Anti-CD3 Antibodies and Methods of Use Thereof

FIELD OF THE INVENTION

This invention relates generally to fully human anti-CD3 antibodies as well as to methods for use thereof.

BACKGROUND OF THE INVENTION

The body's immune system serves as a defense against a variety of conditions, including, *e.g.*, injury, infection and neoplasia, and is mediated by two separate but interrelated systems, the cellular and humoral immune systems. Generally speaking, the humoral system is mediated by soluble products, termed antibodies or immunoglobulins, which have the ability to combine with and neutralize products recognized by the system as being foreign to the body. In contrast, the cellular immune system involves the mobilization of certain cells, termed T-cells that serve a variety of therapeutic roles.

The immune system of both humans and animals include two principal classes of lymphocytes: the thymus derived cells (T cells), and the bone marrow derived cells (B cells). Mature T cells emerge from the thymus and circulate between the tissues, lymphatics, and the bloodstream. T cells exhibit immunological specificity and are directly involved in cell-mediated immune responses (such as graft rejection). T cells act against or in response to a variety of foreign structures (antigens). In many instances these foreign antigens are expressed on host cells as a result of infection. However, foreign antigens can also come from the host having been altered by neoplasia or infection. Although T cells do not themselves secrete antibodies, they are usually required for antibody secretion by the second class of lymphocytes, B cells.

There are various subsets of T cells, which are generally defined by antigenic determinants found on their cell surfaces, as well as functional activity and foreign antigen recognition. Some subsets of T cells, such as $CD8^+$ cells, are killer/suppressor cells that play a regulating function in the immune system, while others, such as $CD4^+$ cells, serve to promote inflammatory and humoral responses.

Human peripheral T lymphocytes can be stimulated to undergo mitosis by a variety of agents including foreign antigens, monoclonal antibodies and lectins such as phytohemayglutinin and concanavalin A. Although activation presumably occurs by binding of the mitogens to specific sites on cell membranes, the nature of these receptors, and their mechanism of activation, is not completely elucidated. Induction of proliferation is only one indication of T cell activation. Other indications of activation, defined as alterations in the basal or resting state of the cell, include increased lymphokine production and cytotoxic cell activity.

T cell activation is a complex phenomenon that depends on the participation of a variety of cell surface molecules expressed on the responding T cell population. For example, the antigen-specific T cell receptor (TcR) is composed of a disulfide-linked heterodimer, containing two clonally distributed, integral membrane glycoprotein chains, alpha and beta (α and β), or gamma and delta (γ and δ), non-covalently associated with a complex of low molecular weight invariant proteins, commonly designated as CD3 (once referred to as T3).

The TcR alpha and beta chains determine antigen specificities. The CD3 structures represent accessory molecules that are the transducing elements of activation signals initiated upon binding of the TcR alpha beta (TcR $\alpha\beta$) to its ligand. There are both constant regions of the glycoprotein chains of TcR, and variable regions (polymorphisms). Polymorphic TcR variable regions define subsets of T cells, with distinct specificities. Unlike antibodies that recognize whole or smaller fragments of foreign proteins as antigens, the TcR complex interacts with only small peptides of the antigen, which must be presented in the context of major histocompatibility complex (MHC) molecules. These MHC proteins represent another highly polymorphic set of molecules randomly dispersed throughout the species. Thus, activation usually requires the tripartite interaction of the TcR and foreign peptidic antigen bound to the major MHC proteins.

SUMMARY OF THE INVENTION

The present invention provides fully human monoclonal antibodies specifically directed against CD3. Exemplary monoclonal antibodies include 28F11, 27H5, 23F10 and 15C3 described herein. Alternatively, the monoclonal antibody is an antibody that binds to the same epitope as 28F11, 27H5, 23F10 or 15C3. The antibodies are respectively referred to herein is huCD3 antibodies. The huCD3 antibody has one or more of the following characteristics: the antibody binds to CD3 positive (CD3+) cells but not CD3 negative (CD3-) cells; the huCD3 antibody induces antigenic modulation which involves alteration (*e.g.*, decrease) of the cell surface expression level or activity of CD3 or the T cell receptor (TcR); the huCD3 antibody inhibits binding of the murine anti-human OKT3 monoclonal antibody to T-lymphocytes; or the huCD3 antibody binds an epitope of CD3 that wholly or partially includes the amino acid sequence EMGGITQTPYKVSISGT (SEQ ID NO:21). The huCD3 antibodies of the invention compete with the murine anti-CD3 antibody OKT3 for binding to CD3, and exposure to the huCD3 antibody removes or masks CD3 and/or TcR without affecting cell surface expression of CD2, CD4 or CD8. The masking of CD3 and/or TcR results in the loss or reduction of T-cell activation, which is desirable in autoimmune diseases where uncontrolled T-cell activation occurs. Down-regulation of CD3 results in a prolonged effect of reduced T cell activation, *e.g.*, for a period of at least several months, as compared with the transient suppression that is observed when using a traditional immunosuppressive agent, *e.g.*, cyclosporin.

Antigenic modulation refers to the redistribution and elimination of the CD3-T cell receptor complex on the surface of a cell, *e.g.*, a lymphocyte. Decrease in the level of cell surface expression or activity of the TcR on the cell is meant that the amount or function of the TcR is reduced. Modulation of the level of cell surface expression or activity of CD3 is meant that the amount of CD3 on the cell surface or function of CD3 is altered, *e.g.*, reduced. The amount of CD3 or the TcR expressed at the plasma membrane of the cell is reduced, for example, by internalization of CD3 or the TcR upon contact of the cell with the huCD3 antibody. Alternatively, upon contact of a cell with the huCD3 antibody, CD3 or the TcR is masked.

Inhibiting the binding of the murine anti-human OKT3 monoclonal antibody to a T-lymphocyte is defined as a decrease in the ability of the murine OKT3 antibody to form a complex with CD3 on the cell surface of a T-lymphocyte.

A huCD3 antibody contains a heavy chain variable having the amino acid sequence of SEQ ID NOS: 2, 6, 10 or 22 and a light chain variable having the amino acid sequence of SEQ ID NOS: 4, 8, 16-20 or 25-26. Preferably, the three heavy chain CDRs include an amino acid sequence at least 90%, 92%, 95%, 97% 98%, 99% or more identical a sequence selected from the group consisting of GYGMH (SEQ ID NO:27); VIWYDGSKKYYVDSVKG (SEQ ID NO:28); QMGYWHFDL (SEQ ID NO:29); SYGMH (SEQ ID NO:33); IIWYDGSKKNYADSVKG (SEQ ID NO:34); GTGYNWFDP (SEQ ID NO:35); and AIWYNGRKQDYADSVKG (SEQ ID NO:44) and a light chain with three CDR that include an amino acid sequence at least 90%, 92%, 95%, 97% 98%, 99% or more identical to a sequence selected from the group consisting of the amino acid sequence of RASQSVSSYLA (SEQ ID NO:30); DASNRAT (SEQ ID NO:31); QQRSNWPPLT (SEQ ID NO:32); RASQSVSSSYLA (SEQ ID NO:36); GASSRAT (SEQ ID NO:37); QQYGSSPIT (SEQ ID NO:38); RASQGISSALA (SEQ ID NO:39); YASSLQS (SEQ ID NO:40); QQYYSTLT (SEQ ID NO:41); DASSLGS (SEQ ID NO:42); WASQGISSYLA (SEQ ID NO:43); QQRSNWPWT (SEQ ID NO:45); DASSLES (SEQ ID NO:46); and QQFNSYPIT (SEQ ID NO:47). The antibody binds CD3.

A huCD3 antibody of the invention exhibits at least two or more (*i.e.*, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more) of the following characteristics: the antibody contains a variable heavy chain region (V_H) encoded by a human DP50 V_H germline gene sequence, or a nucleic acid sequence that is homologous to the human DP50 V_H germline gene sequence; the antibody contains a variable light chain region (V_L) encoded by a human L6 V_L germline gene sequence, or a nucleic acid sequence homologous to the human L6 V_L germline gene sequence; the antibody contains a V_L encoded by a human L4/18a V_L germline gene sequence, or a nucleic acid sequence homologous to the human L4/18a V_L germline gene sequence; the antibody includes a V_H CDR1 region comprising the amino acid sequence YGMH (SEQ ID NO:58); the

antibody includes a V_H CDR2 region comprising the amino acid sequence DSVKG (SEQ ID NO:59); the antibody includes a V_H CDR2 region comprises the amino acid sequence $IWYX_1GX_2X_3X_4X_5Y$ X_6DSVKG (SEQ ID NO:60); the antibody includes a V_H CDR3 region comprising the amino acid sequence $X_AX_BGYX_CX_DFDX_E$ (SEQ ID NO:61); the antibody includes a V_H CDR3 region comprising the amino acid sequence GTGYNWFDP (SEQ ID NO:62) or the amino acid sequence QMGYWHFDL (SEQ ID NO:63); the antibody includes the amino acid sequence VTVSS (SEQ ID NO:64) at a position that is C-terminal to the CDR3 region, wherein the position is in a variable region C-terminal to the CDR3 region; the antibody includes the amino acid sequence GTLVTVSS (SEQ ID NO:65) at a position that is C-terminal to CDR3 region, wherein the position is in a variable region C-terminal to the CDR3 region; the antibody includes the amino acid sequence WGRGTLVTVSS (SEQ ID NO:66) at a position that is C-terminal to CDR3 region, wherein the position is in a variable region C-terminal to the CDR3 region; the antibody binds an epitope that wholly or partially includes the amino acid sequence EMGGITQTPYKVSISGT (SEQ ID NO:67); and the antibody includes a mutation in the heavy chain at an amino acid residue at position 234, 235, 265, or 297 or combinations thereof, and wherein the release of cytokines from a T-cell in the presence of said antibody is reduced as compared to the release of cytokines from a T-cell in the presence of an antibody that does not include a mutation in the heavy chain at position 234, 235, 265 or 297 or combinations thereof. The numbering of the heavy chain residues described herein is that of the EU index (*see* Kabat *et al.*, "Proteins of Immunological Interest", US Dept. of Health & Human Services (1983)), as shown, *e.g.*, in U.S. Patent Nos. 5,624,821 and 5,648,260, the contents of which are hereby incorporated in its entirety by reference.

In some aspects, the huCD3 antibody contains an amino acid mutation. The mutation is in the constant region. The mutation results in an antibody that has an altered effector function. An effector function of an antibody is altered by altering, *i.e.*, enhancing or reducing, the affinity of the antibody for an effector molecule such as an Fc receptor or a complement component. By altering an effector function of an antibody, it is possible to control various aspects of the immune response, *e.g.*, enhancing or suppressing various reactions of the immune system. For example, the mutation results

in an antibody that is capable of reducing cytokine release from a T-cell. For example, the mutation is in the heavy chain at amino acid residue 234, 235, 265, or 297 or combinations thereof. Preferably, the mutation results in an alanine residue at either position 234, 235, 265 or 297, or a glutamate residue at position 235, or a combination thereof. The term "cytokine" refers to all human cytokines known within the art that bind extracellular receptors expressed on the cell surface and thereby modulate cell function, including but not limited to IL-2, IFN-gamma, TNF-a, IL-4, IL-5, IL-6, IL-9, IL-10, and IL-13.

The release of cytokines can lead to a toxic condition known as cytokine release syndrome (CRS), a common clinical complication that occurs, *e.g.*, with the use of an anti-T cell antibody such as ATG (anti-thymocyte globulin) and OKT3 (a murine anti-human CD3 antibody). This syndrome is characterized by the excessive release of cytokines such as TNF, IFN-gamma and IL-2 into the circulation. The CRS occurs as a result of the simultaneous binding of the antibodies to CD3 (via the variable region of the antibody) and the Fc Receptors and/or complement receptors (via the constant region of the antibody) on other cells, thereby activating the T cells to release cytokines that produce a systemic inflammatory response characterized by hypotension, pyrexia and rigors. Symptoms of the CRS include fever, chills, nausea, vomiting, hypotension, and dyspnea. Thus, the huCD3 antibody of the invention contains one or more mutations that prevent heavy chain constant region-mediated release of one or more cytokine(s) *in vivo*.

The fully human CD3 antibodies of the invention include, for example, a L^{234} L^{235} → A^{234} E^{235} mutation in the Fc region, such that cytokine release upon exposure to the huCD3 antibody is significantly reduced or eliminated (*see e.g.*, Figures 11A, 11B). As described below in Example 4, the L^{234} L^{235} → A^{234} E^{235} mutation in the Fc region of the huCD3 antibodies of the invention reduces or eliminates cytokine release when the huCD3 antibodies are exposed to human leukocytes, whereas the mutations described below maintain significant cytokine release capacity. For example, a significant reduction in cytokine release is defined by comparing the release of cytokines upon exposure to the huCD3 antibody having a L^{234} L^{235} → A^{234} E^{235} mutation in the Fc region to level of cytokine release upon exposure to another anti-CD3 antibody having one or

more of the mutations described below. Other mutations in the Fc region include, for example, L^{234} L^{235} → A^{234} A^{235}, L^{235} → E^{235}, N^{297} → A^{297}, and D^{265} → A^{265}.

Alternatively, the huCD3 antibody is encoded by a nucleic acid that includes one or more mutations that replace a nucleic acid residue with a germline nucleic acid residue. By "germline nucleic acid residue" is meant the nucleic acid residue that naturally occurs in a germline gene encoding a constant or variable region. "Germline gene" is the DNA found in a germ cell (*i.e.*, a cell destined to become an egg or in the sperm). A "germline mutation" refers to a heritable change in a particular DNA that has occurred in a germ cell or the zygote at the single-cell stage, and when transmitted to offspring, such a mutation is incorporated in every cell of the body. A germline mutation is in contrast to a somatic mutation which is acquired in a single body cell. In some cases, nucleotides in a germline DNA sequence encoding for a variable region are mutated (*i.e.*, a somatic mutation) and replaced with a different nucleotide. Thus, the antibodies of the invention include one or more mutations that replace a nucleic acid with the germline nucleic acid residue. Germline antibody genes include, for example, DP50 (Accession number: IMGT/EMBL/GenBank/ DDBJ:L06618), L6 (Accession number: IMGT/EMBL/GenBank/DDBJ:X01668) and L4/18a (Accession number: EMBL/GenBank/DDBJ: Z00006).

The heavy chain of a huCD3 antibody is derived from a germ line V (variable) gene such as, for example, the DP50 germline gene. The nucleic acid and amino acid sequences for the DP50 germline gene include, for example, the nucleic acid and amino acid sequences shown below:

tgattcatgg agaaatagag agactgagtg tgagtgaaca tgagtgagaa aaactggatt tgtgtggcat tttctgataa cggtgtcctt ctgtttgcag gtgtccagtg tcaggtgcag ctggtggagt ctgggggagg cgtggtccag cctgggaggt ccctgagact ctcctgtgca gcgtctggat tcaccttcag tagctatggc atgcactggg tccgccaggc tccaggcaag gggctggagt gggtggcagt tatatggtat gatggaagta ataaatacta tgcagactcc gtgaagggcc gattcaccat ctccagagac aattccaaga acacgctgta tctgcaaatg aacagcctga gagccgagga cacggctgtg tattactgtg cgagagacac ag (SEQ ID NO: 68)

VQCQVQLVES GGGVVQPGRS LRLSCAASGF TFSSYGMHWV RQAPGKGLEW VAVIWYDGSN KYYADSVKGR FTISRDNSKN TLYLQMNSLR AEDTAVYYCA R (SEQ ID NO: 69)

The huCD3 antibodies of the invention include a variable heavy chain (V_H) region encoded by a human DP50 V_H germline gene sequence. A DP50 V_H germline gene sequence is shown, *e.g.*, in SEQ ID NO:48 in Figure 5. The huCD3 antibodies of the invention include a V_H region that is encoded by a nucleic acid sequence that is at least 80% homologous to the DP50 V_H germline gene sequence. Preferably, the nucleic acid sequence is at least 90%, 95%, 96%, 97% homologous to the DP50 V_H germline gene sequence, and more preferably, at least 98%, 99% homologous to the DP50 V_H germline gene sequence. The V_H region of the huCD3 antibody is at least 80% homologous to the amino acid sequence of the V_H region encoded by the DP50 V_H germline gene sequence. Preferably, the amino acid sequence of V_H region of the huCD3 antibody is at least 90%, 95%, 96%, 97% homologous to the amino acid sequence encoded by the DP50 V_H germline gene sequence, and more preferably, at least 98%, 99% homologous to the sequence encoded by the DP50 V_H germline gene sequence.

The huCD3 antibodies of the invention also include a variable light chain (V_L) region encoded by a human L6 or L4/18a V_L germline gene sequence. A human L6 V_L germline gene sequence is shown, *e.g.*, in SEQ ID NO:74 in Figure 6, and a human L4/18a V_L germline gene sequence is shown, for example, in SEQ ID NO:53 in Figure 7. Alternatively, the huCD3 antibodies include a V_L region that is encoded by a nucleic acid sequence that is at least 80% homologous to either the L6 or L4/18a V_L germline gene sequence. Preferably, the nucleic acid sequence is at least 90%, 95%, 96%, 97% homologous to either the L6 or L4/18a V_L germline gene sequence, and more preferably, at least 98%, 99% homologous to either the L6 or L4/18a V_L germline gene sequence. The V_L region of the huCD3 antibody is at least 80% homologous to the amino acid sequence of the V_L region encoded by either the L6 or L4/18a V_L germline gene sequence. Preferably, the amino acid sequence of V_L region of the huCD3 antibody is at least 90%, 95%, 96%, 97% homologous to the amino acid sequence encoded by either the L6 or L4/18a V_L germline gene sequence, and more preferably, at least 98%, 99% homologous to the sequence encoded by either the L6 or L4/18a V_L germline gene sequence.

The huCD3 antibodies of the invention have, for example, partially conserved amino acid sequences that are derived from the DP50 germline. For example, the CDR1

region of huCD3 antibodies of the invention have at least the contiguous amino acid sequence YGMH (SEQ ID NO: 58).

The CDR2 of the huCD3 antibodies includes, *e.g.*, at least the contiguous amino acid sequence DSVKG (SEQ ID NO:59) . For example, the CDR2 region includes the contiguous amino acid sequence $IWYX_1GX_2X_3X_4X_5YX_6DSVKG$ (SEQ ID NO:60), where X_1, X_2, X_3, X_4, X_5 and X_6 represent any amino acid. For example, X_1, X_2, X_3 and X_4 are hydrophilic amino acids. In some huCD3 antibodies of the invention, X_1 is asparagine or aspartate, X_2 is arginine or serine, X_3 is lysine or asparagine, X_4 is lysine or glutamine, X_5 is aspartate, asparagine or tyrosine, and/or X_6 is valine or alanine. For example, the V_H CDR2 region includes an amino acid sequence selected from the group consisting of AIWYNGRKQDYADSVKG (SEQ ID NO:69), IIWYDGSKKNYADSVKG (SEQ ID NO:70), VIWYDGSKKYYVDSVKG (SEQ ID NO:71) and VIWYDGSNKYYADSVKG (SEQ ID NO:72).

The CDR3 region of huCD3 antibodies contain, for example, at least the contiguous amino acid sequence $X_AX_BGYX_CX_DFDX_E$ (SEQ ID NO:61), where X_A, X_B, X_C, X_D, and X_E represent any amino acid. In some huCD3 antibodies of the invention, X_A and X_B are neutral amino acids, X_D is an aromatic amino acid, and/or wherein X_E is a hydrophobic amino acid. For example, X_A is glycine or glutamine, X_B is threonine or methionine, X_C is asparagine or tryptophan, X_D is tryptophan or histidine, and/or X_E is proline or leucine. For example, the CDR3 region includes either the contiguous amino acid sequence GTGYNWFDP (SEQ ID NO:62) or the contiguous amino acid sequence QMGYWHFDL (SEQ ID NO: 63).

The huCD3 antibodies include a framework 2 region (FRW2) that contains the amino acid sequence WVRQAPGKGLEWV (SEQ ID NO:73). huCD3 antibodies of the invention include a framework 3 region (FRW3) that contains the amino acid sequence RFTISRDNSKNTLYLQMNSLRAEDTAVYYCA (SEQ ID NO:74).

Some huCD3 antibodies include the contiguous amino acid sequence VTVSS (SEQ ID NO:64) at a position that is C-terminal to CDR3 region. For example, the antibody contains the contiguous amino acid sequence GTLVTVSS (SEQ ID NO:65) at a position that is C-terminal to the CDR3 region. Other huCD3 antibodies include the contiguous amino acid sequence WGRGTLVTVSS (SEQ ID NO: 66) at a position that is

C-terminal to the CDR3 region. The arginine residue in SEQ ID NO:66 is shown, for example, in the V_H sequences for the 28F11 huCD3 antibody (SEQ ID NO:2) and the 23F10 huCD3 antibody (SEQ ID NO:6).

In another aspect, the invention provides methods of treating, preventing or alleviating a symptom of an immune-related disorder by administering an huCD3 antibody to a subject. Optionally, the subject is further administered with a second agent such as, but not limited to, anti-inflammatory compounds or immunosuppressive compounds. For example, subjects with Type I diabetes or Latent Autoimmune Diabetes in the Adult (LADA), are also administered a second agent, such as, for example, GLP-1 or a beta cell resting compound (*i.e.*, a compound that reduces or otherwise inhibits insulin release, such as potassium channel openers).

Suitable compounds include, but are not limited to methotrexate, cyclosporin A (including, for example, cyclosporin microemulsion), tacrolimus, corticosteroids, statins, interferon beta, Remicade (Infliximab), Enbrel (Etanercept) and Humira (Adalimumab).

The subject is suffering from or is predisposed to developing an immune related disorder, such as, for example, an autoimmune disease or an inflammatory disorder.

In another aspect, the invention provides methods of administering the huCD3 antibody of the invention to a subject prior to, during and/or after organ or tissue transplantation. For example, the huCD3 antibody of the invention is used to treat or prevent rejection after organ or tissue transplantation.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a series of representations of the nucleotide sequence and amino acid sequences for the variable light and variable heavy regions of the huCD3 antibody 28F11. Figure 1A depicts the nucleotide sequence encoding the variable region of the heavy chain, and Figure 1B represents the amino acid sequence encoded by the nucleotide sequence shown in Figure 1A, wherein the CDRs are highlighted with boxes. Figure 1C depicts the nucleotide sequence encoding the variable region of the light chain, and Figure 1D represents the amino acid sequence encoded by the nucleotide sequence shown in Figure 1C, wherein the CDRs are indicated by boxes.

Figure 2 is series of representations of the nucleotide sequence and amino acid sequences for the variable light and variable heavy regions of the huCD3 antibody 23F10, with Figure 2A representing the nucleotide sequence encoding the variable region of the heavy chain, Figure 2B representing the amino acid sequence encoded by the nucleotide sequence shown in Figure 2A, Figure 2C representing the nucleotide sequence encoding the variable region of the light chain, and Figure 2D representing the amino acid sequence encoded by the nucleotide sequence shown in Figure 2C.

Figure 3 is series of representations of the nucleotide sequence and amino acid sequences for the variable light and variable heavy regions of the huCD3 antibody 27H5. Figure 3A represents the nucleotide sequence encoding the variable region of the heavy chain; Figure 3B represents the amino acid sequence encoded by the nucleotide sequence shown in Figure 3A; Figure 3C represents the five nucleotide sequences encoding the variable region of the light chain for the 27H5 clone; Figure 3D represents the five amino acid sequences encoded by the nucleotide sequences shown in Figure 3C; and Figure 3E is an alignment of the five light chains from the clone 27H5, wherein an asterisk (*) in the last row (labeled KEY) represents a conserved amino acid in that column; a colon (:) in the KEY row represents a conservative mutation; and a period (.) in the KEY row represents a semiconservative mutation.

Figure 4 is a is series of representations of the nucleotide sequence and amino acid sequences for the variable light and variable heavy regions of the huCD3 antibody 15C3, with Figure 4A representing the nucleotide sequence encoding the variable region of the heavy chain, Figure 4B representing the amino acid sequence encoded by the nucleotide sequence shown in Figure 4A, Figure 4C representing the two nucleotide sequences encoding the variable region of the light chain for the 15C3 clone, and Figure 4D representing the two amino acid sequences encoded by the nucleotide sequences shown in Figure 4C.

Figure 5 is an alignment depicting the variable heavy chain regions of the 15C3, 27H5 and 28F11 huCD3 antibodies as well as the DP-50 germline sequence, the human heavy joining 5-02 sequence, and the human heavy joining 2 sequence. The CDR regions are indicated for each sequence.

Figure 6 is an alignment depicting the VκIII variable regions of the 15C3 (variable light chain 1, *i.e.*, "VL1") and 28F11 huCD3 antibodies, as well as the L6 germline sequence, the human kappa joining 4 sequence and the human kappa joining 1 sequence. The CDR regions are indicated for each sequence.

Figure 7 is an alignment depicting the VκI variable regions of the 15C3 (variable light chain 2, *i.e.*, "VL2") and 27H5 VL2 huCD3 antibodies, as well as the L4/18a germline sequence, the human kappa joining 4 sequence and the human kappa joining 5 sequence. The CDR regions are indicated for each sequence.

Figure 8 is an alignment depicting the VκII variable regions of the 27H5 VL1 huCD3 antibody and DPK22, as well as human kappa joining 5 sequence. The CDR regions are indicated for each sequence.

Figure 9A is a graph depicting antibody binding to CD3 molecules at the surface of Jurkat cells using a variety of anti-CD3 antibodies, including the 28F11, 27H5VL1, 27H5VL2, 15C3VL1 and 15C3VL2 huCD3 antibodies of the invention. Figure 9B is a graph depicting the ability of a variety of anti-CD3 antibodies, including the 28F11, 27H5VL1, 27H5VL2, 15C3VL1 and 15C3VL2 huCD3 antibodies of the invention, to inhibit the binding of the murine anti-CD3 antibody OKT3 to CD3 positive cells. Figure 9C is a graph depicting the antigenic modulation of CD3 and TCR from the surface of human peripheral blood T cells by a variety of anti-CD3 antibodies, including the 28F11, 27H5VL1, 27H5VL2, 15C3VL1 and 15C3VL2 huCD3 antibodies of the invention. Figure 9D is a graph depicting the effect of a variety anti-CD3 antibodies, including the 28F11, 27H5VL1, 27H5VL2, 15C3VL1 and 15C3VL2 huCD3 antibodies of the invention, on T-cell proliferation.

Figure 10 is an illustration depicting the binding pattern of the fully human monoclonal antibody 28F11 on a peptide array derived from the amino acid sequence of the CD3 epsilon chain.

Figure 11 is a series of graphs depicting the level of cytokine release upon exposure to wild-type 28F11 huCD3 antibody (28F11WT), a mutated 28F11 huCD3 antibody having a L^{234} L^{235} → A^{234} A^{235} mutation (28F11AA), and a mutated 28F11 huCD3 antibody having a L^{234} L^{235} → A^{234} E^{235} mutation (28F11AE). Figure 11A

depicts the level of TNF-alpha release upon exposure to these antibodies, and Figure 11B depicts the level of interferon gamma release.

DETAILED DESCRIPTION

The present invention provides fully human monoclonal antibodies specific against CD3 epsilon chain (CD3ε). The antibodies are respectively referred to herein is huCD3 antibodies.

CD3 is a complex of at least five membrane-bound polypeptides in mature T-lymphocytes that are non-covalently associated with one another and with the T-cell receptor. The CD3 complex includes the gamma, delta, epsilon, zeta, and eta chains (also referred to as subunits). Non-human monoclonal antibodies have been developed against some of these chains, as exemplified by the murine antibodies OKT3, SP34, UCHT1 or 64.1. (*See e.g.*, June, *et al.*, J. Immunol. 136:3945-3952 (1986); Yang, *et al.*, J. Immunol. 137:1097-1100 (1986); and Hayward, *et al.*, Immunol. 64:87-92 (1988)).

The huCD3 antibodies of the invention were produced by immunizing two lines of transgenic mice, the HuMab™ mice and the KM™ mice (Medarex, Princeton NJ).

The huCD3 antibodies of the invention have one or more of the following characteristics: the huCD3 antibody binds to CD3 positive (CD3+) cells but not CD3 negative (CD3-) cells; the huCD3 antibody induces antigenic modulation which involves alterations of the cell surface expression levels of CD3 and the T cell receptor (TcR); or the huCD3 antibody inhibits binding of the murine anti-human OKT3 monoclonal antibody to T-lymphocytes. The huCD3 antibodies of the invention compete with the murine anti-CD3 antibody OKT3 for binding to CD3, and exposure to the huCD3 antibody removes or masks CD3 and/or TcR without affecting cell surface expression of CD2, CD4 or CD8. The masking of CD3 and/or TcR results in the loss or reduction of T-cell activation.

The huCD3 antibodies of the invention bind to a CD3 that wholly or partially includes the amino acid residues from position 27 to position 43 of the processed human CD3 epsilon subunit (*i.e.*, without the leader sequence). The amino acid sequence of the human CD3 epsilon subunit is shown, for example, in GenBank Accession Nos.

NP_000724; AAA52295; P07766; A32069; CAA27516; and AAH49847. For example, the huCD3 antibody binds a CD3 epitope that wholly or partially includes the amino acid sequence of EMGGITQTPYKVSISGT (SEQ ID NO: 67). An exemplary huCD3 monoclonal antibody that binds to this epitope is the 28F11 antibody described herein. The 28F11 antibody includes a heavy chain variable region (SEQ ID NO:2) encoded by the nucleic acid sequence shown below in SEQ ID NO:1, and a light chain variable region (SEQ ID NO:4) encoded by the nucleic acid sequence shown in SEQ ID NO:3 (Figures 1A-1D).

The amino acids encompassing the complementarity determining regions (CDR) as defined by Chothia et al. 1989, E.A. Kabat et al., 1991 are highlighted with boxes below (*see also* Figures 1B and 1D and Figures 5 and 6). (*See* Chothia, C, *et al.*, Nature 342:877-883 (1989); Kabat, EA, *et al.*, Sequences of Protein of immunological interest, Fifth Edition, US Department of Health and Human Services, US Government Printing Office (1991)). The heavy chain CDRs of the 28F11 antibody have the following sequences: GYGMH (SEQ ID NO:27) VIWYDGSKKYYVDSVKG (SEQ ID NO:28) and QMGYWHFDL (SEQ ID NO:29). The light chain CDRs of the 28F11 antibody have the following sequences: RASQSVSSYLA (SEQ ID NO:30) DASNRAT (SEQ ID NO:31) and QQRSNWPPLT (SEQ ID NO:32).

>28F11 VH nucleotide sequence: (SEQ ID NO: 1)

CAGGTGCAGCTGGTGGAGTCCGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT
CTCCTGTGCAGCGTCTGGATTCAAGTTCAGTGGCTATGGCATGCACTGGGTCCGCCAGG
CTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAAGAAATAC
TATGTAGACTCCGTGAAGGGCCGCTTCACCATCTCCAGAGACAATTCCAAGAACACGCT
GTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAC
AAATGGGCTACTGGCACTTCGATCTCTGGGGCCGTGGCACCCTGGTCACTGTCTCCTCA

>28F11 VH amino acid sequence: (SEQ ID NO: 2)

QVQLVESGGGVVQPGRSLRLSCAASGFKFSGYGMHWVRQAPGKGLEWVAVIWYDGSKKY
YVDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARQMGYWHFDLWGRGTLVTVSS

>28F11 VL nucleotide sequence: (SEQ ID NO: 3)

GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCAC
CCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTACCAACAGAAAC
CTGGCCAGGCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCA
GCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGA

GCCTGAAGATTTTGCAGTTTATTACTGTCAGCAGCGTAGCAACTGGCCTCCGCTCACTT
TCGGCGGAGGGACCAAGGTGGAGATCAAA

>28F11 VL amino acid sequence: (SEQ ID NO: 4)
EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIP
ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPLTFGGGTKVEIK

The 23F10 antibody includes a heavy chain variable region (SEQ ID NO:6) encoded by the nucleic acid sequence shown below in SEQ ID NO:5, and a light chain variable region (SEQ ID NO:8) encoded by the nucleic acid sequence shown in SEQ ID NO:7.

The amino acids encompassing the CDR as defined by Chothia et al. 1989, E.A. Kabat et al., 1991 are highlighted with boxes below. (*see also* Figures 2B, 2D). The heavy chain CDRs of the 23F10 antibody have the following sequences: GYGMH (SEQ ID NO:27) VIWYDGSKKYYVDSVKG (SEQ ID NO:28) and QMGYWHFDL (SEQ ID NO:29). The light chain CDRs of the 23F10 antibody have the following sequences: RASQSVSSYLA (SEQ ID NO:30) DASNRAT (SEQ ID NO:31) and QQRSNWPPLT (SEQ ID NO:32).

>23F10 VH nucleotide sequence: (SEQ ID NO: 5)
CAGGTGCAGCTGGTGCAGTCCGGGGGAGGCGTGGTCCAGTCTGGGAGGTCCCTGAGACT
CTCCTGTGCAGCGTCTGGATTCAAGTTCAGTGGCTATGGCATGCACTGGGTCCGCCAGG
CTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAAGAAATAC
TATGTAGACTCCGTGAAGGGCCGCTTCACCATCTCCAGAGACAATTCCAAGAACACGCT
GTATCTGCAAATGAACAGCCTGAGAGGCGAGGACACGGCTGTGTATTACTGTGCGAGAC
AAATGGGCTACTGGCACTTCGATCTCTGGGGCCGTGGCACCCTGGTCACTGTCTCCTCA

>23F10 VH amino acid sequence: (SEQ ID NO: 6)
QVQLVQSGGGVVQSGRSLRLSCAASGFKFSGYGMHWVRQAPGKGLEWVAVIWYDGSKKY
YVDSVKGRFTISRDNSKNTLYLQMNSLRGEDTAVYYCARQMGYWHFDLWGRGTLVTVSS

>23F10 VL nucleotide sequence: (SEQ ID NO: 7)
GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCAC
CCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTACCAACAGAAAC
CTGGCCAGGCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCA
GCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGA

GCCTGAAGATTTTGCAGTTTATTACTGTCAGCAGCGTAGCAACTGGCCTCCGCTCACTT
TCGGCGGAGGGACCAAGGTGGAGATCAAA

>23F10 VL amino acid sequence: (SEQ ID NO: 8)
EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIP
ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPLTFGGGTKVEIK

The 27H5 antibody includes a heavy chain variable region (SEQ ID NO:10) encoded by the nucleic acid sequence shown below in SEQ ID NO:9, and a light chain variable region selected from the amino acid sequences shown below in SEQ ID NOS: 16-20 and encoded by the nucleic acid sequences shown in SEQ ID NO:11-15. As described herein in Example 2, a single clonal hybridoma derived from the HuMAb® transgenic mice can produce multiple light chains for a single heavy chain. Each combination of heavy and light chains produced is tested for optimal functioning, as described herein in Example 2.

The amino acids encompassing the CDR as defined by Chothia et al. 1989, E.A. Kabat et al., 1991 are highlighted with boxes below. (*see also* Figures 3B, 3D, 5, and 7-8). The heavy chain CDRs of the 27H5 antibody have the following sequences: SYGMH (SEQ ID NO:33) IIWYDGSKKNYADSVKG (SEQ ID NO:34) and GTGYNWFDP (SEQ ID NO:35). The light chain CDRs of the 27H5 antibody have the following sequences: RASQSVSSSYLA (SEQ ID NO:36); GASSRAT (SEQ ID NO:37); QQYGSSPIT (SEQ ID NO:38); RASQGISSALA (SEQ ID NO:39); YASSLQS (SEQ ID NO:40); QQYYSTLT (SEQ ID NO:41); DASSLGS (SEQ ID NO:42); and WASQGISSYLA (SEQ ID NO:43).

>27H5 VH nucleotide sequence: (SEQ ID NO: 9)
CAGGTGCAGCTGGTGGAGTCCGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT
CTCCTGTGCAGCGTCTGGATTCACCTTCAGAAGCTATGGCATGCACTGGGTCCGCCAGG
CTCCAGGCAAGGGGCTGGAGTGGGTGGCAATTATATGGTATGATGGAAGTAAAAAAAAC
TATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCT
GTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG
GAACTGGGTACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
>27H5 VH amino acid sequence: (SEQ ID NO: 10)
QVQLVESGGGVVQPGRSLRLSCAASGFTFRSYGMHWVRQAPGKGLEWVAIIWYDGSKKN
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGTGYNWFDPWGQGTLVTVSS

>27H5 VL1 nucleotide sequence: (SEQ ID NO: 11)

GAAATTGTGTTGACACAGTCTCCACGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCAC
CCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGA
AACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATC
CCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACT
GGACCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCGATCACCT
TCGGCCAAGGGACACGACTGGAGATTAAA

>27H5 VL2 nucleotide sequence: (SEQ ID NO: 12)

GACATCCTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCAC
CATCACTTGCCGGGCAAGTCAGGGCATTAGCAGTGCTTTAGCCTGGTATCAGCAGAAAC
CAGGGAAAGCTCCTAAGCTCCTGATCTATTATGCATCCAGTTTGCAAAGTGGGGTCCCA
TCAAGGTTCAGCGGCAGTGGATCTGGGACGGATTACACTCTCACCATCAGCAGCCTGCA
GCCTGAAGATTTTGCAACTTATTACTGTCAACAGTATTATAGTACCCTCACTTTCGGCG
GAGGGACCAAGGTGGAGATCAAA

>27H5 VL3 nucleotide sequence: (SEQ ID NO: 13)

GACATCGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCAC
CATCACTTGCCGGGCAAGTCAGGGCATTAGCAGTGCTTTAGCCTGGTATCAGCAGAAAC
CAGGGAAAGCTCCTAAGCTCCTGATCTATGATGCCTCCAGTTTGGGAAGTGGGGTCCCA
TCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCA
GCCTGAAGATTTTGCAACTTATTACTGTCAACAGTATTATAGTACCCTCACTTTCGGCG
GAGGGACCAAGGTGGAGATCAAA

>27H5 VL4 nucleotide sequence: (SEQ ID NO: 14)

GACATCCAGATGACCCAGTCTCCATTCTCCCTGTCTGCATCTGTAGGAGACAGAGTCAC
CATCACTTGCTGGGCCAGTCAGGGCATTAGCAGTTATTTAGCCTGGTATCAGCAAAAAC
CAGCAAAAGCCCCTAAGCTCTTCATCTATTATGCATCCAGTTTGCAAAGTGGGGTCCCA
TCAAGGTTCAGCGGCAGTGGATCTGGGACGGATTACACTCTCACCATCAGCAGCCTGCA
GCCTGAAGATTTTGCAACTTATTACTGTCAACAGTATTATAGTACCCTCACTTTCGGCG
GAGGGACCAAGGTGGAGATCAAA

>27H5 VL5 nucleotide sequence: (SEQ ID NO: 15)

GACATCGAGATGACCCAGTCTCCATTCTCCCTGTCTGCATCTGTAGGAGACAGAGTCAC
CATCACTTGCTGGGCCAGTCAGGGCATTAGCAGTTATTTAGCCTGGTATCAGCAAAAAC
CAGCAAAAGCCCCTAAGCTCTTCATCTATTATGCATCCAGTTTGCAAAGTGGGGTCCCA
TCAAGGTTCAGCGGCAGTGGATCTGGGACGGATTACACTCTCACCATCAGCAGCCTGCA
GCCTGAAGATTTTGCAACTTATTACTGTCAACAGTATTATAGTACCCTCACTTTCGGCG
GAGGGACCAAGGTGGAGATCAAA

>27H5 VL1 amino acid sequence: (SEQ ID NO: 16)

EIVLTQSPRTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGI
PDRFSGSGSGTDFTLTISRLDPEDFAVYYCQQYGSSPITFGQGTRLEIK

>27H5 VL2 amino acid sequence: (SEQ ID NO: 17)
DILMTQSPSSLSASVGDRVTITC[RASQGISSALA]WYQQKPGKAPKLLIY[YASSLQS]GVP
SRFSGSGSGTDYTLTISSLQPEDFATYYC[QQYYSTLT]FGGGTKVEIK

>27H5 VL3 amino acid sequence: (SEQ ID NO: 18)
DIVMTQSPSSLSASVGDRVTITC[RASQGISSALA]WYQQKPGKAPKLLIY[DASSLGS]GVP
SRFSGSGSGTDFTLTISSLQPEDFATYYC[QQYYSTLTF]GGGTKVEIK

>27H5 VL4 amino acid sequence: (SEQ ID NO: 19)
DIQMTQSPFSLSASVGDRVTITC[WASQGISSYLA]WYQQKPAKAPKLFIY[YASSLQS]GVP
SRFSGSGSGTDYTLTISSLQPEDFATYYC[QQYYSTLTF]GGGTKVEIK

>27H5 VL5 amino acid sequence: (SEQ ID NO: 20)
DIEMTQSPFSLSASVGDRVTITC[WASQGISSYLA]WYQQKPAKAPKLFIY[YASSLQS]GVP
SRFSGSGSGTDYTLTISSLQPEDFATYYC[QQYYSTLTF]GGGTKVEIK

The 15C3 antibody includes a heavy chain variable region (SEQ ID NO:22) encoded by the nucleic acid sequence shown below in SEQ ID NO:21, and a light chain variable region selected from the amino acid sequences shown below in SEQ ID NOS: 25-26 and encoded by the nucleic acid sequences shown in SEQ ID NO:23-24. As described herein in Example 2, a single clonal hybridoma derived from the HuMAb® transgenic mice can produce multiple light chains for a single heavy chain. Each combination of heavy and light chains produced is tested for optimal functioning, as described herein in Example 2.

The amino acids encompassing the CDR as defined by Chothia et al. 1989, E.A. Kabat et al., 1991 are highlighted with boxes below. (*see also* Figures 4B, 4D, and 5-7). The heavy chain CDRs of the 15C3 antibody have the following sequences: SYGMH (SEQ ID NO:33) AIWYNGRKQDYADSVKG (SEQ ID NO:44) and GTGYNWFDP (SEQ ID NO:35). The light chain CDRs of the 15C3 antibody have the following sequences: RASQSVSSYLA (SEQ ID NO:30); DASNRAT (SEQ ID NO:31); QQRSNWPWT (SEQ ID NO:45); RASQGISSALA (SEQ ID NO:39); DASSLES (SEQ ID NO:46); QQFNSYPIT (SEQ ID NO:47).

>15C3 VH nucleotide sequence: (SEQ ID NO: 21)

CAGGTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCCGGGAGGTCCCTGAGACT
CTCCTGTGTAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGG
CTCCAGGCAAGGGGCTGGAGTGGGTGGCAGCTATATGGTATAATGGAAGAAAACAAGAC
TATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCT
GTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTACGAGGG
GAACTGGGTACAATTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

>15C3 VH amino acid sequence: (SEQ ID NO: 22)

QVQLVQSGGGVVQPGRSLRLSCVASGFTFSSYGMHWVRQAPGKGLEWVAAIWYNGRKQD
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRGTGYNWFDPWGQGTLVTVSS

>15C3 VL1 nucleotide sequence: (SEQ ID NO: 23)

GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCAC
CCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTACCAACAGAAAC
CTGGCCAGGCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCA
GCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGA
GCCTGAAGATTTTGCAGTTTATTACTGTCAGCAGCGTAGCAACTGGCCGTGGACGTTCG
GCCAAGGGACCAAGGTGGAAATCAAA

>15C3 VL2 nucleotide sequence: (SEQ ID NO: 24)

GCCATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTATGAGACAGAGTCAC
CATCACTTGCCGGGCAAGTCAGGGCATTAGCAGTGCTTTAGCCTGGTATCAGCAGAAAC
CAGGGAAAGCTCCTAAGCTCCTGATCTATGATGCCTCCAGTTTGGAAAGTGGGGTCCCA
TCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCA
GCCTGAAGATTTTGCAACTTATTACTGTCAACAGTTTAATAGTTACCCTATCACCTTCG
GCCAAGGGACACGACTGGAGATTAAA

>15C3 VL1 amino acid sequence: (SEQ ID NO: 25)

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIP
ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPWTFGQGTKVEIK

>15C3 VL2 amino acid sequence: (SEQ ID NO: 26)

AIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKAPKLLIYDASSLESGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCQQFNSYPITFGQGTRLEIK

huCD3 antibodies of the invention also include antibodies that include a heavy chain variable amino acid sequence that is at least 90%, 92%, 95%, 97% 98%, 99% or more identical the amino acid sequence of SEQ ID NO:2, 6, 10 or 22 and/or a light chain

variable amino acid that is at least 90%, 92%, 95%, 97% 98%, 99% or more identical the amino acid sequence of SEQ ID NO:4, 8, 16-20 or 25-26.

Alternatively, the monoclonal antibody is an antibody that binds to the same epitope as 28F11, 27H5, 23F10 or 15C3.

Unless otherwise defined, scientific and technical terms used in connection with the present invention shall have the meanings that are commonly understood by those of ordinary skill in the art. Further, unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular. Generally, nomenclatures utilized in connection with, and techniques of, cell and tissue culture, molecular biology, and protein and oligo- or polynucleotide chemistry and hybridization described herein are those well known and commonly used in the art. Standard techniques are used for recombinant DNA, oligonucleotide synthesis, and tissue culture and transformation (*e.g.*, electroporation, lipofection). Enzymatic reactions and purification techniques are performed according to manufacturer's specifications or as commonly accomplished in the art or as described herein. The foregoing techniques and procedures are generally performed according to conventional methods well known in the art and as described in various general and more specific references that are cited and discussed throughout the present specification. *See e.g.,* Sambrook *et al.* Molecular Cloning: A Laboratory Manual (2d ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989)). The nomenclatures utilized in connection with, and the laboratory procedures and techniques of, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well known and commonly used in the art. Standard techniques are used for chemical syntheses, chemical analyses, pharmaceutical preparation, formulation, and delivery, and treatment of patients.

As utilized in accordance with the present disclosure, the following terms, unless otherwise indicated, shall be understood to have the following meanings:

As used herein, the term "antibody" refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single

chain, F_{ab}, $F_{ab'}$ and $F_{(ab')2}$ fragments, and an F_{ab} expression library. By "specifically bind" or "immunoreacts with" is meant that the antibody reacts with one or more antigenic determinants of the desired antigen and does not react (i.e., bind) with other polypeptides or binds at much lower affinity ($K_d > 10^{-6}$) with other polypeptides.

The basic antibody structural unit is known to comprise a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kDa) and one "heavy" chain (about 50-70 kDa). The amino-terminal portion of each chain includes a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The carboxy-terminal portion of each chain defines a constant region primarily responsible for effector function. Human light chains are classified as kappa and lambda light chains. Heavy chains are classified as mu, delta, gamma, alpha, or epsilon, and define the antibody's isotype as IgM, IgD, IgA, and IgE, respectively. Within light and heavy chains, the variable and constant regions are joined by a "J" region of about 12 or more amino acids, with the heavy chain also including a "D" region of about 10 more amino acids. *See* generally, Fundamental Immunology Ch. 7 (Paul, W., ea., 2nd ed. Raven Press, N.Y. (1989)). The variable regions of each light/heavy chain pair form the antibody binding site.

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

In general, antibody molecules obtained from humans relate to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG_1, IgG_2, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain.

The term "antigen-binding site," or "binding portion" refers to the part of the immunoglobulin molecule that participates in antigen binding. The antigen binding site is

formed by amino acid residues of the N-terminal variable ("V") regions of the heavy ("H") and light ("L") chains. Three highly divergent stretches within the V regions of the heavy and light chains, referred to as "hypervariable regions," are interposed between more conserved flanking stretches known as "framework regions," or "FRs". Thus, the term "FR" refers to amino acid sequences which are naturally found between, and adjacent to, hypervariable regions in immunoglobulins. In an antibody molecule, the three hypervariable regions of a light chain and the three hypervariable regions of a heavy chain are disposed relative to each other in three dimensional space to form an antigen-binding surface. The antigen-binding surface is complementary to the three-dimensional surface of a bound antigen, and the three hypervariable regions of each of the heavy and light chains are referred to as "complementarity-determining regions," or "CDRs." The assignment of amino acids to each domain is in accordance with the definitions of Kabat Sequences of Proteins of Immunological Interest (National Institutes of Health, Bethesda, Md. (1987 and 1991)), or Chothia &Lesk J. Mol. Biol. 196:901-917 (1987), Chothia *et al.* Nature 342:878-883 (1989).

As used herein, the term "epitope" includes any protein determinant capable of specific binding to an immunoglobulin, an scFv, or a T-cell receptor. The term "epitope" includes any protein determinant capable of specific binding to an immunoglobulin or T-cell receptor. Epitopic determinants usually consist of chemically active surface groupings of molecules such as amino acids or sugar side chains and usually have specific three dimensional structural characteristics, as well as specific charge characteristics. An antibody is said to specifically bind an antigen when the dissociation constant is ≤ 1 μM; preferably ≤ 100 nM and most preferably ≤ 10 nM.

As used herein, the terms "immunological binding," and "immunological binding properties" refer to the non-covalent interactions of the type which occur between an immunoglobulin molecule and an antigen for which the immunoglobulin is specific. The strength, or affinity of immunological binding interactions can be expressed in terms of the dissociation constant (K_d) of the interaction, wherein a smaller K_d represents a greater affinity. Immunological binding properties of selected polypeptides are quantified using methods well known in the art. One such method entails measuring the rates of antigen-binding site/antigen complex formation and dissociation, wherein those rates depend on

the concentrations of the complex partners, the affinity of the interaction, and geometric parameters that equally influence the rate in both directions. Thus, both the "on rate constant" (K_{on}) and the "off rate constant" (K_{off}) can be determined by calculation of the concentrations and the actual rates of association and dissociation. (*See* Nature 361:186-87 (1993)). The ratio of K_{off} /K_{on} enables the cancellation of all parameters not related to affinity, and is equal to the dissociation constant K_d. (*See, generally*, Davies et al. (1990) Annual Rev Biochem 59:439-473). An antibody of the present invention is said to specifically bind to a CD3 epitope when the equilibrium binding constant (K_d) is ≤1 μM, preferably ≤ 100 nM, more preferably ≤ 10 nM, and most preferably ≤ 100 pM to about 1 pM, as measured by assays such as radioligand binding assays or similar assays known to those skilled in the art.

Those skilled in the art will recognize that it is possible to determine, without undue experimentation, if a human monoclonal antibody has the same specificity as a human monoclonal antibody of the invention (*e.g.*, monoclonal antibody 28F11, 27H5, 23F10 or 15C3) by ascertaining whether the former prevents the latter from binding to a CD3 antigen polypeptide. If the human monoclonal antibody being tested competes with a human monoclonal antibody of the invention, as shown by a decrease in binding by the human monoclonal antibody of the invention, then the two monoclonal antibodies bind to the same, or a closely related, epitope. Another way to determine whether a human monoclonal antibody has the specificity of a human monoclonal antibody of the invention is to pre-incubate the human monoclonal antibody of the invention with the CD3 antigen polypeptide with which it is normally reactive, and then add the human monoclonal antibody being tested to determine if the human monoclonal antibody being tested is inhibited in its ability to bind the CD3 antigen polypeptide. If the human monoclonal antibody being tested is inhibited then, in all likelihood, it has the same, or functionally equivalent, epitopic specificity as the monoclonal antibody of the invention.

Various procedures known within the art are used for the production of the monoclonal antibodies directed against a protein such as a CD3 protein, or against derivatives, fragments, analogs homologs or orthologs thereof. (*See, e.g.*, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Fully human antibodies are

antibody molecules in which the entire sequence of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies are prepared, for example, using the procedures described below in Example 1. Human monoclonal antibodies can be also prepared by using trioma technique; the human B-cell hybridoma technique (*see* Kozbor, et al., 1983 Immunol Today 4: 72); and the EBV hybridoma technique to produce human monoclonal antibodies (*see* Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized and may be produced by using human hybridomas (*see* Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

Antibodies are purified by well-known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

It is desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating immune-related diseases. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). (*See* Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992)). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. (*See* Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989)).

The invention also includes F_v, F_{ab}, $F_{ab'}$ and $F_{(ab')2}$ huCD3 fragments, single chain huCD3 antibodies, bispecific huCD3 antibodies and heteroconjugate huCD3 antibodies.

Bispecific antibodies are antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for CD3. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., EMBO J., 10:3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (*e.g.* tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created

on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (*e.g.* alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (*e.g.* $F(ab')_2$ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody $F(ab')_2$ molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to

form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (*e.g.* CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this

purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi, ^{131}I, ^{131}In, ^{90}Y, and ^{186}Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. (*See* WO94/11026).

Those of ordinary skill in the art will recognize that a large variety of possible moieties can be coupled to the resultant antibodies or to other molecules of the invention. (*See, for example*, "Conjugate Vaccines", Contributions to Microbiology and

Immunology, J. M. Cruse and R. E. Lewis, Jr (eds), Carger Press, New York, (1989), the entire contents of which are incorporated herein by reference).

Coupling is accomplished by any chemical reaction that will bind the two molecules so long as the antibody and the other moiety retain their respective activities. This linkage can include many chemical mechanisms, for instance covalent binding, affinity binding, intercalation, coordinate binding and complexation. The preferred binding is, however, covalent binding. Covalent binding is achieved either by direct condensation of existing side chains or by the incorporation of external bridging molecules. Many bivalent or polyvalent linking agents are useful in coupling protein molecules, such as the antibodies of the present invention, to other molecules. For example, representative coupling agents can include organic compounds such as thioesters, carbodiimides, succinimide esters, diisocyanates, glutaraldehyde, diazobenzenes and hexamethylene diamines. This listing is not intended to be exhaustive of the various classes of coupling agents known in the art but, rather, is exemplary of the more common coupling agents. (*See* Killen and Lindstrom, Jour. Immun. 133:1335-2549 (1984); Jansen et al., Immunological Reviews 62:185-216 (1982); and Vitetta et al., Science 238:1098 (1987). Preferred linkers are described in the literature. (*See, for example*, Ramakrishnan, S. et al., Cancer Res. 44:201-208 (1984) describing use of MBS (M-maleimidobenzoyl-N-hydroxysuccinimide ester). *See also*, U.S. Patent No. 5,030,719, describing use of halogenated acetyl hydrazide derivative coupled to an antibody by way of an oligopeptide linker. Particularly preferred linkers include: (i) EDC (1-ethyl-3-(3-dimethylamino-propyl) carbodiimide hydrochloride; (ii) SMPT (4-succinimidyloxycarbonyl-alpha-methyl-alpha-(2-pridyl-dithio)-toluene (Pierce Chem. Co., Cat. (21558G); (iii) SPDP (succinimidyl-6 [3-(2-pyridyldithio) propionamido]hexanoate (Pierce Chem. Co., Cat #21651G); (iv) Sulfo-LC-SPDP (sulfosuccinimidyl 6 [3-(2-pyridyldithio)-propianamide] hexanoate (Pierce Chem. Co. Cat. #2165-G); and (v) sulfo-NHS (N-hydroxysulfo-succinimide: Pierce Chem. Co., Cat. #24510) conjugated to EDC.

The linkers described above contain components that have different attributes, thus leading to conjugates with differing physio-chemical properties. For example, sulfo-NHS esters of alkyl carboxylates are more stable than sulfo-NHS esters of aromatic

carboxylates. NHS-ester containing linkers are less soluble than sulfo-NHS esters. Further, the linker SMPT contains a sterically hindered disulfide bond, and can form conjugates with increased stability. Disulfide linkages, are in general, less stable than other linkages because the disulfide linkage is cleaved *in vitro*, resulting in less conjugate available. Sulfo-NHS, in particular, can enhance the stability of carbodimide couplings. Carbodimide couplings (such as EDC) when used in conjunction with sulfo-NHS, forms esters that are more resistant to hydrolysis than the carbodimide coupling reaction alone.

The term "isolated polynucleotide" as used herein shall mean a polynucleotide of genomic, cDNA, or synthetic origin or some combination thereof, which by virtue of its origin the "isolated polynucleotide" (1) is not associated with all or a portion of a polynucleotide in which the "isolated polynucleotide" is found in nature, (2) is operably linked to a polynucleotide which it is not linked to in nature, or (3) does not occur in nature as part of a larger sequence.

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

The term "polypeptide" is used herein as a generic term to refer to native protein, fragments, or analogs of a polypeptide sequence. Hence, native protein fragments, and analogs are species of the polypeptide genus. Preferred polypeptides in accordance with the invention comprise the human heavy chain immunoglobulin molecules represented by Figures 1B, 2B, 3B and 4B and the human light chain immunoglobulin molecules represented by Figures 1D, 2D, 3D and 4D, as well as antibody molecules formed by combinations comprising the heavy chain immunoglobulin molecules with light chain immunoglobulin molecules, such as kappa light chain immunoglobulin molecules, and vice versa, as well as fragments and analogs thereof.

The term "naturally-occurring" as used herein as applied to an object refers to the fact that an object can be found in nature. For example, a polypeptide or polynucleotide sequence that is present in an organism (including viruses) that can be isolated from a

source in nature and which has not been intentionally modified by man in the laboratory or otherwise is naturally-occurring.

The term "operably linked" as used herein refers to positions of components so described are in a relationship permitting them to function in their intended manner. A control sequence "operably linked" to a coding sequence is ligated in such a way that expression of the coding sequence is achieved under conditions compatible with the control sequences.

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

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

The term "naturally occurring nucleotides" referred to herein includes deoxyribonucleotides and ribonucleotides. The term "modified nucleotides" referred to herein includes nucleotides with modified or substituted sugar groups and the like. The

term "oligonucleotide linkages" referred to herein includes Oligonucleotides linkages such as phosphorothioate, phosphorodithioate, phosphoroselerloate, phosphorodiselenoate, phosphoroanilothioate, phoshoraniladate, phosphoronmidate, and the like. *See e.g.*, LaPlanche *et al.* Nucl. Acids Res. 14:9081 (1986); Stec *et al.* J. Am. Chem. Soc. 106:6077 (1984), Stein *et al.* Nucl. Acids Res. 16:3209 (1988), Zon *et al.* Anti Cancer Drug Design 6:539 (1991); Zon *et al.* Oligonucleotides and Analogues: A Practical Approach, pp. 87-108 (F. Eckstein, Ed., Oxford University Press, Oxford England (1991)); Stec *et al.* U.S. Patent No. 5,151,510; Uhlmann and Peyman Chemical Reviews 90:543 (1990). An oligonucleotide can include a label for detection, if desired.

The term "selectively hybridize" referred to herein means to detectably and specifically bind. Polynucleotides, oligonucleotides and fragments thereof in accordance with the invention selectively hybridize to nucleic acid strands under hybridization and wash conditions that minimize appreciable amounts of detectable binding to nonspecific nucleic acids. High stringency conditions can be used to achieve selective hybridization conditions as known in the art and discussed herein. Generally, the nucleic acid sequence homology between the polynucleotides, oligonucleotides, and fragments of the invention and a nucleic acid sequence of interest will be at least 80%, and more typically with preferably increasing homologies of at least 85%, 90%, 95%, 99%, and 100%. Two amino acid sequences are homologous if there is a partial or complete identity between their sequences. For example, 85% homology means that 85% of the amino acids are identical when the two sequences are aligned for maximum matching. Gaps (in either of the two sequences being matched) are allowed in maximizing matching gap lengths of 5 or less are preferred with 2 or less being more preferred. Alternatively and preferably, two protein sequences (or polypeptide sequences derived from them of at least 30 amino acids in length) are homologous, as this term is used herein, if they have an alignment score of at more than 5 (in standard deviation units) using the program ALIGN with the mutation data matrix and a gap penalty of 6 or greater. *See* Dayhoff, M.O., in Atlas of Protein Sequence and Structure, pp. 101-110 (Volume 5, National Biomedical Research Foundation (1972)) and Supplement 2 to this volume, pp. 1-10. The two sequences or parts thereof are more preferably homologous if their amino acids are greater than or equal to 50% identical when optimally aligned using the ALIGN program. The term

"corresponds to" is used herein to mean that a polynucleotide sequence is homologous (*i.e.,* is identical, not strictly evolutionarily related) to all or a portion of a reference polynucleotide sequence, or that a polypeptide sequence is identical to a reference polypeptide sequence. In contradistinction, the term "complementary to" is used herein to mean that the complementary sequence is homologous to all or a portion of a reference polynucleotide sequence. For illustration, the nucleotide sequence "TATAC" corresponds to a reference sequence "TATAC" and is complementary to a reference sequence "GTATA".

The following terms are used to describe the sequence relationships between two or more polynucleotide or amino acid sequences: "reference sequence", "comparison window", "sequence identity", "percentage of sequence identity", and "substantial identity". A "reference sequence" is a defined sequence used as a basis for a sequence comparison a reference sequence may be a subset of a larger sequence, for example, as a segment of a full-length cDNA or gene sequence given in a sequence listing or may comprise a complete cDNA or gene sequence. Generally, a reference sequence is at least 18 nucleotides or 6 amino acids in length, frequently at least 24 nucleotides or 8 amino acids in length, and often at least 48 nucleotides or 16 amino acids in length. Since two polynucleotides or amino acid sequences may each (1) comprise a sequence (*i.e.,* a portion of the complete polynucleotide or amino acid sequence) that is similar between the two molecules, and (2) may further comprise a sequence that is divergent between the two polynucleotides or amino acid sequences, sequence comparisons between two (or more) molecules are typically performed by comparing sequences of the two molecules over a "comparison window" to identify and compare local regions of sequence similarity. A "comparison window", as used herein, refers to a conceptual segment of at least 18 contiguous nucleotide positions or 6 amino acids wherein a polynucleotide sequence or amino acid sequence may be compared to a reference sequence of at least 18 contiguous nucleotides or 6 amino acid sequences and wherein the portion of the polynucleotide sequence in the comparison window may comprise additions, deletions, substitutions, and the like (*i.e.,* gaps) of 20 percent or less as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Optimal alignment of sequences for aligning a comparison window may

be conducted by the local homology algorithm of Smith and Waterman Adv. Appl. Math. 2:482 (1981), by the homology alignment algorithm of Needleman and Wunsch J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson and Lipman Proc. Natl. Acad. Sci. (U.S.A.) 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, (Genetics Computer Group, 575 Science Dr., Madison, Wis.), Geneworks, or MacVector software packages), or by inspection, and the best alignment (*i.e.*, resulting in the highest percentage of homology over the comparison window) generated by the various methods is selected.

The term "sequence identity" means that two polynucleotide or amino acid sequences are identical (*i.e.*, on a nucleotide-by-nucleotide or residue-by-residue basis) over the comparison window. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over the window of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, U or I) or residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the comparison window (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The terms "substantial identity" as used herein denotes a characteristic of a polynucleotide or amino acid sequence, wherein the polynucleotide or amino acid comprises a sequence that has at least 85 percent sequence identity, preferably at least 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison window of at least 18 nucleotide (6 amino acid) positions, frequently over a window of at least 24-48 nucleotide (8-16 amino acid) positions, wherein the percentage of sequence identity is calculated by comparing the reference sequence to the sequence which may include deletions or additions which total 20 percent or less of the reference sequence over the comparison window. The reference sequence may be a subset of a larger sequence.

As used herein, the twenty conventional amino acids and their abbreviations follow conventional usage. *See* Immunology - A Synthesis (2nd Edition, E.S. Golub and D.R. Gren, Eds., Sinauer Associates, Sunderland7 Mass. (1991)). Stereoisomers (*e.g.*, D-

amino acids) of the twenty conventional amino acids, unnatural amino acids such as α-, α-disubstituted amino acids, N-alkyl amino acids, lactic acid, and other unconventional amino acids may also be suitable components for polypeptides of the present invention. Examples of unconventional amino acids include: 4 hydroxyproline, γ-carboxyglutamate, ε-N,N,N-trimethyllysine, ε -N-acetyllysine, O-phosphoserine, N- acetylserine, N-formylmethionine, 3-methylhistidine, 5-hydroxylysine, σ-N-methylarginine, and other similar amino acids and imino acids (*e.g.*, 4- hydroxyproline). In the polypeptide notation used herein, the lefthand direction is the amino terminal direction and the righthand direction is the carboxy-terminal direction, in accordance with standard usage and convention.

Similarly, unless specified otherwise, the lefthand end of single- stranded polynucleotide sequences is the 5' end the lefthand direction of double-stranded polynucleotide sequences is referred to as the 5' direction. The direction of 5' to 3' addition of nascent RNA transcripts is referred to as the transcription direction sequence regions on the DNA strand having the same sequence as the RNA and which are 5' to the 5' end of the RNA transcript are referred to as "upstream sequences", sequence regions on the DNA strand having the same sequence as the RNA and which are 3' to the 3' end of the RNA transcript are referred to as "downstream sequences".

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

Preferably, residue positions which are not identical differ by conservative amino acid substitutions.

Conservative amino acid substitutions refer to the interchangeability of residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide- containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and tryptophan; a group of amino acids

having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur- containing side chains is cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine valine, glutamic- aspartic, and asparagine-glutamine.

As discussed herein, minor variations in the amino acid sequences of antibodies or immunoglobulin molecules are contemplated as being encompassed by the present invention, providing that the variations in the amino acid sequence maintain at least 75%, more preferably at least 80%, 90%, 95%, and most preferably 99%. In particular, conservative amino acid replacements are contemplated. Conservative replacements are those that take place within a family of amino acids that are related in their side chains. Genetically encoded amino acids are generally divided into families: (1) acidic amino acids are aspartate, glutamate; (2) basic amino acids are lysine, arginine, histidine; (3) non-polar amino acids are alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan, and (4) uncharged polar amino acids are glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine. The hydrophilic amino acids include arginine, asparagine, aspartate, glutamine, glutamate, histidine, lysine, serine, and threonine. The hydrophobic amino acids include alanine, cysteine, isoleucine, leucine, methionine, phenylalanine, proline, tryptophan, tyrosine and valine. Other families of amino acids include (i) serine and threonine, which are the aliphatic-hydroxy family; (ii) asparagine and glutamine, which are the amide containing family; (iii) alanine, valine, leucine and isoleucine, which are the aliphatic family; and (iv) phenylalanine, tryptophan, and tyrosine, which are the aromatic family. For example, it is reasonable to expect that an isolated replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, a threonine with a serine, or a similar replacement of an amino acid with a structurally related amino acid will not have a major effect on the binding or properties of the resulting molecule, especially if the replacement does not involve an amino acid within a framework site. Whether an amino acid change results in a functional peptide can readily be determined by assaying the specific activity of the polypeptide derivative. Assays are described in detail herein. Fragments or analogs of antibodies or immunoglobulin molecules can be readily prepared by those of ordinary skill in the art. Preferred amino- and carboxy-termini of fragments or analogs occur near boundaries of

functional domains. Structural and functional domains can be identified by comparison of the nucleotide and/or amino acid sequence data to public or proprietary sequence databases. Preferably, computerized comparison methods are used to identify sequence motifs or predicted protein conformation domains that occur in other proteins of known structure and/or function. Methods to identify protein sequences that fold into a known three-dimensional structure are known. Bowie *et al.* Science 253:164 (1991). Thus, the foregoing examples demonstrate that those of skill in the art can recognize sequence motifs and structural conformations that may be used to define structural and functional domains in accordance with the invention.

Preferred amino acid substitutions are those which: (1) reduce susceptibility to proteolysis, (2) reduce susceptibility to oxidation, (3) alter binding affinity for forming protein complexes, (4) alter binding affinities, and (4) confer or modify other physicochemical or functional properties of such analogs. Analogs can include various muteins of a sequence other than the naturally-occurring peptide sequence. For example, single or multiple amino acid substitutions (preferably conservative amino acid substitutions) may be made in the naturally- occurring sequence (preferably in the portion of the polypeptide outside the domain(s) forming intermolecular contacts. A conservative amino acid substitution should not substantially change the structural characteristics of the parent sequence (*e.g.*, a replacement amino acid should not tend to break a helix that occurs in the parent sequence, or disrupt other types of secondary structure that characterizes the parent sequence). Examples of art-recognized polypeptide secondary and tertiary structures are described in Proteins, Structures and Molecular Principles (Creighton, Ed., W. H. Freeman and Company, New York (1984)); Introduction to Protein Structure (C. Branden and J. Tooze, eds., Garland Publishing, New York, N.Y. (1991)); and Thornton et at. Nature 354:105 (1991).

The term "polypeptide fragment" as used herein refers to a polypeptide that has an amino terminal and/or carboxy-terminal deletion, but where the remaining amino acid sequence is identical to the corresponding positions in the naturally-occurring sequence deduced, for example, from a full length cDNA sequence. Fragments typically are at least 5, 6, 8 or 10 amino acids long, preferably at least 14 amino acids long' more preferably at least 20 amino acids long, usually at least 50 amino acids long, and even

more preferably at least 70 amino acids long. The term "analog" as used herein refers to polypeptides which are comprised of a segment of at least 25 amino acids that has substantial identity to a portion of a deduced amino acid sequence and which has at least one of the following properties: (1) specific binding to CD3, under suitable binding conditions, (2) ability to block appropriate CD3 binding, or (3) ability to inhibit CD3-expressing cell growth *in vitro* or in vivo. Typically, polypeptide analogs comprise a conservative amino acid substitution (or addition or deletion) with respect to the naturally- occurring sequence. Analogs typically are at least 20 amino acids long, preferably at least 50 amino acids long or longer, and can often be as long as a full-length naturally-occurring polypeptide.

Peptide analogs are commonly used in the pharmaceutical industry as non-peptide drus with properties analogous to those of the template peptide. These types of non-peptide compound are termed "peptide mimetics" or "peptidomimetics". Fauchere, J. Adv. Drug Res. 15:29 (1986), Veber and Freidinger TINS p.392 (1985); and Evans *et al.* J. Med. Chem. 30:1229 (1987). Such compounds are often developed with the aid of computerized molecular modeling. Peptide mimetics that are structurally similar to therapeutically useful peptides may be used to produce an equivalent therapeutic or prophylactic effect. Generally, peptidomimetics are structurally similar to a paradigm polypeptide (*i.e.,* a polypeptide that has a biochemical property or pharmacological activity), such as human antibody, but have one or more peptide linkages optionally replaced by a linkage selected from the group consisting of: -- CH_2NH--, --CH_2S-, --CH_2-CH_2--, --CH=CH--(cis and trans), --$COCH_2$--, $CH(OH)CH_2$--, and -CH_2SO--, by methods well known in the art. Systematic substitution of one or more amino acids of a consensus sequence with a D-amino acid of the same type (*e.g.,* D-lysine in place of L-lysine) may be used to generate more stable peptides. In addition, constrained peptides comprising a consensus sequence or a substantially identical consensus sequence variation may be generated by methods known in the art (Rizo and Gierasch Ann. Rev. Biochem. 61:387 (1992)); for example, by adding internal cysteine residues capable of forming intramolecular disulfide bridges which cyclize the peptide.

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

As used herein, the terms "label" or "labeled" refers to incorporation of a detectable marker, *e.g.*, by incorporation of a radiolabeled amino acid or attachment to a polypeptide of biotinyl moieties that can be detected by marked avidin (*e.g.*, streptavidin containing a fluorescent marker or enzymatic activity that can be detected by optical or calorimetric methods). In certain situations, the label or marker can also be therapeutic. Various methods of labeling polypeptides and glycoproteins are known in the art and may be used. Examples of labels for polypeptides include, but are not limited to, the following: radioisotopes or radionuclides (*e.g.*, ^{3}H, ^{14}C, ^{15}N, ^{35}S, ^{90}Y, ^{99}Tc, ^{111}In, ^{125}I, ^{131}I), fluorescent labels (*e.g.*, FITC, rhodamine, lanthanide phosphors), enzymatic labels (*e.g.*, horseradish peroxidase, p-galactosidase, luciferase, alkaline phosphatase), chemiluminescent, biotinyl groups, predetermined polypeptide epitopes recognized by a secondary reporter (*e.g.*, leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags). In some embodiments, labels are attached by spacer arms of various lengths to reduce potential steric hindrance. The term "pharmaceutical agent or drug" as used herein refers to a chemical compound or composition capable of inducing a desired therapeutic effect when properly administered to a patient.

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

The term "antineoplastic agent" is used herein to refer to agents that have the functional property of inhibiting a development or progression of a neoplasm in a human, particularly a malignant (cancerous) lesion, such as a carcinoma, sarcoma, lymphoma, or leukemia. Inhibition of metastasis is frequently a property of antineoplastic agents.

As used herein, "substantially pure" means an object species is the predominant species present (*i.e.*, on a molar basis it is more abundant than any other individual species in the composition), and preferably a substantially purified fraction is a

composition wherein the object species comprises at least about 50 percent (on a molar basis) of all macromolecular species present.

Generally, a substantially pure composition will comprise more than about 80 percent of all macromolecular species present in the composition, more preferably more than about 85%, 90%, 95%, and 99%. Most preferably, the object species is purified to essential homogeneity (contaminant species cannot be detected in the composition by conventional detection methods) wherein the composition consists essentially of a single macromolecular species.

The term patient includes human and veterinary subjects.

Human Antibodies and Humanization of Antibodies

A huCD3 antibody is generated, for example, by immunizing xenogenic mice capable of developing fully human antibodies (*see* Example 1). An IgG huCD3 antibody is generated, for example, by converting an IgM anti-CD3 antibody produced by a transgenic mouse (*see* Example 2). Alternatively, such a huCD3 antibody is developed, for example, using phase-display methods using antibodies containing only human sequences. Such approaches are well-known in the art, *e.g.*, in WO92/01047 and U.S. Pat. No. 6,521,404, which are hereby incorporated by reference. In this approach, a combinatorial library of phage carrying random pairs of light and heavy chains are screened using natural or recombinant source of CD3 or fragments thereof.

This invention includes methods to produce a huCD3 antibody by a process wherein at least one step of the process includes immunizing a transgenic, non-human animal with human CD3 protein. Some of the endogenous heavy and/or kappa light chain loci of this xenogenic non-human animal have been disabled and are incapable of the rearrangement required to generate genes encoding immunoglobulins in response to an antigen. In addition, at least one human heavy chain locus and at least one human light chain locus have been stably transfected into the animal. Thus, in response to an administered antigen, the human loci rearrange to provide genes encoding human variable regions immunospecific for the antigen. Upon immunization, therefore, the xenomouse produces B-cells that secrete fully human immunoglobulins.

A variety of techniques are well-known in the art for producing xenogenic non-human animals. For example, see U.S. Pat. No. 6,075,181 and No. 6,150,584. By one

strategy, the xenogeneic (human) heavy and light chain immunoglobulin genes are introduced into the host germ line (*e.g.*, sperm or oocytes) and, in separate steps, the corresponding host genes are rendered non-functional by inactivation using homologous recombination. Human heavy and light chain immunoglobulin genes are reconstructed in an appropriate eukaryotic or prokaryotic microorganism, and the resulting DNA fragments are introduced into the appropriate host, for example, the pronuclei of fertilized mouse oocytes or embryonic stem cells. Inactivation of the endogenous host immunoglobulin loci is achieved by targeted disruption of the appropriate loci by homologous recombination in the host cells, particularly embryonic stem cells or pronuclei of fertilized mouse oocytes. The targeted disruption can involve introduction of a lesion or deletion in the target locus, or deletion within the target locus accompanied by insertion into the locus, *e.g.*, insertion of a selectable marker. In the case of embryonic stem cells, chimeric animals are generated which are derived in part from the modified embryonic stem cells and are capable of transmitting the genetic modifications through the germ line. The mating of hosts with introduced human immunoglobulin loci to strains with inactivated endogenous loci will yield animals whose antibody production is purely xenogeneic, e.g., human.

In an alternative strategy, at least portions of the human heavy and light chain immunoglobulin loci are used to replace directly the corresponding endogenous immunoglobulin loci by homologous recombination in embryonic stem cells. This results in simultaneous inactivation and replacement of the endogenous immunoglobulin. This is followed by the generation of chimeric animals in which the embryonic stem cell-derived cells can contribute to the germ lines.

For example, a B cell clone that expresses human anti-CD3 antibody is removed from the xenogenic non-human animal and immortalized according to various methods known within the art. Such B cells may be derived directly from the blood of the animal or from lymphoid tissues, including but not restricted to spleen, tonsils, lymph nodes, and bone marrow. The resultant, immortalized B cells may be expanded and cultured in vitro to produce large, clinically applicable quantities of huCD3 antibody. Alternatively, genes encoding the immunoglobulins with one or more human variable regions can be recovered and expressed in a differing cell type, including but not restricted to a

mammalian cell culture system, in order to obtain the antibodies directly or individual chains thereof, composed of single chain F_v molecules.

In addition, the entire set of fully human anti-CD3 antibodies generated by the xenogenic non-human animal may be screened to identify one such clone with the optimal characteristics. Such characteristics include, for example, binding affinity to the human CD3 protein, stability of the interaction as well as the isotype of the fully human anti-CD3 antibody. Clones from the entire set which have the desired characteristics then are used as a source of nucleotide sequences encoding the desired variable regions, for further manipulation to generate antibodies with the-se characteristics, in alternative cell systems, using conventional recombinant or transgenic techniques.

This general strategy was demonstrated in connection with generation of the first XenoMouse™ strains as published in 1994. *See* Green *et al.* Nature Genetics 7:13-21 (1994). This approach is further discussed and delineated in U.S. Patent Application Serial Nos. 07/466,008, filed January 12, 1990, 07/610,515, filed November 8, 1990, 07/919,297, filed July 24, 1992, 07/922,649, filed July 30, 1992, filed 08/031,801, filed March 15,1993, 08/112,848, filed August 27, 1993, 08/234,145, filed April 28, 1994, 08/376,279, filed January 20, 1995, 08/430, 938, April 27, 1995, 08/464,584, filed June 5, 1995, 08/464,582, filed June 5, 1995, 08/463,191, filed June 5, 1995, 08/462,837, filed June 5, 1995, 08/486,853, filed June 5, 1995, 08/486,857, filed June 5, 1995, 08/486,859, filed June 5, 1995, 08/462,513, filed June 5, 1995, 08/724,752, filed October 2, 1996, and 08/759, 620, filed December 3, 1996 and U.S. Patent Nos. 6,162,963, 6,150,584, 6, 114,598, 6,075,181, and 5,939,598 and Japanese Patent Nos. 3 068 180 B2, 3 068 506 B2, and 3 068 507 B2. *See* also Mendez *et al.* Nature Genetics 15:146-156 (1997) and Green and Jakobovits J. Exp. Med.: 188:483-495 (1998). *See* also European Patent No., EP 0 463 151 B1, grant published June 12, 1996, International Patent Application No., WO 94/02602, published February 3, 1994, International Patent Application No., WO 96/34096, published October 31, 1996, WO 98/24893, published June 11, 1998, WO 00/76310, published December 21,2000.

In an alternative approach, others have utilized a "minilocus" approach. In the minilocus approach, an exogenous Ig locus is mimicked through the inclusion of pieces (individual genes) from the Ig locus. Thus, one or more VH genes, one or more D_H

genes, one or more J_H genes, a mu constant region, and a second constant region (preferably a gamma constant region) are formed into a construct for insertion into an animal. This approach is described in U.S. Patent No. 5,545,807 to Surani *et al.* and U.S. Patent Nos. 5,545,806, 5,625,825, 5,625,126, 5,633,425, 5,661,016, 5,770,429, 5,789,650, 5,814,318, 5,877, 397, 5,874,299, and 6,255,458 each to Lonberg and Kay, U.S. Patent No. 5,591,669 and 6,023.010 to Krimpenfort and Berns, U.S. Patent Nos. 5, 612,205, 5,721,367, and 5,789,215 to Berns *et al.*, and U.S. Patent No. 5, 643,763 to Choi and Dunn, and GenPharm International U.S. Patent Application Serial Nos. 07/574,748, filed August 29, 1990, 07/575,962, filed August 31, 1990, 07/810,279, filed December 17, 1991, 07/853,408, filed March 18, 1992, 07/904,068, filed June 23, 1992, 07/990,860, filed December 16, 1992, 08/053,131, filed April 26, 1993, 08/096,762, filed July 22, 1993, 08/155,301, filed November 18, 1993, 081161,739, filed December 3, 1993, 08/165,699, filed December 10, 1993, 08/209,741, filed March 9, 1994. *See* also European Patent No. 0 546 073 B1, International Patent Application Nos. WO 92/03918, WO 92/22645, WO 92/22647, WO 92/22670, WO 93/12227, WO 94/00569, WO 94/25585, WO 96/14436, WO 97/13852, and WO 98/24884 and U.S. Patent No. 5,981,175. *See* further Taylor *et al.*, 1992, Chen *et al.*, 1993, Tuaillon *et al.*, 1993, Choi *et al.*, 1993, Lonberg *et al.*, (1994), Taylor *et al.*, (1994), and Tuaillon *et al.*, (1995), Fishwild *et al.*, (1996).

An advantage of the minilocus approach is the rapidity with which constructs including portions of the Ig locus can be generated and introduced into animals. Commensurately, however, a significant disadvantage of the minilocus approach is that, in theory, insufficient diversity is introduced through the inclusion of small numbers of V, D, and J genes. Indeed, the published work appears to support this concern. B-cell development and antibody production of animals produced through use of the minilocus approach appear stunted. Therefore, research surrounding the present invention has consistently been directed towards the introduction of large portions of the Ig locus in order to achieve greater diversity and in an effort to reconstitute the immune repertoire of the animals.

Kirin has also demonstrated the generation of human antibodies from mice in which, through microcell fusion, large pieces of chromosomes, or entire chromosomes, have been introduced. *See* European Patent Application Nos. 773 288 and 843 961.

Human anti-mouse antibody (HAMA) responses have led the industry to prepare chimeric or otherwise humanized antibodies. While chimeric antibodies have a human constant region and a immune variable region, it is expected that certain human anti-chimeric antibody (HACA) responses will be observed, particularly in chronic or multi-dose utilizations of the antibody. Thus, it would be desirable to provide fully human antibodies against CD3 in order to vitiate concerns and/or effects of HAMA or HACA response.

The production of antibodies with reduced immunogenicity is also accomplished via humanization and display techniques using appropriate libraries. It will be appreciated that murine antibodies or antibodies from other species can be humanized or primatized using techniques well known in the art. *See e.g.*, Winter and Harris Immunol Today 14:43 46 (1993) and Wright *et al.* Crit, Reviews in Immunol. 12125-168 (1992). The antibody of interest may be engineered by recombinant DNA techniques to substitute the CH1, CH2, CH3, hinge domains, and/or the framework domain with the corresponding human sequence (*See* WO 92102190 and U.S. Patent Nos. 5,530,101, 5,585,089, 5, 693,761, 5,693,792, 5,714,350, and 5,777,085). Also, the use of Ig cDNA for construction of chimeric immunoglobulin genes is known in the art (Liu *et al.* P.N.A.S. 84:3439 (1987) and J. Immunol. 139:3521 (1987)). mRNA is isolated from a hybridoma or other cell producing the antibody and used to produce cDNA. The cDNA of interest may be amplified by the polymerase chain reaction using specific primers (U.S. Pat. Nos. 4,683, 195 and 4,683,202). Alternatively, a library is made and screened to isolate the sequence of interest. The DNA sequence encoding the variable region of the antibody is then fused to human constant region sequences. The sequences of human constant regions genes may be found in Kabat *et al.* (1991) Sequences of Proteins of immunological Interest, N.I.H. publication no. 91-3242. Human C region genes are readily available from known clones. The choice of isotype will be guided by the desired effecter functions, such as complement fixation, or activity in antibody-dependent cellular cytotoxicity. Preferred isotypes are IgGl, IgG3 and IgG4. Either of the human

light chain constant regions, kappa or lambda, may be used. The chimeric, humanized antibody is then expressed by conventional methods.

Antibody fragments, such as Fv, $F(ab')_2$ and Fab may be prepared by cleavage of the intact protein, *e.g.*, by protease or chemical cleavage. Alternatively, a truncated gene is designed. For example, a chimeric gene encoding a portion of the $F(ab')_2$ fragment would include DNA sequences encoding the CH1 domain and hinge region of the H chain, followed by a translational stop codon to yield the truncated molecule.

Consensus sequences of H and L J regions may be used to design oligonucleotides for use as priers to introduce useful restriction sites into the J region for subsequent linkage of V region segments to human C region segments. C region cDNA can be modified by site directed mutagenesis to place a restriction site at the analogous position in the human sequence.

Expression vectors include plasmids, retroviruses, YACs, EBV derived episomes, and the like. A convenient vector is one that encodes a functionally complete human CH or CL immunoglobulin sequence, with appropriate restriction sites engineered so that any VH or VL -31 sequence can be easily inserted and expressed. In such vectors, splicing usually occurs between the splice donor site in the inserted J region and the splice acceptor site preceding the human C region, and also at the splice regions that occur within the human CH exons. Polyadenylation and transcription termination occur at native chromosomal sites downstream of the coding regions. The resulting chimeric antibody may be joined to any strong promoter, including retroviral LTRs, *e.g.*, SV-40 early promoter, (Okayama *et al.* Mol. Cell. Bio. 3:280 (1983)), Rous sarcoma virus LTR (Gorman *et al.* P.N.A.S. 79:6777 (1982)), and moloney murine leukemia virus LTR (Grosschedl *et al.* Cell 41:885 (1985)). Also, as will be appreciated, native Ig promoters and the like may be used.

Further, human antibodies or antibodies from other species can be generated through display type technologies, including, without limitation, phage display, retroviral display, ribosomal display, and other techniques, using techniques well known in the art and the resulting molecules can be subjected to additional maturation, such as affinity maturation, as such techniques are well known in the art. Wright and Harris, supra., Hanes and Plucthau PEAS USA 94:4937-4942 (1997) (ribosomal display), Parmley and

Smith Gene 73:305-318 (1988) (phage display), Scott TIB5 17:241-245 (1992), Cwirla *et al.* PNAS USA 87:6378-6382 (1990), Russel *et al.* Nucl. Acids Research 21:1081-1085 (1993), Hoganboom *et al.* Immunol. Reviews 130:43-68 (1992), Chiswell and McCafferty TIBTECH; 10:80-8A (1992), and U.S. Patent No. 5,733,743. If display technologies are utilized to produce antibodies that are not human, such antibodies can be humanized as described above.

Using these techniques, antibodies can be generated to CD3 expressing cells, CD3 itself, forms of CD3, epitopes or peptides thereof, and expression libraries thereto (*See e.g.,* U.S. Patent No. 5,703,057) which can thereafter be screened as described above for the activities described above.

Design and Generation of Other Therapeutics

In accordance with the present invention and based on the activity of the antibodies that are produced and characterized herein with respect to CD3, the design of other therapeutic modalities beyond antibody moieties is facilitated. Such modalities include, without limitation, advanced antibody therapeutics, such as bispecific antibodies, immunotoxins, and radiolabeled therapeutics, generation of peptide therapeutics, gene therapies, particularly intrabodies, antisense therapeutics, and small molecules.

For example, in connection with bispecific antibodies, bispecific antibodies can be generated that comprise (i) two antibodies one with a specificity to CD3 and another to a second molecule that are conjugated together, (ii) a single antibody that has one chain specific to CD3 and a second chain specific to a second molecule, or (iii) a single chain antibody that has specificity to CD3 and the other molecule. Such bispecific antibodies can be generated using techniques that are well known for example, in connection with (i) and (ii) *See e.g.,* Fanger *et al.* Immunol Methods 4:72-81 (1994) and Wright and Harris, supra, and in connection with (iii) *See e.g.,* Traunecker *et al.* Int. J. Cancer (Suppl.) 7:51-52 (1992). In each case, the second specificity can be made to the heavy chain activation receptors, including, without limitation, CD16 or CD64 (*See e.g.,* Deo *et al.* 18:127 (1997)) or CD89 (*See e.g.,* Valerius *et al.* Blood 90:4485-4492 (1997)). Bispecific antibodies prepared in accordance with the foregoing would be likely to kill cells expressing CD3, and particularly those cells in which the CD3 antibodies of the invention are effective.

In connection with immunotoxins, antibodies can be modified to act as immunotoxins utilizing techniques that are well known in the art. *See e.g.,* Vitetta Immunol Today 14:252 (1993). *See* also U.S. Patent No. 5,194,594. In connection with the preparation of radiolabeled antibodies, such modified antibodies can also be readily prepared utilizing techniques that are well known in the art. *See e.g.,* Junghans *et al.* in Cancer Chemotherapy and Biotherapy 655-686 (2d edition, Chafner and Longo, eds., Lippincott Raven (1996)). *See* also U.S. Patent Nos. 4,681,581, 4,735,210, 5,101,827,5,102,990 (RE 35,500), 5, 648,471, and 5,697,902. Each of immunotoxins and radiolabeled molecules would be likely to kill cells expressing CD3, and particularly those cells in which the antibodies of the invention are effective.

In connection with the generation of therapeutic peptides, through the utilization of structural information related to CD3 and antibodies thereto, such as the antibodies of the invention or screening of peptide libraries, therapeutic peptides can be generated that are directed against CD3. Design and screening of peptide therapeutics is discussed in connection with Houghten *et al.* Biotechniques 13:412-421 (1992), Houghten PNAS USA 82:5131-5135 (1985), Pinalla *et al.* Biotechniques 13:901-905 (1992), Blake and Litzi-Davis BioConjugate Chem. 3:510-513 (1992). Immunotoxins and radiolabeled molecules can also be prepared, and in a similar manner, in connection with peptidic moieties as discussed above in connection with antibodies. Assuming that the CD3 molecule (or a form, such as a splice variant or alternate form) is functionally active in a disease process, it will also be possible to design gene and antisense therapeutics thereto through conventional techniques. Such modalities can be utilized for modulating the function of CD3. In connection therewith the antibodies of the present invention facilitate design and use of functional assays related thereto. A design and strategy for antisense therapeutics is discussed in detail in International Patent Application No. WO 94/29444. Design and strategies for gene therapy are well known. However, in particular, the use of gene therapeutic techniques involving intrabodies could prove to be particularly advantageous. *See e.g.,* Chen *et al.* Human Gene Therapy 5:595-601 (1994) and Marasco Gene Therapy 4:11-15 (1997). General design of and considerations related to gene therapeutics is also discussed in International Patent Application No. WO 97/38137.

Knowledge gleaned from the structure of the CD3 molecule and its interactions with other molecules in accordance with the present invention, such as the antibodies of the invention, and others can be utilized to rationally design additional therapeutic modalities. In this regard, rational drug design techniques such as X-ray crystallography, computer-aided (or assisted) molecular modeling (CAMM), quantitative or qualitative structure-activity relationship (QSAR), and similar technologies can be utilized to focus drug discovery efforts. Rational design allows prediction of protein or synthetic structures which can interact with the molecule or specific forms thereof which can be used to modify or modulate the activity of CD3. Such structures can be synthesized chemically or expressed in biological systems. This approach has been reviewed in Capsey *et al.* Genetically Engineered Human Therapeutic Drugs (Stockton Press, NY (1988)). Further, combinatorial libraries can be designed and synthesized and used in screening programs, such as high throughput screening efforts.

Therapeutic Administration and Formulations

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

2):1-60 (2000), Charman WN "Lipids, lipophilic drugs, and oral drug delivery-some emerging concepts." J Pharm Sci.89(8):967-78 (2000), Powell *et al.* "Compendium of excipients for parenteral formulations" PDA J Pharm Sci Technol. 52:238-311 (1998) and the citations therein for additional information related to formulations, excipients and carriers well known to pharmaceutical chemists.

Therapeutic formulations of the invention, which include a huCD3 antibody of the invention, are used to treat or alleviate a symptom associated with an immune-related disorder, such as, for example, an autoimmune disease or an inflammatory disorder.

Autoimmune diseases include, for example, Acquired Immunodeficiency Syndrome (AIDS, which is a viral disease with an autoimmune component), alopecia areata, ankylosing spondylitis, antiphospholipid syndrome, autoimmune Addison's disease, autoimmune hemolytic anemia, autoimmune hepatitis, autoimmune inner ear disease (AIED), autoimmune lymphoproliferative syndrome (ALPS), autoimmune thrombocytopenic purpura (ATP), Behcet's disease, cardiomyopathy, celiac sprue-dermatitis hepetiformis; chronic fatigue immune dysfunction syndrome (CFIDS), chronic inflammatory demyelinating polyneuropathy (CIPD), cicatricial pemphigold, cold agglutinin disease, crest syndrome, Crohn's disease, Degos' disease, dermatomyositis-juvenile, discoid lupus, essential mixed cryoglobulinemia, fibromyalgia-fibromyositis, Graves' disease, Guillain-Barré syndrome, Hashimoto's thyroiditis, idiopathic pulmonary fibrosis, idiopathic thrombocytopenia purpura (ITP), IgA nephropathy, insulin-dependent diabetes mellitus, juvenile chronic arthritis (Still's disease), juvenile rheumatoid arthritis, Ménière's disease, mixed connective tissue disease, multiple sclerosis, myasthenia gravis, pernacious anemia, polyarteritis nodosa, polychondritis, polyglandular syndromes, polymyalgia rheumatica, polymyositis and dermatomyositis, primary agammaglobulinemia, primary biliary cirrhosis, psoriasis, psoriatic arthritis, Raynaud's phenomena, Reiter's syndrome, rheumatic fever, rheumatoid arthritis, sarcoidosis, scleroderma (progressive systemic sclerosis (PSS), also known as systemic sclerosis (SS)), Sjögren's syndrome, stiff-man syndrome, systemic lupus erythematosus, Takayasu arteritis, temporal arteritis/giant cell arteritis, ulcerative colitis, uveitis, vitiligo and Wegener's granulomatosis.

Inflammatory disorders, include, for example, chronic and acute inflammatory disorders. Examples of inflammatory disorders include Alzheimer's disease, asthma, atopic allergy, allergy, atherosclerosis, bronchial asthma, eczema, glomerulonephritis, graft vs. host disease, hemolytic anemias, osteoarthritis, sepsis, stroke, transplantation of tissue and organs, vasculitis, diabetic retinopathy and ventilator induced lung injury.

In one embodiment, the huCD3 antibody compositions of the invention are administered in conjunction with a second agent such as, for example, GLP-1 or a beta cell resting compound (*i.e.*, a compound that reduces or otherwise inhibits insulin release, such as potassium channel openers). Examples of suitable GLP-1 compounds are described in *e.g.*, the published application U.S. 20040037826, and suitable beta cell resting compounds are described in published application U.S. 20030235583, each of which is hereby incorporated by reference in its entirety.

In another embodiment, the huCD3 antibody compositions used to treat an immune-related disorder are administered in combination with any of a variety of known anti-inflammatory and/or immunosuppressive compounds. Suitable known compounds include, but are not limited to methotrexate, cyclosporin A (including, for example, cyclosporin microemulsion), tacrolimus, corticosteroids, statins, interferon beta, Remicade (Infliximab), Enbrel (Etanercept) and Humira (Adalimumab).

For example, in the treatment of rheumatoid arthritis, the huCD3 antibody compositions of the invention can be co-administered with corticosteroids, methotrexate, cyclosporin A, statins, Remicade (Infliximab), Enbrel (Etanercept) and/or Humira (Adalimumab).

In the treatment of uveitis, the huCD3 antibody compositions can be administered in conjunction with, *e.g.*, corticosteroids, methotrexate, cyclosporin A, cyclophosphamide and/or statins. Likewise, patients afflicted with a disease such as Crohn's Disease or psoriasis can be treated with a combination of a huCD3 antibody composition of the invention and Remicaid (Infliximab), and/or Humira (Adalimumab).

Patients with multiple sclerosis can receive a combination of a huCD3 antibody composition of the invention in combination with, *e.g.*, glatiramer acetate (Copaxone), interferon beta-1a (Avonex), interferon beta-1a (Rebif), interferon beta-1b (Betaseron or

Betaferon), mitoxantrone (Novantrone), dexamethasone (Decadron), methylprednisolone (Depo-Medrol), and/or prednisone (Deltasone) and/or statins.

The present invention also provides methods of treating or alleviating a symptom associated with an immune-related disorder or a symptom associated with rejection following organ transplantation. For example, the compositions of the invention are used to treat or alleviate a symptom of any of the autoimmune diseases and inflammatory disorders described herein.

The therapeutic compositions of the invention are also used as immunosuppression agents in organ or tissue transplantation. As used herein, "immunosuppression agent" refers to an agent whose action on the immune system leads to the immediate or delayed reduction of the activity of at least one pathway involved in an immune response, whether this response is naturally occurring or artificially triggered, whether this response takes place as part of the innate immune system, the adaptive immune system, or both. These immunosuppressive huCD3 antibody compositions are administered to a subject prior to, during and/or after organ or tissue transplantation. For example, a huCD3 antibody of the invention is used to treat or prevent rejection after organ or tissue transplantation.

In one embodiment, the immunosuppressive huCD3 antibody compositions of the invention are administered in conjunction with a second agent such as, for example, GLP-1 or a beta cell resting compound, as described above.

In another embodiment, these immunosuppressive huCD3 antibody compositions are administered in combination with any of a variety of known anti-inflammatory and/or immunosuppressive compounds. Suitable anti-inflammatory and/or immunosuppressive compounds for use with the huCD3 antibodies of the invention include, but are not limited to, methotrexate, cyclosporin A (including, for example, cyclosporin microemulsion), tacrolimus, corticosteroids and statins.

In yet another embodiment of the invention, a huCD3 antibody is administered to a human individual upon detection of the presence of auto-reactive antibodies within the human individual. Such auto-reactive antibodies are known within the art as antibodies with binding affinity to one or more proteins expressed endogenously within the human individual. In one aspect of the invention, the human individual is tested for the presence

of auto-reactive antibodies specifically involved in one or more autoimmune diseases as are well known within the art. In one specific embodiment, a human patient is tested for the presence of antibodies against insulin, glutamic acid decarboxylase and/or the IA-2 protein, and subsequently administered with a huCD3 antibody upon positive detection of one or more such auto-reactive antibodies.

In another embodiment of the invention, a huCD3 antibody is administered into human subjects to prevent, reduce or decrease the recruitment of immune cells into human tissues. A huCD3 antibody of the invention is administered to a subject in need thereof to prevent and treat conditions associated with abnormal or deregulated immune cell recruitment into tissue sites of human disease.

In another embodiment of the invention, a huCD3 antibody is administered into human subjects to prevent, reduce or decrease the extravasation and diapedesis of immune cells into human tissues. Thus, the huCD3 antibodies of the invention are administered to prevent and/or treat conditions associated with abnormal or deregulated immune cell infiltration into tissue sites of human disease.

In another embodiment of the invention, a huCD3 antibody is administered into human subjects to prevent, reduce or decrease the effects mediated by the release of cytokines within the human body. The term "cytokine" refers to all human cytokines known within the art that bind extracellular receptors upon the cell surface and thereby modulate cell function, including but not limited to IL-2, IFN-g, TNF-a, IL-4, IL-5, IL-6, IL-9, IL-10, and IL-13.

The release of cytokines can lead to a toxic condition known as the cytokine release syndrome (CRS), a common clinical complication that occurs, *e.g.*, with the use of an anti-T cell antibody such as ATG (anti-thymocyte globulin) and OKT3 (a murine anti-human CD3 antibody). This syndrome is characterized by the excessive release of cytokines such as TNF, IFN-gamma and IL-2 into the circulation. The CRS occurs as a result of the simultaneous binding of the antibodies to CD3 (via the variable region of the antibody) and the Fc Receptors and/or complement receptors (via the constant region of the antibody) on other cells, thereby activating the T cells to release cytokines that produce a systemic inflammatory response characterized by hypotension, pyrexia and rigors. Symptoms of CRS include fever, chills, nausea, vomiting, hypotension, and

dyspnea. Thus, a huCD3 antibody of the invention contains one or more mutations designed to prevent abnormal release and production of one or more cytokine(s) *in vivo*.

In another embodiment of the invention, a huCD3 antibody is administered into human subjects to prevent, reduce or decrease the effects mediated by the release of cytokine receptors within the human body. The term "cytokine receptor" refers to all human cytokine receptors within the art that bind one or more cytokine(s), as defined herein, including but not limited to receptors of the aforementioned cytokines. Thus, a huCD3 antibody of the invention is administered to treat and/or prevent conditions mediated through abnormal activation, binding or ligation of one or more cytokine receptor(s) within the human body. It is further envisioned that administration of the huCD3 antibody in vivo will deplete the intracellular signaling mediated by cytokine receptor(s) within such human subject.

In one aspect of the invention, a huCD3 antibody is administered to a human individual upon decrease of pancreatic beta-cell function therein. In one embodiment, the individual is tested for beta-cell function, insulin secretion or c-peptide levels as are known within the art. Subsequently, upon notice of sufficient decrease of either the indicator, the human individual is administered with a sufficient dosage regimen of a huCD3 antibody to prevent further progression of autoimmune destruction of beta-cell function therein.

Diagnostic and Prophylactic Formulations

The fully human anti-CD3 MAbs of the invention are used in diagnostic and prophylactic formulations. In one embodiment, a huCD3 MAb of the invention is administered to patients that are at risk of developing one of the aforementioned autoimmune diseases. A patient's predisposition to one or more of the aforementioned autoimmune diseases can be determined using genotypic, serological or biochemical markers. For example, the presence of particular HLA subtypes and serological autoantibodies (against insulin, GAD65 and IA-2) are indicative of Type I diabetes.

In another embodiment of the invention, a huCD3 antibody is administered to human individuals diagnosed with one or more of the aforementioned autoimmune diseases. Upon diagnosis, a huCD3 antibody is administered to mitigate or reverse the effects of autoimmunity. In one such example, a human individual diagnosed with Type I

diabetes is administered with sufficient dose of a huCD3 antibody to restore pancreatic function and minimize damage of autoimmune infiltration into the pancreas. In another embodiment, a human individual diagnosed with rheumatoid arthritis is administered with a huCD3 antibody to reduce immune cell infiltration into and destruction of limb joints.

Antibodies of the invention are also useful in the detection of CD3 in patient samples and accordingly are useful as diagnostics. For example, the huCD3 antibodies of the invention are used in *in vitro* assays, *e.g.*, ELISA, to detect CD3 levels in a patient sample.

In one embodiment, a huCD3 antibody of the invention is immobilized on a solid support (*e.g.*, the well(s) of a microtiter plate). The immobilized antibody serves as a capture antibody for any CD3 that may be present in a test sample. Prior to contacting the immobilized antibody with a patient sample, the solid support is rinsed and treated with a blocking agent such as mink protein or albumin to prevent nonspecific adsorption of the analyte.

Subsequently the wells were treated with a test sample suspected of containing the antigen, or with a solution containing a standard amount of the antigen. Such a sample may be, *e.g.*, a serum sample from a subject suspected of having levels of circulating antigen considered to be diagnostic of a pathology. After rinsing away the test sample or standard, the solid support is treated with a second antibody that is detectably labeled. The labeled second antibody serves as a detecting antibody. The level of detectable label is measured, and the concentration of CD3 antigen in the test sample is determined by comparison with a standard curve developed from the standard samples.

It will be appreciated that based on the results obtained using the huCD3 antibodies of the invention in an *in vitro* diagnostic assay, it is possible to stage a disease (*e.g.*, an autoimmune or inflammatory disorder) in a subject based on expression levels of the CD3 antigen. For a given disease, samples of blood are taken from subjects diagnosed as being at various stages in the progression of the disease, and/or at various points in the therapeutic treatment of the disease. Using a population of samples that provides statistically significant results for each stage of progression or therapy, a range

of concentrations of the antigen that may be considered characteristic of each stage is designated.

All publications and patent documents cited herein are incorporated herein by reference as if each such publication or document was specifically and individually indicated to be incorporated herein by reference. Citation of publications and patent documents is not intended as an admission that any is pertinent prior art, nor does it constitute any admission as to the contents or date of the same. The invention having now been described by way of written description, those of skill in the art will recognize that the invention can be practiced in a variety of embodiments and that the foregoing description and examples below are for purposes of illustration and not limitation of the claims that follow.

EXAMPLES

The following examples, including the experiments conducted and results achieved are provided for illustrative purposes only and are not to be construed as limiting upon the present invention.

EXAMPLE 1: Generation of huCD3 antibodies

Immunization Strategies: To generate a fully human huCD3 antibody, two lines of transgenic mice were utilized, the HuMab® mice and the KM™ mice (Medarex, Princeton NJ). Initial immunization strategies followed well-documented protocols from the literature for generating mouse antibodies. (*See e.g.*, Kung P, *et al.*, *Science*; 206(4416): 347-9 (1979); Kung PC, *et al.*, *Transplant Proc.* (3 Suppl 1):141-6 (1980); Kung PC, *et al.*, *Int J Immunopharmacol.*3(3):175-81 (1981)). The standard protocols known in the art failed to produce fully human anti-CD3 antibodies in the HuMAb® or the KM mouse™. For example, the following immunization strategies were unsuccessful and did not produce functional antibodies in either the HuMAb® or KM mice™:

- immunization with thymocytes only or T-cells only
- immunization with recombinant human CD3 material only
- immunization with recombinant CD3 material in Freund's adjuvant

- immunization with cell in Freund's adjuvant
- immunization with thymocytes or T-cells co-administered with soluble CD3
- immunization with thymocytes or T-cells co-administered with recombinant CD3-expressing cells

When these prior art immunization strategies are used in a BALB/c mouse rather than a HuMAb® or KM™ mouse, these strategies produce a murine anti-CD3 antibody rather than a human anti-CD3 antibody.

Accordingly, novel immunization strategies were developed by varying the following parameters:

- types of immunogens employed
- frequency of injection
- types of adjuvants employed
- types of co-stimulation techniques employed
- routes of immunization employed
- types of secondary lymphoid tissue used for fusion

A series of novel immunization strategies were developed, including for example, (i) immunization with a viral particle expressing CD3 only, and (ii) immunization with co-stimulatory signals (*e.g.*, CD40, CD27 or combinations thereof) co-administered with T cells, thymocytes, or with cells that have been transfected to express recombinant CD3.

In a first novel immunization strategy, referred to herein as the "hyper-boost protocol", a HuMAb® mouse (Medarex, Inc., Princeton, NJ) or a KM™ mouse (Medarex, Inc., Kirin) was immunized by first injecting human cells, *e.g.*, thymocytes or T-cells. At time points ranging from 1 to 8 weeks after injection of the thymocytes and/or T-cells, the mice received one or more subsequent "hyper-boost" injections. The hyper-boost injection included, for example, soluble CD3 protein (*e.g.*, recombinant soluble CD3 protein), additional injections of thymocytes or T-cells, CD3-transfected cells, viral particles expressing high levels of CD3, and combinations thereof. For example, the hyper-boost injection contained a combination of soluble CD3 protein and CD3-transfected cells.

Preferably, in the hyper-boost immunization protocols, the immunized mice received two final hyper-boost injections at –6 and –3 days prior to fusion of the lymph nodes and/or spleen. For example, in the KM mouse™, the fused tissue is derived from the spleen, and in the HuMAb® mouse, the fused tissue is derived from lymph nodes and/or splenic tissue.

In one example of the hyper-boost immunization protocol, one HuMAb™ mouse was immunized three times with human thymocytes (~10^6 cells) on days 0, 7 and 28. The Chinese ovarian cells line (CHO) transfected with the cDNA encoding human CD3 δ and ε chains (CHO/CD3, ~10^6 cells) was then injected on days 47 and 65. Another boost with a viral particle expressing high levels of CD3δε at its surface was given on day 79. Finally, the mouse was injected with soluble recombinant human CD3δε on day 121 and 124 before fusion of the lymph nodes on day 127.

All immunizations were given subcutaneously with Ribi (Corixa Corp., Seattle WA) as an adjuvant. A total of $8.5x10^6$ cells were fused. Only seven out of 470 hybridomas screened produced a fully human anti-CD3 antibody, and all of the fully human anti-CD3 antibodies were IgM molecules. Two of these anti-CD3 antibodies were selected as a therapeutic clinical candidates (Figures 1-3).

In a second example of the hyper-boost immunization protocol, one KM™ mouse was immunized twice with soluble recombinant human CD3δε on days 0 and 25. Human thymocytes (~10^6 cells) were then used for boosting on days 40, 49 and 56. The soluble recombinant CD3δε was injected twice on days 70, 77, 84 and 91. The mouse T cell line transfected with the cDNA encoding human CD3 δ and ε chains (EL4/CD3, ~10^6 cells) was then injected on day 98. Finally, the mouse was injected with soluble recombinant human CD3δε on day 101 before fusion of the spleen on day 104. Immunizations were administered intraperitoneally with Alum as an adjuvant, except on day 70 where Ribi adjuvant was used. CpG was used as a costimulatory agent on day 0, 25, 84 and 91. A total of $1.27x10^8$ cells were fused. Only five out of 743 hybridomas screened produced a fully human anti-CD3 antibody, and all of antibodies produced were IgG molecules. One of the fully human anti-CD3 antibodies was selected as a therapeutic clinical candidate (Figure 4).

Selection Criteria: Therapeutic clinical candidates were selected using the following criteria. First, antibody-binding to CD3 positive cells versus CD3 negative cells was analyzed. For this, Jurkat CD3 positive cells (J+) and Jurkat negative cells (J-) were incubated with the different antibodies and binding was assessed by flow cytometry (Figure 9A). Second, a competition assay in which the ability of the candidate antibody to inhibit the binding of the murine anti-human OKT3 monoclonal antibody to CD3 positive cells was assessed using J+ cells and competition was assessed by flow cytometry (Figure 9B). Next, antigenic modulation of CD3 and the TCR from the surface of human peripheral blood T cells was assessed by flow cytometry (Figure 9C). Finally, a T-cell proliferation assay was performed using human peripheral blood T cells dyed with CFSE and cell division was assessed by flow cytometry (Figure 9D).

Example 2: Isotype Switching of Human Anti-CD3 Antibodies

Some huCD3 antibodies produced using the novel protocols described in Example 1 were IgM antibodies. These IgM antibodies were "converted" to an IgG antibody, preferably to an IgG1 antibody. For example, the IgM antibodies were converted by a cloning procedure in which the VDJ region of the gene encoding the IgM antibody was cloned into an IgG1 heavy chain gene obtained from a vector that contains a gene encoding allotype F gamma1. For conversion of the light chain, the IgM sequence was cloned into a vector containing the kappa region. In Medarex mice, *e.g.*, the HuMAb® mouse, multiple light chains are produced, due to a lack of allelic exclusion.

Each combination of heavy and light chains was transfected into 293T cells using the FuGENE 6 (Roche Diagnostics) transfection agent according to the manufacturer's guidelines. The secreted monoclonal antibodies were tested for optimized functionality, *e.g.*, target antigen binding, using the selection criteria described in Example 1.

EXAMPLE 3: Antigenic Modulation Using the huCD3 antibodies

The huCD3 antibodies of the invention are capable of antigenic modulation, which is defined as the redistribution and elimination of the CD3-TCR complex induced by antibody binding. Cell surface expression of other molecules on T cells, including, for

example, CD4 is not altered by exposure to an anti-CD3 antibody of the invention (Figure 9C).

EXAMPLE 4: Reducing the toxic cytokine release syndrome generated by huCD3 antibodies

Preferably, the huCD3 antibodies of the invention include a mutation in the Fc region, such that the mutation alters cytokine release syndrome. As described above, the cytokine release syndrome (CRS) is a common immediate complication that occurs with the use of an anti-T cell antibody such as ATG (anti-thymocyte globulin) and OKT3 (a murine anti-CD3 antibody). This syndrome is characterized by the excessive release of cytokines such as TNF, IFN-gamma and IL-2 into the circulation. The cytokines released by the activated T cells produce a type of systemic inflammatory response similar to that found in severe infection characterized by hypotension, pyrexia and rigors. Symptoms of CRS include, for example, fever, chills, nausea, vomiting, hypotension, and dyspnea.

The huCD3 antibodies of the invention contain one or more mutations that prevent heavy chain constant region-mediated release of one or more cytokine(s) *in vivo*. In one embodiment, the huCD3 antibodies of the invention are IgG molecules having one or more of the following mutations in a modified IgG γ1 backbone: "γ1 N297A", in which the asparagine residue at position 297 is replaced with an alanine residue; "γ1 L234/A, L235/A", in which the leucine residues at positions 234 and 235 are replaced with alanine residues; "γ1 L234/A; L235/E", in which the leucine residue at position 234 is replaced with an alanine residue, while the leucine residue at position 235 is replaced with a glutamic acid residue; "γ1 L235/E" in which the leucine residue at position 235 is replaced with a glutamic acid residue; and "γ1 D265/A" in which the aspartic acid residue at position 265 is replaced with an alanine residue. The numbering of the heavy chain residues described herein is that of the EU index (*see* Kabat *et al.*, "Proteins of Immunological Interest", US Dept. of Health & Human Services (1983)), as shown, *e.g.*, in U.S. Patent Nos. 5,624,821 and 5,648,260, the contents of which are hereby incorporated in its entirety by reference.

Other IgG γ1 backbone modifications that can be used in the huCD3 antibodies of the invention include, for example, "A330/S" in which the alanine residue at position 330

is replaced with a serine residue, and/or "P331/S" in which the proline residue at position 331 is replaced with a serine residue.

The fully human CD3 antibodies of the invention having a L^{234} L^{235} → A^{234} E^{235} mutation in the Fc region have a unique function – elimination of cytokine release in the presence of the huCD3 antibody. Prior studies have actually taught away from the use of an L → E mutation (*see e.g.*, Xu et al., Cellular Immunology, 200, pp. 16-26 (2000), at p. 23). However, these particular two mutations at positions 234 and 235 (*i.e.*, L^{234} L^{235} → A^{234} E^{235}) eliminated the cytokine release syndrome, as assessed peripheral human blood mononuclear cell *in vitro* assay system (Figures 11A, 11B). In this assay, peripheral human blood mononuclear cells were isolated using a ficoll gradient, labeled with CFSE and the CFSE-labeled cells were then plated into 96 well plates. The various monoclonal antibodies were added at various dilutions and incubated for 72 hours at 37 °C. After 6 hours, 50 µl of supernatant was removed to evaluate TNF release by ELISA. After 48 hours, 50 µl of supernatant was removed to evaluate IFN-γ release by ELISA. After 72 hours, the cells were harvested and proliferation was assessed by FACS using CFSE-labeling intensity.

Thus, contrary to wild type heavy chains, and contrary to a series of other mutations that had been described by others (*e.g.*, TolerX (aglycosylation mutation), Bluestone (L^{234} L^{235} → A^{234} A^{235} mutation) (*see e.g.*, US Pat. No. 5,885,573)), which all retain a significant level of cytokine release effect, the L^{234} L^{235} → A^{234} E^{235} mutations of the huCD3 antibodies of the invention do not exhibit cytokine release phenomenon. The level of remaining cytokine release effect was 100 % for the wild type Fc, about 50 to 60% for the Bluestone (L^{234} L^{235} → A^{234} A^{235}) mutation and undetectable for Ala/Glu Fc mutations described herein (Figure 11A, 11B).

EXAMPLE 5: Peptide Array Identification of the huCD3 Antibody-Binding Epitope

The synthesis and ELISA screening of large numbers of peptides have been used to determine the amino acid residues involved in the epitope for various monoclonal antibodies. (*See e.g.*, Geysen *et al.*, J Immunol Methods, vol. 102(2):259-74 (1987)). In the experiments described herein, arrays of overlapping peptides derived from the amino acid sequence of the CD3 epsilon chain were purchased from Jerini (Berlin, Germany)

and subsequently tested for a pattern of binding by the fully human anti-CD3 mAbs of the invention.

The peptides in the arrays were produced using the "SPOT synthesis" technique for direct chemical synthesis on membrane supports (*see* Frank and Overwin, Meth Mol Biol , vol. 66:149-169 (1996); Kramer and Schneider-Mergener, Meth Mol Biol, vol. 87:25-39 (1998)). The linear 14-mer peptides were covalently bound to a Whatman 50 cellulose support by the C-terminus, leaving the N-terminus free (*i.e.*, unbound). Using standard western blotting techniques, these solid phase-bound peptides revealed that the 28F11 monoclonal recognized an overlapping set of amino acids in proximity to the N terminus (Fig. 10).

OTHER EMBODIMENTS

While the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

What is claimed is:

1. An isolated fully human monoclonal CD3 antibody, wherein said antibody has the following characteristics:
   a. binds to CD3 positive (CD3+) cells but not CD3 negative (CD3-) cells;
   b. modulates the cell surface expression level or activity of CD3;
   c. decreases the cell surface expression level or activity of the T cell receptor; and
   d. includes at least two mutations in the heavy chain at position 234 and at position 235 of the heavy chain of an IgG1 backbone, wherein the mutation at position 234 results in an alanine residue and the mutation at position 235 results in an alanine or glutamic acid residue, and wherein the mutations reduce the release of cytokines from a T-cell.

2. The antibody of claim 1, wherein said antibody inhibits binding of the murine anti-human OKT3 monoclonal antibody to a T-lymphocyte.

3. The antibody of claim 1, wherein said antibody binds an epitope that wholly or partially includes the amino acid sequence EMGGITQTPYKVSISGT (SEQ ID NO:67).

4. The antibody of claim 1, wherein said antibody further comprises an additional mutation in the heavy chain at an amino acid residue at position 265 or 297 of the heavy chain of an IgG1 backbone or combinations thereof, and reduces the release of cytokines from a T-cell.

5. The antibody of claim 4, wherein said additional mutation results in an alanine residue at position 265 or 297.

6. The antibody of claim 1, wherein said antibody is an IgGγ1 isotype.

7. The antibody of claim 1, wherein said antibody has a heavy chain with three complementarity determining regions (CDRs), comprising a VH CDR1 comprising an amino acid sequence selected from the group consisting of the amino acid sequences of GYGMH (SEQ ID NO:27) and SYGMH (SEQ ID NO:33); a VH CDR2 comprising an amino acid sequence selected from the group consisting of

VIWYDGSKKYYVDSVKG (SEQ ID NO:28), IIWYDGSKKNYADSVKG (SEQ ID NO:34), and AIWYNGRKQDYADSVKG (SEQ ID NO:44); and a VH CDR3 comprising an amino acid sequence selected from the group consisting of QMGYWHFDL (SEQ ID NO:29) and GTGYNWFDP (SEQ ID NO:35); and a light chain with three CDRs, comprising a VL CDR1 comprising an amino acid sequence selected from the group consisting of the amino acid sequences of RASQSVSSYLA (SEQ ID NO:30), RASQSVSSSYLA (SEQ ID NO:36), RASQGISSALA (SEQ ID NO:39), and WASQGISSYLA (SEQ ID NO:43); a VL CDR2 comprising an amino acid sequence selected from the group consisting of DASNRAT (SEQ ID NO:31), GASSRAT (SEQ ID NO:37), YASSLQS (SEQ ID NO:40), DASSLGS (SEQ ID NO:42), and DASSLES (SEQ ID NO:46); and a VL CDR3 comprising an amino acid sequence selected from the group consisting of QQRSNWPPLT (SEQ ID NO:32); QQYGSSPIT (SEQ ID NO:38),QQYYSTLT (SEQ ID NO:41),QQRSNWPWT (SEQ ID NO:45),and QQFNSYPIT (SEQ ID NO:47).

8. An isolated fully human monoclonal antibody, wherein said antibody has a heavy chain with three CDRs comprising a VH CDR1 region comprising the amino acid sequence of GYGMH (SEQ ID NO:27); a VH CDR2 region comprising the amino acid sequence of VIWYDGSKKYYVDSVKG (SEQ ID NO:28); a VH CDR3 region comprising the amino acid sequence of QMGYWHFDL (SEQ ID NO:29); a VL CDR1 region comprising the amino acid sequence of RASQSVSSYLA (SEQ ID NO:30); a VL CDR2 region comprising the amino acid sequence of DASNRAT (SEQ ID NO:31); and a VL CDR1 region comprising the amino acid sequence of QQRSNWPPLT (SEQ ID NO:32), wherein said antibody binds CD3.

9. The antibody of claim 1 or claim 8, wherein said antibody comprises a heavy chain variable amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 6, 10 and 22 and a light chain variable amino acid sequence selected from the group consisting of SEQ ID NOS: 4, 8, 16-20, 25 and 26.

10. The antibody of claim 1 or claim 8, wherein said antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 2 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 4.

11. An isolated fully human monoclonal antibody, wherein said antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 2 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 4, wherein said antibody binds CD3.

12. The antibody of claim 1 or claim 8, wherein said antibody comprises a framework 2 region (FWR2) comprising the amino acid sequence WVRQAPGKGLEWV (SEQ ID NO:73).

13. The antibody of claim 1 or claim 8, wherein said antibody comprises a framework 3 region (FRW3) comprising the amino acid sequence RFTISRDNSKNTLYLQMNSLRAEDTAVYYCA (SEQ ID NO:74).

14. The antibody of claim 1 or claim 8, wherein said antibody comprises a variable region located C-terminal to the CDR3 region, wherein said variable region comprises the amino acid sequence VTVSS (SEQ ID NO:64) at a position that is C-terminal to the CDR3 region.

15. The antibody of claim 14, wherein said antibody comprises a variable region located C-terminal to the CDR3 region, wherein said variable region comprises the amino acid sequence GTLVTVSS (SEQ ID NO:65) at a position that is C-terminal to the CDR3 region.

16. The antibody of claim 14, wherein said antibody comprises a variable region located C-terminal to the CDR3 region, wherein said variable region comprises the amino acid sequence WGRGTLVTVSS (SEQ ID NO:66) at a position that is C-terminal to the CDR3 region.

17. The antibody of claim 8, wherein said antibody binds an epitope that wholly or partially includes the amino acid sequence EMGGITQTPYKVSISGT (SEQ ID NO:67).

18. The antibody of claim 8, wherein said antibody further comprises a mutation in the heavy chain at an amino acid residue at position 234, 235, 265, or 297 of the heavy chain an IgG1 backbone or combinations thereof, and wherein the release of cytokines from a T-cell in the presence of said antibody is reduced as compared to the

release of cytokines from a T-cell in the presence of an antibody that does not include a mutation in the heavy chain at position 234, 235, 265 or 297 of the heavy chain an IgG1 backbone or combinations thereof.

19. The antibody of claim 18, wherein said mutation results in an alanine or glutamic acid residue at said position.

20. The antibody of claim 18, wherein said antibody contains at least a first mutation is at position 234 and a second mutation is at position 235 of the heavy chain an IgG1 backbone, and wherein said first mutation results in an alanine residue at position 234 of the heavy chain an IgG1 backbone and said second mutation results in a glutamic acid residue at position 235 of the heavy chain an IgG1 backbone.