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CA 2454361 A1 2003/05/01

(21) 2 454 361

(12) DEMANDE DE BREVET CANADIEN
CANADIAN PATENT APPLICATION

(13) A1

(86) Date de dépôt PCT/PCT Filing Date: 2002/07/19
(87) Date publication PCT/PCT Publication Date: 2003/05/01
(85) Entrée phase nationale/National Entry: 2004/01/19
(86) N° demande PCT/PCT Application No.: US 2002/023002
(87) N° publication PCT/PCT Publication No.: 2003/035696
(30) Priorité/Priority: 2001/07/19 (09/910,483) US

(51) Cl.Int.[7]/Int.Cl.[7] C07K 16/28, A61P 31/12, A61K 39/395, C12N 15/13, C12N 15/63, C07K 16/46

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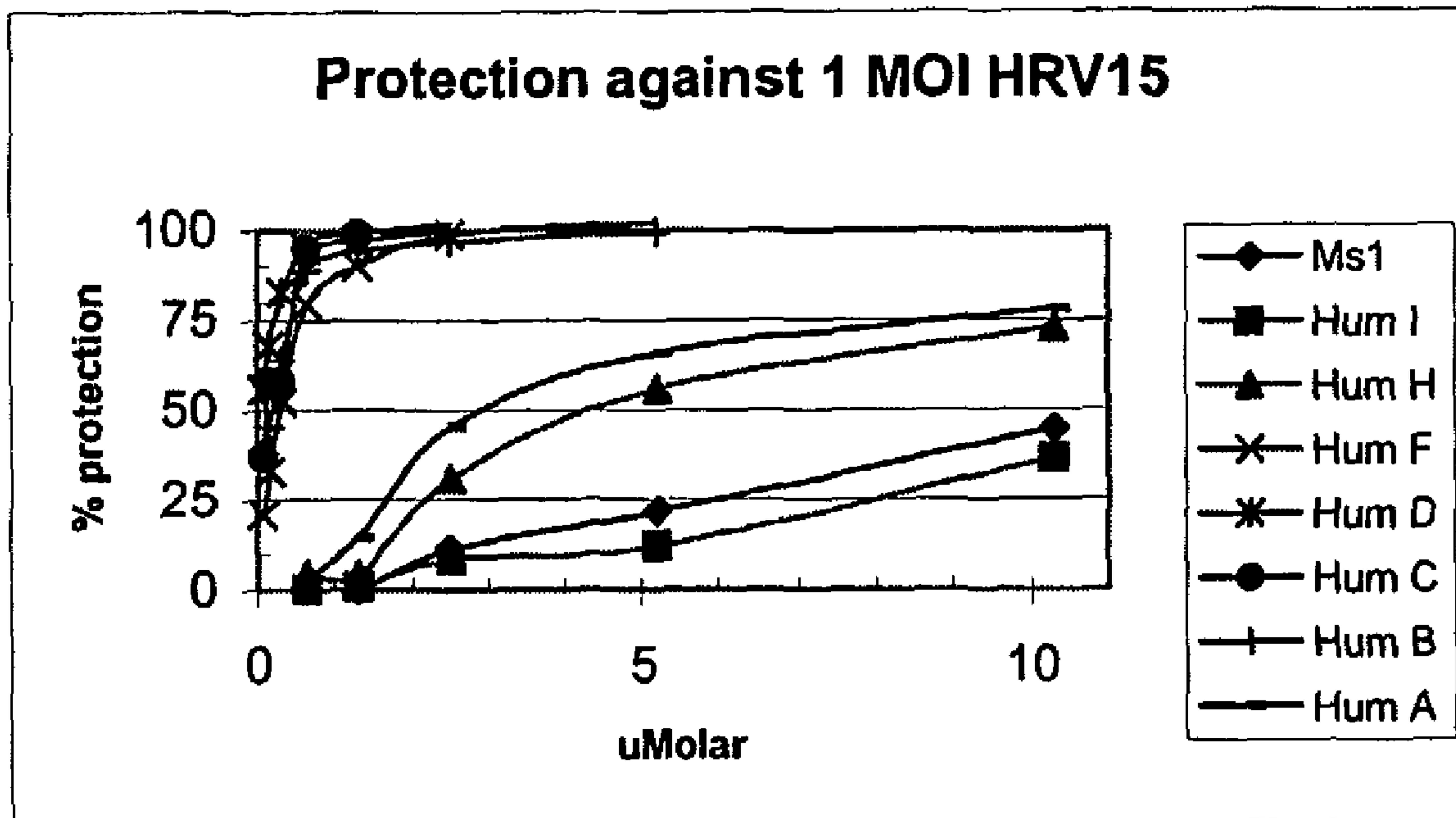
(54) Titre : ANTICORPS HUMANISES
(54) Title: HUMANIZED ANTIBODIES AGAINST ICAM-1, THEIR PRODUCTION AND USES



(57) Abrégé/Abstract:
The invention provides humanized antibodies, for example, those that that bind ICAM-1, methods of use and methods of producing the antibodies. Antibodies include sequences having a V_H and V_L domain selected from HumA, HumB, HumC, HumD, HumE, HumF, HumG, HumH, HumI, Hum40 and Hum50.

CA 02454361 2004-01-19

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

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
1 May 2003 (01.05.2003)

PCT

(10) International Publication Number
WO 03/035696 A3

(51) International Patent Classification[7]: C07K 16/28, 16/46, C12N 15/13, 15/63, A61K 39/395, A61P 31/12

(21) International Application Number: PCT/US02/23002

(22) International Filing Date: 19 July 2002 (19.07.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
09/910,483 19 July 2001 (19.07.2001) US

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(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

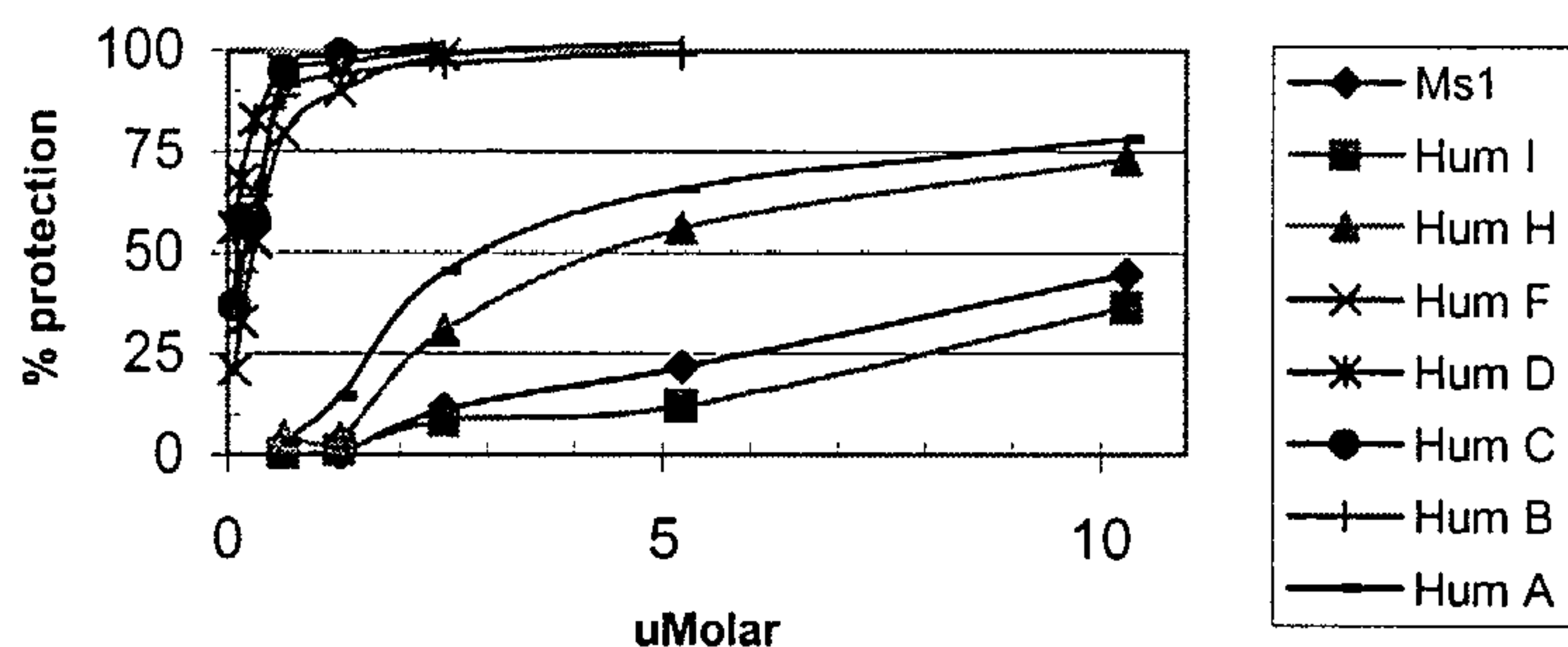
(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *with international search report*

(88) Date of publication of the international search report: 27 November 2003

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: HUMANIZED ANTIBODIES AGAINST ICAM-1, THEIR PRODUCTION AND USES



(57) Abstract: The invention provides humanized antibodies, for example, those that that bind ICAM-1, methods of use and methods of producing the antibodies. Antibodies include sequences having a V_H and V_L domain selected from HumA, HumB, HumC, HumD, HumE, HumF, HumG, HumH, HumI, Hum40 and Hum50.

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Humanized Antibodies

FIELD OF THE INVENTION

5 The invention relates to humanized antibody compositions and methods of making and using humanized antibodies.

BACKGROUND

Monoclonal antibodies have become an important class of therapeutic proteins. 10 However, foreign immunoglobulins used in humans can elicit an anti-globulin response which may interfere with therapy or cause allergic or immune complex hypersensitivity. To avoid this problem, a monoclonal antibody may be "humanized," and this is typically carried out by CDR grafting.

CDR's, also called hypervariable regions, are present in immunoglobulin light 15 and heavy chains and are flanked by "framework" regions. CDR grafting was first described in Jones *et al.* ((1986) *Nature* 321:522-525). In this and later publications, the CDRs of three mouse antibodies were grafted onto the variable domain framework of the human immunoglobulin NEW (V_H) and REI (V_L). The resulting humanized antibodies had the same antigen specificity and a similar affinity as the parental murine monoclonal 20 antibody (mAb) (Jones *et al. supra*; Verhoeyen *et al.* (1988) *Science* 239:1534-1536; Riechmann *et al.* (1988) *Nature* 332:323-327; U.S. Patent No. 5,225,539).

CDR grafting has been described by Queen and coworkers who reported the humanization of four murine monoclonal antibodies (Queen *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86:10029-10033; Co *et al.* (1991) *Proc. Natl. Acad. Sci. USA* 88:2869- 25 2873; Co *et al.* (1992) *J. Immunol.*148:1149-1154; and U.S. Patent Nos. 5,585,089; 5,693,761; and 5,693,762). Murine residues were inserted in the human framework in order to maintain affinity and, in each case the original antigen specificity was maintained. The affinities of the humanized antibodies ranged from 1/3 to 3 times of the parental unmodified murine antibodies.

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SUMMARY

The invention provides humanized antibodies that bind ICAM-1. In one embodiment, the antibody has a V_H and V_L domain selected from: SEQ ID NO:1 and 3

(HumA); SEQ ID NO:4 and 5 (HumB); SEQ ID NO:6 and 7 (HumC); SEQ ID NO:8 and 9 (HumD); SEQ ID NO:10 and 11 (HumE); SEQ ID NO:12 and 13 (HumF); SEQ ID NO:14 and 15 (HumG); SEQ ID NO:16 and 17 (HumH); and SEQ ID NO:18 and 19 (HumI); and SEQ ID NO:5 and 20 (Hum40); and SEQ ID NO:5 and 21 (Hum50). Subsequences of antibodies that bind ICAM-1 are provided, for example, single chain, Fab, Fab' and $(Fab)_2$ fragments. In particular aspects, the humanized antibody has greater affinity for ICAM-1 than the parental (non-human) antibody. Varaint and modified forms of antibodies that bind ICAM-1 are also provided, for example, antibodies having a V_H and V_L domain selected from: SEQ ID NO:1 and 3 (HumA); SEQ ID NO:4 and 5 (HumB); SEQ ID NO:6 and 7 (HumC); SEQ ID NO:8 and 9 (HumD); SEQ ID NO:10 and 11 (HumE); SEQ ID NO:12 and 13 (HumF); SEQ ID NO:14 and 15 (HumG); SEQ ID NO:16 and 17 (HumH); and SEQ ID NO:18 and 19 (HumI); and SEQ ID NO:5 and 20 (Hum40); and SEQ ID NO:5 and 21 (Hum50), having one or more amino acid substitutions, insertions or deletions.

The invention also provides humanized antibodies that bind ICAM-1 and inhibit pathogen infection of cells expressing ICAM-1. Such invention antibodies include antibodies that provide equal or greater protection from pathogen infection than parental (non-human) antibody. In particular aspects, a humanized antibody has a protective efficacy equal to or at least 2 times greater, 5 times greater, 10 times greater, 20 times greater, 30 times greater than the non-humanized antibody. In other aspects, the pathogen is human rhinovirus (HRV), coxackie A virus, respiratory syncytial virus (RSV), or malaria.

The humanized antibodies of the invention include intact immunoglobulin molecules, comprising 2 full-length heavy chains and 2 full-length light chains, for example, IgG, IgA, IgM, IgE, and IgD, and subsequences that inhibit pathogen infection. Particular subsequences include, for example, single chain, Fab, Fab' or $(Fab)_2$ fragment.

The humanized antibodies of the invention include multispecific or multifunctional antibodies. In one aspect, such an antibody is formed by linking a humanized antibody to one or more identical or different antibodies to form a multimer (e.g. using a linker). Antibody multimers include a homo- or hetero-dimer, trimer,

tetramer or any other higher order oligomer. Antibody multimers that include different antibodies are human, humanized or non-human. Multimeric forms include antibody oligomers that form via a multimerization domain (e.g. a human amino acid sequence) or a covalent bond. Antibody multimers that include a multimerization domain further include forms having a linker located between the multimerization domain and the antibody.

The invention additionally provides methods for producing humanized antibodies. In one embodiment, a method includes: selecting a human framework sequence as an acceptor, wherein said sequence has 50% or more identity (e.g., 50-55%, 55-60%, 60-65%, 65-70%, 70-75%, 75-80%, 80-85%, 85-90%, 90-95%, or more identity) to a non-human donor antibody framework region; grafting a CDR from the donor non-human antibody (e.g., murine) onto the human framework; comparing the vernier zone residues of the human acceptor and the non-human donor framework regions; and maintaining one or more of the human acceptor residues in the vernier zone when the donor non-human and human residues are structurally or chemically similar, or substituting one or more of the vernier zone residues with a residue that is different from both the donor non-human vernier zone residue and acceptor human vernier zone residue if the donor non-human vernier zone residue is structurally or chemically dissimilar to the human residue, wherein the different residue is structurally or chemically similar to the donor non-human vernier zone residue. In additional embodiments, human framework acceptor sequences are selected from a consenus sequence, for example, from V_H domain subgroup I and subgroup II consensus sequences.

Nucleic acid sequences encoding humanized antibodies, subsequences and modified forms thereof (e.g., amino acid additions, deletions or substitutions) are also provided. Nucleic acid sequences further include expression cassettes in which nucleic acid encoding humanized antibodies are operably linked to an expression control element. Vectors and cells (prokaryotic and eukaryotic) that include the nucleic acids also are provided.

The invention further provides pharmaceutical compositions including humanized antibodies, subsequences, multimers, variants and modified forms, and nucleic acids

encoding them, and a pharmaceutically acceptable carrier. In particular aspects, the pharmaceutically acceptable carrier is compatible with inhalation or nasal delivery to a subject.

The invention further provides methods of inhibiting pathogen infection of a cell. 5 In one embodiment, a method includes contacting a pathogen or a cell with an amount of a humanized antibody, subsequence, multimer, variant or modified form sufficient to inhibit pathogen infection of the cell. In one aspect, the cell expresses ICAM-1. In another aspect, the cell (e.g., epithelial cell) is present in a subject.

The invention also provides methods of inhibiting HRV infection of a cell. In one 10 embodiment, a method includes contacting HRV or a cell susceptible to HRV infection with an amount of a humanized antibody, subsequence, multimer, variant or modified form effective to inhibit HRV infection of the cell (e.g., epithelial cell). In one aspect, the cell is present in a subject. In another aspect, the cell is present in a subject having or at risk of having asthma. In yet another aspect, the subject is a newborn or between the 15 ages of 1 to 5, 5 to 10 or 10 to 18. In still another aspect, the antibody, subsequence, multimer, variant or modified form binds to an antigen present on the surface of the cell (e.g., ICAM-1). In various additional aspects, the humanized antibody is administered locally, via inhalation or intranasaly.

The invention also provides methods of inhibiting HRV infection, inhibiting HRV 20 progression or treating HRV infection of a subject. In one embodiment, a method includes administering to a subject having or at risk of having HRV infection an amount of a humanized antibody, subsequence, multimer, variant or modified form effective to inhibit HRV infection, inhibit HRV progression or treat HRV infection of the subject. In one aspect, the subject has or is at risk of having asthma. In another aspect, the subject is 25 a newborn or between the ages of 1 to 5, 5 to 10 or 10 to 18. In various additional aspects, the humanized antibody is administered locally, via inhalation or intranasaly.

The invention additionally provides methods of decreasing or inhibiting one or more symptoms of the common cold in a subject. In one embodiment, a method includes administering to a subject having a common cold an amount of a humanized antibody, 30 subsequence, multimer, variant or modified form effective to decrease or inhibit one or

more symptoms of the common cold in the subject. In one aspect, the subject has or is at risk of having asthma. In another aspect, the subject is a newborn or between the ages of 1 to 5, 5 to 10 or 10 to 18. In various additional aspects, the humanized antibody is administered locally, via inhalation or intranasaly.

5

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the amino acid sequences of murine 1A6 antibody heavy and light chain (SEQ ID NO:77 and 79) and human consensus sequence of heavy chain subgroup III (Hum3; SEQ ID NO:78) and light chain kappa subgroup I (HumκI; SEQ ID
10 NO:80). Asterisks denote amino acid differences between human and mouse sequence. CDR amino acids as defined by Kabat and Chothia are in bold face.

Figure 2 shows the amino acid sequences of murine 1A6 antibody (SEQ ID NO:77), humanized 1A6 (HumB; SEQ ID NO:4) and human consensus sequences of heavy chain subgroup III (Hum3; (SEQ ID NO:78) and light chain kappa subgroup I
15 (HumκI; (SEQ ID NO:80). Asterisks and bold face amino acids are as previously indicated.

Figure 3 shows the cDNA sequences of humanized scFVA (HumA) antibody (SEQ ID NO:2). Restriction sites are indicated by underlining; CCATGG Nco I site; GGATCC BamH I site; GTTAAC Hpa I site. Bold face amino acids are as previously
20 indicated.

Figure 4 shows protection from HRV15 infection with mouse 1A6 scFv antibody (Ms1) and humanized 1A6 scFv antibodies HumA, HumB, HumC, HumD, HumF, HumH and HumI.

Figure 5 shows amino acid sequences of murine 1A6 V_H domain (SEQ ID
25 NO:77) and human consensus sequences of V_H domain subgroup I (Hum1; (SEQ ID NO:82) and subgroup II (Hum2; SEQ ID NO:81). Bold face amino acids are as previously indicated.

Figure 6 shows the V_H domain amino acid sequences of murine 1A6 antibody (SEQ ID NO:77), humanized 1A6 (Hum40; SEQ ID NO:20) and human consensus

sequences of heavy chain subgroup II (Hum2; SEQ ID NO:81). Asterisks and bold face amino acids are as previously indicated.

Figure 7 shows the V_H domain amino acid sequences of murine 1A6 antibody (SEQ ID NO:77), humanized 1A6 (Hum50; SEQ ID NO:21) and human consensus
5 sequences of heavy chain subgroup I (Hum1; SEQ ID NO:82). Asterisks and bold face amino acids are as previously indicated.

DETAILED DESCRIPTION

The present invention is based, at least in part, upon producing humanized
10 antibodies. More particularly, complementarity determining region (CDR) from a non-human antibody are grafted into a human framework region. Following grafting, one or more amino acids of the antibody is mutated to a human amino acid or is mutated to a non-human amino acid having structural similarity to the amino acid it replaces. For example, mutating a murine amino acid to a human amino acid in a framework region or
15 CDR of the grafted antibody can produce a humanized antibody having increased antigen binding affinity relative to the non-human or grafted antibody. Humanized antibodies are not immunogenic or are less immunogenic than non-human antibodies when administered to human subjects. Therefore, humanized antibodies are useful in a variety of therapeutic and diagnostic applications. For example, as exemplified herein, a
20 humanized antibody of the invention protects cells from HRV infection, a virus that can cause the common cold, and other associated disorders (e.g. otitis media, bronchitis, sinusitis etc.).

Thus, in accordance with the invention, there are provided humanized antibodies. In one embodiment, a humanized antibody binds to ICAM-1. In one aspect, a humanized
25 antibody that binds ICAM-1 protects against pathogen infection of cells expressing ICAM-1. In other aspects, a humanized antibody has a V_H and V_L domain selected from: SEQ ID NO:1 and 3 (HumA); SEQ ID NO:4 and 5 (HumB); SEQ ID NO:6 and 7 (HumC); SEQ ID NO:8 and 9 (HumD); SEQ ID NO:10 and 11 (HumE); SEQ ID NO:12 and 13 (HumF); SEQ ID NO:14 and 15 (HumG); SEQ ID NO:16 and 17 (HumH); and
30 SEQ ID NO:18 and 19 (HumI); and SEQ ID NO:5 and 20 (Hum40); and SEQ ID NO:5 and 21 (Hum50). In another embodiment, a humanized antibody has a greater or less

affinity for the antigen than the donor non-human antibody. In various aspects, affinities range from greater or less affinity for the antigen than either the donor or recombinant antibody. In particular aspects, humanized antibody has an antigen binding affinity 2- to 4-fold, 5-fold, 5- to 8-fold, 5- to 10-fold, 8- to 15-fold, 10- to 20-fold, 20- to 40-fold, 20-60-fold, 20- to 100-fold or greater than the parental antibody.

Human antibody sequence regions can be used for producing humanized antibodies of the invention. For example, a "consensus sequence," an antibody sequence having the most frequently occurring amino acid residues at particular positions in an antibody or an antibody region, may be used. As an example, human variable region domain sequences are described in Kabat (*Sequences of Proteins of Immunological Interest.* 4th Ed.US Department of Health and Human Services. Public Health Service (1987)). Sequences that are completely determined in the framework regions, 1-23, 35-49, and 57-88 in the light chains, and in the framework regions, 1-30, 36-49, and 66-94, in the heavy chains, are included in the survey. For the fourth framework region, 98-107 in the light chain and 103-113 in the heavy chain, residues that can be derived from the known J-minigene segments are surveyed.

At the end of the survey, the most frequently occurring residue at a given position is chosen as the residue in the consensus sequence. Consensus sequences may therefore be identified by surveying amino acid residues at each position of a plurality of antibodies; the most frequently occurring amino acid at a given position in the region of interest is a part of the consensus. In many instances, more than one residue will be found at high frequency at a given position. In such cases, if the amino acid that occurs at least one-fourth as frequently as the most frequently occurring the amino acid residue is considered a part of the consensus sequence.

The published consensus sequence of human V_H subgroup III is based on a survey of 22 known human V_H III sequences, the consensus sequence of human V_H subgroup I is based on 6 known human V_H I sequences, and the consensus sequence of human V_H subgroup II is based on 10 known sequences in the same group. The published consensus sequence of human V_L kappa-chain subgroup I, based on a survey of 30 known human kappa I sequences (Padlan (1994) *Mol. Immunol.* 31:169-217; Padlan (1991) *Mol.*

Immunol. 28:489-498). The human consensus sequences were previously used to humanize two antibodies (Carter *et al.* (1992) *Proc. Natl. Acad. Sci. USA* 89:4285-4289; Presta *et al.* (1993) *J. Immunol.*151: 2623-2632). These human V_H subgroup I, II and III sequences, and V_L -kappa subgroup I consensus sequences are selected as frameworks, respectively, to humanize mAb1A6 as described in Examples 1 and 8. Thus, consensus sequences known in the art, as exemplified for human V_H subgroup I, II and III or V_L -kappa subgroup I, are selected as acceptor frameworks for producing humanized antibody in accordance with the invention.

Any mouse, rat, guinea pig, goat, non-human primate (e.g., ape, chimpanzee, macaque, orangutan, etc.) or other non-human animal antibody may be used as a CDR donor for producing humanized antibody. Murine antibodies secreted by hybridoma cell lines can also be used. Donor CDRs are selected based upon the antigen to which the antibody binds. Thus, donor CDRs include sequences from antibodies that bind to pathogens, such as bacteria, viruses, protozoa and other microorganisms. Donor CDRs also include antibodies that bind to molecules to which the pathogens bind, for example, cell surface proteins (e.g., adhesion proteins, receptor proteins, immune-recognition/modulation proteins such as HLA, tumor associated antigens, etc.). In one particular example, the donor antibody is a mouse monoclonal antibody 1A6 (mAb1A6), which specifically binds to ICAM-1.

"Complementarity determining regions" or "CDRs" are among the sequences that can be grafted into framework sequences. CDRs refer to sequence regions that confer antibody specificity and affinity. CDRs are also generally known as supervariable regions or hypervariable loops. CDR regions of antibodies have been mapped and are defined as in Kabat (*Sequences of Proteins of Immunological Interest.* 4th Ed.US Department of Health and Human Services. Public Health Service (1987)) and Chothia and Lesk ((1987) J. Mol. Biol. 186:651-663)). In particular, for heavy chain, CDR1 is defined as H26-H35, CDR2 is H50-65 and CDR3 is H95-H102; for light chain, CDR 1 is L24-L34, CDR2 is L50-L56 and CDR3 is L89-L97. The amino acids are numbered according to the scheme described in Kabat (*Sequences of Proteins of Immunological Interest.* 4th Ed.US Department of Health and Human Services. Public Health Service (1987)). Variable region domains typically comprise the amino-terminal approximately

105-115 amino acids a of a naturally-occurring immunoglobulin chain (e.g., amino acids 1-110). Variable domains shorter or longer than these exemplary sequence lengths may also be used.

Thus, the invention provides humanized antibodies, methods of making the
5 antibodies and methods of using the antibodies, including therapeutic and diagnostic methods. In one embodiment, a humanized antibody has increased affinity for the antigen relative to non-humanized antibody (e.g., less than 1.18×10^{-6} M in K_D against ICAM-1, less than 1×10^{-7} M in K_D, less than 5×10^{-7} M in K_D, less than 1×10^{-8} M in K_D, less than 5×10^{-8} M in K_D or less than 1×10^{-9} M in K_D). In various aspects, a
10 humanized antibody includes a V_H and V_L domain selected from: SEQ ID NO:1 and 3 (HumA); SEQ ID NO:4 and 5 (HumB); SEQ ID NO:6 and 7 (HumC); SEQ ID NO:8 and 9 (HumD); SEQ ID NO:10 and 11 (HumE); SEQ ID NO:12 and 13 (HumF); SEQ ID NO:14 and 15 (HumG); SEQ ID NO:16 and 17 (HumH); and SEQ ID NO:18 and 19 (HumI); and SEQ ID NO:5 and 20 (Hum40); and SEQ ID NO:5 and 21 (Hum50); and
15 antigen binding subsequences thereof. In various additional aspects, an antibody subsequence comprises Fab, Fab', $(Fab')_2$, Fv, and single chain antibody (SCA), *e.g.*, scFv fragments.

The humanized antibodies of the invention also include antibody multimers. In various aspects, a multimer comprises a dimer, trimer, tetramer or other higher order
20 oligomer. In other aspects, multimers comprise combinations of the same antibodies (homo-oligomers) and different antibodies (hetero-oligomers), the different antibodies being human, humanized or non-human.

The terms "protein," "polypeptide" and "peptide" are used interchangeably herein to refer to two or more covalently linked amino acids, also referred to as "residues,"
25 through an amide bond or equivalent. Polypeptides are of unlimited length and may be comprised of L- or D-amino acids as well as mixtures thereof. Amino acids may be linked by non-natural and non-amide chemical bonds including, for example, those formed with glutaraldehyde, N-hydoxysuccinimide esters, bifunctional maleimides, or N,N'-dicyclohexylcarbodiimide (DCC). Non-amide bonds include, for example,
30 ketomethylene, aminomethylene, olefin, ether, thioether and the like (see, e.g., Spatola

(1983) in Chemistry and Biochemistry of Amino Acids, Peptides and Proteins, Vol. 7, pp 267-357, "Peptide and Backbone Modifications," Marcel Decker, NY). Polypeptides may have one or more cyclic structures such as an end-to-end amide bond between the amino and carboxy- terminus of the molecule or intra- or inter-molecular disulfide bond.
5 Polypeptides may be modified in vitro or *in vivo*, e.g., post-translationally modified to include, for example, sugar residues, phosphate groups, ubiquitin, fatty acids or lipids. Polypeptides further include amino acid structural and functional analogues, for example, peptidomimetics having synthetic or non-natural amino acids or amino acid analogues.

The term "antibody" refers to a protein that binds to other molecules (antigens)
10 via heavy and light chain variable domains, V_H and V_L, respectively. Antibodies include IgG, IgD, IgA, IgM and IgE. The antibodies may be intact immunoglobulin molecules, two full length heavy chains linked by disulfide bonds to two full length light chains, as well as subsequences (i.e. fragments) of immunoglobulin molecules, with our without constant region, that bind to an epitope of an antigen, or subsequences thereof (i.e.
15 fragments) of immunoglobulin molecules, with or without constant region, that bind to an epitope of an antigen. Antibodies may comprise full length heavy and light chain variable domains, V_H and V_L, individually or in any combination. For example, each of a a V_H and V_L domain selected from: SEQ ID NO:1 and 3 (HumA); SEQ ID NO:4 and 5 (HumB); SEQ ID NO:6 and 7 (HumC); SEQ ID NO:8 and 9 (HumD); SEQ ID NO:10
20 and 11 (HumE); SEQ ID NO:12 and 13 (HumF); SEQ ID NO:14 and 15 (HumG); SEQ ID NO:16 and 17 (HumH); and SEQ ID NO:18 and 19 (HumI); and SEQ ID NO:5 and 20 (Hum40); and SEQ ID NO:5 and 21 (Hum50) are included individually and in any combination.

Polypeptide sequences can be made using recombinant DNA technology of
25 polypeptide encoding nucleic acids via cell expression or in vitro translation, or chemical synthesis of polypeptide chains using methods known in the art. Antibodies according to the invention, including humanized sequences and subsequences can be expressed from recombinantly produced antibody-encoding nucleic acid (see, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1989; Harlow and
30 Lane, *Using Antibodies: A Laboratory Manual,* Cold Spring Harbor Laboratory, 1999; Fitzgerald *et al., J.A.C.S.* 117:11075 (1995); Gram *et al., Proc. Natl. Acad. Sci. USA*

89:3576-80 (1992)). For example, as described in Example 3, cDNA encoding humanized antibody sequences can be expressed in bacteria in order to produce invention antibodies. Antibodies may also be produced by expressing encoding nucleic acids in mammalian, insect, and plant cells. Polypeptide sequences including antibodies can also be produced by a chemical synthesizer (see, e.g., Applied Biosystems, Foster City, CA).

As used herein, the term "subsequence" or "fragment" means a portion of the full length molecule. For example, a subsequence of an antibody is one or more amino acid less in length than full length polypeptide (e.g. one or more internal or terminal amino acid deletions from either amino or carboxy-termini). Subsequences therefore can be any length up to the full length molecule.

Specific examples of antibody subsequences include, for example, Fab, Fab', $(Fab')_2$, Fv, or single chain antibody (SCA) fragment (*e.g.,* scFv). Subsequences include portions which retain at least part of the function or activity of full length sequence. For example, an antibody subsequence will retain the ability to selectively bind to an antigen even though the binding affinity of the subsequence may be greater or less than the binding affinity of the full length antibody. Subsequences can comprise a portion of any of the invention humanized sequences, for example, a portion of V_H and V_L domain selected from: SEQ ID NO:1 and 3 (HumA); SEQ ID NO:4 and 5 (HumB); SEQ ID NO:6 and 7 (HumC); SEQ ID NO:8 and 9 (HumD); SEQ ID NO:10 and 11 (HumE); SEQ ID NO:12 and 13 (HumF); SEQ ID NO:14 and 15 (HumG); SEQ ID NO:16 and 17 (HumH); and SEQ ID NO:18 and 19 (HumI); and SEQ ID NO:5 and 20 (Hum40); and SEQ ID NO:5 and 21 (Hum50).

Pepsin or papain digestion of whole antibodies can be used to generate antibody fragments. In particular, an Fab fragment consists of a monovalent antigen-binding fragment of an antibody molecule, and can be produced by digestion of a whole antibody molecule with the enzyme papain, to yield a fragment consisting of an intact light chain and a portion of a heavy chain. An $(Fab')_2$ fragment of an antibody can be obtained by treating a whole antibody molecule with the enzyme pepsin, without subsequent reduction. An Fab' fragment of an antibody molecule can be obtained from $(Fab')_2$ by reduction with a thiol reducing agent, which yields a molecule consisting of an intact

light chain and a portion of a heavy chain. Two Fab' fragments are obtained per antibody molecule treated in this manner.

An Fv fragment is a fragment containing the variable region of a light chain V_L and the variable region of a heavy chain V_H expressed as two chains. The association may be non-covalent or may be covalent, such as a chemical cross-linking agent or an intermolecular disulfide bond (Inbar et al., (1972) *Proc. Natl. Acad Sci.* USA 69:2659; Sandhu (1992) *Crit. Rev. Biotech.* 12:437).

A single chain antibody ("SCA") is a genetically engineered or enzymatically digested antibody containing the variable region of a light chain V_L and the variable region of a heavy chain, optionally linked by a flexible linker, such as a polypeptide sequence, in either V_L-linker-V_H orientation or in V_H-linker-V_L orientation. Alternatively, a single chain Fv fragment can be produced by linking two variable domains via a disulfide linkage between two cysteine residues. Methods for producing scFv antibodies are described, for example, by Whitlow et al., (1991) In: Methods: A Companion to Methods in Enzymology 2:97; U.S. Patent No. 4,946,778; and Pack et al., (1993) *Bio/Technology* 11:1271.

Other methods of producing antibody subsequences, such as separation of heavy chains to form monovalent light-heavy chain fragments, further cleavage of fragments, or other enzymatic, chemical, or genetic techniques may also be used, provided that the subsequences bind to the antigen to which the intact antibody binds.

As used herein, the term "bind" or "binding" means that the compositions referred to have affinity for each other. "Specific binding" is where the binding is selective between two molecules. A particular example of specific binding is that which occurs between an antibody and an antigen. Typically, specific binding can be distinguished from non-specific when the dissociation constant (K_D) is less than about 1×10^{-5} M or less than about 1×10^{-6} M or 1×10^{-7} M. Specific binding can be detected, for example, by ELISA, immunoprecipitation, coprecipitation, with or without chemical crosslinking, two-hybrid assays and the like. Appropriate controls can be used to distinguish between "specific" and "non-specific" binding.

Invention antibodies, including full length antibodies, subsequences (e.g., single chain forms) may be present as dimer, trimers, tetramers, pentamers, hexamers or any other higher order oligomer that retains at least a part of antigen binding activity of monomer. Multimers can comprise heteromeric or homomeric combinations of full length antibody, subsequences, unmodified or modified as set forth herein and known in the art. Antibody multimers are useful for increasing antigen avidity in comparison to monomer due to the multimer having multiple antigen binding sites. Antibody multimers are also useful for producing oligomeric (e.g., dimer, trimer, tertamer, etc.) combinations of different antibodies thereby producing compositions of antibodies that are multifunctional (e.g., bifunctional, trifunctional, tetrafunctional, etc.).

The term "multifunctional" means that the composition referred to has two or more activities or functions (e.g., antigen binding, enzyme activity, ligand or receptor binding, toxin, etc.). For example, an antibody that binds to a particular antigen which also has an attached polypeptide with enzyme activity (e.g., luciferase, acetyltransferase, galactosidase, peroxidase, etc.) is one particular example of a muiltifunctional antibody.

Multifunctional antibodies further include multispecific (e.g., bispecific, trispecific, tetraspecific, etc.) forms. The term "multispecific" means an antibody that binds to two or more different antigenic epitopes. The term "multispecific" means that the antibody contains two or more variable region sequences that bind to different epitopes. The different epitopes may be present on the same antigen or different antigens. For example, a multispecific antibody oligomer comprises a mixture of two or more antibodies each having different epitope binding specificity and which form a multimer. Multispecific antibodies may be comprised of individual antigen binding polypeptides each of which have distinct variable domains. For example, one of the antibodies may have two variable domains each of which recognizes a different epitope.

Candidate functions for multifunctional antibodies other than antigen binding and in addition to enzyme activity include, for example, detectable moieties such as radioisotopes and amino acid sequences (e.g., ^{35}S, ^{131}I, T7, immunoglobulin or polyhistidine tags, toxins (e.g., ricin, cholera, pertussis), cell surface proteins such as receptors, ligands (substrates, agonists and antagonists), adhesion proteins (e.g.,

streptavidin, avidin, lectins), growth factors, differentiative factors and chemotactic factors.

Multifunctional humanized antibodies can be produced through chemical crosslinking of the selected molecules (which have been produced by synthetic means or by expression of nucleic acid that encode the polypeptides) or through recombinant DNA technology combined with in vitro, or cellular expression of the polypeptide, and subsequent oligomerization. Multispecific antibodies can be similarly produced through recombinant technology and expression, fusion of hybridomas that produce antibodies with different epitopic specificities, or expression of multiple nucleic acid encoding antibody variable chains with different epitopic specificities in a single cell.

Antibodies may be either joined directly or indirectly through covalent or non-covalent binding, e.g. via a multimerization domain, to produce multimers. A "multimerization domain" mediates non-covalent protein-protein interactions. Specific examples include coiled-coil (e.g., leucine zipper structures) and alpha-helical protein sequences. Sequences that mediate protein-protein binding via Van der Waals' forces, hydrogen bonding or charge-charge bonds are also contemplated as multimerization domains. Additional examples include basic-helix-loop-helix domains and other protein sequences that mediate heteromeric or homomeric protein-protein interactions among nucleic acid binding proteins (e.g., DNA binding transcription factors, such as TAFs). One specific example of a multimerization domain is p53 residues 319 to 360 which mediate tetramer formation. Another example is human platelet factor 4, which self-assembles into tetramers. Yet another example is extracellular protein TSP4, a member of the thrombospondin family, which can form pentamers. Additional specific examples are the leucine zippers of jun, fos, and yeast protein GCN4.

Humanized antibodies may be directly linked to each other via a chemical cross linking agent or can be connected via a linker sequence (e.g., a peptide sequence) to form multimers. As used herein, "linker" or "spacer" refers to a molecule or group of molecules that connects two or more molecules to each other. A flexible linker allows rotation of the two molecules linked to each other to the extent that the molecules do not block each others function. For example, a linker such as an amino acid sequence attached to a humanized antibody which is itself attached to a multimerization domain,

allows the antibody to bind to antigen without significant steric interference from the multimers of the oligomer. Non-peptide linkers include chemical cross linking agents and polyethylene glycol.

One specific example of a peptide linker is an immunoglobulin hinge sequence. Additional specific examples are polylyisne, ployglutamic acid and mixtures of randomized amino acid sequences. Linker amino acid sequences may be fully human, humanized or non-human amino acid sequences, unmodified or modified as set forth herein. The invention therefore further provides humanized antibodies that include a linker sequence. Linker sequences include, for example, sequences from about 2 to 10, 10 to 20, 10 to 30, 25 to 50, 30 to 60 and 50 to 75 amino acids in length.

Antibodies also include modified forms such as sequences having one or more amino acid substitutions, additions or deletions, provided the modification does not destroy function, e.g., does not destroy antigen binding activity; the antibody retains, at least in part, antigen binding activity. For example, a modified humanized antibody will retain, at least in part, affinity for the antigen to which unmodified antibody binds. The term "modification" therefore denotes an alteration of a molecule that does not destroy an activity of the modified molecule.

Modifications therefore include, for example, amino acid additions, insertions, deletions and substitutions. An example of an addition is where one or more amino acids are added to the N- or C-terminal end of a humanized antibody. An example of an insertion is where an amino acid is inserted into the sequence. An example of a deletion is where one or more amino acids are deleted from the N- or C-terminal end, or internally within the sequence.

The invention therefore also provides modified forms of the humanized antibodies, including one or more amino acid additions, insertions, deletions and substitutions. In one embodiment, a humanized antibody has one or more amino acid substitutions of a sequence set forth in SEQ ID NO:1 and 3 (HumA); SEQ ID NO:4 and 5 (HumB); SEQ ID NO:6 and 7 (HumC); SEQ ID NO:8 and 9 (HumD); SEQ ID NO:10 and 11 (HumE); SEQ ID NO:12 and 13 (HumF); SEQ ID NO:14 and 15 (HumG); SEQ ID NO:16 and 17 (HumH); and SEQ ID NO:18 and 19 (HumI); and SEQ ID NO:5 and

20 (Hum40); and SEQ ID NO:5 and 21 (Hum50), provided that the substituted antibody is capable of antigen binding. In a particular aspect, one or more of the amino acid substitutions are conservative amino acid substitutions. In another aspect, the substitution comprises 1-3, 3-5 or 5-10 amino acids. In yet another aspect, the substitution is with a human amino acid. In still another aspect, the substitution is with a non-human amino acid which is structurally similar to the non-human residue, for example, where a non-human vernier zone amino acid of the framework acceptor (e.g., murine acceptor) is structurally dissimilar to the human counterpart vernier zone amino acid.

Exemplary amino acid substitutions include conservative amino acid substitutions. The term "conservative substitution" means the replacement of one amino acid by a biologically or chemically or structurally similar residue. Biologically similar means that the substitution is compatible with biological activity, e.g., for a humanized antibody, antigen binding. Structurally similar means that the amino acids have side chains with similar length, such as alanine, glycine and serine, or having similar size. Chemical similarity means that the residues have the same charge or are both hydrophilic or hydrophobic. Particular examples of conservative substitutions include the substitution of one hydrophobic residue, such as isoleucine, valine, leucine or methionine for another, or the substitution of one polar residue for another, such as the substitution of arginine for lysine, glutamic for aspartic acids, or glutamine for asparagine, serine for threonine, and the like.

Modifications also include derivatized sequences, for example, amino acids in which free amino groups form amine hydrochlorides, p-toluene sulfonyl groups, cabrobenzoxy groups; the free carboxy groups from salts, methyl and ethyl esters; free hydroxl groups that form O-acyl or O-alkyl derivatives, as well as naturally occurring amino acid derivatives, for example, 4-hydroxyproline, for proline, 5-hydroxylysine for lysine, homoserine for serine, ornithine for lysine, etc. Also included are modifications that confer covalent bonding, for example, a disulfide linkage between two cysteine residues thereby producing a cyclic polypeptide. Modifications can be produced using any of a variety of methods well known in the art (*e.g.*, PCR based sited-directed,

deletion and insertion mutagenesis, chemical modification and mutagenesis, cross-linking, etc.).

Modifications also include addition of functional entities such as tags (e.g., polyhistidine, T7, immunoglubulin, etc.), gold particles, covalently or non-covalently attached to the humanized antibodies or subsequences or multimers. Thus, the invention provides modified humanized antibodies having one or more activities (e.g., retain at least part of the antigen binding activity) of unmodified parent antibody. Modifications include radioactive or alternatively non-radioactive detectable labels attached to or incorporated into the molecule.

The term "identical" or "identity" means that two or more referenced entities are the same. Thus, where two nucleic acid sequences are identical, they have the same sequence. "Areas of identity" means that a portion of two or more referenced entities are the same. Thus, where two nucleic acid sequences are identical over one or more parts of their sequence, they share identity in these areas. The term "substantial identity" means that the identity is structurally or functionally significant. That is, the identity is such that the molecules are structurally identical or perform the same function (e.g., biological function) even though the molecules differ. Due to variation in the amount of sequence conservation between structurally and functionally related proteins, the amount of sequence identity for substantial identity will depend upon the type of region/domain and its function. For nucleic acid sequences, 50% sequence homology and above may constitute substantial homology. Substantial homology for proteins can be significantly less, for example, as little as 30% sequence homology, but typically is more, e.g., 50%, 60%, 75%, 85% or more.

The extent of identity between two sequences can be ascertained using various computer programs and mathematical algorithms known in the art. Such algorithms that calculate percent sequence identity (homology) generally account for sequence gaps and mismatches over the comparison region. For example, a BLAST (*e.g.*, BLAST 2.0) search algorithm (see, *e.g.*, Altschul *et al.* (1990) *J. Mol. Biol.* 215:403-10, publicly available through NCBI at http:/www.ncbi.nlm.nih.gov) has exemplary search parameters as follows: Mismatch -2; gap open 5; gap extension 2. For polypeptide sequence

comparisons, a BLASTP algorithm is typically used in combination with a scoring matrix, such as PAM100, PAM 250, BLOSUM 62 and the like.

As used herein, the term “isolated,” when used as a modifier of invention compositions (e.g., antibodies, subsequences, modified forms, multimers, nucleic acids encoding same, cells, vectors, etc.), means that the compositions are made by the hand of man and are separated from their naturally occurring *in vivo* environment. Generally, compositions so separated are substantially free of one or more materials with which they normally associate with in nature, for example, one or more protein, nucleic acid, lipid, carbohydrate, cell membrane. An “isolated” antibody can also be “substantially pure” when free of most or all of the materials with which they may normally associate with in nature. Thus, an isolated molecule that also is substantially pure does not include polypeptides or polynucleotides present among millions of other sequences, such as antibodies of an antibody library or nucleic acids in a genomic or cDNA library, for example. Purity can be at least about 60% or more by mass. The purity can also be about 70% or 80% or more, and can be greater, for example, 90% or more. Purity can be determined by any appropriate method, including, for example, UV spectroscopy, chromatography (*e.g.*, HPLC, gas phase), gel electrophoresis (*e.g.*, silver or coomassie staining) and sequence analysis (nucleic acid and peptide).

The invention additionally provides methods for producing humanized antibodies. In one embodiment, a method includes: selecting a human framework sequence as an acceptor, wherein said sequence has 50% or more identity (e.g., 50-55%, 55-60%, 60-65%, 65-70%, 70-75%, 75-80%, 80-85%, 85-90%, 90-95%, or more identity) to a non-human donor antibody framework region; grafting a CDR from the donor non-human antibody (e.g., murine) onto the human framework; comparing the vernier zone residues of the human acceptor and the non-human donor framework regions; and maintaining one or more of the human acceptor residues in the vernier zone when the donor non-human and human residues are structurally or chemically similar, or substituting one or more of the vernier zone residues with a residue that is different from both the donor non-human vernier zone residue and acceptor human vernier zone residue if the donor non-human vernier zone residue is structurally or chemically dissimilar to the human residue, wherein the different residue is structurally or chemically similar to the donor non-human

vernier zone residue. In other words, if the donor non-human vernier zone residue is structurally or chemically dissimilar to the acceptor human vernier zone residue, then this vernier zone residue is modified to a residue that is different from both the donor non-human vernier zone residue and the acceptor human vernier zone residue, yet structurally or chemically similar to the donor non-human vernier zone residue. In additional embodiments, human framework acceptor sequences are selected from consensus sequences, for example, from V_H domain subgroup I and subgroup II consensus sequenes.

The invention also provides nucleic acids encoding invention humanized antibodies, including high affinity humanized antibodies, subsequences, modified forms and multimers thereof. In various embodiments, a nucleic acid encodes a polypeptide set forth in SEQ ID NO:1 and 3 (HumA); SEQ ID NO:4 and 5 (HumB); SEQ ID NO:6 and 7 (HumC); SEQ ID NO:8 and 9 (HumD); SEQ ID NO:10 and 11 (HumE); SEQ ID NO:12 and 13 (HumF); SEQ ID NO:14 and 15 (HumG); SEQ ID NO:16 and 17 (HumH); and SEQ ID NO:18 and 19 (HumI); and SEQ ID NO:5 and 20 (Hum40); and SEQ ID NO:5 and 21 (Hum50).

As used herein, a "nucleic acid" refers to at least two or more ribo- or deoxy-ribonucleic acid base pairs that are linked through a phosphoester bond or equivalent. Nucleic acids include polynucleotides and polynculeosides. Nucleic acids include single, double or triplex, circular or linear, molecules. A nucleic acid molecule may belong exclusively or in a mixture to any group of nucleotide-containing molecules, as exemplified by, but not limited to, the following groups of nucleic acid molecules: RNA, DNA, cDNA, genomic nucleic acids, non-genomic nucleic acids, naturally occurring and non naturally occurring nucleic acids and synthetic nucleic acids. This includes, by way of example, nucleic acids associated with any organelle, such as the mitochondria, ribosomal RNA, and nucleic acid molecules comprised chimerically of one or more components that are not naturally occurring along with naturally occurring components.

Additionally, a "nucleic acid molecule" may contain in part one or more non-nucleotide-based components as exemplified by, but not limited to, amino acids and

sugars. Thus, by way of example, but not limitation, a ribozyme that is in part nucleotide-based and in part protein-based is considered a "nucleic acid molecule."

Nucleic acids can be of any length. Nucleic acid lengths typically range from about 20 to 10 Kb, 10 to 5Kb, 1 to 5 Kb or less, 1000 to about 500 base pairs or less in 5 length. Nucleic acids can also be shorter, for example, 100 to about 500 base pairs, or from about 12 to 25, 25 to 50, 50 to 100, 100 to 250, or about 250 to 500 base pairs in length.

As a result of the degeneracy of the genetic code, nucleic acids include sequences and subsequences degenerate with respect to nucleic acids that encode SEQ ID NO:1 and 10 3 (HumA); SEQ ID NO:4 and 5 (HumB); SEQ ID NO:6 and 7 (HumC); SEQ ID NO:8 and 9 (HumD); SEQ ID NO:10 and 11 (HumE); SEQ ID NO:12 and 13 (HumF); SEQ ID NO:14 and 15 (HumG); SEQ ID NO:16 and 17 (HumH); and SEQ ID NO:18 and 19 (HumI); and SEQ ID NO:5 and 20 (Hum40); and SEQ ID NO:5 and 21 (Hum50), and subsequences thereof. Nucleic acids also include sequences complementary to a 15 sequence that encodes SEQ ID NO:1 and 3 (HumA); SEQ ID NO:4 and 5 (HumB); SEQ ID NO:6 and 7 (HumC); SEQ ID NO:8 and 9 (HumD); SEQ ID NO:10 and 11 (HumE); SEQ ID NO:12 and 13 (HumF); SEQ ID NO:14 and 15 (HumG); SEQ ID NO:16 and 17 (HumH); and SEQ ID NO:18 and 19 (HumI); and SEQ ID NO:5 and 20 (Hum40); and SEQ ID NO:5 and 21 (Hum50), and subsequences thereof. Nucleic acid subsequences 20 have from about 15 to 25, 25 to 50 or 50 to 100 nucleotides. Such nucleic acids are useful for hybridization to detect the presence or an amount of humanized antibody in a sample (*in vitro*, cell, culture medium, tissue or organ, serum, in a subject, etc.).

The invention further includes nucleic acids that hybridize at high stringency to nucleic acids that encode SEQ ID NO:1 and 3 (HumA); SEQ ID NO:4 and 5 (HumB); 25 SEQ ID NO:6 and 7 (HumC); SEQ ID NO:8 and 9 (HumD); SEQ ID NO:10 and 11 (HumE); SEQ ID NO:12 and 13 (HumF); SEQ ID NO:14 and 15 (HumG); SEQ ID NO:16 and 17 (HumH); and SEQ ID NO:18 and 19 (HumI); and SEQ ID NO:5 and 20 (Hum40); and SEQ ID NO:5 and 21 (Hum50), subsequences thereof and nucleic acid sequences complementary thereto. Hybridizing nucleic acids are also useful for detecting 30 the presence or an amount of humanized antibody in a sample.

The term "hybridize" refers to the binding between complementary nucleic acids. Sequences will generally have more than about 50% homology to a nucleic acid that encodes SEQ ID NO:1 and 3 (HumA); SEQ ID NO:4 and 5 (HumB); SEQ ID NO:6 and 7 (HumC); SEQ ID NO:8 and 9 (HumD); SEQ ID NO:10 and 11 (HumE); SEQ ID
5 NO:12 and 13 (HumF); SEQ ID NO:14 and 15 (HumG); SEQ ID NO:16 and 17 (HumH); and SEQ ID NO:18 and 19 (HumI); and SEQ ID NO:5 and 20 (Hum40); and SEQ ID NO:5 and 21 (Hum50). The region between related sequences can extend over at least about 30 base pairs, or about 50 base pairs, or about 100 to 200 or more residues.

As is understood by those skilled in the art, the T_M (melting temperature) refers to
10 the temperature at which binding between complementary sequences is no longer stable. For two sequences to bind, the temperature of a hybridization reaction must be less than the calculated T_M for the sequences. The T_M is influenced by the amount of sequence complementarity, length, composition (%GC), type of nucleic acid (RNA vs. DNA), and the amount of salt, detergent and other components in the reaction (*e.g.*, formamide). All
15 of these factors are considered in establishing appropriate hybridization conditions (see, *e.g.*, the hybridization techniques and formula for calculating T_M described in Sambrook *et al.*, 1989, *supra*).

Typically, wash conditions are adjusted so as to attain the desired degree of hybridization stringency. Thus, hybridization stringency can be determined empirically,
20 for example, by washing under particular conditions, *e.g.*, at low stringency conditions or high stringency conditions. Optimal conditions for selective hybridization will vary depending on the particular hybridization reaction involved. An example of high stringency hybridization conditions are as follows: 2X SSC/0.1% SDS at about 37°C or 42°C (hybridization conditions); 0.5X SSC/0.1% SDS at about room temperature (low
25 stringency wash); 0.5X SSC/0.1% SDS at about 42°C (moderate stringency wash); and 0.1 X SSC/0.1% SDS at about 65°C (high stringency wash).

Nucleic acids of the invention can be produced using various standard cloning and chemical synthesis techniques. Such techniques include, but are not limited to: 1) nucleic acid amplification, *e.g.*, polymerase chain reaction (PCR), with genomic DNA or
30 cDNA targets using primers (*e.g.*, a degenerate primer mixture) capable of annealing to

antibody sequence; 2) chemical synthesis of nucleic acid sequences which can then be cloned into a plasmid, propagated amplified and purified and; 3) computer searches of databases for related sequences. Purity of nucleic acids can be determined through sequencing, gel electrophoresis and the like.

5 The invention further provides expression cassettes comprising a nucleic acid encoding a humanized antibody operably linked to an expression control element. As used herein, the term "operably linked" refers to a physical or a functional relationship between the elements referred to that permit them to operate in their intended fashion. Thus, an expression control element "operably linked" to a nucleic acid means that the 10 control element modulates transcription and as appropriate, translation of the transcript.

There need not be physical linkage to nucleic acid in order to control expression. Thus, physical linkage is not required for the elements to be operably linked. For example, a minimal element can be linked to a nucleic acid encoding a humanized antibody. A second element that controls expression of an operably linked nucleic acid 15 encoding a protein that functions "in trans" to bind to the minimal element can influence expression of the humanized antibody. Because the second element regulates expression of humanized antibody, the second element is operably linked to the nucleic acid encoding the humanized antibody.

The term "expression control element" refers to nucleic acid that influences 20 expression of an operably linked nucleic acid. Promoters and enhancers are particular non-limiting examples of expression control elements. A "promotor sequence" is a DNA regulatory region capable of initiating transcription of a downstream (3' direction) coding sequence. The promoter sequence includes a minimum number of bases necessary to initiate transcription. Enhancers also regulate gene expression but can function a distance 25 from the transcription start site of the gene to which it is operably linked. Enhancers also function at either 5' or 3' ends of the gene, as well as within the gene (e.g., in introns or coding sequences).

An expression control element can confer expression in a manner that is "constitutive," such that transcription of the operably linked nucleic acid occurs without 30 the presence of a signal or stimuli. Expression control elements can confer expression in

a manner that is "regulatable," that is, a signal or stimuli increases or decreases expression of the operably linked nucleic acid. A regulatable element that increases expression of the operably linked nucleic acid in response to a signal or stimuli is also referred to as an "inducible element" A regulatable element that decreases expression of 5 the operably linked nucleic acid in response to a signal or stimuli is referred to as a "repressible element" (*i.e.*, the signal decreases expression such that when the signal, is removed or absent, expression is increased).

Expression control elements include elements active in a particular tissue or cell type, referred to herein as a "tissue-specific expression control elements." Tissue-10 specific expression control elements are typically active in specific cell or tissue because they are recognized by transcriptional activator proteins, or other regulators of transcription, that are unique to a specific cell or tissue type.

Expression control elements additionally include elements that confer expression at a particular stage of the cell cycle or differentiation. Accordingly, the invention further 15 includes expression control elements that confer constitutive, regulatable, tissue-specific, cell cycle specific, and differentiation stage specific expression.

Expression control elements include full-length nucleic acid sequences, such as native promoter and enhancer elements, as well as subsequences or nucleotide variants thereof (e.g., substituted/mutated or other forms that differ from native sequences) which 20 retain all or part of full-length or non-variant control element function (confer regulation, *e.g.*, retain some amount of inducibility in response to a signal or stimuli).

For bacterial systems, constitutive promoters such as T7 and the like, as well as inducible promoters such as pL of bacteriophage λ, plac, ptrp, ptac (ptrp-lac hybrid promoter) may be used. In insect cell systems, constitutive or inducible promoters (*e.g.*, 25 ecdysone) may be used. In yeast, constitutive or inducible promoters may be used (see, *e.g.*, Ausubel *et al.*, In: Current Protocols in Molecular Biology, Vol. 2, Ch. 13, ed., Greene Publish. Assoc. & Wiley Interscience, 1988; Grant *et al.,* (1987) In: Methods in Enzymology, 153:516-544, eds. Wu & Grossman, 31987, Acad. Press, N.Y.; Glover, DNA Cloning, Vol. II, Ch. 3, IRL Press, Wash., D.C., 1986; Bitter (1987) In: Methods in 30 Enzymology, 152:673-684, eds. Berger & Kimmel, Acad. Press, N.Y.; and, Strathern *et*

al., The Molecular Biology of the Yeast Saccharomyces (1982) eds. Cold Spring Harbor Press, Vols. I and II). A constitutive yeast promoter such as ADH or LEU2 or an inducible promoter such as GAL may be used (R. Rothstein In: DNA Cloning, A Practical Approach, Vol.11, Ch. 3, ed. D.M. Glover, IRL Press, Wash., D.C., 1986).

5 For mammalian cells, constitutive promoters of viral or other origins may be used. For example, SV40, or viral long terminal repeats (LTRs) and the like, or inducible promoters derived from the genome of mammalian cells (*e.g.*, metallothionein IIA promoter; heat shock promoter, steroid/thyroid hormone/retinoic acid response elements) or from mammalian viruses (*e.g.*, the adenovirus late promoter; the inducible mouse
10 mammary tumor virus LTR) can be used for expression.

The invention also provides transformed cells and progeny thereof into which a nucleic acid molecule encoding humanized antibody has been introduced by means of recombinant DNA techniques in vitro, *ex vivo* or *in vivo*. The transformed cells can be propagated and the introduced nucleic acid transcribed, or encoded protein expressed. It
15 is understood that a progeny cell may not be identical to the parental cell, since there may be mutations that occur during replication. Transformed cells include but are not limited to prokaryotic and eukaryotic cells such as bacteria, fungi, plant, insect, and animal (e.g., mammalian, including human) cells. The cells may be present in culture, in a cell, tissue or organ *ex vivo* or present in a subject.

20 The term "transformed" means a genetic change in a cell following incorporation of nucleic acid (*e.g.*, a transgene) exogenous to the cell. Thus, a "transformed cell" is a cell into which, or a progeny of which a nucleic acid molecule has been introduced by means of recombinant DNA techniques. Cell transformation to produce host cells may be carried out as described herein or using techniques known in the art. Accordingly,
25 methods of producing cells containing the nucleic acids and cells expressing the humanized antibodies of the invention are also provided.

Typically cell transformation employs a vector. The term "vector," refers to, *e.g.*, a plasmid, virus, such as a viral vector, or other vehicle known in the art that can be manipulated by insertion or incorporation of a nucleic acid, for genetic manipulation (*i.e.*,
30 "cloning vectors"), or can be used to transcribe or translate the inserted polynucleotide

(*i.e.*, "expression vectors"). Such vectors are useful for introducing nucleic acids, including a nucleic acid that encodes a humanized antibody operably linked with an expression control element, and expressing the encoded protein *in vitro* (e.g., in solution or in solid phase), in cells or *in vivo*.

5 A vector generally contains at least an origin of replication for propagation in a cell. Control elements, including expression control elements as set forth herein, present within a vector, are included to facilitate transcription and translation. The term "expression control element" is intended to include, at a minimum, one or more components whose presence can influence expression, and can include components other 10 than or in addition to promoters or enhancers, for example, leader sequences and fusion partner sequences, internal ribosome binding sites (IRES) elements for the creation of multigene, or polycistronic, messages, splicing signal for introns, maintenance of the correct reading frame of the gene to permit in-frame translation of mRNA, polyadenylation signal to provide proper polyadenylation of the transcript of a gene of 15 interest, stop codons, etc.

Vectors can include a selection marker. As is known in the art, "selection marker" means a gene that allows for the selection of cells containing the gene. "Positive selection" refers to a process whereby only cells that contain the selection marker will survive upon exposure to the positive selection. Drug resistance is one example of a 20 positive selection marker; cells containing the marker will survive in culture medium containing the selection drug, and cells which do not contain the marker will die. Such markers include drug resistance genes such as *neo*, which confers resistance to G418, *hygr*, which confers resistance to hygromycin, or *puro* which confers resistance to puromycin, among others. Other positive selection marker genes include genes that 25 allow identification or screening of cells containing the marker. These genes include genes for fluorescent proteins (GFP), the lacZ gene, the alkaline phosphatase gene, and surface markers such as CD8, among others.

Vectors can contain negative selection markers. "Negative selection" refers to a process whereby cells containing a negative selection marker are killed upon exposure to 30 an appropriate negative selection agent. For example, cells which contain the herpes

simplex virus-thymidine kinase (*HSV-tk*) gene (Wigler *et al., Cell* 11:223 (1977)) are sensitive to the drug gancyclovir (GANC). Similarly, the *gpt* gene renders cells sensitive to 6-thioxanthine.

Additional selection systems may be used, including, but not limited to the
5 hypoxanthine-guanine phosphoribosyltransferase gene (Szybalska *et al., Proc. Natl. Acad. Sci. USA* 48:2026 (1962)), and the adenine phosphoribosyltransferase (Lowy *et al., Cell* 22:817 (1980)) genes. Additional selectable genes have been described, namely trpB, which allows cells to utilize indole in place of tryptophan; hisD, which allows cells to utilize histinol in place of histidine (Hartman *et al., Proc. Natl. Acad. Sci. USA*
10 **85**:8047 (1988)); and ODC (ornithine decarboxylase), which confers resistance to the ornithine decarboxylase inhibitor, 2-(difluoromethyl)-DL-ornithine, DFMO (McConlogue (1987) In: Current Communications in Molecular Biology, Cold Spring Harbor Laboratory, ed.).

Vectors included are those based on viral vectors, such as retroviral, adeno-
15 associated virus, adenovirus, reovirus, lentivirus, rotavirus genomes, simian virus 40 (SV40) or bovine papilloma virus, etc., modified for introducing and expressing a nucleic acid in a cell (Cone *et al., Proc. Natl. Acad. Sci.* USA 81:6349 (1984)). (Eukaryotic Viral Vectors, Cold Spring Harbor Laboratory, Gluzman ed., 1982; Sarver *et al., Mol. Cell. Biol.* 1:486 (1981)). Additional viral vectors useful for expression include parvovirus,
20 rotavirus, Norwalk virus, coronaviruses, paramyxo and rhabdoviruses, togavirus (e.g., sindbis virus and semliki forest virus) and vesicular stomatitis virus.

Mammalian expression systems further include vectors specifically designed for *in vivo* and *ex vivo* expression. Such systems include adeno-associated virus (AAV) vectors (U.S. Patent No. 5,604,090). AAV vectors have previously been shown to
25 provide expression of Factor IX in humans and in mice at levels sufficient for therapeutic benefit (Kay *et al., Nat. Genet.* 24:257 (2000); Nakai *et al., Blood* 91:4600 (1998)). Adenoviral vectors (U.S. Patent Nos. 5,700,470, 5,731,172 and 5,928,944), herpes simplex virus vectors (U.S. Patent No. 5,501,979) and retroviral (e.g., lentivirus vectors are useful for infecting dividing as well as non-dividing cells and foamy virues) vectors
30 (U.S. Patent Nos. 5,624,820, 5,693,508, 5,665,577, 6,013,516 and 5,674,703 and WIPO

publications WO92/05266 and WO92/14829) and papilloma virus vectors (e.g., human and bovine papilloma virus) have all been employed in gene therapy (U.S. Patent No. 5,719,054). Vectors also include cytomegalovirus (CMV) based vectors (U.S. Patent No. 5,561,063). Vectors that efficiently deliver genes to cells of the intestinal tract have been developed and also may be used (see, *e.g.*, U.S. Patent Nos. 5,821,235, 5,786,340 and 6,110,456).

In yeast, vectors that facilitate integration of foreign nucleic acid sequences into a chromosome, via homologous recombination, for example, are known in the art and can be used. Yeast artificial chromosomes (YAC) are typically used when the inserted nucleic acids are too large for more conventional vectors (*e.g.*, greater than about 12 kb).

Introduction of nucleic acid encoding humanized antibody and humanized antibody into target cells can also be carried out by conventional methods known in the art such as osmotic shock (*e.g.*, calcium phosphate), electroporation, microinjection, cell fusion, etc. Introduction of nucleic acid and polypeptide *in vitro*, *ex vivo* and *in vivo* can also be accomplished using other techniques. For example, a polymeric substance, such as polyesters, polyamine acids, hydrogel, polyvinyl pyrrolidone, ethylene-vinylacetate, methylcellulose, carboxymethylcellulose, protamine sulfate, or lactide/glycolide copolymers, polylactide/glycolide copolymers, or ethylenevinylacetate copolymers. A nucleic acid can be entrapped in microcapsules prepared by coacervation techniques or by interfacial polymerization, for example, by the use of hydroxymethylcellulose or gelatin-microcapsules, or poly (methylmethacrolate) microcapsules, respectively, or in a colloid drug delivery system. Colloidal dispersion systems include macromolecule complexes, nano-capsules, microspheres, beads, and lipid-based systems, including oil-in-water emulsions, micelles, mixed micelles, and liposomes.

The use of liposomes for introducing various compositions into cells, including nucleic acids, is known to those skilled in the art (see, *e.g.*, U.S. Patent Nos. 4,844,904, 5,000,959, 4,863,740, and 4,975,282). A carrier comprising a natural polymer, or a derivative or a hydrolysate of a natural polymer, described in WO 94/20078 and U.S. Patent No. 6,096,291, is suitable for mucosal delivery of molecules, such as polypeptides and polynucleotides. Piperazine based amphilic cationic lipids useful for gene therapy

also are known (see, *e.g.*, U.S. Patent No. 5,861,397). Cationic lipid systems also are known (see, *e.g.*, U.S. Patent No. 5,459,127). Accordingly, viral and non-viral vector means of delivery into cells or tissue, *in vitro, in vivo* and *ex vivo* are included.

The invention further provides kits comprising one or more compositions of the invention, including pharmaceutical formulations, packaged into suitable packaging material. In one embodiment, a kit includes a humanized antibody or subsequence. In another embodiment, a kit includes a nucleic acid encoding humanized antibody or subsequence. In additional embodiments, a kit includes nucleic acids that further include an expression control element; an expression vector; a viral expression vector; an adeno-associated virus expression vector; an adenoviral expression vector; and a retroviral expression vector. In yet an additional embodiment, a kit includes a cell that expresses a humanized antibody or subsequence.

In additional embodiments, a kit includes a label or packaging insert including instructions for expressing a humanized antibody or a nucleic acid encoding a humanized antibody in cells in vitro, *in vivo*, or *ex vivo*. In yet additional embodiments, a kit includes a label or packaging insert including instructions for treating a subject (e.g., a subject having or at risk of having asthma) with a humanized antibody or a nucleic acid encoding a humanized antibody *in vivo*, or *ex vivo*.

As used herein, the term "packaging material" refers to a physical structure housing the components of the kit. The packaging material can maintain the components sterilely, and can be made of material commonly used for such purposes (*e.g.*, paper, corrugated fiber, glass, plastic, foil, ampules, etc.). The label or packaging insert can include appropriate written instructions, for example, practicing a method of the invention, e.g., treating the common cold. Kits of the invention therefore can additionally include instructions for using the kit components in a method of the invention.

Instructions can include instructions for practicing any of the methods of the invention described herein. Thus, invention pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration to a subject. Instructions may additionally include indications of a satisfactory clinical

endpoint or any adverse symptoms that may occur, or additional information required by the Food and Drug Administration for use on a human subject.

The instructions may be on "printed matter," e.g., on paper or cardboard within the kit, on a label affixed to the kit or packaging material, or attached to a vial or tube 5 containing a component of the kit. Instructions may comprise voice or video tape and additionally be included on a computer readable medium, such as a disk (floppy diskette or hard disk), optical CD such as CD- or DVD-ROM/RAM, magnetic tape, electrical storage media such as RAM and ROM and hybrids of these such as magnetic/optical storage media.

10 Invention kits can additionally include a buffering agent, a preservative, or a protein/nucleic acid stabilizing agent. The kit can also include control components for assaying for activity, *e.g.,* a control sample or a standard. Each component of the kit can be enclosed within an individual container or in a mixture and all of the various containers can be within single or multiple packages. For example, an invention 15 composition can be packaged into a hand pump container or pressurized (e.g., aerosol) container for spraying the composition into the throat or nasal or sinus passages of a subject.

The humanized antibodies of the invention, including subsequences, modified forms, multimers and nucleic acids encoding them, can be incorporated into 20 pharmaceutical compositions. Such pharmaceutical compositions are useful for administration to a subject *in vivo* or *ex vivo*, and for providing therapy for a physiological disorder or condition treatable with a humanized antibody.

Pharmaceutical compositions include "pharmaceutically acceptable" and "physiologically acceptable" carriers, diluents or excipients. As used herein the terms 25 "pharmaceutically acceptable" and "physiologically acceptable" include solvents (aqueous or non-aqueous), solutions, emulsions, dispersion media, coatings, isotonic and absorption promoting or delaying agents, compatible with pharmaceutical administration. Such formulations can be contained in a liquid; emulsion, suspension, syrup or elixir, or solid form; tablet (coated or uncoated), capsule (hard or soft), powder, granule, crystal, or

microbead. Supplementary active compounds (e.g., preservatives, antibacterial, antiviral and antifungal agents) can also be incorporated into the compositions.

Pharmaceutical compositions can be formulated to be compatible with a particular local or systemic route of administration. Thus, pharmaceutical compositions include
5 carriers, diluents, or excipients suitable for administration by particular routes.

Specific non-limiting examples of routes of administration for compositions of the invention are inhalation or intranasal delivery. Additional routes include parenteral, e.g., intravenous, intradermal, subcutaneous, oral, transdermal (topical), transmucosal, and rectal administration.

10 Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic
15 acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide.

Pharmaceutical compositions for injection include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous
20 preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, NJ) or phosphate buffered saline (PBS). The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyetheylene glycol, and the like), and suitable
25 mixtures thereof. Fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Antibacterial and antifungal agents include, for example, parabens, chlorobutanol, phenol, ascorbic acid and thimerosal. Isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride can be included

in the composition. Including an agent which delays absorption, for example, aluminum monostearate and gelatin can prolong absorption of injectable compositions.

Sterile injectable solutions can be prepared by incorporating the active compound in the required amount in an appropriate solvent with one or a combination of above 5 ingredients followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle containing a basic dispersion medium and other ingredients as above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation include, for example, vacuum drying and freeze-drying which yields a powder of the active ingredient plus any 10 additional desired ingredient from a previously sterile-filtered solution thereof.

For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished 15 through the use of nasal sprays, inhalation devices (e.g., aspirators) or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

Invention humanized antibodies, including subsequences and modified forms and nucleic acids encoding them, can be prepared with carriers that protect against rapid 20 elimination from the body, such as a controlled release formulation or a time delay material such as glyceryl monostearate or glyceryl stearate. The compositions can also be delivered using implants and microencapsulated delivery systems to achieve local or systemic sustained delivery or controlled release.

Biodegradable, biocompatable polymers can be used, such as ethylene vinyl 25 acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to cells or tissues using antibodies or viral coat proteins) can also be used as pharmaceutically

acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811.

Additional pharmaceutical formulations appropriate for the compositions for administration in the methods of the invention are known in the art (see, *e.g.*,
5 Remington's Pharmaceutical Sciences (1990) 18th ed., Mack Publishing Co., Easton, PA; The Merck Index (1996) 12th ed., Merck Publishing Group, Whitehouse, NJ; and Pharmaceutical Principles of Solid Dosage Forms, Technonic Publishing Co., Inc., Lancaster, Pa., (1993)).

The pharmaceutical formulations can be packaged in dosage unit form for ease of
10 administration and uniformity of dosage. "Dosage unit form" as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the pharmaceutical carrier or excipient.

Humanized antibodies of the invention include antibodies that protect against
15 virus infection of cells. For example, HumA, HumB, HumC, HumD, HumF, HumH and HumI protect against HRV infection of cells (FIG. 4). Thus, in another embodiment, the invention provides antibodies that protect against human rhinovirus (HRV) infection of cells. In one embodiment, an antibody has a protective efficacy equal to or at least 2 to 5 times greater than the non-humanized antibody. In another embodiment, an antibody has
20 a protective efficacy at least 5 to 10 times greater than the non-humanized antibody. In yet another embodiment, an antibody has a protective efficacy at least 10 to 20 times greater than the non-humanized antibody. In still another embodiment, an antibody has a protective efficacy at least 20 to 30 times greater than the non-humanized antibody.

As used herein, "human rhinovirus" or "HRV" means major and minor group
25 human serotypes of rhinoviruses that have been identified (see, e.g., Hamparian *et al.*, (1987) *Virology* 159:191) and those that are identified later as falling within this class of virus. Major group HRV binds to ICAM-1 and minor group HRV binds low density lipoprotein (LDL) receptor.

As used herein, the term "protective efficacy" is the amount of an antibody which
30 can protect 50% of susceptible cells from infection (i.e. EC_{50}) under experimental

conditions (see, e.g., Example 5). For example, for HRV, protective efficacy in EC_{50} is the amount of antibody that protects 50% of hela cells from HRV infection. Thus, a humanized antibody having a protective efficacy 5 times greater than another antibody (e.g., non-humanized) can be used in an amount 5 fold less than non-humanized antibody
5 while still providing the same degree of protection from infection.

Humanized antibodies of the invention include antibodies that bind to ICAM-1. Although not wishing to be bound by theory, it is believed that antibody binding to ICAM-1 inhibits viral binding or the ability to infect or penetrate the cell thereby inhibiting viral infection or proliferation. Such antibodies are therefore useful for
10 inhibiting pathogens such as viruses (e.g., HRV and coxackie A virus, respiratory syncytial virus (RSV)), bacteria, fungi and protozoa (e.g., malaria) that bind to ICAM-1. Thus, the antibodies are useful for inhibiting HRV infection as well as for inhibiting any microorganism or other pathogens in which ICAM-1 receptor participates. Accordingly, the invention provides antibodies that inhibit pathogen infection of cells where infection
15 is mediated, at least in part, by binding to ICAM-1, and methods for inhibiting pathogen infection of cells where infection is mediated, at least in part, by binding to ICAM-1.

In one embodiment, a method includes contacting a virus or cell with an amount of humanized antibody that binds to ICAM-1 sufficient to inhibit viral infection of the cell. In one aspect, the cell is an epithelial cell. In another embodiment, a method
20 includes administering to a subject an amount of humanized antibody that binds to ICAM-1 sufficient to inhibit viral infection of the subject. In various aspects, the virus is HRV, coxackie A virus and respiratory syncytial virus. In yet another embodiment, a method includes administering to a subject an amount of humanized antibody that binds to ICAM-1 sufficient to inhibit infection of the subject by a pathogen.

25 The invention also provides methods for inhibiting infection, inhibiting progression or treating a pathogenic infection of a subject. In one embodiment, a method includes administering to a subject having or at risk of having an HRV infection an amount of humanized antibody sufficient to inhibit, inhibit progression or to treat HRV infection of the subject. In another embodiment, a method includes administering to a
30 subject having or at risk of having an coxackie A virus or respiratory syncytial virus

infection an amount of humanized antibody sufficient to inhibit infection, inhibit progression or to treat coxackie A virus or respiratory syncytial virus infection of the subject. In still another embodiment, a method includes administering to a subject having or at risk of having malaria an amount of humanized antibody sufficient to inhibit, inhibit 5 progression or to treat malaria of the subject. In various aspects, a humanized antibody has a V_H and V_L domain selected from: SEQ ID NO:1 and 3 (HumA); SEQ ID NO:4 and 5 (HumB); SEQ ID NO:6 and 7 (HumC); SEQ ID NO:8 and 9 (HumD); SEQ ID NO:10 and 11 (HumE); SEQ ID NO:12 and 13 (HumF); SEQ ID NO:14 and 15 (HumG); SEQ ID NO:16 and 17 (HumH); and SEQ ID NO:18 and 19 (HumI); and SEQ ID NO:5 and 10 20 (Hum40); and SEQ ID NO:5 and 21 (Hum50), and antigen binding subsequences thereof.

The invention further provides methods of decreasing or inhibiting one or more symptoms of a pathogen infection (e.g., caused by HRV, coxackie A virus, respiratory syncytial virus or malaria). In one embodiment, a method includes administering to a 15 subject having one or more symptoms associated with HRV, coxackie A virus, respiratory syncytial virus or malaria an amount of a humanized antibody sufficient to decrease or inhibit or prevent one or more symptoms associated with HRV, coxackie A virus, respiratory syncytial virus or malaria in the subject. Symptoms decreased or inhibited or prevented include, for example, for HRV, one or more of fever, congestion, 20 cough, nasal drip, sore throat, and the like associated with the common cold. In another embodiment, a method includes administering to a subject having otitis media an amount of a humanized antibody sufficient to decrease or inhibit or prevent one or more symptoms of otitis media in the subject. In yet another embodiment, a method includes administering to a subject having bronchitis an amount of a humanized antibody 25 sufficient to decrease or inhibit or prevent one or more symptoms of bronchitis in the subject. In still another embodiment, a method includes administering to a subject having sinusitis an amount of a humanized antibody sufficient to decrease or inhibit or prevent one or more symptoms of sinusitis in the subject. In a further embodiment, a method includes administering to a subject having or at risk of having asthma an amount of a 30 humanized antibody sufficient to decrease or inhibit or prevent asthma exacerbation. In

one aspect, the humanized antibody is administered locally. In another aspect, the humanized antibody is administered via inhalation or intranasaly.

In addition to inhibiting pathogens that function directly or indirectly through ICAM-1, invention humanized antibodies can be used to treat undesirable physiological conditions, such as disease or disorders in which ICAM-1 plays a role. For example, LFA-1 interaction with ICAM-1 participates in inflammation. Thus, an invention antibody may be used to inhibit this interaction thereby modulating (e.g., decrease) local or systemic inflammation. Furthermore, ICAM-1 plays a role in other immune response pathways, cancer and metastasis. Thus, an invention antibody may be used to reduce or prevent organ transplant rejection or autoimmune diseases or cancer or metastasis. Accordingly, the invention provides antibodies that modulate immune responsiveness (e.g., inflammation) and other cellular processes in which ICAM-1 participates and methods for modulating immune response pathways.

The methods of the invention may be practiced prior to infection (i.e. prophylaxis) or after infection, before or after acute or chronic symptoms of the infection or physiological condition or disorder develops (e.g., before organ transplantation). Administering a composition prior to or immediately following development of symptoms may lessen the severity of the symptoms in the subject. Administering a composition prior to development of symptoms in the subject may decrease contagiousness of the subject thereby decreasing the likelihood of other subjects becoming infected from the infected subject.

The term “subject” refers to animals, typically mammalian animals, such as a non-human primate (gorillas, chimpanzees, orangutans, macaques, gibbons), a domestic animal (dogs and cats), a farm animal (horses, cows, goats, sheep, pigs), experimental animal (mouse, rat, rabbit, guinea pig) and humans. Human subjects include adults, and children, for example, newborns and older children, for example, between the ages of 1 and 5, 5 and 10 and 10 and 18. Human subjects may include those having or at risk of having a viral infection, such as HRV, and which develops one or more symptoms of the infection, for example, those typically associated with the common cold. Human subjects include those having or at risk of having asthma, including asthmatics suffering from

chronic asthma prior to or following suffering an acute asthma attack. Subjects include disease model animals (e.g., such as mice and non-human primates) for testing *in vivo* efficacy of humanized antibodies of the invention (e.g., an HRV animal model, an asthma animal model, an organ transplant model, an autoimmune disorder model, cancer model, 5 etc.).

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable 10 methods and materials are described herein.

All publications, patents and other references cited herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control.

As used herein, the singular forms "a", "and," and "the" include plural referents 15 unless the context clearly indicates otherwise. Thus, for example, reference to "a transformed cell" includes a plurality of such cells and reference to "a humanized antibody" can include reference to one or more such cells or antibodies, and so forth.

A number of embodiments of the invention have been described. Nevertheless, it will be understood that various modifications may be made without departing from the 20 spirit and scope of the invention. Accordingly, the following examples are intended to illustrate but not limit the scope of invention described in the claims.

EXAMPLES

Example 1

25 This example describes the strategy for humanizing 1A6.

Mouse monoclonal antibody 1A6 (mAb1A6) was developed by Colonno et al., and has been shown to bind specifically to ICAM-1 and protect cells against infection by human rhinovirus (HRV) major group (Colonno RJ, et al. (1991) European Patent Application #91201243.2; Publication number: 0 459 577 A2, which also describes the 30 sequence of mouse mAb1A6). The parental mouse monoclonal antibody 1A6 was

synthesized in the form of scFv. The purified protein, Msc1A6, has an affinity of 1.18 x 10^{-6} M in K_D against ICAM-1 (Table 4).

To humanize mAb1A6, selected human VH subgroup III and VL-kappa subgroup I consensus sequences were selected as the acceptor VH and VL frameworks,
5 respectively (Padlan (1994) *Molecular Immunol.* 31:169-217; Padlan (1991) *Molecular Immunol.* 28:489-498). These human sequences have previously been used to humanize two antibodies (Carter *et al.* (1992) *Proc. Natl. Acad. Sci. USA* 89:4285-4289; Presta *et al.* (1993) J. Immunol. 151:2623-2632).

Among a total of 82 amino acid residues in the heavy chain framework, the
10 human VH III consensus sequence and mAb1A6 antibody share 54 identical amino acid residues, which amounts to 66% identity. Among 81 light chain framework residues, the human κ I consensus sequence and mAb1A6 antibody have 52 amino acid residues in common, which equals to 64.2% identity. (FIG. 1).

Among a total of 57 framework amino acid residues that are different between
15 mAb1A6 and human consensus sequences, 49 of them are either located on the surface of the antibody molecule, or are residues with similar characteristics, therefore human consensus residues can be used to replace mouse residues. The remaining six positions, VH 37, 69, 71, 73, 94 and VL 49, belong to the "Vernier" zone as described by Toote and Winter (1992, *J. Mol. Biol.* 224:487-499). Because "Vernier" zone residues form a layer
20 underlying the CDRs and may impact on the structure of CDRs and the affinity of the antibody, residues at these positions were chosen based on molecular model building of the antibody.

VL 49:

Inspection reveals that this position is both at the center of the antibody
25 combining site and at the light chain/heavy chain interface. Substituting an ideal residue at this position can improve antigen binding by both providing additional direct binding contact and by improving the character of the interface. Tyrosine, found in human antibodies at this position, does both. Model building suggests that Y49 can form both Van der Waals and H bond contact with ICAM. Y49 also can interact with heavy chain
30 W102, completing a network of interacting aromatic residues that provide both binding

interaction and flexibility at the light chain/heavy chain interface. Therefore, human consensus residue tyrosine at this position is superior to the parental mouse residue lysine.

VH 37:

5 This residue is at the interface between the light and heavy chains. Comparing to the parental mouse residue methionine, the human consensus residue valine intrudes less on the interface, potentially providing additional flexibility. Flexibility at the interface can enhance binding affinity by increasing conformational adaptability of the antibody.

VH 69:

10 This residue is packed in the interior of the variable domain. The murine residue, methionine, makes a potentially destabilizing contact with the backbone of a neighboring beta strand. In contrast, the human residue isoleucine packs well in the interior of the protein.

VH 73:

15 Molecular modeling indicates that the human consensus residue, aspartic acid (D73) can interact with K30 of heavy chain CDR1. Since model building suggests that K30 is not involved directly in antigen binding, this stabilizing change is predicted to be either neutral or beneficial.

VH 71 and VH94:

20 Structural inspection indicated that both of these positions require a residue with a small side chain for maintenance of proper antibody conformation. Therefore, the human consensus residue at this position, arginine, is not appropriate. Serine and glycine were selected for position 71.

According to Chothia *et al.*, the residue at VH94 is involved in the canonical
25 structure of H1 or CDR1 (defined as VH26-VH32). The CDR1 of 1A6 belongs to the canonical structure 1 and family 1 (Chothia and Lesk (1987) *J. Mol. Biol.* 186:651-663; Chothia *et al.* (1992) *J. Mol. Biol.* 227:799-817; Chothia *et al.* (1989) *Nature* 342:877-883). Corresponding to this canonical structure, human sequences showed three possible residues at VH94 position: arginine, threonine or alanine (Chothia *et al.* (1992) *J. Mol.*

Biol. 227:799-817). Since arginine is not appropriate for this particular antibody, alanine, threonine and another small residue, aspartic acid were chosen.

Finally, molecular model building indicates that a portion of the CDR2 in the VH domain, VH60-64, does not have direct contact with the antigen. Therefore mouse
5 residues at these positions (DPKVQ) can be replaced by human residues ADSVK.

Example 2

This example describes the preparation of several humanized scFv expression constructs.

The humanized scFvA (HumA) cDNA (FIG. 3) containing 750 bp was
10 synthesized using a series of overlapping oligonucleotides. These overlapping oligonucleotides (Table 1) were designed to encode the amino acids of the variable region of the heavy (V_H) and light (V_L) chains linked by a linker(($G_4S)_4$) with a Bam H1 site. The heavy chain and light chain were cloned separately in TOPO 2.1 vector. After DNA sequencing conformation, the heavy and light chain were subcloned into expression
15 vector (pBAD/pIII A) to form full length DNA.

The oligonucleotides were first annealed in six groups consisting of oligo AVH1/AVH2, oligo AVH3/AVH4, oligo AVH5/AVH6 for heavy chain, and oligo AVL1/AVL2, oligo AVL3/AVL4, oligo AVL5/AVL6 for the light chain. Each annealed group was extended with the Klenow fragment of DNA polymerase. The annealed and
20 extended products of group 1-3 were pooled with oligo AVH7 as overlapping templates that were amplified via polymerase chain reaction (PCR) using the high-fidelity thermostable DNA polymerase (Roche) with oligo AVH8 and AVH9 as primers. The annealed and extended products of group 4-6 were pooled with oligo AVL7 as overlapping templates that were also amplified via polymerase chain reaction (PCR)
25 using oligo AVL8 and AVL9 as primers. The PCR products were directly inserted into the TA cloning vector pCR2.1-TOPO (Invitrogen) and transferred into TOP10 competent cells. The plasmids with inserts were isolated and sequenced.

The light chain and the heavy chain DNA fragments were isolated from their cloning vector by digestion with Nco I/Bam H I and Bam H I/Hpa I respectively, and
30 cloned into expression vector pBAD/pIII A cutting with Nco I / Sal I (blunted) to be in

frame with the carboxy-terminal His tag. Both strands of the expression construct pBAD-HumA was sequenced (MWG Biotech, Inc.).

All other human scFv expression constructs (HumB to H) were made with the same procedure as HumA described above except using different oligonucleotides (Table 1).

For HumB, using BVH6 and BVH7 to replace AVH6 and AVH7; for HumC, using CVH5, CVH6 and CVH7 to replace AVH5, AVH6 and AVH7; for HumD, using DVH6 and DVH7 to replace AVH6 and AVH7; for HumE, using EVH4, EVH5, EVH6 and EVH7 to replace AVH4, AVH5, AVH6 and AVH7; for HumF, using FVH6 and FVH7 to replace AVH6 and AVH7; for HumG, using GVL3, GVL4, GVH5, GVH6 and GVH7 to replace AVL3, AVL4, AVH5, AVH6 and AVH7; for HumH, using HVL3, HVL4, HVH4, HVH5, HVH6 and HVH7 to replace AVL3, AVL4, AVH4, AVH5, AVH6 and AVH7; for HumI, using IVL3, IVL4, IVH4, IVH5, IVH6 and IVH7 to replace AVL3, AVL4, AVH4, AVH5, AVH6 and AVH7.

Table 1. Oligonucleotides for humanized scFvs

Oligonucleotides for the light (V_L) chain of HumA:

AVL-1 (SEQ ID NO:26):
CGAACCATGGGCGATATCCAGATGACCCAATCTCCGTCTAGCCTGAGCGCCAGTGTTGGTG
AVL-2 (SEQ ID NO:27):
GTGAAGATTATTACTGATAGATTGGCTGGCGCGGCAAGTAATGGTAACTCGATCACCAACAC
TGGCGCTCAG
AVL-3 (SEQ ID NO:28):
CTATCAGTAATAATCTTCACTGGTATCAACAAAAACCGGGTAAAGCTCCGAAACTTCTTATCT
ATCACGCC
AVL-4 (SEQ ID NO:29):
CCCGAGCCAGAGCCAGAGAAGCGGCTCGGAACGCCGCTAATGCTCTGAGAGGCGTGATAG
ATAAGAAG
AVL-5 (SEQ ID NO:30):
CTCTGGCTCTGGCTCGGGCACGGACTTTACCCTTACCATCAGCTCTCTTCAGCCGGAAGAC
TTTGCCACC
AVL-6 (SEQ ID NO:31):
CCTTGACCGAAGGTATACGGCCAGCTATTAGACTGCTGACAATAATAGGTGGCAAAGTCTTC
CGGC
AVL-7 (SEQ ID NO:32):
GTATACCTTCGGTCAAGGTACCAAGGTCGAGATTAAGCGCGGCGGTGGCGGTTCTGGTGGC
GGTGGTAGCG
AVL-8 (SEQ ID NO:33): CGAACCATGGGCGATATCCAGATGACCCAATC
AVL-9 (SEQ ID NO:34): CGGATCCACCGCCACCGCTACCACCGCCACCAG

<u>Oligonucleotides for the heavy (V_H) chain of HumA:</u>

AVH-1 (SEQ ID NO:35):
GGTGGCGGT<u>GGATCC</u>GGTGGCGGTGGCAGCGAAGTTCAACTTGTTGAGTCTGGTGGCGGT
CTGGTTCAGCCGG

5 AVH-2 (SEQ ID NO:36):
GTCCTTAATGTTGAAACCGCTTGCTGCGCAAGACAGGCGCAGAGAGCCACCCGGCTGAACC
AGACCGCCAC

AVH-3 (SEQ ID NO:37):
GGTTTCAACATTAAGGACACCTACATCCATTGGGTGAGGCAAGCTCCGGGTAAGGGTCTGG

10 AGTGGG

AVH-4 (SEQ ID NO:38):
GGCCCTTCACGCTGTCAGCGTAAATGGTGTTGTCGTTTGCCGGGTCGATACGTGCCACCCA
CTCCAGACCCTTACC

AVH-5 (SEQ ID NO:39):

15 CGCTGACAGCGTGAAGGGCCGTTTTACTATTTCTAGCGACGACTCTAAGAACACCGCGTAC
CTTCAGATGAACTCTCTGCG

AVH-6 (SEQ ID NO:40):
CCAGTAGCCAGAGTCCGTGCAGTAGTAGACGGCGGTGTCCTCGGCACGCAGAGAGTTCAT
CTGAAGG

20 AVH-7 (SEQ ID NO:41):
GGACTCTGGCTACTGGTTTGCCTACTGGGGCCAGGGCACGCTTGTCACCGTCTCTTCTGGT
TAAC

AVH-8 (SEQ ID NO:42):GGTGGCGGTGGATCCGGT

AVH-9 (SEQ ID NO:43):GGGTTAACCAGAAGAGACGG

Oligonucleotides for making other human scFv (Hum B-I):

BVH-6 (SEQ ID NO:44):
CCAGTAGCCAGAGGCCGTGCAGTAGTAGACGGCGGTGTCCTCGGCACGCAGAGAGTTCAT
5 CTGAAGG
BVH-7 (SEQ ID NO:45):
GGCCTCTGGCTACTGGTTTGCCTACTGGGGCCAGGGCACGCTTGTCACCGTCTCTTCTGGT
TAAC
CVH-5 (SEQ ID NO:46):
10 CGCTGACAGCGTGAAGGGCCGTTTTACTATTTCTGGCGACGACTCTAAGAACACCGCGTAC
CTTCAGATGAACTCTCTGCG
CVH-6 (SEQ ID NO:47):
CCAGTAGCCAGAGGTCGTGCAGTAGTAGACGGCGGTGTCCTCGGCACGCAGAGAGTTCAT
CTGAAGG
15 CVH-7 (SEQ ID NO:48):
GACCTCTGGCTACTGGTTTGCCTACTGGGGCCAGGGCACGCTTGTCACCGTCTCTTCTGGT
TAAC
DVH-6 (SEQ ID NO:49):
CCAGTAGCCAGAGGTCGTGCAGTAGTAGACGGCGGTGTCCTCGGCACGCAGAGAGTTCAT
20 CTGAAGG
DVH-7 (SEQ ID NO:50):
GACCTCTGGCTACTGGTTTGCCTACTGGGGCCAGGGCACGCTTGTCACCGTCTCTTCTGGT
TAAC
EVH-4 (SEQ ID NO:51):
25 GGCCCTGCACCTTCGGATCGTAAATGGTGTTGTCGTTTGCCGGGTCGATACGTGCCACCCA
CTCCAGACCCTTACC
EVH-5 (SEQ ID NO:53):
CGATCCGAAGGTGCAGGGCCGTTTTACTATTTCTGCGGACGACTCTAAGAACACCGCGTAC
CTTCAGATGAACTCTCTGCG
30 EVH-6 (SEQ ID NO:54):
CCAGTAGCCAGAGGTCGTGCAGTAGTAGACGGCGGTGTCCTCGGCACGCAGAGAGTTCAT
CTGAAGG
EVH-7 (SEQ ID NO:55):
GACCTCTGGCTACTGGTTTGCCTACTGGGGCCAGGGCACGCTTGTCACCGTCTCTTCTGGT
35 TAAC
FVH-6 (SEQ ID NO:56):
CCAGTAGCCAGAGGTCGTGCAGTAGTAGACGGCGGTGTCCTCGGCACGCAGAGAGTTCAT
CTGAAGG
FVH-7 (SEQ ID NO:57):
40 GACCTCTGGCTACTGGTTTGCCTACTGGGGCCAGGGCACGCTTGTCACCGTCTCTTCTGGT
TAAC
GVL-3 (SEQ ID NO:58):
CTATCAGTAATAATCTTCACTGGTATCAACAAAAACCGGGTAAAGCTCCGAAACTTCTTATCA
AACACGCC
45 GVL-4 (SEQ ID NO:59):
CCCGAGCCAGAGCCAGAGAAGCGGCTCGGAACGCCGCTAATGCTCTGAGAGGCGTGAAAG
ATAAGAAG
GVH-5 (SEQ ID NO:60):
CGCTGACAGCGTGAAGGGCCGTTTTACTATTTCTGCGGACGACTCTAAGAACACCGCGTAC
50 CTTCAGATGAACTCTCTGCG
GVH-6 (SEQ ID NO:61):
CCAGTAGCCAGAGGTCGTGCAGTAGTAGACGGCGGTGTCCTCGGCACGCAGAGAGTTCAT
CTGAAGG

GVH-7 (SEQ ID NO:62):
GACCTCTGGCTACTGGTTTGCCTACTGGGGCCAGGGCACGCTTGTCACCGTCTCTTCTGGT
TAAC
HVL-3 (SEQ ID NO:63):
5 CTATCAGTAATAATCTTCACTGGTATCAACAAAAACCGGGTAAAGCTCCGAAACTTCTTATCA
AACACGCC
HVL-4 (SEQ ID NO:64):
CCCGAGCCAGAGCCAGAGAAGCGGCTCGGAACGCCGCTAATGCTCTGAGAGGCGTGAAAG
ATAAGAAG
10 HVH-4 (SEQ ID NO:65):
GGCCCTGCACCTTCGGATCGTAAATGGTGTTGTCGTTTGCCGGGTCGATACGTGCCACCCA
CTCCAGACCCTTACC
HVH-5 (SEQ ID NO:66):
CGATCCGAAGGTGCAGGGCCGTTTTACTATTTCTGCGGACGACTCTAAGAACACCGCGTAC
15 CTTCAGATGAACTCTCTGCG
HVH-6 (SEQ ID NO:67):
CCAGTAGCCAGAGGTCGTGCAGTAGTAGACGGCGGTGTCCTCGGCACGCAGAGAGTTCAT
CTGAAGG
HVH-7 (SEQ ID NO:68):
20 GACCTCTGGCTACTGGTTTGCCTACTGGGGCCAGGGCACGCTTGTCACCGTCTCTTCTGGT
TAAC
IVL-3 (SEQ ID NO:69):
CTATCAGTAATAATCTTCACTGGTATCAACAAAAACCGGGTAAAGCTCCGAAACTTCTTATCA
AACACGCC
25 IVL-4 (SEQ ID NO:70):
CCCGAGCCAGAGCCAGAGAAGCGGCTCGGAACGCCGCTAATGCTCTGAGAGGCGTGAAAG
ATAAGAAG
IVH-4 (SEQ ID NO:71):
GGCCCTGCACCTTCGGATCGTAAATGGTGTTGTCGTTTGCCGGGTCGATACGTGCCACCCA
30 CTCCAGACCCTTACC
IVH-5 (SEQ ID NO:72):
CGATCCGAAGGTGCAGGGCCGTTTTACTATGTCTGCGGACACCTCTAAGAACACCGCGTAC
CTTCAGATGAACTCTCTGCG
IVH-6 (SEQ ID NO:73):
35 CCAGTAGCCAGAGGTCGTGCAGTAGTAGACGGCGGTGTCCTCGGCACGCAGAGAGTTCAT
CTGAAGG
IVH-7 (SEQ ID NO:74):
GACCTCTGGCTACTGGTTTGCCTACTGGGGCCAGGGCACGCTTGTCACCGTCTCTTCTGGT
TAAC
40

Molecular model building enabled synthesis of 9 versions of humanized antibodies in the form of scFv (HumA-HumI, summarized in Tables 2 and 3). Four of the humanized antibodies, HumA-HumD, do not have parental mouse framework residues, and five of them, HumE-HumI, contain various number of parental mouse residues in the 45 framework. The sequence of HumB is compared against parental mouse 1A6 and human consensus framework in FIG. 2.

Table 2. Humanization Constructs

Position	L49	H37	H60-64	H69	H71	H73	H94
Human / Mouse	Y/K	V/M	ADSVK/DPKVQ (SEQ ID NO:75 and 76)	I/M	R/A	D/T	R/T
HumA	Y	V	ADSVK	I	S	D	D
HumB	Y	V	ADSVK	I	S	D	A
HumC	Y	V	ADSVK	I	G	D	T
HumD	Y	V	ADSVK	I	S	D	T
HumE	Y	V	DPKVQ	I	A	D	T
HumF	Y	V	ADSVK	I	A	D	T
HumG	K	V	ADSVK	I	A	D	T
HumH	K	V	DPKVQ	I	A	D	T
HumI	K	M	DPKVQ	M	A	T	T

Table 3. Amino Acid Sequences of Humanized Antibody

Hum A:

5 **VH Domain** (SEQ ID NO:1)

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser (Gly Phe Asn Ile Lys Asp Thr Tyr Ile His) Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala (Arg Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr Ala Asp Ser Val Lys Gly) Arg Phe Thr Ile Ser Ser Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

10 Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Asp (Ser Gly Tyr Trp Phe Ala Tyr) Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

VL Domain (SEQ ID NO:3)

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys (Arg Ala Ser Gln Ser Ile Ser Asn Asn Leu His) Trp Tyr Gln Gln Lys Pro

15 Gly Lys Ala Pro Lys Leu Leu Ile Tyr (His Ala Ser Gln Ser Ile Ser) Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

Glu Asp Phe Ala Thr Tyr Tyr Cys (Gln Gln Ser Asn Ser Trp Pro Tyr Thr) Phe Gly Gln

Gly Thr Lys Val Glu Ile Lys Arg

Hum B:
VH Domain (SEQ ID NO:4)
5 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu

Ser Cys Ala Ala Ser (Gly Phe Asn Ile Lys Asp Thr Tyr Ile His) Trp Val Arg Gln Ala

Pro Gly Lys Gly Leu Glu Trp Val Ala (Arg Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr Ala

Asp Ser Val Lys Gly) Arg Phe Thr Ile Ser Ser Asp Asp Ser Lys Asn Thr Ala Tyr Leu

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ala (Ser Gly Tyr
10 Trp Phe Ala Tyr) Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

VL Domain (SEQ ID NO:5)
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr

Ile Thr Cys (Arg Ala Ser Gln Ser Ile Ser Asn Asn Leu His) Trp Tyr Gln Gln Lys Pro
15
Gly Lys Ala Pro Lys Leu Leu Ile Tyr (His Ala Ser Gln Ser Ile Ser) Gly Val Pro Ser

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

20 Glu Asp Phe Ala Thr Tyr Tyr Cys (Gln Gln Ser Asn Ser Trp Pro Tyr Thr) Phe Gly Gln

Gly Thr Lys Val Glu Ile Lys Arg

Hum C:
25 **VH Domain** (SEQ ID NO:6)
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu

Ser Cys Ala Ala Ser (Gly Phe Asn Ile Lys Asp Thr Tyr Ile His) Trp Val Arg Gln Ala

Pro Gly Lys Gly Leu Glu Trp Val Ala (Arg Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr Ala

Asp Ser Val Lys Gly) Arg Phe Thr Ile Ser Gly Asp Asp Ser Lys Asn Thr Ala Tyr Leu

30 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Thr (Ser Gly Tyr
Trp Phe Ala Tyr) Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

VL Domain (SEQ ID NO:7)
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr

35 Ile Thr Cys (Arg Ala Ser Gln Ser Ile Ser Asn Asn Leu His) Trp Tyr Gln Gln Lys Pro

Gly Lys Ala Pro Lys Leu Leu Ile Tyr (His Ala Ser Gln Ser Ile Ser) Gly Val Pro Ser

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

5 Glu Asp Phe Ala Thr Tyr Tyr Cys (Gln Gln Ser Asn Ser Trp Pro Tyr Thr) Phe Gly Gln

Gly Thr Lys Val Glu Ile Lys Arg

10 **Hum D:**

VH Domain (SEQ ID NO:8)

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu

Ser Cys Ala Ala Ser (Gly Phe Asn Ile Lys Asp Thr Tyr Ile His) Trp Val Arg Gln Ala

Pro Gly Lys Gly Leu Glu Trp Val Ala (Arg Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr Ala

15 Asp Ser Val Lys Gly) Arg Phe Thr Ile Ser Ser Asp Asp Ser Lys Asn Thr Ala Tyr Leu

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Thr (Ser Gly Tyr

Trp Phe Ala Tyr) Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

VL Domain (SEQ ID NO:9)

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr

20 Ile Thr Cys (Arg Ala Ser Gln Ser Ile Ser Asn Asn Leu His) Trp Tyr Gln Gln Lys Pro

Gly Lys Ala Pro Lys Leu Leu Ile Tyr (His Ala Ser Gln Ser Ile Ser) Gly Val Pro Ser

25 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

Glu Asp Phe Ala Thr Tyr Tyr Cys (Gln Gln Ser Asn Ser Trp Pro Tyr Thr) Phe Gly Gln

Gly Thr Lys Val Glu Ile Lys Arg

30 **Hum E:**

VH Domain (SEQ ID NO:10)

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu

Ser Cys Ala Ala Ser (Gly Phe Asn Ile Lys Asp Thr Tyr Ile His) Trp Val Arg Gln Ala

35 Pro Gly Lys Gly Leu Glu Trp Val Ala (Arg Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr

Asp Pro Lys Val Gln Gly) Arg Phe Thr Ile Ser Ala Asp Asp Ser Lys Asn Thr Ala Tyr

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Thr (Ser Gly

Tyr Trp Phe Ala Tyr) Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

VL Domain (SEQ ID NO:11)

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr

Ile Thr Cys (Arg Ala Ser Gln Ser Ile Ser Asn Asn Leu His) Trp Tyr Gln Gln Lys Pro

5 Gly Lys Ala Pro Lys Leu Leu Ile Tyr (His Ala Ser Gln Ser Ile Ser) Gly Val Pro Ser

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

Glu Asp Phe Ala Thr Tyr Tyr Cys (Gln Gln Ser Asn Ser Trp Pro Tyr Thr) Phe Gly Gln

10 Gly Thr Lys Val Glu Ile Lys Arg

Hum F:
VH Domain (SEQ ID NO:12)

15 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu

Ser Cys Ala Ala Ser (Gly Phe Asn Ile Lys Asp Thr Tyr Ile His) Trp Val Arg Gln Ala

Pro Gly Lys Gly Leu Glu Trp Val Ala (Arg Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr Ala

Asp Ser Val Lys Gly) Arg Phe Thr Ile Ser Ala Asp Asp Ser Lys Asn Thr Ala Tyr Leu

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Thr (Ser Gly Tyr

20 Trp Phe Ala Tyr) Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

VL Domain (SEQ ID NO:13)

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr

Ile Thr Cys (Arg Ala Ser Gln Ser Ile Ser Asn Asn Leu His) Trp Tyr Gln Gln Lys Pro

25 Gly Lys Ala Pro Lys Leu Leu Ile Tyr (His Ala Ser Gln Ser Ile Ser) Gly Val Pro Ser

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

30 Glu Asp Phe Ala Thr Tyr Tyr Cys (Gln Gln Ser Asn Ser Trp Pro Tyr Thr) Phe Gly Gln

Gly Thr Lys Val Glu Ile Lys Arg

Hum G:

35 **VH Domain** (SEQ ID NO:14)

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu

Ser Cys Ala Ala Ser (Gly Phe Asn Ile Lys Asp Thr Tyr Ile His) Trp Val Arg Gln Ala

Pro Gly Lys Gly Leu Glu Trp Val Ala (Arg Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr Ala

Asp Ser Val Lys Gly) Arg Phe Thr Ile Ser Ala Asp Asp Ser Lys Asn Thr Ala Tyr Leu

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Thr (Ser Gly Tyr Trp Phe Ala Tyr) Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

VL Domain (SEQ ID NO:15)

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

15 **Hum H:**

VH Domain (SEQ ID NO:16)

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
Ser Cys Ala Ala Ser (Gly Phe Asn Ile Lys Asp Thr Tyr Ile His) Trp Val Arg Gln Ala
Pro Gly Lys Gly Leu Glu Trp Val Ala (Arg Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr
20 Asp Pro Lys Val Gln Gly) Arg Phe Thr Ile Ser Ala Asp Asp Ser Lys Asn Thr Ala Tyr
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Thr (Ser Gly
Tyr Trp Phe Ala Tyr) Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

VL Domain (SEQ ID NO:17)

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
25
Ile Thr Cys (Arg Ala Ser Gln Ser Ile Ser Asn Asn Leu His) Trp Tyr Gln Gln Lys Pro
Gly Lys Ala Pro Lys Leu Leu Ile Lys (His Ala Ser Gln Ser Ile Ser) Gly Val Pro Ser
30 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
Glu Asp Phe Ala Thr Tyr Tyr Cys (Gln Gln Ser Asn Ser Trp Pro Tyr Thr) Phe Gly Gln
Gly Thr Lys Val Glu Ile Lys Arg
35

Hum I:

VH Domain (SEQ ID NO:18)

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
Ser Cys Ala Ala Ser (Gly Phe Asn Ile Lys Asp Thr Tyr Ile His) Trp Met Arg Gln Ala

Pro Gly Lys Gly Leu Glu Trp Val Ala (Arg Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr Asp Pro Lys Val Gln Gly) Arg Phe Thr Met Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Thr (Ser Gly Tyr Trp Phe Ala Tyr) Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

5 **VL Domain** (SEQ ID NO:19)

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys (Arg Ala Ser Gln Ser Ile Ser Asn Asn Leu His) Trp Tyr Gln Gln Lys Pro

10 Gly Lys Ala Pro Lys Leu Leu Ile Lys (His Ala Ser Gln Ser Ile Ser) Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys (Gln Gln Ser Asn Ser Trp Pro Tyr Thr) Phe Gly Gln

15 Gly Thr Lys Val Glu Ile Lys Arg

The CDR residues are included within brackets.

20 **Example 3**

This example describes expression and purification of humanized 1A6 single chain antibody proteins.

For production of the humanized 1A6 scFv, TOP10 cells transformed with desired expression construct were grown in shaker flasks in TB medium (Bio 101) until they

25 reached an OD_{600} of 0.8. Protein expression was induced with 0.02% arabinose for eighteen hours at room temperature. Cells were pelleted by centrifugation at 4,000 g for 15 minutes. Cell pellets were resuspended in $1/50^{th}$ volume of lysis buffer (20 mM sodium phosphate, 1% Triton X-100, 500 mM NaCl, 40 mM imidazole, 2 mM 2-mercaptoethanol), 0.2 mM PMSF, 1mg/ml lysozyme and incubated on ice for 30 minutes.

30 The cell suspension was sonicated and another aliquot of PMSF was added. The cell debris was pelleted by centrifugation at 12,000 x g and the clarified sonicate was filtered and fractionated by metal affinity chromatography. Induced histidine-tagged proteins were bound to a Hi Trap™ metal chelating column (Amersham/Pharmacia) equilibrated with Ni^{2+} according to the manufacturer's instructions. The column was then washed

35 with four column volumes of buffer consisting of 100 mM imidazole, 20 mM sodium phosphate, pH 7.4, 500 mM NaCl. Fractions of proteins eluted from the column in 500

mM Imidazole, 20 mM sodium phosphate, pH 7.4 were collected, pooled and dialyzed at 4 °C against phosphate buffered saline (PBS)/2mM EDTA, then dialyzed against PBS.

Example 4

This example describes studies measuring binding affinity of humanized single
5 chain antibody proteins for ICAM-1.

To evaluate the binding affinity of histidine-tagged human single chain (hsc) proteins soluble ICAM was used in an ELISA assay. A 96-well EIA plate (Corning, Inc.) was coated with 100 µl/well soluble ICAM-1 (Bender MedSystems) at 1 µg/ml in 0.1 M $NaHCO_3$. After washing with TBST (50 mM Tris, pH8.0, 150 mM NaCl, 0.05% Tween-
10 20), the plate was blocked with 3% non-fat milk in TBST at 37 °C for 1 hour. After washing with TBST, the plate was incubated with scFv samples (100 µl /well) diluted in 1% non-fat milk / TBST solution at room temperature for 1 hour. After washing with TBST, the horse radish peroxidase-conjugated anti-His (C-term) antibody (Invitrogen) diluted 1:2000 in 1% non-fat milk/TBST was added and the plate was incubated at room
15 temperature for 1 hour. The plate was washed thoroughly with TBST and 100 µl/well 3,3',5,5'-tetramethybenzidine substrate solution (Kirkegaard and Perry Laboratories) was added. After 5 min incubation, the color development was stopped by adding 100 ml/well 0.12 N HCl and the absorbance of the wells at 450 nm was measured by a plate reader (ICN).

20 Binding studies revealed that all of the humanized scFv proteins (hsc) demonstrate greater than ten times higher binding affinity for ICAM-1 than the parental mouse scFv (Table 4).

Table 4. Mouse 1A6 scFv and Humanized 1A6 scFv

25

ScFv	K_D (M)	EC 50 (µM)*
Msc1A6	1.18×10^{-6}	> 10
HumA	1.50×10^{-7}	2.8
HumB	2.62×10^{-8}	0.19
HumC	5.80×10^{-8}	0.22

HumD	2.33×10^{-8}	0.05
HumF	4.60×10^{-8}	0.29
HumH	2.09×10^{-8}	4.2
HumI	1.50×10^{-7}	>10

5

* 50% protection of HeLa cells against HRV15 infection at 1 MOI.

Example 5

This example describes data demonstrating that humanized 1A6 antibodies
10 protect against HRV infection. This example also describes data that demonstrate that protection was significantly greater than mouse1A6 antibody.

HeLa cells were plated at 1×10^5 cells per well of a 48-well tissue culture dish and cultured for 24 hours. Culture medium was aspirated and 100μl of humanized 1A6 proteins was added to each well at the dilution indicated. The plates were incubated for
15 one hour in a 37°C incubator, the protein solution removed, 200μl HRV15 (at MOI of 1) was added and the plates incubated for one hour at 33°C. The cells were then washed and 1 ml/well growth medium added. The infected cells were incubated at 33°C for 48 hours. The medium was then aspirated and the remaining viable cells stained with crystal violet. Finally, the crystal violet was extracted with 2 ml methanol per well, and the
20 extracted stain determined by measuring the A_{570}. The percentage protection was calculated for each point in triplicate using the formula:

$$\% \text{ protection} = \frac{(100)(\text{Absorbance of sample- Absorbance of virus only})}{(\text{Absorbance of uninfected cells- Absorbance of virus only})}$$

25

The protective efficacy was quantified as EC_{50}, which is the dose of an antibody protein which can protect 50% of hela cells from HRV infection. EC_{50} of several humanized 1A6 proteins are summarized in Table 4, and the data from this protection assay is shown in FIG. 4. This assay revealed that the EC50 of Hum19 scFv protein was
30 more than sixty times higher than that of the parental mouse 1A6 scFv protein (FIG. 4). In vitro protection results correlate well with the antibody binding affinity.

Example 6

This example describes additional strategies for humanizing 1A6.

Two additional versions of humanized 1A6 were produced by grafting the CDR loops of the V_H domain onto two different human consensus framework sequences, Hum40 and Hum50. Hum40 is a humanized 1A6 resulting from CDR grafting onto the human consensus V_H subgroup II (Hum2) and Hum50 is a humanized 1A6 resulting from CDR grafting onto the human consensus V_H subgroup I (Hum1) (Padlan (1991) *Mol. Immunol.* 28:489-498; FIG. 5).

Hum40:

The human V_H subgroup II (Hum2) shares 50 identical amino acid residues among 82 framework residues with the murine 1A6 V_H sequence, which amounts to 61% identity (FIG. 5 and 6). Among the 32 amino acid residues that differ between the murine 1A6 and HumII, six of them belong to the "Vernier" zone (Foote and Vinter, (1992), *J. Mol. Biol.* 224:487-499), and may affect the antigen-binding affinity. The critical "Vernier" zone residues are V_H 67, 69, 71, 78, 93 and 94.

Analysis of the amino acids at V_H 67, 69 78 and 93 positions reveals that the human consensus residues and the murine residues have very similar properties. Thus, human consensus residues are used to replace murine residues at these positions. Structural analysis reveals that residues at V_H 71 and 94 should have small side chains, which rules out the human consensus residues, lysine and arginine at these two positions. Serine and alanine, both having small side chains, were therefore selected for V_H71 and V_H94 respectively. As a result, the V_H domain of Hum40 contains all human consensus residues at framework positions except for V_H71 and V_H94. Residues that are unrelated to either murine or human residues were chosen at V_H71 and V_H94 because of their structural features (FIG. 6).

Hum50:

The human V_H subgroup I (Hum1) shares 62 identical amino acid residues among 82 framework residues with the murine 1A6 V_H sequence, which amounts to 76% identity (FIG. 5 and 7). Among the 20 amino acid residues that differ between the

murine 1A6 and Hum1, four of them belong to the "Vernier" zone (Foote and Vinter, (1992), *J. Mol. Biol.* 224:487-499), and may affect the antigen-binding affinity. The critical "Vernier" zone residues are V_H 48, 67, 93 and 94. Analysis of the amino acids at V_H 48, 67 and 93 positions reveals that the human consensus residues and the murine
5 residues have very similar properties. Thus, human consensus residues are used to replace murine residues at these positions. Structural analysis reveals that the residue at V_H 94 should have a small side chain, which rules out the human consensus residue arginine. Alanine was therefore selected for V_H94. As a result, Hum50 contains all human consensus residues at framework positions except for V_H94 (FIG. 7).

10 **Example 7**

This example describes the preparation of humanized 1A6 Fab protein.

Three expression constructs were made: Fab19, Fab40 and Fab50. Fab19 is composed of variable domains (V_H and V_L) derived from humanized 1A6, HumB (see Table 3), which is based on human consensus sequence of heavy chain V_H subgroup III
15 and human light chain κ subgroup I. Fab40 and Fab50 contain Hum40 and Hum50 V_H domains respectively and the same light chains as Fab19. The amino acid sequence of the heavy chain variable domain of Fab19, Fab40 and Fab50 are listed in Table 5, and the corresponding gene sequences are listed in Table 6

Gene segments of the light chain variable domain (V_L) and the light chain
20 constant region (C_L) that was derived from human κ_1 light chain constant region (Palm and Hilschmann, 1975, *Z. Physiol. Chem.* 356:167-191) were synthesized separately by PCR amplification. After sequencing conformation, the two gene segments were fused together to form the light chain V_L-C_L gene. A similar approach was used to clone the gene segment containing the heavy chain variable domain (V_H) and the heavy chain
25 constant region (C_H) that is based on the sequence of the C_H1 domain of human IgG1 (Ellison *et al.*, 1982, *Nucl. Acids Res.* 10:4071).

An expression vector was designed for production of Fab proteins. The V_H and V_L domains are precisely fused on their 5' ends to a gene segment encoding the enterotoxin II signal sequence. The intervening sequence in the dicistronic gene contains
30 a ribosome entry site, while the 3' end of the gene contains the bacteriophage λ t_0

transcriptional terminator. The isopropyl-1-thio-β-D-galactopyranoside (IPTG)-inducible ptac promoter was used to drive expression of this dicistronic message.

For production of the humanized 1A6 Fab proteins, JM83 cells transformed with desired expression construct were grown in shaker flasks in TB medium (Bio 101) until
5 they reached an OD_{600} of 1.2. Protein expression was induced with 0.2 mM IPTG for eighteen hours at room temperature. Cells were pelleted by centrifugation at 4,000 g for 15 minutes. Cell pellets were resuspended in lysis buffer (50 mM Tris, pH 8.0 , 1.0 M NaCl, 5 mM EDTA, 0.2 mM PMSF, 1mg/ml lysozyme) to 10-15% solution and incubated on ice for 20 minutes. The cell suspension was sonicated and another aliquot
10 of PMSF was added. The cell debris was removed by centrifugation at 12,000 x g and the clarified sonicate filtered and fractionated by affinity chromatography, using Protein A agarose for Fab19 and Protein G agarose for Fab40 and Fab50. After washing the protein A or protein G columns with 50 mM Tris, pH 8.0 , 2.0 M NaCl, 5 mM EDTA, the bound protein was eluted from the columns with 0.1 N Glycine, pH 2.5, and collected in the
15 tubes containing 1/10 volume 0.1 M Tris, pH 9.0. The protein fractions were pooled and then dialyzed against TBS.

Table 5. Amino Acid Sequences of Fab19, Fab40 and Fab50

V_L Domain of Fab19, Fab40 and Fab50 (SEQ ID NO:5):

20 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
Ile Thr Cys (Arg Ala Ser Gln Ser Ile Ser Asn Asn Leu His) Trp Tyr Gln Gln Lys Pro
Gly Lys Ala Pro Lys Leu Leu Ile Tyr (His Ala Ser Gln Ser Ile Ser) Gly Val Pro Ser
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
Glu Asp Phe Ala Thr Tyr Tyr Cys (Gln Gln Ser Asn Ser Trp Pro Tyr Thr) Phe Gly Gln
25 Gly Thr Lys Val Glu Ile Lys Arg

V_H Domain of Fab19 (SEQ ID NO:4):

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu

Ser Cys Ala Ala Ser (Gly Phe Asn Ile Lys Asp Thr Tyr Ile His) Trp Val Arg Gln Ala

30 Pro Gly Lys Gly Leu Glu Trp Val Ala (Arg Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr Ala

Asp Ser Val Lys Gly) Arg Phe Thr Ile Ser Ser Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ala (Ser Gly Tyr Trp Phe Ala Tyr) Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

5 V_H Domain of Fab40 (SEQ ID NO:20):

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Thr Leu Thr Cys Thr Val Ser (Gly Phe Asn Ile Lys Asp Thr Tyr Ile His) Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly (Arg Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr Asp Pro Lys Val Gln Gly) Arg Val Thr Ile Thr Ser Asp Thr Ser Lys Asn Gln Val Ser Leu Asn Leu
10 Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Ala (Ser Gly Tyr Trp Phe Ala Tyr) Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

VH Domain of Fab50 (SEQ ID NO:21):

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

20

The CDR residues are included within brackets.

Table 6. The Variable Domain Gene Sequences of Fab19, Fab40 and Fab50

25

V_L gene of Fab19, Fab40 and Fab50 (SEQ ID NO:22):

GATATCCAGATGACCCAATCTCCGTCTAGCCTGAGCGCCAGTGTTGGTGATCG
AGTTACCATTACTTGCCGCGCCAGCCAATCTATCAGTAATAATCTTCACTGGT
30 ATCAACAAAAACCGGGTAAAGCTCCGAAACTTCTTATCTATCACGCCTCTCA
GAGCATTAGCGGCGTTCCGAGCCGCTTCTCTGGCTCTGGCTCGGGCACGGAC
TTTACCCTTACCATCAGCTCTCTTCAGCCGGAAGACTTTGCCACCTATTATTGT
CAGCAGTCTAATAGCTGGCCGTATACCTTCGGTCAAGGTACCAAGGTCGAGA
TTAAGCGG

V_H gene of Fab19 (SEQ ID NO:23):
GAAGTTCAACTTGTTGAGTCTGGTGGCGGTCTGGTTCAGCCCGGGGGCTCTCT
GCGCCTGTCTTGCGCAGCAAGCGGTTTCAACATTAAGGACACCTACATCCATT
5 GGGTGAGGCAAGCTCCGGGTAAGGGTCTGGAGTGGGTGGCACGTATCGACCC
GGCAAACGACAACACCATTTACGCTGACAGCGTGAAGGGCCGTTTTACTATT
TCTAGCGACGACTCTAAGAACACCGCGTACCTTCAGATGAACTCTCTGCGTG
CCGAGGACACCGCCGTCTACTACTGCACGGCCTCTGGCTACTGGTTTGCCTAC
TGGGGCCAGGGCACGCTTGTCACCGTCTCGAGC
10

V_H gene of Fab40 (SEQ ID NO:24):

CAGGTTCAACTTCAGGAGTCTGGTCCGGGTCTGGTTAAACCCTCTGAGACCTT
GACCCTTACCTGCACGGTTAGCGGTTTCAACATTAAGGACACCTACATCCATT
15 GGATTAGGCAACCGCCGGGTAAGGGTCTGGAGTGGATTGGCCGTATCGACCC
GGCAAACGACAACACCATTTACGACCCGAAGGTGCAAGGTCGTGTTACCATT
ACCTCTGACACCTCTAAGAACCAGGTGTCTCTCAATCTCAATAGCGTTACAGC
GGCTGACACCGCCGTCTACTACTGCGCCGCATCTGGCTACTGGTTTGCCTACT
GGGGCCAGGGCACGCTTGTCACCGTCTCGAGC
20

V_H gene of Fab50 (SEQ ID NO:25):

CAGGTTCAACTTGTGCAGTCTGGTGCAGAGGTGAAGAAACCCGGCGCATCTG
TGAAGGTGTCTTGCAAAGCAAGCGGTTTCAACATTAAGGACACCTACATCCA
25 TTGGGTTAGGCAAGCGCCGGGTCAAGGTCTGGAGTGGGTGGGCCGTATCGAC
CCGGCAAACGACAACACCATTTACGACCCGAAGGTGCAAGGTCGTGTTACCA
TGACCGCAGACACCTCTACAAACACCGCGTACATGGAGCTGTCTTCTCTGCGT
TCTGAGGACACCGCCGTCTACTACTGCGCCGCATCTGGCTACTGGTTTGCCTA
CTGGGGCCAGGGCACGCTTGTCACCGTCTCGAGC
30

Example 8

This example describes measuring binding affinities of humanized 1A6 Fab proteins against their antigen ICAM-1.

Binding affinities of Fab proteins were evaluated using an ELISA assay. A 96-well EIA plate (Corning, Inc.) was coated with 100 μl/well soluble ICAM-1 (Bender MedSystems) at 1 μg/ml in 0.1 M $NaHCO_3$. After washing with TBST (50 mM Tris, pH8.0, 150 mM NaCl, 0.05% Tween-20), the plate was blocked with 3% non-fat milk in
5 TBST at room temperature for 1 hour. After washing with TBST, the plate was incubated with the horseradish peroxidase-conjugated anti-human IgG Fab specific antibody (Sigma, A-0923) diluted 1:3,000 in 1% non-fat milk/TBST at room temperature for 1 hour. The plate was washed thoroughly with TBST and 100 μl/well 3,3',5,5'-tetramethylbenzidine substrate solution (Kirkegaard and Perry Laboratories) was added.
10 After 10 min incubation, the color development was stopped by adding 100 ml/well 0.12 N HCl. The absorbance at 450 nm was measured by a plate reader (ICN), and then plotted against antibody concentration. The affinity constant (K_D), also called equilibrium dissociation constant, is equal to the concentration of a Fab protein that gives rise to ICAM-1 binding at 50% of the saturation level.

15 Binding studies revealed that Fab19 has much higher binding affinity for ICAM-1 than its scFv form (HumB, see Table 4). The binding affinities of three humanized Fab proteins are in the following order: Fab19 > Fab40 > Fab50.

Table 7. Binding affinity of Humanized 1A6 Fab

20

Sample	K_D (M)
Fab19	9.3×10^{-9}
Fab 40	5.1×10^{-8}
Fab 50	1.3×10^{-7}

25

What is claimed is:

1. A humanized antibody that binds ICAM-1, said antibody having a V_H and V_L domain selected from: SEQ ID NO:1 and 3 (HumA); SEQ ID NO:4 and 5 (HumB); SEQ ID NO:6 and 7 (HumC); SEQ ID NO:8 and 9 (HumD); SEQ ID NO:10 and 11 (HumE); SEQ ID NO:12 and 13 (HumF); SEQ ID NO:14 and 15 (HumG); SEQ ID NO:16 and 17 (HumH); and SEQ ID NO:18 and 19 (HumI); and SEQ ID NO:5 and 20 (Hum40); and SEQ ID NO:5 and 21 (Hum50).
2. A subsequence of the antibody of claim 1, said antibody subsequence capable of binding an ICAM-1 epitope.
3. The humanized antibody of claim 2, wherein the antibody subsequence comprises a single chain, Fab, Fab' or $(Fab)_2$ fragment.
4. The humanized antibody of claim 1, said antibody having one or more amino acid substitutions, provided that said antibody is capable of binding an ICAM-1 epitope.
5. A humanized antibody that binds ICAM-1 and inhibits pathogen infection of cells expressing ICAM-1.
6. The humanized antibody of claim 5, said antibody having a protective efficacy at least 2 times greater than the non-humanized antibody.
7. The humanized antibody of claim 5, said antibody having a protective efficacy at least 5 times greater than the non-humanized antibody.
8. The humanized antibody of claim 5, said antibody having a protective efficacy at least 10 times greater than the non-humanized antibody.
9. The humanized antibody of claim 5, said antibody having a protective efficacy at least 20 times greater than the non-humanized antibody.
10. The humanized antibody of claim 5, said antibody having a protective efficacy at least 30 times greater than the non-humanized antibody.
11. The humanized antibody of claim 5, wherein the pathogen is human rhinovirus (HRV).
12. The humanized antibody of claim 5, wherein the pathogen is coxackie A virus, respiratory syncytial virus, or malaria.

13. The humanized antibody of claim 5, wherein the antibody is an intact immunoglobulin molecule comprising 2 full-length heavy chains and 2 full-length light chains.
14. The humanized antibody of claim 5, wherein the antibody is an antibody subsequence that binds to ICAM-1.
15. The humanized antibody of claim 14, wherein the antibody subsequence comprises a single chain, Fab, Fab' or $(Fab)_2$ fragment.
16. The humanized antibody of claim 5, wherein the antibody is multispecific or multifunctional.
17. The humanized antibody of claim 5, wherein the antibody is linked to one or more identical or different antibodies to form a multimer.
18. The humanized antibody of claim 17, wherein the multimer comprises a homo- or hetero-dimer, trimer, or tetramer or pentamer.
19. The humanized antibody of claim 17, wherein the multimer is formed via a multimerization domain.
20. The humanized antibody of claim 19, wherein the multimerization domain comprises a human amino acid sequence.
21. The humanized antibody of claim 19, further comprising a linker located between the multimerization domain and the antibody.
22. A humanized antibody that inhibits human rhinovirus (HRV) infection of cells comprising a V_H and V_L domain selected from: SEQ ID NO:1 and 3 (HumA); SEQ ID NO:4 and 5 (HumB); SEQ ID NO:6 and 7 (HumC); SEQ ID NO:8 and 9 (HumD); SEQ ID NO:10 and 11 (HumE); SEQ ID NO:12 and 13 (HumF); SEQ ID NO:14 and 15 (HumG); SEQ ID NO:16 and 17 (HumH); and SEQ ID NO:18 and 19 (HumI); and SEQ ID NO:5 and 20 (Hum40); and SEQ ID NO:5 and 21 (Hum50); or a subsequence thereof.
23. The humanized antibody of claim 22, wherein the antibody is an immunoglobulin molecule comprising 2 full-length heavy chain polypeptides and 2 full-length light chain polypeptides.
24. The humanized antibody of claim 22, wherein the subsequence comprises a single chain, Fab, Fab' or $(Fab)_2$ fragment.

25. The humanized antibody of claim 22, wherein the antibody is linked with other identical or different antibodies to form a multimer.
26. The humanized antibody of claim 25, wherein the multimer comprises a homo- or hetero-dimer, trimer, or tetramer.
27. The humanized antibody of claim 25, wherein the different antibodies are human, humanized or non-human.
28. A nucleic acid sequence encoding a humanized antibody of claim 1 or 22 or a subsequence thereof.
29. An expression cassette comprising the nucleic acid sequence of claim 28 operably linked to an expression control element.
30. A vector comprising the nucleic acid sequence of claim 29.
31. The vector of claim 29, wherein the nucleic acid sequence is operably linked to an expression control element.
32. A cell comprising the nucleic acid sequence of claim 28.
33. The cell of claim 31, wherein the cell is prokaryotic or eukaryotic.
34. A pharmaceutical composition comprising a humanized antibody of claim 1 or 5, and a pharmaceutically acceptable carrier.
35. The pharmaceutical composition of claim 34, wherein the carrier is compatible with inhalation or nasal delivery to a subject.
36. A method of inhibiting pathogen infection of a cell comprising contacting a pathogen or a cell with an amount of a humanized antibody of claim 1 sufficient to inhibit pathogen infection of the cell.
37. The method of claim 36, wherein the cell is present in a subject.
38. The method of claim 37, wherein the cell is an epithelial cell.
39. The method of claim 37, wherein the cell expresses ICAM-1.
40. A method of inhibiting HRV infection of a cell comprising contacting HRV or a cell susceptible to HRV infection with an amount of a humanized antibody of claim 21 effective to inhibit HRV infection of the cell.
41. The method of claim 40, wherein the cell is present in a subject.
42. The method of claim 41, wherein the subject has or is at risk of having asthma.

43. The method of claim 40, wherein the antibody binds to an antigen present on the surface of the cell.
44. The method of claim 40, wherein the cell expresses ICAM-1.
45. The method of claim 40, wherein the cell is an epithelial cell.
46. The method of claim 40, wherein the humanized antibody is administered locally.
47. The method of claim 40, wherein the humanized antibody is administered via inhalation or intranasaly.
48. A method of inhibiting HRV infection, inhibiting HRV progression or treating HRV infection of a subject comprising administering to a subject having or at risk of having HRV infection an amount of a humanized antibody of claim 22 effective to inhibit, inhibit progression or treat HRV infection of the subject.
49. The method of claim 48, wherein the humanized antibody is administered locally.
50. The method of claim 48, wherein the humanized antibody is administered via inhalation or intranasaly.
51. The method of claim 48, wherein the subject has or is at risk of having asthma.
52. The method of claim 48, wherein the subject is a newborn or between the ages of 1 to 5, 5 to 10 or 10 to 18.
53. A method of decreasing or inhibiting one or more symptoms of the common cold in a subject comprising administering to a subject having a common cold an amount of a humanized antibody of claim 22 effective to decrease or inhibit one or more symptoms of the common cold in the subject.
54. The method of claim 53, wherein the humanized antibody is administered locally.
55. The method of claim 53, wherein the humanized antibody is administered via inhalation or intranasaly.
56. The method of claim 53, wherein the subject has or is at risk of having asthma.
57. The method of claim 53, wherein the subject is a newborn or between the ages of 1 to 5, 5 to 10 or 10 to 18.
58. A method for producing humanized antibody comprising:
    a) selecting a human framework sequence as an acceptor, wherein said sequence has 50% or more identity to a non-human donor antibody framework region;

b) grafting a CDR from the donor non-human antibody onto the human framework;

c) comparing the vernier zone residues of the human acceptor and the non-human donor framework regions; and

d) maintaining one or more of the human acceptor residues in the vernier zone when the donor non-human and acceptor human residues are structurally or chemically similar, or substituting one or more of the vernier zone residues with a residue that is different from both the donor non-human vernier zone residue and acceptor human vernier zone residue if the donor non-human vernier zone residue is structurally or chemically dissimilar to the human residue, wherein the different residue is structurally or chemically similar to the donor non-human vernier zone residue.

59. The method of claim 58, wherein the human framework acceptor sequences is selcted from a V_H domain subgroup I or subgroup II consensus sequence.

Figure 1

V_H Domain

	1 11 21 31 41
Mouse1A6	EVQLQQSGAE LVKPGASVKL SCTAS**GFNIK** **DTYIH**WMKQR PEQGLEW I **GR**
	* * * * * * * * * * * * * * * * * * *
Hum3	EVQLVESGGG LVQPGGSLRL SCAAS**GFNFS** ----------WVRQA PGKGLEWVA—
	51 a 61 71 81 abc 91
Mouse1A6	**IDPANDNTIYD** **PKVQG**KATMT ADTSS NTAYL QLSSLTSEDTAVY YCTT
	* * * * * * * * * * * * *
Hum3	-------------------**A** **DSVKG**RF T IS RDDSKNTAYL QMNSLRAEDTAVY YCTT
	103 111
Mouse1A6	**SGYWFA** **Y**WGQGTLVT VSA
	*
Hum3	-------------- --WGQGTLVT VSS

V_L Domain

	1 11 21 31 41 51
Mouse1A6	DIVLTQSPAT LSVTPGDSVS LSC**RASQSIS** **NNLH**WYQQKS HESPRLLIK**H** **ASQ**
	* * * * * * * * * * * * * * * * * *
HumκI	DIQMTQSPSS LSASVGDRVT ITC------------- -------- WYQQKP GKAPKLLIY -- -----
	61 71 81 91 101
Mouse1A6	**SISG** I PS RFSGSGSGTD FTLSINSVET EDFGMFFC**QQ** **SNSWPYT**FGG GTKLEIKR
	* * * * * * * * * * * *
HumκI	----GVPS RFSGSGSGTD FTLTISSLQP EDFATYYC ---- -------------- FGQ GTKVEIKR

Figure 2

V$_H$ Domain

```
        1                11              21              31                41
Mouse   EVQLQQSGAE LVKPGASVKL SCTASGFNIK DTYIHWMKQR PEQGLEWI GR
            * *   * *    *   *  * *    *                * * *  * *    * *
HumB    EVQLVESGGG LVQPGGSLRL SCAASGFNIK DTYIHWVRQA PGKGLEWVAR

Hum3    EVQLVESGGG LVQPGGSLRL SCAASGFNFS ----------WVRQA PGKGLEWVA—
        51 a           61                71           81  a bc              91
Mouse   IDPANDNTIYD PKVQGKATMT ADTSS NTAYL QS NSLTSEDTAVY YCT T
                      * *  * *  * .. *  *          *   * * *          *
HumB    IDPANDNTIYA DSVKG RFT IS  SDDSKNTAYL QMNSLRAEDTAVY YCTA
                                  *                                   *
Hum3    -------------------A DSVKG RFT IS RDDSKNTAYL QMNSLRAEDTAVY YCTR
                 103          111
Mouse   SGYWFA YWGQGTLVT VSS

HumB    SGYWFA YWGQGTLVT VSS

Hum3    -------------- --WGQGTLVT VSS
```

V$_L$ Domain

```
        1               11               21              31                 41             51
Mouse   DIVLTQSPAT LSVTPGDSVS LSCRASQSIS NNLHWYQQKS HESPRLLIKH ASQ
          * *       **      * **    *   *  **                       *  ** *  *      *
HumB    DIQMTQSPSS LSASVGDRVT ITCRASQSIS NNLHWYQQKP GKAPKLLIYH ASQ

HumκI   DIQMTQSPSS LSASVGDRVT ITC------------- -------- WYQQKP GKAPKLLIY -- -----
                   61              71             81              91                101
Mouse   SISG I PS RFSGSGSGTD FTLSINSVET EDFGMFFCQQ SNSWPYTFGG GTKLEIKR
           *                      * *  * * *   * * **                   *      *
HumB    SISGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SNSWPYTFGQ GTKVEIKR

HumκI   ----GVPS RFSGSGSGTD FTLTISSLQP EDFATYYC ---- -------------- FGQ GTKVEIKR
```

Figure 3

CGAACCATGGGCGATATCCAGATGACCCAATCTCCGTCTAGCCTGAGCGCCA
GTGTTGGTGATCGAGTTACCATTACTTGCCGCGCCAGCCAATCTATCAGTAAT
AATCTTCACTGGTATCAACAAAAACCGGGTAAAGCTCCGAAACTTCTTATCTA
TCACGCCTCTCAGAGCATTAGCGGCGTTCCGAGCCGCTTCTCTGGCTCTGGCT
CGGGCACGGACTTTACCCTTACCATCAGCTCTCTTCAGCCGGAAGACTTTGCC
ACCTATTATTGTCAGCAGTCTAATAGCTGGCCGTATACCTTCGGTCAAGGTAC
CAAGGTCGAGATTAAGCGCGGCGGTGGCGGTTCTGGTGGCGGTGGTAGCGGT
GGCGGTGGATCCGGTGGCGGTGGCAGCGAAGTTCAACTTGTTGAGTCTGGTG
GCGGTCTGGTTCAGCCGGGTGGCTCTCTGCGCCTGTCTTGCGCAGCAAGCGGT
TTCAACATTAAGGACACCTACATCCATTGGGTGAGGCAAGCTCCGGGTAAGG
GTCTGGAGTGGGTGGCACGTATCGACCCGGCAAACGACAACACCATTTACGC
TGACAGCGTGAAGGGCCGTTTTACTATTTCTAGCGACGACTCTAAGAACACCG
CGTACCTTCAGATGAACTCTCTGCGTGCCGAGGACACCGCCGTCTACTACTGC
ACGGACTCTGGCTACTGGTTTGCCTACTGGGGCCAGGGCACGCTTGTCACCGT
CTCTTCTGGTTAACCC

Figure 4

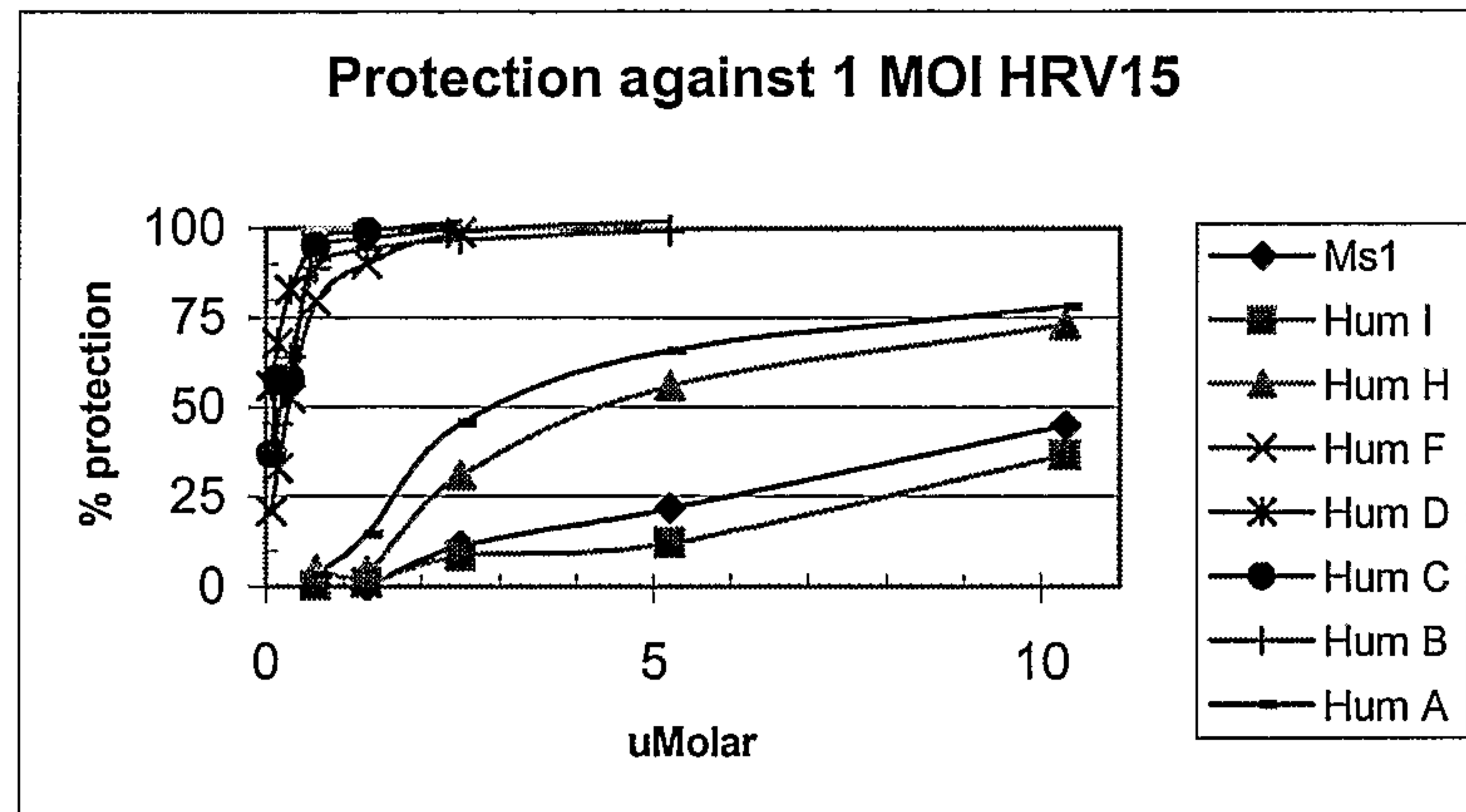


Figure 5

```
                              10                  20
M1A6 VH:    E V Q L Q Q S G A E L V K P G A S V K L S C T A S
Hum2:       Q V Q L Q E S G P G L V K P S E T L T L T C T V S

Hum1:       Q V Q L V Q S G A E V K K P G A S V K V S C K A S


                    30                  40                  50
M1A6 VH:    G F N I K D T Y I H W M K Q R P E Q G L E W I G R
Hum2:       G F S I S           W I R Q P P G K G L E W I G
Hum1:       G G T F S           W V R Q A P G Q G L E W V G


                                        66      70
M1A6 VH:    I D P A N D N T I Y D P K V Q G K A T M T A D T S
Hum2:                                       R V T I T K D T S

Hum1:                                       R V T M T A D T S


                      80    a b c               90
M1A6 VH:    S N T A Y L Q L S S L T S E D T A V Y Y C T T S G
Hum2:       K N Q V S L N L N S V T A A D T A V Y Y C A A
Hum1:       T N T A Y M E L S S L R S E D T A V Y Y C A A


                      103           110
M1A6 VH:    Y W F A Y W G Q G T L V T V S S
Hum2:                 W G Q G T L V T V S S
Hum1:                 W G Q G T L V T V S S
```

Figure 6

V_H Domain

```
        1           11          21          31           41
Mouse   EVQLQQSGAE  LVKPGASVKL  SCTASGFNIK  DTYIHWMKQR  PEQGLEWI GR
        *    *  * *    *****   *  *                  * * *   * *
Hum40   QVQLQESGPG  LVKPSETLTL  TCTVSGFNIK  DTYIHW I RQP  PGKGLEWI GR

Hum2    QVQLQESGPG  LVKPSETLTL  TCTVSGFSIS  ----------W I RQP  PGKGLEWI G---

        51 a          61          71           81 a bc        91
Mouse   IDPANDNTIYD  PKVQGKATMT  ADTSSNTAYL  QL SSLTSEDTAVY  YCT T
                           ** *  *    * * * *  *  * *  **      * *
Hum40   IDPANDNTIYD  PKVQG RVT I T  SDTSKNQVSL  NL NSVTAADTAVY  YCAA
                                 *                                *
Hum2    --------------------------------- RVT I T  KDTSKNQVSL  NLNSVTAADTAVY  YCAR

                   103         111
Mouse   SGYWFA  YWGQGTLVT  VSA
                              *
Hum40   SGYWFA  YWGQGTLVT  VSS

Hum2    -------------- --WGQGTLVT  VSS
```

Figure 7

V_H Domain

1 11 21 31 41

Mouse EVQLQQSGAE LVKPGASVKL SCTAS**GFNIK DTYIH**WMKQR PEQGLEW I G**R**

* * * * * * * * * * *

Hum50 QVQLVQSGAE VKKPGASVKV SCKAS**GFNIK DTYIH**WVRQA PGQGLEWVG**R**

Hum1 QVQLVQSGAE VKKPGASVKV SCKAS**GYTFS** ----------WVRQA PGQGLEWVG---

51 a 61 71 81 a bc 91

Mouse **IDPANDNTIYD PKVQG**KATMT ADTSSNTAYL QLSSLTSEDTAVY YCT T

* * * * * * * *

Hum50 **IDPANDNTIYD PKVQG**RVTM T ADTSTNTAYM ELSSLRSEDTAVY YCAA

*

Hum1 --------------------------------- RVT MT ADTSTNTAYM ELSSLRSEDTAVY YCAR

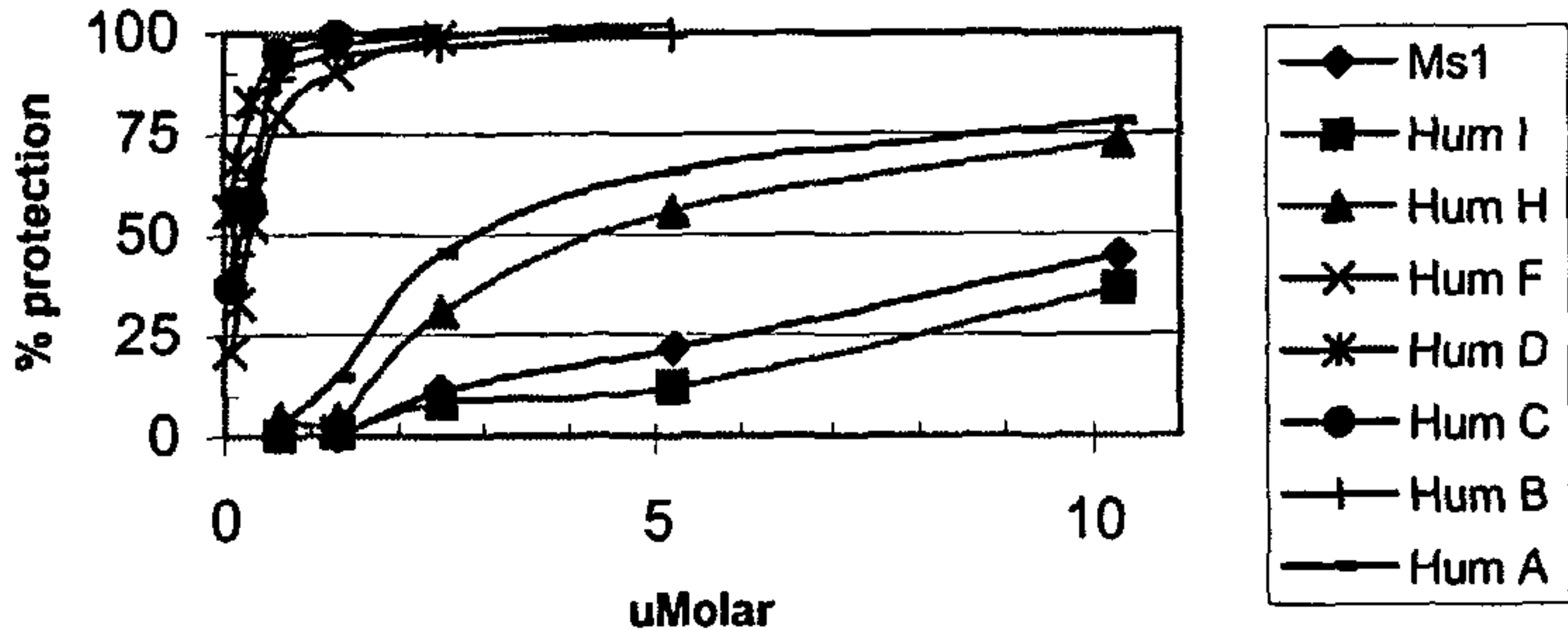
103 111

Mouse **SGYWFA Y**WGQGTLVT VSA

*

Hum50 **SGYWFA Y**WGQGTLVT VSS

Hum1 -------------- --WGQGTLVT VSS



Protection against 1 MOI HRV15
100
75
50
25
0
% protection
0
5
10
uMolar
Ms1
Hum I
Hum H
Hum F
Hum D
Hum C
Hum B
Hum A