1B320	pDR000007336	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGATATC CAGATGACACAGACTACATCCTCCCTGTCTGCC TCTCTGGGAGACAGAGTCACCATCAGTTGCAG TGCAAGTCAGGGCATTAGCAATTATTTAAACT GGTATCAGCAGAAACCAGATGGAACTGTTAAA CTCCTGATCTATTACACATCAAGTTTACACTCA GGAGTCCCATCAAGGTTCAGTGGCAGTGGGTC TGGGACAGATTATTCTCTCACCATCAGCAACCT GGAACCTGAAGATATTGCCACTTACTATTGTCA GCAGTATAGTAAGCTTCCGTACACGTTCGGAG GGGGGACCAAGCTGGAAATAAAACGGGCTGA TGCTGCACCGACTGTGTCCATCTTCCCACCATC CAGTGAGCAGTTAACATCTGGAGGTGCCTCAG TCGTGTGCTTCTTGAACAACTTCTACCCCAAAG ACATCAATGTCAAGTGGAAGATTGATGGCAGT GAACGACAAAATGGCGTCCTGAACAGTTGGAC TGATCAGGACAGCAAAGACAGCACCTACAGCA TGAGCAGCACCCTCACGTTGACCAAGGACGAG TATGAACGACATAACAGCTATACCTGTGAGGC CACTCACAAGACATCAACTTCACCCATTGTCA AGAGCTTCAACAGGAATGAGTGTTAG	1261
SM1B321	pDR000027048	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC CAGATGACCCAGAGCCCCGCCAGCCTGAGCGC CTCTGTGGGCGAGACAGTGACCATCATCTGCC GGGCCAGCGAGAACATCTACAGCTACCTGGCC TGGTATCAGCAGAAGCAGGGCAAGAGCCCCCA GCTGCTGGTGTACAACGCCAAGACCCTGGTGG AAGGCGTGCCCAGCAGATTCAGCGGCAGCGGC TCCGGCACCCAGTTCAGCCTGAAGATCAACAG CCTGCAGCCCGAGGACTTCGGCAGCTACTACT GCCAGCACCACTACGGCAGCCCCTACACCTTC GGCGGAGGCACCAAGCTGGAAATCAAGCGGG CTGATGCTGCACCGACTGTGTCCATCTTCCCAC	1262

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		CATCCAGTGAGCAGTTAACATCTGGAGGTGCC TCAGTCGTGTGCTTCTTGAACAACTTCTACCCC AAAGACATCAATGTCAAGTGGAAGATTGATGG CAGTGAACGACAAAATGGCGTCCTGAACAGTT GGACTGATCAGGACAGCAAAGACAGCACCTAC AGCATGAGCAGCACCCTCACGTTGACCAAGGA CGAGTATGAACGACATAACAGCTATACCTGTG AGGCCACTCACAAGACATCAACTTCACCCATT GTCAAGAGCTTCAACAGGAATGAGTGTTAG	
SM1B322	pDR000007338	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATT GTGATGACCCAGTCTCACAAATTCATGTCCAC ATCAGTAGGAGACAGGGTCAGCATCACCTGCA AGGCCAGTCAGGATGTGAGTACTGCTGTAGCC TGGTATCAACAGAAACCAGGACAATCTCCTAA ACTACTGATTTACTCGGCATCCTACCGGTACAC TGGAGTCCCTGATCGCTTCACTGGCAGTGGATC TGGGACGGATTTCACTTTCACCATCAGCAGTGT GCAGGCTGAAGACCTGGCAGTTTATTACTGTC AGCAACATTATAGTACTCCGTGGACGTTCGGT GGAGGCACCAAGCTGGAAATCAAACGGGCTG ATGCTGCACCGACTGTGTCCATCTTCCCACCAT CCAGTGAGCAGTTAACATCTGGAGGTGCCTCA GTCGTGTGCTTCTTGAACAACTTCTACCCCAAA GACATCAATGTCAAGTGGAAGATTGATGGCAG TGAACGACAAAATGGCGTCCTGAACAGTTGGA CTGATCAGGACAGCAAAGACAGCACCTACAGC ATGAGCAGCACCCTCACGTTGACCAAGGACGA GTATGAACGACATAACAGCTATACCTGTGAGG CCACTCACAAGACATCAACTTCACCCATTGTCA AGAGCTTCAACAGGAATGAGTGTTAG	1263
SM1B323	pDR000029310	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGAGAC AACCGTGACCCAGAGCCCCGCCAGCCTGAGCA TGGCCATCGGCGAGAAAGTGACCATCCGGTGC ATCACCAGCACCGACATCGACGACGACATGAA CTGGTATCAGCAGAAGCCCGGCGAGCCCCCCA AGCTGCTGATCAGCGAGGGCAACACCCTGCGG CCTGGCGTGCCCAGCAGATTCAGCAGCAGCGG CTACGGCACCGACTTCGTGTTCACCATCGAGA ACATGCTGAGCGAGGACGTGGCCGACTACTAC TGCCTGCAGAGCGACAACCTGCCCTACACCTT CGGCGGAGGCACCAAGCTGGAAATCAAGCGG GCTGATGCTGCACCGACTGTGTCCATCTTCCCA CCATCCAGTGAGCAGTTAACATCTGGAGGTGC CTCAGTCGTGTGCTTCTTGAACAACTTCTACCC CAAAGACATCAATGTCAAGTGGAAGATTGATG GCAGTGAACGACAAAATGGCGTCCTGAACAGT	1264

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		TGGACTGATCAGGACAGCAAAGACAGCACCTA CAGCATGAGCAGCACCCTCACGTTGACCAAGG ACGAGTATGAACGACATAACAGCTATACCTGT GAGGCCACTCACAAGACATCAACTTCACCCAT TGTCAAGAGCTTCAACAGGAATGAGTGTTAG	
SM1B324	pDR000029309	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC GTGATGACCCAGAGCCCCAGCAGCCTGTCCGT GTCTGCCGGCGAGAAAGTGACCATGAGCTGCA AGAGCAGCCAGAGCCTGCTGAACAGCGGCAAC CAGAAGAACTACCTGGCCTGGTATCAGCAGAA GCCCGGCCAGCCCCCCAAGCTGCTGATCTACG GCGCCAGCACCAGAGAAAGCGGCGTGCCCGAC AGATTCACCGGCAGCGGCTCCGGCACCGACTT CACCCTGACCATCAGCAGCGTGCAGGCCGAGG ACCTGGCCGTGTACTACTGCCAGAACGACCAC AGCTACCCCCCCACCTTCGGCGGAGGCACCAA GCTGGAAATCAAGCGGGCTGATGCTGCACCGA CTGTGTCCATCTTCCCACCATCCAGTGAGCAGT TAACATCTGGAGGTGCCTCAGTCGTGTGCTTCT TGAACAACTTCTACCCCAAAGACATCAATGTC AAGTGGAAGATTGATGGCAGTGAACGACAAA ATGGCGTCCTGAACAGTTGGACTGATCAGGAC AGCAAAGACAGCACCTACAGCATGAGCAGCAC CCTCACGTTGACCAAGGACGAGTATGAACGAC ATAACAGCTATACCTGTGAGGCCACTCACAAG ACATCAACTTCACCCATTGTCAAGAGCTTCAAC AGGAATGAGTGTTAG	1265
SM1B325	pDR000029308	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC CAGATGACCCAGAGCCCCAGCAGCCTGAGCGC CAGCCTGGGCGAGAGAGTGTCCCTGACCTGCC GGGCCAGCCAGGACATCGGCAACAGCCTGAAC TGGCTGCAGCAGAAGCCCGACGGCACCATCAA GCGGCTGATCTACGCCACCAGCAACCTGGACA GCGGCGTGCCCAAGCGGTTCAGCGGCAGCAGA TCCGGCAGCGACTACAGCCTGACCATCAGCAG CCTGGAAAGCGAGGACTTCGTGAACTACTACT GCCTGCAGTTCGCCAGCAGCCCCCTGACCTTCG GCACCGGCACCAAGCTGGAAATCAAGCGGGCT GATGCTGCACCGACTGTGTCCATCTTCCCACCA TCCAGTGAGCAGTTAACATCTGGAGGTGCCTC AGTCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGGCA GTGAACGACAAAATGGCGTCCTGAACAGTTGG ACTGATCAGGACAGCAAAGACAGCACCTACAG CATGAGCAGCACCCTCACGTTGACCAAGGACG AGTATGAACGACATAACAGCTATACCTGTGAG	1266

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		GCCACTCACAAGACATCAACTTCACCCATTGTC AAGAGCTTCAACAGGAATGAGTGTTAG	
SM1B326	pDR000007289	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATT CAGATGACTCAGTCTCCAGCCTCCCTATCTGTA TCTGTGGGAGAAACTGTCACCATCACATGTCG AGCAAGTGAAAATATTTACAGTAATTTAGCAT GGTATCAGCAGAAACAGGGAAAATCTCCTCAG CTCCTGGTCTATGCTGCAACAAACTTAGCAGAT GGTGTGCCATCAAGGTTCAGTGGCAGTGGATC AGGCACACAGTATTCCCTCAAGATCAACAGCC TGCAGTCTGAAGATTTTGGGAGTTATTACTGTC AACATTTTTGGGGTACTCCGTACACGTTCGGAG GGGGGACCAAGCTGGAAATAAAACGGGCTGA TGCTGCACCGACTGTGTCCATCTTCCCACCATC CAGTGAGCAGTTAACATCTGGAGGTGCCTCAG TCGTGTGCTTCTTGAACAACTTCTACCCCAAAG ACATCAATGTCAAGTGGAAGATTGATGGCAGT GAACGACAAAATGGCGTCCTGAACAGTTGGAC TGATCAGGACAGCAAAGACAGCACCTACAGCA TGAGCAGCACCCTCACGTTGACCAAGGACGAG TATGAACGACATAACAGCTATACCTGTGAGGC CACTCACAAGACATCAACTTCACCCATTGTCA AGAGCTTCAACAGGAATGAGTGTTAG	1267
SM1B327	pDR000029307	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCCAGATC GTGCTGACCCAGAGCCCCGCCATCATGAGCGC CAGCCCTGGCGAGAAAGTGACCATGACCTGCA GCGCCAGCAGCAACGTGTCCTACATGCACTGG TTCCAGCAGAAGTCCGGCACCAGCCCCAAGCG GTGGATCTACGACACCAGCAAGCTGGCCAGCG GCGTGCCCGCCAGATTTTCTGGCAGCGGCAGC GGCACCAGCTACAGCCTGACCGTGTCCAGCAT GGAAGCCGAGGACGCCGCCACCTACTACTGCC AGCAGTGGTCCAGCAACCCCCGGACCTTCGGC GGAGGCACCAAGCTGGAAATCAAGCGGGCTG ATGCTGCACCGACTGTGTCCATCTTCCCACCAT CCAGTGAGCAGTTAACATCTGGAGGTGCCTCA GTCGTGTGCTTCTTGAACAACTTCTACCCCAAA GACATCAATGTCAAGTGGAAGATTGATGGCAG TGAACGACAAAATGGCGTCCTGAACAGTTGGA CTGATCAGGACAGCAAAGACAGCACCTACAGC ATGAGCAGCACCCTCACGTTGACCAAGGACGA GTATGAACGACATAACAGCTATACCTGTGAGG CCACTCACAAGACATCAACTTCACCCATTGTCA AGAGCTTCAACAGGAATGAGTGTTAG	1268
SM1B328	pDR000027029	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC	1269

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		CAGATGACCCAGAGCCCCAGCAGCCTGAGCGC CAGCCTGGGCGAGAGAGTGTCCCTGACCTGCC GGGCCAGCCAGGACATCGGCAGCTACCTGAAC TGGCTGCAGCAGGAACCCGACGGCACCATCAA GCGGCTGATCTACGCCACCAGCTCCCTGGACA GCGGCGTGCCCAAGCGGTTCAGCGGCAGCAGA TCTGGCGCCGACTACAGCCTGACCATCAGCAG CCTGGAAAGCGAGGACTTCGTGGACTACTACT GCCTGCAGTACGCCACCTCCCCCTGGACCTTCG GCGGAGGCACCAAGCTGGAAATCAAGCGGGCT GATGCTGCACCGACTGTGTCCATCTTCCCACCA TCCAGTGAGCAGTTAACATCTGGAGGTGCCTC AGTCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGGCA GTGAACGACAAAATGGCGTCCTGAACAGTTGG ACTGATCAGGACAGCAAAGACAGCACCTACAG CATGAGCAGCACCCTCACGTTGACCAAGGACG AGTATGAACGACATAACAGCTATACCTGTGAG GCCACTCACAAGACATCAACTTCACCCATTGTC AAGAGCTTCAACAGGAATGAGTGTTAG	
SM1B329	pDR000029306	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC CAGATGACCCAGAGCAGCAGCTACCTGAGCGT GTCCCTGGGCGGCAGAGTGACCATCACATGCA AGGCCAGCGACCACATCAACAACTGGCTGGCC TGGTATCAGCAGAAGCCCGGCAACGCCCCCAG ACTGCTGATCAGCGGCGCCACCAGCCTGGAAA CCGGCGTGCCAAGCAGATTCAGCGGCAGCGGC TCCGGCAAGGACTACACCCTGAGCATCACCAG CCTGCAGACCGAGGACGTGGCCACCTACTACT GCCAGCAGTACTGGTCCACCCCCTACACCTTCG GCGGAGGCACCAAGCTGGAAATCAAGCGGGCT GATGCTGCACCGACTGTGTCCATCTTCCCACCA TCCAGTGAGCAGTTAACATCTGGAGGTGCCTC AGTCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGGCA GTGAACGACAAAATGGCGTCCTGAACAGTTGG ACTGATCAGGACAGCAAAGACAGCACCTACAG CATGAGCAGCACCCTCACGTTGACCAAGGACG AGTATGAACGACATAACAGCTATACCTGTGAG GCCACTCACAAGACATCAACTTCACCCATTGTC AAGAGCTTCAACAGGAATGAGTGTTAG	1270
SM1B330	pDR000029305	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCCAGATC GTGCTGACCCAGAGCCCTGCCCTGATGAGCGC CAGCCCTGGCGAGAAAGTGACCATGACCTGCA GCGCCAGCAGCAGCGTGTCCTACATGTACTGG TATCAGCAGAAGCCCAGAAGCAGCCCCAAGCT	1271

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		GAAGTACGCCAGCAACCTGGCCAGCGGCGTGC CCGCCAGATTTTCTGGCAGCGGCAGCGGCACC AGCTACAGCCTGACCATCAGCAGCATGGAAGC CGAGGACGCCGCCACCTACTACTGCCAGCAGT GGTCCAGCAACCCCCCCATCACCTTCGGAGCC GGCACCAAGCTGGAACTGAAGCGGGCTGATGC TGCACCGACTGTGTCCATCTTCCCACCATCCAG TGAGCAGTTAACATCTGGAGGTGCCTCAGTCG TGTGCTTCTTGAACAACTTCTACCCCAAAGACA TCAATGTCAAGTGGAAGATTGATGGCAGTGAA CGACAAAATGGCGTCCTGAACAGTTGGACTGA TCAGGACAGCAAAGACAGCACCTACAGCATGA GCAGCACCCTCACGTTGACCAAGGACGAGTAT GAACGACATAACAGCTATACCTGTGAGGCCAC TCACAAGACATCAACTTCACCCATTGTCAAGA GCTTCAACAGGAATGAGTGTTAG	
SM1B331	pDR000027141	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC GTGATGACCCAGAGCCCCGCCACCCTGAGCGT GACCCCTGGCGATAGAGTGTCCCTGAGCTGCC GGGCCAGCCAGAGCATCAGCGACTACCTGCAC TGGTATCAGCAGAAGTCCCACGAGAGCCCCAG ACTGCTGATTAAGTACGACAGCCAGTCCATCA GCGGCATCCCCAGCAGATTCAGCGGCAGCGGC TCCGGCTCCGACTTCACCCTGAGCATCAACAG CGTGGAACCCGAGGACGTGGGCGTGTACTACT GCCAGAACGGCCACCGGTTCCCTTTCACCTTCG GCGGAGGCACCAAGCTGGAAATCAAGCGGGCT GATGCTGCACCGACTGTGTCCATCTTCCCACCA TCCAGTGAGCAGTTAACATCTGGAGGTGCCTC AGTCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGGCA GTGAACGACAAAATGGCGTCCTGAACAGTTGG ACTGATCAGGACAGCAAAGACAGCACCTACAG CATGAGCAGCACCCTCACGTTGACCAAGGACG AGTATGAACGACATAACAGCTATACCTGTGAG GCCACTCACAAGACATCAACTTCACCCATTGTC AAGAGCTTCAACAGGAATGAGTGTTAG	1272
SM1B332	pDR000029304	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCCAGATC GTGCTGACCCAGAGCCCCGCCATCATGAGCGC CAGCCCTGGCGAGAAAGTGACCCTGACCTGCA GCGCCAGCAGCAGCGTGTCCAGCAGCTACCTG TTCTGGTATCAGCAGAAGCCCGGCAGCAGCCC CAAGCTGTGGATCTACAGCACCAGCAACCTGG CCAGCGGCGTGCCCGTGCGGTTTAGCGGCAGC GGCTTTGGCACCAGCTACAGCCTGACCATCAG CCGGATGGAAGCCGAGGACGCCGCCAGCTACT	1273

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		TCTGCCACCAGTGGTCCAGCTACCCCCCCACCT TCGGAGCCGGCACCAAGCTGGAACTGAAGCGG GCTGATGCTGCACCGACTGTGTCCATCTTCCCA CCATCCAGTGAGCAGTTAACATCTGGAGGTGC CTCAGTCGTGTGCTTCTTGAACAACTTCTACCC CAAAGACATCAATGTCAAGTGGAAGATTGATG GCAGTGAACGACAAAATGGCGTCCTGAACAGT TGGACTGATCAGGACAGCAAAGACAGCACCTA CAGCATGAGCAGCACCCTCACGTTGACCAAGG ACGAGTATGAACGACATAACAGCTATACCTGT GAGGCCACTCACAAGACATCAACTTCACCCAT TGTCAAGAGCTTCAACAGGAATGAGTGTTAG	
SM1B333	pDR000029303	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC GTGCTGACCCAGAGCCCTGCCAGCCTGGCCGT GTCTCTGGGCCAGAGAGCCACCATCAGCTGCC GGGCCAGCGAGAGCGTGGACAGCTACGGCAA CAGCTTCATGCACTGGTATCAGCAGAAGCCCG GCCAGCCCCCCAAGCTGCTGATCTACCTGGCC AGCAACCTGGAAAGCGGCGTGCCCGCCAGATT CAGCGGCAGCGGCAGCAGAACCGACTTCACCC TGACCATCGACCCCGTGGAAGCCGACGACGCC GCCACCTACTACTGCCAGCAGAACAACGAGGA CCCCTACACCTTCGGCGGAGGCACCAAGCTGG AAATCAAGCGGGCTGATGCTGCACCGACTGTG TCCATCTTCCCACCATCCAGTGAGCAGTTAACA TCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAAC AACTTCTACCCCAAAGACATCAATGTCAAGTG GAAGATTGATGGCAGTGAACGACAAAATGGCG TCCTGAACAGTTGGACTGATCAGGACAGCAAA GACAGCACCTACAGCATGAGCAGCACCCTCAC GTTGACCAAGGACGAGTATGAACGACATAACA GCTATACCTGTGAGGCCACTCACAAGACATCA ACTTCACCCATTGTCAAGAGCTTCAACAGGAA TGAGTGTTAG	1274
SM1B334	pDR000029302	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACGTG CTGATGACCCAGACCCCCCTGAGCCTGCCCGT GTCTCTGGGCGATCAGGCCAGCATCAGCTGCC GGTCCAGCCAGAGCATCGTGTACAGCAACGGC AACACCTACCTGGACTGGTATCTGCAGAAGCC CGGCCAGCCCCCCAAGCTGCTGATCTACAAGG TGTCCAACCGGTTCAGCGGCGTGCCCGACAGA TTCAGCGGCAGCGGCTCCGGCACCGACTTCAT CCTGAAGATCAGCCGGGTGGAAGCCGAGGACC TGGGCGTGTACTACTGTTTTCAGGGCAGCCAC GTGCCCTGGACCTTCGGCGGAGGCACCAAGCT GGAAATCAAGCGGGCTGATGCTGCACCGACTG	1275

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		TGTCCATCTTCCCACCATCCAGTGAGCAGTTAA CATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGA ACAACTTCTACCCCAAAGACATCAATGTCAAG TGGAAGATTGATGGCAGTGAACGACAAAATGG CGTCCTGAACAGTTGGACTGATCAGGACAGCA AAGACAGCACCTACAGCATGAGCAGCACCCTC ACGTTGACCAAGGACGAGTATGAACGACATAA CAGCTATACCTGTGAGGCCACTCACAAGACAT CAACTTCACCCATTGTCAAGAGCTTCAACAGG AATGAGTGTTAG	
SM1B335	pDR000029301	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACGTG GTGGTCACCCAGACCCCCCTGAGCCTGCCCGT GTCCTTCGGCGACCAGGTGTCCATCAGCTGCA GAAGCAGCCAGAGCCTGGCCAACAGCTACGGC AACACCTACCTGAGCTGGTATCTGCACAAGCC CGGCCAGAGCCCCCAGCTGCTGATCTACGGCA TCAGCAACCGGTTCAGCGGCGTGCCCGACAGA TTCAGCGGCAGCGGCTCCGGCACCGACTTCAC CCTGAAGATCAGCACCATCAAGCCCGAGGACC TGGGCATGTACTACTGTCTGCAGGGCACCCAC CAGCCCTACACCTTCGGCGGAGGCACCAAGCT GGAAATCAAGCGGGCTGATGCTGCACCGACTG TGTCCATCTTCCCACCATCCAGTGAGCAGTTAA CATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGA ACAACTTCTACCCCAAAGACATCAATGTCAAG TGGAAGATTGATGGCAGTGAACGACAAAATGG CGTCCTGAACAGTTGGACTGATCAGGACAGCA AAGACAGCACCTACAGCATGAGCAGCACCCTC ACGTTGACCAAGGACGAGTATGAACGACATAA CAGCTATACCTGTGAGGCCACTCACAAGACAT CAACTTCACCCATTGTCAAGAGCTTCAACAGG AATGAGTGTTAG	1276
SM1B336	pDR000029300	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC GTGATGAGCCAGAGCCCCAGCAGCCTGGCCGT GTCCGTGGGCGAGAAAGTGACCATGAGCTGCA AGAGCAGCCAGAGCGTGCTGTACAACAGCAAC CAGCGGAACTACCTGGCCTGGTATCAGCAGAA GCCCGGCCAGTCCCCCAAGCTGCTGATCTACT GGGCCAGCACCCGCGAGAGCGGCGTGCCAGAT AGAAGCACAGGCAGCGGCAGCGGCACCGACTT CACCCTGACCATCAGCAGCGTGCAGGCCGAGG ATCTGGCCGTGTACTACTGCCACCAGTACCTGA GCAGCTACACCTTCGGCGGAGGCACCAAGCTG GAAATCAAGCGGGCTGATGCTGCACCGACTGT GTCCATCTTCCCACCATCCAGTGAGCAGTTAAC ATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAA	1277

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		CAACTTCTACCCCAAAGACATCAATGTCAAGT GGAAGATTGATGGCAGTGAACGACAAAATGGC GTCCTGAACAGTTGGACTGATCAGGACAGCAA AGACAGCACCTACAGCATGAGCAGCACCCTCA CGTTGACCAAGGACGAGTATGAACGACATAAC AGCTATACCTGTGAGGCCACTCACAAGACATC AACTTCACCCATTGTCAAGAGCTTCAACAGGA ATGAGTGTTAG	
SM1B337	pDR000029299	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC GTGATGACCCAGAGCCACAAGTTCATGAGCAC CAGCGTGGGCGACCGGGTGTCCATCACATGCA AGGCCAGCCAGGACGTGGGCACCGCCGTGGCC TGGTATCAGCAGAAGCCCGGCCAGAGCCCCAA GCTGCTGATCTACTGGGCCAGCACCAGACACA CCGGCGTGCCCGACAGATTCACAGGCAGCGGC AGCGGCACCGACTTCACCCTGACCATCAGCAA CGTGCAGAGCGAGGACCTGGCCGACTACTTCT GCCAGCAGTACAGCAGCTACCCCCTGACCTTC GGAGCCGGCACCAAGCTGGAACTGAAGCGGG CTGATGCTGCACCGACTGTGTCCATCTTCCCAC CATCCAGTGAGCAGTTAACATCTGGAGGTGCC TCAGTCGTGTGCTTCTTGAACAACTTCTACCCC AAAGACATCAATGTCAAGTGGAAGATTGATGG CAGTGAACGACAAAATGGCGTCCTGAACAGTT GGACTGATCAGGACAGCAAAGACAGCACCTAC AGCATGAGCAGCACCCTCACGTTGACCAAGGA CGAGTATGAACGACATAACAGCTATACCTGTG AGGCCACTCACAAGACATCAACTTCACCCATT GTCAAGAGCTTCAACAGGAATGAGTGTTAG	1278
SM1B338	pDR000029319	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC GTGCTGACCCAGAGCCCTGCCAGCCTGGCCGT GTCTCTGGGCCAGAGAGCCACCATCAGCTGCC GGGCCAGCGAGAGCGTGGACAGCTACGGCAA CAGCTTCATGCACTGGTATCAGCAGAAGCCCG GCCAGCCCCCCAAGCTGCTGATCTACCGGGCC AGCAACCTGGAAAGCGGCATCCCCGCCAGATT CAGCGGCAGCGGCAGCCGGACCGACTTCACCC TGACCATCAACCCCGTGGAAGCCGACGACGTG GCCACCTACTACTGCCAGCAGAGCAACGAGGA CCCCCCCTGGACCTTCGGCGGAGGCACCAAGC TGGAAATCAAGCGGGCTGATGCTGCACCGACT GTGTCCATCTTCCCACCATCCAGTGAGCAGTTA ACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTG AACAACTTCTACCCCAAAGACATCAATGTCAA GTGGAAGATTGATGGCAGTGAACGACAAAATG GCGTCCTGAACAGTTGGACTGATCAGGACAGC	1279

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		AAAGACAGCACCTACAGCATGAGCAGCACCCT CACGTTGACCAAGGACGAGTATGAACGACATA ACAGCTATACCTGTGAGGCCACTCACAAGACA TCAACTTCACCCATTGTCAAGAGCTTCAACAG GAATGAGTGTTAG	
SM1B339	pDR000029319	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC GTGCTGACCCAGAGCCCTGCCAGCCTGGCCGT GTCTCTGGGCCAGAGAGCCACCATCAGCTGCC GGGCCAGCGAGAGCGTGGACAGCTACGGCAA CAGCTTCATGCACTGGTATCAGCAGAAGCCCG GCCAGCCCCCCAAGCTGCTGATCTACCGGGCC AGCAACCTGGAAAGCGGCATCCCCGCCAGATT CAGCGGCAGCGGCAGCCGGACCGACTTCACCC TGACCATCAACCCCGTGGAAGCCGACGACGTG GCCACCTACTACTGCCAGCAGAGCAACGAGGA CCCCCCCTGGACCTTCGGCGGAGGCACCAAGC TGGAAATCAAGCGGGCTGATGCTGCACCGACT GTGTCCATCTTCCCACCATCCAGTGAGCAGTTA ACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTG AACAACTTCTACCCCAAAGACATCAATGTCAA GTGGAAGATTGATGGCAGTGAACGACAAAATG GCGTCCTGAACAGTTGGACTGATCAGGACAGC AAAGACAGCACCTACAGCATGAGCAGCACCCT CACGTTGACCAAGGACGAGTATGAACGACATA ACAGCTATACCTGTGAGGCCACTCACAAGACA TCAACTTCACCCATTGTCAAGAGCTTCAACAG GAATGAGTGTTAG	1280
SM1B340	pDR000029298	ATGGAGACACATTCTCAGGTCTTTGTATACATG TTGCTGTGGTTGTCTGGTGTCGAGGGCGACATC CAGATGACCCAGACCACCAGCAGCCTGAGCGC CAGCCTGGGCGACAGAGTGACCATCAGCTGCC GGGCCAGCCAGGACATCGACAACTACCTGAAC TGGTATCAGCAGAAACCCGACGGCACCGTGAA GCTGCTGATCAGCTACACCAGCCGGCTGCACA GCGGCGTGCCCAGCAGATTTTCTGGCAGCGGC AGCGGCACCGACTACAGCCTGACCATCTCCAA CCTGGAACAGGAAGATTTCGCTACCTACTTCTG TCAGCAGGGCTACACCCTGCCCTGGACCTTCG GCGGAGGCACCAAGCTGGAAATCAAGCGGGCT GATGCTGCACCGACTGTGTCCATCTTCCCACCA TCCAGTGAGCAGTTAACATCTGGAGGTGCCTC AGTCGTGTGCTTCTTGAACAACTTCTACCCCAA AGACATCAATGTCAAGTGGAAGATTGATGGCA GTGAACGACAAAATGGCGTCCTGAACAGTTGG ACTGATCAGGACAGCAAAGACAGCACCTACAG CATGAGCAGCACCCTCACGTTGACCAAGGACG AGTATGAACGACATAACAGCTATACCTGTGAG	1281

mAB/Fab name	Construct ID	Light Chain Primary Transcript	SEQ ID NO:
		GCCACTCACAAGACATCAACTTCACCCATTGTC AAGAGCTTCAACAGGAATGAGTGTTAG	

WHAT IS CLAIMED:

1. An antibody or binding portion thereof that binds *Staphylococcus aureus* Leukocidin AB comprising a heavy chain variable region, wherein said heavy chain variable region comprises:

a complementarity-determining region 1 (CDR-H1) comprising an amino acid sequence of any one of SEQ ID NOs: 1-20, or a modified amino acid sequence of any one of SEQ ID NOs: 1-20, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 1-20;

a complementarity-determining region 2 (CDR-H2) comprising an amino acid sequence of any one of SEQ ID NOs: 21-41, or a modified amino acid sequence of any one of SEQ ID NOs: 21-41, said modified sequences having at least 80% sequence identity to any one of SEQ ID NOs: 21-41; and

a complementarity-determining region 3 (CDR-H3) comprising an amino acid sequence of any one of SEQ ID NOs: 42-62 or a modified amino acid sequence of any one of SEQ ID NO:42-62 said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 42-62.

2. The antibody or binding portion thereof of claim 1, wherein said heavy chain variable region is selected from the group consisting of:

(i) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 1, the CDR-H2 of SEQ ID NO: 21, and the CDR-H3 of SEQ ID NO: 42;

(ii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 2, the CDR-H2 of SEQ ID NO: 22, and the CDR-H3 of SEQ ID NO: 43;

(iii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 2, the CDR-H2 of SEQ ID NO: 22, and the CDR-H3 of SEQ ID NO: 45;

(iv) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 3, the CDR-H2 of SEQ ID NO: 23, and the CDR-H3 of SEQ ID NO: 44;

(v) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 4, the CDR-H2 of SEQ ID NO: 24, and the CDR-H3 of SEQ ID NO: 46;

(vi) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 5, the CDR-H2 of SEQ ID NO: 25, and the CDR-H3 of SEQ ID NO: 47;

(vii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 6, the CDR-H2 of SEQ ID NO: 26, and the CDR-H3 of SEQ ID NO: 48;

(viii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 7, the CDR-H2 of SEQ ID NO: 27, and the CDR-H3 of SEQ ID NO: 49;

(ix) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 8, the CDR-H2 of SEQ ID NO: 28, and the CDR-H3 of SEQ ID NO: 50;

(x) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO:9 , the CDR-H2 of SEQ ID NO: 29, and the CDR-H3 of SEQ ID NO: 51;

(xi) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 10, the CDR-H2 of SEQ ID NO: 30, and the CDR-H3 of SEQ ID NO: 52;

(xii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 11, the CDR-H2 of SEQ ID NO: 31, and the CDR-H3 of SEQ ID NO: 53;

(xiii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 12, the CDR-H2 of SEQ ID NO: 32, and the CDR-H3 of SEQ ID NO: 54;

(xiv) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 13, the CDR-H2 of SEQ ID NO: 33, and the CDR-H3 of SEQ ID NO: 55;

(xv) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 14, the CDR-H2 of SEQ ID NO: 34, and the CDR-H3 of SEQ ID NO: 56;

(xvi) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 14, the CDR-H2 of SEQ ID NO: 35, and the CDR-H3 of SEQ ID NO: 56;

(xvii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 15, the CDR-H2 of SEQ ID NO: 36, and the CDR-H3 of SEQ ID NO: 57;

(xviii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 16, the CDR-H2 of SEQ ID NO: 37, and the CDR-H3 of SEQ ID NO: 58;

(xix) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 17, the CDR-H2 of SEQ ID NO: 38, and the CDR-H3 of SEQ ID NO: 59;

(xx) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 18, the CDR-H2 of SEQ ID NO:39, and the CDR-H3 of SEQ ID NO: 60;

(xxi) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 19, the CDR-H2 of SEQ ID NO: 40, and the CDR-H3 of SEQ ID NO: 61; and

(xxii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 20, the CDR-H2 of SEQ ID NO: 41, and the CDR-H3 of SEQ ID NO: 62.

3. The antibody or binding portion thereof of claim 1 further comprising:

a light chain variable region, wherein said light chain variable region comprises:

a complementarity-determining region 1 (CDR-L1) having an amino acid sequence of any one of SEQ ID NOs: 63-87, or a modified amino acid sequence of any one of SEQ ID NO: 63-87, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 63-87;

a complementarity-determining region 2 (CDR-L2) having an amino acid sequence of any one of SEQ ID NOs: 88-105, or a modified amino acid sequence of any one of SEQ ID NO: 88-105, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 88-105; and

a complementarity-determining region 3 (CDR-L3) having an amino acid sequence of any one of SEQ ID NOs: 106-135 or a modified amino acid sequence of any one of SEQ ID NO: 106-135, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 106-135.

4. The antibody or binding portion thereof of claim 3, wherein said light chain variable region is selected from the group consisting of:

(i) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 63, the CDR-L2 of SEQ ID NO: 88, and the CDR-L3 of SEQ ID NO: 106;

(ii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 64, the CDR-L2 of SEQ ID NO: 89, and the CDR-L3 of SEQ ID NO: 107;

(iii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 65, the CDR-L2 of SEQ ID NO: 90, and the CDR-L3 of SEQ ID NO: 108;

(iv) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 66, the CDR-L2 of SEQ ID NO: 91, and the CDR-L3 of SEQ ID NO: 109;

(v) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 67, the CDR-L2 of SEQ ID NO: 88, and the CDR-L3 of SEQ ID NO: 110;

(vi) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 68, the CDR-L2 of SEQ ID NO: 92, and the CDR-L3 of SEQ ID NO: 111;

(vii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 69, the CDR-L2 of SEQ ID NO: 93, and the CDR-L3 of SEQ ID NO: 112;

(viii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 70, the CDR-L2 of SEQ ID NO: 94, and the CDR-L3 of SEQ ID NO: 113;

(ix) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 71, the CDR-L2 of SEQ ID NO: 95, and the CDR-L3 of SEQ ID NO: 114;

(x) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 72, the CDR-L2 of SEQ ID NO: 96, and the CDR-L3 of SEQ ID NO: 115;

(xi) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 73, the CDR-L2 of SEQ ID NO: 97, and the CDR-L3 of SEQ ID NO: 116;

(xii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 66, the CDR-L2 of SEQ ID NO: 92, and the CDR-L3 of SEQ ID NO: 117;

(xiii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 74, the CDR-L2 of SEQ ID NO: 89, and the CDR-L3 of SEQ ID NO: 118;

(xiv) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 75, the CDR-L2 of SEQ ID NO: 98, and the CDR-L3 of SEQ ID NO: 119;

(xv) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 76, the CDR-L2 of SEQ ID NO: 96, and the CDR-L3 of SEQ ID NO: 120;

(xvi) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 77, the CDR-L2 of SEQ ID NO: 99, and the CDR-L3 of SEQ ID NO: 121;

(xvii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 78, the CDR-L2 of SEQ ID NO: 100, and the CDR-L3 of SEQ ID NO: 122;

(xviii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 78, the CDR-L2 of SEQ ID NO: 99, and the CDR-L3 of SEQ ID NO: 123;

(xix) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 79, the CDR-L2 of SEQ ID NO: 101, and the CDR-L3 of SEQ ID NO: 124;

(xx) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 80, the CDR-L2 of SEQ ID NO: 96, and the CDR-L3 of SEQ ID NO: 120;

(xxi) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 66, the CDR-L2 of SEQ ID NO: 92, and the CDR-L3 of SEQ ID NO: 125;

(xxii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 71, the CDR-L2 of SEQ ID NO: 95, and the CDR-L3 of SEQ ID NO: 114;

(xxiii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 81, the CDR-L2 of SEQ ID NO: 102, and the CDR-L3 of SEQ ID NO: 126;

(xxiv) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 69, the CDR-L2 of SEQ ID NO: 93, and the CDR-L3 of SEQ ID NO: 127;

(xxv) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 79, the CDR-L2 of SEQ ID NO: 101, and the CDR-L3 of SEQ ID NO: 128;

(xxvi) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 82, the CDR-L2 of SEQ ID NO: 103, and the CDR-L3 of SEQ ID NO: 129;

(xxvii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 75, the CDR-L2 of SEQ ID NO: 98, and the CDR-L3 of SEQ ID NO: 119;

(xxviii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 83, the CDR-L2 of SEQ ID NO: 104, and the CDR-L3 of SEQ ID NO: 130;

(xxix) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 84, the CDR-L2 of SEQ ID NO: 88, and the CDR-L3 of SEQ ID NO: 131;

(xxx) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 74, the CDR-L2 of SEQ ID NO: 89, and the CDR-L3 of SEQ ID NO: 132;

(xxxi) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 74, the CDR-L2 of SEQ ID NO: 89, and the CDR-L3 of SEQ ID NO: 133;

(xxxii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 66, the CDR-L2 of SEQ ID NO: 92, and the CDR-L3 of SEQ ID NO: 125;

(xxxiii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 70, the CDR-L2 of SEQ ID NO: 94, and the CDR-L3 of SEQ ID NO: 113;

(xxxiv) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 85, the CDR-L2 of SEQ ID NO: 105, and the CDR-L3 of SEQ ID NO: 134;

(xxxv) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 86, the CDR-L2 of SEQ ID NO: 96, and the CDR-L3 of SEQ ID NO: 135; and

(xxxvi) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 87, the CDR-L2 of SEQ ID NO: 99, and the CDR-L3 of SEQ ID NO: 122.

5. The antibody or binding portion thereof of claim 1, wherein said antibody comprises a variable light (VL) chain and a variable heavy (VH) chain, wherein said VL chain comprises an amino acid sequence selected from SEQ ID NOs: 136-176 or an amino acid sequence that is at least 80% identical to any one of the amino acid sequence selected from SEQ ID NOs: 136-176, and said VH chain comprises an amino acid sequence selected from SEQ ID NOs: 177-217 or an amino acid sequence that is at least 80% identical to any one of the amino acid sequence selected from SEQ ID NOs: 177-217.

6. The antibody or binding portion thereof of claim 1, wherein said antibody neutralizes *S. aureus* leukocidin AB cytolytic activity.

7. The antibody or binding portion thereof of claim 6, wherein said antibody comprises:

a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 11, the CDR-H2 of SEQ ID NO: 31, and the CDR-H3 of SEQ ID NO: 53 and

a light chain variable region comprising the CDR-L1 of SEQ ID NO: 66, the CDR-L2 of SEQ ID NO: 92, and the CDR-L3 of SEQ ID NO: 117.

8. An antibody or binding portion thereof that competes for leukocidin AB binding with a monoclonal antibody, wherein said monoclonal antibody comprises a heavy chain variable region comprising a CDR-H1 of SEQ ID NO: 11, a CDR-H2 of SEQ ID NO: 31, and a CDR-H3 of SEQ ID NO: 53, and a light chain variable region comprising a CDR-L1 of SEQ ID NO: 66, a CDR-L2 of SEQ ID NO: 92, and a CDR-L3 of SEQ ID NO: 117

9. An antibody or binding portion thereof that binds *Staphylococcus aureus* Leukocidin E comprising a heavy chain variable region, wherein said heavy chain variable region comprises:

a complementarity-determining region 1 (CDR-H1) comprising an amino acid sequence of any one of SEQ ID NOs: 287-291, or a modified amino acid sequence of any one of SEQ ID NOs: 287-291, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 287-291;

a complementarity-determining region 2 (CDR-H2) comprising an amino acid sequence of any one of SEQ ID NOs: 292-296, or a modified amino acid sequence of any one of SEQ ID NOs: 292-296, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 292-296; and

a complementarity-determining region 3 (CDR-H3) comprising an amino acid sequence of any one of SEQ ID NOs: 297-302 or a modified amino acid sequence of any one of SEQ ID NO: 297-302 said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 297-302.

10. The antibody or binding portion thereof of claim 9, wherein said heavy chain variable region is selected from the group consisting of:

(i) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 287, the CDR-H2 of SEQ ID NO: 292, and the CDR-H3 of SEQ ID NO: 297;

(ii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 288, the CDR-H2 of SEQ ID NO: 292, and the CDR-H3 of SEQ ID NO: 298;

(iii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 289, the CDR-H2 of SEQ ID NO: 293, and the CDR-H3 of SEQ ID NO: 299;

(iv) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 288, the CDR-H2 of SEQ ID NO: 294, and the CDR-H3 of SEQ ID NO: 300;

(v) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 290, the CDR-H2 of SEQ ID NO: 295, and the CDR-H3 of SEQ ID NO: 301;

(vi) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 288, the CDR-H2 of SEQ ID NO: 294, and the CDR-H3 of SEQ ID NO: 300; and

(vii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 291, the CDR-H2 of SEQ ID NO: 296, and the CDR-H3 of SEQ ID NO: 302.

11. The antibody or binding portion thereof of claim 9 further comprising:

a light chain variable region, wherein said light chain variable region comprises:

a complementarity-determining region 1 (CDR-L1) having an amino acid sequence of any one of SEQ ID NOs: 303-309, or a modified amino acid sequence of any one of SEQ ID NO: 303-309, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 303-309;

a complementarity-determining region 2 (CDR-L2) having an amino acid sequence of any one of SEQ ID NOs: 310-313, or a modified amino acid sequence of any one of SEQ ID NO: 310-313, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 310-313; and

a complementarity-determining region 3 (CDR-L3) having an amino acid sequence of any one of SEQ ID NOs: 314-323, or a modified amino acid sequence of any one of SEQ ID NO: 314-323, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 314-323.

12. The antibody or binding portion thereof of claim 11, wherein said light chain variable region is selected from the group consisting of:

(i) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 303, the CDR-L2 of SEQ ID NO: 310, and the CDR-L3 of SEQ ID NO: 314;

(ii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 304, the CDR-L2 of SEQ ID NO: 311, and the CDR-L3 of SEQ ID NO: 315;

(iii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 305, the CDR-L2 of SEQ ID NO: 310, and the CDR-L3 of SEQ ID NO: 316;

(iv) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 306, the CDR-L2 of SEQ ID NO: 311, and the CDR-L3 of SEQ ID NO: 317

(v) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 306, the CDR-L2 of SEQ ID NO: 311, and the CDR-L3 of SEQ ID NO: 318;

(vi) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 303, the CDR-L2 of SEQ ID NO: 310, and the CDR-L3 of SEQ ID NO: 319;

(vii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 307, the CDR-L2 of SEQ ID NO: 312, and the CDR-L3 of SEQ ID NO: 320;

(viii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 308, the CDR-L2 of SEQ ID NO: 311, and the CDR-L3 of SEQ ID NO: 321;

(ix) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 306, the CDR-L2 of SEQ ID NO: 311, and the CDR-L3 of SEQ ID NO: 322; and

(x) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 309, the CDR-L2 of SEQ ID NO: 313, and the CDR-L3 of SEQ ID NO: 323.

13. The antibody or binding portion thereof of claim 9, wherein said antibody comprises a variable light (VL) chain and a variable heavy (VH) chain, wherein said VL chain comprises an amino acid sequence selected from SEQ ID NOs: 324-335 or an amino acid sequence that is at least 80% identical to any one of the amino acid sequence selected from SEQ ID NOs: 324-335, and said VH chain comprises an amino acid sequence selected from SEQ ID NOs: 336-347 or an amino acid sequence that is at least 80% identical to any one of the amino acid sequence selected from SEQ ID NOs: 336-347.

14. The antibody or binding portion thereof of claim 9, wherein said antibody neutralizes *S. aureus* leukocidin ED cytolytic activity.

15. The antibody or binding portion thereof of claim 9, wherein said antibody comprises:

a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 290, the CDR-H2 of SEQ ID NO: 295, and the CDR-H3 of SEQ ID NO: 301 and

a light chain variable region comprising the CDR-L1 of SEQ ID NO: 308, the CDR-L2 of SEQ ID NO: 311, and the CDR-L3 of SEQ ID NO: 321.

16. An antibody or binding portion thereof that competes for leukocidin E binding with a monoclonal antibody, wherein said monoclonal antibody comprises a heavy chain variable region comprising a CDR-H1 of SEQ ID NO: 290, a CDR-H2 of SEQ ID NO: 295, and a CDR-H3 of SEQ ID NO: 301, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 308, the CDR-L2 of SEQ ID NO: 311, and the CDR-L3 of SEQ ID NO: 321.

17. An antibody or binding portion thereof that binds *Staphylococcus aureus* Leukocidin D comprising a heavy chain variable region, wherein said heavy chain variable region comprises:

a complementarity-determining region 1 (CDR-H1) comprising an amino acid sequence of any one of SEQ ID NOs: 372-374, or a modified amino acid sequence of any one of SEQ ID NOs: 372-374, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 372-374;

a complementarity-determining region 2 (CDR-H2) comprising an amino acid sequence of any one of SEQ ID NOs: 375-379, or a modified amino acid sequence of any one of SEQ ID NOs: 375-379, said modified sequences having at least 80% sequence identity to any one of SEQ ID NOs: 375-379; and

a complementarity-determining region 3 (CDR-H3) comprising an amino acid sequence of any one of SEQ ID NOs: 380-383, or a modified amino acid sequence of any one of SEQ ID NO: 380-383, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 380-383.

18. The antibody or binding portion thereof of claim 17, wherein said heavy chain variable region is selected from the group consisting of:

(i) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 372, the CDR-H2 of SEQ ID NO: 375, and the CDR-H3 of SEQ ID NO: 380;

(ii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 372, the CDR-H2 of SEQ ID NO: 376, and the CDR-H3 of SEQ ID NO: 381;

(iii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 372, the CDR-H2 of SEQ ID NO: 377, and the CDR-H3 of SEQ ID NO: 380;

(iv) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 373, the CDR-H2 of SEQ ID NO: 378, and the CDR-H3 of SEQ ID NO: 382; and

(v) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 374, the CDR-H2 of SEQ ID NO: 379, and the CDR-H3 of SEQ ID NO: 383.

19. The antibody or binding portion thereof of claim 17 further comprising:

a light chain variable region, wherein said light chain variable region comprises:

a complementarity-determining region 1 (CDR-L1) having an amino acid sequence of any one of SEQ ID NOs: 384-387, or a modified amino acid sequence of any one of SEQ ID NO: 384-387, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 384-387;

a complementarity-determining region 2 (CDR-L2) having an amino acid sequence of any one of SEQ ID NOs: 388-391, or a modified amino acid sequence of any one of SEQ ID NO: 388-391, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 388-391; and

a complementarity-determining region 3 (CDR-L3) having an amino acid sequence of any one of SEQ ID NOs: 392-397, or a modified amino acid sequence of any one of SEQ ID NO: 392-397, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 392-397

20. The antibody or binding portion thereof of claim 19, wherein said light chain variable region is selected from the group consisting of:

(i) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 384, the CDR-L2 of SEQ ID NO: 388, and the CDR-L3 of SEQ ID NO: 392;

(ii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 385, the CDR-L2 of SEQ ID NO: 389, and the CDR-L3 of SEQ ID NO: 393;

(iii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 386, the CDR-L2 of SEQ ID NO: 390, and the CDR-L3 of SEQ ID NO: 394;

(iv) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 387, the CDR-L2 of SEQ ID NO: 390, and the CDR-L3 of SEQ ID NO: 395;

(v) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 386, the CDR-L2 of SEQ ID NO: 388, and the CDR-L3 of SEQ ID NO: 396;

(vi) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 386, the CDR-L2 of SEQ ID NO: 391, and the CDR-L3 of SEQ ID NO: 397; and

(vii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 386, the CDR-L2 of SEQ ID NO: 388, and the CDR-L3 of SEQ ID NO: 392.

21. The antibody or binding portion thereof of claim 17, wherein said antibody comprises a variable light (VL) chain and a variable heavy (VH) chain, wherein said VL chain comprises an amino acid sequence selected from SEQ ID NOs: 398-405 or an amino acid sequence that is at least 80% identical to any one of the amino acid sequence selected from SEQ ID NOs: 398-405, and said VH chain comprises an amino acid sequence selected from SEQ ID NOs: 406-413 or an amino acid sequence that is at least 80% identical to any one of the amino acid sequence selected from SEQ ID NOs: 406-413.

22. The antibody or binding portion thereof of claim 17, wherein said antibody neutralizes *S. aureus* leukocidin ED cytolytic activity.

23. The antibody or binding portion thereof of claim 22, wherein said antibody comprises:

(i) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 373, the CDR-H2 of SEQ ID NO: 378, and the CDR-H3 of SEQ ID NO: 382, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 387, the CDR-L2 of SEQ ID NO: 390, and the CDR-L3 of SEQ ID NO: 395;

(ii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 372, the CDR-H2 of SEQ ID NO: 375, and the CDR-H3 of SEQ ID NO: 380, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 386, the CDR-L2 of SEQ ID NO: 388, and the CDR-L3 of SEQ ID NO: 396;

(iii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 374, the CDR-H2 of SEQ ID NO: 379, and the CDR-H3 of SEQ ID NO: 383, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 386, the CDR-L2 of SEQ ID NO: 391, and the CDR-L3 of SEQ ID NO: 397; or

(iv) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 372, the CDR-H2 of SEQ ID NO: 375, and the CDR-H3 of SEQ ID NO: 380, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 386, the CDR-L2 of SEQ ID NO: 388, and the CDR-L3 of SEQ ID NO: 392.

24. An antibody or binding portion thereof that competes for leukocidin E binding with a monoclonal antibody, wherein said monoclonal antibody is selected from a monoclonal antibody comprising:

(i) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 373, the CDR-H2 of SEQ ID NO: 378, and the CDR-H3 of SEQ ID NO: 382, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 387, the CDR-L2 of SEQ ID NO: 390, and the CDR-L3 of SEQ ID NO: 395;

(ii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 372, the CDR-H2 of SEQ ID NO: 375, and the CDR-H3 of SEQ ID NO: 380, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 386, the CDR-L2 of SEQ ID NO: 388, and the CDR-L3 of SEQ ID NO: 396;

(iii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 374, the CDR-H2 of SEQ ID NO: 379, and the CDR-H3 of SEQ ID NO: 383, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 386, the CDR-L2 of SEQ ID NO: 391, and the CDR-L3 of SEQ ID NO: 397; or

(iv) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 372, the CDR-H2 of SEQ ID NO: 375, and the CDR-H3 of SEQ ID NO: 380, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 386, the CDR-L2 of SEQ ID NO: 388, and the CDR-L3 of SEQ ID NO: 392

25. An antibody or binding portion thereof that binds *Staphylococcus aureus* gamma-hemolysin A (HlgA) comprising a heavy chain variable region, wherein said heavy chain variable region comprises:

a complementarity-determining region 1 (CDR-H1) comprising an amino acid sequence of any one of SEQ ID NOs: 430-432, or a modified amino acid sequence of any one of SEQ ID NOs: 430-432, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 430-432;

a complementarity-determining region 2 (CDR-H2) comprising an amino acid sequence of any one of SEQ ID NOs: 433-435, or a modified amino acid sequence of any one of SEQ ID NOs: 433-435, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 433-435; and

a complementarity-determining region 3 (CDR-H3) comprising an amino acid sequence of any one of SEQ ID NOs: 436-438, or a modified amino acid sequence of any one of SEQ ID NO: 436-438, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 436-438.

26. The antibody or binding portion thereof of claim 25, wherein said heavy chain variable region is selected from the group consisting of:

(i) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 430, the CDR-H2 of SEQ ID NO: 433, and the CDR-H3 of SEQ ID NO: 436;

(ii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 431, the CDR-H2 of SEQ ID NO: 434, and the CDR-H3 of SEQ ID NO: 437; and

(iii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 432, the CDR-H2 of SEQ ID NO: 435, and the CDR-H3 of SEQ ID NO: 438;

27. The antibody or binding portion thereof of claim 25 further comprising:

a light chain variable region, wherein said light chain variable region comprises:

a complementarity-determining region 1 (CDR-L1) having an amino acid sequence of any one of SEQ ID NOs: 439-440, or a modified amino acid sequence of any one of SEQ ID NO: 439-440, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 439-440;

a complementarity-determining region 2 (CDR-L2) having an amino acid sequence of any one of SEQ ID NOs: 441-443, or a modified amino acid sequence of any one of SEQ ID NO: 441-443, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 441-443; and

a complementarity-determining region 3 (CDR-L3) having an amino acid sequence of any one of SEQ ID NOs: 444-445 or a modified amino acid sequence of any one of SEQ ID NO: 444-445, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 444-445.

28. The antibody or binding portion thereof of claim 27, wherein said light chain variable region is selected from the group consisting of:

(i) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 439 , the CDR-L2 of SEQ ID NO: 441 , and the CDR-L3 of SEQ ID NO: 444;

(ii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 440, the CDR-L2 of SEQ ID NO: 442, and the CDR-L3 of SEQ ID NO: 445; and

(iii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 439, the CDR-L2 of SEQ ID NO: 443, and the CDR-L3 of SEQ ID NO: 444.

29. The antibody or binding portion thereof of claim 25, wherein said antibody comprises a variable light (VL) chain and a variable heavy (VH) chain, wherein said VL chain comprises an amino acid sequence selected from SEQ ID NOs: 446-451 or an amino acid sequence that is at least 80% identical to any one of the amino acid sequence selected from SEQ ID NOs: 446-451, and said VH chain comprises an amino acid sequence selected from SEQ ID NOs: 452-457 or an amino acid sequence that is at least 80% identical to any one of the amino acid sequence selected from SEQ ID NOs: 452-457.

30. The antibody or binding portion thereof of claim 25, wherein said antibody neutralizes *S. aureus* HlgAB cytolytic activity.

31. The antibody or binding portion thereof of claim 30, wherein said antibody comprises:

a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 432, the CDR-H2 of SEQ ID NO: 435, and the CDR-H3 of SEQ ID NO: 438 and

a light chain variable region comprising the CDR-L1 of SEQ ID NO: 439, the CDR-L2 of SEQ ID NO: 441, and the CDR-L3 of SEQ ID NO: 444.

32. An antibody or binding portion thereof that competes for HlgA binding to a monoclonal antibody, wherein said monoclonal antibody comprises:

a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 432, the CDR-H2 of SEQ ID NO: 435, and the CDR-H3 of SEQ ID NO: 438 and

a light chain variable region comprising the CDR-L1 of SEQ ID NO: 439, the CDR-L2 of SEQ ID NO: 441, and the CDR-L3 of SEQ ID NO: 444.

33. An antibody or binding portion thereof that binds *Staphylococcus aureus* gamma-hemolysin C (HlgC) comprising a heavy chain variable region, wherein said heavy chain variable region comprises:

a complementarity-determining region 1 (CDR-H1) comprising an amino acid sequence of SEQ ID NO: 470, or a modified amino acid sequence of SEQ ID NO: 470, said modified sequence having at least 80% sequence identity to SEQ ID NO: 470;

a complementarity-determining region 2 (CDR-H2) comprising an amino acid sequence of SEQ ID NO: 471, or a modified amino acid sequence of SEQ ID NO: 471, said modified sequence having at least 80% sequence identity to SEQ ID NO: 471; and

a complementarity-determining region 3 (CDR-H3) comprising an amino acid sequence of SEQ ID NO: 472 or a modified amino acid sequence of SEQ ID NO: 472, said modified sequence having at least 80% sequence identity to SEQ ID NO: 472.

34. The antibody or binding portion thereof of claim 33 further comprising:

a light chain variable region, wherein said light chain variable region comprises:

a complementarity-determining region 1 (CDR-L1) having an amino acid sequence of any one of SEQ ID NOs: 473-477, or a modified amino acid sequence of any one of SEQ ID NO: 473-477, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 473-477;

a complementarity-determining region 2 (CDR-L2) having an amino acid sequence of any one of SEQ ID NOs: 478-482, or a modified amino acid sequence of any one of SEQ ID NO: 478-482, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 478-482; and

a complementarity-determining region 3 (CDR-L3) having an amino acid sequence of any one of SEQ ID NOs: 483-487, or a modified amino acid sequence of any one of SEQ ID NO: 483-487, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 483-487.

35. The antibody or binding portion thereof of claim 34, wherein said light chain variable region is selected from the group consisting of:

(i) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 473, the CDR-L2 of SEQ ID NO: 478, and the CDR-L3 of SEQ ID NO: 483;

(ii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 474, the CDR-L2 of SEQ ID NO: 479, and the CDR-L3 of SEQ ID NO: 484;

(iii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 475, the CDR-L2 of SEQ ID NO: 480, and the CDR-L3 of SEQ ID NO: 485;

(iv) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 476, the CDR-L2 of SEQ ID NO: 481, and the CDR-L3 of SEQ ID NO: 486

(v) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 474, the CDR-L2 of SEQ ID NO: 482, and the CDR-L3 of SEQ ID NO: 487; and

(vi) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 477, the CDR-L2 of SEQ ID NO: 480, and the CDR-L3 of SEQ ID NO: 485.

36. The antibody or binding portion thereof of claim 33, wherein said antibody comprises a variable light (VL) chain and a variable heavy (VH) chain, wherein said VL chain comprises an amino acid sequence selected from SEQ ID NOs: 488-493 or an amino acid sequence that is at least 80% identical to any one of the amino acid sequence selected from SEQ ID NOs: 488-493, and said VH chain comprises an amino acid sequence selected from SEQ ID NOs: 494-499 or an amino acid sequence that is at least 80% identical to any one of the amino acid sequence selected from SEQ ID NOs: 494-499.

37. The antibody or binding portion thereof of claim 33, wherein said antibody neutralizes *S. aureus* HlgCB cytolytic activity.

38. The antibody or binding portion thereof of claim 37, wherein said antibody comprises:

a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 470, the CDR-H2 of SEQ ID NO: 471, and the CDR-H3 of SEQ ID NO: 472 and

a light chain variable region comprising the CDR-L1 of SEQ ID NO: 474, the CDR-L2 of SEQ ID NO: 479, and the CDR-L3 of SEQ ID NO: 484.

39. An antibody or binding portion thereof that competes for HlgC binding with a monoclonal antibody, wherein said monoclonal antibody comprises:

a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 470, the CDR-H2 of SEQ ID NO: 471, and the CDR-H3 of SEQ ID NO: 472 and

a light chain variable region comprising the CDR-L1 of SEQ ID NO: 474, the CDR-L2 of SEQ ID NO: 479, and the CDR-L3 of SEQ ID NO: 484.

40. An antibody or binding portion thereof that binds *Staphylococcus aureus* Leukocidin E/HlgA comprising a heavy chain variable region, wherein said heavy chain variable region comprises:

a complementarity-determining region 1 (CDR-H1) comprising an amino acid sequence of any one of SEQ ID NOs: 513-529, or a modified amino acid sequence of any one of SEQ ID NOs: 513-529, said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 513-529;

a complementarity-determining region 2 (CDR-H2) comprising an amino acid sequence of any one of SEQ ID NOs: 530-548, or a modified amino acid sequence of any one of

SEQ ID NOs: 530-548, said modified sequences having at least 80% sequence identity to any one of SEQ ID NOs: 530-548; and

a complementarity-determining region 3 (CDR-H3) comprising an amino acid sequence of any one of SEQ ID NOs: 549-568 or a modified amino acid sequence of any one of SEQ ID NO: 549-568 said modified sequence having at least 80% sequence identity to any one of SEQ ID NOs: 549-568.

41. The antibody or binding portion thereof of claim 40, wherein said heavy chain variable region is selected from the group consisting of:

(i) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 513, the CDR-H2 of SEQ ID NO: 530, and the CDR-H3 of SEQ ID NO: 549;

(ii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 514, the CDR-H2 of SEQ ID NO: 531, and the CDR-H3 of SEQ ID NO: 550;

(iii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 515, the CDR-H2 of SEQ ID NO: 532, and the CDR-H3 of SEQ ID NO: 551;

(iv) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 516, the CDR-H2 of SEQ ID NO: 533, and the CDR-H3 of SEQ ID NO: 552;

(v) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 517, the CDR-H2 of SEQ ID NO: 534, and the CDR-H3 of SEQ ID NO: 553;

(vi) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 514, the CDR-H2 of SEQ ID NO: 535, and the CDR-H3 of SEQ ID NO: 554;

(vii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 518, the CDR-H2 of SEQ ID NO: 536, and the CDR-H3 of SEQ ID NO: 555;

(viii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 519, the CDR-H2 of SEQ ID NO: 537, and the CDR-H3 of SEQ ID NO: 556;

(ix) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 520, the CDR-H2 of SEQ ID NO: 538, and the CDR-H3 of SEQ ID NO: 557;

(x) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 521, the CDR-H2 of SEQ ID NO: 539, and the CDR-H3 of SEQ ID NO: 558;

(xi) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 522, the CDR-H2 of SEQ ID NO: 540, and the CDR-H3 of SEQ ID NO: 558;

(xii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 523, the CDR-H2 of SEQ ID NO: 541, and the CDR-H3 of SEQ ID NO: 559;

(xiii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 524, the CDR-H2 of SEQ ID NO: 542, and the CDR-H3 of SEQ ID NO: 560;

(xiv) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 525, the CDR-H2 of SEQ ID NO: 543, and the CDR-H3 of SEQ ID NO: 561;

(xv) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 526, the CDR-H2 of SEQ ID NO: 544, and the CDR-H3 of SEQ ID NO: 562;

(xvi) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 527, the CDR-H2 of SEQ ID NO: 545, and the CDR-H3 of SEQ ID NO: 563;

(xvii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 528, the CDR-H2 of SEQ ID NO: 546, and the CDR-H3 of SEQ ID NO: 564;

(xviii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 525, the CDR-H2 of SEQ ID NO: 533, and the CDR-H3 of SEQ ID NO: 565;

(xix) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 520, the CDR-H2 of SEQ ID NO: 547, and the CDR-H3 of SEQ ID NO: 566;

(xx) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 529, the CDR-H2 of SEQ ID NO: 548, and the CDR-H3 of SEQ ID NO: 567; and

(xxi) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 528, the CDR-H2 of SEQ ID NO: 546, and the CDR-H3 of SEQ ID NO: 568.

42. The antibody or binding portion thereof of claim 40 further comprising:

a light chain variable region, wherein said light chain variable region comprises:

a complementarity-determining region 1 (CDR-L1) having an amino acid sequence of any one of SEQ ID NOs: 569-600, or a modified amino acid sequence of any one of SEQ ID NO: 569-600, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 569-600;

a complementarity-determining region 2 (CDR-L2) having an amino acid sequence of any one of SEQ ID NOs: 601-621, or a modified amino acid sequence of any one of SEQ ID NO: 601-621, said modified sequence having at least 80% sequence identity to any one of SEQ ID NO: 601-621; and

a complementarity-determining region 3 (CDR-L3) having an amino acid sequence of any one of SEQ ID NOs: 622-654, or a modified amino acid sequence of any one of SEQ ID NO: 622-654, said having at least 80% sequence identity to any one of SEQ ID NO: 622-654.

43. The antibody or binding portion thereof of claim 42, wherein said light chain variable region is selected from the group consisting of:

(i) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 569, the CDR-L2 of SEQ ID NO: 601, and the CDR-L3 of SEQ ID NO: 622;

(ii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 570, the CDR-L2 of SEQ ID NO: 602, and the CDR-L3 of SEQ ID NO: 623;

(iii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 571, the CDR-L2 of SEQ ID NO: 603, and the CDR-L3 of SEQ ID NO: 624;

(iv) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 572, the CDR-L2 of SEQ ID NO:604 , and the CDR-L3 of SEQ ID NO: 625

(v) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 573, the CDR-L2 of SEQ ID NO: 605, and the CDR-L3 of SEQ ID NO: 626;

(vi) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 574, the CDR-L2 of SEQ ID NO: 606, and the CDR-L3 of SEQ ID NO: 627;

(vii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 575, the CDR-L2 of SEQ ID NO: 607, and the CDR-L3 of SEQ ID NO: 628;

(viii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 576, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 629;

(ix) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 577, the CDR-L2 of SEQ ID NO: 607, and the CDR-L3 of SEQ ID NO: 630;

(x) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 578, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 631;

(xi) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 579, the CDR-L2 of SEQ ID NO: 602, and the CDR-L3 of SEQ ID NO: 632;

(xii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 580, the CDR-L2 of SEQ ID NO: 607, and the CDR-L3 of SEQ ID NO: 633;

(xiii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 581, the CDR-L2 of SEQ ID NO: 609, and the CDR-L3 of SEQ ID NO: 634;

(xiv) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 582, the CDR-L2 of SEQ ID NO: 610, and the CDR-L3 of SEQ ID NO: 635;

(xv) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 579, the CDR-L2 of SEQ ID NO: 602, and the CDR-L3 of SEQ ID NO: 636;

(xvi) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 583, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 631;

(xvii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 584, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 631;

(xviii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 585, the CDR-L2 of SEQ ID NO: 611, and the CDR-L3 of SEQ ID NO: 637;

(xix) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 579, the CDR-L2 of SEQ ID NO: 602, and the CDR-L3 of SEQ ID NO: 638;

(xx) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 586, the CDR-L2 of SEQ ID NO: 612, and the CDR-L3 of SEQ ID NO: 639;

(xxi) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 587, the CDR-L2 of SEQ ID NO: 613, and the CDR-L3 of SEQ ID NO: 640;

(xxii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 588, the CDR-L2 of SEQ ID NO: 614, and the CDR-L3 of SEQ ID NO: 641;

(xxiii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 589, the CDR-L2 of SEQ ID NO: 615, and the CDR-L3 of SEQ ID NO: 642;

(xxiv) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 590, the CDR-L2 of SEQ ID NO: 601, and the CDR-L3 of SEQ ID NO: 643;

(xxv) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 581, the CDR-L2 of SEQ ID NO: 609, and the CDR-L3 of SEQ ID NO: 634;

(xxvi) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 591, the CDR-L2 of SEQ ID NO: 616, and the CDR-L3 of SEQ ID NO: 644;

(xxvii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 592, the CDR-L2 of SEQ ID NO: 601, and the CDR-L3 of SEQ ID NO: 645;

(xxviii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 593, the CDR-L2 of SEQ ID NO: 617, and the CDR-L3 of SEQ ID NO: 646;

(xxix) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 594, the CDR-L2 of SEQ ID NO: 618, and the CDR-L3 of SEQ ID NO: 647;

(xxx) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 595, the CDR-L2 of SEQ ID NO: 619, and the CDR-L3 of SEQ ID NO: 648;

(xxxi) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 596, the CDR-L2 of SEQ ID NO: 620, and the CDR-L3 of SEQ ID NO: 649;

(xxxii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 574, the CDR-L2 of SEQ ID NO: 621, and the CDR-L3 of SEQ ID NO: 650;

(xxxiii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 597, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 625;

(xxxiv) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 573, the CDR-L2 of SEQ ID NO: 605, and the CDR-L3 of SEQ ID NO: 651;

(xxxv) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 598, the CDR-L2 of SEQ ID NO: 607, and the CDR-L3 of SEQ ID NO: 652;

(xxxvi) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 599, the CDR-L2 of SEQ ID NO: 607, and the CDR-L3 of SEQ ID NO: 653;

(xxxvii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 574, the CDR-L2 of SEQ ID NO: 606, and the CDR-L3 of SEQ ID NO: 627; and

(xxxviii) a light chain variable region comprising the CDR-L1 of SEQ ID NO: 600, the CDR-L2 of SEQ ID NO: 602, and the CDR-L3 of SEQ ID NO: 654.

44. The antibody or binding portion thereof of claim 40, wherein said antibody comprises a variable light (VL) chain and a variable heavy (VH) chain, wherein said VL chain comprises an amino acid sequence selected from SEQ ID NOs: 655-693 or an amino acid sequence that is at least 80% identical to any one of the amino acid sequence selected from SEQ ID NOs: 655-693, and said VH chain comprises an amino acid sequence selected from SEQ ID NOs: 694-732 or an amino acid sequence that is at least 80% identical to any one of the amino acid sequence selected from SEQ ID NOs: 694-732.

45. The antibody or binding portion thereof of claim 40, wherein said antibody neutralizes *S. aureus* leukotoxin ED and/or gamma-hemolysin cytolytic activity.

46. The antibody or binding portion thereof of claim 45, wherein said antibody is selected from the group consisting of:

(i) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 519, the CDR-H2 of SEQ ID NO: 537, and the CDR-H3 of SEQ ID NO: 556, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 576, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 629;

(ii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 521, the CDR-H2 of SEQ ID NO: 539, and the CDR-H3 of SEQ ID NO: 558, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 578, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 631;

(iii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 522, the CDR-H2 of SEQ ID NO: 540, and the CDR-H3 of SEQ ID NO: 558, and a light chain

variable region comprising the CDR-L1 of SEQ ID NO: 583, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 631;

(iv) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 523, the CDR-H2 of SEQ ID NO: 541, and the CDR-H3 of SEQ ID NO: 559, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 584, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 631;

(v) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 524, the CDR-H2 of SEQ ID NO: 542, and the CDR-H3 of SEQ ID NO: 560, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 589, the CDR-L2 of SEQ ID NO: 615, and the CDR-L3 of SEQ ID NO:642;

(vi) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 525, the CDR-H2 of SEQ ID NO: 543, and the CDR-H3 of SEQ ID NO: 561 and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 590, the CDR-L2 of SEQ ID NO: 601, and the CDR-L3 of SEQ ID NO: 643; and

(vii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 527, the CDR-H2 of SEQ ID NO: 545 and the CDR-H3 of SEQ ID NO: 563, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 596, the CDR-L2 of SEQ ID NO: 620, and the CDR-L3 of SEQ ID NO: 649.

47. An antibody or binding portion thereof that competes for HlgA binding with a monoclonal antibody, wherein said monoclonal antibody is selected from the group consisting of:

(i) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 519, the CDR-H2 of SEQ ID NO: 537, and the CDR-H3 of SEQ ID NO: 556, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 576, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 629;

(ii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 521, the CDR-H2 of SEQ ID NO: 539, and the CDR-H3 of SEQ ID NO: 558, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 578, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 631;

(iii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 522, the CDR-H2 of SEQ ID NO: 540, and the CDR-H3 of SEQ ID NO: 558, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 583, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 631;

(iv) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 523, the CDR-H2 of SEQ ID NO: 541, and the CDR-H3 of SEQ ID NO: 559, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 584, the CDR-L2 of SEQ ID NO: 608, and the CDR-L3 of SEQ ID NO: 631;

(v) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 524, the CDR-H2 of SEQ ID NO: 542, and the CDR-H3 of SEQ ID NO: 560, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 589, the CDR-L2 of SEQ ID NO: 615, and the CDR-L3 of SEQ ID NO:642;

(vi) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 525, the CDR-H2 of SEQ ID NO: 543, and the CDR-H3 of SEQ ID NO: 561 and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 590, the CDR-L2 of SEQ ID NO: 601, and the CDR-L3 of SEQ ID NO: 643; and

(vii) a heavy chain variable region comprising the CDR-H1 of SEQ ID NO: 527, the CDR-H2 of SEQ ID NO: 545 and the CDR-H3 of SEQ ID NO: 563, and a light chain variable region comprising the CDR-L1 of SEQ ID NO: 596, the CDR-L2 of SEQ ID NO: 620, and the CDR-L3 of SEQ ID NO: 649.

48. The antibody or binding portion thereof of any one of claims 1-47, wherein said antibody or binding portion thereof is a chimeric antibody or binding portion thereof.

49. The antibody or binding portion thereof of any one of claims 1-47, wherein said antibody or binding portion thereof is a humanized antibody or binding portion thereof.

50. The antibody or binding portion thereof of any one of claims 1-47, wherein said antibody or binding portion thereof is a monoclonal antibody or binding portion thereof.

51. The antibody or binding portion thereof of any one of claims 1-47, wherein said antibody or binding portion thereof is selected from the group consisting of: a disulfide linked Fv, a scFv, a CDR-grafted antibody, a diabody, a multi-specific antibody, a Fab, a Fab′, a bispecific antibody, a $F(ab')_2$, and a Fv.

52. An isolated nucleic acid molecule encoding the antibody or binding portion thereof of any one of claims 1-47.

53. A vector comprising the isolated nucleic acid molecule of claim 52.

54. A host cell comprising the vector of claim 53.

55. A pharmaceutical composition comprising:
the antibody or binding portion thereof of any one of claims 1-51, and
a pharmaceutical carrier.

56. A pharmaceutical composition comprising:
the isolated nucleic acid molecule of claim 52 or vector of claim 53, and
a pharmaceutical carrier.

57. A method of treating a staphylococcal infection in a subject comprising:
administering to a subject in need thereof, the pharmaceutical composition of claim 55 or claim 56 in an amount effective to treat the staphylococcal infection.

58. The method of claim 57 further comprising:
selecting a subject having a staphylococcal infection prior to said administering.

59. The method of claim 57, wherein the staphylococcal infection is a methicillin-resistant *Staphylococcus aureus* infection or a methicillin-sensitive *Staphylococcus aureus* infection.

60. The method of claim 57 further comprising:
administering one or more agents selected from the group consisting of an anti-infective agent, an antibiotic agent, and an antimicrobial agent in conjunction with said administering the pharmaceutical composition.

61. A method of inhibiting the onset of staphylococcal infection in a subject comprising:
administering to a subject in need thereof, the pharmaceutical composition of claim 55 or claim 56 in an amount effective to inhibit the onset of staphylococcal infection in a subject.

62. The method of claim 61 further comprising:

selecting a subject at risk for staphylococcal infection prior to said administering.

63. The method of claim 61, wherein the staphylococcal infection is a methicillin-resistant *Staphylococcus aureus* infection or a methicillin-sensitive *Staphylococcus aureus* infection.

64. A method for detecting *Staphylococcus aureus* in a biological sample comprising:

contacting the antibody or binding portion thereof of any one of claims 1-51 with the biological sample; and

detecting presence or absence of a staphylococcal bi-component toxin in the biological sample based on said contacting, thereby detecting *S. aureus* in the biological sample.

65. The method of claim 64, wherein the biological sample is from a subject, said method further comprising:

diagnosing a staphylococcal infection in the subject based on said detecting.

66. A diagnostic kit comprising:

the antibody or binding portion thereof of any one of claims 1-51

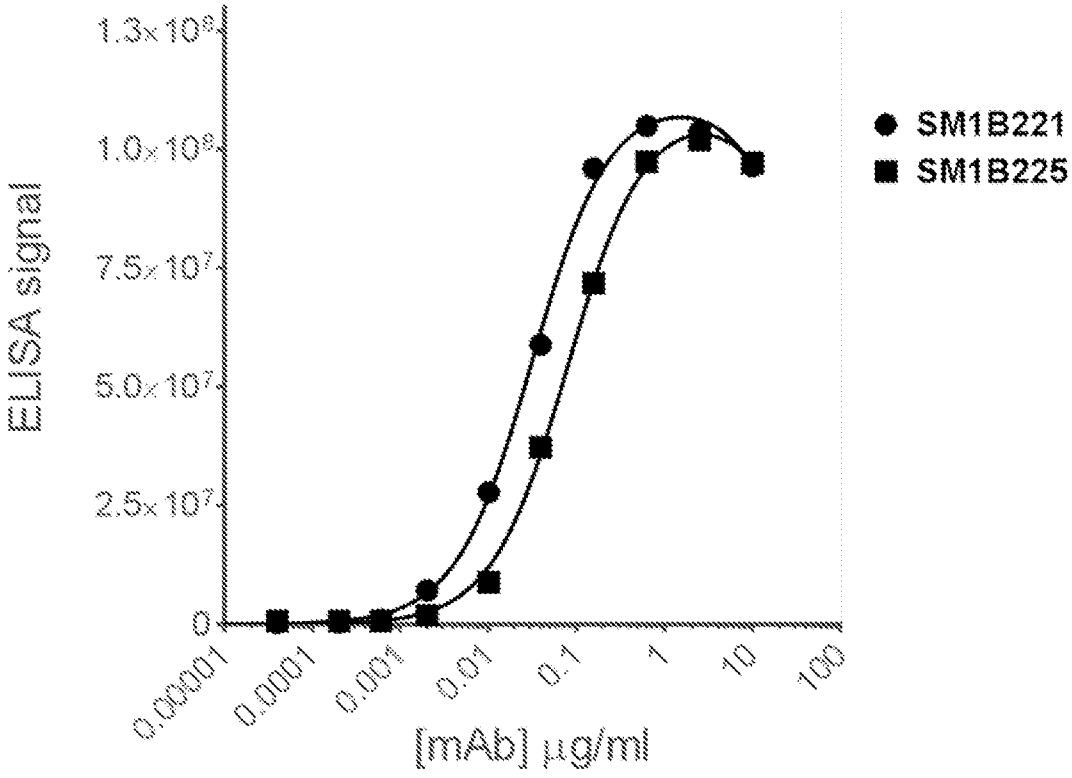

1.3×10⁸
1.0×10⁸
7.5×10⁷
5.0×10⁷
2.5×10⁷
0
ELISA signal
0.00001
0.0001
0.001
0.01
0.1
1
10
100
[mAb] µg/ml
SM1B221
SM1B225

FIG. 1A

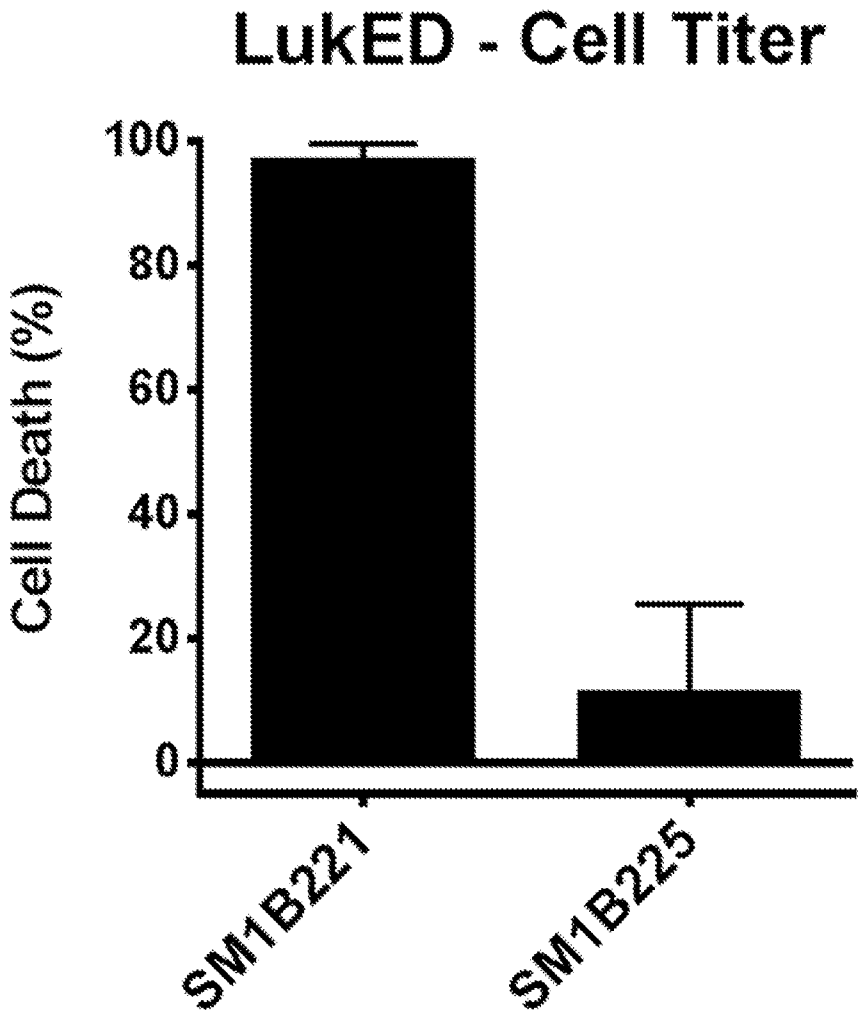


FIG. 1B

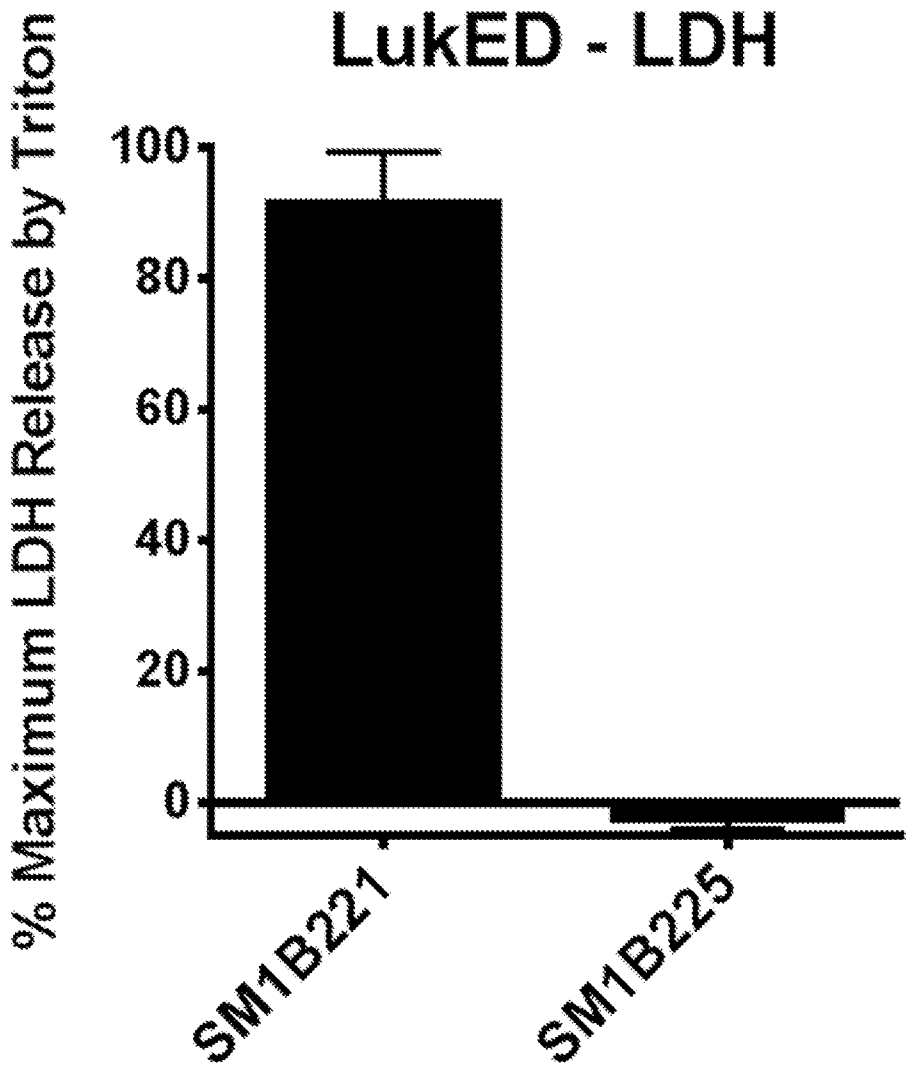
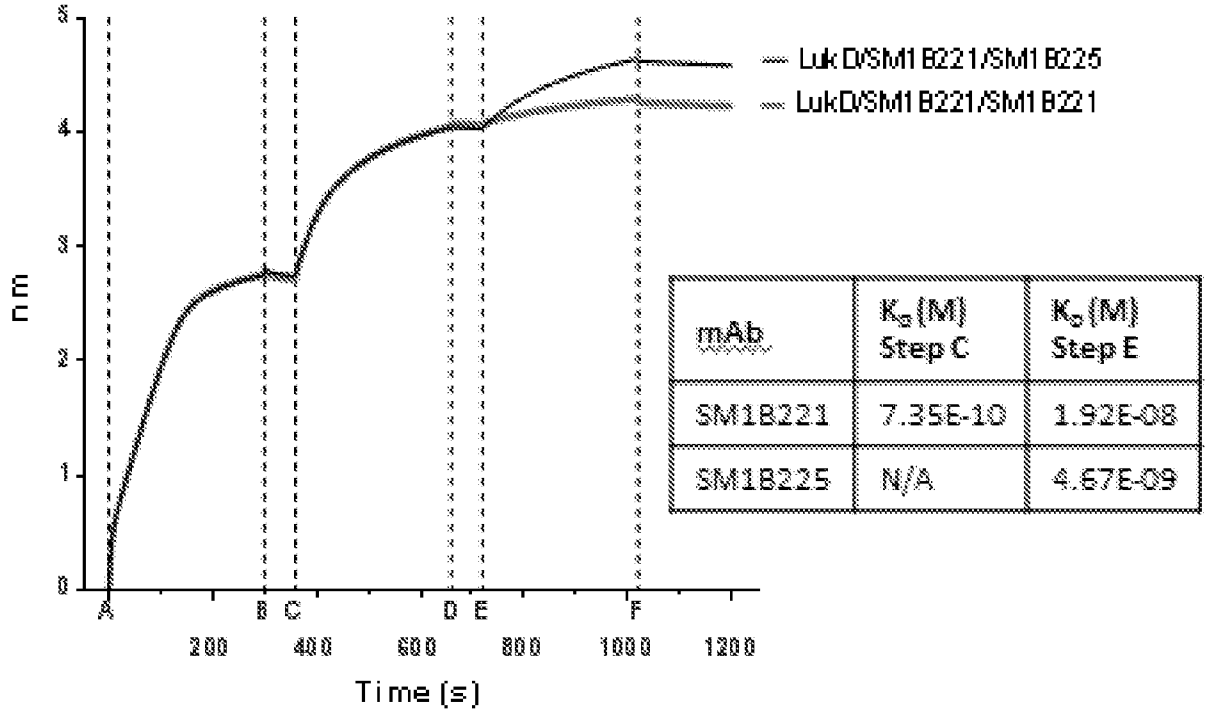

LukED - LDH
% Maximum LDH Release by Triton
100
80
60
40
20
0
SM1B221
SM1B225

FIG. 1C

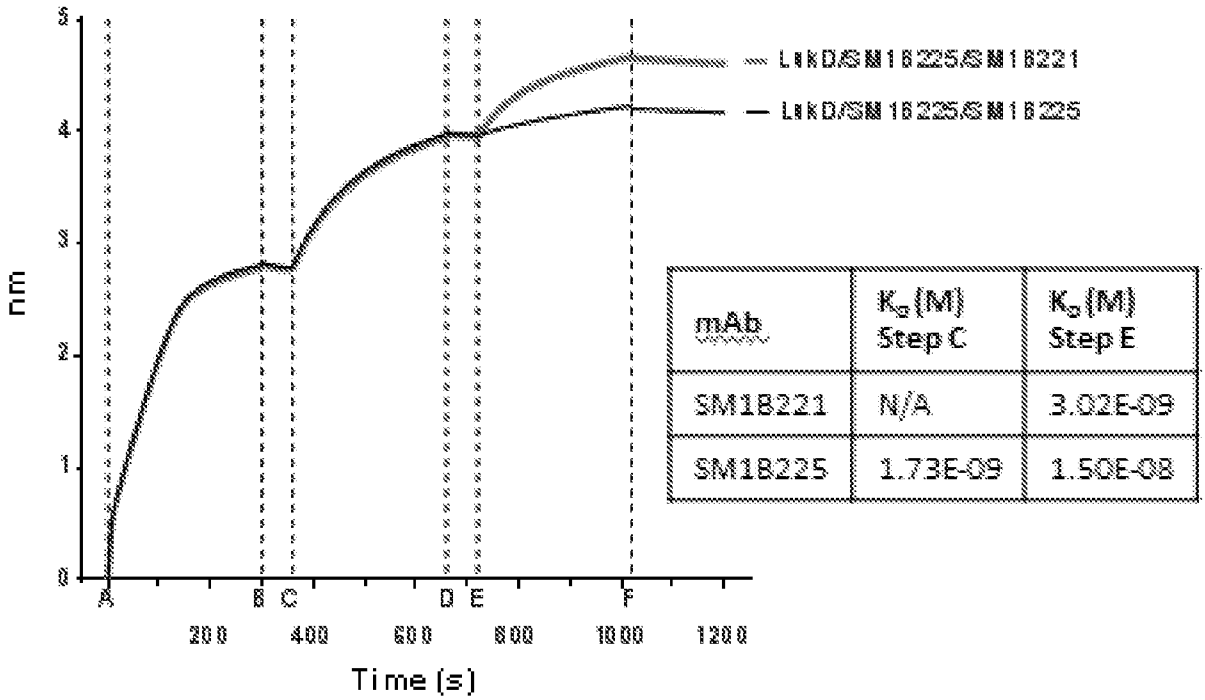


mAb	K_D (M) Step C	K_D (M) Step E
SM1B221	7.35E-10	1.92E-08
SM1B225	N/A	4.67E-09

Binding steps:

A: Loading of biotinylated LukD
B: Baseline (PBS)
C: Association of SM1B221
D: Baseline (PBS)
E: Association of SM1B221 (grey) or SM1B225 (black)
F: Dissociation (PBS)

FIG. 1D



mAb	K_D (M) Step C	K_D (M) Step E
SM1B221	N/A	3.02E-09
SM1B225	1.73E-09	1.50E-08

Binding steps:

A: Loading of biotinylated LukD
B: Baseline (PBS)
C: Association of SM1B225
D: Baseline (PBS)
E: Association of SM1B221 (grey)
or SM1B225 (black)
F: Dissociation (PBS)

FIG. 1E

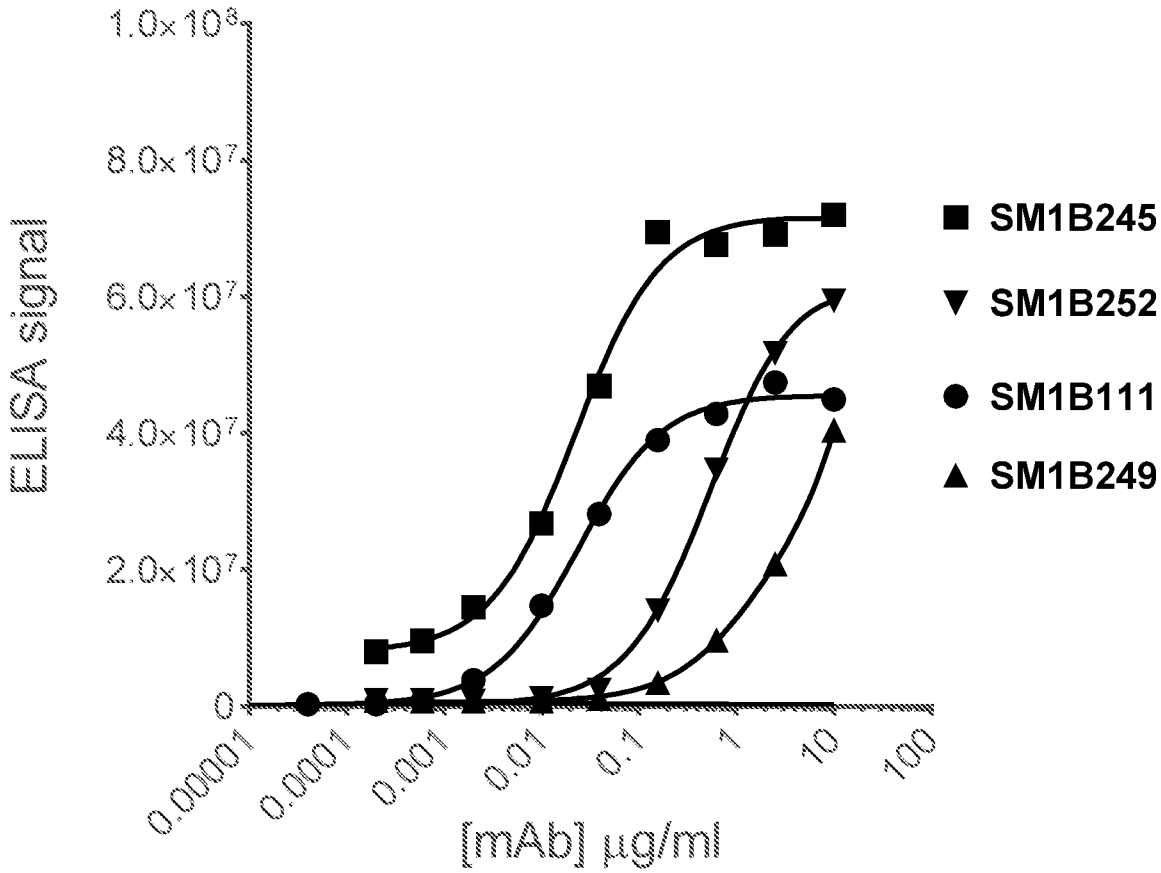

1.0×10⁸
8.0×10⁷
6.0×10⁷
4.0×10⁷
2.0×10⁷
0
ELISA signal
0.00001
0.0001
0.001
0.01
0.1
1
10
100
[mAb] µg/ml
SM1B245
SM1B252
SM1B111
SM1B249

FIG. 2A

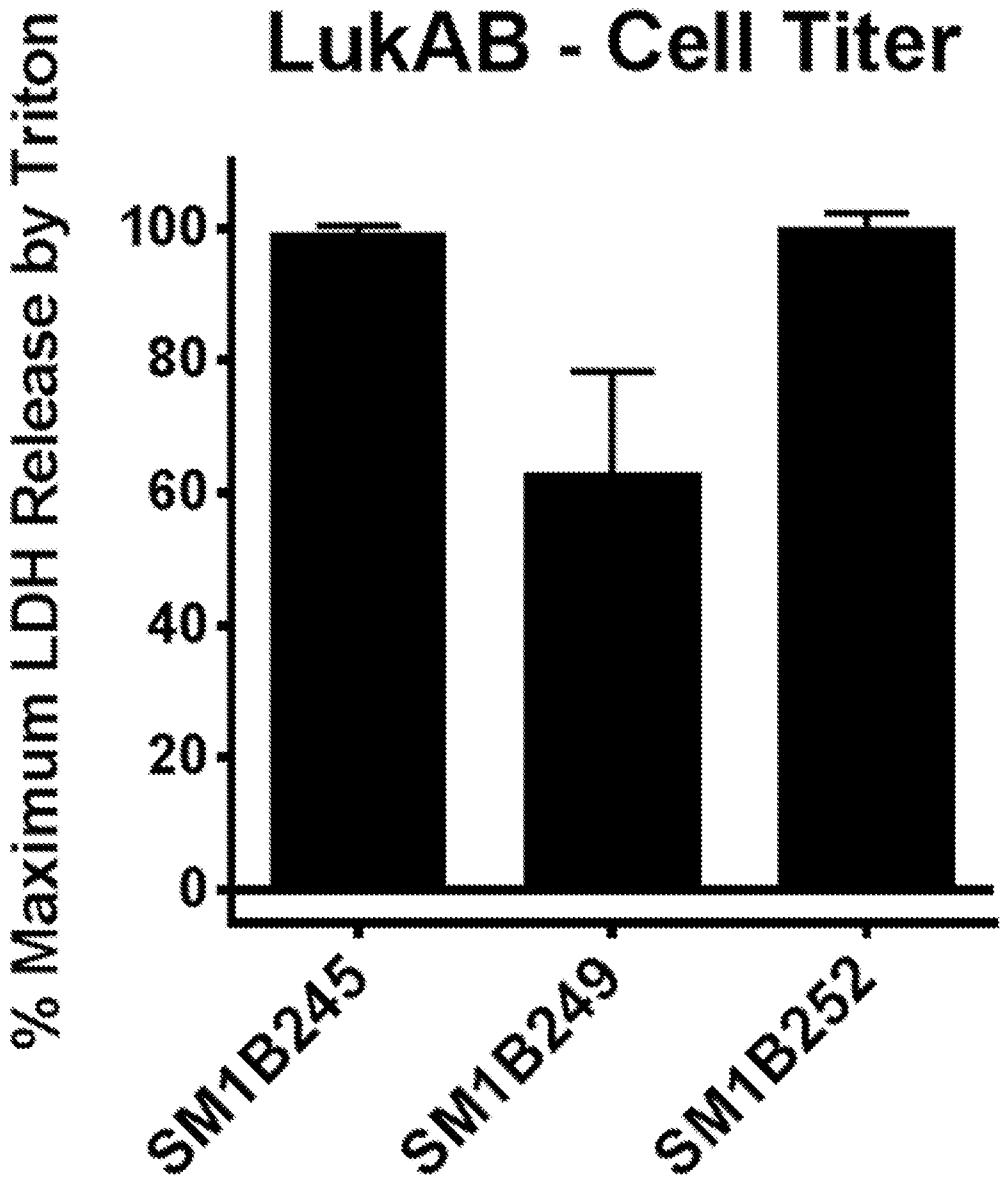

LukAB - Cell Titer
% Maximum LDH Release by Triton
100
80
60
40
20
0
SM1B245
SM1B249
SM1B252

FIG. 2B

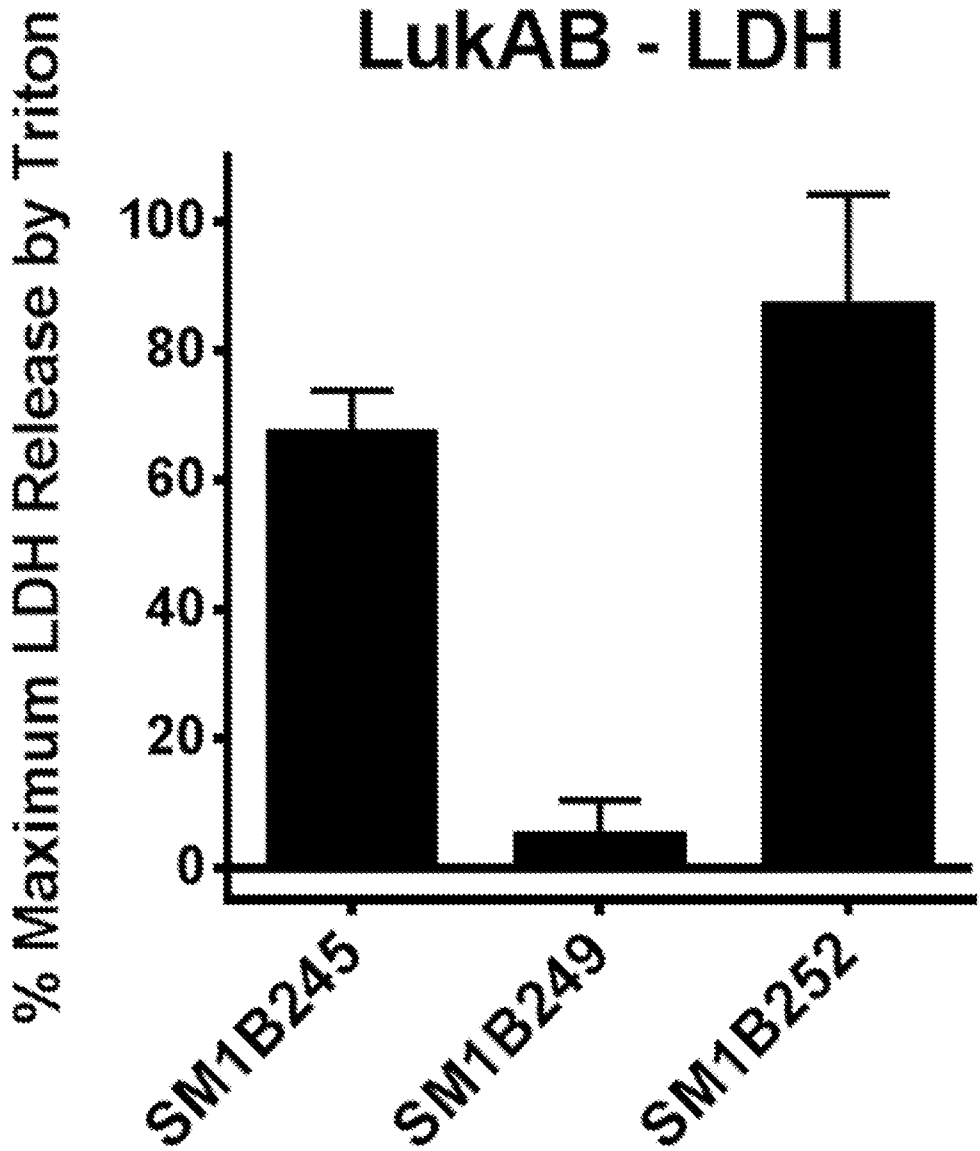

LukAB - LDH
% Maximum LDH Release by Triton
100
80
60
40
20
0
SM1B245
SM1B249
SM1B252

FIG. 2C

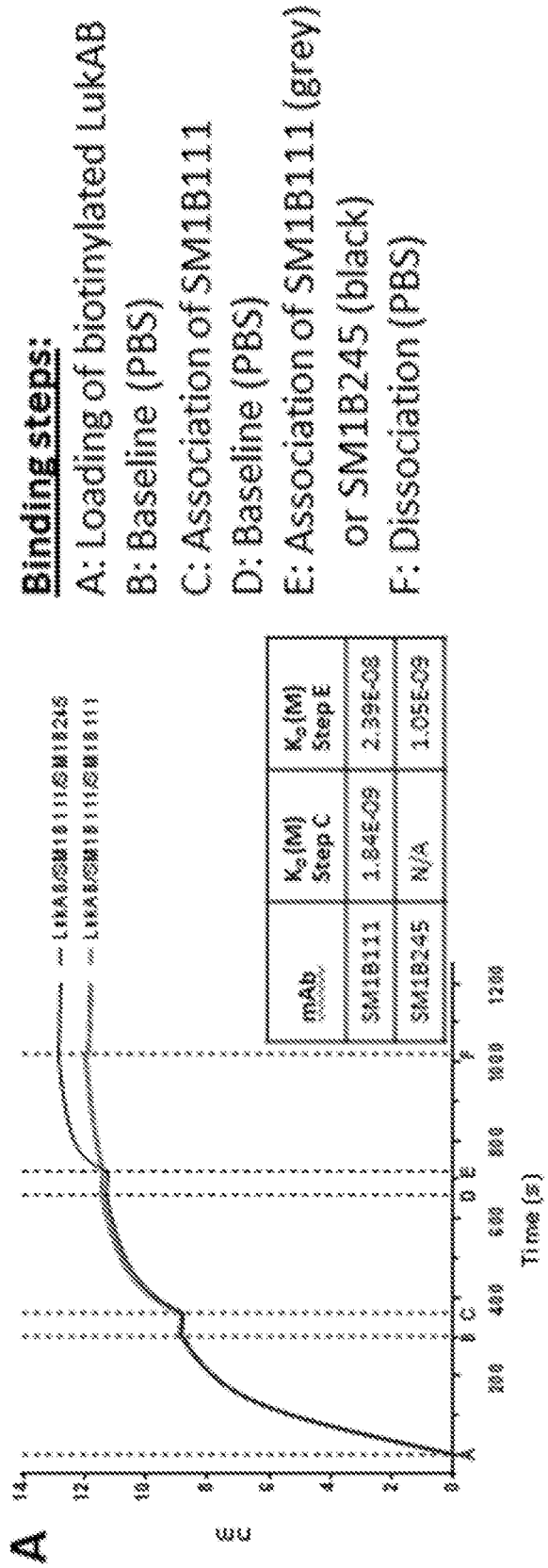

Binding steps:
A: Loading of biotinylated LukAB
B: Baseline (PBS)
C: Association of SM1B111
D: Baseline (PBS)
E: Association of SM1B111 (grey) or SM1B245 (black)
F: Dissociation (PBS)
A
nm
Time (s)
mAb
K_D (M) Step C
K_D (M) Step E
SM1B111
1.84E-09
2.39E-08
SM1B245
N/A
1.05E-09

FIG. 2D

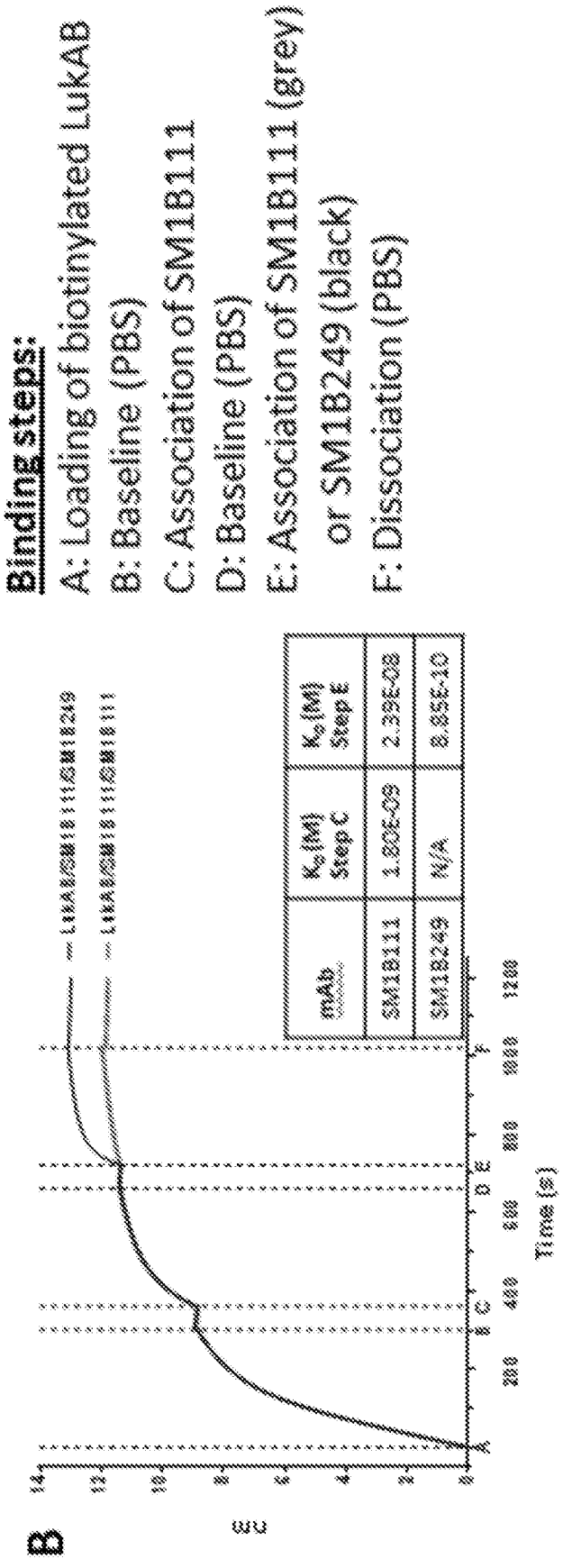

Binding steps:
A: Loading of biotinylated LukAB
B: Baseline (PBS)
C: Association of SM1B111
D: Baseline (PBS)
E: Association of SM1B111 (grey) or SM1B249 (black)
F: Dissociation (PBS)
B
nm
Time (s)
mAb
K_D (M) Step C
K_D (M) Step E
SM1B111
1.80E-09
2.39E-08
SM1B249
N/A
8.85E-10

FIG. 2E

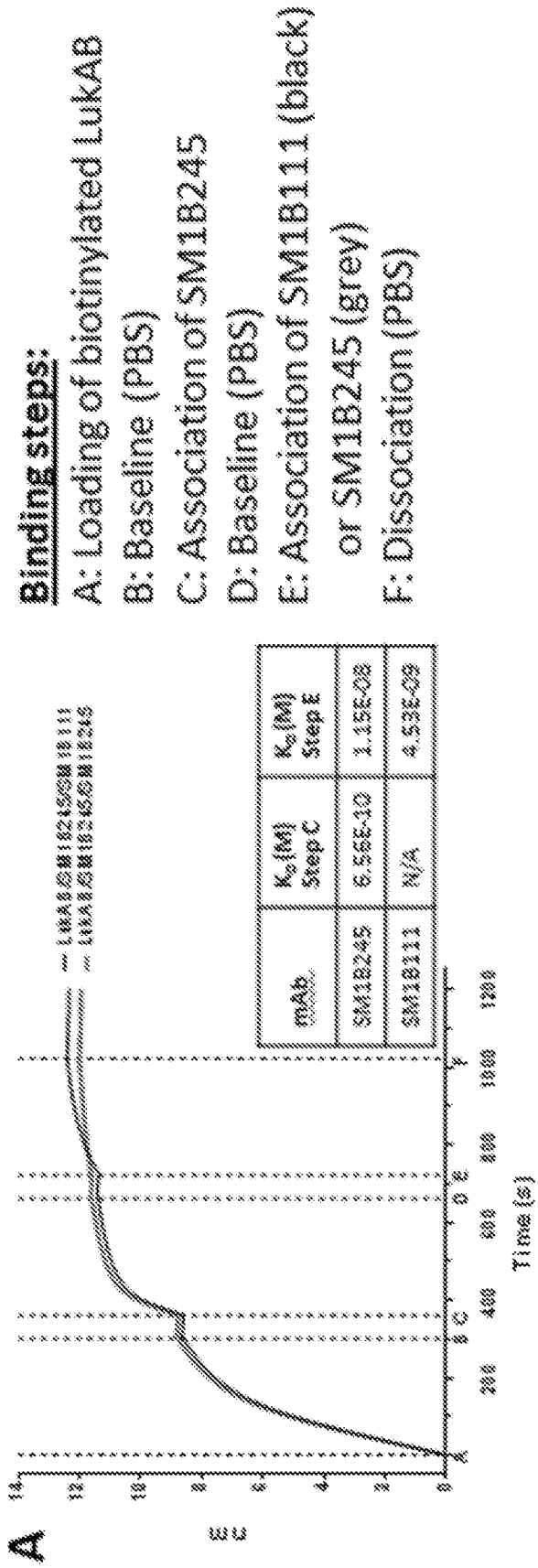

Binding steps:
A: Loading of biotinylated LukAB
B: Baseline (PBS)
C: Association of SM1B245
D: Baseline (PBS)
E: Association of SM1B111 (black) or SM1B245 (grey)
F: Dissociation (PBS)
A
nm
Time (s)
mAb
KD (M) Step C
KD (M) Step E
SM1B245
6.56E-10
1.15E-08
SM1B111
N/A
4.53E-09

FIG. 2F

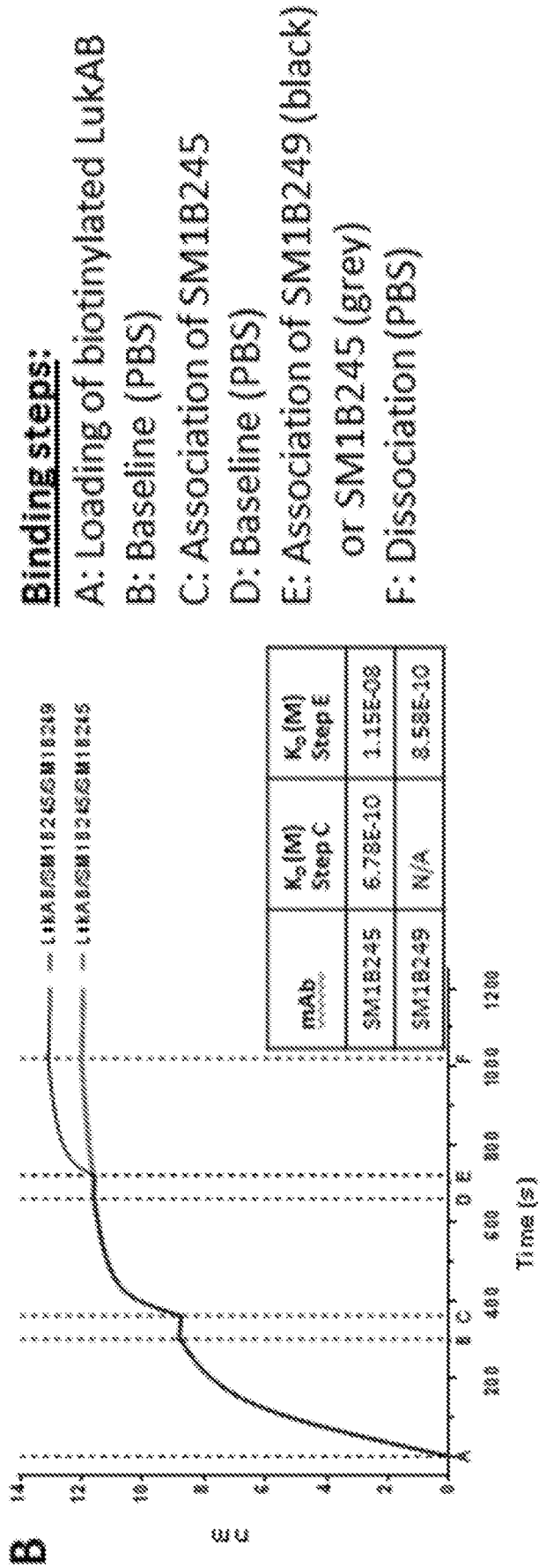

B
nm
Time (s)
A
B
C
D
E
F
Binding steps:
A: Loading of biotinylated LukAB
B: Baseline (PBS)
C: Association of SM1B245
D: Baseline (PBS)
E: Association of SM1B249 (black)
or SM1B245 (grey)
F: Dissociation (PBS)
mAb
K_D(M) Step C
K_D(M) Step E
SM1B245
6.78E-10
1.15E-08
SM1B249
N/A
8.58E-10

FIG. 2G

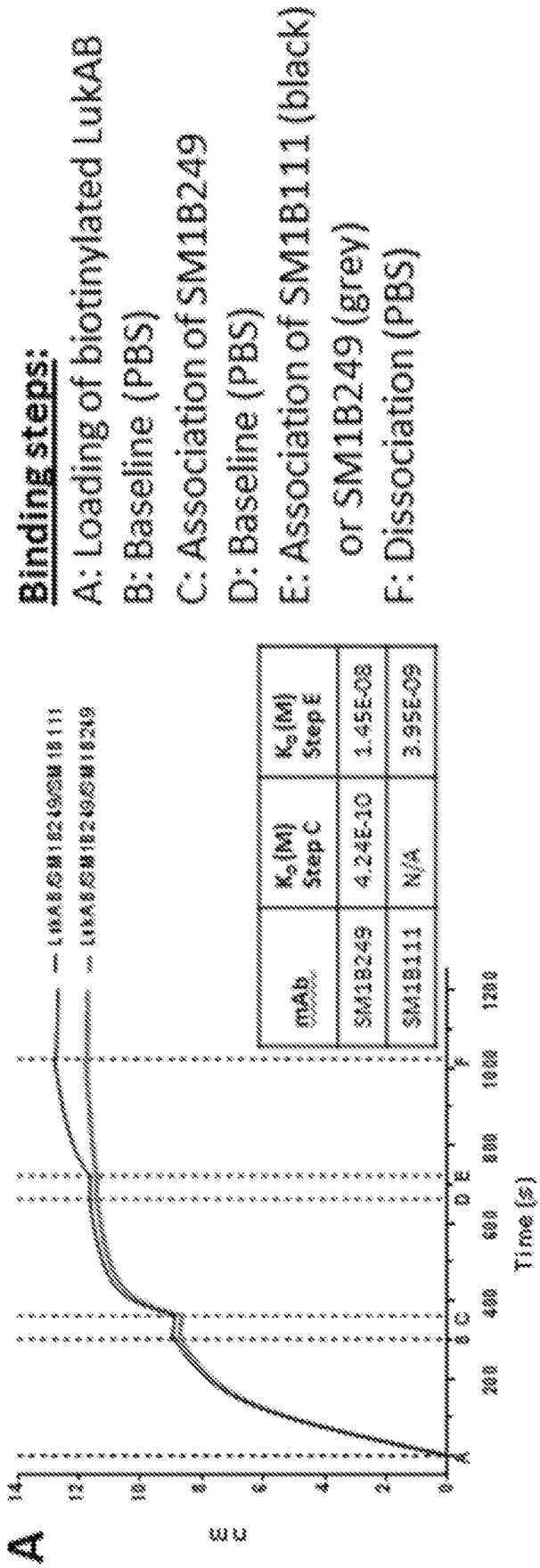

A
nm
Time (s)
A
B
C
D
E
F
mAb
K_D (M) Step C
K_D (M) Step E
SM18249
4.24E-10
1.45E-03
SM18111
N/A
3.95E-09
Binding steps:
A: Loading of biotinylated LukAB
B: Baseline (PBS)
C: Association of SM18249
D: Baseline (PBS)
E: Association of SM18111 (black) or SM18249 (grey)
F: Dissociation (PBS)

FIG. 2H

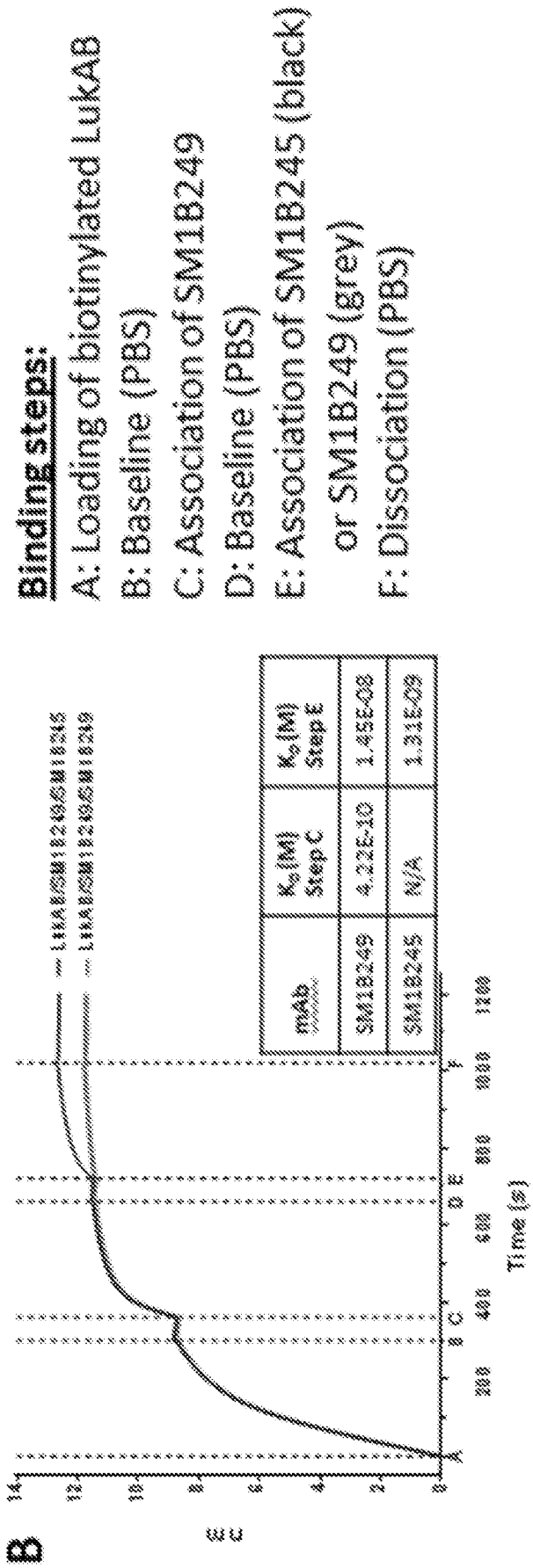

Binding steps:
A: Loading of biotinylated LukAB
B: Baseline (PBS)
C: Association of SM1B249
D: Baseline (PBS)
E: Association of SM1B245 (black)
or SM1B249 (grey)
F: Dissociation (PBS)
B
nm
Time (s)
A
B
C
D
E
F
mAb
K_D (M) Step C
K_D (M) Step E
SM1B249
4.22E-10
1.45E-08
SM1B245
N/A
1.31E-09

FIG. 2I

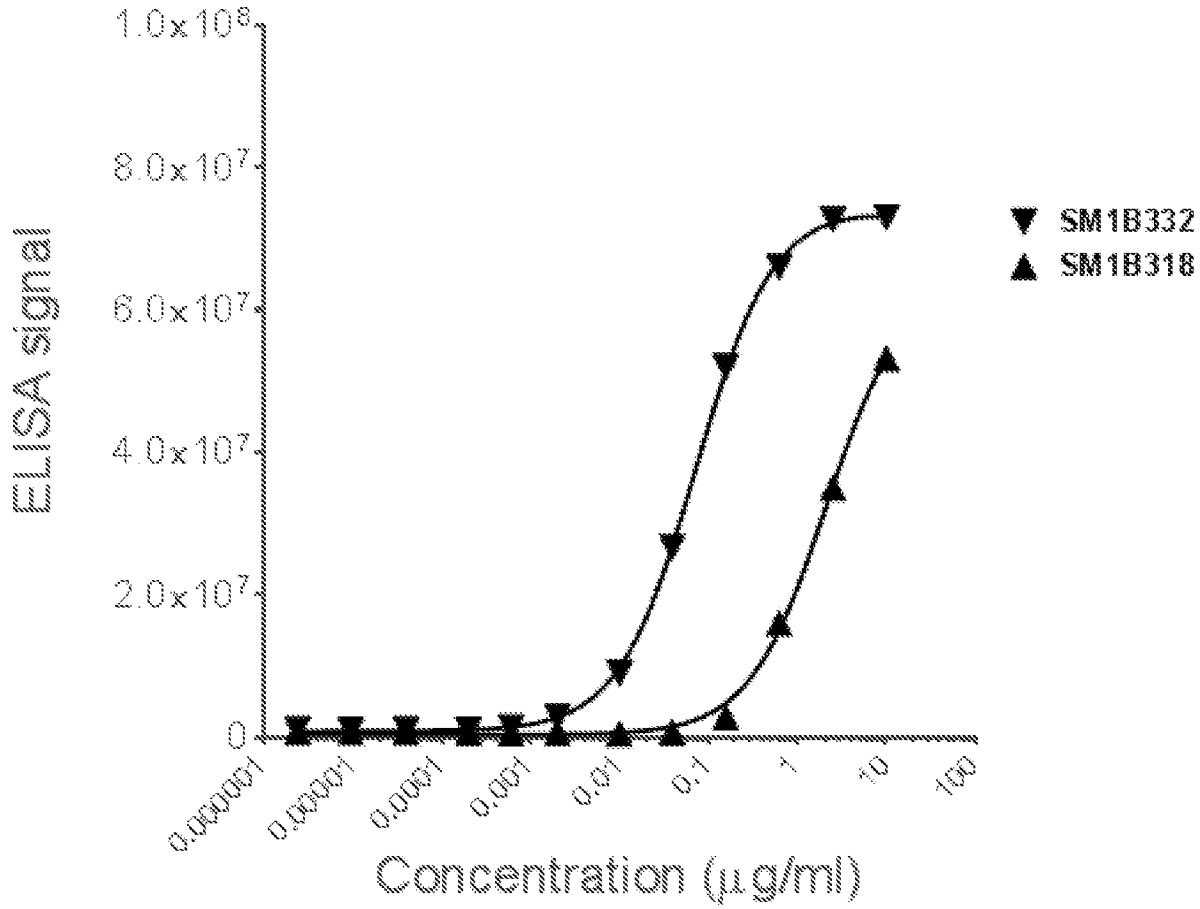
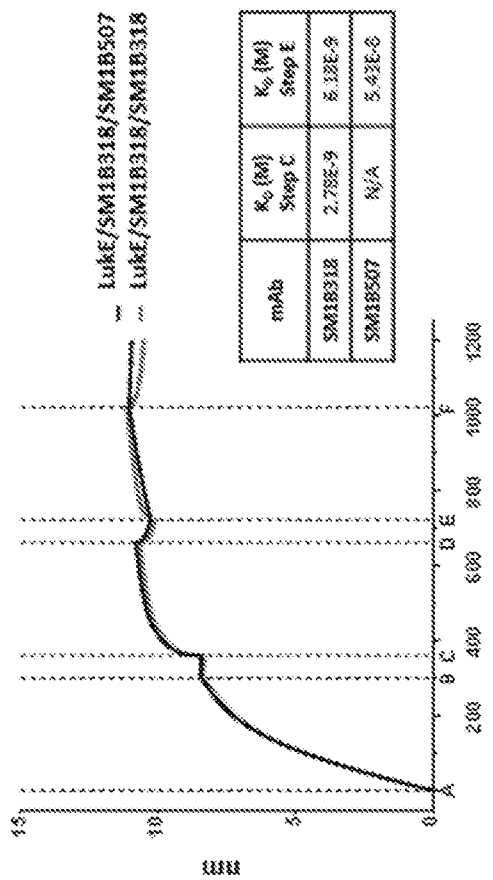
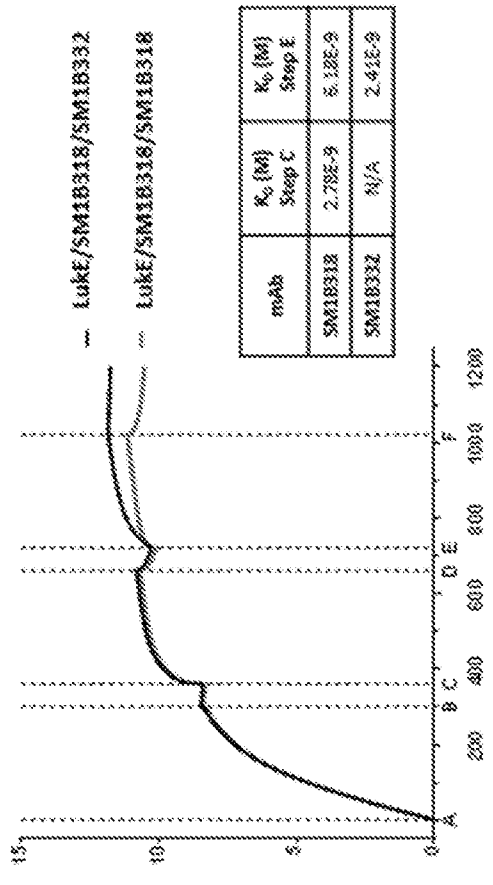

1.0x10^8
8.0x10^7
6.0x10^7
4.0x10^7
2.0x10^7
0
ELISA signal
0.000001
0.00001
0.0001
0.001
0.01
0.1
1
10
100
Concentration (µg/ml)
SM1B332
SM1B318

FIG. 3A





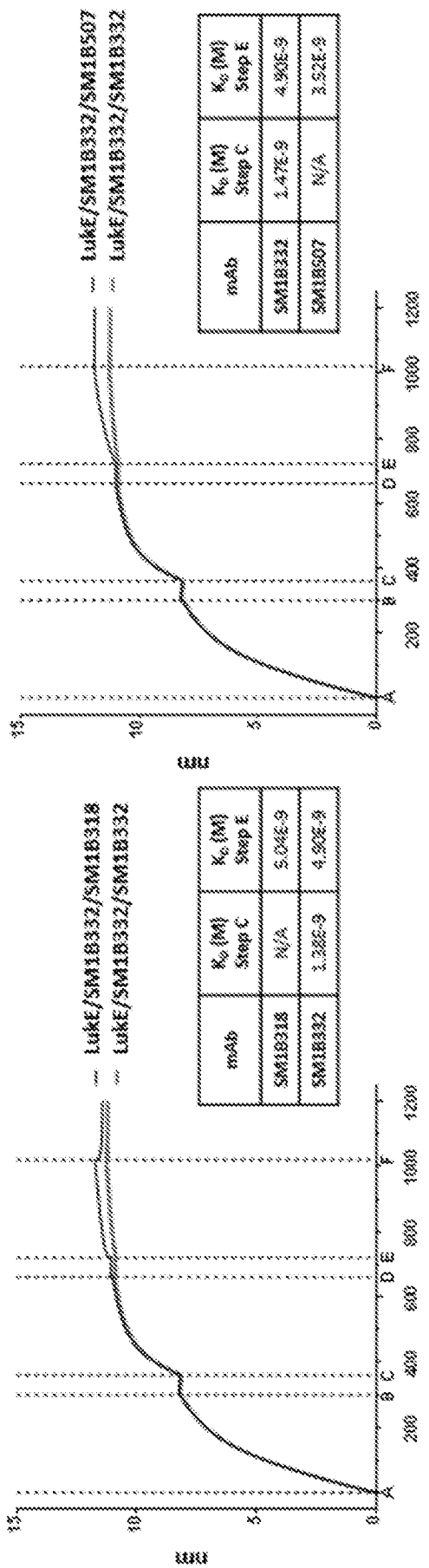
Binding steps:

A: Loading of biotinylated LukE
B: Baseline (PBS)
C: Association of SM1B318
D: Baseline (PBS)
E: Association of SM1B318 (grey) or SM1B332 (black)
F: Dissociation (PBS)

Binding steps:

A: Loading of biotinylated LukE
B: Baseline (PBS)
C: Association of SM1B318
D: Baseline (PBS)
E: Association of SM1B318 (grey) or SM1B507 (black)
F: Dissociation (PBS)

FIG. 3B



Binding steps:

A: Loading of biotinylated LukE
B: Baseline (PBS)
C: Association of SM1B332
D: Baseline (PBS)
E: Association of SM1B332 (grey) or SM1B318 (black)
F: Dissociation (PBS)

Binding steps:

A: Loading of biotinylated LukE
B: Baseline (PBS)
C: Association of SM1B332
D: Baseline (PBS)
E: Association of SM1B332 (grey) or SM1B507 (black)
F: Dissociation (PBS)

FIG. 3C

mAb	K_D (M) Step C	K_D (M) Step E
SM1B332	N/A	8.07E-10
SM1B507	3.02E-9	7.65E-9

Binding steps:

A: Loading of biotinylated LukE
B: Baseline (PBS)
C: Association of SM1B507
D: Baseline (PBS)
E: Association of SM1B507 (grey) or SM1B332 (black)
F: Dissociation (PBS)

mAb	K_D (M) Step C	K_D (M) Step E
SM1B318	N/A	4.15E-9
SM1B507	1.73E-9	7.65E-9

Binding steps:

A: Loading of biotinylated LukE
B: Baseline (PBS)
C: Association of SM1B507
D: Baseline (PBS)
E: Association of SM1B507 (grey) or SM1B318 (black)
F: Dissociation (PBS)

FIG. 3D

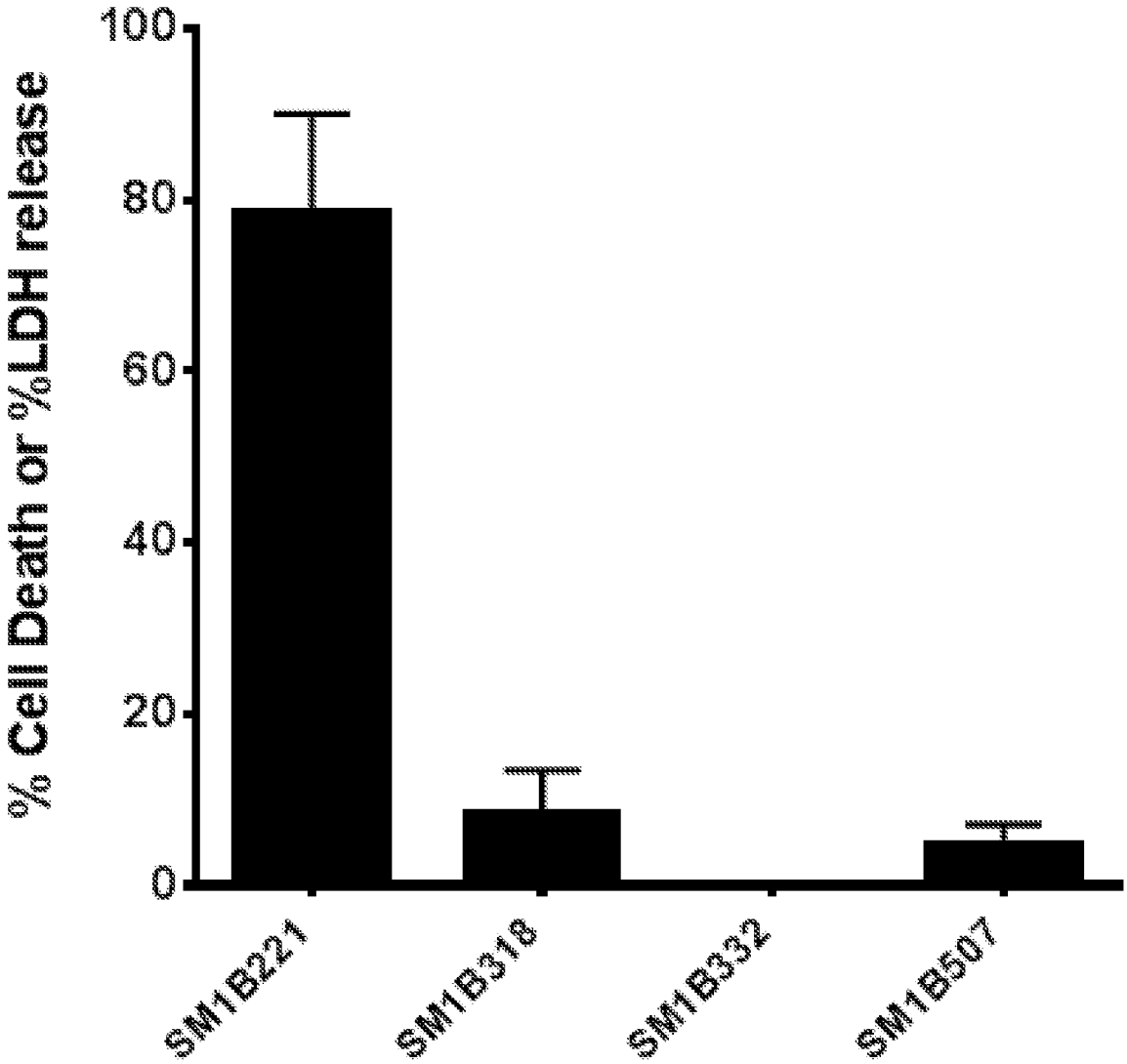

% Cell Death or %LDH release
100
80
60
40
20
0
SM1B221
SM1B318
SM1B332
SM1B507

FIG. 3E

AA residues in LukE (SEQ ID # 826)	Protected Sequence	Fab SM1B438	Fab SM1B440	Fab SM1B709
60-68	KMQGFINSR	-	+	-
74-82	VKGSGYELT	-	-	++
115-158	TTDVGQTLGYNIGGNFQS APSIGGNGSFNYSKTISYT QKSYVSE	-	+	-
192-206	VQSPNGPTGSAREYF	-	-	++
207-219	APDNQLPPLVQSG	++	++	-
207-224	APDNQLPPLVQSGFNPSF	-	++	-
255-275	LFPRTGIYAERKHNAFVN RNF	-	-	++

"-" indicates no detectable reduction in deuterium uptake upon Fab binding.
"+" indicates detectable reduction in deuterium uptake upon Fab binding.
"++" indicates significant reduction in deuterium uptake upon Fab binding.

FIG. 4