LAG-3-Binding Molecules and Methods of Use Thereof

Cross-Reference to Related Applications:

[0001] This application claims priority to U.S. Patent Appln. Serial Nos. 62/255,094 filed on November 13, 2015; pending) and 62/172,277 (filed on June 8, 2015; pending), each of which applications is herein incorporated by reference in its entirety.

Reference to Sequence Listing:

[0002] This application includes one or more Sequence Listings pursuant to 37 C.F.R. 1.821 et seq., which are disclosed in computer-readable media (file name: 1301_0121PCT_Sequence_Listing_ST25.txt, created on May 18, 2016, and having a size of 105,774 bytes), which file is herein incorporated by reference in its entirety.

Field of the Invention:

[0003] The present invention is directed to LAG-3 binding molecules that comprise the LAG-3-binding domain of selected anti-LAG-3 antibodies: LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5, or LAG-3 mAb 6 that are capable of binding to both cynomolgus monkey LAG-3 and to human LAG-3. The invention particularly concerns LAG-3 binding molecules that are humanized or chimeric versions of such antibodies, or that comprise LAG-3 binding-fragments of such anti-LAG-3 antibodies (especially immunocongugates, diabodies, BiTEs, bispecific antibodies, *etc.*). The invention particularly concerns such LAG-3-binding molecules that are additionally capable of binding an epitope of a molecule involved in regulating an immune check point that is present on the surface of an immune cell. The present invention also pertains to methods of using such LAG-3 binding molecules to detect LAG-3 or to stimulate an immune response. The present invention also pertains to methods of combination therapy in which a LAG-3-binding molecule that comprises one or more LAG-3-binding domain(s) of such selected anti-LAG-3 antibodies is administered in combination with one or more additional molecules that are effective

in stimulating an immune response to thereby further enhance, stimulate or upregulate such immune response in a subject.

Background of the Invention:

I. Cell Mediated Immune Responses

[0004] The immune system of humans and other mammals is responsible for providing protection against infection and disease. Such protection is provided both by a humoral immune response and by a cell-mediated immune response. The humoral response results in the production of antibodies and other biomolecules that are capable of recognizing and neutralizing foreign targets (antigens). In contrast, the cell-mediated immune response involves the activation of macrophages, Natural Killer cells (NK), and antigen-specific cytotoxic T-lymphocytes by T-cells, and the release of various cytokines in response to the recognition of an antigen (Dong, C. *et al.* (2003) "*Immune Regulation by Novel Costimulatory Molecules*," Immunolog. Res. 28(1):39-48).

[0005] The ability of T-cells to optimally mediate an immune response against an antigen requires two distinct signaling interactions (Viglietta, V. *et al.* (2007) "*Modulating Co-Stimulation*," Neurotherapeutics 4:666-675; Korman, A.J. *et al.* (2007) "*Checkpoint Blockade in Cancer Immunotherapy*," Adv. Immunol. 90:297-339). First, antigen that has been arrayed on the surface of Antigen-Presenting Cells (**APC**) must be presented to an antigen-specific naïve $CD4^+$ T-cell. Such presentation delivers a signal via the T-Cell Receptor (**TCR**) that directs the T-cell to initiate an immune response that will be specific to the presented antigen. Second, a series of costimulatory and inhibitory signals, mediated through interactions between the APC and distinct T-cell surface molecules, triggers first the activation and proliferation of the T-cells and ultimately their inhibition. Thus, the first signal confers specificity to the immune response whereas the second signal serves to determine the nature, magnitude and duration of the response.

[0006] The immune system is tightly controlled by costimulatory and co-inhibitory ligands and receptors. These molecules provide the second signal for T-cell activation and provide a balanced network of positive and negative signals to maximize immune responses against infection while limiting immunity to self (Wang, L. *et al.*

(2011) "*VISTA, A Novel Mouse Ig Superfamily Ligand That Negatively Regulates T-Cell Responses*," J. Exp. Med. 10.1084/jem.20100619:1-16; Lepenies, B. *et al.* (2008) "*The Role Of Negative Costimulators During Parasitic Infections*," Endocrine, Metabolic & Immune Disorders - Drug Targets 8:279-288). The inhibitory pathways crucial for maintaining self-tolerance and modulating the duration and amplitude of immune responses are collectively referred to as immune checkpoints. Of particular importance is binding between the B7.1 (CD80) and B7.2 (CD86) ligands of the Antigen-Presenting Cell and the CD28 and CTLA-4 receptors of the $CD4^+$ T-lymphocyte (Sharpe, A.H. *et al.* (2002) "*The B7-CD28 Superfamily*," Nature Rev. Immunol. 2:116-126; Dong, C. *et al.* (2003) "*Immune Regulation by Novel Costimulatory Molecules*," Immunolog. Res. 28(1):39-48; Lindley, P.S. *et al.* (2009) "*The Clinical Utility Of Inhibiting CD28-Mediated Costimulation*," Immunol. Rev. 229:307-321). Binding of B7.1 or of B7.2 to CD28 stimulates T-cell activation; binding of B7.1 or B7.2 to CTLA-4 inhibits such activation (Dong, C. *et al.* (2003) "*Immune Regulation by Novel Costimulatory Molecules*," Immunolog. Res. 28(1):39-48; Lindley, P.S. *et al.* (2009) "*The Clinical Utility Of Inhibiting CD28-Mediated Costimulation*," Immunol. Rev. 229:307-321; Greenwald, R.J. *et al.* (2005) "*The B7 Family Revisited*," Ann. Rev. Immunol. 23:515-548). CD28 is constitutively expressed on the surface of T-cells (Gross, J., *et al.* (1992) "*Identification And Distribution Of The Costimulatory Receptor CD28 In The Mouse*," J. Immunol. 149:380–388), whereas CTLA-4 expression is rapidly upregulated following T-cell activation (Linsley, P. *et al.* (1996) "*Intracellular Trafficking Of CTLA4 And Focal Localization Towards Sites Of TCR Engagement*," Immunity 4:535–543). Since CTLA-4 is the higher affinity receptor (Sharpe, A.H. *et al.* (2002) "*The B7-CD28 Superfamily*," Nature Rev. Immunol. 2:116-126), binding first initiates T-cell proliferation (via CD28) and then inhibits it (via nascent expression of CTLA-4), thereby dampening the effect when proliferation is no longer needed.

[0007] Further investigations into the ligands of the CD28 receptor have led to the identification and characterization of a set of related B7 molecules (the "B7 Superfamily") (Sharpe, A.H. *et al.* (2002) "*The B7-CD28 Superfamily*," Nature Rev. Immunol. 2:116-126; Greenwald, R.J. *et al.* (2005) "*The B7 Family Revisited*," Ann. Rev. Immunol. 23:515-548; Collins, M. *et al.* (2005) "*The B7 Family Of Immune-*

Regulatory Ligands," Genome Biol. 6:223.1-223.7; Loke, P. *et al.* (2004) "*Emerging Mechanisms Of Immune Regulation: The Extended B7 Family And Regulatory T-Cells*." Arthritis Res. Ther. 6:208-214; Korman, A.J. *et al.* (2007) "*Checkpoint Blockade in Cancer Immunotherapy*," Adv. Immunol. 90:297-339; Flies, D.B. *et al.* (2007) "*The New B7s: Playing a Pivotal Role in Tumor Immunity*," J. Immunother. 30(3):251-260; Agarwal, A. *et al.* (2008) "*The Role Of Positive Costimulatory Molecules In Transplantation And Tolerance*," Curr. Opin. Organ Transplant. 13:366-372; Wang, S. *et al.* (2004) "*Co-Signaling Molecules Of The B7-CD28 Family In Positive And Negative Regulation Of T Lymphocyte Responses*," Microbes Infect. 6:759-766). There are currently several known members of the family: B7.1 (CD80), B7.2 (CD86), the inducible co-stimulator ligand (ICOS-L), the programmed death-1 ligand (PD-L1; B7-H1), the programmed death-2 ligand (PD-L2; B7-DC), B7-H3, B7-H4 and B7-H6 (Collins, M. *et al.* (2005) "*The B7 Family Of Immune-Regulatory Ligands*," Genome Biol. 6:223.1-223.7; Flajnik, M.F. *et al.* (2012) "*Evolution Of The B7 Family: Co-Evolution Of B7H6 And Nkp30, Identification Of A New B7 Family Member, B7H7, And Of B7's Historical Relationship With The MHC*," Immunogenetics 64(8):571-90).

II. Lymphocyte Activation Gene-3 ("LAG-3")

[0008] The Lymphocyte Activation Gene 3 encodes a cell surface receptor protein that is referred to as "LAG-3," or CD223 (Triebel, F. *et al.* (1990) "*LAG-3, A Novel Lymphocyte Activation Gene Closely Related To CD4*," J. Exp. Med. 171(5):1393-1405). LAG-3 is expressed by activated CD4+ and CD8+ T-cells and by NK cells, and is constitutively expressed by plasmacytoid dendritic cells. LAG-3 is not expressed by B cells, monocytes or any other cell types tested (Workman, C.J. *et al.* (2009) "*LAG-3 Regulates Plasmacytoid Dendritic Cell Homeostasis*," J. Immunol. 182(4):1885-1891).

[0009] LAG-3 has been found to be closely related to the T-cell co-receptor CD4 (Triebel, F. *et al.* (1990) "*LAG-3, A Novel Lymphocyte Activation Gene Closely Related To CD4*," J. Exp. Med. 171(5):1393-1405; Grosso, J.F. *et al.* (2009) "*Functionally Distinct LAG-3 and PD-1 Subsets on Activated and Chronically Stimulated CD8 T-Cells*," J. Immunol. 182(11):6659-6669; Huang, C.T. *et al.* (2004) "*Role Of LAG-3 In*

Regulatory T-Cells," Immunity 21:503-513; Workman, C.J. *et al.* (2009) "*LAG-3 Regulates Plasmacytoid Dendritic Cell Homeostasis*," J. Immunol. 182(4):1885-1891). Like CD4, LAG-3 also binds to MHC class II molecules but does so with significantly higher affinity (Workman, C.J. *et al.* (2002) "*Phenotypic Analysis Of The Murine CD4-Related Glycoprotein, CD223 (LAG-3)*," Eur. J. Immunol. 32:2255-2263; Huard, B. *et al.* (1995) "*CD4/Major Histocompatibility Complex Class II Interaction Analyzed With CD4- And Lymphocyte Activation Gene-3 (LAG-3)-Ig Fusion Proteins*," Eur. J. Immunol. 25:2718-2721; Huard, B. *et al.* (1994) "*Cellular Expression And Tissue Distribution Of The Human LAG-3- Encoded Protein, An MHC Class II Ligand*," Immunogenetics 39:213-217).

[0010] Studies have shown that LAG-3 plays an important role in negatively regulating T-cell proliferation, function and homeostasis (Workman, C.J. *et al.* (2009) "*LAG-3 Regulates Plasmacytoid Dendritic Cell Homeostasis*," J. Immunol. 182(4):1885-1891; Workman, C.J. *et al.* (2002) "*Cutting Edge: Molecular Analysis Of The Negative Regulatory Function Of Lymphocyte Activation Gene-3*," J. Immunol. 169:5392-5395; Workman, C.J. *et al.* (2003) "T*he CD4-Related Molecule, LAG-3 (CD223), Regulates The Expansion Of Activated T-Cells*," Eur. J. Immunol. 33:970-979; Workman, C.J. (2005) "*Negative Regulation Of T-Cell Homeostasis By Lymphocyte Activation Gene-3 (CD223)*," J. Immunol. 174:688-695; Hannier, S. *et al.* (1998) "*CD3/TCR Complex-Associated Lymphocyte Activation Gene-3 Molecules Inhibit CD3/TCR Signaling*," J. Immunol. 161:4058-4065; Huard, B. *et al.* (1994) "*Lymphocyte-Activation Gene 3/Major Histocompatibility Complex Class II Interaction Modulates The Antigenic Response Of CD4+ T Lymphocytes*," Eur. J. Immunol. 24:3216-3221).

[0011] Studies have suggested that inhibiting LAG-3 function through antibody blockade can reverse LAG-3-mediated immune system inhibition and partially restore effector function (Grosso, J.F. *et al.* (2009) "*Functionally Distinct LAG-3 and PD-1 Subsets on Activated and Chronically Stimulated CD8 T-Cells*," J. Immunol. 182(11):6659-6669; Grosso, J.F. *et al.* (2007) "*LAG-3 Regulates CD8+ T-Cell Accumulation And Effector Function During Self And Tumor Tolerance*," J. Clin. Invest. 117:3383-3392). LAG-3 has been found to negatively regulate T-cell expansion

via inhibition of TCR-induced calcium fluxes, and controls the size of the memory T-cell pool (Matsuzaki, J. *et al.* (2010) "*Tumor-Infiltrating NY-ESO-1-Specific CD8+ T-Cells Are Negatively Regulated By LAG-3 and PD-1 In Human Ovarian Cancer*," Proc. Natl. Acad. Sci. (U.S.A.) 107(17):7875-7880; Workman C.J., *et al.* (2004) "*Lymphocyte Activation Gene-3 (CD223) Regulates The Size Of The Expanding T-Cell Population Following Antigen Activation in vivo*," J. Immunol. 172:5450-5455).

[0012] However, despite all such prior advances, a need remains for improved compositions capable of more vigorously directing the body's immune system to attack cancer cells or pathogen-infected cells, especially at lower therapeutic concentrations. For although the adaptive immune system can be a potent defense mechanism against cancer and disease, it is often hampered by immune suppressive mechanisms in the tumor microenvironment, such as the expression of LAG-3. Furthermore, co-inhibitory molecules expressed by tumor cells, immune cells, and stromal cells in the tumor milieu can dominantly attenuate T-cell responses against cancer cells. Thus, a need remains for potent LAG-3-binding molecules. In particular, a need exists for LAG-3-binding molecules that a desirable binding kinetic profile, bind different LAG-3 epitopes and/or exhibit single agent activity that could provide improved therapeutic value to patients suffering from cancer or other diseases and conditions. The present invention is directed to these and other goals.

Summary:

[0013] The present disclosure is directed to LAG-3 binding molecules that comprise the LAG-3-binding domain of selected anti-LAG-3 antibodies: LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5, or LAG-3 mAb 6 that are capable of binding to both cynomolgus monkey LAG-3 and to human LAG-3. The disclosure particularly concerns LAG-3 binding molecules that are humanized or chimeric versions of such antibodies, or that comprise LAG-3 binding-fragments of such anti-LAG-3 antibodies (especially immunocongugates, diabodies, BiTEs, bispecific antibodies, *etc.*). The disclosure particularly concerns such LAG-3-binding molecules that are additionally capable of binding an epitope of a molecule involved in regulating an immune check point that is present on the surface of an immune cell. The present disclosure also pertains to methods of using such LAG-3-binding molecules to

detect LAG-3 or to stimulate an immune response. The present disclosure also pertains to methods of combination therapy in which a LAG-3-binding molecule that comprises one or more LAG-3-binding domain(s) of such selected anti-LAG-3 antibodies is administered in combination with one or more additional molecules that are effective in stimulating an immune response to thereby further enhance, stimulate or upregulate such immune response in a subject.

[0014] In detail, the disclosure provides a LAG-3-binding molecule that is capable of binding both to human LAG-3 and to cynomolgus monkey LAG-3, wherein said LAG-3-binding molecule comprises a Variable Heavy Chain Domain and a Variable Light Chain Domain, wherein: said Variable Heavy Chain Domain comprises a CDR_H1 Domain, a CDR_H2 Domain and a CDR_H3 Domain, and said Variable Light Chain Domain comprises a CDR_L1 Domain, a CDR_L2 Domain, and a CDR_L3 Domain, wherein:

(A) (1) the CDR_H1 Domain, CDR_H2 Domain, and CDR_H3 Domain are the Heavy Chain CDRs of LAG-3 mAb 1, and respectively have the amino acid sequences: **SEQ ID NO:8**, **SEQ ID NO:9**, and **SEQ ID NO:10**; and

(2) the CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain are the Light Chain CDRs of LAG-3 mAb 1, and respectively have the amino acid sequences: **SEQ ID NO:13**, **SEQ ID NO:14**, and **SEQ ID NO:15**;

or

(B) (1) the CDR_H1 Domain, CDR_H2 Domain, and CDR_H3 Domain are the Heavy Chain CDRs of hLAG-3 mAb 1, and respectively have the amino acid sequences: **SEQ ID NO:8**, **SEQ ID NO:9**, and **SEQ ID NO:10**; and

(2) the CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain are the Light Chain CDRs of hLAG-3 mAb 1, and respectively have the amino acid sequences: **SEQ ID NO:28**, **SEQ ID NO:14**, and **SEQ ID NO:15**;

or

(C) (1) the CDR_H1 Domain, CDR_H2 Domain, and CDR_H3 Domain are the Heavy Chain CDRs of LAG-3 mAb 2, and respectively have the amino acid sequences: **SEQ ID NO:31**, **SEQ ID NO:32**, and **SEQ ID NO:33**; and

(2) the CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain are the Light Chain CDRs of LAG-3 mAb 2, and, respectively have the amino acid sequences: **SEQ ID NO:36**, **SEQ ID NO:37**, and **SEQ ID NO:38;**

or

(D) (1) the CDR_H1 Domain, CDR_H2 Domain, and CDR_H3 Domain are the Heavy Chain CDRs of LAG-3 mAb 3, and respectively have the amino acid sequences: **SEQ ID NO:41**, **SEQ ID NO:42**, and **SEQ ID NO:43**; and

(2) the CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain are the Light Chain CDRs of LAG-3 mAb 3, and, respectively have the amino acid sequences: **SEQ ID NO:46**, **SEQ ID NO:47**, and **SEQ ID NO:48**;

or

(E) (1) the CDR_H1 Domain, CDR_H2 Domain, and CDR_H3 Domain are the Heavy Chain CDRs of LAG-3 mAb 4, and respectively have the amino acid sequences: **SEQ ID NO:51**, **SEQ ID NO:52**, and **SEQ ID NO:53**; and

(2) the CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain are the Light Chain CDRs of LAG-3 mAb 4, and, respectively have the amino acid sequences: **SEQ ID NO:56**, **SEQ ID NO:57**, and **SEQ ID NO:58**;

or

(F) (1) the CDR_H1 Domain, CDR_H2 Domain, and CDR_H3 Domain are the Heavy Chain CDRs of LAG-3 mAb 5, and respectively have the amino acid sequences: **SEQ ID NO:61**, **SEQ ID NO:62**, and **SEQ ID NO:63**; and

(2) the CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain are the Light Chain CDRs of LAG-3 mAb 5, and, respectively have the amino acid sequences: **SEQ ID NO:66**, **SEQ ID NO:67**, and **SEQ ID NO:68**;

or

(G) (1) the CDR_H1 Domain, CDR_H2 Domain, and CDR_H3 Domain are the Heavy Chain CDRs of LAG-3 mAb 6 VH1, and respectively have the amino acid sequences: **SEQ ID NO:71**, **SEQ ID NO:72**, and **SEQ ID NO:73**; and

(2) the CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain are the Light Chain CDRs of LAG-3 mAb 6, and, respectively have the amino acid sequences: **SEQ ID NO:76**, **SEQ ID NO:77**, and **SEQ ID NO:78**;

or

(H) (1) the CDR_H1 Domain, CDR_H2 Domain, and CDR_H3 Domain are the Heavy Chain CDRs of LAG-3 hAb 6, and respectively have the amino acid sequences: **SEQ ID NO:71**, **SEQ ID NO:72**, and **SEQ ID NO:73**; and

(2) the CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain are the Light Chain CDRs of hLAG-3 hAb 6, and respectively have the amino acid sequences: **SEQ ID NO:87**, **SEQ ID NO:77**, and **SEQ ID NO:78**.

[0014a] In one aspect, the present disclosure refers to a LAG-3-binding molecule that is capable of binding both to human LAG-3 and to cynomolgus monkey LAG-3, wherein said LAG-3-binding molecule is an antibody or comprises an antigen-binding fragment thereof that comprises a Variable Heavy Chain Domain and a Variable Light Chain Domain of an antibody that specifically binds human LAG-3 with an equilibrium binding constant (KD) of about 0.05 nM or less, wherein:

said Variable Heavy Chain Domain comprises a CDR_H1 Domain, a CDR_H2 Domain and a CDR_H3 Domain, and said Variable Light Chain Domain comprises a CDR_L1 Domain, a CDR_L2 Domain, and a CDR_L3 Domain, wherein:

(A) (1) the CDR_H1 Domain, CDR_H2 Domain, and CDR_H3 Domain are the Heavy Chain CDRs of LAG-3 mAb 1, and respectively have the amino acid sequences: **SEQ ID NO:8**, **SEQ ID NO:9**, and **SEQ ID NO:10**; and

(2) the CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain are the Light Chain CDRs of LAG-3 mAb 1, and respectively have the amino acid sequences: **SEQ ID NO:13**, **SEQ ID NO:14**, and **SEQ ID NO:15**;

(B) (1) the CDR_H1 Domain, CDR_H2 Domain, and CDR_H3 Domain are the Heavy Chain CDRs of hLAG-3 mAb 1, and respectively have the amino acid sequences: **SEQ ID NO:8**, **SEQ ID NO:9**, and **SEQ ID NO:10**; and

(2) the CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain are the Light Chain CDRs of hLAG-3 mAb 1, and respectively have the amino acid sequences: **SEQ ID NO:28**, **SEQ ID NO:14**, and **SEQ ID NO:15**;

(C) (1) the CDR_H1 Domain, CDR_H2 Domain, and CDR_H3 Domain are the Heavy Chain CDRs of LAG-3 mAb 6 VH1, and respectively have the amino acid sequences: **SEQ ID NO:71**, **SEQ ID NO:72**, and **SEQ ID NO:73**; and

(2) the CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain are the Light Chain CDRs of LAG-3 mAb 6, and, respectively have the amino acid sequences: **SEQ ID NO:76**, **SEQ ID NO:77**, and **SEQ ID NO:78**;

or

(D) (1) the CDR_H1 Domain, CDR_H2 Domain, and CDR_H3 Domain are the Heavy Chain CDRs of hLAG-3 mAb 6, and respectively have the amino acid sequences: **SEQ ID NO:71**, **SEQ ID NO:72**, and **SEQ ID NO:73**; and

(2) the CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain are the Light Chain CDRs of hLAG-3 mAb 6, and respectively have the amino acid sequences: **SEQ ID NO:87**, **SEQ ID NO:77**, and **SEQ ID NO:78**;

wherein said LAG-3-binding molecule is capable of binding both to human LAG-3 and to cynomolgus monkey LAG-3, and is capable of binding to human LAG-3 with an equilibrium binding constant (KD) of about 0.05 nM or less.

[0014b] In another aspect, the present disclosure refers to a LAG-3-binding molecule that is capable of binding both to human LAG-3 and to cynomolgus monkey LAG-3, wherein said LAG-3-binding molecule is an antibody or comprises an antigen-binding fragment thereof that comprises a Variable Heavy Chain Domain and a Variable Light Chain Domain, wherein:

(A) (1) said Variable Heavy Chain Domain comprises the amino acid sequence of **SEQ ID NO:16** or **SEQ ID NO:18**; and

(2) said Variable Light Chain Domain comprises the amino acid sequence of **SEQ ID NO:24** or **SEQ ID NO:26**; or

(B) (1) said Variable Heavy Chain Domain comprises the amino acid sequence of **SEQ ID NO:79**; and

(2) said Variable Light Chain Domain comprises the amino acid sequence of **SEQ ID NO:83**.

[0015] The disclosure further concerns the examples of such LAG-3-binding molecules wherein the Heavy Chain Variable Domain has the amino acid sequence of **SEQ ID NO:6**, **SEQ ID NO:29**, **SEQ ID NO:39**, **SEQ ID NO:49**, or **SEQ ID NO:59**.

[0016] The disclosure further concerns the examples of such LAG-3-binding molecules wherein the Light Chain Variable Domain has the amino acid sequence of **SEQ ID NO:11**, **SEQ ID NO:34**, **SEQ ID NO:44**, **SEQ ID NO:54**, or **SEQ ID NO:64**.

[0017] The disclosure further concerns the examples of such LAG-3-binding molecules wherein the Heavy Chain Variable Domain has the amino acid sequence of **SEQ ID NO:16**, **SEQ ID NO:18**, **SEQ ID NO:79**, or **SEQ ID NO:80**.

[0018] The disclosure further concerns the examples of such LAG-3-binding molecules wherein the Light Chain Variable Domain has the amino acid sequence of **SEQ ID NO:20**, **SEQ ID NO:22**, **SEQ ID NO:24**, **SEQ ID NO:26**, **SEQ ID NO:83**, or **SEQ ID NO:85.**

[0019] The disclosure further concerns the examples of all such LAG-3-binding molecules wherein the molecule is an antibody, and especially wherein the molecule is a chimeric antibody or a humanized antibody.

[0020] The disclosure further concerns the example wherein the LAG-3-binding molecule is a bispecific binding molecule, capable of simultaneously binding to human LAG-3 and to a second epitope, and particularly concerns the example wherein the second epitope is an epitope of a molecule involved in regulating an immune check point present on the surface of an immune cell (especially wherein the second epitope is an epitope of B7-H3, B7-H4, BTLA, CD40, CD40L, CD47, CD70, CD80, CD86, CD94, CD137, CD137L, CD226, CTLA-4, Galectin-9, GITR, GITRL, HHLA2, ICOS, ICOSL, KIR, LAG-3, LIGHT, MHC class I or II, NKG2a, NKG2d, OX40, OX40L, PD1H, PD-1, PD-L1, PD-L2, PVR, SIRPa, TCR, TIGIT, TIM-3 or VISTA, and most particularly wherein the second epitope is an epitope of CD137, OX40, PD-1, TIGIT or TIM-3).

[0021] The disclosure further concerns the example of such LAG-3-binding molecules wherein the molecule is a diabody, and especially, wherein the diabody is a covalently bonded complex that comprises two, or three, or four, or five, or more than five polypeptide chains. The disclosure further concerns the example of such anti-LAG-3-binding molecules wherein the molecule is a trivalent binding molecule, the trivalent binding molecule being a covalently bonded complex that comprises three, four, five or more polypeptide chains. The disclosure additionally concerns the example of such LAG-3-binding molecules in which the molecule comprises an Fc Region. The disclosure additionally concerns the example of such LAG-3-binding molecules in which the molecule comprises an Albumin-Binding Domain, and especially a deimmunized Albumin-Binding Domain.

[0022] The disclosure further concerns the examples of all such LAG-3-binding molecules wherein the molecule comprises an Fc (Fraction Crystalizable) Region, and wherein the Fc Region is a variant Fc Region that comprises one or more amino acid modifications that reduces the affinity of the variant Fc Region for an FcγR and/or enhances serum half-life, and more particularly, wherein the modifications comprise at least one amino acid substitution selected from the group consisting of:

(1) L234A;

(2) L235A;

(3) L234A and L235A;

(4) M252Y; M252Y and S254T;
(5) M252Y and T256E;
(6) M252Y, S254T and T256E; or
(7) K288D and H435K;
wherein the numbering is that of the EU index according to Kabat.

[0022a] In one aspect, the present disclosure refers to a pharmaceutical composition comprising an effective amount of any of the above-described LAG-3-binding molecules, and a pharmaceutically acceptable carrier.

[0023] The disclosure further concerns the examples in which any of the above-described LAG-3-binding molecules is used to stimulate a T-cell mediate immune response. The disclosure additionally concerns the examples in which any of the above-described LAG-3-binding molecules is used in the treatment of a disease or condition associated with a suppressed immune system, especially cancer or an infection.

[**0023a**] In one aspect, the present disclosure refers to any of the above-described LAG-3-binding molecules, or the above-described pharmaceutical composition, for use in stimulating a T-cell-mediated immune response of a subject in need thereof. In another aspect, the present disclosure refers to any of the above-described LAG-3-binding molecules, or the above-described pharmaceutical composition, for use in treating a disease or condition associated with a suppressed immune system.

[0024] The disclosure particularly concerns such use in the treatment or diagnosis or prognosis of cancer, wherein the cancer is characterized by the presence of a cancer cell selected from the group consisting of a cell of: an adrenal gland tumor, an AIDS-associated cancer, an alveolar soft part sarcoma, an astrocytic tumor, bladder cancer, bone cancer, a brain and spinal cord cancer, a metastatic brain tumor, a breast cancer, a carotid body tumors, a cervical cancer, a chondrosarcoma, a chordoma, a chromophobe renal cell carcinoma, a clear cell carcinoma, a colon cancer, a colorectal cancer, a cutaneous benign fibrous histiocytoma, a desmoplastic small round cell tumor, an ependymoma, a Ewing's tumor, an extraskeletal myxoid chondrosarcoma, a fibrogenesis imperfecta ossium, a fibrous dysplasia of the bone, a gallbladder or bile duct cancer, gastric cancer, a gestational trophoblastic disease, a germ cell tumor, a head and neck cancer, hepatocellular carcinoma, an islet cell tumor, a Kaposi's Sarcoma, a kidney cancer, a leukemia, a lipoma/benign lipomatous tumor, a liposarcoma/malignant lipomatous tumor, a liver cancer, a lymphoma, a lung cancer, a medulloblastoma, a melanoma, a meningioma, a multiple endocrine neoplasia, a multiple myeloma, a myelodysplastic syndrome, a neuroblastoma, a neuroendocrine tumors, an ovarian cancer, a pancreatic cancer, a papillary thyroid carcinoma, a parathyroid tumor, a pediatric cancer, a peripheral nerve sheath tumor, a phaeochromocytoma, a pituitary tumor, a prostate cancer, a posterious uveal melanoma, a rare hematologic disorder, a renal metastatic cancer, a rhabdoid tumor, a

rhabdomysarcoma, a sarcoma, a skin cancer, a soft-tissue sarcoma, a squamous cell cancer, a stomach cancer, a synovial sarcoma, a testicular cancer, a thymic carcinoma, a thymoma, a thyroid metastatic cancer, and a uterine cancer.

[0025] The disclosure particularly concerns such use in the treatment or diagnosis or prognosis of cancer, wherein the cancer is colorectal cancer, hepatocellular carcinoma, glioma, kidney cancer, breast cancer, multiple myeloma, bladder cancer, neuroblastoma; sarcoma, non-Hodgkin's lymphoma, non-small cell lung cancer, ovarian cancer, pancreatic cancer, a rectal cancer, acute myeloid leukemia (AML), chronic myelogenous leukemia (CML), acute B lymphoblastic leukemia (B-ALL), chronic lymphocytic leukemia (CLL), hairy cell leukemia (HCL), blastic plasmacytoid dendritic cell neoplasm (BPDCN), non-Hodgkin's lymphomas (NHL), including mantel cell leukemia (MCL), and small lymphocytic lymphoma (SLL), Hodgkin's lymphoma, systemic mastocytosis, or Burkitt's lymphoma.

[0026] The disclosure further concerns the examples in which any of the above-described LAG-3-binding molecules is detectably labeled and is used in the detection of LAG-3.

Brief Description of the Drawings:

[0027] **Figure 1** provides a schematic of a representative covalently bonded diabody having two epitope-binding sites composed of two polypeptide chains, each having an E-coil or K-coil Heterodimer-Promoting Domain. A cysteine residue may be present in a linker and/or in the Heterodimer-Promoting Domain as shown in **Figure 3B**. VL and VH Domains that recognize the same epitope are shown using the same shading or fill pattern.

[0028] **Figure 2** provides a schematic of a representative covalently bonded diabody molecule having two epitope-binding sites composed of two polypeptide chains, each having a CH2 and CH3 Domain, such that the associated chains form all or part of an Fc Region. VL and VH Domains that recognize the same epitope are shown using the same shading or fill pattern.

[0029] **Figures 3A-3C** provide schematics showing representative tetravalent diabodies having four epitope-binding sites composed of two pairs of polypeptide chains (*i.e.*, four polypeptide chains in all). One polypeptide of each pair possesses a CH2 and CH3 Domain, such that the associated chains form all or part of an Fc Region. VL and VH Domains that recognize the same epitope are shown using the same shading or fill pattern. The two pairs of polypeptide chains may be same. In such embodiments wherein the VL and VH Domains recognize different epitopes (as shown in **Figures 3A-3C**) the resulting molecule possesses four epitope-binding sites and is bispecific and bivalent with respect to each bound epitope. In such embodiments wherein the VL and VH Domains recognize the same epitope (*e.g.*, the same VL Domain CDRs and the same VH Domain CDRs are used on both chains), the resulting molecule possesses four epitope-binding sites and is monospecific and tetravalent with respect to a single epitope. Alternatively, the two pairs of polypeptides may be different. In such embodiments wherein the VL and VH Domains of each pair of polypeptides recognize different epitopes (as shown in **Figure 3C**), the resulting molecule possesses four epitope-binding sites and is tetraspecific and monovalent with respect to each bound epitope. **Figure 3A** shows an Fc diabody which contains a peptide Heterodimer-Promoting Domain comprising a cysteine residue. **Figure 3B** shows an Fc Region-containing diabody, which contains E-coil and K-coil Heterodimer-Promoting Domains comprising a cysteine residue and a linker (with an optional cysteine residue). **Figure 3C**, shows an Fc Region-containing diabody, which contains antibody CH1 and CL domains.

[0030] **Figures 4A and 4B** provide schematics of a representative covalently bonded diabody molecule having two epitope-binding sites composed of three polypeptide chains. Two of the polypeptide chains possess a CH2 and CH3 Domain, such that the associated chains form all or part of an Fc Region. The polypeptide chains comprising the VL and VH Domain further comprise a Heterodimer-Promoting Domain. VL and VH Domains that recognize the same epitope are shown using the same shading or fill pattern.

[0031] **Figure 5** provides the schematics of a representative covalently bonded diabody molecule having four epitope-binding sites composed of five polypeptide

chains. Two of the polypeptide chains possess a CH2 and CH3 Domain, such that the associated chains form an Fc Region that comprises all or part of an Fc Region. The polypeptide chains comprising the linked VL and VH Domains further comprise a Heterodimer-Promoting Domain. VL and VH Domains that recognize the same epitope are shown using the same shading or fill pattern.

[0032] **Figures 6A-6F** provide schematics of representative Fc Region-containing trivalent binding molecules having three epitope-binding sites. **Figures 6A** and **6B**, respectively, illustrate schematically the domains of trivalent binding molecules comprising two diabody-type binding domains and a Fab-type binding domain having different domain orientations in which the diabody-type binding domains are N-terminal or C-terminal to an Fc Region. The molecules in **Figures 6A** and **6B** comprise four chains. **Figures 6C** and **6D**, respectively, illustrate schematically the domains of trivalent binding molecules comprising two diabody-type binding domains N-terminal to an Fc Region, and a Fab-type binding domain in which the light chain and heavy chain are linked via polypeptide linker spacer, or an scFv-type binding domain. The trivalent binding molecules in **Figures 6E** and **6F**, respectively illustrate schematically the domains of trivalent binding molecules comprising two diabody-type binding domains C-terminal to an Fc Region, and a linked Fab-type binding domain, or an scFv-type binding domain in which the diabody-type binding domains are. The trivalent binding molecules in **Figures 6C-6F** comprise three chains. VL and VH Domains that recognize the same epitope are shown using the same shading or fill pattern.

[0033] **Figures 7A-7C** show the binding characteristics of LAG-3 mAb 1 and LAG-3 mAb 6 to cynomolgous monkey LAG-3. Biacore binding curves of hLAG-3 mAb 6 (1.1) (**Figure 7A**), hLAG-3 mAb 1 (1.4) (**Figure 7B**) and LAG-3 mAb A (**Figure 7C**) demonstrating that hLAG-3 mAb 6 (1.1) exhibits better binding to cynomolgous monkey LAG-3 (RU; Response Units).

[0034] **Figures 8A-8D** show that LAG-3 mAb 1 and LAG-3 mAb 6 bind an epitope that is distinct from the one bound by the reference antibody LAG 3 mAb A. the binding profiles of labeled LAG-3 mAb 1, LAG-3 mAb 6 and LAG-3 mAb A in

the absence of a competitor antibody (**Figure 8A**), in the presence of excess LAG-3 mAb 1 (**Figure 8B**), excess LAG-3 mAb 6 (**Figure 8C**), or LAG-3 mAb A (**Figure 8D**) (RU; Response Units).

[0035] **Figures 9A-9B** show that the isolated antibodies inhibit the binding of soluble human LAG-3 (shLAG-3) to MHC class II as determined in an ELISA assay. **Figure 9A** shows the inhibition curves of LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, and LAG-3 mAb 5. **Figure 9B** shows the inhibition curves of LAG-3 mAb A, humanized hLAG-3 1 (1.4), and hLAG-3 6 (1.1) (RLU; Relative Luminesence Units).

[0036] **Figures 10A-10C** show that the isolated antibodies inhibit the binding of shLAG-3 to the surface of MHC class II expressing Daudi cells. **Figure 10A** shows the inhibition curves of LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5, and the reference antibody LAG-3 mAb A. **Figure 10B** shows the inhibition curves of LAG-3 mAb 1, LAG-3 mAb 6 and LAG-3 mAb A. **Figure 10C** shows the inhibition curves of LAG-3 mAb 1 and humanized hLAG-3 1 (1.4), hLAG-3 1 (1.2), hLAG-3 1 (2.2), hLAG-3 1 (1.1). Each figure represents a separate experiment; MFI, mean fluorescence intensity.

[0037] **Figures 11A-11C** show that expression of LAG-3 is upregulated in stimulated CD4+ T-cells. Flow cytometric analysis of LAG-3 expression on unstimulated CD4+ T-cells (**Figure 11A**) and CD3/CD28 bead-stimulated CD4+ T-cells from two different donors (**Figures 11B** and **11C**) on day 11 and 14, respectively. All cells were co-stained with anti-CD4 antibody.

[0038] **Figure 12 (Panels A-F)** show that the isolated anti-LAG-3 antibodies bind to stimulated but not unstimulated T-cells. Flow cytometric analysis of CD3/CD28 stimulated CD4+ T-cells (**Panels A-C**) and unstimulated CD4+ T-cells (**Panels D-F**) labeled with LAG-3 mAb 1 (**Panels A** and **D**), LAG-3 mAb 2 (**Panels B** and **E**), or LAG-3 mAb 3 (**Panels C** and **F**). All cells were co-stained with anti-CD4 antibody.

[0039] **Figure 13 (Panels A-D)** show that the isolated anti-LAG-3 antibodies bind to stimulated but not unstimulated T-cells. Flow cytometric analysis of CD3/CD28 stimulated CD4+ T-cells (**Panels A-B**) and unstimulated CD4+ T-cells (**Panels C-D**) labeled with LAG-3 mAb 4 (**Panels A** and **C**), or LAG-3 mAb 5 (**Panels B** and **D**). All cells were co-stained with anti-CD4 antibody.

[0040] **Figure 14 (Panels A-D)** show that expression of LAG-3 and PD-1 is upregulated on *Staphylococcus aureus* enterotoxin type B antigen (SEB)-stimulated peripheral blood mononuclear cells (PBMCs) from a representative donor D:34765. Flow cytometric analysis of SEB-stimulated PBMCs from a representative donor 48 hours after primary stimulation (**Panels A-B**) labeled with anti-LAG-3/anti-CD3 antibodies (**Panel A**), or anti-PD-1/anti-CD3 antibodies (**Panel B**) and on day five post-SEB-stimulation (**Panels C-D**) cells treated with SEB alone (**Panel C**) or with isotype control antibody (**Panel D**) during the secondary stimulation, labeled with anti-LAG-3/anti-PD-1 antibodies.

[0041] **Figure 15 (Panels A-D)** show that expression of LAG-3 and PD-1 is upregulated on SEB-stimulated PBMCs from another representative donor D:53724. Flow cytometric analysis of SEB-stimulated PBMCs from a representative donor 48 hours after primary stimulation (**Panels A-B**) labeled with anti-LAG-3/anti-CD3 antibodies (**Panel A**), or anti-PD-1/anti-CD3 antibodies (**Panel B**) and on day five post-SEB-stimulation (**Panels C-D**) cells treated with SEB alone (**Panel C**) or with isotype control antibody (**Panel D**) labeled with anti-LAG-3/anti-PD-1 antibodies.

[0042] **Figures 16A-16B** shows that LAG-3 mAb 1 is able to stimulate cytokine production to levels comparable to treatment with anti-PD-1 antibodies. IFNγ (**Figure 16A**) and TNFα (**Figure 16B**), secretion profiles from SEB-stimulated PBMCs treated with anti-LAG-3 or anti-PD-1 antibodies.

[0043] **Figure 17** shows that LAG-3 mAb 1 is able to stimulate cytokine production to levels comparable to treatment with anti-PD-1 antibodies and that treatment with LAG-3 mAb 1 in combination with an anti-PD-1 provided the largest enhancement of cytokine release. IFNγ secretion profiles from SEB-stimulated PBMCs treated with anti-LAG-3 and anti-PD-1 antibodies alone and in combination.

[0044] **Figures 18A-18B** shows binding the anti-LAG-3 antibodies hLAG-3 mAb 6 (1.1), and LAG-3 mAb A to endogenous LAG-3 expressed on SEB stimulated cynomolgus monkey PBMCs from two donors (Figures 18A and 18B). The anti-PD-1 antibody PD-1 mAb A was included as a positive control for SEB stimulation.

Detailed Description of the Invention:

[0045] The present invention is directed to LAG-3 binding molecules that comprise the LAG-3-binding domain of selected anti-LAG-3 antibodies: LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5, or LAG-3 mAb 6 that are capable of binding to both cynomolgus monkey LAG-3 and to human LAG-3. The invention particularly concerns LAG-3 binding molecules that are humanized or chimeric versions of such antibodies, or that comprise LAG-3 binding-fragments of such anti-LAG-3 antibodies (especially immunocongugates, diabodies, BiTEs, bispecific antibodies, *etc.*). The invention particularly concerns such LAG-3-binding molecules that are additionally capable of binding an epitope of a molecule involved in regulating an immune check point that is present on the surface of an immune cell. The present invention also pertains to methods of using such LAG-3 binding molecules to detect LAG-3 or to stimulate an immune response. The present invention also pertains to methods of combination therapy in which a LAG-3-binding molecule that comprises one or more LAG-3-binding domain(s) of such selected anti-LAG-3 antibodies is administered in combination with one or more additional molecules that are effective in stimulating an immune response to thereby further enhance, stimulate or upregulate such immune response in a subject.

I. Antibodies and Their Binding Domains

[0046] The antibodies of the present invention are immunoglobulin molecules capable of immunospecific binding to a target, such as a carbohydrate, polynucleotide, lipid, polypeptide, *etc.*, through at least one epitope recognition site, located in the Variable Domain of the immunoglobulin molecule.

[0047] As used herein, the term "**antibody**" refers to an immunoglobulin molecule capable of immunospecific binding to a polypeptide or protein or a non-protein molecule due to the presence on such molecule of a particular domain or moiety

or conformation (an "**epitope**"). An epitope-containing molecule may have immunogenic activity, such that it elicits an antibody production response in an animal; such molecules are termed "**antigens**"). Epitope-containing molecules need not necessarily be immunogenic.

[0048] The binding domains of the present invention bind to epitopes in an "**immunospecific**" manner. As used herein, an antibody, diabody or other epitope-binding molecule is said to "**immunospecifically**" bind (or to exhibit "**specific**" binding to) a region of another molecule (*i.e.*, an epitope) if it reacts or associates more frequently, more rapidly, with greater duration and/or with greater affinity with that epitope relative to alternative epitopes. For example, an antibody that specifically binds to a LAG-3 epitope is an antibody that binds such LAG-3 epitope with greater affinity, avidity, more readily, and /or with greater duration than it binds to other LAG-3 epitopes or to a non-LAG-3 epitope. It is also understood by reading this definition that, for example, an antibody (or moiety or epitope) that immunospecifically binds to a first target may or may not specifically or preferentially bind to a second target. As such, "immunospecific binding" does not necessarily require (although it can include) exclusive binding. Generally, but not necessarily, reference to binding means "specific" binding. Two molecules are said to be capable of binding to one another in a "**physiospecific**" manner, if such binding exhibits the specificity with which receptors bind to their respective ligands. The ability of an antibody to immunospecifically bind to an epitope may be determined by, for example, an immunoassay.

[0049] Natural antibodies (such as IgG antibodies) are composed of two **Light Chains** complexed with two **Heavy Chains**. Each light chain contains a Variable Domain (**VL**) and a Constant Domain (**CL**). Each heavy chain contains a Variable Domain (**VH**), three Constant Domains (**CH1**, **CH2** and **CH3**), and a "**Hinge**" Domain ("**H**") located between the **CH1** and **CH2** Domains. The basic structural unit of naturally occurring immunoglobulins (*e.g.*, IgG) is thus a tetramer having two light chains and two heavy chains, usually expressed as a glycoprotein of about 150,000 Da. The amino-terminal ("N-terminal") portion of each chain includes a Variable Domain of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The carboxy-terminal ("C-terminal") portion of each chain defines a constant region,

with light chains having a single Constant Domain and heavy chains usually having three Constant Domains and a Hinge Domain. Thus, the structure of the light chains of an IgG molecule is n-VL-CL-c and the structure of the IgG heavy chains is n-VH-CH1-H-CH2-CH3-c (where n and c represent, respectively, the N-terminus and the C-terminus of the polypeptide). The ability of an antibody to bind an epitope of an antigen depends upon the presence and amino acid sequence of the antibody's VL and VH Domains. Interaction of an antibody light chain and an antibody heavy chain and, in particular, interaction of its VL and VH Domains forms one of the two epitope-binding sites of a natural antibody. Natural antibodies are capable of binding to only one epitope species (*i.e.*, they are monospecific), although they can bind multiple copies of that species (*i.e.*, exhibiting bivalency or multivalency). The Variable Domains of an IgG molecule consist of the complementarity determining regions (**CDR**), which contain the residues in contact with epitope, and non-CDR segments, referred to as framework segments (**FR**), which in general maintain the structure and determine the positioning of the CDR loops so as to permit such contacting (although certain framework residues may also contact antigen). Thus, the V_L and VH Domains have the structure n-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4-c. Polypeptides that are (or may serve as) the first, second and third CDR of an antibody Light Chain are herein respectively designated **CDR_L1 Domain**, **CDR_L2 Domain**, and **CDR_L3 Domain**. Similarly, polypeptides that are (or may serve as) the first, second and third CDR of an antibody heavy chain are herein respectively designated **CDR_H1 Domain**, **CDR_H2 Domain**, and **CDR_H3 Domain**. Thus, the terms CDR_L1 Domain, CDR_L2 Domain, CDR_L3 Domain, CDR_H1 Domain, CDR_H2 Domain, and CDR_H3 Domain are directed to polypeptides that when incorporated into a protein cause that protein to be able to bind to a specific epitope regardless of whether such protein is an antibody having light and heavy chains or a diabody or a single-chain binding molecule (*e.g.*, an scFv, a BiTe, *etc.*), or is another type of protein. Accordingly, as used herein, the term "**Epitope-Binding Domain**" refers to that portion of an epitope-binding molecule that is responsible for the ability of such molecule to immunospecifically bind an epitope. An epitope-binding fragment may contain 1, 2, 3, 4, 5 or all 6 of the CDR Domains of such antibody and, although capable of immunospecifically binding to such epitope, may exhibit an immunospecificity, affinity or selectivity toward such epitope that differs from that of

such antibody. Preferably, however, an epitope-binding fragment will contain all 6 of the CDR Domains of such antibody. An epitope-binding fragment of an antibody may be a single polypeptide chain (*e.g.*, an scFv), or may comprise two or more polypeptide chains, each having an amino terminus and a carboxy terminus (*e.g.*, a diabody, a Fab fragment, an $F(ab')_2$ fragment, *etc.*).

[0050] As used herein, the term "**antibody**" encompasses monoclonal antibodies, multispecific antibodies, human antibodies, humanized antibodies, synthetic antibodies, chimeric antibodies, polyclonal antibodies, camelized antibodies, single-chain Fvs (scFv), single-chain antibodies, immunologically active antibody fragments (*e.g.*, antibody fragments capable of binding to an epitope, *e.g.*, Fab fragments, Fab' fragments, $F(ab')_2$ fragments, Fv fragments, fragments containing a V_L and/or V_H domain, or that contain 1, 2, or 3 of the complementary determining regions (CDRs) of such VL domain (*i.e.*, CDR_L1, CDR_L2, and/or CDR_L3) or VH domain (*i.e.*, CDR_H1, CDR_H2, and/or CDR_H3)) that specifically bind an antigen, *etc.*, bi-functional or multi-functional antibodies, disulfide-linked bispecific Fvs (sdFv), intrabodies, and diabodies, and epitope binding fragments of any of the above. In particular, the term "antibody" is intended to encompass immunoglobulin molecules and immunologically active fragments of immunoglobulin molecules, *i.e.*, molecules that contain an epitope-binding site. Immunoglobulin molecules can be of any type (*e.g.*, IgG, IgE, IgM, IgD, IgA and IgY), class (*e.g.*, IgG_1, IgG_2, IgG_3, IgG_4, IgA_1 and IgA_2) or subclass (see, *e.g.*, United States Patent Publication Nos.: 20040185045; 20050037000; 20050064514; 20050215767; 20070004909; 20070036799; 20070077246; and 20070244303). The last few decades have seen a revival of interest in the therapeutic potential of antibodies, and antibodies have become one of the leading classes of biotechnology-derived drugs (Chan, C.E. *et al.* (2009) "*The Use Of Antibodies In The Treatment Of Infectious Diseases*," Singapore Med. J. 50(7):663-666). Over 200 antibody-based drugs have been approved for use or are under development.

[0051] The anti-LAG-3 antibodies of the present invention include humanized, chimeric or caninized variants of antibodies LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5, or LAG-3 mAb 6.

[0052] The term "**chimeric antibody**" refers to an antibody in which a portion of a heavy and/or light chain is identical to or homologous with an antibody from one species (*e.g.*, mouse) or antibody class or subclass, while the remaining portion is identical to or homologous with an antibody of another species (*e.g.*, human) or antibody class or subclass, so long as they exhibit the desired biological activity. Chimeric antibodies of interest herein include "**primatized**" antibodies comprising variable domain antigen binding sequences derived from a non-human primate (*e.g.*, Old World Monkey, Ape, *etc.*) and human constant region sequences.

[0053] The term "**monoclonal antibody**" as used herein refers to an antibody of a population of substantially homogeneous antibodies, *i.e.*, the individual antibodies comprising the population are identical except for possible antibodies possessing naturally occurring mutations that may be present in minor amounts, and the term "**polyclonal antibody**" as used herein refers to an antibody obtained from a population of heterogeneous antibodies. The term "monoclonal" indicates the character of the antibody as being a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method (*e.g.*, by hybridoma, phage selection, recombinant expression, transgenic animals, *etc.*). The term includes whole immunoglobulins as well as the fragments *etc*. described above under the definition of "antibody." Methods of making monoclonal antibodies are known in the art. One method which may be employed is the method of Kohler, G. *et al.* (1975) "*Continuous Cultures Of Fused Cells Secreting Antibody Of Predefined Specificity*," Nature 256:495-497 or a modification thereof. Typically, monoclonal antibodies are developed in mice, rats or rabbits. The antibodies are produced by immunizing an animal with an immunogenic amount of cells, cell extracts, or protein preparations that contain the desired epitope. The immunogen can be, but is not limited to, primary cells, cultured cell lines, cancerous cells, proteins, peptides, nucleic acids, or tissue. Cells used for immunization may be cultured for a period of time (*e.g.*, at least 24 hours) prior to their use as an immunogen. Cells may be used as immunogens by themselves or in combination with a non-denaturing adjuvant, such as Ribi (see, *e.g.*, Jennings, V.M. (1995) "*Review of Selected Adjuvants Used in Antibody Production*," ILAR J. 37(3):119-125). In general, cells should be kept intact and preferably viable when used as immunogens. Intact cells may allow antigens to be better detected than

ruptured cells by the immunized animal. Use of denaturing or harsh adjuvants, *e.g.*, Freud's adjuvant, may rupture cells and therefore is discouraged. The immunogen may be administered multiple times at periodic intervals such as, bi-weekly, or weekly, or may be administered in such a way as to maintain viability in the animal (*e.g.*, in a tissue recombinant). Alternatively, existing monoclonal antibodies and any other equivalent antibodies that are immunospecific for a desired pathogenic epitope can be sequenced and produced recombinantly by any means known in the art. In one embodiment, such an antibody is sequenced and the polynucleotide sequence is then cloned into a vector for expression or propagation. The sequence encoding the antibody of interest may be maintained in a vector in a host cell and the host cell can then be expanded and frozen for future use. The polynucleotide sequence of such antibodies may be used for genetic manipulation to generate the monospecific or multispecific (*e.g.*, bispecific, trispecific and tetraspecific) molecules of the invention as well as an affinity optimized, a chimeric antibody, a humanized antibody, and/or a caninized antibody, to improve the affinity, or other characteristics of the antibody.

[0054] The term "**scFv**" refers to single-chain Variable Domain fragments. scFv molecules are made by linking Light and/or Heavy Chain Variable Domain using a short linking peptide. Bird *et al.* (1988) ("*Single-Chain Antigen-Binding Proteins*," Science 242:423-426) describes example of linking peptides which bridge approximately 3.5 nm between the carboxy terminus of one Variable Domain and the amino terminus of the other Variable Domain. Linkers of other sequences have been designed and used (Bird *et al.* (1988) "*Single-Chain Antigen-Binding Proteins*," Science 242:423-426). Linkers can in turn be modified for additional functions, such as attachment of drugs or attachment to solid supports. The single-chain variants can be produced either recombinantly or synthetically. For synthetic production of scFv, an automated synthesizer can be used. For recombinant production of scFv, a suitable plasmid containing polynucleotide that encodes the scFv can be introduced into a suitable host cell, either eukaryotic, such as yeast, plant, insect or mammalian cells, or prokaryotic, such as E. coli. Polynucleotides encoding the scFv of interest can be made by routine manipulations such as ligation of polynucleotides. The resultant scFv can be isolated using standard protein purification techniques known in the art.

[0055] The invention particularly encompasses humanized variants of the anti-LAG-3 antibodies of the invention and multispecific binding molecules comprising the same. The term "**humanized**" antibody refers to a chimeric molecule, generally prepared using recombinant techniques, having an epitope-binding site of an immunoglobulin from a non-human species and a remaining immunoglobulin structure of the molecule that is based upon the structure and /or sequence of a human immunoglobulin. The epitope-binding site may comprise either complete variable domains fused onto constant domains or only the CDRs grafted onto appropriate framework regions in the variable domains. Epitope-binding sites may be wild-type or modified by one or more amino acid substitutions. This eliminates the constant region as an immunogen in human individuals, but the possibility of an immune response to the foreign variable region remains (LoBuglio, A.F. *et al.* (1989) "*Mouse/Human Chimeric Monoclonal Antibody In Man: Kinetics And Immune Response*," Proc. Natl. Acad. Sci. (U.S.A.) 86:4220-4224). Another approach focuses not only on providing human-derived constant regions, but modifying the variable regions as well so as to reshape them as closely as possible to human form. It is known that the variable regions of both heavy and light chains contain three CDRs which vary in response to the antigens in question and determine binding capability, flanked by four framework regions (FRs) which are relatively conserved in a given species and which putatively provide a scaffolding for the CDRs. When non-human antibodies are prepared with respect to a particular antigen, the variable regions can be "reshaped" or "humanized" by grafting CDRs derived from a non-human antibody on the FRs present in the human antibody to be modified. Application of this approach to various antibodies has been reported by Sato, K. *et al.* (1993) "*Reshaping A Human Antibody To Inhibit The Interleukin 6-Dependent Tumor Cell Growth*," Cancer Res 53:851-856. Riechmann, L. *et al.* (1988) "*Reshaping Human Antibodies for Therapy*," Nature 332:323-327; Verhoeyen, M. *et al.* (1988) "*Reshaping Human Antibodies: Grafting An Antilysozyme Activity*," Science 239:1534-1536; Kettleborough, C. A. *et al.* (1991) "*Humanization Of A Mouse Monoclonal Antibody By CDR-Grafting: The Importance Of Framework Residues On Loop Conformation*," Protein Engineering 4:773-3783; Maeda, H. *et al.* (1991) "*Construction Of Reshaped Human Antibodies With HIV-Neutralizing Activity*," Human Antibodies Hybridoma 2:124-134; Gorman, S. D. *et al.* (1991) "*Reshaping A*

Therapeutic CD4 Antibody," Proc. Natl. Acad. Sci. (U.S.A.) 88:4181-4185; Tempest, P.R. *et al.* (1991) "*Reshaping A Human Monoclonal Antibody To Inhibit Human Respiratory Syncytial Virus Infection in vivo*," Bio/Technology 9:266-271; Co, M. S. *et al.* (1991) "*Humanized Antibodies For Antiviral Therapy*," Proc. Natl. Acad. Sci. (U.S.A.) 88:2869-2873; Carter, P. *et al.* (1992) "*Humanization Of An Anti-p185her2 Antibody For Human Cancer Therapy*," Proc. Natl. Acad. Sci. (U.S.A.) 89:4285-4289; and Co, M.S. *et al.* (1992) "*Chimeric And Humanized Antibodies With Specificity For The CD33 Antigen*," J. Immunol. 148:1149-1154. In some embodiments, humanized antibodies preserve all CDR sequences (for example, a humanized mouse antibody which contains all six CDRs from the mouse antibodies). In other embodiments, humanized antibodies have one or more CDRs (one, two, three, four, five or six) that are altered in their amino acid sequence(s) relative to the original antibody, which are also termed one or more CDRs "**derived from**" one or more CDRs from the original antibody (*i.e.*, derived from such CDRs, derived from knowledge of the amino acid sequences of such CDRs, *etc.*). A polynucleotide sequence that encodes the variable domain of an antibody may be used to generate such derivatives and to improve the affinity, or other characteristics of such antibodies. The general principle in humanizing an antibody involves retaining the basic sequence of the epitope-binding portion of the antibody, while swapping the non-human remainder of the antibody with human antibody sequences. There are four general steps to humanize a monoclonal antibody. These are: (1) determining the nucleotide and predicted amino acid sequence of the starting antibody light and heavy variable domains (2) designing the humanized antibody or caninized antibody, *i.e.*, deciding which antibody framework region to use during the humanizing or canonizing process (3) the actual humanizing or caninizing methodologies/techniques and (4) the transfection and expression of the humanized antibody. See, for example, U.S. Patents Nos. 4,816,567; 5,807,715; 5,866,692; and 6,331,415.

[0056] The epitope-binding site of the molecules of the present invention may comprise a complete Variable Domain fused to a Constant Domain or only the complementarity determining regions (CDRs) of such Variable Domain grafted to appropriate framework regions. Epitope-binding sites may be wild-type or modified by one or more amino acid substitutions. This eliminates the constant region as an

immunogen in human individuals, but the possibility of an immune response to the foreign variable domain remains (LoBuglio, A.F. *et al.* (1989) "*Mouse/Human Chimeric Monoclonal Antibody In Man: Kinetics And Immune Response*," Proc. Natl. Acad. Sci. (U.S.A.) 86:4220-4224). Another approach focuses not only on providing human-derived constant regions, but modifying the variable domains as well so as to reshape them as closely as possible to human form. It is known that the variable domains of both heavy and light chains contain three complementarity determining regions (CDRs) which vary in response to the antigens in question and determine binding capability, flanked by four framework regions (FRs) which are relatively conserved in a given species and which putatively provide a scaffolding for the CDRs. When non-human antibodies are prepared with respect to a particular antigen, the variable domains can be "reshaped" or "humanized" by grafting CDRs derived from non-human antibody on the FRs present in the human antibody to be modified. Application of this approach to various antibodies has been reported by Sato, K. *et al.* (1993) Cancer Res 53:851-856. Riechmann, L. *et al.* (1988) "*Reshaping Human Antibodies for Therapy*," Nature 332:323-327; Verhoeyen, M. *et al.* (1988) "*Reshaping Human Antibodies: Grafting An Antilysozyme Activity*," Science 239:1534-1536; Kettleborough, C. A. *et al.* (1991) "*Humanization Of A Mouse Monoclonal Antibody By CDR-Grafting: The Importance Of Framework Residues On Loop Conformation*," Protein Engineering 4:773-3783; Maeda, H. *et al.* (1991) "*Construction Of Reshaped Human Antibodies With HIV-Neutralizing Activity*," Human Antibodies Hybridoma 2:124-134; Gorman, S. D. *et al.* (1991) "*Reshaping A Therapeutic CD4 Antibody*," Proc. Natl. Acad. Sci. (U.S.A.) 88:4181-4185; Tempest, P.R. *et al.* (1991) "*Reshaping A Human Monoclonal Antibody To Inhibit Human Respiratory Syncytial Virus Infection in vivo*," Bio/Technology 9:266-271; Co, M. S. *et al.* (1991) "*Humanized Antibodies For Antiviral Therapy*," Proc. Natl. Acad. Sci. (U.S.A.) 88:2869-2873; Carter, P. *et al.* (1992) "*Humanization Of An Anti-p185her2 Antibody For Human Cancer Therapy*," Proc. Natl. Acad. Sci. (U.S.A.) 89:4285-4289; and Co, M.S. *et al.* (1992) "*Chimeric And Humanized Antibodies With Specificity For The CD33 Antigen*," J. Immunol. 148:1149-1154. In some embodiments, humanized antibodies preserve all CDR sequences (for example, a humanized mouse antibody which contains all six CDRs from the mouse antibodies). In other embodiments, humanized antibodies have

one or more CDRs (one, two, three, four, five, or six) which differ in sequence relative to the original antibody.

[0057] A number of "humanized" antibody molecules comprising an epitope-binding site derived from a non-human immunoglobulin have been described, including chimeric antibodies having rodent or modified rodent Variable Domain and their associated complementarity determining regions (CDRs) fused to human Constant Domains (see, for example, Winter *et al.* (1991) "*Man-made Antibodies*," Nature 349:293-299; Lobuglio *et al.* (1989) "*Mouse/Human Chimeric Monoclonal Antibody In Man: Kinetics And Immune Response*," Proc. Natl. Acad. Sci. (U.S.A.) 86:4220-4224 (1989), Shaw *et al.* (1987) "*Characterization Of A Mouse/Human Chimeric Monoclonal Antibody (17-1A) To A Colon Cancer Tumor-Associated Antigen*," J. Immunol. 138:4534-4538, and Brown *et al.* (1987) "*Tumor-Specific Genetically Engineered Murine/Human Chimeric Monoclonal Antibody*," Cancer Res. 47:3577-3583). Other references describe rodent CDRs grafted into a human supporting framework region (FR) prior to fusion with an appropriate human antibody Constant Domain (see, for example, Riechmann, L. *et al.* (1988) "*Reshaping Human Antibodies for Therapy*," Nature 332:323-327; Verhoeyen, M. *et al.* (1988) "*Reshaping Human Antibodies: Grafting An Antilysozyme Activity*," Science 239:1534-1536; and Jones *et al.* (1986) "*Replacing The Complementarity-Determining Regions In A Human Antibody With Those From A Mouse*," Nature 321:522-525). Another reference describes rodent CDRs supported by recombinantly veneered rodent framework regions. See, for example, European Patent Publication No. 519,596. These "humanized" molecules are designed to minimize unwanted immunological response towards rodent anti-human antibody molecules, which limits the duration and effectiveness of therapeutic applications of those moieties in human recipients. Other methods of humanizing antibodies that may also be utilized are disclosed by Daugherty *et al.* (1991) "*Polymerase Chain Reaction Facilitates The Cloning, CDR-Grafting, And Rapid Expression Of A Murine Monoclonal Antibody Directed Against The CD18 Component Of Leukocyte Integrins*," Nucl. Acids Res. 19:2471-2476 and in U.S. Patents Nos. 6,180,377; 6,054,297; 5,997,867; and 5,866,692.

II. Fcγ Receptors (FcγRs)

[0058] The CH2 and CH3 Domains of the two heavy chains interact to form the **Fc Region**, which is a domain that is recognized by cellular **Fc Receptors** including but not limited to Fc gamma Receptors **(FcγRs)**. As used herein, the term "Fc Region" is used to define a C-terminal region of an IgG heavy chain. The amino acid sequence of the CH2-CH3 Domain of an exemplary human IgG1 is (**SEQ ID NO:1**):

```
231       240           250           260           270           280
APELLGGPSV    FLFPPKPKDT    LMISRTPEVT    CVVVDVSHED    PEVKFNWYVD

          290           300           310           320           330
GVEVHNAKTK    PREEQYNSTY    RVVSVLTVLH    QDWLNGKEYK    CKVSNKALPA

          340           350           360           370           380
PIEKTISKAK    GQPREPQVYT    LPPSREEMTK    NQVSLTCLVK    GFYPSDIAVE

          390           400           410           420           430
WESNGQPENN    YKTTPPVLDS    DGSFFLYSKL    TVDKSRWQQG    NVFSCSVMHE

          440       447
ALHNHYTQKS    LSLSPGX
```

as numbered by the EU index according to Kabat, wherein, X is a lysine (K) or is absent.

[0059] The amino acid sequence of the CH2-CH3 Domain of an exemplary human IgG2 is (**SEQ ID NO:2**):

```
231       240           250           260           270           280
APPVA-GPSV    FLFPPKPKDT    LMISRTPEVT    CVVVDVSHED    PEVQFNWYVD

          290           300           310           320           330
GVEVHNAKTK    PREEQFNSTF    RVVSVLTVVH    QDWLNGKEYK    CKVSNKGLPA

          340           350           360           370           380
PIEKTISKTK    GQPREPQVYT    LPPSREEMTK    NQVSLTCLVK    GFYPSDISVE

          390           400           410           420           430
WESNGQPENN    YKTTPPMLDS    DGSFFLYSKL    TVDKSRWQQG    NVFSCSVMHE

          440       447
ALHNHYTQKS    LSLSPGX
```

as numbered by the EU index according to Kabat, wherein, X is a lysine (K) or is absent.

[0060] The amino acid sequence of the CH2-CH3 Domain of an exemplary human IgG3 is (**SEQ ID NO:3**):

```
231      240          250          260          270          280
APELLGGPSV   FLFPPKPKDT   LMISRTPEVT   CVVVDVSHED   PEVQFKWYVD

         290          300          310          320          330
GVEVHNAKTK   PREEQYNSTF   RVVSVLTVLH   QDWLNGKEYK   CKVSNKALPA

         340          350          360          370          380
PIEKTISKTK   GQPREPQVYT   LPPSREEMTK   NQVSLTCLVK   GFYPSDIAVE

         390          400          410          420          430
WESSGQPENN   YNTTPPMLDS   DGSFFLYSKL   TVDKSRWQQG   NIFSCSVMHE

         440       447
ALHNRFTQKS   LSLSPGX
```

as numbered by the EU index according to Kabat, wherein, X is a lysine (K) or is absent.

[0061] The amino acid sequence of the CH2-CH3 Domain of an exemplary human IgG4 is (**SEQ ID NO:4**):

```
231      240          250          260          270          280
APEFLGGPSV   FLFPPKPKDT   LMISRTPEVT   CVVVDVSQED   PEVQFNWYVD

         290          300          310          320          330
GVEVHNAKTK   PREEQFNSTY   RVVSVLTVLH   QDWLNGKEYK   CKVSNKGLPS

         340          350          360          370          380
SIEKTISKAK   GQPREPQVYT   LPPSQEEMTK   NQVSLTCLVK   GFYPSDIAVE

         390          400          410          420          430
WESNGQPENN   YKTTPPVLDS   DGSFFLYSRL   TVDKSRWQEG   NVFSCSVMHE

         440       447
ALHNHYTQKS   LSLSLGX
```

as numbered by the EU index according to Kabat, wherein, X is a lysine (K) or is absent.

[0062] Throughout the present specification, the numbering of the residues in the constant region of an IgG heavy chain is that of the EU index according to Kabat *et al.*, SEQUENCES OF PROTEINS OF IMMUNOLOGICAL INTEREST, 5th Ed. Public Health Service, NH1, MD (1991) ("**Kabat**"), expressly incorporated herein by references. The "EU index according to Kabat" refers to the numbering of the human IgG1 EU antibody. Amino acids from the Variable Domains of the mature heavy and light chains of

immunoglobulins are designated by the position of an amino acid in the chain, and the CDRs are identified as defined by Kabat (it will be understood that CDR_H1 as defined by Chothia, C. & Lesk, A. M. ((1987) "*Canonical structures for the hypervariable regions of immunoglobulins*,". J. Mol. Biol. 196:901-917) begins five residues earlier). Kabat described numerous amino acid sequences for antibodies, identified an amino acid consensus sequence for each subgroup, and assigned a residue number to each amino acid. Kabat's numbering scheme is extendible to antibodies not included in his compendium by aligning the antibody in question with one of the consensus sequences in Kabat by reference to conserved amino acids. This method for assigning residue numbers has become standard in the field and readily identifies amino acids at equivalent positions in different antibodies, including chimeric or humanized variants. For example, an amino acid at position 50 of a human antibody light chain occupies the equivalent position to an amino acid at position 50 of a mouse antibody light chain.

[0063] Polymorphisms have been observed at a number of different positions within antibody constant regions (*e.g.*, Fc positions, including but not limited to positions 270, 272, 312, 315, 356, and 358 as numbered by the EU index according to Kabat), and thus slight differences between the presented sequence and sequences in the prior art can exist. Polymorphic forms of human immunoglobulins have been well-characterized. At present, 18 Gm allotypes are known: G1m (1, 2, 3, 17) or G1m (a, x, f, z), G2m (23) or G2m (n), G3m (5, 6, 10, 11, 13, 14, 15, 16, 21, 24, 26, 27, 28) or G3m (b1, c3, b3, b0, b3, b4, s, t, g1, c5, u, v, g5) (Lefranc, *et al.*, "*The Human IgG Subclasses: Molecular Analysis Of Structure, Function And Regulation.*" Pergamon, Oxford, pp. 43-78 (1990); Lefranc, G. *et al.*, 1979, Hum. Genet.: 50, 199-211). It is specifically contemplated that the antibodies of the present invention may be incorporate any allotype, isoallotype, or haplotype of any immunoglobulin gene, and are not limited to the allotype, isoallotype or haplotype of the sequences provided herein. Furthermore, in some expression systems the C-terminal amino acid residue (bolded above) of the CH3 Domain may be post-translationally removed. Accordingly, the C-terminal residue of the CH3 Domain is an optional amino acid residue in the LAG-3-binding molecules of the invention. Specifically encompassed by the instant invention are LAG-3-binding molecules lacking the C-terminal residue of the CH3

Domain. Also specifically encompassed by the instant invention are such constructs comprising the C-terminal lysine residue of the CH3 Domain.

[0064] Activating and inhibitory signals are transduced through the ligation of an Fc Region to a cellular Fc Receptor (FcγR). The ability of such ligation to result in diametrically opposing functions results from structural differences among the different receptor isoforms. Two distinct domains within the cytoplasmic signaling domains of the receptor called immunoreceptor tyrosine-based activation motifs (ITAMs) and immunoreceptor tyrosine-based inhibitory motifs (ITIMS) account for the different responses. The recruitment of different cytoplasmic enzymes to these structures dictates the outcome of the FcγR-mediated cellular responses. ITAM-containing FcγR complexes include FcγRI, FcγRIIA, FcγRIIIA, whereas ITIM-containing complexes only include FcγRIIB. Human neutrophils express the FcγRIIA gene. FcγRIIA clustering via immune complexes or specific antibody cross-linking serves to aggregate ITAMs along with receptor-associated kinases which facilitate ITAM phosphorylation. ITAM phosphorylation serves as a docking site for Syk kinase, activation of which results in activation of downstream substrates (*e.g.*, PI_3K). Cellular activation leads to release of proinflammatory mediators. The FcγRIIB gene is expressed on B lymphocytes; its extracellular domain is 96% identical to FcγRIIA and binds IgG complexes in an indistinguishable manner. The presence of an ITIM in the cytoplasmic domain of FcγRIIB defines this inhibitory subclass of FcγR. Recently the molecular basis of this inhibition was established. When co-ligated along with an activating FcγR, the ITIM in FcγRIIB becomes phosphorylated and attracts the SH2 domain of the inositol polyphosphate 5'-phosphatase (SHIP), which hydrolyzes phosphoinositol messengers released as a consequence of ITAM-containing FcγR- mediated tyrosine kinase activation, consequently preventing the influx of intracellular Ca^{++}. Thus cross-linking of FcγRIIB dampens the activating response to FcγR ligation and inhibits cellular responsiveness. B-cell activation, B-cell proliferation and antibody secretion is thus aborted.

III. Bispecific Antibodies, Multispecific Diabodies and DART® Diabodies

[0065] The functionality of antibodies can be enhanced by generating multispecific antibody-based molecules that can simultaneously bind two separate and

distinct antigens (or different epitopes of the same antigen) and/or by generating antibody-based molecule having higher valency (*i.e.*, more than two binding sites) for the same epitope and/or antigen.

[0066] In order to provide molecules having greater capability than natural antibodies, a wide variety of recombinant bispecific antibody formats have been developed (see, *e.g.*, PCT Publication Nos. WO 2008/003116, WO 2009/132876, WO 2008/003103, WO 2007/146968, WO 2009/018386, WO 2012/009544, WO 2013/070565), most of which use linker peptides either to fuse a further epitope-binding fragment (*e.g.*, an scFv, VL, VH, *etc.*) to, or within the antibody core (IgA, IgD, IgE, IgG or IgM), or to fuse multiple epitope-binding fragments (*e.g.*, two Fab fragments or scFvs). Alternative formats use linker peptides to fuse an epitope-binding fragment (*e.g.*, an scFv, VL, VH, *etc.*) to a dimerization domain such as the CH2-CH3 Domain or alternative polypeptides (WO 2005/070966, WO 2006/107786A WO 2006/107617A, WO 2007/046893). Typically, such approaches involve compromises and trade-offs. For example, PCT Publications Nos. WO 2013/174873, WO 2011/133886 and WO 2010/136172 disclose that the use of linkers may cause problems in therapeutic settings, and teaches a trispecific antibody in which the CL and CH1 Domains are switched from their respective natural positions and the VL and VH Domains have been diversified (WO 2008/027236; WO 2010/108127) to allow them to bind to more than one antigen. Thus, the molecules disclosed in these documents trade binding specificity for the ability to bind additional antigen species. PCT Publications Nos. WO 2013/163427 and WO 2013/119903 disclose modifying the CH2 Domain to contain a fusion protein adduct comprising a binding domain. The document notes that the CH2 Domain likely plays only a minimal role in mediating effector function. PCT Publications Nos. WO 2010/028797, WO2010028796 and WO 2010/028795 disclose recombinant antibodies whose Fc Regions have been replaced with additional VL and VH Domains, so as to form trivalent binding molecules. PCT Publications Nos. WO 2003/025018 and WO2003012069 disclose recombinant diabodies whose individual chains contain scFv Domains. PCT Publications No. WO 2013/006544 discloses multivalent Fab molecules that are synthesized as a single polypeptide chain and then subjected to proteolysis to yield heterodimeric structures. Thus, the molecules disclosed in these documents trade all or some of the capability of

mediating effector function for the ability to bind additional antigen species. PCT Publications Nos. WO 2014/022540, WO 2013/003652, WO 2012/162583, WO 2012/156430, WO 2011/086091, WO 2008/024188, WO 2007/024715, WO 2007/075270, WO 1998/002463, WO 1992/022583 and WO 1991/003493 disclose adding additional binding domains or functional groups to an antibody or an antibody portion (*e.g.*, adding a diabody to the antibody's light chain, or adding additional VL and VH Domains to the antibody's light and heavy chains, or adding a heterologous fusion protein or chaining multiple Fab Domains to one another). Thus, the molecules disclosed in these documents trade native antibody structure for the ability to bind additional antigen species.

[0067] The art has additionally noted the capability to produce **diabodies** that differ from such natural antibodies in being capable of binding two or more different epitope species (*i.e.*, exhibiting bispecificity or multispecificity in addition to bivalency or multivalency) (see, *e.g.*, Holliger *et al.* (1993) "*'Diabodies': Small Bivalent And Bispecific Antibody Fragments,*" Proc. Natl. Acad. Sci. (U.S.A.) 90:6444-6448; US 2004/0058400 (Hollinger *et al.*); US 2004/0220388 / WO 02/02781 (Mertens *et al.*); Alt *et al.* (1999) FEBS Lett. 454(1-2):90-94; Lu, D. *et al.* (2005) "*A Fully Human Recombinant IgG-Like Bispecific Antibody To Both The Epidermal Growth Factor Receptor And The Insulin-Like Growth Factor Receptor For Enhanced Antitumor Activity*," J. Biol. Chem. 280(20):19665-19672; WO 02/02781 (Mertens *et al.*); Olafsen, T. *et al.* (2004) "*Covalent Disulfide-Linked Anti-CEA Diabody Allows Site-Specific Conjugation And Radiolabeling For Tumor Targeting Applications*," Protein Eng. Des. Sel. 17(1):21-27; Wu, A. *et al.* (2001) "*Multimerization Of A Chimeric Anti-CD20 Single Chain Fv-Fv Fusion Protein Is Mediated Through Variable Domain Exchange*," Protein Engineering 14(2):1025-1033; Asano *et al.* (2004) "*A Diabody For Cancer Immunotherapy And Its Functional Enhancement By Fusion Of Human Fc Domain*," Abstract 3P-683, J. Biochem. 76(8):992; Takemura, S. *et al.* (2000) "*Construction Of A Diabody (Small Recombinant Bispecific Antibody) Using A Refolding System,*" Protein Eng. 13(8):583-588; Baeuerle, P.A. *et al.* (2009) "*Bispecific T-Cell Engaging Antibodies For Cancer Therapy*," Cancer Res. 69(12):4941-4944).

[0068] The design of a diabody is based on the antibody derivative known as a single-chain Variable Domain fragment (**scFv**). Such molecules are made by linking Light and/ or Heavy chain Variable Domains by using a short linking peptide. Linkers can in turn be modified for additional functions, such as attachment of drugs or attachment to solid supports. The single-chain variants can be produced either recombinantly or synthetically. For synthetic production of scFv, an automated synthesizer can be used. For recombinant production of scFv, a suitable plasmid containing polynucleotide that encodes the scFv can be introduced into a suitable host cell, either eukaryotic, such as yeast, plant, insect or mammalian cells, or prokaryotic, such as *E. coli*. Polynucleotides encoding the scFv of interest can be made by routine manipulations such as ligation of polynucleotides. The resultant scFv can be isolated using standard protein purification techniques known in the art.

[0069] The provision of non-monospecific diabodies provides a significant advantage over antibodies, including but not limited to, the capacity to co-ligate and co-localize cells that express different epitopes. Bispecific diabodies thus have wide-ranging applications including therapy and immunodiagnosis. Bispecificity allows for great flexibility in the design and engineering of the diabody in various applications, providing enhanced avidity to multimeric antigens, the cross-linking of differing antigens, and directed targeting to specific cell types relying on the presence of both target antigens. Due to their increased valency, low dissociation rates and rapid clearance from the circulation (for diabodies of small size, at or below ~50 kDa), diabody molecules known in the art have also shown particular use in the field of tumor imaging (Fitzgerald *et al.* (1997) *"Improved Tumour Targeting By Disulphide Stabilized Diabodies Expressed In Pichia pastoris,"* Protein Eng. 10:1221).

[0070] The bispecificity of diabodies has led to their use for co-ligating differing cells, for example, the cross-linking of cytotoxic T-cells to tumor cells (Staerz *et al.* (1985) *"Hybrid Antibodies Can Target Sites For Attack By T Cells,"* Nature 314:628-631, and Holliger *et al.* (1996) *"Specific Killing Of Lymphoma Cells By Cytotoxic T-Cells Mediated By A Bispecific Diabody,"* Protein Eng. 9:299-305; Marvin *et al.* (2005) "*Recombinant Approaches To IgG-Like Bispecific Antibodies*," Acta Pharmacol. Sin. 26:649-658). Alternatively, or additionally, bispecific diabodies can be used to co-

ligate receptors on the surface of different cells or on a single cell. Co-ligation of different cells and/or receptors is useful to modulation effector functions and/or immune cell signaling. Multispecific molecules (*e.g.*, bispecific diabodies) comprising epitope-binding sites may be directed to a surface determinant of any immune cell such as B7-H3 (CD276), B7-H4 (VTCN1), BTLA (CD272), CD3, CD8, CD16, CD27, CD32, CD40, CD40L, CD47, CD64, CD70 (CD27L), CD80 (B7-1), CD86 (B7-2), CD94 (KLRD1), CD137 (4-1BB), CD137L (4-1BBL), CD226, CTLA-4 (CD152), Galectin-9, GITR, GITRL, HHLA2, ICOS (CD278), ICOSL (CD275), Killer Activation Receptor (KIR), LAG-3 (CD223), LIGHT (TNFSF14, CD258), MHC class I or II, NKG2a, NKG2d, OX40 (CD134), OX40L (CD134L), PD1H, PD-1 (CD279), PD-L1 (B7-H1, CD274), PD-L2 (B7-CD, CD273), PVR (NECL5, CD155), SIRPa, TCR, TIGIT, TIM-3 (HAVCR2), and/or VISTA (PD-1H), which are expressed on T lymphocytes, Natural Killer (NK) cells, Antigen-presenting cells or other mononuclear cell. In particular, epitope-binding sites directed to a cell surface receptor that is involved in regulating an immune checkpoint (or the ligand thereof) are useful in the generation of bispecific or multispecific binding molecules which antagonize or block the inhibitory signaling of immune checkpoint molecules and thereby stimulate, upregulate or enhance, immune responses in a subject. Molecules involved in regulating immune checkpoints include, but are not limited to B7-H3, B7-H4, BTLA, CD40, CD40L, CD47, CD70, CD80, CD86, CD94, CD137, CD137L, CD226, CTLA-4, Galectin-9, GITR, GITRL, HHLA2, ICOS, ICOSL, KIR, LAG-3, LIGHT, MHC class I or II, NKG2a, NKG2d, OX40, OX40L, PD1H, PD-1, PD-L1, PD-L2, PVR, SIRPa, TCR, TIGIT, TIM-3 and/or VISTA.

[0071] However, the above advantages come at a salient cost. The formation of such non-monospecific diabodies requires the successful assembly of two or more distinct and different polypeptides (*i.e.*, such formation requires that the diabodies be formed through the heterodimerization of different polypeptide chain species). This fact is in contrast to monospecific diabodies, which are formed through the homodimerization of identical polypeptide chains. Because at least two dissimilar polypeptides (*i.e.*, two polypeptide species) must be provided in order to form a non-monospecific diabody, and because homodimerization of such polypeptides leads to inactive molecules (Takemura, S. *et al.* (2000) "*Construction Of A Diabody (Small*

Recombinant Bispecific Antibody) Using A Refolding System," Protein Eng. 13(8):583-588), the production of such polypeptides must be accomplished in such a way as to prevent covalent bonding between polypeptides of the same species (*i.e.*, so as to prevent homodimerization) (Takemura, S. *et al.* (2000) "*Construction Of A Diabody (Small Recombinant Bispecific Antibody) Using A Refolding System,*" Protein Eng. 13(8):583-588). The art has therefore taught the non-covalent association of such polypeptides (see, *e.g.*, Olafsen *et al.* (2004) *"Covalent Disulfide-Linked Anti-CEA Diabody Allows Site-Specific Conjugation And Radiolabeling For Tumor Targeting Applications,"* Prot. Engr. Des. Sel. 17:21-27; Asano *et al.* (2004) "*A Diabody For Cancer Immunotherapy And Its Functional Enhancement By Fusion Of Human Fc Domain*," Abstract 3P-683, J. Biochem. 76(8):992; Takemura, S. *et al.* (2000) "*Construction Of A Diabody (Small Recombinant Bispecific Antibody) Using A Refolding System,*" Protein Eng. 13(8):583-588; Lu, D. *et al.* (2005) "*A Fully Human Recombinant IgG-Like Bispecific Antibody To Both The Epidermal Growth Factor Receptor And The Insulin-Like Growth Factor Receptor For Enhanced Antitumor Activity*," J. Biol. Chem. 280(20):19665-19672).

[0072] However, the art has recognized that bispecific diabodies composed of non-covalently associated polypeptides are unstable and readily dissociate into non-functional monomers (see, *e.g.*, Lu, D. *et al.* (2005) "*A Fully Human Recombinant IgG-Like Bispecific Antibody To Both The Epidermal Growth Factor Receptor And The Insulin-Like Growth Factor Receptor For Enhanced Antitumor Activity*," J. Biol. Chem. 280(20):19665-19672).

[0073] In the face of this challenge, the art has succeeded in developing stable, covalently bonded heterodimeric non-monospecific diabodies, termed **DART® (Dual Affinity Re-Targeting Reagents)** diabodies; see, *e.g.*, United States Patent Publications No. 2013-0295121; 2010-0174053 and 2009-0060910; European Patent Publication No. EP 2714079; EP 2601216; EP 2376109; EP 2158221 and PCT Publications No. WO 2012/162068; WO 2012/018687; WO 2010/080538; WO 2008/157379; WO 2006/113665 and Sloan, D.D. *et al.* (2015) "*Targeting HIV Reservoir in Infected CD4 T Cells by Dual-Affinity Re-targeting Molecules (DARTs) that Bind HIV Envelope and Recruit Cytotoxic T Cells*," PLoS Pathog.

11(11):e1005233. doi: 10.1371/journal.ppat.1005233; Al Hussaini, M. *et al.* (2015) "*Targeting CD123 In AML Using A T-Cell Directed Dual-Affinity Re-Targeting (DART®) Platform*," Blood 127(1):122-131; Chichili, G.R. *et al.* (2015) "*A CD3xCD123 Bispecific DART For Redirecting Host T Cells To Myelogenous Leukemia: Preclinical Activity And Safety In Nonhuman Primates*," Sci. Transl. Med. 7(289):289ra82; Moore, P.A. *et al.* (2011) "*Application Of Dual Affinity Retargeting Molecules To Achieve Optimal Redirected T-Cell Killing Of B-Cell Lymphoma*," Blood 117(17):4542-4551; Veri, M.C. *et al.* (2010) "*Therapeutic Control Of B Cell Activation Via Recruitment Of Fcgamma Receptor IIb (CD32B) Inhibitory Function With A Novel Bispecific Antibody Scaffold*," Arthritis Rheum. 62(7):1933-1943; Johnson, S. *et al.* (2010) "*Effector Cell Recruitment With Novel Fv-Based Dual-Affinity Re-Targeting Protein Leads To Potent Tumor Cytolysis And in vivo B-Cell Depletion*," J. Mol. Biol. 399(3):436-449; Marvin, J.S. *et al.* (2005) "*Recombinant Approaches To IgG-Like Bispecific Antibodies,*" Acta Pharmacol. Sin. 26:649-658; Olafsen, T. *et al.* (2004) "*Covalent Disulfide-Linked Anti-CEA Diabody Allows Site-Specific Conjugation And Radiolabeling For Tumor Targeting Applications*," Prot. Engr. Des. Sel. 17:21-27; Holliger, P. *et al.* (1993) "'*Diabodies': Small Bivalent And Bispecific Antibody Fragments,*" Proc. Natl. Acad. Sci. (U.S.A.) 90:6444-6448. Such diabodies comprise two or more covalently complexed polypeptides and involve engineering one or more cysteine residues into each of the employed polypeptide species that permit disulfide bonds to form and thereby covalently bond two polypeptide chains. For example, the addition of a cysteine residue to the C-terminus of such constructs has been shown to allow disulfide bonding between the polypeptide chains, stabilizing the resulting heterodimer without interfering with the binding characteristics of the bivalent molecule.

[0074] Each of the two polypeptides of the simplest bispecific **DART®** diabody comprises three domains. The first polypeptide comprises (in the N-terminal to C-terminal direction): (i) a First Domain that comprises a binding region of a Light Chain Variable Domain of a first immunoglobulin (VL1), (ii) a Second Domain that comprises a binding region of a Heavy Chain Variable Domain of a second immunoglobulin (VH2), and (iii) a Third Domain that contains a cysteine residue (or a cysteine-containing domain) and a Heterodimer-Promoting Domain that serves to promote

heterodimerization with the second polypeptide of the diabody and to covalently bond the diabody's first and second polypeptides to one another. The second polypeptide contains (in the N-terminal to C-terminal direction): (i) a First Domain that comprises a binding region of a Light Chain Variable Domain of the second immunoglobulin (VL2), (ii) a Second Domain that comprises a binding region of a Heavy Chain Variable Domain of the first immunoglobulin (VH1), and (iii) a Third Domain that contains a cysteine residue (or a cysteine-containing domain) and a complementary Heterodimer-Promoting Domain that complexes with the Heterodimer-Promoting Domain of the first polypeptide chain in order to promote heterodimerization with the first polypeptide chain. The cysteine residue (or a cysteine-containing domain) of the third domain of the second polypeptide chain serves to promote the covalent bonding of the second polypeptide chain to the first polypeptide chain of the diabody. Such molecules are stable, potent and have the ability to simultaneously bind two or more antigens. In one embodiment, the Third Domains of the first and second polypeptides each contain a cysteine residue, which serves to bind the polypeptides together via a disulfide bond. **Figure 1** provides a schematic of such a diabody, which utilizes E-coil/K-coil Heterodimer-Promoting domains and a cysteine containing linker for covalent bonding. As provided in **Figure 2** and **Figures 3A-3C**, one or both of the polypeptides may additionally possesses the sequence of a CH2-CH3 Domain, such that complexing between the two diabody polypeptides forms an Fc Region that is capable of binding to the Fc receptor of cells (such as B lymphocytes, dendritic cells, natural killer cells, macrophages, neutrophils, eosinophils, basophils and mast cells). As provided in more detail below, the CH2 and/or CH3 Domains of such polypeptide chains need not be identical in sequence, and advantageously are modified to foster complexing between the two polypeptide chains.

[0075] Many variations of such molecules have been described (see, *e.g.*, United States Patent Publications No. 2015/0175697; 2014/0255407; 2014/0099318; 2013/0295121; 2010/0174053 and 2009/0060910; European Patent Publication No. EP 2714079; EP 2601216; EP 2376109; EP 2158221 and PCT Publications No. WO 2012/162068; WO 2012/018687; WO 2010/080538). These Fc Region-containing **DART®** diabodies may comprise two pairs of polypeptide chains. The first polypeptide chain comprises (in the N-terminal to C-terminal direction): (i) a First

Domain that comprises a binding region of a Light Chain Variable Domain of a first immunoglobulin (VL1), (ii) a Second Domain that comprises a binding region of a Heavy Chain Variable Domain of a second immunoglobulin (VH2), (iii) a Third Domain that contains a cysteine residue (or a cysteine-containing domain) and a serves to promote heterodimerization with the second polypeptide of the diabody and to covalently bond the diabody's first and second polypeptides to one another, and (iv) a CH2-CH3 Domain. The second polypeptide contains (in the N-terminal to C-terminal direction): (i) a First Domain that comprises a binding region of a Light Chain Variable Domain of the second immunoglobulin (VL2), (ii) a Second Domain that comprises a binding region of a Heavy Chain Variable Domain of the first immunoglobulin (VH1), and (iii)) a Third Domain that contains a cysteine residue (or a cysteine-containing domain) and a Heterodimer-Promoting Domain that promotes heterodimerization with the first polypeptide chain. Here, two first polypeptides complex with each other to form an Fc Region. **Figures 3A-3C** provide schematics of three variations of such diabodies utilizing different Heterodimer-Promoting Domains.

[0076] Other Fc-Region-containing DART® diabodies may comprise three polypeptide chains. The first polypeptide of such DART® diabodies contains three domains: (i) a VL1-containing Domain, (ii) a VH2-containing Domain and (iii) a Domain containing a CH2-CH3 sequence. The second polypeptide of such DART® diabodies contains: (i) a VL2-containing Domain, (ii) a VH1-containing Domain and (iii) a Domain that promotes heterodimerization and covalent bonding with the diabody's first polypeptide chain. The third polypeptide of such DART® diabodies comprises a CH2-CH3 sequence. Thus, the first and second polypeptide chains of such DART® diabodies associate together to form a VL1/VH1 binding site that is capable of binding to the epitope, as well as a VL2/VH2 binding site that is capable of binding to the second epitope. Such more complex DART® molecules also possess cysteine-containing domains which function to form a covalently bonded complex. Thus, the first and second polypeptides are bonded to one another through a disulfide bond involving cysteine residues in their respective Third Domains. Notably, the first and third polypeptide chains complex with one another to form an Fc Region that is stabilized via a disulfide bond. **Figures 4A-4B** provide schematics of such diabodies comprising three polypeptide chains.

[0077] Still other Fc-Region-containing DART® diabodies may comprise five polypeptide chains which may comprise the binding regions from the Light and Heavy Chain Variable Domains of up to three different immunoglobulins (referred to as VL1/VH1, VL2/VH2 and VL3/VH3). For example, the first polypeptide chain of such diabodies may contain: (i) a VH1-containing domain, (ii) a CH1-containing domain, and (iii) a Domain containing a CH2-CH3 sequence. The second and fifth polypeptide chains of such diabodies may contain: (i) a VL1-containing domain, and (ii) a CL-containing domain. The third polypeptide chain of such diabodies may contain: (i) a VH1-containing domain, (ii) a CH1-containing domain, (iii) a Domain containing a CH2-CH3 sequence, (iv) a VL2-containing Domain, (v) a VH3-containing Domain and (vi) a Heterodimer-Promoting Domain, where the Heterodimer-Promoting Domains promote the dimerization of the third chain with the fourth chain. The fourth polypeptide of such diabodies may contain: (i) a VL3-containing Domain, (ii) a VH2-containing Domain and (iii) a Domain that promotes heterodimerization and covalent bonding with the diabody's third polypeptide chain. Here, the first and third polypeptides complex with each other to form an Fc Region. Such more complex DART® molecules also possess cysteine-containing domains which function to form a covalently bonded complex, such that each polypeptide chain is bonded to at least one addition polypeptide chain through a disulfide bond involving cysteine residues. Preferably, such domains are ordered in the N-terminal to C-terminal direction. **Figure 5** provides schematics of such diabodies comprising five polypeptide chains

[0078] Alternative constructs are known in the art for applications where a tetravalent molecule is desirable but an Fc is not required including, but not limited to, tetravalent tandem antibodies, also referred to as "**TandAbs**" (see, *e.g.* United States Patent Publications Nos. 2005-0079170, 2007-0031436, 2010-0099853, 2011-020667 2013-0189263; European Patent Publication Nos. EP 1078004, EP 2371866, EP 2361936 and EP 1293514; PCT Publications Nos. WO 1999/057150, WO 2003/025018, and WO 2013/013700) which are formed by the homo-dimerization of two identical chains each possessing a VH1, VL2, VH2, and VL2 Domain.

[0079] Recently, trivalent structures incorporating two diabody-type binding domains and one non-diabody-type domain and an Fc Region have been described (see,

e.g., PCT Application No: PCT/US15/33076, titled "Tri-Specific Binding Molecules and Methods of Use Thereof," filed May 29, 2015; and PCT/US15/33081, titled "Tri-Specific Binding Molecules That Specifically Bind to Multiple Cancer Antigens and Methods of Use Thereof," filed May 29, 2015). Such trivalent molecules may be utilized to generate monospecific, bispecific or trispecific molecules. **Figures 6A-6F** provide schematics of such trivalent molecules comprising 3 or 4 polypeptide chains.

IV. The LAG-3-Binding Molecules of the Present Invention

[0080] The preferred LAG-3-binding molecules of the present invention include antibodies, diabodies, BiTEs, *etc.* and are capable of binding to a continuous or discontinuous (*e.g.*, conformational) portion (**epitope**) of human LAG-3. The LAG-3-binding molecules of the present invention will preferably also exhibit the ability to bind to LAG-3 molecules of one or more non-human species, in particular, primate species (and especially a primate species, such as cynomolgus monkey). A representative human LAG-3 polypeptide (NCBI Sequence NP_002277.4; including a 22 amino acid residue signal sequence (shown underlined) and the 503 amino acid residue mature protein) has the amino acid sequence (**SEQ ID NO:5**):

MWEAQFLGLL FLQPLWVAPV KPLQPGAEVP VVWAQEGAPA QLPCSPTIPL
QDLSLLRRAG VTWQHQPDSG PPAAAPGHPL APGPHPAAPS SWGPRPRRYT
VLSVGPGGLR SGRLPLQPRV QLDERGRQRG DFSLWLRPAR RADAGEYRAA
VHLRDRALSC RLRLRLGQAS MTASPPGSLR ASDWVILNCS FSRPDRPASV
HWFRNRGQGR VPVRESPHHH LAESFLFLPQ VSPMDSGPWG CILTYRDGFN
VSIMYNLTVL GLEPPTPLTV YAGAGSRVGL PCRLPAGVGT RSFLTAKWTP
PGGGPDLLVT GDNGDFTLRL EDVSQAQAGT YTCHIHLQEQ QLNATVTLAI
ITVTPKSFGS PGSLGKLLCE VTPVSGQERF VWSSLDTPSQ RSFSGPWLEA
QEAQLLSQPW QCQLYQGERL LGAAVYFTEL SSPGAQRSGR APGALPAGHL
LLFLILGVLS LLLLVTGAFG FHLWRRQWRP RRFSALEQGI HPPQAQSKIE
ELEQEPEPEP EPEPEPEPEP EPEQL

[0081] In certain embodiments the LAG-3-binding molecules of the invention are characterized by any (one or more) of the following criteria:

(1) specifically binds human LAG-3 as endogenously expressed on the surface of a stimulated human T-cell;

(2) specifically binds human LAG-3 with an equilibrium binding constant (K_D) of 40 nM or less;

(3) specifically binds human LAG-3 with an equilibrium binding constant (K_D) of 0.5 nM or less;

(4) specifically binds non-human primate LAG-3 (*e.g.*, LAG-3 of cynomolgus monkey);

(5) specifically binds non-human primate LAG-3 with an equilibrium binding constant (K_D) of 50 nM or less;

(6) specifically binds non-human primate LAG-3 with an equilibrium binding constant (K_D) of 5 nM or less;

(7) inhibits (*i.e.*, blocks or interferes with) the binding of LAG-3 to MHC class II;

(8) stimulates an immune response;

(9) stimulates antigen specific T-cell response as a single agent;

(10) synergizes with an anti-PD-1 antibody to stimulate an antigen specific T-cell response;

(11) binds the same epitope of LAG-3 as the anti-LAG-3 antibody LAG-3 mAb 1 or LAG-3 mAb 6 and/or

(12) does not compete with the anti-LAG-3 antibody 257F (BMS 986016, Medarex/BMS) for LAG-3 binding (*e.g.*, as measured by Biacore Analysis).

[0082] As used here the term "antigen specific T-cell response" refers to responses by a T-cell that result from stimulation of the T-cell with the antigen for which the T-cell is specific. Non-limiting examples of responses by a T-cell upon antigen specific stimulation include proliferation and cytokine production (*e.g.*, TNF-α, IFN-γ production). The ability of a molecule to stimulate an antigen specific T-cell response may be determined, for example, using the *Staphylococcus aureus* Enterotoxin type B antigen ("**SEB**")-stimulated PBMC assay described herein.

[0083] The preferred LAG-3-binding molecules of the present invention possess the VH and/or VL Domains of murine anti-LAG-3 monoclonal antibodies "**LAG-3 mAb 1**," "**LAG-3 mAb 2**," "**LAG-3 mAb 3**," "**LAG-3 mAb 4**," "**LAG-3 mAb 5**," and/or "**LAG-3 mAb 6**" and more preferably possess 1, 2 or all 3 of the CDR_{H}s of the VH Domain and/or 1, 2 or all 3 of the CDR_{L}s of the VL Domain of such anti-LAG-3

monoclonal antibodies. Such preferred LAG-3-binding molecules include bispecific (or multispecific) antibodies, chimeric or humanized antibodies, BiTes, diabodies, *etc*, and such binding molecules having variant Fc Regions.

[0084] The invention particularly relates to LAG-3-binding molecules comprising a LAG-3 binding domain that possess:

(A) (1) the three CDR_{HS} of the VH Domain of the anti-LAG-3 antibody LAG-3 mAb 1, or hLAG-3 mAb 1 VL4;

(2) the three CDR_{LS} of the VL Domain of the anti-LAG-3 antibody LAG-3 mAb 1;

(3) the three CDR_{HS} of the VH Domain of the anti-LAG-3 antibody LAG-3 mAb 1 and the three CDR_{LS} of the VL Domain of the anti-LAG-3 antibody LAG-3 mAb 1;

(4) the VH Domain of the anti-LAG-3 antibody LAG-3 mAb 1;

(5) the VL Domain of the anti-LAG-3 antibody LAG-3 mAb 1;

(6) the VH and VL Domains of the anti-LAG-3 antibody LAG-3 mAb 1;

(B) (1) the three CDR_{HS} of the VH Domain of the anti-LAG-3 antibody LAG-3 mAb 2;

(2) the three CDR_{LS} of the VL Domain of the anti-LAG-3 antibody LAG-3 mAb 2;

(3) the three CDR_{HS} of the VH Domain of the anti-LAG-3 antibody LAG-3 mAb 2 and the three CDR_{LS} of the VL Domain of the anti-LAG-3 antibody LAG-3 mAb 2;

(4) the VH Domain of the anti-LAG-3 antibody LAG-3 mAb 2;

(5) the VL Domain of the anti-LAG-3 antibody LAG-3 mAb 2;

(6) the VH and VL Domains of the anti-LAG-3 antibody LAG-3 mAb 2;

(C) (1) the three CDR_{HS} of the VH Domain of the anti-LAG-3 antibody LAG-3 mAb 3;

(2) the three CDR_{LS} of the VL Domain of the anti-LAG-3 antibody LAG-3 mAb 3;

(3) the three CDR_{HS} of the VH Domain of the anti-LAG-3 antibody LAG-3 mAb 3 and the three CDR_{LS} of the VL Domain of the anti-LAG-3 antibody LAG-3 mAb 3;

(4) the VH Domain of the anti-LAG-3 antibody LAG-3 mAb 3;

(5) the VL Domain of the anti-LAG-3 antibody LAG-3 mAb 3;

(6) the VH and VL Domains of the anti-LAG-3 antibody LAG-3 mAb 3;

(D) (1) the three CDR_{HS} of the VH Domain of the anti-LAG-3 antibody LAG-3 mAb 4;

(2) the three CDR_{LS} of the VL Domain of the anti-LAG-3 antibody LAG-3 mAb 4;

(3) the three CDR_{HS} of the VH Domain of the anti-LAG-3 antibody LAG-3 mAb 4 and the three CDR_{LS} of the VL Domain of the anti-LAG-3 antibody LAG-3 mAb 4;

(4) the VH Domain of the anti-LAG-3 antibody LAG-3 mAb 4;

(5) the VL Domain of the anti-LAG-3 antibody LAG-3 mAb 4;

(6) the VH and VL Domains of the anti-LAG-3 antibody LAG-3 mAb 4;

(E) (1) the three CDR_{HS} of the VH Domain of the anti-LAG-3 antibody LAG-3 mAb 5;

(2) the three CDR_{LS} of the VL Domain of the anti-LAG-3 antibody LAG-3 mAb 5;

(3) the three CDR_{HS} of the VH Domain of the anti-LAG-3 antibody LAG-3 mAb 5 and the three CDR_{LS} of the VL Domain of the anti-LAG-3 antibody LAG-3 mAb 5;

(4) the VH Domain of the anti-LAG-3 antibody LAG-3 mAb 5;

(5) the VL Domain of the anti-LAG-3 antibody LAG-3 mAb 5;

(6) the VH and VL Domains of the anti-LAG-3 antibody LAG-3 mAb 5;

(F) (1) the three CDR_{HS} of the VH Domain of the anti-LAG-3 antibody LAG-3 mAb 6;

(2) the three CDR_{LS} of the VL Domain of the anti-LAG-3 antibody LAG-3 mAb 6;

(3) the three CDR_{HS} of the VH Domain of the anti-LAG-3 antibody LAG-3 mAb 6 and the three CDR_{LS} of the VL Domain of the anti-LAG-3 antibody LAG-3 mAb 6;

(4) the VH Domain of the anti-LAG-3 antibody LAG-3 mAb 6;

(5) the VL Domain of the anti-LAG-3 antibody LAG-3 mAb 6;

(6) the VH and VL Domains of the anti-LAG-3 antibody LAG-3 mAb 6,

(G) (1) the three CDR_{LS} of the VL Domain of the anti-LAG-3 antibody hLAG-3 mAb 1 VL4;

(2) the three CDR_{HS} of the VH Domain of the anti-LAG-3 antibody LAG-3 mAb 1 and the three CDRs of the VL Domain of the anti-LAG-3 antibody hLAG-3 mAb 1 VL4;

or

that binds, or competes for binding with, the epitope that LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5 or LAG-3 mAb 6 immunospecifically binds.

A. The Anti-LAG-3 Antibody LAG-3 mAb 1

1. Murine Anti-Human Antibody LAG-3 mAb 1

[0085] The amino acid sequence of the VH Domain of LAG-3 mAb 1 (**SEQ ID NO:6**) is shown below (CDR_H residues are shown underlined).

QIQLVQSGPE LKKPGETVKI SCKASGYTFR **NYGMN**WVKQA PGKVLKWMG**W**
INTYTGESTY ADDFEGRFAF SLGTSASTAY LQINILKNED TATYFCAR**ES**
LYDYYSMDYW GQGTSVTVSS

CDR_H1 of LAG-3 mAb 1 (**SEQ ID NO:8**): **NYGMN**

CDR_H2 of LAG-3 mAb 1 (**SEQ ID NO:9**): **WINTYTGESTYADDFEG**

CDR_H3 of LAG-3 mAb 1 (**SEQ ID NO:10**): **ESLYDYYSMDY**

[0086] An exemplary polynucleotide that encodes the VH Domain of LAG-3 mAb 1 is **SEQ ID NO:7** (nucleotides encoding the CDR_H residues are shown underlined):

cagatccagt tggtgcagtc tggacctgag ctgaagaagc ctggagagac
agtcaagatc tcctgcaagg cttctgggta taccttcaga **aactatggaa**
tgaactgggt gaagcaggct ccaggaaagg ttttaaagtg gatgggc**tgg**
ataaacacct acactggaga gtcaacatat gctgatgact tcgagggacg
gtttgccttc tctttgggaa cctctgccag cactgcctat ttgcagatca
acatcctcaa aaatgaggac acggctacat atttctgtgc aaga**gaatcc**
ctctatgatt actattctat ggactactgg ggtcaaggaa cctcagtcac
cgtctcctca

[0087] The amino acid sequence of the VL Domain of LAG-3 mAb 1 (**SEQ ID NO:11**) is shown below (CDR_L residues are shown underlined):

DVVVTQTPLT LSVTIGQPAS ISC**KSSQSLL HSDGKTYLN**W LLQRPGQSPE
RLIY**LVSELD S**GVPDRFTGS GSGTDFTLKI SRVEAEDLGV YYC**WQGTHFP**
YTFGGGTKLE IK

CDR_L1 of LAG-3 mAb 1 (**SEQ ID NO:13**): **KSSQSLLHSDGKTYLN**

CDR_L2 of LAG-3 mAb 1 (**SEQ ID NO:14**): **LVSELDS**

CDR_L3 of LAG-3 mAb 1 (**SEQ ID NO:15**): **WQGTHFPYT**

[0088] An exemplary polynucleotide that encodes the VL Domain of LAG-3 mAb 1 is **SEQ ID NO:12** (nucleotides encoding the CDR_L residues are shown underlined):

gatgttgtgg tgacccagac tccactcact ttgtcggtta ccattggaca
accagcctcc atctcttgc**a agtcaagtca gagcctctta catagtgatg**
gaaagacata tttgaattgg ttgttacaga ggccaggcca gtctccagag
cgcctaatct at**ctggtgtc tgaactggac tct**ggagtcc ctgacaggtt
cactggcagt ggatcaggga cagatttcac actgaaaatc agcagagtgg
aggctgagga tttgggagtt tattattgc**t ggcaaggtac acattttccg**
tacacgttcg gaggggggac caagctggaa ataaaa

2. Humanization of the Anti-LAG-3 Antibody LAG-3 mAb 1 to Form "hLAG-3 mAb 1"

[0089] The above-described murine anti-LAG-3 antibody LAG-3mAb 1 was humanized in order to demonstrate the capability of humanizing an anti-LAG-3 antibody so as to decrease its antigenicity upon administration to a human recipient.

The humanization yielded two humanized VH Domains, designated herein as "**hLAG-3 mAb 1 VH-1,**" and "**hLAG-3 mAb 1 VH-2**," and four humanized VL Domains designated herein as "**hLAG-3 mAb 1 VL-1**," "**hLAG-3 mAb 1 VL-2**," "**hLAG-3 mAb 1 VL-3**," and "**hLAG-3 mAb 1 VL-4**." Any of the humanized VL Domains may be paired with the humanized VH Domains. Accordingly, any antibody comprising one of the humanized VL Domains paired with the humanized VH Domain is referred to generically as "**hLAG-3 mAb 1**," and particular combinations of humanized VH/VL Domains are referred to by reference to the specific VH/VL Domains, for example a humanized antibody comprising hLAG-3 mAb 1 VH-1 and hLAG-3 mAb 1 VL-2 is specifically referred to as "**hLAG-3 mAb 1(1.2)**."

[0090] The amino acid sequence of the VH Domain of **hLAG-3 mAb 1 VH-1** (**SEQ ID NO:16**) is shown below (CDR_H residues are shown underlined):

QVQLVQSGAE VKKPGASVKV SCKASGYTFT **NYGMN**WVRQA PGQGLEWMG**W**
INTYTGESTY ADDFEGRFVF SMDTSASTAY LQISSLKAED TAVYYCAR**ES**
LYDYYSMDYW GQGTTVTVSS

[0091] An exemplary polynucleotide that encodes **hLAG-3 mAb 1 VH-1** is **SEQ ID NO:17** (nucleotides encoding the CDR_H residues are shown underlined):

caggtgcaac tggttcaatc cggcgccgag gtgaaaaagc ctggcgcctc
cgtgaaagtg tcctgtaagg catctgggta tacgttcaca **aattatggta**
tgaactgggt gcgacaggca ccagggcagg gactggaatg gatgggg**tgg**
atcaatactt atacaggcga gagtacttat gctgacgatt tcgagggcag
atttgtcttc tccatggaca ccagcgctag taccgcttat ctccagatta
gttctctcaa ggcggaggac acagctgttt attattgtgc ccgc**gagagt**
ttgtatgact actatagcat ggattactgg ggacaaggta caaccgtgac
agtgagttcc

[0092] The amino acid sequence of the VH Domain of **hLAG-3 mAb 1 VH-2** (**SEQ ID NO:18**) is shown below (CDR_H residues are shown underlined):

QVQLVQSGAE VKKPGASVKV SCKASGYTFT **NYGMN**WVRQA PGQGLEWMG**W**
INTYTGESTY ADDFEGRFVF SMDTSASTAY LQISSLKAED TAVYFCAR**ES**
LYDYYSMDYW GQGTTVTVSS

[0093] An exemplary polynucleotide that encodes **hLAG-3 mAb 1 VH-2** is **SEQ ID NO:19** (nucleotides encoding the CDR_H residues are shown underlined):

caggtgcaac tggttcaatc cggcgccgag gtgaaaaagc ctggcgcctc
cgtgaaagtg tcctgtaagg catctgggta tacgttcaca **aattatggta**

tgaactgggt gcgacaggca ccagggcagg gactggaatg gatgggg**tgg**
atcaatactt atacaggcga gagtacttat gctgacgatt tcgagggcag
atttgtcttc tccatggaca ccagcgctag taccgcttat ctccagatta
gttctctcaa ggcggaggac acagctgttt atttctgtgc ccgc**gagagt**
ttgtatgact actatagcat ggattactgg ggacaaggta caaccgtgac
agtgagttcc

[0094] The amino acid sequence of the VL Domain of **hLAG-3 mAb 1 VL-1** (**SEQ ID NO:20**) is shown below (CDR_L residues are shown underlined):

DIVMTQTPLS LSVTPGQPAS ISC**KSSQSLL HSDGKTYLN**W LLQKPGQSPE
RLIY**LVSELD S**GVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYC**WQGTHFP**
YTFGGGTKVE IK

[0095] An exemplary polynucleotide that encodes **hLAG-3 mAb 1 VL-1** is **SEQ ID NO:21** (nucleotides encoding the CDR_L residues are shown underlined):

gatatcgtta tgactcagac accactgtca ctgagtgtga ccccaggtca
gcccgctagt atttcctgt**a aatcatccca gtccctcctg catagcgatg**
gaaagaccta tttgaactgg cttctgcaga aaccaggcca aagtccagag
agattgatct ac**ctcgtttc agaactcgac agt**ggagtgc ccgatcgctt
ctcagggtcc ggctctggga ctgattttac tctcaagatc tcaagagtgg
aggccgagga cgtcggggtt tactactgt**t ggcagggtac ccacttccct**
tatacatttg gcggaggcac aaaagtggag attaaa

[0096] The amino acid sequence of the VL Domain of **hLAG-3 mAb 1 VL-2** (**SEQ ID NO:22**) is shown below (CDR_L residues are shown underlined):

DIVMTQTPLS LSVTPGQPAS ISC**KSSQSLL HSDGKTYLN**W LLQRPGQSPE
RLIY**LVSELD S**GVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYC**WQGTHFP**
YTFGGGTKVE IK

[0097] An exemplary polynucleotide that encodes **hLAG-3 mAb 1 VL-2** is **SEQ ID NO:23** (nucleotides encoding the CDR_L residues are shown underlined):

gatatcgtta tgactcagac accactgtca ctgagtgtga ccccaggtca
gcccgctagt atttcctgt**a aatcatccca gtccctcctg catagcgatg**
gaaagaccta tttgaactgg cttctgcaga gaccaggcca aagtccagag
agattgatct ac**ctcgtttc agaactcgac agt**ggagtgc ccgatcgctt
ctcagggtcc ggctctggga ctgattttac tctcaagatc tcaagagtgg
aggccgagga cgtcggggtt tactactgt**t ggcagggtac ccacttccct**
tatacatttg gcggaggcac aaaagtggag attaaa

[0098] The amino acid sequence of the VL Domain of **hLAG-3 mAb 1 VL-3** (**SEQ ID NO:24**) is shown below (CDR_L residues are shown underlined):

DIVMTQTPLS LSVTPGQPAS ISC**KSSQSLL HSDGKTYLN**W LLQKPGQPPE
RLIY**LVSELD S**GVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYC**WQGTHFP**
YTFGGGTKVE IK

[0099] An exemplary polynucleotide that encodes **hLAG-3 mAb 1 VL-3** is **SEQ ID NO:25 (**nucleotides encoding the CDR_L residues are shown underlined**)**:

gatatcgtta tgactcagac accactgtca ctgagtgtga ccccaggtca
gcccgctagt atttcctgt**a aatcatccca gtccctcctg catagcgatg**
gaaagaccta tttgaactgg cttctgcaga aaccaggcca accgccagag
agattgatct ac**ctcgtttc agaactcgac agt**ggagtgc ccgatcgctt
ctcagggtcc ggctctggga ctgattttac tctcaagatc tcaagagtgg
aggccgagga cgtcggggtt tactactgt**t ggcagggtac ccacttccct**
tatacatttg gcggaggcac aaaagtggag attaaa

[00100] The amino acid sequence of the VL Domain of **hLAG-3 mAb 1 VL-4 (SEQ ID NO:26)** is shown below (CDR_L residues are shown underlined):

DIVMTQTPLS LSVTPGQPAS ISC**KSSQSLL HSDAKTYLN**W LLQKPGQPPE
RLIY**LVSELD S**GVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYC**WQGTHFP**
YTFGGGTKVE IK

[00101] An exemplary polynucleotide that encodes **hLAG-3 mAb 1 VL-4** is **SEQ ID NO:27 (**nucleotides encoding the CDR_L residues are shown underlined**)**:

gatatcgtta tgactcagac accactgtca ctgagtgtga ccccaggtca
gcccgctagt atttcctgt**a aatcatccca gtccctcctg catagcgatg**
caaagaccta tttgaactgg cttctgcaga aaccaggcca accgccagag
agattgatct ac**ctcgtttc agaactcgac agt**ggagtgc ccgatcgctt
ctcagggtcc ggctctggga ctgattttac tctcaagatc tcaagagtgg
aggccgagga cgtcggggtt tactactgt**t ggcagggtac ccacttccct**
tatacatttg gcggaggcac aaaagtggag attaaa

[00102] The CDR_L1 of the VL Domain of hLAG-3 mAb 1 VL-4 comprises an glycine to alanine amino acid substitution and has the amino acid sequence: KSSQSLLHSD**A**KTYLN **(SEQ ID NO:28)**, the substituted alanine is shown underlined). It is contemplated that a similar substitution may be incorporated into any of the LAG-3 mAb 1 CDR_L1 Domains described above.

B. The Anti-LAG-3 Antibody LAG-3 mAb 2

[00103] The amino acid sequence of the VH Domain of LAG-3 mAb 2 **(SEQ ID NO:29)** is shown below (CDR_H residues are shown underlined):

EVQLQQSGPE LVKPGASVKI SCKTSGYTFT **DYNIH**WLRQS HGESLEWIG**Y**
IYPYSGDIGY NQKFKNRATL TVDNSSSTAY MDLRSLTSED SAVFYCAR**WH**
RNYFGPWFAY WGQGTPVTVS A

CDR$_H$1 of LAG-3 mAb 2 (**SEQ ID NO:31**): **DYNIH**

VH CDR$_H$2 of LAG-3 mAb 2 (**SEQ ID NO:32**): **YIYPYSGDIGYNQKFKN**

VH CDR$_H$3 of LAG-3 mAb 2 (**SEQ ID NO:33**): **WHRNYFGPWFAY**

[00104] An exemplary polynucleotide that encodes the VH Domain of LAG-3 mAb 2 is **SEQ ID NO:30** (nucleotides encoding the CDR$_H$ residues are shown underlined):

gaggtccagc ttcagcagtc aggacctgag ctggtgaaac ctggggcctc
agtgaagatt tcctgcaaga cttctggata cacatttact **gactacaaca**
tacactggtt gaggcagagc catggagaga gccttgagtg gattgga**tat**
atttatcctt acagtggtga tattggatac aaccagaagt tcaagaacag
ggccacattg actgtagaca attcctccag cacagcctac atggatctcc
gcagcctgac atctgaagac tctgcagtct tttactgtgc aaga**tggcac**
aggaactact ttggcccctg gtttgcttac tggggccaag ggactccggt
cactgtctct gca

[00105] The amino acid sequence of the VL Domain of LAG-3 mAb 2 (**SEQ ID NO:34**) is shown below (CDR$_L$ residues are shown underlined):

DIVLTQSPAS LAVSLGQRAT ISC**KASQSVD YDGESYMN**WY QQKPGQPPKL
LIY**VVSNLES** GIPARFSGSG SGTDFTLNIH PVEEEDAATY YC**QQSSEDPL**
TFGAGTKLEL K

CDR$_L$1 of LAG-3 mAb 2 (**SEQ ID NO:36**): **KASQSVDYDGESYMN**

CDR$_L$2 of LAG-3 mAb 2 (**SEQ ID NO:37**): **VVSNLES**

CDR$_L$3 of LAG-3 mAb 2 (**SEQ ID NO:38**): **QQSSEDPLT**

[00106] An exemplary polynucleotide that encodes the VL Domain of LAG-3 mAb 2 is **SEQ ID NO:35** (nucleotides encoding the CDR$_L$ residues are shown underlined):

gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca
gagggccacc atctcctgc**a aggccagcca aagtgttgat tatgatggtg**
aaagttatat gaactggtac caacagaaac caggacagcc acccaaactc
ctcatttat**g ttgtatccaa tctagaatct** gggatcccag ccaggtttag
tggcagtggg tctgggacag acttcaccct caacatccat cctgtggagg

aggaggatgc tgcaacctat tactgtcagc aaagtagtga ggatccgctc
acgttcggtg ctgggaccaa gctggagctg aaa

C. The Anti-LAG-3 Antibody LAG-3 mAb 3

[00107] The amino acid sequence of the VH Domain of LAG-3 mAb 3 (**SEQ ID NO:39**) is shown below (CDR_H residues are shown underlined):

EVRLQQSGPE LVKPGASVKI SCKASGYTFT **DYNIH**WVRQS HGQSLEWIG**Y**
IYPYNGDTGY NQKFKTKATL TVDNSSNTAY MELRSLASED SAVYYCTR**WS**
RNYFGPWFAY WGQGTLVTVS A

CDR_H1 of LAG-3 mAb 3 (**SEQ ID NO:41**): **DYNIH**

CDR_H2 of LAG-3 mAb 3 (**SEQ ID NO:42**): **YIYPYNGDTGYNQKFKT**

CDR_H3 of LAG-3 mAb 3 (**SEQ ID NO:43**): **WSRNYFGPWFAY**

[00108] An exemplary polynucleotide that encodes the VH Domain of LAG-3 mAb 3 is **SEQ ID NO:40** (nucleotides encoding the CDR_H residues are shown underlined):

gaggtccggc ttcagcagtc aggacctgag ctggtgaaac ctggggcctc
agtgaagata tcctgcaagg cttctggata cacattcact **gactacaaca**
ttcactgggt gaggcagagc catggacaga gccttgagtg gattgga**tat**
atttatcctt ataatggtga tactggctac aaccagaagt tcaagaccaa
ggccacattg actgtagaca attcctccaa cacagcctac atggaactcc
gcagcctggc atctgaagac tctgcagtct attactgtac aaga**tggagc**
aggaactact ttggcccctg gtttgcttac tggggccaag ggactctggt
cactgtctct gca

[00109] The amino acid sequence of the VL Domain of LAG-3 mAb 3 (**SEQ ID NO:44**) is shown below (CDR_L residues are shown underlined):

DIVLTQSPTS LAVSLGQRAT ISC**KASQSVD YDGDSYMN**WY QQKPGQPPKL
LIY**AASNLES** GIPARFSGSG SGTDFTLNIH PVEEEDAATY YC**QQSSEDPL**
TFGAGTKLEL K

CDR_L1 of LAG-3 mAb 3 (**SEQ ID NO:46**): **KASQSVDYDGDSYMN**

CDR_L2 of LAG-3 mAb 3 (**SEQ ID NO:47**): **AASNLES**

CDR_L3 of LAG-3 mAb 3 (**SEQ ID NO:48**): **QQSSEDPLT**

[00110] An exemplary polynucleotide that encodes the VL Domain of LAG-3 mAb 3 is **SEQ ID NO:45** (nucleotides encoding the CDR_H residues are shown underlined):

gacattgtgc tgacccaatc tccaacttct ttggctgtgt ctctagggca
gagggccacc atctcctgca aggccagcca aagtgttgat tatgatggtg
atagttatat gaactggtat caacagaaac caggacagcc acccaaactc
ctcatctatg ctgcatccaa tctagaatct gggatcccag ccaggtttag
tggcagtggg tctgggacag acttcaccct caacatccat cctgtggagg
aggaggatgc tgcaacctat tactgtcagc aaagtagtga ggatccgctc
acgttcggtg ctgggaccaa gctggagctg aaa

D. The Anti-LAG-3 Antibody LAG-3 mAb 4

[00111] The amino acid sequence of the VH Domain of LAG-3 mAb 4 (**SEQ ID NO:49**) is shown below (CDR_H residues are shown underlined):

EVQLHQSGPE LVKPGASVKI SCKTSGYTFT DYNIHWVKQS HGKSLEWIGY
IYPYNGDAGY NQNFKTKATL TVDNSSSTAY MELRSLTSED SAVYYCARWN
MNYFGPWFAY WGQGTLVTVS A

CDR_H1 of LAG-3 mAb 4 (**SEQ ID NO:51**): **DYNIH**

CDR_H2 of LAG-3 mAb 4 (**SEQ ID NO:52**): **YIYPYNGDAGYNQNFKT**

CDR_H3 of LAG-3 mAb 4 (**SEQ ID NO:53**): **WNMNYFGPWFAY**

[00112] An exemplary polynucleotide that encodes the VH Domain of LAG-4 mAb 4 is **SEQ ID NO:50** (nucleotides encoding the CDR_H residues are shown underlined):

gaggtccagc ttcaccagtc aggacctgag ctggtgaaac ctggggcctc
agtgaagata tcctgcaaga cttctggata cactttcact gactacaaca
tacactgggt gaagcagagc catggaaaga gccttgagtg gattggatat
atttatcctt acaatggtga tgctggctac aaccagaact tcaagaccaa
ggccacattg actgtagaca attcctccag cacagcctac atggagctcc
gcagcctgac atctgaggac tctgcagtct attactgtgc aagatggaac
atgaactact ttggcccctg gtttgcttac tggggccaag ggactctggt
cactgtctct gcg

[00113] The amino acid sequence of the VL Domain of LAG-3 mAb 4 (**SEQ ID NO:54**) is shown below (CDR_L residues are shown underlined):

DIVLTQSPAS LAVSLGQRAT ISC**KASQSVD YDGVTYIN**WY QQKPGQPPKL LIF**AASNLES** GIPARFSGSG SGTDFTLNIH PVEEEDAATY YC**QQSNEDPL T**FGAGTKLEL K

CDR_L1 of LAG-3 mAb 4 (**SEQ ID NO:56**): **KASQSVDYDGVTYIN**

CDR_L2 of LAG-3 mAb 4 (**SEQ ID NO:7570**): **AASNLES**

CDR_L3 of LAG-3 mAb 4 (**SEQ ID NO:58**): **QQSNEDPLT**

[00114] An exemplary polynucleotide that encodes the VL Domain of LAG-3 mAb 4 is **SEQ ID NO:55** (nucleotides encoding the CDR_L residues are shown underlined):

gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc atctcctgc**a aggccagcca aagtgttgat tatgatggtg ttacttatat caac**tggtac caacagaaac caggacagcc acccaaactc ctcatctttg**g ctgcatccaa tctagaatct** gggatcccag ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat cctgtggagg aggaggatgc tgcaacctat tactgt**cagc aaagtaatga ggatccgctc acg**ttcggtg ctgggaccaa gctggagctg aaa

E. The Anti-LAG-3 Antibody LAG-3 mAb 5

[00115] The amino acid sequence of the VH Domain of LAG-3 mAb 5 (**SEQ ID NO:59**) is shown below (CDR_H residues are shown underlined):

EVQLQQSGPE LVKPGASVKI SCKASGYTFT **DYNIH**WVKQS PGKSLEWIG**Y IYPYSGDFGY NQKFKS**KATL TVDNSSSTAY MDLRSLTSED SAVFYCAR**WH RNYFGPWFAY** WGQGTLVTVS A

CDR_H1 of LAG-3 mAb 5 (**SEQ ID NO:61**): **DYNIH**

CDR_H2 of LAG-3 mAb 5 (**SEQ ID NO:62**): **YIYPYSGDFGYNQKFKS**

CDR_H3 of LAG-3 mAb 5 (**SEQ ID NO:63**): **WHRNYFGPWFAY**

[00116] An exemplary polynucleotide that encodes the VH Domain of LAG-3 mAb 5 is **SEQ ID NO:60** (nucleotides encoding the CDR_H residues are shown underlined):

gaggtccagc ttcagcagtc aggacctgag ctggtgaaac ctggggcctc agtgaagatt tcctgcaaag cttctggata cacatttact **gactacaaca**

tacactgggt gaagcagagc cctggaaaga gccttgaatg gattggatat atttatcctt acagtggtga ttttggatac aaccagaagt tcaagagcaa ggccacattg actgtagaca attcctccag cacagcctac atggatctcc gcagcctgac atctgaggac tctgcagtct tttactgtgc aagatggcac aggaactact ttggcccctg gtttgcttac tggggccaag ggactctggt cactgtctct gca

[00117] The amino acid sequence of the VL Domain of LAG-3 mAb 5 (**SEQ ID NO:64**) is shown below (CDR_L residues are shown underlined):

DIVLTQSPAS LAVSLGQRAT ISCKASQSVD YDGESYMNWY QQKPGQPPKL LIYVVSNLES GIPARFSGSG SGTDFTLNIH PVEEEDAATY YCQQSSEDPL TFGAGTKLEL K

CDR_L1 of LAG-3 mAb 5 (**SEQ ID NO:66**): KASQSVDYDGESYMN

CDR_L2 of LAG-3 mAb 5 (**SEQ ID NO:67**): VVSNLES

CDR_L3 of LAG-3 mAb 5 (**SEQ ID NO:68**): QQSSEDPLT

[00118] An exemplary polynucleotide that encodes the VL Domain of LAG-3 mAb 5 is **SEQ ID NO:65** (nucleotides encoding the CDR_L residues are shown underlined):

gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc atctcctgca aggccagcca agtgttgat tatgatggtg aaagttatat gaactggtac caacagaaac caggacagcc acccaaactc ctcatttatg ttgtttccaa tctagaatct gggatcccag ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat cctgtggagg aggaggatgc tgcaacctat tactgtcagc aaagtagtga ggatccgctc acgttcggtg ctgggaccaa gctggagctg aaa

F. The Anti-LAG-3 Antibody LAG-3 mAb 6

1. Murine Anti-Human Antibody LAG-3 mAb 6

[00119] The amino acid sequence of the VH Domain of LAG-3 mAb 6 (**SEQ ID NO:69**) is shown below (CDR_H residues are shown underlined):

EVLLQQSGPE LVKPGASVKI PCKASGYTFT DYNMDWVKQS HGESLEWIGD INPDNGVTIY NQKFEGKATL TVDKSSSTAY MELRSLTSED TAVYYCAREA DYFYFDYWGQ GTTLTVSS

CDR_H1 of LAG-3 mAb 6 (**SEQ ID NO:71**): DYNMD

CDR_H2 of LAG-3 mAb 6 (**SEQ ID NO:72**): DINPDNGVTIYNQKFEG

CDR_H3 of LAG-3 mAb 6 (**SEQ ID NO:72**): **EADYFYFDY**

[00120] An exemplary polynucleotide that encodes the VH Domain of LAG-3 mAb 6 is **SEQ ID NO:70** (nucleotides encoding the CDR_H residues are shown underlined):

gaggtcctgc tgcaacagtc tggacctgag ctggtgaagc ctggggcttc
agtgaagata ccctgcaagg cttctggata cacattcact **gactacaaca**
tggactgggt gaagcagagc catggagaga gccttgagtg gattgga**gat**
attaatcctg acaatggtgt tactatctac aaccagaagt ttgagggcaa
ggccacactg actgtagaca agtcctccag tacagcctac atggagctcc
gcagcctgac atctgaggac actgcagtct attactgtgc aaga**gaggcg**
gattacttct actttgacta ctggggccaa ggcaccactc tcacagtctc
ctca

[00121] The amino acid sequence of the VL Domain of LAG-3 mAb 6 (**SEQ ID NO:74**) is shown below (CDR_L residues are shown underlined):

DIVMTQSHRF MSTSVGDRVS ITC**KASQDVS SVVA**WYQQKP GQSPKLLIF**S**
ASYRYTGVPD RFTGSGSGTD FTFTISSVQA ADLAVYYC**QQ HYSTPWT**FGG
GTKLEIK

CDR_L1 of LAG-3 mAb 6 (**SEQ ID NO:76**): **KASQDVSSVVA**

CDR_L2 of LAG-3 mAb 6 (**SEQ ID NO:77**): **SASYRYT**

CDR_L3 of LAG-3 mAb 6 (**SEQ ID NO:78**): **QQHYSTPWT**

[00122] An exemplary polynucleotide that encodes the VL Domain of LAG-3 mAb 6 is **SEQ ID NO:75** (nucleotides encoding the CDRs are shown underlined):

gacattgtga tgacccagtc tcacagattc atgtccacat cagttggaga
cagggtcagc atcacctgc**a aggccagtca ggatgtgagt tctgttgtag**
cctggtatca acagaaacca ggacaatctc ctaaattact gattttt**tcg**
gcatcctacc ggtacactgg agtccctgat cgcttcactg gcagtggatc
tgggacggat ttcactttca ccatcagcag tgtgcaggct gcagacctgg
cagtttatta ctgt**cagcaa cattatagta ctccgtggac g**ttcggtgga
ggcaccaagc tggaaatcaa a

2. Humanization of the Anti-LAG-3 Antibody LAG-3 mAb 6 to Form "hLAG-3 mAb 6"

[00123] The above-described murine anti-LAG-3 antibody LAG-3mAb 6 was humanized in order to demonstrate the capability of humanizing an anti-LAG-3 antibody so as to decrease its antigenicity upon administration to a human recipient.

The humanization yielded two humanized VH Domains, designated herein as "**hLAG-3 mAb 6 VH-1,**" and "**hLAG-3 mAb 6 VH-2**," and two humanized VL Domains designated herein as "**hLAG-3 mAb 6 VL-1**," and "**hLAG-3 mAb 6 VL-2**." Any of the humanized VL Domains may be paired with either of the humanized VH Domains. Accordingly, any antibody comprising one of the humanized VL Domains paired with the humanized VH Domain is referred to generically as "**hLAG-3 mAb 6**," and particular combinations of humanized VH/VL Domains are referred to by reference to the specific VH/VL Domains, for example a humanized antibody comprising hLAG-3 mAb 6 VH-1 and hLAG-3 mAb 6 VL-2 is specifically referred to as "**hLAG-3 mAb 6(1.2)**."

[00124] The amino acid sequence of the VH Domain of **hLAG-3 mAb 6 VH-1** (**SEQ ID NO:79**) is shown below (CDR_H residues are shown underlined):

QVQLVQSGAE VKKPGASVKV SCKASGYTFT **DYNMD**WVRQA PGQGLEWMG**D**
INPDNGVTIY NQKFEGRVTM TTDTSTSTAY MELRSLRSDD TAVYYCAR**EA**
DYFYFDYWGQ GTTLTVSS

[00125] An exemplary polynucleotide that encodes **hLAG-3 mAb 6 VH-1** is **SEQ ID NO:80** (nucleotides encoding the CDR_H residues are shown underlined):

caggtccagc tggtgcagtc tggcgccgaa gtgaagaaac ctggcgcaag
cgtgaaggtg tcctgcaagg ccagcggcta caccttcacc **gactacaaca**
tggactgggt ccgacaggcc ccaggacagg gcctggaatg gatgggc**gac**
atcaaccccg acaacggcgt gaccatctac aaccagaaat tcgagggcag
agtgaccatg accaccgaca ccagcaccag caccgcctac atggaactgc
ggtccctgcg gagcgacgac accgccgtgt actactgcgc caga**ggccc**
gactacttct acttcgacta ctggggccag ggcaccaccc tgaccgtgtc
ctcc

[00126] An amino acid sequence of the VH Domain of **hLAG-3 mAb 6 VH-2** (**SEQ ID NO:81**) is shown below (CDR_H residues are shown underlined):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS **DYNMD**WVRQA PGKGLEWVS**D**
INPDNGVTIY NQKFEGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCAR**EA**
DYFYFDYWGQ GTTLTVSS

[00127] An exemplary polynucleotide that encodes **hLAG-3 mAb 6 VH-2** is **SEQ ID NO:82** (nucleotides encoding the CDR_H residues are shown underlined):

gaggtccagc tggtggaatc tggcggcgga ctggtcaagc ctggcggcag
cctgagactg agctgcgctg ccagcggctt caccttcagc **gactacaaca**

tggactgggt ccgacaggcc cctggcaagg gcctggaatg ggtgtcc**gac atcaaccccg acaacggcgt gaccatctac aaccagaagt tcgagggc**cg gttcaccatc agccgggaca acgccaagaa cagcctgtac ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caga**gaggcc gactacttct acttcgacta c**tggggccag ggcaccaccc tgaccgtgtc ctcc

[00128] The amino acid sequence of the VL Domain of **hLAG-3 mAb 6 VL-1** (**SEQ ID NO:83**) is shown below (CDR_L residues are shown underlined):

DIQMTQSPSS LSASVGDRVT ITC**RASQDVS SVVA**WYQQKP GKAPKLLIY**S ASYRYT**GVPS RFSGSGSGTD FTLTISSLQP EDFATYYC**QQ HYSTPWT**FGG GTKLEIK

[00129] An exemplary polynucleotide that encodes **hLAG-3 mAb 6 VL-1** is **SEQ ID NO:84** (nucleotides encoding the CDR_L residues are shown underlined):

gacatccaga tgacccagag ccccagcagc ctgagcgcca gcgtgggcga cagagtgacc atcacctgt**c gggccagcca ggatgtgtcc agcgtggtgg cc**tggtatca gcagaagccc ggcaaggccc ccaagctgct gatctac**agc gccagctacc ggtacaca**gg cgtgcccagc agattcagcg gcagcggctc cggcaccgac ttcaccctga ccatcagcag cctgcagccc gaggacttcg ccacctacta ctgc**cagcag cactacagca ccccctggac c**ttcggcgga ggcaccaagc tggaaatcaa g

[00130] The amino acid sequence of the VL Domain of **hLAG-3 mAb 6 VL-2** (**SEQ ID NO:85**) is shown below (CDR_L residues are shown underlined):

DIVMTQSPSS LSASVGDRVT ITC**RASQDVS SVVA**WYQQKP GKAPKLLIY**S ASYRYT**GVPD RFSGSGSGTD FTFTISSLQP EDIAVYYC**QQ HYSTPWT**FGG GTKLEIK

[00131] An exemplary polynucleotide that encodes **hLAG-3 mAb 6 VL-2** is **SEQ ID NO:86** (nucleotides encoding the CDR_L residues are shown underlined):

gacatcgtga tgacccagag ccccagcagc ctgagcgcca gcgtgggcga
cagagtgacc atcacctgt**c gggccagcca ggatgtgtcc agcgtggtgg**
cctggtatca gcagaagccc ggcaaggccc ccaagctgct gatctac**agc**
gccagctacc ggtacacagg cgtgcccgat agattcagcg gcagcggctc
cggcaccgac ttcaccttca ccatcagcag cctgcagccc gaggacatcg
ccgtttacta ctgc**cagcag cactacagca ccccctggac c**ttcggcgga
ggcaccaagc tggaaatcaa g

[00132] The CDR_L1 of the VL Domain of hLAG-3 mAb 2 VL-1 and VL-2 comprises an lysine to arginine amino acid substitution and has the amino acid

sequence: RASQDVSSVVA (**SEQ ID NO:87**), the substituted arginine is shown underlined). It is contemplated that a similar substitution may be incorporated into any of the LAG-3 mAb 6 CDR_L1 Domains described above.

[00133] Minor changes to the amino acid sequence of the VH and/or VL Domains provided herein are contemplated. For example, the C-terminal amino acid residue of any of the VH and/or VL Domains described herein may be substituted to facilitate sub-cloning.

V. Anti-LAG-3 Antibodies LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5, and/or LAG-3 mAb 6 and Their Derivatives Having an Engineered Fc Region

[00134] In traditional immune function, the interaction of antibody-antigen complexes with cells of the immune system results in a wide array of responses, ranging from effector functions such as antibody dependent cytotoxicity, mast cell degranulation, and phagocytosis to immunomodulatory signals such as regulating lymphocyte proliferation and antibody secretion. All of these interactions are initiated through the binding of the Fc Region of antibodies or immune complexes to specialized cell surface receptors on hematopoietic cells. The diversity of cellular responses triggered by antibodies and immune complexes results from the structural heterogeneity of the three Fc receptors: FcγRI (CD64), FcγRII (CD32), and FcγRIII (CD16). FcγRI (CD64), FcγRIIA (CD32A) and FcγRIII (CD16) are activating (*i.e.*, immune system enhancing) receptors; FcγRIIB (CD32B) is an inhibiting (*i.e.*, immune system dampening) receptor. In addition, interaction with the neonatual Fc Receptor (FcRn) mediates the recycling of IgG molecules from the endosome to the cell surface and release into the blood. The amino acid sequence of exemplary IgG1 (**SEQ ID NO:1**), IgG2 (**SEQ ID NO:2**), IgG3 (**SEQ ID NO: 3**), and IgG4 (**SEQ ID NO:4**) are presented above.

[00135] Modification of the Fc Region normally leads to an altered phenotype, for example altered serum half-life, altered stability, altered susceptibility to cellular enzymes or altered effector function. It may be desirable to modify an antibody or other binding molecule of the present invention with respect to effector function, for example, so as to enhance the effectiveness of such molecule in treating cancer. Reduction or

elimination of effector function is desirable in certain cases, for example in the case of antibodies whose mechanism of action involves blocking or antagonism, but not killing of the cells bearing a target antigen. Increased effector function is generally desirable when directed to undesirable cells, such as tumor and foreign cells, where the FcγRs are expressed at low levels, for example, tumor-specific B cells with low levels of FcγRIIB (*e.g.*, non-Hodgkin's lymphoma, CLL, and Burkitt's lymphoma). In said embodiments, molecules of the invention with conferred or altered effector function activity are useful for the treatment and/or prevention of a disease, disorder or infection where an enhanced efficacy of effector function activity is desired.

[00136] In certain embodiments, the LAG-3-binding molecules of the present invention comprise an Fc Region that possesses one or more modifications (*e.g.*, substitutions, deletions, or insertions) to the sequence of amino acids of a wild-type Fc Region (*e.g.*, **SEQ ID NO:1**), which reduce the affinity and avidity of the Fc Region and, thus, the molecule of the invention, for one or more FcγR receptors. In other embodiments, the molecules of the invention comprise an Fc Region that possesses one or more modifications to the amino acids of the wild-type Fc Region, which increase the affinity and avidity of the Fc Region and, thus, the molecule of the invention, for one or more FcγR receptors. In other embodiments, the molecules comprise a variant Fc Region wherein said variant confers or mediates increased antibody dependent cell mediated cytotoxicity (ADCC) activity and/or an increased binding to FcγRIIA, relative to a molecule comprising no Fc Region or comprising a wild-type Fc Region. In alternate embodiments, the molecules comprise a variant Fc Region wherein said variant confers or mediates decreased ADCC activity (or other effector function) and/or an increased binding to FcγRIIB, relative to a molecule comprising no Fc Region or comprising a wild-type Fc Region. In some embodiments, the invention encompasses LAG-3-binding molecules comprising a variant Fc Region, which variant Fc Region does not show a detectable binding to any FcγR, relative to a comparable molecule comprising the wild-type Fc Region. In other embodiments, the invention encompasses LAG-3-binding molecules comprising a variant Fc Region, which variant Fc Region only binds a single FcγR, preferably one of FcγRIIA, FcγRIIB, or FcγRIIIA. Any such increased affinity and/or avidity is preferably assessed by measuring *in vitro* the extent of detectable binding to the FcγR or FcγR-related activity in cells that express low levels

of the FcγR when binding activity of the parent molecule (without the modified Fc Region) cannot be detected in the cells, or in cells which express non-FcγR receptor target antigens at a density of 30,000 to 20,000 molecules/cell, at a density of 20,000 to 10,000 molecules/cell, at a density of 10,000 to 5,000 molecules/cell, at a density of 5,000 to 1,000 molecules/cell, at a density of 1,000 to 200 molecules/cell or at a density of 200 molecules/cell or less (but at least 10, 50, 100 or 150 molecules/cell).

[00137] The LAG-3-binding molecules of the present invention may comprise a variant Fc Region having altered affinities for an activating and/or inhibitory Fcγ receptor. In one embodiment, the LAG-3-binding molecule comprises a variant Fc Region that has increased affinity for FcγRIIB and decreased affinity for FcγRIIIA and/or FcγRIIA, relative to a comparable molecule with a wild-type Fc Region. In another embodiment, the LAG-3-binding molecule of the present invention comprise a variant Fc Region, which has decreased affinity for FcγRIIB and increased affinity for FcγRIIIA and/or FcγRIIA, relative to a comparable molecule with a wild-type Fc Region. In yet another embodiment, the LAG-3-binding molecules of the present invention comprise a variant Fc Region that has decreased affinity for FcγRIIB and decreased affinity for FcγRIIIA and/or FcγRIIA, relative to a comparable molecule with a wild-type Fc Region. In still another embodiment, the LAG-3-binding molecules of the present invention comprise a variant Fc Region, which has unchanged affinity for FcγRIIB and decreased (or increased) affinity for FcγRIIIA and/or FcγRIIA, relative to a comparable molecule with a wild-type Fc Region.

[00138] In certain embodiments, the LAG-3-binding molecules of the present invention comprise a variant Fc Region having an altered affinity for FcγRIIIA and/or FcγRIIA such that the immunoglobulin has an enhanced effector function. Non-limiting examples of effector cell functions include antibody dependent cell mediated cytotoxicity, antibody dependent phagocytosis, phagocytosis, opsonization, opsonophagocytosis, cell binding, rosetting, C1q binding, and complement dependent cell mediated cytotoxicity.

[00139] In a preferred embodiment, the alteration in affinity or effector function is at least 2-fold, preferably at least 4-fold, at least 5-fold, at least 6-fold, at least 7-fold,

at least 8-fold, at least 9-fold, at least 10-fold, at least 50-fold, or at least 100-fold, relative to a comparable molecule comprising a wild-type Fc Region. In other embodiments of the invention, the variant Fc Region immunospecifically binds one or more FcRs with at least 65%, preferably at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 100%, at least 125%, at least 150%, at least 175%, at least 200%, at least 225%, or at least 250% greater affinity relative to a molecule comprising a wild-type Fc Region. Such measurements can be in vivo or in vitro assays, and in a preferred embodiment are in vitro assays such as ELISA or surface plasmon resonance assays.

[00140] In different embodiments, the LAG-3-binding molecules of the present invention comprise a variant Fc Region wherein said variant agonizes at least one activity of an FcγR receptor, or antagonizes at least one activity of an FcγR receptor. In a preferred embodiment, the molecules comprise a variant that antagonizes one or more activities of FcγRIIB, for example, B-cell receptor-mediated signaling, activation of B-cells, B-cell proliferation, antibody production, intracellular calcium influx of B cells, cell cycle progression, FcγRIIB-mediated inhibition of FcεRI signaling, phosphorylation of FcγRIIB, SHIP recruitment, SHIP phosphorylation and association with Shc, or activity of one or more downstream molecules (*e.g.*, MAP kinase, JNK, p38, or Akt) in the FcγRIIB signal transduction pathway. In another embodiment, the LAG-3-binding molecules of the present invention comprise a variant that agonizes one or more activities of FcεRI, for example, mast cell activation, calcium mobilization, degranulation, cytokine production, or serotonin release.

[00141] In certain embodiments, the molecules comprise an Fc Region comprising regions from two or more IgG isotypes (*e.g.*, IgG1, IgG2, IgG3 and IgG4). As used herein, an Fc Region is said to be of a particular IgG isotype if its amino acid sequence is most homologous to that isotype relative to other IgG isotypes. The various IgG isotypes exhibit differing physical and functional properties including serum half-life, complement fixation, FcγR binding affinities and effector function activities (*e.g.*, ADCC, CDC, *etc.*) due to differences in the amino acid sequences of their hinge and/or Fc Regions, for example as described in Flesch and Neppert (1999) J. Clin. Lab. Anal. 14:141-156; Chappel *et al.* (1993) J. Biol. Chem. 33:25124-25131; Chappel *et al.*

(1991) Proc. Natl. Acad. Sci. (U.S.A.) 88:9036-9040; or Brüggemann *et al.* (1987) J. Exp. Med 166:1351-1361. This type of variant Fc Region may be used alone, or in combination with an amino acid modification, to affect Fc-mediated effector function and/or binding activity. In combination, the amino acid modification and IgG hinge/Fc Region may display similar functionality (*e.g.*, increased affinity for FcγRIIA) and may act additively or, more preferably, synergistically to modify the effector functionality in the molecule of the invention, relative to a molecule of the invention comprising a wild-type Fc Region. In other embodiments, the amino acid modification and IgG Fc Region may display opposite functionality (*e.g.*, increased and decreased affinity for FcγRIIA, respectively) and may act to selectively temper or reduce a specific functionality in the molecule of the invention, relative to a molecule of the invention not comprising an Fc Region or comprising a wild-type Fc Region of the same isotype.

[00142] In a preferred specific embodiment, the LAG-3-binding molecules of the present invention comprise a variant Fc Region, wherein said variant Fc Region comprises at least one amino acid modification relative to a wild-type Fc Region, such that said molecule has an altered affinity for an FcR, provided that said variant Fc Region does not have a substitution at positions that make a direct contact with FcγR based on crystallographic and structural analysis of Fc-FcR interactions such as those disclosed by Sondermann *et al.* (2000) Nature 406:267-73. Examples of positions within the Fc Region that make a direct contact with FcγR are amino acid residues 234-239 (hinge region), amino acid residues 265-269 (B/C loop), amino acid residues 297-299 (C'/E loop), and amino acid residues 327-332 (F/G loop). In some embodiments, the molecules of the invention comprise variant Fc Regions comprise modification of at least one residue that does not make a direct contact with an FcγR based on structural and crystallographic analysis, *e.g.*, is not within the Fc-FcγR binding site.

[00143] Variant Fc Regions are well known in the art, and any known variant Fc Region may be used in the present invention to confer or modify the effector function exhibited by a molecule of the invention comprising an Fc Region (or portion thereof) as functionally assayed, *e.g.*, in an NK dependent or macrophage dependent assay. For example, Fc Region variants identified as altering effector function are disclosed in PCT Publications No. WO 04/063351; WO 06/088494; WO 07/024249; WO

06/113665; WO 07/021841; WO 07/106707; and WO 2008/140603, and any suitable variant disclosed therein may be used in the present molecules.

[00144] In certain embodiments, the LAG-3-binding molecules of the present invention comprise a variant Fc Region, having one or more amino acid modifications in one or more regions, which modification(s) alter (relative to a wild-type Fc Region) the **Ratio of Affinities** of the variant Fc Region to an activating FcγR (such as FcγRIIA or FcγRIIIA) relative to an inhibiting FcγR (such as FcγRIIB):

$$\text{Ratio of Affinities} = \frac{\text{Wild-Type to Variant Change in Affinity to Fc}\gamma\text{R}_{\text{Activating}}}{\text{Wild-Type to Variant Change in Affinity to Fc}\gamma\text{R}_{\text{Inhibiting}}}$$

[00145] Particularly preferred are LAG-3-binding molecules of the present invention that possess a variant Fc Region (relative to the wild-type Fc Region) in which the variant Fc Region has a Ratio of Affinities greater than 1. Such molecules have particular use in providing a therapeutic or prophylactic treatment of a disease, disorder, or infection, or the amelioration of a symptom thereof, where an enhanced efficacy of effector cell function (*e.g.*, ADCC) mediated by FcγR is desired, *e.g.*, cancer or infectious disease. In contrast, a variant Fc Region having a Ratio of Affinities less than 1 mediates decreased efficacy of effector cell function. **Table 1** lists exemplary single, double, triple, quadruple and quintuple mutations by whether their Ratio of Affinities is greater than or less than 1.

Table 1 Exemplary Single and Multiple Mutations Listed by Ratio of Affinities				
Single	**Double**	**Triple**	**Quadruple**	**Quintuple**
Ratio of Affinities > 1				
F243L	F243L & R292P	F243L, P247L & N421K	L234F, F243L, R292P & Y300L	L235V, F243L, R292P, Y300L & P396L
D270E	F243L & Y300L	F243L, R292P & Y300L	L235I, F243L, R292P & Y300L	L235P, F243L, R292P, Y300L & P396L
R292G	F243L & P396L	F243L, R292P & V305I	L235Q, F243L, R292P & Y300L	F243L, R292P, V305I, Y300L & P396L
R292P	D270E & P396L	F243L, R292P & P396L	F243L, P247L, D270E & N421K	
	R292P & Y300L	F243L, Y300L & P396L	F243L, R255L, D270E & P396L	
	R292P & V305I	P247L, D270E & N421K	F243L, D270E, G316D & R416G	
	R292P & P396L	R255L, D270E & P396L	F243L, D270E, K392T & P396L	
	Y300L & P396L	D270E, G316D & R416G	F243L, D270E, P396L & Q419H	
	P396L & Q419H	D270E, K392T & P396L	F243L, R292P, Y300L, & P396L	
		D270E, P396L & Q419H	F243L, R292P, V305I & P396L	
		V284M, R292L & K370N	P247L, D270E, Y300L & N421K	
		R292P, Y300L & P396L	R255L, D270E, R292G & P396L	
			R255L, D270E, Y300L & P396L	
			D270E, G316D, P396L & R416G	

Table 1 Exemplary Single and Multiple Mutations Listed by Ratio of Affinities				
Single	**Double**	**Triple**	**Quadruple**	**Quintuple**
Ratio of Affinities < 1				
Y300L	F243L & P396L	F243L, R292P & V305I		
P396L	P247L & N421K			
	R255L & P396L			
	R292P & V305I			
	K392T & P396L			
	P396L & Q419H			

[00146] In a specific embodiment, in variant Fc Regions, any amino acid modifications (*e.g.*, substitutions) at any of positions 235, 240, 241, 243, 244, 247, 262, 263, 269, 298, 328, or 330 and preferably one or more of the following residues: A240, I240, L241, L243, H244, N298, I328 or V330. In a different specific embodiment, in variant Fc Regions, any amino acid modifications (*e.g.*, substitutions) at any of positions 268, 269, 270, 272, 276, 278, 283, 285, 286, 289, 292, 293, 301, 303, 305, 307, 309, 331, 333, 334, 335, 337, 338, 340, 360, 373, 376, 416, 419, 430, 434, 435, 437, 438 or 439 and preferably one or more of the following residues: H280, Q280, Y280, G290, S290, T290, Y290, N294, K295, P296, D298, N298, P298, V298, I300 or L300.

[00147] In a preferred embodiment, in variant Fc Regions that bind an FcγR with an altered affinity, any amino acid modifications (*e.g.*, substitutions) at any of positions 255, 256, 258, 267, 268, 269, 270, 272, 276, 278, 280, 283, 285, 286, 289, 290, 292, 293, 294, 295, 296, 298, 300, 301, 303, 305, 307, 309, 312, 320, 322, 326, 329, 330, 332, 331, 333, 334, 335, 337, 338, 339, 340, 359, 360, 373, 376, 416, 419, 430, 434, 435, 437, 438 or 439. Preferably, the variant Fc Region has any of the following residues: A256, N268, Q272, D286, Q286, S286, A290, S290, A298, M301, A312, E320, M320, Q320, R320, E322, A326, D326, E326, N326, S326, K330, T339, A333, A334, E334, H334, L334, M334, Q334, V334, K335, Q335, A359, A360 or A430.

[00148] In a different embodiment, in variant Fc Regions that bind an FcγR (via its Fc Region) with a reduced affinity, any amino acid modifications (*e.g.*, substitutions) at any of positions 252, 254, 265, 268, 269, 270, 278, 289, 292, 293, 294, 295, 296, 298, 300, 301, 303, 322, 324, 327, 329, 333, 335, 338, 340, 373, 376, 382, 388, 389, 414, 416, 419, 434, 435, 437, 438 or 439.

[00149] In a different embodiment, in variant Fc Regions that bind an FcγR (via its Fc Region) with an enhanced affinity, any amino acid modifications (*e.g.*, substitutions) at any of positions 280, 283, 285, 286, 290, 294, 295, 298, 300, 301, 305, 307, 309, 312, 315, 331, 333, 334, 337, 340, 360, 378, 398 or 430. In a different embodiment, in variant Fc Regions that binds FcγRIIA with an enhanced affinity, any of the following residues: A255, A256, A258, A267, A268, N268, A272, Q272, A276, A280, A283, A285, A286, D286, Q286, S286, A290, S290, M301, E320, M320, Q320, R320, E322, A326, D326, E326, S326, K330, A331, Q335, A337 or A430.

[00150] Preferred variants include one or more modifications at any of positions: 228, 230, 231, 232, 233, 234, 235, 239, 240, 241, 243, 244, 245, 247, 262, 263, 264, 265, 266, 271, 273, 275, 281, 284, 291, 296, 297, 298, 299, 302, 304, 305, 313, 323, 325, 326, 328, 330 or 332.

[00151] Particularly preferred variants include one or more modifications selected from groups A-AI:

A	228E, 228K, 228Y or 228G;
B	230A, 230E, 230Y or 230G;
C	231E, 231K, 231Y, 231P or 231G;
D	232E, 232K, 232Y, 232G;
E	233D;
F	234I or 234F;
G	235D, 235Q, 235P, 235I or 235V;
H	239D, 239E, 239N or 239Q;
I	240A, 240I, 240M or 240T;
J	243R, 243, 243Y, 243L, 243Q, 243W, 243H or 243I;
K	244H;
L	245A;
M	247G, 247V or 247L;
N	262A, 262E, 262I, 262T, 262E or 262F;
O	263A, 263I, 263M or 263T;

P	264F, 264E, 264R, 264I, 264A, 264T or 264W;
Q	265F, 265Y, 265H, 265I, 265L, 265T, 265V, 265N or 265Q;
R	266A, 266I, 266M or 266T;
S	271D, 271E, 271N, 271Q, 271K, 271R, 271S, 271T, 271H, 271A, 271V, 271L, 271I, 271F, 271M, 271Y, 271W or 271G;
T	273I;
U	275L or 275W;
V	281D, 281K, 281Y or 281P;
W	284E, 284N, 284T, 284L, 284Y or284M;
X	291D, 291E, 291Q, 291T, 291H, 291I or 291G;
Y	299A, 299D, 299E, 299F, 299G, 299H, 299I, 299K, 299L, 299M, 299N, 299P, 299Q, 299R, 299S, 299V, 299W or 299Y;
Z	302I;
AA	304D, 304N, 304T, 304H or 304L
AB	305I;
AC	313F;
AD	323I;
AE	325A, 325D, 325E, 325G, 325H, 325I, 325L, 325K, 325R, 325S, 325F, 325M, 325T, 325V, 325Y, 325W or 325P;
AF	328D, 328Q, 328K, 328R, 328S, 328T, 328V, 328I, 328Y, 328W, 328P, 328G, 328A, 328E, 328F, 328H, 328M or 328N;
AG	330L, 330Y, 330I or 330V;
AH	332A, 332D, 332E, 332H, 332N, 332Q, 332T, 332K, 332R, 332S, 332V, 332L, 332F, 332M, 332W, 332P, 332G or 332Y; and
AI	336E, 336K or 336Y

[00152] Still more particularly preferred variants include one or more modifications selected from Groups 1-105:

Group	Variant	Group	Variant
1	A330L / I332E	54	S239D / D265L / N297D / I332E
2	D265F / N297E / I332E	55	S239D / D265T / N297D / I332E
3	D265Y / N297D / I332E	56	S239D / D265V / N297D / I332E
4	D265Y / N297D / T299L / I332E	57	S239D / D265Y / N297D / I332E
5	F241E / F243Q / V262T / V264F	58	S239D / I332D
6	F241E / F243Q / V262T / V264E / I332E	59	S239D / I332E
7	F241E / F243R / V262E / V264R	60	S239D / I332E / A330I

8	F241E / F243R / V262E / V264R / I332E	61	S239D / I332N
9	F241E / F243Y / V262T / V264R	62	S239D / I332Q
10	F241E / F243Y / V262T / V264R / I332E	63	S239D / N297D / I332E
11	F241L / F243L / V262I / V264I	64	S239D / N297D / I332E / A330Y
12	F241L / V262I	65	S239D / N297D / I332E / A330Y / F241S / F243H / V262T / V264T
13	F241R / F243Q / V262T / V264R	66	S239D / N297D / I332E / K326E
14	F241R / F243Q / V262T / V264R / I332E	67	S239D / N297D / I332E / L235D
15	F241W / F243W / V262A / V264A	68	S239D / S298A / I332E
16	F241Y / F243Y / V262T / V264T	69	S239D / V264I / A330L / I332E
17	F241Y / F243Y / V262T / V264T / N297D / I332E	70	S239D / V264I / I332E
18	F243L / V262I / V264W	71	S239D / V264I / S298A / I332E
19	P243L / V264I	72	S239E / D265N
20	L328D / I332E	73	S239E / D265Q
21	L328E / I332E	74	S239E / I332D
22	L328H / I332E	75	S239E / I332E
23	L328I / I332E	76	S239E / I332N
24	L328M / I332E	77	S239E / I332Q
25	L328N / I332E	78	S239E / N297D / I332E
26	L328Q / I332E	79	S239E / V264I / A330Y / I332 E
27	L328T / I332E	80	S239E / V264I / I332 E
28	L328V / I332E	81	S239E / V264I / S298A / A330Y / I332E
29	N297D / A330Y / I332E	82	S239N / A330L / I332E
30	N297D / I332E	83	S239N / A330Y / I332E
31	N297D / I332E / S239D / A330L	84	S239N / I332D
32	N297D / S298A / A330Y / I 332E	85	S239N / I332E
33	N297D / T299L / I332E	86	S239N / I332N
34	N297D / T299F / I332E / N297D / T299H / I332E	87	S239N / I332Q
35	N297D / T299I / I332E	88	S239N1S298A / I332E
36	N297D / T299L / I332E	89	S239Q / I332D
37	N297D / T299V / I332E	90	S239Q / I332E
38	N297E / I332E	91	S239Q / I332N

39	N297S / I332E	92	S239Q / I332Q
40	P230A / E233D / I332E	93	S239Q / V264I / I332E
41	P244H / P245A / P247V	94	S298A / I332E
42	S239D / A330L / I332E	95	V264E / N297D / I332E
43	S239D / A330Y / I332E	96	V264I / A330L / I332E
44	S239D / A330Y / I332E / K326E	97	V264I / A330Y / I332E
45	S239D / A330Y / I332E / K326T	98	V264I / I332E
46	S239D / A330Y / I332E / L234I	99	V264I / S298A / I332E
47	S239D / A330Y / I332E / L235D	100	Y296D / N297D / I332E
48	S239D / A330Y / I332E / V240I	101	Y296E / N297D / I332 E
49	S239D / A330Y / I332E / V264T	102	Y296H / N297D / I332E
50	S239D / A330Y / I332E / V266I	103	Y296N / N297D / I332E
51	S239D / D265F / N297D / I332E	104	Y296Q / N297I / I332E
52	S239D / D265H / N297D / I332E	105	Y296T / N297D / I332E
53	S239D / D265I / N297D / I332E		

[00153] In one embodiment, a LAG-3 binding molecule of the invention will comprise a variant Fc Region having at least one modification in the Fc Region. In certain embodiments, the variant Fc Region comprises at least one substitution selected from the group consisting of L235V, F243L, R292P, Y300L, V305I, and P396L, wherein said numbering is that of the EU index according to Kabat.

[00154] In a specific embodiment, the variant Fc Region comprises:

(A) at least one substitution selected from the group consisting of F243L, R292P, Y300L, V305I, and P396L;

(B) at least two substitutions selected from the group consisting of:

(1) F243L and P396L;

(2) F243L and R292P; and

(3) R292P and V305I;

(C) at least three substitutions selected from the group consisting of:

(1) F243L, R292P and Y300L;

(2) F243L, R292P and V305I;

(3) F243L, R292P and P396L; and

(4) R292P, V305I and P396L;

(D) at least four substitutions selected from the group consisting of:

(1) F243L, R292P, Y300L and P396L; and

(2) F243L, R292P, V305I and P396L; or

(E) at least the five substitutions selected from the group consisting of:

(1) F243L, R292P, Y300L, V305I and P396L; and

(2) L235V, F243L, R292P, Y300L and P396L.

[00155] In another specific embodiment, the variant Fc Region comprises substitutions of:

(A) F243L, R292P, and Y300L;

(B) L235V, F243L, R292P, Y300L, and P396L; or

(C) F243L, R292P, Y300L, V305I, and P396L.

[00156] In one embodiment, a LAG-3-binding molecule of the invention comprises a variant Fc Region that exhibits decreased (or substantially no) binding to FcγRIA (CD64), FcγRIIA (CD32A), FcγRIIB (CD32B), FcγRIIIA (CD16a) or FcγRIIIB (CD16b) (relative to the binding exhibited by the wild-type IgG1 Fc Region (**SEQ ID NO:1**)). In one embodiment, a LAG-3-binding molecule of the invention will comprise a variant Fc Region that exhibits reduced (or substantially no) binding to an FcγR (*e.g.*, FcγRIIIA) and reduced (or substantially no) ADCC effector function. In certain embodiments, the variant Fc Region comprises at least one substitution selected from the group consisting of L234A, L235A, D265A, N297Q, and N297G. In a specific embodiment, the variant Fc Region comprises the substitution of L234A; L235A; L234A and L235A; D265A; N297Q, or N297G.

[00157] In a different embodiment, a LAG-3-binding molecule of the invention comprises an Fc Region which inherently exhibits decreased (or substantially no) binding to FcγRIIIA (CD16a) and/or reduced effector function (relative to the binding exhibited by the wild-type IgG1 Fc Region (**SEQ ID NO:1**)). In a specific embodiment, a LAG-3-binding molecule of the present invention comprises an IgG2

Fc Region (**SEQ ID NO:2**) or an IgG4 Fc Region (**SEQ ID:NO:4**). When an IgG4 Fc Region in utilized, the instant invention also encompasses the introduction of a stabilizing mutation, such the IgG4 hinge region S228P substitution (see, *e.g.*, **SEQ ID NO:117:** ESKYGPPCPPCP, (Lu *et al.*, (2008) "*The Effect Of A Point Mutation On The Stability Of Igg4 As Monitored By Analytical Ultracentrifugation*," J. Pharmaceutical Sciences 97:960-969) to reduce the incidence of strand exchange. Other stabilizing mutations known in the art may be introduced into an IgG4 Fc Region (Peters, P *et al.*, (2012) "*Engineering an Improved IgG4 Molecule with Reduced Disulfide Bond Heterogeneity and Increased Fab Domain Thermal Stability*," J. Biol. Chem., 287:24525-24533; PCT Patent Publication No: WO 2008/145142).

[00158] In other embodiments, the invention encompasses the use of any Fc variant known in the art, such as those disclosed in Jefferis, B.J. *et al.* (2002) "*Interaction Sites On Human IgG*-Fc *For FcgammaR: Current Models*," Immunol. Lett. 82:57-65; Presta, L.G. *et al.* (2002) "*Engineering Therapeutic Antibodies For Improved Function*," Biochem. Soc. Trans. 30:487-90; Idusogie, E.E. *et al.* (2001) "*Engineered Antibodies With Increased Activity To Recruit Complement*," J. Immunol. 166:2571-75; Shields, R.L. *et al.* (2001) "*High Resolution Mapping Of The Binding Site On Human IgG1 For Fc Gamma RI, Fc Gamma RII, Fc Gamma RIII, And FcRn And Design Of IgG1 Variants With Improved Binding To The Fc gamma R*," J. Biol. Chem. 276:6591-6604; Idusogie, E.E. *et al.* (2000) "*Mapping Of The C1q Binding Site On Rituxan, A Chimeric Antibody With A Human IgG Fc*," J. Immunol. 164:4178-84; Reddy, M.P. *et al.* (2000) "*Elimination Of Fc Receptor-Dependent Effector Functions Of A Modified IgG4 Monoclonal Antibody To Human CD4*," J. Immunol. 164:1925-1933; Xu, D. *et al.* (2000) "*In Vitro Characterization of Five Humanized OKT3 Effector Function Variant Antibodies*," Cell. Immunol. 200:16-26; Armour, K.L. *et al.* (1999) "*Recombinant human IgG Molecules Lacking Fcgamma Receptor I Binding And Monocyte Triggering Activities*," Eur. J. Immunol. 29:2613-24; Jefferis, R. *et al.* (1996) "*Modulation Of Fc(Gamma)R And Human Complement Activation By IgG3-Core Oligosaccharide Interactions*," Immunol. Lett. 54:101-04; Lund, J. *et al.* (1996) "*Multiple Interactions Of IgG With Its Core Oligosaccharide Can Modulate Recognition By Complement And Human Fc Gamma Receptor I And Influence The Synthesis Of Its Oligosaccharide Chains*," J. Immunol. 157:4963-4969; Hutchins *et al.*

(1995) "*Improved Biodistribution, Tumor Targeting, And Reduced Immunogenicity In Mice With A Gamma 4 Variant Of Campath-1H*," Proc. Natl. Acad. Sci. (U.S.A.) 92:11980-84; Jefferis, R. *et al.* (1995) "*Recognition Sites On Human IgG For Fc Gamma Receptors: The Role Of Glycosylation*," Immunol. Lett. 44:111-17; Lund, J. *et al.* (1995) "*Oligosaccharide-Protein Interactions In IgG Can Modulate Recognition By Fc Gamma Receptors*," FASEB J. 9:115-19; Alegre, M.L. *et al.* (1994) "*A Non-Activating "Humanized" Anti-CD3 Monoclonal Antibody Retains Immunosuppressive Properties In Vivo*," Transplantation 57:1537-1543; Lund *et al.* (1992) "*Multiple Binding Sites On The CH2 Domain Of IgG For Mouse Fc Gamma R11*," Mol. Immunol. 29:53-59; Lund *et al.* (1991) "*Human Fc Gamma RI And Fc Gamma RII Interact With Distinct But Overlapping Sites On Human IgG*," J. Immunol. 147:2657-2662; Duncan, A.R. *et al.* (1988) "*Localization Of The Binding Site For The Human High-Affinity Fc Receptor On IgG*," Nature 332:563-564; US Patent Nos. 5,624,821; 5,885,573; 6,194,551; 7,276,586; and 7,317,091; and PCT Publications WO 00/42072 and PCT WO 99/58572.

[00159] In some embodiments, the molecules of the invention further comprise one or more glycosylation sites, so that one or more carbohydrate moieties are covalently attached to the molecule. Preferably, the molecules of the invention with one or more glycosylation sites and/or one or more modifications in the Fc Region confer or have an enhanced antibody mediated effector function, *e.g.*, enhanced ADCC activity, compared to the unmodified antibody. In some embodiments, the invention further comprises molecules comprising one or more modifications of amino acids that are directly or indirectly known to interact with a carbohydrate moiety of the Fc Region, including but not limited to amino acids at positions 241, 243, 244, 245, 245, 249, 256, 258, 260, 262, 264, 265, 296, 299, or 301. Amino acids that directly or indirectly interact with a carbohydrate moiety of an Fc Region are known in the art, *see*, *e.g.*, Jefferis *et al.*, 1995 *Immunology Letters*, 44: 111-7, which is incorporated herein by reference in its entirety.

[00160] In another embodiment, the invention encompasses molecules that have been modified by introducing one or more glycosylation sites into one or more sites of the molecules, preferably without altering the functionality of the molecules, *e.g.*,

binding activity to target antigen or FcγR. Glycosylation sites may be introduced into the variable and/or constant region of the molecules of the invention. As used herein, "glycosylation sites" include any specific amino acid sequence in an antibody to which an oligosaccharide (*i.e.*, carbohydrates containing two or more simple sugars linked together) will specifically and covalently attach. Oligosaccharide side chains are typically linked to the backbone of an antibody via either N-or O-linkages. N-linked glycosylation refers to the attachment of an oligosaccharide moiety to the side chain of an asparagine residue. O-linked glycosylation refers to the attachment of an oligosaccharide moiety to a hydroxyamino acid, *e.g.*, serine, threonine. The molecules of the invention may comprise one or more glycosylation sites, including N-linked and O-linked glycosylation sites. Any glycosylation site for N-linked or O-linked glycosylation known in the art may be used in accordance with the instant invention. An exemplary N-linked glycosylation site that is useful in accordance with the methods of the present invention is the amino acid sequence: Asn-X-Thr/Ser, wherein X may be any amino acid and Thr/Ser indicates a threonine or a serine. Such a site or sites may be introduced into a molecule of the invention using methods well known in the art to which this invention pertains (see for example, *IN VITRO* MUTAGENESIS, RECOMBINANT DNA: A SHORT COURSE, J. D. Watson, *et al.* W.H. Freeman and Company, New York, 1983, chapter 8, pp. 106-116, which is incorporated herein by reference in its entirety. An exemplary method for introducing a glycosylation site into a molecule of the invention may comprise: modifying or mutating an amino acid sequence of the molecule so that the desired Asn-X-Thr/Ser sequence is obtained.

[00161] In some embodiments, the invention encompasses methods of modifying the carbohydrate content of a molecule of the invention by adding or deleting a glycosylation site. Methods for modifying the carbohydrate content of antibodies (and molecules comprising antibody domains, *e.g.,* Fc Region) are well known in the art and encompassed within the invention, *see*, *e.g.*, U.S. Patent No. 6,218,149; EP 0 359 096 B1; U.S. Publication No. US 2002/0028486; WO 03/035835; U.S. Publication No. 2003/0115614; U.S. Patent No. 6,218,149; U.S. Patent No. 6,472,511; all of which are incorporated herein by reference in their entirety. In other embodiments, the invention encompasses methods of modifying the carbohydrate content of a molecule of the invention by deleting one or more endogenous carbohydrate moieties of the molecule.

In a specific embodiment, the invention encompasses shifting the glycosylation site of the Fc Region of an antibody, by modifying positions adjacent to 297. In a specific embodiment, the invention encompasses modifying position 296 so that position 296 and not position 297 is glycosylated.

[00162] Effector function can also be modified by techniques such as by introducing one or more cysteine residues into the Fc Region, thereby allowing interchain disulfide bond formation in this region to occur, resulting in the generation of a homodimeric antibody that may have improved internalization capability and/or increased complement-mediated cell killing and ADCC (Caron, P.C. *et al.* (1992) "*Engineered Humanized Dimeric Forms Of IgG Are More Effective Antibodies*," J. Exp. Med. 176:1191-1195; Shopes, B. (1992) "*A Genetically Engineered Human IgG Mutant With Enhanced Cytolytic Activity*," J. Immunol. 148(9):2918-2922. Homodimeric antibodies with enhanced antitumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff, E.A. *et al.* (1993) "*Monoclonal Antibody Homodimers: Enhanced Antitumor Activity In Nude Mice*," Cancer Research 53:2560-2565. Alternatively, an antibody can be engineered which has dual Fc Regions and may thereby have enhanced complement lysis and ADCC capabilities (Stevenson, G.T. *et al.* (1989) "*A Chimeric Antibody With Dual Fc Regions (bisFabFc) Prepared By Manipulations At The IgG Hinge*," Anti-Cancer Drug Design 3:219-230).

[00163] The serum half-life of the molecules of the present invention comprising Fc Regions may be increased by increasing the binding affinity of the Fc Region for FcRn. The term "half-life" as used herein means a pharmacokinetic property of a molecule that is a measure of the mean survival time of the molecules following their administration. Half-life can be expressed as the time required to eliminate fifty percent (50%) of a known quantity of the molecule from a subject's body (*e.g.*, human patient or other mammal) or a specific compartment thereof, for example, as measured in serum, *i.e.*, circulating half-life, or in other tissues. In general, an increase in half-life results in an increase in mean residence time (MRT) in circulation for the molecule administered.

[00164] In some embodiments, the LAG-3-binding molecules of the present invention comprise a variant Fc Region that comprises at least one amino acid modification relative to a wild-type Fc Region and that exhibit an increased half-life (relative to a wild-type Fc Region).

[00165] In some embodiments, the LAG-3-binding molecules of the present invention comprise a variant Fc Region that comprises a half-life-extending amino acid substitution at one or more positions selected from the group consisting of 238, 250, 252, 254, 256, 257, 256, 265, 272, 286, 288, 303, 305, 307, 308, 309, 311, 312, 317, 340, 356, 360, 362, 376, 378, 380, 382, 413, 424, 428, 433, 434, 435, and 436, as numbered by the EU index according to Kabat. Numerous specific mutations capable of increasing the half-life of an Fc Region-containing molecule are known in the art and include, for example M252Y, S254T, T256E, and combinations thereof. For example, see the mutations described in U.S. Patent Nos. 6,277,375, 7,083,784; 7,217,797, 8,088,376; U.S. Publication Nos. 2002/0147311; 2007/0148164; and International Publication Nos. WO 98/23289 WO 2009/058492, and WO 2010/033279, which are herein incorporated by reference in their entireties. Fc Region-containing molecules with enhanced half-life also include those with substitutions at two or more of Fc Region residues 250, 252, 254, 256, 257, 288, 307, 308, 309, 311, 378, 428, 433, 434, 435 and 436. In particular, two or more substitutions selected from: T250Q, M252Y, S254T, T256E, K288D, T307Q, V308P, A378V, M428L, N434A, H435K, and Y436I.

[00166] In a specific embodiment, the variant Fc Region comprises substitutions of:

(A) 252Y, 254T and 256E;
(B) M252Y and S254T;
(C) M252Y and T256E;
(D) 250Q and 428L;
(E) T307Q and N434A;
(F) A378V and N434A;
(G) N434A and Y436I;
(H) V308P and N434A; or

(I) K288D and H435K.

[00167] The instant invention further encompasses variant Fc Regions comprising:

(A) one or more mutations which alter effector function and/or FcγR; and

(B) one or more mutations which extend serum half-life.

VI. Bispecific LAG-3-Binding Molecules of the Present Invention

[00168] One embodiment of the present invention relates to bispecific binding molecules that are capable of binding to a "**first epitope**" and a "**second epitope**," wherein the first epitope is an epitope of human LAG-3 and the second epitope is the same or a different epitope of LAG-3, or is an epitope of another molecule that is present on the surface of an immune cell (such as a T lymphocyte) and is involved in regulating an immune checkpoint. In certain embodiments, the second epitope is preferably not an epitope of LAG-3. In one embodiment, the second epitope is an epitope of B7-H3, B7-H4, BTLA, CD3, CD8, CD16, CD27, CD32, CD40, CD40L, CD47, CD64, CD70, CD80, CD86, CD94, CD137, CD137L, CD226, CTLA-4, Galectin-9, GITR, GITRL, HHLA2, ICOS, ICOSL, KIR, LAG-3, LIGHT, MHC class I or II, NKG2a, NKG2d, OX40, OX40L, PD1H, PD-1, PD-L1, PD-L2, PVR, SIRPa, TCR, TIGIT, TIM-3 or VISTA. In a specific embodiment, the second epitope is CD137, PD-1, OX40, TIGIT, or TIM-3. In certain embodiments, such bispecific molecules comprise more than two epitope-binding sites. Such bispecific molecules may, for example, bind two or more different epitopes of LAG-3 and at least one epitope of a molecule that is not LAG-3.

[00169] The instant invention encompasses bispecific antibodies capable of simultaneously binding to LAG-3 and the second epitope (*e.g.* B7-H3, B7-H4, BTLA, CD40, CD80, CD86, CD137, CTLA-4, ICOS, KIR, MHC class I or II, OX40, PD-1, PD-L1, TCR, TIM-3, *etc.*). In some embodiments, the bispecific antibody capable of simultaneously binding to PD-1 and the second epitope is produced using any of the methods described in PCT Publication Nos. WO 1998/002463, WO 2005/070966, WO 2006/107786 WO 2007/024715, WO 2007/075270, WO 2006/107617, WO 2007/046893, WO 2007/146968, WO 2008/003103, WO 2008/003116, WO

2008/027236, WO 2008/024188, WO 2009/132876, WO 2009/018386, WO 2010/028797, WO2010028796, WO 2010/028795, WO 2010/108127, WO 2010/136172, WO 2011/086091, WO 2011/133886, WO 2012/009544, WO 2013/003652, WO 2013/070565, WO 2012/162583, WO 2012/156430, WO 2013/174873, and WO 2014/022540, each of which is hereby incorporated herein by reference in its entirety.

1. Bispecific Diabodies Lacking Fc Regions

[00170] One embodiment of the present invention relates to bispecific monovalent diabodies that comprise, and most preferably consist of, a first polypeptide chain and a second polypeptide chain, whose sequences permit the polypeptide chains to covalently bind to each other to form a covalently associated diabody that is capable of simultaneously binding to a first epitope ("**Epitope 1**") and a second epitope (**Epitope 2**"), such epitopes not being identical to one another. Such bispecific diabodies thus comprise "**VL1**" / "**VH1**" domains that are capable of binding to the first epitope ($\mathbf{VL_{Epitope\ 1}}$ / $\mathbf{VH_{Epitope\ 1}}$) and "**VL2**" / "**VH2**" domains that are capable of binding to the second epitope ($\mathbf{VL_{Epitope\ 2}}$ / $\mathbf{VH_{Epitope\ 2}}$). The notation "**VL1**" and "**VH1**" denote respectively, the Variable Light Chain Domain and Variable Heavy Chain Domain that bind the "first" epitope of such bispecific diabody. Similarly, the notation "**VL2**" and "**VH2**" denote respectively, the Variable Light Chain Domain and Variable Heavy Chain Domain that bind the "second" epitope of such bispecific diabody. In one embodiment, Epitope 1 of such diabody molecules is an epitope of LAG-3 and Epitope 2 of such diabody molecules is not an epitope of LAG-3 (for example, it is an epitope of B7-H3, B7-H4, BTLA, CD40, CD80, CD86, CD137, CTLA-4, ICOS, KIR, MHC class I or II, OX40, PD-1, PD-L1, TCR, TIM-3, *etc.*).

[00171] The VL Domain of the first polypeptide chain of such LAG-2 binding diabodies interacts with the VH Domain of the second polypeptide chain to form a first functional epitope-binding site that is specific for a first antigen (*i.e.*, either LAG-3 or an antigen that contains the second epitope). Likewise, the VL Domain of the second polypeptide chain interacts with the VH Domain of the first polypeptide chain in order to form a second functional epitope-binding site that is specific for a second antigen (*i.e.*, either an antigen that contains the second epitope or LAG-3). Thus, the selection

of the VL and VH Domains of the first and second polypeptide chains is coordinated, such that the two polypeptide chains of the diabody collectively comprise VL and VH Domains capable of binding to both an epitope of LAG-3 and to the second epitope (*i.e.*, they collectively comprise VL_{LAG-3}/VH_{LAG-3} and $VL_{Epitope\ 2}$/ $VH_{Epitope\ 2}$ Domains). It is irrelevant whether a particular pair of binding domains (*i.e.*, $\mathbf{VL_{Epitope\ 1}}$ / $\mathbf{VH_{Epitope\ 1}}$ or $\mathbf{VL_{Epitope\ 2}}$ / $\mathbf{VH_{Epitope\ 2}}$) an epitope of an antigen having Epitope 1 or an epitope of an antigen having Epitope 2) is designated as the first vs. the second epitope of the diabody; such notation having relevance only with respect to the presence and orientation of domains of the polypeptide chains of the binding molecules of the present invention

[00172] The first polypeptide chain of an embodiment of such bispecific monovalent diabodies comprises, in the N-terminal to C-terminal direction, an N-terminus, the VL Domain of a monoclonal antibody capable of binding to either the first epitope or the VL Domain of a monoclonal antibody capable of binding to the second epitope (*i.e.*, either VL_{LAG-3} or $VL_{Epitope\ 2}$), a first intervening spacer peptide (Linker 1), a VH Domain of a monoclonal antibody capable of binding to either the second epitope (if such first polypeptide chain contains VL_{LAG-3}) or a VH Domain of a monoclonal antibody capable of binding to the first epitope (if such first polypeptide chain contains $VL_{Epitope\ 2}$), a second intervening spacer peptide (Linker 2), optionally comprising a cysteine residue, a Heterodimer-Promoting Domain and a C-terminus (**Figure 1**).

[00173] The second polypeptide chain of this embodiment of bispecific monovalent diabodies comprises, in the N-terminal to C-terminal direction, an N-terminus, a VL Domain of a monoclonal antibody capable of binding to LAG-3 or a VL Domain of a monoclonal antibody capable of binding to the second epitope (*i.e.*, either VL_{LAG-3} or $VL_{Epitope\ 2}$, and being the VL Domain not selected for inclusion in the first polypeptide chain of the diabody), an intervening linker peptide (Linker 1), a VH Domain of a monoclonal antibody capable of binding to either the second epitope (if such second polypeptide chain contains VL_{LAG-3}) or a VH Domain of a monoclonal antibody capable of binding to LAG-3 (if such second polypeptide chain contains

$VL_{Epitope\ 2}$), a second intervening spacer peptide (Linker 2) optionally containing a cysteine residue, a Heterodimer-Promoting Domain, and a C-terminus (**Figure 1**).

[00174] Most preferably, the length of the intervening linker peptide (*e.g.*, Linker 1) that separates such VL and VH Domains) is selected to substantially or completely prevent the VL and VH Domains of the polypeptide chain from binding to one another. Thus the VL and VH Domains of the first polypeptide chain are substantially or completely incapable of binding to one another. Likewise, the VL and VH Domains of the second polypeptide chain are substantially or completely incapable of binding to one another. A preferred intervening spacer peptide (Linker 1) has the sequence (**SEQ ID NO:88**): GGGSGGGG.

[00175] The length and composition of the second intervening linker peptide (Linker 2) is selected based on the choice of heterodimer-promoting domains. Typically, the second intervening linker peptide (Linker 2) will comprise 3-20 amino acid residues. In particular, where the heterodimer-promoting domains do not comprise a cysteine residue a cysteine-containing second intervening linker peptide (Linker 2) is utilized. The cysteine-containing second intervening spacer peptide (Linker 2) will contain 1, 2, 3 or more than 3 cysteine residue(s). A preferred cysteine-containing spacer peptide (Linker 2) has the sequence is **SEQ ID NO:89**: GGCGGG. Alternatively, Linker 2 does not comprise a cysteine (*e.g.*, GGG, GGGS (**SEQ ID NO:90**), LGGGSG (**SEQ ID NO:91**), GGGSGGGSGGG (**SEQ ID NO:92**), ASTKG (**SEQ ID NO:93**), LEPKSS (**SEQ ID NO:94**), APSSS (**SEQ ID NO:95**), *etc.*) and a Cysteine-Containing Heterodimer-Promoting Domain, as described below is used. Optionally, both a cysteine-containing Linker 2 and a cysteine-containing Heterodimer-Promoting Domain are used.

[00176] The Heterodimer-Promoting Domains may be GVEPKSC (**SEQ ID NO:96**) or VEPKSC (**SEQ ID NO:97**) or AEPKSC (**SEQ ID NO:98**) on one polypeptide chain and GFNRGEC (**SEQ ID NO:99**) or FNRGEC (**SEQ ID NO:100**) on the other polypeptide chain (US2007/0004909).

[00177] More preferably, however, the Heterodimer-Promoting Domains of such diabodies are formed from one, two, three or four tandemly repeated coil domains of opposing charge that comprise a sequence of at least six, at least seven or at least eight amino acid residues such that the Heterodimer-Promoting Domain possesses a net charge (Apostolovic, B. *et al.* (2008) "*pH-Sensitivity of the E3/K3 Heterodimeric Coiled Coil*," Biomacromolecules 9:3173–3180; Arndt, K.M. *et al.* (2001) "*Helix-stabilized Fv (hsFv) Antibody Fragments: Substituting the Constant Domains of a Fab Fragment for a Heterodimeric Coiled-coil Domain*," J. Molec. Biol. 312:221-228; Arndt, K.M. *et al.* (2002) "*Comparison of In Vivo Selection and Rational Design of Heterodimeric Coiled Coils*," Structure 10:1235-1248; Boucher, C. *et al.* (2010) "*Protein Detection By Western Blot Via Coiled–Coil Interactions*," Analytical Biochemistry 399:138-140; Cachia, P.J. *et al.* (2004) "*Synthetic Peptide Vaccine Development: Measurement Of Polyclonal Antibody Affinity And Cross-Reactivity Using A New Peptide Capture And Release System For Surface Plasmon Resonance Spectroscopy*," J. Mol. Recognit. 17:540-557; De Crescenzo, G.D. *et al.* (2003) "*Real-Time Monitoring of the Interactions of Two-Stranded de novo Designed Coiled-Coils: Effect of Chain Length on the Kinetic and Thermodynamic Constants of Binding*," Biochemistry 42:1754-1763; Fernandez-Rodriquez, J. *et al.* (2012) "*Induced Heterodimerization And Purification Of Two Target Proteins By A Synthetic Coiled-Coil Tag*," Protein Science 21:511-519; Ghosh, T.S. *et al.* (2009) "*End-To-End And End-To-Middle Interhelical Interactions: New Classes Of Interacting Helix Pairs In Protein Structures*," Acta Crystallographica D65:1032-1041; Grigoryan, G. *et al.* (2008) "*Structural Specificity In Coiled-Coil Interactions*," Curr. Opin. Struc. Biol. 18:477-483; Litowski, J.R. *et al.* (2002) "*Designing Heterodimeric Two-Stranded α-Helical Coiled-Coils: The Effects Of Hydrophobicity And α-Helical Propensity On Protein Folding, Stability, And Specificity*," J. Biol. Chem. 277:37272-37279; Steinkruger, J.D. *et al.* (2012) "*The d'--d--d' Vertical Triad is Less Discriminating Than the a'--a--a' Vertical Triad in the Antiparallel Coiled-coil Dimer Motif*," J. Amer. Chem. Soc. 134(5):2626–2633; Straussman, R. *et al.* (2007) "*Kinking the Coiled Coil – Negatively Charged Residues at the Coiled-coil Interface*," J. Molec. Biol. 366:1232-1242; Tripet, B. *et al.* (2002) "*Kinetic Analysis of the Interactions between Troponin C and the C-terminal Troponin I Regulatory Region and Validation of a New Peptide*

Delivery/Capture System used for Surface Plasmon Resonance," J. Molec. Biol. 323:345–362; Woolfson, D.N. (2005) "*The Design Of Coiled-Coil Structures And Assemblies*," Adv. Prot. Chem. 70:79-112; Zeng, Y. *et al.* (2008) "*A Ligand-Pseudoreceptor System Based On de novo Designed Peptides For The Generation Of Adenoviral Vectors With Altered Tropism*," J. Gene Med. 10:355-367).

[00178] Such repeated coil domains may be exact repeats or may have substitutions. For example, the coil domain of the Heterodimer-Promoting Domain of the first polypeptide chain may comprise a sequence of eight amino acid residues selected to confer a negative charge to such Heterodimer-Promoting Domain, and the coil domain of the Heterodimer-Promoting Domain of the second polypeptide chain may comprise a sequence of eight amino acid residues selected to confer a positive charge to such Heterodimer-Promoting Domain. It is immaterial which coil is provided to the first or second polypeptide chains, provided that, when both polypeptide chains are provided with such Heterodimer-Promoting Domains, a coil of opposite charge is used for the other polypeptide chain. The positively charged amino acid may be lysine, arginine, histidine, *etc.* and/or the negatively charged amino acid may be glutamic acid, aspartic acid, *etc.* The positively charged amino acid is preferably lysine and/or the negatively charged amino acid is preferably glutamic acid. It is possible for only a single Heterodimer-Promoting Domain to be employed (since such domain will inhibit homodimerization and thereby promote heterodimerization), however, it is preferred for both the first and second polypeptide chains of the diabodies of the present invention to contain Heterodimer-Promoting Domains.

[00179] In a preferred embodiment, one of the Heterodimer-Promoting Domains will comprise four tandem "E-coil" helical domains (**SEQ ID NO:101**: EVAALEK-EVAALEK-EVAALEK-EVAALEK), whose glutamate residues will form a negative charge at pH 7, while the other of the Heterodimer-Promoting Domains will comprise four tandem "K-coil" helical domains (**SEQ ID NO:102**: KVAALKE-KVAALKE-KVAALKE-KVAALKE), whose lysine residues will form a positive charge at pH 7. The presence of such charged domains promotes association between the first and second polypeptides, and thus fosters heterodimer formation. Especially preferred is a Heterodimer-Promoting Domain in which one of the four tandem "E-coil" helical

domains of **SEQ ID NO:101** has been modified to contain a cysteine residue: EVAACEK-EVAALEK-EVAALEK-EVAALEK (**SEQ ID NO:103**). Likewise, especially preferred is a Heterodimer-Promoting Domain in which one of the four tandem "K-coil" helical domains of **SEQ ID NO:102** has been modified to contain a cysteine residue: KVAACKE-KVAALKE-KVAALKE-KVAALKE (**SEQ ID NO:104**).

[00180] As disclosed in WO 2012/018687, in order to improve the *in vivo* pharmacokinetic properties of diabodies, a diabody may be modified to contain a polypeptide portion of a serum-binding protein at one or more of the termini of the diabody. Most preferably, such polypeptide portion of a serum-binding protein will be installed at the C-terminus of the diabody. Albumin is the most abundant protein in plasma and has a half-life of 19 days in humans. Albumin possesses several small molecule binding sites that permit it to non-covalently bind to other proteins and thereby extend their serum half-lives. The Albumin-Binding Domain 3 (ABD3) of protein G of Streptococcus strain G148 consists of 46 amino acid residues forming a stable three-helix bundle and has broad albumin-binding specificity (Johansson, M.U. *et al.* (2002) "*Structure, Specificity, And Mode Of Interaction For Bacterial Albumin-Binding Module*s," J. Biol. Chem. 277(10):8114-8120. Thus, a particularly preferred polypeptide portion of a serum-binding protein for improving the *in vivo* pharmacokinetic properties of a diabody is the Albumin-Binding Domain (ABD) from streptococcal protein G, and more preferably, the Albumin-Binding Domain 3 (ABD3) of protein G of Streptococcus strain G148 (**SEQ ID NO:105**): LAEAKVLANR ELDKYGVSDY YKNLIDNAKS AEGVKALIDE ILAALP.

[00181] As disclosed in WO 2012/162068 (herein incorporated by reference), "**deimmunized**" variants of **SEQ ID NO:105** have the ability to attenuate or eliminate MHC class II binding. Based on combinational mutation results, the following combinations of substitutions are considered to be preferred substitutions for forming such a deimmunized ABD: 66D/70S +71A; 66S/70S +71A; 66S/70S +79A; 64A/65A/71A; 64A/65A/71A+66S; 64A/65A/71A+66D; 64A/65A/71A+66E; 64A/65A/79A+66S; 64A/65A/79A+66D; 64A/65A/79A+66E. Variant ABDs having the modifications L64A, I65A and D79A or the modifications N66S, T70S and D79A. Variant deimmunized ABD having the amino acid sequence:

LAEAKVLANR ELDKYGVSDY YKNLI**D**$_{66}$NAK**S**$_{70}$ **A**$_{71}$EGVKALIDE ILAALP **(SEQ ID NO:106)**,

or the amino acid sequence:

LAEAKVLANR ELDKYGVSDY YKN**A**$_{64}$**A**$_{65}$NNAKT VEGVKALI**A**$_{79}$E ILAALP **(SEQ ID NO:107)**,

or the amino acid sequence:

LAEAKVLANR ELDKYGVSDY YKNLI**S**$_{66}$NAK**S**$_{70}$ VEGVKALI**A**$_{79}$E ILAALP **(SEQ ID NO:108)**,

are particularly preferred as such deimmunized ABD exhibit substantially wild-type binding while providing attenuated MHC class II binding. Thus, the first polypeptide chain of such a diabody having an ABD contains a third linker (Linker 3) preferably positioned C-terminally to the E-coil (or K-coil) Domain of such polypeptide chain so as to intervene between the E-coil (or K-coil) Domain and the ABD (which is preferably a deimmunized ABD). A preferred sequence for such Linker 3 is **SEQ ID NO:90**: GGGS.

2. Bispecific Diabodies Containing Fc Regions

[00182] One embodiment of the present invention relates to bispecific diabodies comprising an Fc Region capable of simultaneously binding to LAG-3 and a second epitope (*e.g.* B7-H3, B7-H4, BTLA, CD40, CD80, CD86, CD137, CTLA-4, ICOS, KIR, MHC class I or II, OX40, PD-1, PD-L1, TCR, TIM-3, *etc.*). The addition of an IgG CH2-CH3 Domain to one or both of the diabody polypeptide chains, such that the complexing of the diabody chains results in the formation of an Fc Region, increases the biological half-life and/or alters the valency of the diabody. Incorporating an IgG CH2-CH3 Domain onto both of the diabody polypeptides will permit a two-chain bispecific Fc-Region-containing diabody to form (**Figure 2**).

[00183] Alternatively, incorporating an IgG CH2-CH3 Domain onto only one of the diabody polypeptides will permit a more complex four-chain bispecific Fc Region-containing diabody to form (**Figures 3A-3C**). **Figure 3C** shows a representative four-chain diabody possessing the Constant Light (CL) Domain and the Constant Heavy CH1 Domain, however fragments of such domains as well as other polypeptides may

alternatively be employed (see, *e.g.*, **Figures 3A and 3B**, United States Patent Publications No. 2013-0295121; 2010-0174053 and 2009-0060910; European Patent Publication No. EP 2714079; EP 2601216; EP 2376109; EP 2158221 and PCT Publications No. WO 2012/162068; WO 2012/018687; WO 2010/080538). Thus, for example, in lieu of the CH1 Domain, one may employ a peptide having the amino acid sequence GVEPKSC (**SEQ ID NO:96**) VEPKSC (**SEQ ID NO:97**), or AEPKSC (**SEQ ID NO:98**), derived from the hinge domain of a human IgG, and in lieu of the CL Domain, one may employ the C-terminal 6 amino acids of the human kappa light chain, GFNRGEC (**SEQ ID NO:99**) or FNRGEC (**SEQ ID NO:100**). A representative peptide containing four-chain diabody is shown in **Figure 3A**. Alternatively, or in addition, one may employ a peptide comprising tandem coil domains of opposing charge such as the "E-coil" helical domains (**SEQ ID NO:101**: EVAALEK-EVAALEK-EVAALEK-EVAALEK or **SEQ ID NO:103:** EVAACEK-EVAALEK-EVAALEK-EVAALEK); and the "K-coil" domains (**SEQ ID NO:102**: KVAALKE-KVAALKE-KVAALKE-KVAALKE or **SEQ ID NO:104:** KVAACKE-KVAALKE-KVAALKE-KVAALKE). A representative coil domain containing four-chain diabody is shown in **Figure 3B**.

[00184] The Fc Region-containing diabody molecules of the present invention generally include additional intervening linker peptides (Linkers). Typically, the additional Linkers will comprise 3-20 amino acid residues. Additional or alternative linkers that may be employed in the Fc Region-containing diabody molecules of the present invention include: GGGS (**SEQ ID NO:90**), LGGGSG (**SEQ ID NO:91**), GGGSGGGSGGG (**SEQ ID NO:92**), ASTKG (**SEQ ID NO:93**), DKTHTCPPCP (**SEQ ID NO:109**), LEPKSS (**SEQ ID NO:94**), APSSS (**SEQ ID NO:95**), and APSSSPME (**SEQ ID NO:110**), LEPKSADKTHTCPPC (**SEQ ID NO:111**), GGC, and GGG. **SEQ ID NO:94** may be used in lieu of GGG or GGC for ease of cloning. Additionally, the amino acid GGG, or **SEQ ID NO:94** may be immediately followed by **SEQ ID NO:109** to form the alternate linkers: GGGDKTHTCPPCP (**SEQ ID NO:112**); and LEPKSSDKTHTCPPCP; (**SEQ ID NO:113**). Fc Region-containing diabody molecule of the present invention may incorporate an IgG hinge region in addition to or in place of a linker. Exemplary hinge regions include: EPKSCDKTHTCPPCP (**SEQ ID NO:114**) from IgG1, ERKCCVECPPCP (**SEQ ID NO:115**) from IgG2,

ESKYGPPCPSCP (**SEQ ID NO:116**) from IgG4, and ESKYGPPCPPCP (**SEQ ID NO:117**) an IgG4 hinge variant comprising a stabilizing substitute to reduce strand exchange.

[00185] As provided in **Figure 3A-3C**, diabodies of the invention may comprise four different chains. The first and third polypeptide chains of such a diabody contain three domains: (i) a VL1-containing Domain, (ii) a VH2-containing Domain, (iii) Heterodimer-Promoting Domain and (iv) a Domain containing a CH2-CH3 sequence. The second and fourth polypeptide chains contain: (i) a VL2-containing Domain, (ii) a VH1-containing Domain and (iii) a Heterodimer-Promoting Domain, where the Heterodimer-Promoting Domains promote the dimerization of the first/third polypeptide chains with the second/fourth polypeptide chains. The VL and/or VH Domains of the third and fourth polypeptide chains, and VL and/or VH Domains of the first and second polypeptide chains may be the same or different so as to permit tetravalent binding that is either monospecific, bispecific or tetraspecific. The notation "**VL3**" and "**VH3**" denote respectively, the Variable Light Chain Domain and Variable Heavy Chain Domain that bind the "third" epitope of such diabody ("**Epitope 3**"). Similarly, the notation "**VL4**" and "**VH4**" denote respectively, the Variable Light Chain Domain and Variable Heavy Chain Domain that bind the "fourth" epitope of such diabody ("**Epitope 4**"). The general structure of the polypeptide chains of a representative four-chain Fc Region-containing diabodies of invention is provided in **Table 2**:

Table 2

Bispecific	2nd Chain	NH_2-VL2-VH1-HPD-COOH
	1st Chain	NH_2-VL1-VH2-HPD-CH2-CH3-COOH
	1st Chain	NH_2-VL1-VH2-HPD-CH2-CH3-COOH
	2nd Chain	NH_2-VL2-VH1-HPD-COOH
Tetraspecific	2nd Chain	NH_2-VL2-VH1-HPD-COOH
	1st Chain	NH_2-VL1-VH2-HPD-CH2-CH3-COOH
	3rd Chain	NH_2-VL3-VH4-HPD-CH2-CH3-COOH
	4th Chain	NH_2-VL4-VH3-HPD-COOH

HPD = Heterodimer-Promoting Domain

[00186] In a specific embodiment, diabodies of the present invention are bispecific, tetravalent (*i.e.*, possess four epitope-binding sites), Fc-containing diabodies (**Figures 3A-3C**) that are composed of four total polypeptide chains. The bispecific, tetravalent, Fc-containing diabodies of the invention comprise two epitope-binding sites immunospecific for LAG-3 (which may be capable of binding to the same epitope of LAG-3 or to different epitopes of LAG-3), and two epitope-binding sites specific for a second epitope (*e.g.*, B7-H3, B7-H4, BTLA, CD40, CD80, CD86, CD137, CTLA-4, ICOS, KIR, MHC class I or II, OX40, PD-1, PD-L1, TCR, TIM-3, *etc.*).

[00187] In a further embodiment, the bispecific Fc Region-containing diabodies may comprise three polypeptide chains. The first polypeptide of such a diabody contains three domains: (i) a VL1-containing Domain, (ii) a VH2-containing Domain and (iii) a Domain containing a CH2-CH3 sequence. The second polypeptide of such diabodies contains: (i) a VL2-containing Domain, (ii) a VH1-containing Domain and (iii) a Domain that promotes heterodimerization and covalent bonding with the diabody's first polypeptide chain. The third polypeptide of such diabodies comprises a CH2-CH3 sequence. Thus, the first and second polypeptide chains of such diabodies associate together to form a VL1/VH1 binding site that is capable of binding to the first epitope, as well as a VL2/VH2 binding site that is capable of binding to the second epitope. The first and second polypeptides are bonded to one another through a disulfide bond involving cysteine residues in their respective Third Domains. Notably, the first and third polypeptide chains complex with one another to form an Fc Region that is stabilized via a disulfide bond. Such diabodies have enhanced potency. **Figures 4A** and **4B** illustrate the structures of such diabodies. Such Fc-Region-containing bispecific diabodies may have either of two orientations (**Table 3**):

Table 3		
First Orientation	3rd Chain	NH_2-CH2-CH3-COOH
	1st Chain	NH_2-VL1-VH2-HPD-CH2-CH3-COOH
	2nd Chain	NH_2-VL2-VH1-HPD-COOH
Second Orientation	3rd Chain	NH_2-CH2-CH3-COOH
	1st Chain	NH_2-CH2-CH3-VL1-VH2-HPD-COOH
	2nd Chain	NH_2-VL2-VH1-HPD-COOH

HPD = Heterodimer-Promoting Domain

[00188] In a specific embodiment, diabodies of the present invention are bispecific, bivalent (*i.e.*, possess two epitope-binding sites), Fc-containing diabodies (**Figures 4A-4B**) that are composed of three total polypeptide chains. The bispecific, bivalent Fc-containing diabodies of the invention comprise one epitope-binding site immunospecific for LAG-3, and one epitope-binding site specific for a second epitope (*e.g.*, B7-H3, B7-H4, BTLA, CD40, CD80, CD86, CD137, CTLA-4, ICOS, KIR, LAG-3 MHC class I or II, OX40, PD-L1, TCR, TIM-3, *etc.*).

[00189] In a further embodiment, the bispecific Fc Region-containing diabodies may comprise a total of five polypeptide chains. In a particular embodiment, two of said five polypeptide chains have the same amino acid sequence. The first polypeptide chain of such diabodies contains: (i) a VH1-containing domain, (ii) a CH1-containing domain, and (iii) a Domain containing a CH2-CH3 sequence. The first polypeptide chain may be the heavy chain of an antibody that contains a VH1 and a heavy chain constant region. The second and fifth polypeptide chains of such diabodies contain: (i) a VL1-containing domain, and (ii) a CL-containing domain. The second and/or fifth polypeptide chains of such diabodies may be light chains of an antibody that contains a VL1 complementary to the VH1 of the first/third polypeptide chain. The first, second and/or fifth polypeptide chains may be isolated from naturally occurring antibodies. Alternatively, they may be constructed recombinantly. The third polypeptide chain of such diabodies contains: (i) a VH1-containing domain, (ii) a CH1-containing domain, (iii) a Domain containing a CH2-CH3 sequence, (iv) a VL2-containing Domain, (v) a VH3-containing Domain and (vi) a Heterodimer-Promoting Domain, where the

Heterodimer-Promoting Domains promote the dimerization of the third chain with the fourth chain. The fourth polypeptide of such diabodies contains: (i) a VL3-containing Domain, (ii) a VH2-containing Domain and (iii) a Domain that promotes heterodimerization and covalent bonding with the diabody's third polypeptide chain.

[00190] Thus, the first and second, and the third and fifth, polypeptide chains of such diabodies associate together to form two VL1/VH1 binding sites capable of binding a first epitope. The third and fourth polypeptide chains of such diabodies associate together to form a VL2/VH2 binding site that is capable of binding to a second epitope, as well as a VL3/VH3 binding site that is capable of binding to a third epitope. The first and third polypeptides are bonded to one another through a disulfide bond involving cysteine residues in their respective constant regions. Notably, the first and third polypeptide chains complex with one another to form an Fc Region. Such diabodies have enhanced potency. **Figure 5** illustrates the structure of such diabodies. It will be understood that the VL1/VH1, VL2/VH2, and VL3/VH3 Domains may be the same or different so as to permit binding that is monospecific, bispecific or trispecific. However, as provided herein, these domains are preferably selected so as to bind LAG-3 and a second epitope (or a second and a third epitope (*e.g.*, B7-H3, B7-H4, BTLA, CD40, CD80, CD86, CD137, CTLA-4, ICOS, KIR, LAG-3 MHC class I or II, OX40, PD-L1, TCR, TIM-3, *etc.*). The second and third epitope may be different epitopes of the same antigen molecule, or may be epitopes of different antigen molecules. Such aspects of the invention are discussed in detail below.

[00191] Thus, the VL and VH Domains of the polypeptide chains are selected so as to form VL/VH binding sites specific for the desired epitopes. The VL/VH binding sites formed by the association of the polypeptide chains may be the same or different so as to permit tetravalent binding that is monospecific, bispecific, trispecific or tetraspecific. In particular, the VL and VH Domains maybe selected such that a bispecific diabody may comprise two binding sites for a first epitope and two binding sites for a second epitope, or three binding sites for a first epitope and one binding site for a second epitope, or two binding sites for a first epitope, one binding site for a second epitope and one binding site for a third epitope (as depicted in **Figure 5**). The

general structure of the polypeptide chains of representative five-chain Fc Region-containing diabodies of invention is provided in **Table 4**:

Table 4

Bispecific (2x2)	2nd Chain	NH_2-VL1-CL-COOH
	1st Chain	NH_2-VH1-CH1-CH2-CH3-COOH
	3rd Chain	NH_2-VH1-CH1-CH2-CH3-VL2-VH2-HPD-COOH
	5nd Chain	NH_2-VL1-CL-COOH
	4th Chain	NH_2-VL2-VH2-HPD-COOH
Bispecific (3x1)	2nd Chain	NH_2-VL1-CL-COOH
	1st Chain	NH_2-VH1-CH1-CH2-CH3-COOH
	3rd Chain	NH_2-VH1-CH1-CH2-CH3-VL1-VH2-HPD-COOH
	5nd Chain	NH_2-VL1-CL-COOH
	4th Chain	NH_2-VL2-VH1-HPD-COOH
Trispecific (2x1x1)	2nd Chain	NH_2-VL1-CL-COOH
	1st Chain	NH_2-VH1-CH1-CH2-CH3-COOH
	3rd Chain	NH_2-VH1-CH1-CH2-CH3-VL2-VH3-HPD-COOH
	5nd Chain	NH_2-VL1-CL-COOH
	4th Chain	NH_2-VL3-VH2-HPD-COOH

HPD = Heterodimer-Promoting Domain

[00192] In a specific embodiment, diabodies of the present invention are bispecific, tetravalent (*i.e.*, possess four epitope-binding sites), Fc-containing diabodies that are composed of five total polypeptide chains having two binding sites for a first epitope and two binding sites for a second epitope. In one embodiment, the bispecific, tetravalent, Fc-containing diabodies of the invention comprise two epitope-binding sites immunospecific for LAG-3 (which may be capable of binding to the same epitope of LAG-3 or to different epitopes of LAG-3), and two epitope-binding sites specific for a second epitope (*e.g.*, B7-H3, B7-H4, BTLA, CD40, CD80, CD86, CD137, CTLA-4, ICOS, KIR, LAG-3 MHC class I or II, OX40, PD-L1, TCR, TIM-3, *etc.*). In another embodiment, the bispecific, tetravalent, Fc-containing diabodies of the invention comprise three epitope-binding sites immunospecific for LAG-3 (which may be capable of binding to the same epitope of LAG-3 or to different epitopes of LAG-3), and one epitope-binding sites specific for a second epitope (*e.g.*, B7-H3, B7-H4, BTLA,

CD40, CD80, CD86, CD137, CTLA-4, ICOS, KIR, LAG-3 MHC class I or II, OX40, PD-L1, TCR, TIM-3, *etc.*). In another embodiment, the bispecific, tetravalent, Fc-containing diabodies of the invention comprise one epitope-binding sites immunospecific for LAG-3, and three epitope-binding sites specific for a second epitope (*e.g.*, B7-H3, B7-H4, BTLA, CD40, CD80, CD86, CD137, CTLA-4, ICOS, KIR, LAG-3 MHC class I or II, OX40, PD-L1, TCR, TIM-3, *etc.*).

3. Bispecific Trivalent Binding Molecules Containing Fc Regions

[00193] A further embodiment of the present invention relates to bispecific, trivalent binding molecules, comprising an Fc Region, and being capable of simultaneously binding to a first epitope, a second epitope and a third epitope, wherein at least one of such epitopes is not identical to another of such epitopes. Such bispecific diabodies thus comprise "**VL1**" / "**VH1**" domains that are capable of binding to the first epitope, "**VL2**" / "**VH2**" domains that are capable of binding to the second epitope and "**VL3**" / "**VH3**" domains that are capable of binding to the third epitope. In one embodiment, one or two of such epitopes is an epitope of LAG-3 and another (or the other) of such epitopes is not an epitope of LAG-3 (for example, an epitope of B7-H3, B7-H4, BTLA, CD40, CD80, CD86, CD137, CTLA-4, ICOS, KIR, LAG-3, MHC class I or II, OX40, PD-1, PD-L1, TCR, TIM-3, etc.). Such bispecific trivalent binding molecules comprise three epitope-binding sites, two of which are diabody-type binding domains, which provide binding Site A and binding Site B, and one of which is a non-diabody-type binding domain, which provides binding Site C (see, *e.g.*, **Figures 6A-6F**, and PCT Application No: PCT/US15/33081; and PCT/US15/33076).

[00194] Typically, the trivalent binding molecules of the present invention will comprise four different polypeptide chains (see **Figures 6A-6B**), however, the molecules may comprise fewer or greater numbers of polypeptide chains, for example, by fusing such polypeptide chains to one another (*e.g.*, via a peptide bond) or by "dividing" such polypeptide chains to form additional polypeptide chains, or by associating fewer or additional polypeptide chains via disulfide bonds. **Figures 6B-6F** illustrate this aspect of the present invention by schematically depicting such molecules having three polypeptide chains. As provided in **Figures 6A-6F**, the trivalent binding

molecules of the present invention may have alternative orientations in which the diabody-type binding domains are N-terminal (**Figures 6A**, **6C** and **6D**) or C-terminal (**Figures 6B**, **6E** and **6F**) to an Fc Region.

[00195] In certain embodiments, the first polypeptide chain of such trivalent binding molecules of the present invention contains: (i) a VL1-containing Domain, (ii) a VH2-containing Domain, (iii) a Heterodimer-Promoting Domain, and (iv) a Domain containing a CH2-CH3 sequence. The VL1 and VL2 Domains are located N-terminal or C-terminal to the CH2-CH3-containing domain as presented in **Table 5** (**Figures 6A** and **6B**). The second polypeptide chain of such embodiments contains: (i) a VL2-containing Domain, (ii) a VH1-containing Domain, and (iii) a Heterodimer-Promoting Domain. The third polypeptide chain of such embodiments contains: (i) a VH3-containing Domain, (ii) a CH1-containing Domain and (iii) a Domain containing a CH2-CH3 sequence. The third polypeptide chain may be the heavy chain of an antibody that contains a VH3 and a heavy chain constant region. The fourth polypeptide of such embodiments contains: (i) a VL3-containing Domain and (ii) a CL-containing Domain. The fourth polypeptide chains may be light chain of an antibody that contains a VL3 complementary to the VH3 of the third polypeptide chain. The third or fourth polypeptide chains may be isolated from naturally occurring antibodies. Alternatively, they may be constructed recombinantly, synthetically or by other means.

[00196] The Variable Light Chain Domain of the first and second polypeptide chains are separated from the Variable Heavy Chain Domains of such polypeptide chains by an intervening spacer linker having a length that is too short to permit their VL1/VH2 (or their VL2/VH1) domains to associate together to form epitope-binding site capable of binding to either the first or second epitope. A preferred intervening spacer peptide (Linker 1) for this purpose has the sequence (**SEQ ID NO:14**): GGGSGGGG. Other Domains of the trivalent binding molecules may be separated by one or more intervening spacer peptides, optionally comprising a cysteine residue. Exemplary linkers useful for the generation of trivalent binding molecules are provided herein and are also provided in PCT Application Nos: PCT/US15/33081; and PCT/US15/33076. Thus, the first and second polypeptide chains of such trivalent binding molecules associate together to form a VL1/VH1 binding site capable of

binding a first epitope, as well as a VL2/VH2 binding site that is capable of binding to a second epitope. The third and fourth polypeptide chains of such trivalent binding molecules associate together to form a VL3/VH3 binding site that is capable of binding to a third epitope.

[00197] As described above, the trivalent binding molecules of the present invention may comprise three polypeptides. Trivalent binding molecules comprising three polypeptide chains may be obtained by linking the domains of the fourth polypeptide N-terminal to the VH3-containing Domain of the third polypeptide. Alternatively, a third polypeptide chain of a trivalent binding molecule of the invention containing the following three domains is utilized: (i) a VL3-containing Domain, (ii) a VH3-containing Domain, and (iii) a Domain containing a CH2-CH3 sequence, wherein the VL3 and VH3 are spaced apart from one another by an intervening spacer peptide that is sufficiently long (at least 9 or more amino acid residues) so as to allow the association of these domains to form an epitope-binding site.

[00198] It will be understood that the VL1/VH1, VL2/VH2, and VL3/VH3 Domains of such diabody molecules may be the same or different so as to permit binding that is monospecific, bispecific or trispecific. However, as provided herein, these domains are preferably selected so as to bind LAG-3 and a second epitope (or a second and third epitope) (preferably, such epitopes are epitopes of B7-H3, B7-H4, BTLA, CD40, CD80, CD86, CD137, CTLA-4, ICOS, KIR, LAG-3 MHC class I or II, OX40, PD-L1, TCR, TIM-3, etc.).

[00199] In particular, the VL and VH Domains maybe selected such that a trivalent binding molecule comprises two binding sites for a first epitope and one binding sites for a second epitope, or one binding site for a first epitope and two binding sites for a second epitope, or one binding site for a first epitope, one binding site for a second epitope and one binding site for a third epitope. The general structure of the polypeptide chains of representative trivalent binding molecules of invention is provided in **Figures 6A-6F** and in **Table 5**:

Table 5		
Four Chain 1st Orientation	2nd Chain	NH_2-VL2-VH1-HPD-COOH
	1st Chain	NH_2-VL1-VH2-HPD-CH2-CH3-COOH
	3rd Chain	NH_2-VH3-CH1-CH2-CH3-COOH
	4th Chain	NH_2-VL3-CL-COOH
Four Chain 2nd Orientation	2nd Chain	NH_2-VL2-VH1-HPD-COOH
	1st Chain	NH_2-CH2-CH3-VL1-VH2-HPD COOH
	3rd Chain	NH_2-VH3-CH1-CH2-CH3-COOH
	4th Chain	NH_2-VL3-CL-COOH
Three Chain 1st Orientation	2nd Chain	NH_2-VL2-VH1-HPD-COOH
	1st Chain	NH_2-VL1-VH2-HPD-CH2-CH3-COOH
	3rd Chain	NH_2-VL3-VH3-HPD-CH2-CH3-COOH
Three Chain 2nd Orientation	2nd Chain	NH_2-VL2-VH1-HPD-COOH
	1st Chain	NH_2-CH2-CH3-VL1-VH2-HPD COOH
	3rd Chain	NH_2-VL3-VH3-HPD-CH2-CH3-COOH

HPD = Heterodimer-Promoting Domain

[00200] One embodiment of the present invention relates to bispecific trivalent binding molecules that comprise two epitope-binding sites for LAG-3 and one epitope-binding site for the second epitope present on a molecule other than LAG-3 (*e.g.* B7-H3, B7-H4, BTLA, CD40, CD80, CD86, CD137, CTLA-4, ICOS, KIR, LAG-3, MHC class I or II, OX40, PD-L1, TCR, TIM-3, *etc.*). The two epitope-binding sites for LAG-3 may bind the same epitope or different epitopes. Another embodiment of the present invention relates to bispecific trivalent binding molecules that comprise, one epitope-binding site for LAG-3 and two epitope-binding sites that bind a second antigen present on a molecule other than LAG-3 (*e.g.* B7-H3, B7-H4, BTLA, CD40, CD80, CD86, CD137, CTLA-4, ICOS, KIR, LAG-3, MHC class I or II, OX40, PD-L1, TCR, TIM-3, *etc.*). The two epitope-binding sites for the second antigen may bind the same epitope or different epitopes of the antigen (*e.g.*, the same or different epitopes of LAG-3). As provided above, such bispecific trivalent binding molecules may comprise three or four polypeptide chains.

VII. Constant Domains and Fc Regions

[00201] Provided herein are antibody Constant Domains useful in the generation of LAG-3-binding molecules (*e.g.*, antibodies, diabodies, trivalent binding molecules, *etc.*) of the invention.

[00202] A preferred CL Domain is a human IgG CL Kappa Domain. The amino acid sequence of an exemplary human CL Kappa Domain is (**SEQ ID NO:118**):

RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC

[00203] Alternatively, an exemplary CL Domain is a human IgG CL Lambda Domain. The amino acid sequence of an exemplary human CL Kappa Domain is (**SEQ ID NO:119**):

QPKAAPSVTL FPPSSEELQA NKATLVCLIS DFYPGAVTVA WKADSSPVKA GVETTPSKQS NNKYAASSYL SLTPEQWKSH RSYSCQVTHE GSTVEKTVAP TECS

[00204] As provided herein, the LAG-3-binding molecules of the invention may comprise an Fc Region. The Fc Region of such molecules of the invention may be of any isotype (*e.g.*, IgG1, IgG2, IgG3, or IgG4). The LAG-3-binding molecules of the invention may further comprise a CH1 Domain and/or a hinge region. When present, the CH1 Domain and/or hinge region may be of any isotype (*e.g.*, IgG1, IgG2, IgG3, or IgG4), and is preferably of the same isotype as the desired Fc Region.

[00205] An exemplary CH1 Domain is a human IgG1 CH Domain. The amino acid sequence of an exemplary human IgG1 CH1 Domain is (**SEQ ID NO:120**):

ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKRV

[00206] An exemplary CH1 Domain is a human IgG2 CH Domain. The amino acid sequence of an exemplary human IgG2 CH1 Domain is (**SEQ ID NO:121**):

ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSNFGTQT YTCNVDHKPS NTKVDKTV

[00207] An exemplary CH1 Domain is a human IgG4 CH1 Domain. The amino acid sequence of an exemplary human IgG4 CH1 Domain is (**SEQ ID NO:122**):

ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTKT YTCNVDHKPS NTKVDKRV

[00208] One exemplary hinge region is a human IgG1 hinge region. The amino acid sequence of an exemplary human IgG1 hinge region is (**SEQ ID NO:114**): EPKSCDKTHTCPPCP.

[00209] Another exemplary hinge region is a human IgG2 hinge region. The amino acid sequence of an exemplary human IgG2 hinge region is (**SEQ ID NO:115**): ERKCCVECPPCP.

[00210] Another exemplary hinge region is a human IgG4 hinge region. The amino acid sequence of an exemplary human IgG4 hinge region is (**SEQ ID NO:116**): ESKYGPPCPSCP. As described herein, an IgG4 hinge region may comprise a stabilizing mutation such as the S228P substitution. The amino acid sequence of an exemplary stabilized IgG4 hinge region is (**SEQ ID NO:117**): ESKYGPPCPPCP.

[00211] The Fc Region of the Fc Region-containing molecules (*e.g.*, antibodies, diabodies, and trivalent molecules) of the present invention may be either a complete Fc Region (*e.g.*, a complete IgG Fc Region) or only a fragment of an Fc Region. Optionally, the Fc Region of the Fc Region-containing molecules of the present invention lacks the C-terminal lysine amino acid residue. In particular, the Fc Region of the Fc Region-containing molecules of the present invention may be an engineered variant Fc Region. Although the Fc Region of the bispecific Fc Region-containing molecules of the present invention may possess the ability to bind to one or more Fc receptors (*e.g.*, FcγR(s)), more preferably such variant Fc Region will have altered binding to FcγRIA (CD64), FcγRIIA (CD32A), FcγRIIB (CD32B), FcγRIIIA (CD16a) or FcγRIIIB (CD16b) (relative to the binding exhibited by a wild-type Fc Region) or will have substantially reduced or no ability to bind to inhibitory receptor(s). Thus, the Fc Region of the Fc Region-containing molecules of the present invention may include some or all of the CH2 Domain and/or some or all of the CH3 Domain of a complete Fc Region, or may comprise a variant CH2 and/or a variant CH3 sequence (that may include, for example, one or more insertions and/or one or more deletions with respect to the CH2 or CH3 domains of a complete Fc Region). Such Fc Regions may comprise non-Fc polypeptide portions, or may comprise portions of non-naturally complete Fc Regions, or may comprise non-naturally occurring orientations of CH2 and/or CH3 Domains (such as, for example, two CH2 domains or two CH3 domains, or in the N-terminal to C-terminal direction, a CH3 Domain linked to a CH2 Domain, *etc.*).

[00212] Fc Region modifications identified as altering effector function are known in the art, including modifications that increase binding to activating receptors (*e.g.*, FcγRIIA (CD16A) and reduce binding to inhibitory receptors (*e.g.*, FcγRIIB (CD32B) (see, *e.g.*, Stavenhagen, J.B. *et al.* (2007) "*Fc Optimization Of Therapeutic Antibodies Enhances Their Ability To Kill Tumor Cells In Vitro And Controls Tumor Expansion In Vivo Via Low-Affinity Activating Fcgamma Receptors*," Cancer Res. 57(18):8882-8890). Exemplary variants of human IgG1 Fc Regions with reduced binding to CD32B and/or increased binding to CD16A contain F243L, R292P, Y300L, V305I or P296L substitutions. These amino acid substitutions may be present in a human IgG1 Fc Region in any combination or subcombination. In one embodiment, the human IgG1 Fc Region variant contains a F243L, R292P and Y300L substitution. In another embodiment, the human IgG1 Fc Region variant contains F243L, R292P, Y300L, V305I and P296L substitutions.

[00213] In particular, it is preferred for the CH2-CH3 Domains of the polypeptide chains of the Fc Region-containing molecules of the present invention to exhibit decreased (or substantially no) binding to FcγRIA (CD64), FcγRIIA (CD32A), FcγRIIB (CD32B), FcγRIIIA (CD16a) or FcγRIIIB (CD16b) (relative to the binding exhibited by the wild-type IgG1 Fc Region (**SEQ ID NO:1**). Variant Fc Regions and mutant forms capable of mediating such altered binding are described above. In a specific embodiment, the Fc Region-containing molecules of the present invention comprise an IgG Fc Region that exhibits reduced ADCC effector function. In a preferred embodiment the CH2-CH3 Domain of the first and/or third polypeptide chains of such molecules include any 1, 2, or 3, of the substitutions: L234A, L235A, N297Q, and N297G. In another embodiment, the human IgG Fc Region variant contains an N297Q substitution, an N297G substitution, L234A and L235A substitutions or a D265A substitution, as these mutations abolish FcR binding. Alternatively, a CH2-CH3 Domain of an Fc Region which inherently exhibits decreased (or substantially no) binding to FcγRIIIA (CD16a) and/or reduced effector function (relative to the binding exhibited by the wild-type IgG1 Fc Region (**SEQ ID NO:1**)) is utilized. In a specific embodiment, the Fc Region-containing molecules of the present invention comprise an IgG2 Fc Region (**SEQ ID NO:2**) or an IgG4 Fc Region (**SEQ ID:NO:4**). When an IgG4 Fc Region in utilized, the instant invention

also encompasses the introduction of a stabilizing mutation, such as the hinge region S228P substitution described above (see, *e.g.*, **SEQ ID NO:117**). Since the N297G, N297Q, L234A, L235A and D265A substitutions abolish effector function, in circumstances in which effector function is desired, these substitutions would preferably not be employed.

[00214] A preferred IgG1 sequence for the CH2 and CH3 Domains of the LAG-3-binding molecules of the invention will have the L234A/L235A substitutions (**SEQ ID NO:123**):

APE**AA**GGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD
GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA
PIEKTISKAK GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE
WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE
ALHNHYTQKS LSLSPG**X**

wherein, **X** is a lysine (K) or is absent.

[00215] In particular, it is preferred for the Fc Regions of the polypeptide chains of the Fc Region-containing molecules of the present invention to exhibit increased serum half-life (relative to the half-life exhibited by the corresponding wild-type Fc). Variant Fc Regions and mutant forms exhibiting extended serum half-life are described above. In a preferred embodiment the CH2-CH3 Domain of the first and/or third polypeptide chains of such Fc Region-containing molecules include any 1, 2, or 3, of the substitutions: M252Y, S254T and T256E. The invention further encompasses Fc Region-containing molecules of the present invention comprising variant Fc Regions comprising:

(A) one or more mutations which alter effector function and/or FcγR; and

(B) one or more mutations which extend serum half-life.

[00216] A preferred IgG1 sequence for the CH2 and CH3 Domains of the Fc Region-containing molecules of the present invention will comprise the substitutions L234A/L235A/M252Y/S254T/T256E (**SEQ ID NO:124**):

APE**AA**GGPSV FLFPPKPKDT L**Y**I**T**R**E**PEVT CVVVDVSHED PEVKFNWYVD
GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA
PIEKTISKAK GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE

WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE
ALHNHYTQKS LSLSPG**X**

wherein, X is a lysine (K) or is absent

[00217] A preferred IgG4 sequence for the CH2 and CH3 Domains of the Fc Region-containing molecules of the present invention will comprise the M252Y/S254T/T256E substitutions (**SEQ ID NO:125**):

APEFLGGPSV FLFPPKPKDT L**Y**I**T**R**E**PEVT CVVVDVSQED PEVQFNWYVD
GVEVHNAKTK PREEQFNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS
SIEKTISKAK GQPREPQVYT LPPSQEEMTK NQVSLTCLVK GFYPSDIAVE
WESNGQPENN YKTTPPVLDS DGSFFLYSRL TVDKSRWQEG NVFSCSVMHE
ALHNHYTQKS LSLSLG**X**

wherein, X is a lysine (K) or is absent

[00218] For diabodies and trivalent binding molecules whose first and third polypeptide chains are not identical), it is desirable to reduce or prevent homodimerization from occurring between the CH2-CH3 Domains of two first polypeptide chains or between the CH2-CH3 Domains of two third polypeptide chains. The CH2 and/or CH3 Domains of such polypeptide chains need not be identical in sequence, and advantageously are modified to foster complexing between the two polypeptide chains. For example, an amino acid substitution (preferably a substitution with an amino acid comprising a bulky side group forming a "knob", *e.g.*, tryptophan) can be introduced into the CH2 or CH3 Domain such that steric interference will prevent interaction with a similarly mutated domain and will obligate the mutated domain to pair with a domain into which a complementary, or accommodating mutation has been engineered, *i.e.*, "the hole" (*e.g.*, a substitution with glycine). Such sets of mutations can be engineered into any pair of polypeptides comprising CH2-CH3 Domains that forms an Fc Region. Methods of protein engineering to favor heterodimerization over homodimerization are well known in the art, in particular with respect to the engineering of immunoglobulin-like molecules, and are encompassed herein (see *e.g.*, Ridgway *et al.* (1996) *"'Knobs-Into-Holes' Engineering Of Antibody CH3 Domains For Heavy Chain Heterodimerization,"* Protein Engr. 9:617-621, Atwell *et al.* (1997) *"Stable Heterodimers From Remodeling The Domain Interface Of A Homodimer Using A Phage Display Library,"* J. Mol. Biol. 270: 26-35, and Xie *et al.* (2005) *"A New Format Of Bispecific Antibody: Highly Efficient Heterodimerization,*

Expression And Tumor Cell Lysis," J. Immunol. Methods 296:95-101; each of which is hereby incorporated herein by reference in its entirety). Preferably the "knob" is engineered into the CH2-CH3 Domains of the first polypeptide chain and the "hole" is engineered into the CH2-CH3 Domains of the third polypeptide chain of diabodies comprising three polypeptide chains. Thus, the "knob" will help in preventing the first polypeptide chain from homodimerizing via its CH2 and/or CH3 Domains. As the third polypeptide chain preferably contains the "hole" substitution it will heterodimerize with the first polypeptide chain as well as homodimerize with itself. This strategy may be utilized for diabodies and trivalent binding molecules comprising three, four or five chains as detailed above, where the "knob" is engineered into the CH2-CH3 Domains of the first polypeptide chain and the "hole" is engineered into the CH2-CH3 Domains of the third polypeptide chain.

[00219] A preferred knob is created by modifying an IgG Fc Region to contain the modification T366W. A preferred hole is created by modifying an IgG Fc Region to contain the modification T366S, L368A and Y407V. To aid in purifying the hole-bearing third polypeptide chain homodimer from the final bispecific heterodimeric Fc Region-containing molecule, the protein A binding site of the CH2 and CH3 Domains of the third polypeptide chain is preferably mutated by amino acid substitution at position 435 (H435R). Thus, the hole-bearing third polypeptide chain homodimer will not bind to protein A, whereas the bispecific heterodimer will retain its ability to bind protein A via the protein A binding site on the first polypeptide chain. In an alternative embodiment, the hole-bearing third polypeptide chain may incorporate amino acid substitutions at positions 434 and 435 (N434A/N435K).

[00220] A preferred IgG1 amino acid sequence for the CH2 and CH3 Domains of the first polypeptide chain of an Fc Region-containing molecule of the present invention will have the "**knob-bearing**" sequence (**SEQ ID NO:126**):

APE**AA**GGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD
GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA
PIEKTISKAK GQPREPQVYT LPPSREEMTK NQVSL**W**C**L**VK GFYPSDIAVE
WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE
ALHN**H**YTQKS LSLSPG**X**

wherein, X is a lysine (K) or is absent

[00221] A preferred IgG1 amino acid sequence for the CH2 and CH3 Domains of the second polypeptide chain of an Fc Region-containing molecule of the present invention having two polypeptide chains (or the third polypeptide chain of an Fc Region-containing molecule having three, four, or five polypeptide chains) will have the "**hole-bearing**" sequence (**SEQ ID NO:127**):

APE**AA**GGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD
GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA
PIEKTISKAK GQPREPQVYT LPPSREEMTK NQVSL**S**C**A**VK GFYPSDIAVE
WESNGQPENN YKTTPPVLDS DGSFFL**V**SKL TVDKSRWQQG NVFSCSVMHE
ALHN**R**YTQKS LSLSPG**X**

wherein, X is a lysine (K) or is absent

[00222] As will be noted, the CH2-CH3 Domains of **SEQ ID NO:126** and **SEQ ID NO:127** include a substitution at position 234 with alanine and 235 with alanine, and thus form an Fc Region exhibit decreased (or substantially no) binding to FcγRIA (CD64), FcγRIIA (CD32A), FcγRIIB (CD32B), FcγRIIIA (CD16a) or FcγRIIIB (CD16b) (relative to the binding exhibited by the wild-type Fc Region (**SEQ ID NO:1**). The invention also encompasses such CH2-CH3 Domains, which comprise alanine residues at positions 234 and/or 235 and/or alternative and/or additional substitutions which modify effector function and/or FγR binding activity of the Fc Region. The invention also encompasses such CH2-CH3 Domains, which further comprise one or more half-live extending amino acid substitutions. In particular, the invention encompasses such hole-bearing and such knob-bearing CH2-CH3 Domains which further comprise the M252Y/S254T/T256E.

[00223] It is preferred that the first polypeptide chain will have a "knob-bearing" CH2-CH3 sequence, such as that of **SEQ ID NO:126**. However, as will be recognized, a "hole-bearing" CH2-CH3 Domain (*e.g.*, **SEQ ID NO:127**) could be employed in the first polypeptide chain, in which case, a "knob-bearing" CH2-CH3 Domain (*e.g.*, **SEQ ID NO:126**) would be employed in the second polypeptide chain of an Fc Region-containing molecule of the present invention having two polypeptide chains (or the third polypeptide chain of an Fc Region-containing molecule having three, four, or five polypeptide chains).

[00224] As detailed above the invention encompasses Fc Region-containing molecules (*e.g.*, antibodies and Fc Region-containing diabodies) having wild type CH2 and CH3 Domains, or having CH2 and CH3 Domains comprising combinations of the substitutions described above. An exemplary amino acid sequence of an IgG1 CH2-CH3 Domain encompassing such variations is (**SEQ ID NO:128**):

APEX_1X_2GGPSV	FLFPPKPKDT	LX_3IX_4RX_5PEVT	CVVVDVSHED
PEVKFNWYVD	GVEVHNAKTK	PREEQYNSTY	RVVSVLTVLH
QDWLNGKEYK	CKVSNKALPA	PIEKTISKAK	GQPREPQVYT
LPPSREEMTK	NQVSLX_6CX_7VK	GFYPSDIAVE	WESNGQPENN
YKTTPPVLDS	DGSFFLX_8SKL	TVDKSRWQQG	NVFSCSVMHE
ALHX_9X_{10}YTQKS	LSLSPGX_{11}		

wherein:

(a) X_1 and X_2 are both L (wild type), or are both A (decreased FcγR binding);

(b) X_3, X_4, and X_5 respectively are M, S and T (wild type), or are Y, T and E (extended half-life),

(c) X_6, X_7, and X_8 respectively are T, L and Y (wild type), or are W, L and Y (knob), or S, A and V (hole);

(d) X_9 and X_{10} respectively are N and H (wild type), or are N and R (no protein A binding), or A and K (no protein A binding); and

(e) X_{11} is K or is absent

[00225] In other embodiments, the invention encompasses LAG-3-binding molecules comprising CH2 and/or CH3 Domains that have been engineered to favor heterodimerization over homodimerization using mutations known in the art, such as those disclosed in PCT Publication No. WO 2007/110205; WO 2011/143545; WO 2012/058768; WO 2013/06867, all of which are incorporated herein by reference in their entirety.

VIII. Reference Antibodies

A. Reference Anti-LAG-3 Antibody

[00226] In order to assess and characterize the novel anti-LAG-3-binding molecules of the present invention, the following reference antibody was employed: **25F7** (BMS-986016, Medarex/BMS, designated herein as "**LAG-3 mAb A**").

1. 25F7 ("LAG-3 mAb A")

[00227] The amino acid sequence of the VH Domain of **25F7** ("**LAG-3 mAb A**") (**SEQ ID NO:129**) is shown below (CDR_H residues are shown underlined):

QVQLQQWGAG LLKPSETLSL TCAVYGGSFS **DYYWN**WIRQP PGKGLEWIG**E**
INHNGNTNSN **PSLKS**RVTLS LDTSKNQFSL KLRSVTAADT AVYYCAF**GYS**
DYEYNWFDPW GQGTLVTVSS

[00228] The amino acid sequence of the VL Domain of **25F7** ("**LAG-3 mAb A**") (**SEQ ID NO:130**) is shown below (CDR_L residues are shown underlined):

EIVLTQSPAT LSLSPGERAT LSC**RASQSIS** **SYLA**WYQQKP GQAPRLLIY**D**
ASNRATGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYC**QQ** **RSNWPLT**FGQ
GTNLEIK

B. Reference Anti-PD-1 Antibodies

[00229] In order to assess and characterize the activity of the novel LAG-3-binding molecules of the present invention in combination with an anti-PD-1 antibody a reference antibody may be used. Antibodies that are immunospecific for PD-1 are known (see, *e.g.*, United States Patents No. 8,008,449; 8,552,154; PCT Patent Publications WO 2012/135408; WO 2012/145549; and WO 2013/014668) and include: nivolumab (also known as 5C4, BMS-936558, ONO-4538, MDX-1106, and marketed as OPDIVO® by Bristol-Myers Squibb) designated herein as "**PD-1 mAb 1**;" pembrolizumab (formerly known as lambrolizumab, also known as MK-3475, SCH-900475, and marketed as KEYTRUDA® by Merck) designated herein as "**PD-1 mAb 2**"; EH12.2H7 (Dana Farber) designated herein as "**PD-1 mAb 3**"; pidilizumab (also known as CT-011, CureTech,) designated herein as "**PD-1 mAb 4**."

1. Nivolumab ("PD-1 mAb 1")

[00230] The amino acid sequence of the Heavy Chain Variable Domain of **PD-1 mAb 1** has the amino acid sequence (**SEQ ID NO:131**) (CDR_H residues are shown underlined):

QVQLVESGGG VVQPGRSLRL DCKASGITFS **NSGMH**WVRQA PGKGLEWVA**V**
IWYDGSKRYY **ADSVKG**RFTI SRDNSKNTLF LQMNSLRAED TAVYYCAT**ND**
DYWGQGTLVT VSS

[00231] The amino acid sequence of the Light Chain Variable Domain of **PD-1 mAb 1** has the amino acid sequence (**SEQ ID NO:132**) (CDR_L residues are shown underlined):

EIVLTQSPAT LSLSPGERAT LSC**RASQSVS SYLA**WYQQKP GQAPRLLIY**D ASNRAT**GIPA RFSGSGSGTD FTLTISSLEP EDFAVYYC**QQ SSNWPRT**FGQ GTKVEIK

2. Pembrolizumab ("PD-1 mAb 2")

[00232] The amino acid sequence of the Heavy Chain Variable Domain of **PD-1 mAb 2** has the amino acid sequence (**SEQ ID NO:133**) (CDR_H residues are shown underlined):

QVQLVQSGVE VKKPGASVKV SCKASGYTFT **NYYMY**WVRQA PGQGLEWMG**G INPSNGGTNF NEKFKN**RVTL TTDSSTTTAY MELKSLQFDD TAVYYCAR**RD YRFDMGFDY**W GQGTTVTVSS

[00233] The amino acid sequence of the Light Chain Variable Domain of **PD-1 mAb 2** has the amino acid sequence (**SEQ ID NO:134**) (CDR_L residues are shown underlined):

EIVLTQSPAT LSLSPGERAT LSC**RASKGVS TSGYSYLH**WY QQKPGQAPRL LIY**LASYLES** GVPARFSGSG SGTDFTLTIS SLEPEDFAVY YC**QHSRDLPL T**FGGGTKVEIK

3. EH12.2H7 ("PD-1 mAb 3")

[00234] The amino acid sequence of the Heavy Chain Variable Domain of **PD-1 mAb 3** has the amino acid sequence (**SEQ ID NO:135**) (CDR_H residues are shown underlined):

QVQLQQSGAE LAKPGASVQM SCKASGYSFT **SSWIH**WVKQR PGQGLEWIG**Y IYPSTGFTEY NQKFKD**KATL TADKSSSTAY MQLSSLTSED SAVYYCA**RWR DSSGYHAMDY** WGQGTSVTVSS

[00235] The amino acid sequence of the Light Chain Variable Domain of **PD-1 mAb 3** has the amino acid sequence (**SEQ ID NO:136**) (CDR_L residues are shown underlined):

DIVLTQSPAS LTVSLGQRAT ISC**RASQSVS TSGYSYMH**WY QQKPGQPPKL LIK**FGSNLES** GIPARFSGSG SGTDFTLNIH PVEEEDTATY YC**QHSWEIPY T**FGGGTKLEI K

4. Pidilizumab ("PD-1 mAb 4")

[00236] The amino acid sequence of the Heavy Chain Variable Domain of **PD-1 mAb 4** has the amino acid sequence (**SEQ ID NO:137**) (CDR_H residues are shown underlined):

QVQLVQSGSE LKKPGASVKI SCKASGYTFT **NYGMN**WVRQA PGQGLQWMG**W**
INTDSGESTY **AEEFKG**RFVF SLDTSVNTAY LQITSLTAED TGMYFCVR**VG**
YDALDYWGQG TLVTVSS

[00237] The amino acid sequence of the Light Chain Variable Domain of **PD-1 mAb 4** has the amino acid sequence (**SEQ ID NO:138**) (CDR_L residues are shown underlined):

EIVLTQSPSS LSASVGDRVT ITC**SARSSVS** **YMH**WFQQKPG KAPKLWIY**RT**
SNLASGVPSR FSGSGSGTSY CLTINSLQPE DFATYYC**QQR** **SSFPLT**FGGG
TKLEIK

IX. Methods of Production

[00238] An anti-LAG-3 polypeptide, and other LAG-3 agonists, antagonists and modulators can be created from the polynucleotides and/or sequences of the LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5, or LAG-3 mAb 6 antibodies by methods known in the art, for example, synthetically or recombinantly. One method of producing such peptide agonists, antagonists and modulators involves chemical synthesis of the polypeptide, followed by treatment under oxidizing conditions appropriate to obtain the native conformation, that is, the correct disulfide bond linkages. This can be accomplished using methodologies well known to those skilled in the art (see, *e.g.*, Kelley, R. F. *et al.* (1990) In: GENETIC ENGINEERING PRINCIPLES AND METHODS, Setlow, J.K. Ed., Plenum Press, N.Y., vol. 12, pp 1-19; Stewart, J.M *et al.* (1984) SOLID PHASE PEPTIDE SYNTHESIS, Pierce Chemical Co., Rockford, IL; see also United States Patents Nos. 4,105,603; 3,972,859; 3,842,067; and 3,862,925).

[00239] Polypeptides of the invention may be conveniently prepared using solid phase peptide synthesis (Merrifield, B. (1986) "S*olid Phase Synthesis*," Science 232(4748):341-347; Houghten, R.A. (1985) "*General Method For The Rapid Solid-Phase Synthesis Of Large Numbers Of Peptides: Specificity Of Antigen-Antibody*

Interaction At The Level Of Individual Amino Acids," Proc. Natl. Acad. Sci. (U.S.A.) 82(15):5131-5135; Ganesan, A. (2006) "*Solid-Phase Synthesis In The Twenty-First Century*," Mini Rev. Med. Chem. 6(1):3-10).

[00240] In yet another alternative, fully human antibodies having one or more of the CDRs of LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5, or LAG-3 mAb 6 or which compete with LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5, or LAG-3 mAb 6 for binding to human LAG-3 or a soluble form thereof may be obtained through the use of commercially available mice that have been engineered to express specific human immunoglobulin proteins. Transgenic animals that are designed to produce a more desirable (*e.g.*, fully human antibodies) or more robust immune response may also be used for generation of humanized or human antibodies. Examples of such technology are XENOMOUSE™ (Abgenix, Inc., Fremont, CA) and HUMAB-MOUSE® and TC MOUSE™ (both from Medarex, Inc., Princeton, NJ).

[00241] In an alternative, antibodies may be made recombinantly and expressed using any method known in the art. Antibodies may be made recombinantly by first isolating the antibodies made from host animals, obtaining the gene sequence, and using the gene sequence to express the antibody recombinantly in host cells (*e.g.*, CHO cells). Another method that may be employed is to express the antibody sequence in plants {*e.g.*, tobacco) or transgenic milk. Suitable methods for expressing antibodies recombinantly in plants or milk have been disclosed (see, for example, Peeters *et al.* (2001) "*Production Of Antibodies And Antibody Fragments In Plants*," Vaccine 19:2756; Lonberg, N. *et al.* (1995) "*Human Antibodies From Transgenic Mice*," Int. Rev. Immunol 13:65-93; and Pollock *et al.* (1999) "*Transgenic Milk As A Method For The Production Of Recombinant Antibodies*," J. Immunol Methods 231:147-157). Suitable methods for making derivatives of antibodies, *e.g.*, humanized, single-chain, *etc.* are known in the art. In another alternative, antibodies may be made recombinantly by phage display technology (see, for example, U.S. Patent Nos. 5,565,332; 5,580,717; 5,733,743; 6,265,150; and Winter, G. *et al.* (1994) "*Making Antibodies By Phage Display Technology*," Annu. Rev. Immunol. 12.433-455).

[00242] The antibodies or protein of interest may be subjected to sequencing by Edman degradation, which is well known to those of skill in the art. The peptide information generated from mass spectrometry or Edman degradation can be used to design probes or primers that are used to clone the protein of interest.

[00243] An alternative method of cloning the protein of interest is by "panning" using purified LAG-3 or portions thereof for cells expressing an antibody or protein of interest that possesses one or more of the CDRs LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5, or LAG-3 mAb 6 or that competes with LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5, or LAG-3 mAb 6 for binding to human LAG-3. The "panning" procedure may be conducted by obtaining a cDNA library from tissues or cells that express LAG-3, overexpressing the cDNAs in a second cell type, and screening the transfected cells of the second cell type for a specific binding to LAG-3 in the presence or absence of LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5, or LAG-3 mAb 6. Detailed descriptions of the methods used in cloning mammalian genes coding for cell surface proteins by "panning" can be found in the art (see, for example, Aruffo, A. *et al.* (1987) "*Molecular Cloning Of A CD28 cDNA By A High-Efficiency COS Cell Expression System*," Proc. Natl. Acad. Sci. (U.S.A.) 84:8573-8577 and Stephan, J. *et al.* (1999) "*Selective Cloning Of Cell Surface Proteins Involved In Organ Development: Epithelial Glycoprotein Is Involved In Normal Epithelial Differentiation*," Endocrinol. 140:5841-5854).

[00244] Vectors containing polynucleotides of interest can be introduced into the host cell by any of a number of appropriate means, including electroporation, transfection employing calcium chloride, rubidium chloride, calcium phosphate, DEAE-dextran, or other substances; microprojectile bombardment; lipofection; and infection (*e.g.*, where the vector is an infectious agent such as vaccinia virus). The choice of introducing vectors or polynucleotides will often depend on features of the host cell.

[00245] Any host cell capable of overexpressing heterologous DNAs can be used for the purpose of isolating the genes encoding the antibody, polypeptide or protein of

interest. Non-limiting examples of suitable mammalian host cells include but are not limited to COS, HeLa, and CHO cells. Preferably, the host cells express the cDNAs at a level of about 5-fold higher, more preferably 10-fold higher, even more preferably 20-fold higher than that of the corresponding endogenous antibody or protein of interest, if present, in the host cells. Screening the host cells for a specific binding to LAG-3 is effected by an immunoassay or FACS. A cell overexpressing the antibody or protein of interest can be identified.

[00246] The invention includes polypeptides comprising an amino acid sequence of the antibodies of this invention. The polypeptides of this invention can be made by procedures known in the art. The polypeptides can be produced by proteolytic or other degradation of the antibodies, by recombinant methods (*i.e.*, single or fusion polypeptides) as described above or by chemical synthesis. Polypeptides of the antibodies, especially shorter polypeptides up to about 50 amino acids, are conveniently made by chemical synthesis. Methods of chemical synthesis are known in the art and are commercially available. For example, an anti-LAG-3 polypeptide could be produced by an automated polypeptide synthesizer employing the solid phase method.

[00247] The invention includes variants of LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5, or LAG-3 mAb 6 antibodies and their polypeptide fragments that bind to LAG-3, including functionally equivalent antibodies and fusion polypeptides that do not significantly affect the properties of such molecules as well as variants that have enhanced or decreased activity. Modification of polypeptides is routine practice in the art and need not be described in detail herein. Examples of modified polypeptides include polypeptides with conservative substitutions of amino acid residues, one or more deletions or additions of amino acids which do not significantly deleteriously change the functional activity, or use of chemical analogs. Amino acid residues that can be conservatively substituted for one another include but are not limited to: glycine/alanine; serine/threonine; valine/isoleucine/leucine; asparagine/glutamine; aspartic acid/glutamic acid; lysine/arginine; and phenylalanine/tyrosine. These polypeptides also include glycosylated and non-glycosylated polypeptides, as well as polypeptides with other post-translational modifications, such as, for example, glycosylation with different

sugars, acetylation, and phosphorylation. Preferably, the amino acid substitutions would be conservative, *i.e.*, the substituted amino acid would possess similar chemical properties as that of the original amino acid. Such conservative substitutions are known in the art, and examples have been provided above. Amino acid modifications can range from changing or modifying one or more amino acids to complete redesign of a region, such as the Variable Domain. Changes in the Variable Domain can alter binding affinity and/or specificity. Other methods of modification include using coupling techniques known in the art, including, but not limited to, enzymatic means, oxidative substitution and chelation. Modifications can be used, for example, for attachment of labels for immunoassay, such as the attachment of radioactive moieties for radioimmunoassay. Modified polypeptides are made using established procedures in the art and can be screened using standard assays known in the art.

[00248] The invention encompasses fusion proteins comprising one or more of the polypeptides or LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5, or LAG-3 mAb 6 antibodies of this invention. In one embodiment, a fusion polypeptide is provided that comprises a light chain, a heavy chain or both a light and heavy chain. In another embodiment, the fusion polypeptide contains a heterologous immunoglobulin constant region. In another embodiment, the fusion polypeptide contains a Light Chain Variable Domain and a Heavy Chain Variable Domain of an antibody produced from a publicly-deposited hybridoma. For purposes of this invention, an antibody fusion protein contains one or more polypeptide domains that specifically bind to LAG-3 and another amino acid sequence to which it is not attached in the native molecule, for example, a heterologous sequence or a homologous sequence from another region.

X. Uses of the LAG-3-Binding Molecules of the Present Invention

[00249] The present invention encompasses compositions, including pharmaceutical compositions, comprising the LAG-3-binding molecules of the present invention (*e.g.*, anti-LAG-3 antibodies, anti-LAG-3 bispecific diabodies, *etc.*), polypeptides derived from such molecules, polynucleotides comprising sequences encoding such molecules or polypeptides, and other agents as described herein.

[00250] As discussed above, LAG-3 plays an important role in negatively regulating T-cell proliferation, function and homeostasis. The LAG-3-binding molecules of the present invention have the ability to inhibit LAG-3 function, and thus reverse the LAG-3-mediated immune system inhibition. As such, LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5, and LAG-3 mAb 6, their humanized derivatives, and molecules comprising their LAG-3-binding fragments (*e.g.*, bispecific diabodies, *etc.*), or that compete for binding with such antibodies, may be used to block LAG-3-mediated immune system inhibition, and thereby promote the activation of the immune system.

[00251] Bispecific LAG-3-binding molecules of the present invention that bind to LAG-3 and another molecule involved in regulating an immune check point present on the cell surface (*e.g.*, PD-1) augment the immune system by blocking immune system inhibition mediated by LAG-3 and such immune check point molecules. Thus, the LAG-3-binding molecules of the invention are useful for augmenting an immune response (*e.g.*, the T-cell mediated immune response) of a subject. In particular, the LAG-3-binding molecules of the invention and may be used to treat any disease or condition associated with an undesirably suppressed immune system, including cancer and diseases that are associated with the presence of a pathogen (*e.g.*, a bacterial, fungal, viral or protozoan infection).

[00252] The cancers that may be treated by the LAG-3-binding molecules of the present invention include cancers characterized by the presence of a cancer cell selected from the group consisting of a cell of: an adrenal gland tumor, an AIDS-associated cancer, an alveolar soft part sarcoma, an astrocytic tumor, bladder cancer, bone cancer, a brain and spinal cord cancer, a metastatic brain tumor, a breast cancer, a carotid body tumors, a cervical cancer, a chondrosarcoma, a chordoma, a chromophobe renal cell carcinoma, a clear cell carcinoma, a colon cancer, a colorectal cancer, a cutaneous benign fibrous histiocytoma, a desmoplastic small round cell tumor, an ependymoma, a Ewing's tumor, an extraskeletal myxoid chondrosarcoma, a fibrogenesis imperfecta ossium, a fibrous dysplasia of the bone, a gallbladder or bile duct cancer, gastric cancer, a gestational trophoblastic disease, a germ cell tumor, a head and neck cancer, hepatocellular carcinoma, an islet cell tumor, a Kaposi's Sarcoma, a kidney cancer, a

leukemia, a lipoma/benign lipomatous tumor, a liposarcoma/malignant lipomatous tumor, a liver cancer, a lymphoma, a lung cancer, a medulloblastoma, a melanoma, a meningioma, a multiple endocrine neoplasia, a multiple myeloma, a myelodysplastic syndrome, a neuroblastoma, a neuroendocrine tumors, an ovarian cancer, a pancreatic cancer, a papillary thyroid carcinoma, a parathyroid tumor, a pediatric cancer, a peripheral nerve sheath tumor, a phaeochromocytoma, a pituitary tumor, a prostate cancer, a posterious uveal melanoma, a rare hematologic disorder, a renal metastatic cancer, a rhabdoid tumor, a rhabdomysarcoma, a sarcoma, a skin cancer, a soft-tissue sarcoma, a squamous cell cancer, a stomach cancer, a synovial sarcoma, a testicular cancer, a thymic carcinoma, a thymoma, a thyroid metastatic cancer, and a uterine cancer.

[00253] In particular, the LAG-3-binding molecules of the present invention may be used in the treatment of colorectal cancer, hepatocellular carcinoma, glioma, kidney cancer, breast cancer, multiple myeloma, bladder cancer, neuroblastoma; sarcoma, non-Hodgkin's lymphoma, non-small cell lung cancer, ovarian cancer, pancreatic cancer and rectal cancer.

[00254] Pathogen-associated diseases that may be treated by the LAG-3-binding molecules of the present invention include chronic viral, bacterial, fungal and parasitic infections. Chronic infections that may be treated by the LAG-3-binding molecules of the present invention include Epstein Barr virus, Hepatitis A Virus (HAV); Hepatitis B Virus (HBV); Hepatitis C Virus (HCV); herpes viruses (*e.g.* HSV-1, HSV-2, HHV-6, CMV), Human Immunodeficiency Virus (HIV), Vesicular Stomatitis Virus (VSV), *Bacilli, Citrobacter, Cholera, Diphtheria, Enterobacter, Gonococci, Helicobacter pylori, Klebsiella, Legionella, Meningococci,* mycobacteria, *Pseudomonas, Pneumonococci,* rickettsia bacteria, *Salmonella, Serratia, Staphylococci, Streptococci, Tetanus, Aspergillus* (*A. fumigatus*, *A. niger*, *etc.*), *Blastomyces dermatitidis, Candida* (*C. albicans*, *C. krusei*, *C. glabrata*, *C. tropicalis*, *etc.*), *Cryptococcus neoformans,* Genus *Mucorales* (*mucor*, *absidia*, *rhizopus*), *Sporothrix schenkii, Paracoccidioides brasiliensis, Coccidioides immitis, Histoplasma capsulatum, Leptospirosis, Borrelia burgdorferi*, helminth parasite (hookworm, tapeworms, flukes,

flatworms (*e.g. Schistosomia*), *Giardia lambia*, *trichinella*, *Dientamoeba Fragilis*, *Trypanosoma brucei, Trypanosoma cruzi,* and *Leishmania donovani*.

[00255] The LAG-3-binding molecules of the invention can be combined with an immunogenic agent such as a tumor vaccine. Such vaccines may comprise purified tumor antigens (including recombinant proteins, peptides, and carbohydrate molecules), autologous or allogeneic tumor cells. A number of tumor vaccine strategies have been described (see for example, Palena, C., *et al.*, (2006) "*Cancer vaccines: preclinical studies and novel strategies*," Adv. Cancer Res. 95, 115-145; Mellman, I., *et al.* (2011) "*Cancer immunotherapy comes of age*," Nature 480, 480–489; Zhang, X. M. *et al.* (2008) "*The Anti-Tumor Immune Response Induced By A Combination of MAGE-3/MAGE-n-Derived Peptides*," Oncol. Rep. 20, 245–252; Disis, M. L. *et al.* (2002) "*Generation of T-cell Immunity to the HER-2/neu Protein After Active Immunization with HER-2/neu Peptide-Based Vaccines*," J. Clin. Oncol. 20:2624-2632; Vermeij, R. *et al.* (2012) "*Potentiation of a p53-SLP Vaccine By Cyclophosphamide In Ovarian Cancer: A Single-Arm Phase II Study*." Int. J. Cancer 131:E670-E680). The LAG-3-binding molecules of the invention can be combined with chemotherapeutic regimes. In these instances, it may be possible to reduce the dose of chemotherapeutic reagent administered (Mokyr. M.B. *et al.* (1998) "*Realization Of The Therapeutic Potential Of CTLA-4 Blockade In Low-Dose Chemotherapy-Treated Tumor-Bearing Mice*," Cancer Research 58: 5301-5304).

[00256] The LAG-3-binding molecules of the invention can be combined with other immunostimulatory molecules such as antibodies which activate host immune responsiveness to provide for increased levels of T-cell activation. In particular, anti-PD-1 antibodies, anti-PD-L1 antibodies and/or an anti-CTLA-4 antibodies have been demonstrated to active the immune system (see, *e.g.*, del Rio, M-L. *et al.* (2005) "*Antibody-Mediated Signaling Through PD-1 Costimulates T Cells And Enhances CD28-Dependent Proliferation*," Eur. J. Immunol 35:3545-3560; Barber, D. L. *et al.* (2006) "*Restoring Function In Exhausted CD8 T Cells During Chronic Viral Infection*," Nature 439, 682–687; Iwai, Y. *et al.* (2002) "*Involvement of PD-L1 On Tumor Cells In The Escape From Host Immune System And Tumor Immunotherapy by PD-L1 blockade*," Proc. Natl Acad. Sci. USA 99, 12293–12297; Leach, D. R., *et al.*,

(1996) "*Enhancement Of Antitumor Immunity By CTLA-4 Blockade*," Science 271, 1734-1736). Additional immunostimulatory molecules that may be combined with the LAG-3-binding molecules of the invention include antibodies to molecules on the surface of dendritic cells that activate dendritic cell (DC) function and antigen presentation, anti-CD40 antibodies able to substitute for T-cell helper activity, and activating antibodies to T-cell costimulatory molecules such as PD-L1, CTLA-4, OX-40 4-1BB, and ICOS (see, for example, Ito *et al.* (2000) "*Effective Priming Of Cytotoxic T Lymphocyte Precursors By Subcutaneous Administration Of Peptide Antigens In Liposomes Accompanied By Anti-CD40 And Anti-CTLA-4 Antibodies*,"Immunobiology 201:527-40; U.S. Pat. No. 5,811,097; Weinberg *et al.* (2000) "*Engagement of the OX-40 Receptor In Vivo Enhances Antitumor Immunity*," Immunol 164:2160-2169; Melero *et al.* (1997) "*Monoclonal Antibodies Against The 4-1BB T-Cell Activation Molecule Eradicate Established Tumors*," Nature Medicine 3: 682-685; Hutloff *et al.* (1999) "*ICOS is An Inducible T-Cell Co-Stimulator Structurally And Functionally Related to CD28*," Nature 397: 263-266; and Moran, A.E. *et al.* (2013) "*The TNFRs OX40, 4-1BB, and CD40 As Targets For Cancer Immunotherapy*," Curr Opin Immunol. 2013 Apr; 25(2): 10.1016/j.coi.2013.01.004), and/or stimulatory Chimeric Antigen Receptors (**CARs**) comprising an antigen binding domain directed against a disease antigen fused to one or more intracellular signaling domains from various costimulatory protein receptors (*e.g.*, CD28, 4-1BB, ICOS, OX40, *etc.*) which serve to stimulate T-cells upon antigen binding (see, for example, Tettamanti, S. *et al.* (2013) "*Targeting Of Acute Myeloid Leukaemia By Cytokine-Induced Killer Cells Redirected With A Novel CD123-Specific Chimeric* Antigen *Receptor*," Br. J. Haematol. 161:389-401; Gill, S. *et al.* (2014) "*Efficacy Against Human Acute Myeloid Leukemia And Myeloablation Of Normal Hematopoiesis In A Mouse Model Using Chimeric Antigen Receptor-Modified T Cells*," Blood 123(15): 2343-2354; Mardiros, A. *et al.* (2013) "*T Cells Expressing CD123-Specific Chimeric Antigen Receptors Exhibit Specific Cytolytic Effector Functions And Antitumor Effects Against Human Acute Myeloid Leukemia*," Blood 122:3138-3148; Pizzitola, I. *et al.* (2014) "*Chimeric Antigen Receptors Against CD33/CD123 Antigens Efficiently Target Primary Acute Myeloid Leukemia Cells in vivo*," Leukemia 28(8):1596-1605).

[00257] LAG-3-binding molecules of the invention can be combined with inhibitory Chimeric Antigen Receptors (**iCARs**) to divert off target immunotherapy responses. iCARs an antigen binding domain directed against a disease antigen fused to one or more intracellular signaling domains from various inhibitory protein receptors (*e.g.*, CTLA-4, PD-1, *etc.*) which serve to constrain T-cell responses upon antigen binding (see, for example, Fedorov V.D. (2013) "*PD-1– and CTLA-4–Based Inhibitory Chimeric Antigen Receptors (iCARs) Divert Off-Target Immunotherapy Responses*," Sci Tranl Med. 5(215):215ra172).

[00258] In particular, the anti-LAG-3 antibodies of the invention are used in combination with an anti-CD137 antibody, an anti-OX40 antibody, an anti-PD-1 antibody, an anti-PD-L1 antibody, an anti-TIGIT antibody, an anti-TIM-3 antibody and/or a cancer vaccine.

[00259] In addition to their utility in therapy, the LAG-3-binding molecules of the present invention may be detectably labeled and used in the detection of LAG-3 in samples or in the imaging of LAG-3 on cells.

XI. Pharmaceutical Compositions

[00260] The compositions of the invention include bulk drug compositions useful in the manufacture of pharmaceutical compositions (*e.g.*, impure or non-sterile compositions) and pharmaceutical compositions (*i.e.*, compositions that are suitable for administration to a subject or patient) that can be used in the preparation of unit dosage forms. Such compositions comprise a prophylactically or therapeutically effective amount of the LAG-3-binding molecules of the present invention, or a combination of such agents and a pharmaceutically acceptable carrier. Preferably, compositions of the invention comprise a prophylactically or therapeutically effective amount of the LAG-3-binding molecules of the present invention and a pharmaceutically acceptable carrier. The invention particularly encompasses such pharmaceutical compositions in which the LAG-3-binding molecule is: a LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5, or LAG-3 mAb 6 antibody; a humanized LAG-3 mAb 1; LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4 LAG-3 mAb 5, or LAG-3 mAb 6 antibody; a LAG-3-binding fragment of any such antibody; or in which the LAG-3-binding

molecule is a bispecific LAG-3 diabody (*e.g.*, a LAG-3 x PD-1 bispecific diabody). Especially encompassed are such molecules that comprise the 3 CDR_{LS} and the 3 CDR_{HS} of LAG-3 mAb 1; or that comprise the 3 CDR_{LS} and the 3 CDR_{HS} of LAG-3 mAb 2; or that comprise the 3 CDR_{LS} and the 3 CDR_{HS} of LAG-3 mAb 3, or that comprise the 3 CDR_{LS} and the 3 CDR_{HS} of LAG-3 mAb 4, or that comprise the 3 CDR_{LS} and the 3 CDR_{HS} of LAG-3 mAb 5, or that comprise the 3 CDR_{LS} and the 3 CDR_{HS} of LAG-3 mAb 6.

[00261] The invention also encompasses such pharmaceutical compositions that additionally include a second therapeutic antibody (*e.g.*, tumor-specific monoclonal antibody) that is specific for a particular cancer antigen, and a pharmaceutically acceptable carrier.

[00262] In a specific embodiment, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly in humans. The term "carrier" refers to a diluent, adjuvant (*e.g.*, Freund's adjuvant (complete and incomplete), excipient, or vehicle with which the therapeutic is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred carrier when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as liquid carriers, particularly for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. These compositions can take the form of solutions, suspensions, emulsion, tablets, pills, capsules, powders, sustained-release formulations and the like.

[00263] Generally, the ingredients of compositions of the invention are supplied either separately or mixed together in unit dosage form, for example, as a dry

lyophilized powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

[00264] The compositions of the invention can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include, but are not limited to those formed with anions such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, *etc.*, and those formed with cations such as those derived from sodium, potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, *etc.*

[00265] The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with a LAG-3-binding molecule of the present invention (and more preferably, a LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5, or LAG-3 mAb 6 antibody; a humanized LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5, or LAG-3 mAb 6 antibody; a LAG-3-binding fragment of any such antibody; or in which the LAG-3-binding molecule is a bispecific LAG-3 diabody (*e.g.*, a LAG-3 x PD-1 bispecific diabody)). Especially encompassed are such molecules that comprise the 3 CDR_{LS} and the 3 CDR_{HS} of LAG-3 mAb 1; or that comprise the 3 CDR_{LS} and the 3 CDR_{HS} of LAG-3 mAb 2; or that comprise the 3 CDR_{LS} and the 3 CDR_{HS} of LAG-3 mAb 3; or that comprise the 3 CDR_{LS} and the 3 CDR_{HS} of LAG-3 mAb 4; or that comprise the 3 CDR_{LS} and the 3 CDR_{HS} of LAG-3 mAb 5; or that comprise the 3 CDR_{LS} and the 3 CDR_{HS} of LAG-3 mAb 6, alone or with such pharmaceutically acceptable carrier. Additionally, one or more other prophylactic or therapeutic agents useful for the treatment of a disease can also be included in the pharmaceutical pack or kit. The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or

biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

[00266] The present invention provides kits that can be used in the above methods. A kit can comprise any of the LAG-3-binding molecules of the present invention. The kit can further comprise one or more other prophylactic and/or therapeutic agents useful for the treatment of cancer, in one or more containers; and/or the kit can further comprise one or more cytotoxic antibodies that bind one or more cancer antigens associated with cancer. In certain embodiments, the other prophylactic or therapeutic agent is a chemotherapeutic. In other embodiments, the prophylactic or therapeutic agent is a biological or hormonal therapeutic.

XII. Methods of Administration

[00267] The compositions of the present invention may be provided for the treatment, prophylaxis, and amelioration of one or more symptoms associated with a disease, disorder or infection by administering to a subject an effective amount of a fusion protein or a conjugated molecule of the invention, or a pharmaceutical composition comprising a fusion protein or a conjugated molecule of the invention. In a preferred aspect, such compositions are substantially purified (*i.e.*, substantially free from substances that limit its effect or produce undesired side effects). In a specific embodiment, the subject is an animal, preferably a mammal such as non-primate (*e.g.*, bovine, equine, feline, canine, rodent, *etc.*) or a primate (*e.g.*, monkey such as, a cynomolgus monkey, human, *etc.*). In a preferred embodiment, the subject is a human.

[00268] Various delivery systems are known and can be used to administer the compositions of the invention, *e.g.*, encapsulation in liposomes, microparticles, microcapsules, recombinant cells capable of expressing the antibody or fusion protein, receptor-mediated endocytosis (See, *e.g.*, Wu *et al.* (1987) *"Receptor-Mediated In Vitro Gene Transformation By A Soluble DNA Carrier System,"* J. Biol. Chem. 262:4429-4432), construction of a nucleic acid as part of a retroviral or other vector, *etc.*

[00269] Methods of administering a molecule of the invention include, but are not limited to, parenteral administration (*e.g.*, intradermal, intramuscular, intraperitoneal,

intravenous and subcutaneous), epidural, and mucosal (*e.g.*, intranasal and oral routes). In a specific embodiment, the LAG-3-binding molecules of the present invention are administered intramuscularly, intravenously, or subcutaneously. The compositions may be administered by any convenient route, for example, by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (*e.g.*, oral mucosa, rectal and intestinal mucosa, *etc.*) and may be administered together with other biologically active agents. Administration can be systemic or local. In addition, pulmonary administration can also be employed, *e.g.*, by use of an inhaler or nebulizer, and formulation with an aerosolizing agent. See, *e.g.*, U.S. Patent Nos. 6,019,968; 5,985, 320; 5,985,309; 5,934,272; 5,874,064; 5,855,913; 5,290,540; and 4,880,078; and PCT Publication Nos. WO 92/19244; WO 97/32572; WO 97/44013; WO 98/31346; and WO 99/66903, each of which is incorporated herein by reference in its entirety.

[00270] The invention also provides that the LAG-3-binding molecules of the present invention are packaged in a hermetically sealed container such as an ampoule or sachette indicating the quantity of the molecule. In one embodiment, such molecules are supplied as a dry sterilized lyophilized powder or water free concentrate in a hermetically sealed container and can be reconstituted, *e.g.*, with water or saline to the appropriate concentration for administration to a subject. Preferably, the LAG-3-binding molecules of the present invention are supplied as a dry sterile lyophilized powder in a hermetically sealed container.

[00271] The lyophilized LAG-3-binding molecules of the present invention should be stored at between 2°C and 8°C in their original container and the molecules should be administered within 12 hours, preferably within 6 hours, within 5 hours, within 3 hours, or within 1 hour after being reconstituted. In an alternative embodiment, such molecules are supplied in liquid form in a hermetically sealed container indicating the quantity and concentration of the molecule, fusion protein, or conjugated molecule. Preferably, such LAG-3-binding molecules when provided in liquid form are supplied in a hermetically sealed container.

[00272] The amount of the composition of the invention which will be effective in the treatment, prevention or amelioration of one or more symptoms associated with a

disorder can be determined by standard clinical techniques. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the condition, and should be decided according to the judgment of the practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from in vitro or animal model test systems.

[00273] As used herein, an "**effective amount**" of a pharmaceutical composition, in one embodiment, is an amount sufficient to effect beneficial or desired results including, without limitation, clinical results such as decreasing symptoms resulting from the disease attenuating a symptom of infection (*e.g.*, viral load, fever, pain, sepsis, *etc.*) or a symptom of cancer (*e.g.*, the proliferation, of cancer cells, tumor presence, tumor metastases, *etc.*), thereby increasing the quality of life of those suffering from the disease, decreasing the dose of other medications required to treat the disease, enhancing the effect of another medication such as via targeting and/or internalization, delaying the progression of the disease, and/ or prolonging survival of individuals.

[00274] An effective amount can be administered in one or more administrations. For purposes of this invention, an effective amount of drug, compound, or pharmaceutical composition is an amount sufficient to reduce the proliferation of (or the effect of) viral presence and to reduce and /or delay the development of the viral disease, either directly or indirectly. In some embodiments, an effective amount of a drug, compound, or pharmaceutical composition may or may not be achieved in conjunction with another drug, compound, or pharmaceutical composition. Thus, an "effective amount" may be considered in the context of administering one or more chemotherapeutic agents, and a single agent may be considered to be given in an effective amount if, in conjunction with one or more other agents, a desirable result may be or is achieved. While individual needs vary, determination of optimal ranges of effective amounts of each component is within the skill of the art.

[00275] For the LAG-3-binding molecules encompassed by the invention (*e.g.*, antibodies, diabodies, *etc.*), the dosage administered to a patient is preferably determined based upon the body weight (kg) of the recipient subject. For the LAG-binding molecules encompassed by the invention, the dosage administered to a patient

is typically from at least about 0.01 μg/kg body weight, at least about 0.05 μg/kg body weight, at least about 0.1 μg/kg body weight, at least about 0.2 μg/kg body weight, at least about 0.5 μg/kg body weight, at least about 1 μg/kg body weight, at least about 2 μg/kg body weight, at least about 3 μg/kg body weight, at least about 5 μg/kg body weight, at least about 10 μg/kg body weight, at least about 20 μg/kg body weight, at least about 30 μg/kg body weight, at least about 50 μg/kg body weight, at least about 100 μg/kg body weight, at least about 250 μg/kg body weight, at least about 750 μg/kg body weight, at least about 1.5 mg/kg body weight, at least about 3 mg/kg body weight, at least about 5 mg/kg body weight, or at least about 10 mg/kg, at least about 30 mg/kg, at least about 50 mg/kg, at least about 75 mg/kg, at least about 100 mg/kg, at least about 125 mg/kg, at least about 150 mg/kg or more body weight. The calculated dose will be administered based on the patient's body weight at baseline. Significant (≥ 10%) change in body weight from baseline or established plateau weight should prompt recalculation of dose.

[00276] In some embodiments, the LAG-3-binding bispecific molecules (*e.g.*, diabodies and trivalent binding molecules) encompassed by the invention, the dosage administered to a patient is typically from at least about 0.3 ng/kg per day to about 0.9 ng/kg per day, from at least about 1 ng/kg per day to about 3 ng/kg per day, from at least about 3 ng/kg per day to about 9 ng/kg per day, from at least about 10 ng/kg per day to about 30 ng/kg per day, from at least about 30 ng/kg per day to about 90 ng/kg per day, from at least about 100 ng/kg per day to about 300 ng/kg per day, from at least about 200 ng/kg per day to about 600 ng/kg per day, from at least about 300 ng/kg per day to about 900 ng/kg per day, from at least about 400 ng/kg per day to about 800 ng/kg per day, from at least about 500 ng/kg per day to about 1000 ng/kg per day, from at least about 600 ng/kg per day to about 1000 ng/kg per day, from at least about 700 ng/kg per day to about 1000 ng/kg per day, from at least about 800 ng/kg per day to about 1000 ng/kg per day, from at least about 900 ng/kg per day to about 1000 ng/kg per day, or at least about 1,000 ng/kg per day. The calculated dose will be administered based on the patient's body weight at baseline. Significant (≥ 10%) change in body weight from baseline or established plateau weight should prompt recalculation of dose.

[00277] In another embodiment, the patient is administered a treatment regimen comprising one or more doses of such prophylactically or therapeutically effective amount of a LAG-3-binding molecule of the present invention, wherein the treatment regimen is administered over 2 days, 3 days, 4 days, 5 days, 6 days or 7 days. In certain embodiments, the treatment regimen comprises intermittently administering doses of the prophylactically or therapeutically effective amount of the LAG-3-binding molecules of the present invention (for example, administering a dose on day 1, day 2, day 3 and day 4 of a given week and not administering doses of the prophylactically or therapeutically effective amount of the LAG-3-binding molecule (and particularly, a LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5, LAG-3 mAb 6 antibody; a humanized LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5, or LAG-3 mAb 6 antibody; a LAG-3-binding fragment of any such antibody; or in which the LAG-3-binding molecule is a bispecific LAG-3 diabody (*e.g.*, a LAG-3 x PD-1 bispecific Fc diabody). Especially encompassed is the administration (on day 5, day 6 and day 7 of the same week) of molecules that comprise the the 3 CDR_{LS} and the 3 CDR_{HS} of LAG-3 mAb 1; or that comprise the 3 CDR_{LS} and the 3 CDR_{HS} of LAG-3 mAb 2; or that comprise the 3 CDR_{LS} and the 3 CDR_{HS} of LAG-3 mAb 3; or that comprise the 3 CDR_{LS} and the 3 CDR_{HS} of LAG-3 mAb 4; or that comprise the 3 CDR_{LS} and the 3 CDR_{HS} of LAG-3 mAb 5; or that comprise the 3 CDR_{LS} and the 3 CDR_{HS} of LAG-3 mAb 6. Typically, there are 1, 2, 3, 4, 5 or more courses of treatment. Each course may be the same regimen or a different regimen.

[00278] In another embodiment, the administered dose escalates over the first quarter, first half or first two-thirds or three-quarters of the regimen(s) (*e.g.*, over the first, second, or third regimens of a 4 course treatment) until the daily prophylactically or therapeutically effective amount of the LAG-3-binding molecule is achieved. **Table 6** provides 5 examples of different dosing regimens described above for a typical course of treatment with a diabody.

Table 6						
Regimen	Day	Diabody Dosage (ng diabody per kg subject weight per day)				
1	1, 2, 3, 4	100	100	100	100	100
	5, 6, 7	none	none	none	none	none
2	1, 2, 3, 4	300	500	700	900	1,000
	5, 6, 7	none	none	none	none	none
3	1, 2, 3, 4	300	500	700	900	1,000
	5, 6, 7	none	none	none	none	none
4	1, 2, 3, 4	300	500	700	900	1,000
	5, 6, 7	none	none	none	none	none

[00279] The dosage and frequency of administration of a LAG-3-binding molecule of the present invention may be reduced or altered by enhancing uptake and tissue penetration of the molecule by modifications such as, for example, lipidation.

[00280] The dosage of a LAG-3-binding molecule of the invention administered to a patient may be calculated for use as a single agent therapy. Alternatively, the molecule may be used in combination with other therapeutic compositions and the dosage administered to a patient are lower than when said molecules are used as a single agent therapy.

[00281] The pharmaceutical compositions of the invention may be administered locally to the area in need of treatment; this may be achieved by, for example, and not by way of limitation, local infusion, by injection, or by means of an implant, said implant being of a porous, non-porous, or gelatinous material, including membranes, such as sialastic membranes, or fibers. Preferably, when administering a molecule of the invention, care must be taken to use materials to which the molecule does not absorb.

[00282] The compositions of the invention can be delivered in a vesicle, in particular a liposome (*See* Langer (1990) *"New Methods Of Drug Delivery,"* Science 249:1527-1533); Treat *et al.*, in LIPOSOMES IN THE THERAPY OF INFECTIOUS DISEASE AND CANCER, Lopez-Berestein and Fidler (eds.), Liss, New York, pp. 353- 365 (1989); Lopez-Berestein, ibid., pp. 3 17-327).

[00283] The compositions of the invention can be delivered in a controlled-release or sustained-release system. Any technique known to one of skill in the art can be used

to produce sustained-release formulations comprising one or more of the LAG-3-binding molecule(s) of the invention. *See*, *e.g.*, U.S. Patent No. 4,526,938; PCT publication WO 91/05548; PCT publication WO 96/20698; Ning *et al.* (1996) *"Intratumoral Radioimmunotheraphy Of A Human Colon Cancer Xenograft Using A Sustained-Release Gel,"* Radiotherapy & Oncology 39:179-189, Song *et al.* (1995) *"Antibody Mediated Lung Targeting Of Long-Circulating Emulsions,"* PDA Journal of Pharmaceutical Science & Technology 50:372-397; Cleek *et al.* (1997) *"Biodegradable Polymeric Carriers For A bFGF Antibody For Cardiovascular Application,"* Pro. Int'l. Symp. Control. Rel. Bioact. Mater. 24:853-854; and Lam *et al.* (1997) *"Microencapsulation Of Recombinant Humanized Monoclonal Antibody For Local Delivery,"* Proc. Int'l. Symp. Control Rel. Bioact. Mater. 24:759-760, each of which is incorporated herein by reference in its entirety. In one embodiment, a pump may be used in a controlled-release system (*See* Langer, *supra*; Sefton, (1987) *"Implantable Pumps,"* CRC Crit. Rev. Biomed. Eng. 14:201-240; Buchwald *et al.* (1980) *"Long-Term, Continuous Intravenous Heparin Administration By An Implantable Infusion Pump In Ambulatory Patients With Recurrent Venous Thrombosis,"* Surgery 88:507-516; and Saudek *et al.* (1989) *"A Preliminary Trial Of The Programmable Implantable Medication System For Insulin Delivery,"* N. Engl. J. Med. 321:574-579). In another embodiment, polymeric materials can be used to achieve controlled-release of the molecules (*see e.g.*, MEDICAL APPLICATIONS OF CONTROLLED RELEASE, Langer and Wise (eds.), CRC Pres., Boca Raton, Florida (1974); CONTROLLED DRUG BIOAVAILABILITY, DRUG PRODUCT DESIGN AND PERFORMANCE, Smolen and Ball (eds.), Wiley, New York (1984); Levy *et al.* (1985) *"Inhibition Of Calcification Of Bioprosthetic Heart Valves By Local Controlled-Release Diphosphonate,"* Science 228:190-192; During *et al.* (1989) *"Controlled Release Of Dopamine From A Polymeric Brain Implant: In Vivo Characterization,"* Ann. Neurol. 25:351-356; Howard *et al.* (1989) *"Intracerebral Drug Delivery In Rats With Lesion-Induced Memory Deficits,"* J. Neurosurg. 7(1):105-112); U.S. Patent No. 5,679,377; U.S. Patent No. 5,916,597; U.S. Patent No. 5,912,015; U.S. Patent No. 5,989,463; U.S. Patent No. 5,128,326; PCT Publication No. WO 99/15154; and PCT Publication No. WO 99/20253). Examples of polymers used in sustained-release formulations include, but are not limited to, poly(2-hydroxy ethyl methacrylate),

poly(methyl methacrylate), poly(acrylic acid), poly(ethylene-co-vinyl acetate), poly(methacrylic acid), polyglycolides (PLG), polyanhydrides, poly(N-vinyl pyrrolidone), poly(vinyl alcohol), polyacrylamide, poly(ethylene glycol), polylactides (PLA), poly(lactide-co-glycolides) (PLGA), and polyorthoesters. A controlled-release system can be placed in proximity of the therapeutic target (*e.g.*, the lungs), thus requiring only a fraction of the systemic dose (see, *e.g.*, Goodson, in MEDICAL APPLICATIONS OF CONTROLLED RELEASE, *supra*, vol. 2, pp. 115-138 (1984)). Polymeric compositions useful as controlled-release implants can be used according to Dunn *et al.* (See U.S. 5,945,155). This particular method is based upon the therapeutic effect of the in situ controlled-release of the bioactive material from the polymer system. The implantation can generally occur anywhere within the body of the patient in need of therapeutic treatment. A non-polymeric sustained delivery system can be used, whereby a non-polymeric implant in the body of the subject is used as a drug delivery system. Upon implantation in the body, the organic solvent of the implant will dissipate, disperse, or leach from the composition into surrounding tissue fluid, and the non-polymeric material will gradually coagulate or precipitate to form a solid, microporous matrix (See U.S. 5,888,533).

[00284] Controlled-release systems are discussed in the review by Langer (1990, *"New Methods Of Drug Delivery,"* Science 249:1527-1533). Any technique known to one of skill in the art can be used to produce sustained-release formulations comprising one or more therapeutic agents of the invention. See, *e.g.*, U.S. Patent No. 4,526,938; International Publication Nos. WO 91/05548 and WO 96/20698; Ning *et al.* (1996) *"Intratumoral Radioimmunotheraphy Of A Human Colon Cancer Xenograft Using A Sustained-Release Gel,"* Radiotherapy & Oncology 39:179-189, Song *et al.* (1995) *"Antibody Mediated Lung Targeting Of Long-Circulating Emulsions,"* PDA Journal of Pharmaceutical Science & Technology 50:372-397; Cleek *et al.* (1997) *"Biodegradable Polymeric Carriers For A bFGF Antibody For Cardiovascular Application,"* Pro. Int'l. Symp. Control. Rel. Bioact. Mater. 24:853-854; and Lam *et al.* (1997) *"Microencapsulation Of Recombinant Humanized Monoclonal Antibody For Local Delivery,"* Proc. Int'l. Symp. Control Rel. Bioact. Mater. 24:759-760, each of which is incorporated herein by reference in its entirety.

[00285] Where the composition of the invention is a nucleic acid encoding a LAG-3-binding molecule of the present invention, the nucleic acid can be administered *in vivo* to promote expression of its encoded LAG-3-binding molecule by constructing it as part of an appropriate nucleic acid expression vector and administering it so that it becomes intracellular, *e.g.*, by use of a retroviral vector (*See* U.S. Patent No. 4,980,286), or by direct injection, or by use of microparticle bombardment (*e.g.*, a gene gun; Biolistic, Dupont), or coating with lipids or cell surface receptors or transfecting agents, or by administering it in linkage to a homeobox-like peptide which is known to enter the nucleus (See *e.g.*, Joliot *et al.* (1991) *"Antennapedia Homeobox Peptide Regulates Neural Morphogenesis,"* Proc. Natl. Acad. Sci. (U.S.A.) 88:1864-1868), *etc.* Alternatively, a nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression by homologous recombination.

[00286] Treatment of a subject with a therapeutically or prophylactically effective amount of a LAG-3-binding molecule of the present invention can include a single treatment or, preferably, can include a series of treatments. In a preferred example, a subject is treated with such a diabody one time per week for between about 1 to 10 weeks, preferably between 2 to 8 weeks, more preferably between about 3 to 7 weeks, and even more preferably for about 4, 5, or 6 weeks. The pharmaceutical compositions of the invention can be administered once a day, twice a day, or three times a day. Alternatively, the pharmaceutical compositions can be administered once a week, twice a week, once every two weeks, once a month, once every six weeks, once every two months, twice a year or once per year. It will also be appreciated that the effective dosage of the molecules used for treatment may increase or decrease over the course of a particular treatment.

Examples:

[00287] Having now generally described the invention, the same will be more readily understood through reference to the following examples, which are provided by way of illustration and are not intended to be limiting of the present invention unless specified. It will be apparent to those skilled in the art that many modifications, both to materials and methods, can be practiced without departing from the scope of the present disclosure.

Example 1: Characterization of Anti-LAG-3 Monoclonal Antibodies LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5, and LAG-3 mAb 6

[00288] Six murine monoclonal antibodies were isolated as being capable of immunespecifically binding to both human and cynomolgus monkey LAG-3, and accorded the designations "**LAG-3 mAb 1**," "**LAG-3 mAb 2**," "**LAG-3 mAb 3**," "**LAG-3 mAb 4**," "**LAG-3 mAb 5**," and "**LAG-3 mAb 6.**" The CDRs of these antibodies were found to differ and are provided above. LAG-3 mAb 1 was humanized yielded two humanized VH Domains, designated herein as "**hLAG-3 mAb 1 VH-1,**" and "**hLAG-3 mAb 1 VH-2**," and four humanized VL Domains designated herein as "**hLAG-3 mAb 1 VL-1**," "**hLAG-3 mAb 1 VL-2**," "**hLAG-3 mAb 1 VL-3**," and "**hLAG-3 mAb 1 VL-4.**" LAG-3 mAb 6 was also humanized yielded two humanized VH Domains, designated herein as "**hLAG-3 mAb 6 VH-1,**" and "**hLAG-3 mAb 6 VH-2**," and two humanized VL Domains designated herein as "**hLAG-3 mAb 6 VL-1**," and "**hLAG-3 mAb 6 VL-2**." As provided above, the humanized heavy and light Variable Domains of a given antibody may be used in any combination and particular combinations of humanized Variable Domains are referred to by reference to the specific VH/VL Domains, for example a humanized antibody comprising hLAG-3 mAb 1 VH-1 and hLAG-3 mAb 1 VL-2 is specifically referred to as "**hLAG-3 mAb 1(1.2)**."

[00289] Full length humanized mAbs were constructed as follows: the C-terminus of a humanized VL Domain was fused to the N-terminus of a human light chain kappa region to generate a light chain and each light chain is paired with a heavy chain comprising a humanized VH Domain of the same antibody fused to the N-terminus of either a human IgG1 Constant Region comprising the L234A/L235A (AA) substitutions or a human IgG4 Constant Region comprising the S228P substitution.

[00290] The amino acid sequence of an exemplary human IgG1 Constant Region comprising the L234A/L235A (AA) substitutions (**SEQ ID NO:139**):

ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV
HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKRVEP
KSCDKTHTCP PCPAPE**AA**GG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS
HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK

EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSREE MTKNQVSLTC
LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW
QQGNVFSCSV MHEALHNHYT QKSLSLSPG**X**
wherein, X is a lysine (K) or is absent

[00291] In **SEQ ID NO:139**, amino acid residues 1-98 correspond to the IgG1 CH1 Domain (**SEQ ID NO:120**), amino acid residues 99-113 correspond to the IgG1 hinge region (**SEQ ID NO: 114**) and amino acid residues 114-329 correspond to the IgG1 CH2-CH3 Domain comprising the L234A/L235A substitutions (underlined) (**SEQ ID NO:123**).

[00292] The amino acid sequence of an exemplary human human IgG4 Constant Region comprising the S228P substitution (**SEQ ID NO:140**):

ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV
HTFPAVLQSS GLYSLSSVVT VPSSSLGTKT YTCNVDHKPS NTKVDKRVES
KYGPPCP**P**CP APEFLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSQED
PEVQFNWYVD GVEVHNAKTK PREEQFNSTY RVVSVLTVLH QDWLNGKEYK
CKVSNKGLPS SIEKTISKAK GQPREPQVYT LPPSQEEMTK NQVSLTCLVK
GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSRL TVDKSRWQEG
NVFSCSVMHE ALHNHYTQKS LSLSLG**X**
wherein, X is a lysine (K) or is absent

[00293] In **SEQ ID NO:140**, amino acid residues 1-98 correspond to the IgG4 CH1 Domain (**SEQ ID NO:122**), amino acid residues 99-110 correspond to the stabilized IgG4 hinge region comprising the S228P substitutions (underlined) (**SEQ ID NO: 117**) and amino acid residues 111-326 correspond to the IgG4 CH2-CH3 Domain (**SEQ ID NO:4**).

[00294] The binding kinetics of the antibodies LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5, LAG-3 mAb 6, several humanized and a reference antibody LAG-3 mAb A was investigated using Biacore analysis. The anti-LAG-3 antibodies were captured and were incubated with His-tagged soluble human LAG-3 (shLAG-3-His) and the kinetics of binding was determined via Biacore analysis. The calculated ka, kd and KD are presented in **Table 7**.

Table 7			
Anti-LAG-3 Antibody	**k_a ($x10^5$)**	**k_d ($x10^{-4}$)**	**KD (nM)**
LAG-3 mAb A	8.7	5.4	0.6
LAG-3 mAb 1[a]	20	0.26	0.013
LAG-3 mAb 1[b]	31	0.27	0.01
LAG-3 mAb 2[a]	11	21	1.9
LAG-3 mAb 3[a]	7.7	34	4.4
LAG-3 mAb 4[a]	12	9.3	0.8
LAG-3 mAb 5[a]	14	13	0.9
LAG-3 mAb 6[a]	42	0.84	0.02
hLAG-3 mAb 1 (1.2)[d, e]	23	0.13	0.01
hLAG-3 mAb 1 (2.2)[d, e]	8.2	2.6	0.3
hLAG-3 mAb 1 (1.1)[d, e]	17	0.74	0.04
hLAG-3 mAb 1 (1.4)[c, e]	16	0.59	0.04
hLAG-3 mAb 1 (1.4)[c, f]	17	0.86	0.05

a = captured on immobilized Fab2 goat-anti-mouse Fc b = captured on immobilized Protein G
c = captured on immobilized Fab2 goat anti-human Fc d = captured on immobilized Protein A
e = human IgG1 (AA) f = IgG4 (S228P)

[00295] In additional studies, the binding kinetics of the humanized antibodies hLAG-3 mAb 1 (1.4) and hLAG-3 mAb 6 (1.1), and a reference antibody LAG-3 mAb A to both human and cynomolgus monkey LAG-3 was investigated using Biacore analysis. In these studies, a soluble LAG-3 fusion protein (the extracelluar domain of human or cynomolgus monkey LAG-3 fused to murine IgG2a) was captured on a Fab2 goat-anti mouse Fc surface and incubated with the anti-LAG-3 antibody and the kinetics of binding was determined via Biacore analysis. The binding curves for LAG-3 mAb A, hLAG-3 mAb 1 (1.4) and hLAG-3 mAb 6 (1.1) binding to cynomolgus monkey LAG-3 are shown in **Figures 7A-7C** respectively, and the calculated ka, kd and KD are presented in **Table 8**. In a separate study, the binding of a bispecific Fc Region-containing diabody comprising hLAG-3 mAb 6 (1.1) to both human and cynomolgus monkey LAG-3 was investigated using Biacore analysis. In this study, the hLAG-3 mAb 6 (1.1) containing diabody was captured on a Fab_2 goat-anti human Fc surface and incubated with soluble LAG-3 fusion protein (the extracelluar domain of human or cynomolgus monkey LAG-3 fused to a His tag) and the kinetics of binding was determined via Biacore analysis. The calculated ka, kd and KD are presented in **Table 8**.

Table 8						
Anti-LAG-3 Antibody	Human			Cynomolgus Monkey		
	k_a ($x10^4$)	k_d ($x10^{-5}$)	KD (nM)	k_a ($x10^4$)	k_d ($x10^{-5}$)	KD (nM)
LAG-3 mAb A	6.2	1.0	0.16	2.4	1100	458
hLAG-3 mAb 1 (1.4)[a]	3.4	<1.0	<0.29	1.9	<1.0	<0.53
hLAG-3 mAb 6 (1.1)[a]	9.9	<1.0	<0.1	8.2	30	3.7
hLAG-3 mAb 6 (1.1)[b]	480	16	0.033	59	78	0.13

a = immobilized human or cynomolgus LAG-3- murine IgG2a fusion protein

b = immobilized Fc Region-containing diabody comprising a hLAG-3 mAb 6 (1.1) epitope-binding domain

[00296] The results demonstrate that LAG-3 mAb 1 and LAG-3 mAb 6 exhibit better binding kinetics than reference antibody LAG-3 mAb A. In addition, humanized LAG-3 mAb 6 exhibits better cross-reactive binding kinetics with cynomolgus monkey LAG-3.

[00297] The epitope specificity of LAG-3 mAb 1, LAG-3 mAb 6 and the reference antibody LAG-3 mAb A was examined using Biacore analysis. In order to determine whether the antibodies bound to different LAG-3 epitopes, shLAG-3-His was captured by mouse anti-PentaHis antibody immobilized on the CM5 sensor chip according to the procedure recommended by the manufacturer. Briefly, the carboxyl groups on the sensor chip surface were activated with an injection of a solution containing 0.2 M N-ethyl-N-(3dietylamino-propyl) carbodimide and 0.05 M N-hydroxy-succinimide. Anti-PentaHis antibody was injected over the activated CM5 surface in 10 mM sodium-acetate, pH 5.0, at a flow rate 5 μL/min, followed by 1 M ethanolamine for deactivation of remaining amine-reactive groups. Binding experiments were performed in HBS-EP buffer, which contains 10 mM HEPES, pH 7.4, 150 mM NaCl, 3 mM EDTA, and 0.005% P20 surfactant. Each antibody (LAG-3 mAb 1, LAG-3 mAb 6 and LAG-2 mAb A) was preinjected over captured hLAG3-His for 180 seconds at a flow rate of 5 μL/min at concentration of 1μM followed by running buffer and injection of competing antibody at the same conditions. Binding response of competing antibody was compared to its binding response to hLAG3-His preinjected with buffer to identify antibodies competing for the same epitope. Regeneration of the immobilized anti-PentaHis surface was performed by pulse injection of 10 mM glycine, pH 1.5. Reference curves were obtained by injection of analytes over the treated surface with

no immobilized protein. Binding curves were generated by BIAevaluation software v4.1 from real-time sensogram data.

[00298] The results of this experiment are shown in **Figures 8A-8D**. The results of this experiment indicate that the biotinylated antibody LAG3 mAb A was capable of binding to shLAG-3-His even in the presence of excess amounts of the non-biotinylated antibodies LAG-3 mAb 1 and LAG-3 mAb 6. In contrast, LAG-3 mAb 1 blocked the binding of LAG-3 mAb 6. Thus, the results show that LAG-3 mAb 1 and LAG-3 mAb 6 likely bind to the same, or over lapping epitopes of LAG-3, and compete with one another for binding to LAG-3. Both LAG-3 mAb 1 and LAG-3 mAb 6 were found to bind to an epitope that is distinct from that bound by LAG-3 mAb A.

[00299] In order to further characterize the anti-LAG3 antibodies, their ability to block binding between LAG-3 and MHC class II was assessed in two different assays. In one assay, the ability of the antibodies to block the binding of a soluble human LAG3-Fc fusion protein to MHC class II immobilized on a surface was examined. For this assay, LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, and LAG-3 mAb 5 each (at 0-67 nM, 2 fold serial dilutions) were mixed with a soluble human LAG-3-Fc fusion protein, (at 5 μg/mL) and were separately incubated with immobilized MHC class II (1 μg/mL). The amount of LAG-3 binding to the immobilized MHC class II was assessed using a goat anti-human Fc gamma-HRP secondary antibody. In additional experiments LAG-3 mAb A and the humanized antibodies, hLAG-3 mAb 1 (1.4) and hLAG-3 mAb 6 (1.1) (at 0.0096-7.0 nM, three fold serial dilutions) were mixed with soluble human LAG-3-His fusion protein (0.2 μg/ml) and assayed for binding to immobilized MHC class II as described above. The results of these experiments are shown in **Figure 9A** and **Figure 9B**.

[00300] In another assay, the ability of the anti-LAG-3 antibodies of the present invention to block the binding of a soluble human LAG3-Fc fusion protein (shLAG-3-Fc) to native MHC class II on a cell surface was examined. For this assay, LAG-3 mAb 1, LAG-3 mAb 2, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 5, and the reference antibody LAG-3 mAb A each (at 0.1-26.7 ng/ml, 2 fold serial dilutions) were mixed with a biotinylated-soluble human LAG-3-Fc fusion protein, (at 0.5 μg/ml) and were

separately incubated with MHC II-positive Daudi cells. The amount of LAG-3 binding to the surface of the Daudi cells was determined using a PE-conjugated Streptavidin secondary antibody by FACS analysis. In additional separate experiments LAG-3 mAb 1, LAG-3 mAb 6 and LAG-3 mAb A; or LAG-3 mAb 1 and the humanized antibodies, hLAG-3 mAb 1 (1.4), hLAG-3 mAb 1 (1.2), hLAG-3 mAb 1 (2.2), and hLAG-3 mAb 1 (1.1) were assayed as described above. The results of these experiments are shown in **Figures 10A-10C**, respectively.

[00301] The results of these inhibition assays (**Figures 9A-9B** and **Figures 10A-10C**) show that all the anti-LAG-3 antibodies tested blocked the binding of a shLAG-3-Fc fusion protein to bind MHC class II.

Example 2: Flow-Cytometry Methodology

[00302] Experiments to determine expression levels of checkpoint inhibitors: PD-1 and LAG-3 on cells in the experiments described below used the following appropriately fluorescent labeled commercial antibodies (phycoerythrin-cyanine7 (PE-Cy7)-conjugated anti-CD4 [clone SK3] or fluorescein isothiocyanate (FITC)-conjugated anti-CD4 [clone RPA-T4], phycoerythrin (PE)-conjugated anti-LAG-3 [clone 3DS223H], phycoerythrin (PE)-conjugated anti-PD-1 [clone EH12.2H7] or allophycocyanin (APC)-conjugated (eBiosciences, or BioLegend)) and the appropriate isotype controls. All antibodies were used at the manufacturer's recommended concentrations. Cell staining was performed in FACS buffer (10% FCS in PBS) on ice for 30 minutes in the dark for the addition of primary antibodies. After two washes, cells were either stained with the appropriate secondary reagent on ice for 30 minutes in the dark or immediately analyzed on a flow cytometer. To exclude dead cells, all samples were co-stained with a viability dye: 7-Aminoactinomycin D (7-AAD) (BD Biosceinces, or BioLegend,) or 4',6-Diamidino-2-Phenylindole, Dihydrochloride (DAPI) (Life Technologies). All samples were analyzed on either a FACS Calibur or Fortessa Flow Cytometer (BD Biosciences) and analyzed using FlowJo Software (TreeStar, Ashland, OR).

Example 3: LAG-3 Expression and Antibody Binding To Stimulated T-Cells

[00303] LAG-3 expression and the ability of the isolated LAG-3 antibodies to specifically bind LAG-3 on the surface of CD3/CD28-stimulated T-cells was examined. T-cells were obtained from peripheral blood mononuclear cell (PBMCs), briefly, PBMCs were purified using the Ficoll-Paque Plus (GE Healthcare) density gradient centrifugation method according to manufacturer's instructions from whole blood obtained under informed consent from healthy donors (Biological Specialty Corporation) and T cells were then purified using the Dynabeads® Untouched Human T Cells Kit (Life Technologies) according to manufacturer's instructions. For stimulation, isolated T cells were cultured for 10-14 days in the presence of recombinant human IL-2 30 U/ml] (Peprotech) and Dynabeads® Human T cell Activator beads (Life Technologies) according to manufacturer's instructions. LAG-3 expression on freshly isolated unstimulated CD4+ T cells, and stimulated CD4+ T cells (taken from culture at day 11 or 14), was examined by flow cytometry as described above, using FITC-conjugated anti-CD4 and PE-conjugated anti-LAG-3.

[00304] The results of these studies are shown in **Figure 11A-11C**. No LAG-3 expression was observed on unstimulated CD4+ T-cells (**Figure 11A**). However, CD3/CD8 stimulated CD4+ T-cells from two different donors (D:58468 and D:43530) exhibited a dramatic increase in LAG-3 expression (**Figure 11B** and **11C**).

[00305] The ability of LAG-3 mAb 1 (**Figure 12, Panels A** and **D**), LAG-3 mAb 2 (**Figure 12, Panels B** and **E**), LAG-3 mAb 3 (**Figure 12, Panels C** and **F**), LAG-3 mAb 4 (**Figure 13, Panels A** and **C**), and LAG-3 mAb 5 (**Figure 13, Panels B** and **D**), to specifically bind to stimulated CD4+ T cells was investigated. Stimulated T cells (prepared as described above from donor D:58468) taken from culture at day 14, and fresh unstimulated cells (prepared as described above from donor D:43530) were subjected to flow cytometry using the isolated anti-LAG-3 antibodies and the following appropriately fluorescent labeled secondary reagent (PC-conjugated anti-mouse-IgG (H+L) (Jackson ImmunoResearch Labs)) and FITC-conjugated anti-CD4. As shown in **Figure 12, Panels A-F** and **Figure 13, Panels A-D**, each of the anti-LAG-3 antibodies examined bound only to stimulated, but not to unstimulated CD4+ T-cells.

[00306] The results of these studies demonstrate that LAG-3 is upregulated on stimulated T-cells and that the anti-LAG-3 antibodies of the present invention specifically bind only stimulated T-cells.

Example 4: Functional Activity of anti-LAG Antibodies

[00307] *Staphylococcus aureus* enterotoxin type B (SEB) is a microbial superantigen capable of activating a large proportion of T-cells (5-30%). SEB binds to MHC II outside the peptide binding grove and thus is MHC II dependent, but unrestricted and TCR mediated. SEB-stimulation of T-cells results in oligoclonal T-cell proliferation and cytokine production (although donor variability may be observed). The expression of anti-LAG-3 and anti-PD-1 antibodies alone and in combination on SEB-stimulated PMBCs was examined.

[00308] PBMCs purified as described above were cultured in RPMI-media + 10% heat inactivated FBS + 1% Penicillin/Streptomycin in T-25 bulk flasks for 2-3 days alone or with SEB (Sigma-Aldrich) at 0.1 ng/ml (primary stimulation). At the end of the first round of SEB-stimulation, PBMCs were washed twice with PBS and immediately plated in 96-well tissue culture plates at a concentration of 1-5 x 10^5 cells/well in media alone, media with SEB at 0.1 ng/ml (secondary stimulation) and no antibody, or media with SEB and a control IgG antibody, and cultured for an additional 2-3 days. At 48 hours post-primary bulk SEB-stimulation, cells were examined for PD-1 and LAG-3 expression by flow cytometry using PE-conjugated anti-LAG-3 and FITC-conjugated anti-CD3; or APC-conjugated anti-PD-1 and FITC-conjugated anti-CD3. At day 5, post-secondary culture in 96-well plate with SEB-stimulation, wells treated with no antibody or with control antibody were examined using flow cytometry for PD-1 and LAG-3 expression using PE-conjugated anti-LAG-3 and APC-conjugated anti-PD-1.

[00309] Flow cytometry results from two representative donors (D:34765 and D:53724) are shown in **Figure 14, Panels A-D** (D:34765) and **Figure 15, Panels A-D** (D:53724). These results demonstrate that LAG-3 and PD-1 are upregulated by 48 hours post-SEB-stimulation with a further enhancement seen at day 5 post culture with SEB-stimulation. In these studies, Donor 1 had more LAG-3/PD-1 double positive

cells after SEB-stimulation. The addition of a control antibody post-SEB-stimulation did not alter LAG-3 or PD-1 expression (compare **Figure 14, Panels C** and **D**, and **Figure 15, Panels C** and **D**).

[00310] Upregulation of the immune check point proteins LAG-3 and PD-1 following SEB-stimulation of PBMCs limits cytokine release upon restimulation. The ability of LAG-3 mAb 1, LAG-3 mAb 3, LAG-3 mAb 4, LAG-3 mAb 6, a PD-1 monoclonal antibody designated "**PD-1 mAb 5**", and the reference antibodies PD-1 mAb 1 (comprising the 235A/235A Fc variant (AA)), PD-1 mAb 2, LAG-3 mAb A, and the commercial anti-LAG3 antibody 17B4 (#LS-C18692, LS Bio, designated "**LAG-3 mAb B**") to enhance cytokine release through checkpoint inhibition was examined.

[00311] PBMCs were stimulated with SEB as described above except during the secondary stimulations cells were plated with no antibody, with an isotype control antibody, or with anti-LAG-3 and anti-PD-1 antibodies alone or in combination. At the end of the second stimulation, supernatants were harvested to measure cytokine secretion using human DuoSet ELISA Kits for IFNγ, TNFα, IL-10, and IL-4 (R&D Systems) according to the manufacture's instructions. **Figures 16A-16B** shows the IFNγ (**Figure 16A**) and TNFα (**Figure 16B**), secretion profiles from SEB-stimulated PBMCs from a representative donor (D:38166), treated with no antibody or one of the following antibodies: isotype control, PD-1 mAb 1, PD-1 mAb 2, LAG-3 mAb A, LAG-3 mAb B, LAG-3 mAb 1, LAG-3 mAb 3, LAG-3 mAb 4, or LAG-3 mAb 6. For this study the antibodies were utilized at 0.009, 0.039, 0.156, 0.625, 2.5, 10, and 40 μg/ml. **Figure 17** shows the IFNγ secretion profiles from SEB-stimulated PBMCs from another representative donor (D:58108), treated with: no antibody; isotype control antibody; PD-1 mAb 2 and/or LAG-3 mAb A; PD-1 mAb 5 and/or LAG-3 mAb 1; or PD-1 mAb 5 and/or LAG-3 mAb 3. For this study the antibodies were used at 10 μg/ml.

[00312] The results of these studies demonstrate that anti-PD-1 antibodies dramatically enhanced immune system function as evidenced by increased IFNγ (**Figure 16A** and **Figure 17**), and TNFα (**Figure 16B**) production from SEB-stimulated PBMCs upon restimulation. Surprisingly, LAG-3 mAb 1 was also seen to increase

cytokine production across multiple donors to levels comparable to the anti-PD-1 antibodies while the reference anti-LAG-3 mAbs, LAG-3 mAb A and LAG-3 mAb B and several of the isolated antibodies (LAG-3 mAb 3, LAG-4, and LAG-6) provided only a slight enhancement of cytokine release. In addition, the combination of anti-LAG-3 antibodies with anti-PD-1 resulted in a further enhancement of cytokine release (**Figure 17**) from SEB-stimulated PBMCs upon restimulation. LAG-3 mAb 1 provided the largest enhancement in cytokine release when combined with an anti-PD-1 antibody as compared to LAG-3 mAb 3 and the reference antibody LAG-3 mAb A.

Example 5: Binding to Endogenous Cynomolgus Monkey LAG-3

[00313] The ability of the humanized antibody hLAG-3 mAb 6 (1.1), and the reference antibody LAG-3 mAb A to bind endogenous LAG-3 expressed on cynomolgus monkey PBMCs by was investigated FACS. For this study PBMCs were isolated from donor cynomolgus monkey whole blood and cultured alone or with SEB stimulation (500 ng/mL) essentially as described above. At 66 hours post-SEB-stimulation cells (unstimulated and stimulated) were stained with hLAG-3 mAb 6 (1.1), LAG-3 mAb A, or PD-1 mAb 1 antibodies (10 fold serial dilutions). The antibodies were detected with goat-anti human Fc-APC labeled secondary antibody. Binding is plotted in **Figure 18A-18B** for two cynomolgus monkey donors.

[00314] SEB stimulation was confirmed by enhanced PD-1 expression as detected with the anti-PD-1 antibody PD-1 mAb 1. The results of these studies demonstrate that hLAG-3 mAb 6 (1.1) binds endogenous LAG-3 expressed on the surface of stimulated cynomolgous monkey PBMCs.

[00315] All publications and patents mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference in its entirety. While the invention has been described in connection with specific embodiments thereof, it will be understood that it is capable of further modifications and this application is intended to cover any variations, uses, or adaptations of the invention following, in general, the principles of the invention and including such departures from the present disclosure as come within known or customary practice

within the art to which the invention pertains and as may be applied to the essential features hereinbefore set forth.

What Is Claimed Is:

Claim 1. A LAG-3-binding molecule that is capable of binding both to human LAG-3 and to cynomolgus monkey LAG-3, wherein said LAG-3-binding molecule is an antibody or comprises an antigen-binding fragment thereof that comprises a Variable Heavy Chain Domain and a Variable Light Chain Domain of an antibody that specifically binds human LAG-3 with an equilibrium binding constant (KD) of about 0.05 nM or less, wherein:

said Variable Heavy Chain Domain comprises a CDR_H1 Domain, a CDR_H2 Domain and a CDR_H3 Domain, and said Variable Light Chain Domain comprises a CDR_L1 Domain, a CDR_L2 Domain, and a CDR_L3 Domain, wherein:

(A) (1) the CDR_H1 Domain, CDR_H2 Domain, and CDR_H3 Domain are the Heavy Chain CDRs of LAG-3 mAb 1, and respectively have the amino acid sequences: **SEQ ID NO:8**, **SEQ ID NO:9**, and **SEQ ID NO:10**; and

(2) the CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain are the Light Chain CDRs of LAG-3 mAb 1, and respectively have the amino acid sequences: **SEQ ID NO:13**, **SEQ ID NO:14**, and **SEQ ID NO:15**;

(B) (1) the CDR_H1 Domain, CDR_H2 Domain, and CDR_H3 Domain are the Heavy Chain CDRs of hLAG-3 mAb 1, and respectively have the amino acid sequences: **SEQ ID NO:8**, **SEQ ID NO:9**, and **SEQ ID NO:10**; and

(2) the CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain are the Light Chain CDRs of hLAG-3 mAb 1, and respectively have the amino acid sequences: **SEQ ID NO:28**, **SEQ ID NO:14**, and **SEQ ID NO:15**;

(C) (1) the CDR_H1 Domain, CDR_H2 Domain, and CDR_H3 Domain are the Heavy Chain CDRs of LAG-3 mAb 6 VH1, and respectively have the amino acid sequences: **SEQ ID NO:71**, **SEQ ID NO:72**, and **SEQ ID NO:73**; and

(2) the CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain are the Light Chain CDRs of LAG-3 mAb 6, and, respectively have the amino acid sequences: **SEQ ID NO:76**, **SEQ ID NO:77**, and **SEQ ID NO:78**;

or

(D) (1) the CDR_H1 Domain, CDR_H2 Domain, and CDR_H3 Domain are the Heavy Chain CDRs of hLAG-3 mAb 6, and respectively have the amino acid sequences: **SEQ ID NO:71**, **SEQ ID NO:72**, and **SEQ ID NO:73**; and

(2) the CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain are the Light Chain CDRs of hLAG-3 mAb 6, and respectively have the amino acid sequences: **SEQ ID NO:87**, **SEQ ID NO:77**, and **SEQ ID NO:78**;

wherein said LAG-3-binding molecule is capable of binding both to human LAG-3 and to cynomolgus monkey LAG-3, and is capable of binding to human LAG-3 with an equilibrium binding constant (KD) of about 0.05 nM or less.

Claim 2. The LAG-3-binding molecule of claim 1, wherein:

(A) (1) the CDR_H1 Domain, CDR_H2 Domain, and CDR_H3 Domain are the Heavy Chain CDRs of LAG-3 mAb 1, and respectively have the amino acid sequences: **SEQ ID NO:8**, **SEQ ID NO:9**, and **SEQ ID NO:10**; and

(2) the CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain are the Light Chain CDRs of LAG-3 mAb 1, and respectively have the amino acid sequences: **SEQ ID NO:13**, **SEQ ID NO:14**, and **SEQ ID NO:15**; or

(B) (1) the CDR_H1 Domain, CDR_H2 Domain, and CDR_H3 Domain are the Heavy Chain CDRs of hLAG-3 mAb 1, and respectively have the amino acid sequences: **SEQ ID NO:8**, **SEQ ID NO:9**, and **SEQ ID NO:10**; and

(2) the CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain are the Light Chain CDRs of hLAG-3 mAb 1, and respectively have the amino acid sequences: **SEQ ID NO:28**, **SEQ ID NO:14**, and **SEQ ID NO:15**.

Claim 3. The LAG-3-binding molecule of claim 1, wherein:

(A) (1) the CDR_H1 Domain, CDR_H2 Domain, and CDR_H3 Domain are the Heavy Chain CDRs of LAG-3 mAb 6, and respectively have the amino acid sequences: **SEQ ID NO:71**, **SEQ ID NO:72**, and **SEQ ID NO:73**; and

(2) the CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain are the Light Chain CDRs of hLAG-3 mAb 6, and respectively have the amino acid sequences: **SEQ ID NO:76**, **SEQ ID NO:77**, and **SEQ ID NO:78**; or

(B) (1) the CDR_H1 Domain, CDR_H2 Domain, and CDR_H3 Domain are the Heavy Chain CDRs of hLAG-3 mAb 6, and respectively have the amino acid sequences: **SEQ ID NO:71**, **SEQ ID NO:72**, and **SEQ ID NO:73**; and

(2) the CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain are the Light Chain CDRs of hLAG-3 mAb 6, and respectively have the amino acid sequences: **SEQ ID NO:87**, **SEQ ID NO:77**, and **SEQ ID NO:78**.

Claim 4. A LAG-3-binding molecule that is capable of binding both to human LAG-3 and to cynomolgus monkey LAG-3, wherein said LAG-3-binding molecule is an antibody or comprises an antigen-binding fragment thereof that comprises a Variable Heavy Chain Domain and a Variable Light Chain Domain, wherein:

(A) (1) said Variable Heavy Chain Domain comprises the amino acid sequence of **SEQ ID NO:16** or **SEQ ID NO:18**; and

(2) said Variable Light Chain Domain comprises the amino acid sequence of **SEQ ID NO:24** or **SEQ ID NO:26**; or

(B) (1) said Variable Heavy Chain Domain comprises the amino acid sequence of **SEQ ID NO:79**; and

(2) said Variable Light Chain Domain comprises the amino acid sequence of **SEQ ID NO:83**.

Claim 5. The LAG-3-binding molecule of any one of claims 1-4, wherein said molecule comprises:

(1) a Heavy Chain Variable Domain comprising the amino acid sequence of **SEQ ID NO:16** or **SEQ ID NO:18**; and

(2) a Light Chain Variable Domain comprising the amino acid sequence of **SEQ ID NO:24** or **SEQ ID NO:26**.

Claim 6. The LAG-3-binding molecule of any one of claims 1-4, wherein said molecule comprises:

(1) a Heavy Chain Variable Domain comprising the amino acid sequence of **SEQ ID NO:79**; and

(2) a Light Chain Variable Domain comprising the amino acid sequence of **SEQ ID NO:83**.

Claim 7. The LAG-3-binding molecule of claim 5, wherein said molecule comprises a Heavy Chain Variable Domain comprising the amino acid sequence of **SEQ ID NO:16**, and a Light Chain Variable Domain comprising the amino acid sequence of **SEQ ID NO:24**,

Claim 8. The LAG-3-binding molecule of claim 5, wherein said molecule comprises a Heavy Chain Variable Domain comprising the amino acid sequence of **SEQ ID NO:16**, and a Light Chain Variable Domain comprising the amino acid sequence of **SEQ ID NO:26**,

Claim 9. The LAG-3-binding molecule of any one of claims 1-8, wherein said molecule is an antibody.

Claim 10. The LAG-3-binding molecule of claim 9, wherein said molecule is a chimeric antibody or a humanized antibody.

Claim 11. The LAG-3-binding molecule of any one of claims 1-8, wherein said molecule is a bispecific binding molecule, capable of simultaneously binding to human LAG-3 and to a second epitope.

Claim 12. The LAG-3-binding molecule of claim 11, wherein said second epitope is an epitope of a molecule involved in regulating an immune check point present on the surface of an immune cell.

Claim 13. The LAG-3-binding molecule of claim 11, wherein said second epitope is an epitope of B7-H3, B7-H4, BTLA, CD40, CD40L, CD47, CD70, CD80, CD86, CD94, CD137, CD137L, CD226, CTLA-4, Galectin-9, GITR, GITRL, HHLA2, ICOS, ICOSL, KIR, LAG-3, LIGHT, MHC class I or II, NKG2a, NKG2d, OX40, OX40L, PD1H, PD-1, PD-L1, PD-L2, PVR, SIRPa, TCR, TIGIT, TIM-3 or VISTA.

Claim 14. The LAG-3-binding molecule of claim 13, wherein said second epitope is an epitope of PD-1.

Claim 15. The LAG-3-binding molecule of any one of claims 11-14, wherein said molecule is:

(a) a diabody, said diabody being a covalently bonded complex that comprises two, or three or four different polypeptide chains; or

(b) a trivalent binding molecule, said trivalent binding molecule being a covalently bonded complex that comprises three, four, or five polypeptide chains.

Claim 16. The LAG-3-binding molecule of any one of claims 1-15, wherein said molecule comprises an Fc Region.

Claim 17. The LAG-3-binding molecule of any one of claims 1-16, wherein said molecule comprises an Albumin-Binding Domain (ABD).

Claim 18. The LAG-3-binding molecule of claim 17, wherein said ABD is a deimmunized ABD.

Claim 19. The LAG-3-binding molecule of claim 16, wherein said Fc Region is a variant Fc Region that comprises:

(a) one or more amino acid modifications that reduce(s) the affinity of said variant Fc Region for an FcγR; and/or

(b) one or more amino acid modifications that enhance(s) the serum half-life of said variant Fc Region.

Claim 20. The LAG-3-binding molecule of claim 19, wherein:

(a) said modifications that reduce(s) the affinity of the variant Fc Region for an FcγR comprise the substitutions:

(1) L234A; L235A; or

(2) L234A and L235A;

and

(b) said modifications that enhance(s) the serum half-life of the variant Fc Region comprise the substitutions:

(1) M252Y and S254T;

(2) M252Y and T256E;

(3) M252Y, S254T and T256E; or

(4) K288D and H435K,

wherein said numbering is that of the EU index according to Kabat.

Claim 21. A pharmaceutical composition comprising an effective amount of the LAG-3-binding molecule of any one of claims 1-20, and a pharmaceutically acceptable carrier.

Claim 22. The LAG-3-binding molecule of any one of claims 1-20, or the pharmaceutical composition of claim 21, for use in stimulating a T-cell-mediated immune response of a subject in need thereof.

Claim 23. The LAG-3-binding molecule of any one of claims 1-20, or the pharmaceutical composition of claim 21, for use in treating a disease or condition associated with a suppressed immune system.

Claim 24. The LAG-3-binding molecule of claim 23, wherein the disease or condition is cancer or an infection.

Claim 25. The LAG-3-binding molecule of claim 24, wherein disease or condition is a cancer selected from the group consisting of: an adrenal gland tumor, an AIDS-associated cancer, an alveolar soft part sarcoma, an astrocytic tumor, bladder cancer, bone cancer, a brain and spinal cord cancer, a metastatic brain tumor, a breast cancer, a carotid body tumors, a cervical cancer, a

chondrosarcoma, a chordoma, a chromophobe renal cell carcinoma, a clear cell carcinoma, a colon cancer, a colorectal cancer, a desmoplastic small round cell tumor, an ependymoma, a Ewing's tumor, an extraskeletal myxoid chondrosarcoma, a gallbladder or bile duct cancer, gastric cancer, a gestational trophoblastic disease, a germ cell tumor, a head and neck cancer, hepatocellular carcinoma, an islet cell tumor, a Kaposi's Sarcoma, a kidney cancer, a leukemia, a liposarcoma/malignant lipomatous tumor, a liver cancer, a lymphoma, a lung cancer, a medulloblastoma, a melanoma, a meningioma, a multiple endocrine neoplasia, a multiple myeloma, a myelodysplastic syndrome, a neuroblastoma, a neuroendocrine tumors, an ovarian cancer, a pancreatic cancer, a papillary thyroid carcinoma, a parathyroid tumor, a pediatric cancer, a peripheral nerve sheath tumor, a pheochromocytoma, a pituitary tumor, a prostate cancer, a posterious uveal melanoma, a renal metastatic cancer, a rhabdoid tumor, a rhabdomyosarcoma, a sarcoma, a skin cancer, a soft-tissue sarcoma, a squamous cell cancer, a stomach cancer, a synovial sarcoma, a testicular cancer, a thymic carcinoma, a thymoma, a thyroid metastatic cancer, and a uterine cancer.

Claim 26. The LAG-3-binding molecule of claim 24, wherein said disease or condition is selected from the group consisting of: colorectal cancer, hepatocellular carcinoma, glioma, kidney cancer, breast cancer, multiple myeloma, bladder cancer, neuroblastoma, sarcoma, non-Hodgkin's lymphoma, non-small cell lung cancer, ovarian cancer, pancreatic cancer, rectal cancer, acute myeloid leukemia (AML), chronic myelogenous leukemia (CML), acute B lymphoblastic leukemia (B-ALL), chronic lymphocytic leukemia (CLL), hairy cell leukemia (HCL), blastic plasmacytoid dendritic cell neoplasm (BPDCN), non-Hodgkin's lymphoma (NHL), including mantel cell leukemia (MCL), and small lymphocytic lymphoma (SLL), Hodgkin's lymphoma, systemic mastocytosis, and Burkitt's lymphoma.

Claim 27. The LAG-3-binding molecule of any one of claims 1-20, or the pharmaceutical composition of claim 21, wherein said molecule is detectably labeled for use in the detection of LAG-3.