DESCRIPTION

METHOD OF MODIFYING ISOELECTRIC POINT OF ANTIBODY VIA AMINO ACID SUBSTITUTION IN CDR

Technical Field

The present invention relates to methods for modifying the isoelectric point (pI) of an antibody while retaining its antigen-binding activity through amino acid substitutions in the CDR; methods for controlling antibody pharmacokinetics in plasma (pharmacokinetics in blood); pharmaceutical compositions comprising as an active ingredient an antibody with a modified isoelectric point; methods for producing the compositions; and such.

The present invention also relates to methods for controlling the plasma half-lives of anti-IL-6 receptor antibodies, anti-glypican 3 antibodies, and anti-IL-31 receptor antibodies by modifying amino acid residues that are exposed on the surface of the CDR regions of the antibodies; antibodies (anti-IL-6 receptor antibodies, anti-glypican 3 antibodies, and anti-IL-31 receptor antibodies) whose plasma half-life is controlled through modification of amino acid residues; pharmaceutical compositions comprising such an antibody as an active ingredient; and methods for producing the compositions.

Furthermore, the present invention relates to pharmaceutical compositions comprising an anti-IL-6 receptor antibody as an active ingredient, methods for producing the compositions, and such.

Background Art

Antibodies are drawing attention as pharmaceuticals as they have long half-life in plasma and few adverse effects. Of them, a number of IgG-type antibody pharmaceuticals are available on the market and many antibody pharmaceuticals are currently under development (Non-patent Documents 1 and 2). Most of the antibody pharmaceuticals available on the market are chimeric antibodies, humanized antibodies, or human antibodies. Currently, many antibody pharmaceuticals are being developed which have more superior characteristics with improved drug efficacy, convenience, and cost from modification of humanized antibodies or human antibodies. Various technologies applicable to these antibody pharmaceuticals have been developed, including those that enhance effector function, antigen-binding activity, phramacokinetics, or stability, and those that reduce the risk of immunogenicity. For methods of enhancing drug efficacy or reducing dosage, techniques that enhance antibody-dependent cell-mediated cytotoxicity (ADCC) or complement-dependent cytotoxicity (CDC) through

amino acid substitution in the Fc domain of an IgG antibody have been reported (Non-patent Documents 3 and 4). Furthermore, affinity maturation has been reported as a technique for enhancing antigen-binding activity or antigen-neutralizing activity (Non-patent Document 5). This technique enables enhancement of antigen-binding activity through introduction of amino acid mutations into the CDR region of a variable region or such.

A problem encountered with current antibody pharmaceuticals is high production cost associated with the administration of extremely large quantities of protein. The preferred form of administration is thought to be subcutaneous formulation for chronic autoimmune diseases. In general, it is necessary that subcutaneous formulations are high concentration formulations. From the perspective of stability or such, the concentration limit for IgG-type antibody formulations is in general thought to be about 100 mg/ml (Non-patent Document 6). Low-cost, convenient antibody pharmaceuticals with more superior characteristics that can be administered subcutaneously in longer intervals can be provided by increasing the half-life of an antibody in the plasma to prolong its therapeutic effect and thereby reduce the amount of protein administered.

FcRn is closely involved in the long plasma half-life of antibodies. The plasma half-life of antibody is known to be different between antibody isotypes. IgG1 and IgG2 have the longest half-life in plasma, while IgG3 and IgG4 have a shorter half-life (Non-patent Document 7). A reported method for prolonging the plasma half-lives of IgG1 and IgG2 antibodies, which have a superior half-life in plasma, comprises substituting amino acids in the constant region to enhance the binding to FcRn (Non-patent Documents 8 to 10). However, introduction of artificial amino acid mutations into a constant region is encountered with the problem of immunogenicity. On the other hand, a method that comprises introducing amino acid mutations into antibody variable regions for improving antibody pharmacokinetics has recently been reported (Patent Document 1).

Patent Document 1 describes that the pharmacokinetics of IgG can be controlled by modifying its isoelectric point, and the plasma half-life of an antibody can be prolonged by reducing the isoelectric point of the antibody without loss of antigen-binding activity through introduction of amino acid substitutions into the antibody variable region framework. Specifically, the isoelectric point of an antibody can be reduced without loss of antigen-binding activity, for example, by introducing amino acid substitutions at H10, H12, H23, H39, H43, and H105, Kabat's numbering. It is also possible to introduce amino acid mutations into other framework sequences without loss of binding activity. In some cases, however, introduction of amino acid substitutions into framework sequences alone is thought to be insufficient for significant reduction of isoelectric point. This is because a human antibody sequence is generally used as a framework sequence after amino acid substitution to reduce immunogenicity,

but human antibody framework sequences are highly conserved and have low diversity, and thus there is little flexibility for amino acid substitution. Therefore, when amino acid substitution into the framework alone is insufficient to reduce the isoelectric point of an antibody, it would be difficult to further reduce the isoelectric point.

In contrast, CDR sequences have an enormous diversity due to somatic mutations, and because they have the diversity needed for acquiring antigen-binding activity, there is significantly greater flexibility for amino acid substitution compared to framework sequences. However, amino acid substitution in CDR sequence is generally known to affect the antigen-binding activity of an antibody, as CDR sequence is the most important factor for strong antigen-binding activity. Thus, it is difficult to reduce the isoelectric point of an antibody by substituting amino acids in its CDR sequence without considerable loss of antigen-binding activity. Furthermore, CDR sequence varies greatly depending on the type of antigen; thus, regardless of antibody specificity, it has been believed to be very difficult to substitute amino acids in an antibody CDR sequence without considerable loss of the antibody's antigen-binding activity. In fact, this can be inferred from many findings described below.

In general, antibodies derived from a nonhuman animal species are humanized by CDR grafting, in which a human framework sequence is grafted to the CDR sequence of the nonhuman animal species. If a humanized antibody obtained by CDR grafting does not have a comparable binding activity as the chimeric antibody, the binding activity can be recovered from substituting a portion of the framework sequence which determines the CDR structure with amino acids of the antibody framework sequence of the nonhuman animal species from which the antibody is derived (Non-patent Document 11). The CDR sequence and structure are very important for the antigen-binding activity and specificity of an antibody. Furthermore, the antigen-binding activity of an antibody is generally known to be reduced when antibody CDR residues are modified by isomerization of aspartic acid residues, deamidation of aspartic acid residues, or oxidation of methionine residues in antibody CDR (Non-patent Document 12), and this also suggests that CDR sequence is very important for the antigen-binding activity of antibodies. In addition, it has been further reported that not only the antigen-binding activity but also the expression level of an antibody is often considerably reduced when amino acid substitutions are introduced into the heavy chain CDR2 sequence of an antibody (Non-patent Documents 13 to 15). In particular, the expression level of an antibody is known to be markedly reduced when amino acid substitution is introduced at H51 (Non-patent Document 16). Furthermore, the antigen-binding activity has been reported to be considerably reduced in almost all cases when mutations are introduced into the heavy chain CDR3 sequence of an antibody (Non-patent Documents 17 and 18). Alternatively, the antigen-binding activity of an antibody is often markedly reduced when amino acids in the antibody CDR are substituted with alanine by

alanine scanning mutagenesis (Non-patent Documents 19 to 23). The effect of alanine substitution on antigen-binding activity is thought to depend on antibody specificity. In sum, the antigen-binding activity of an antibody is generally considered to be reduced by amino acid substitution in the CDR sequence, and there is no previous report on positions of amino acids whose substitution does not significantly reduce the antigen-binding activity of an antibody regardless of its antibody specificity.

In antibody engineering to produce antibody molecules with more superior characteristics, almost all amino acid substitutions introduced into antibody CDR sequences are aimed at affinity maturation. Affinity maturation is a method for obtaining antibodies with improved antigen-binding activity, and is generally conducted by displaying on phages or ribosomes an antibody library comprising randomized CDR sequences derived from the CDR sequences of an antibody molecule and panning on the antigen. This method enables discovery of amino acid substitutions in antibody CDR sequence that improve antigen-binding activity (Non-patent Documents 5 and 24 to 26). However, amino acid substitutions found by the above-described method which improve antigen-binding activity are different depending on the antibody specificity. Thus, there is no previous report on positions of amino acids in CDR sequence whose substitution improves the antigen-binding activity regardless of the antibody specificity. Other than affinity maturation for modifying CDR sequence, methods for improving expression levels of antibodies in mammalian cells by substituting amino acids at specific positions in the CDR sequence (Patent Document 2) are reported. According to Patent Document 2, the expression levels of antibodies in mammalian cells can be improved independently of the antibody specificity by substituting amino acids at specific positions in the CDR sequence with a particular sequence. Alternatively, some reports describe deimmunization where the immunogenicity of an antibody is reduced by avoiding T cell epitopes in the antibody CDR sequence. However, there is no previous report on methods for substituting amino acids in an antibody, regardless of its antibody specificity, to remove T cell epitopes from the CDR sequence without loss of binding activity (Non-patent Documents 27 and 28).

As described above, the antibody CDR sequence is closely involved in antigen binding. Therefore, amino acid substitutions in CDR sequence generally impair binding activity. The effect of amino acid substitution in CDR sequence on antigen binding differs depending on the antibody specificity. Patent Document 1 describes some examples on the control of isoelectric point by amino acid substitution in CDR; however, the antigen-binding activity can be impaired in some kinds of antibodies. Alternatively, methods have been reported for improving the expression of antibodies independently of the antibody specificity by common amino acid substitutions; however, there is no previous report on methods for improving an antibody's

antigen-binding activity or removing T cell epitopes without considerable loss of an antibody's antigen-binding activity. There is absolutely no report on antibody CDR sequences whose amino acids can be substituted without considerable loss of the antibody's antigen-binding activity regardless of the antibody specificity.

Documents of related prior arts for the present invention are described below.

[Non-patent Document 1] Janice M Reichert, Clark J Rosensweig, Laura B Faden & Matthew C Dewitz. Monoclonal antibody successes in the clinic. Nature Biotechnology (2005) 23:1073-1078

[Non-patent Document 2] Pavlou AK, Belsey MJ. The therapeutic antibodies market to 2008. Eur J Pharm Biopharm. 2005 Apr;59(3):389-96

[Non-patent Document 3] Presta LG. Engineering of therapeutic antibodies to minimize immunogenicity and optimize function. Adv Drug Deliv Rev. 2006 Aug 7;58(5-6):640-56

[Non-patent Document 4] Kim SJ, Park Y, Hong HJ. Antibody engineering for the development of therapeutic antibodies. Mol Cells. 2005 Aug 31;20(1):17-29 Review

[Non-patent Document 5] Fujii I. Antibody affinity maturation by random mutagenesis. Methods Mol Biol. (2004) 248:345-59

[Non-patent Document 6] Shire SJ, Shahrokh Z, Liu J. Challenges in the development of high protein concentration formulations. J Pharm Sci. 2004 Jun;93(6):1390-402

[Non-patent Document 7] Salfeld JG. Isotype selection in antibody engineering.Nat Biotechnol. 2007 Dec;25(12):1369-72

[Non-patent Document 8] Hinton PR, Johlfs MG, Xiong JM, Hanestad K, Ong KC, Bullock C, Keller S, Tang MT, Tso JY, Vasquez M, Tsurushita N. Engineered human IgG antibodies with longer serum half-lives in primates. J Biol Chem. 2004 Feb 20;279(8):6213-6

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[Non-patent Document 10] Ghetie V, Popov S, Borvak J, Radu C, Matesoi D, Medesan C, Ober RJ, Ward ES. Increasing the serum persistence of an IgG fragment by random mutagenesis. Nat Biotechnol. 1997 Jul;15(7):637-40

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[Non-patent Document 13] Chen C, Roberts VA, Rittenberg MB. Generation and analysis of random point mutations in an antibody CDR2 sequence: many mutated antibodies lose their

ability to bind antigen. J Exp Med. 1992 Sep 1;176(3):855-66

[Non-patent Document 14] Chen C, Martin TM, Stevens S, Rittenberg MB. Defective secretion of an immunoglobulin caused by mutations in the heavy chain complementarity determining region 2. J Exp Med. 1994 Aug 1;180(2):577-86

[Non-patent Document 15] Wiens GD, Heldwein KA, Stenzel-Poore MP, Rittenberg MB. Somatic mutation in VH complementarity-determining region 2 and framework region 2: differential effects on antigen binding and Ig secretion. J Immunol. 1997 Aug 1;159(3):1293-302

[Non-patent Document 16] Wiens GD, Lekkerkerker A, Veltman I, Rittenberg MB. Mutation of a single conserved residue in VH complementarity-determining region 2 results in a severe Ig secretion defect. J Immunol. 2001 Aug 15;167(4):2179-86

[Non-patent Document 17] Zwick MB, Komori HK, Stanfield RL, Church S, Wang M, Parren PW, Kunert R, Katinger H, Wilson IA, Burton DR. The long third complementarity-determining region of the heavy chain is important in the activity of the broadly neutralizing anti-human immunodeficiency virus type 1 antibody 2F5. J Virol. 2004 Mar;78(6):3155-61

[Non-patent Document 18] Komissarov AA, Marchbank MT, Calcutt MJ, Quinn TP, Deutscher SL. Site-specific mutagenesis of a recombinant anti-single-stranded DNA Fab. Role of heavy chain complementarity-determining region 3 residues in antigen interaction. J Biol Chem. 1997 Oct 24;272(43):26864-70

[Non-patent Document 19] Gerstner RB, Carter P, Lowman HB. Sequence plasticity in the antigen-binding site of a therapeutic anti-HER2 antibody. J Mol Biol. 2002 Aug 30;321(5):851-62

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biotherapeutic molecules. Expert Opin Biol Ther. 2006 Feb;6(2):177-87
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[Non-patent Document 26] Rajpal A, Beyaz N, Haber L, Cappuccilli G, Yee H, Bhatt RR, Takeuchi T, Lerner RA, Crea R. A general method for greatly improving the affinity of antibodies by using combinatorial libraries. Proc Natl Acad Sci U S A. 2005 Jun 14;102(24):8466-71
[Non-patent Document 27] De Groot AS, Knopp PM, Martin W. De-immunization of therapeutic proteins by T-cell epitope modification. Dev Biol (Basel). (2005) 122:171-94
[Non-patent Document 28]
http://www.algonomics.com/proteinengineering/tripole_applications.php
[Patent Document 1] WO/2007/114319
[Patent Document 2] US/2006/0019342

Disclosure of the Invention

[Problems to be Solved by the Invention]

The present invention was achieved in view of the above circumstances. An objective of the present invention is to provide methods for modifying the isoelectric point of a polypeptide comprising an antibody variable region while retaining its antigen-binding activity; methods for controlling antibody half-life in plasma; pharmaceutical compositions comprising as an active ingredient an antibody with controlled plasma half-life; and methods for producing the antibodies and pharmaceutical compositions comprising the antibody as an active ingredient.

Another objective of the present invention is to provide methods for controlling plasma half-lives of anti-IL-6 receptor antibodies, anti-glypican 3 antibodies, and anti-IL-31 receptor antibodies by modifying amino acid residues exposed on the surface of the CDR regions of the antibodies; anti-IL-6 receptor antibodies, anti-glypican 3 antibodies, and anti-IL-31 receptor antibodies whose plasma half-life is controlled by modifying amino acid residues; methods for producing such antibodies; and pharmaceutical compositions comprising such an antibody as an active ingredient.

Furthermore, another objective of the present invention is to provide pharmaceutical compositions that comprise second-generation molecules, which are more superior than the humanized anti-IL-6 receptor IgG1 antibody TOCILIZUMAB, and methods for producing such pharmaceutical compositions. The second-generation molecules have been improved to exhibit enhanced antigen-neutralizing activity and retention in plasma, and thus produce a prolonged therapeutic effect even when the frequency of administration is reduced; and they have also been

improved to have reduced immunogenicity and improved safety and physical properties, by modifying amino acid sequences of the variable and constant regions of TOCILIZUMAB.

[Means for Solving the Problems]

The present inventors conducted dedicated studies on methods for modifying the isoelectric point of polypeptides comprising an antibody variable region while retaining the antigen-binding activity of the variable region. As a result, the present inventors identified specific amino acid positions within the amino acid sequence of a complementarity determining region (CDR) of an antibody variable region, that allow for modification of the isoelectric point while retaining the antigen-binding activity of the variable region. Furthermore, the present inventors discovered that the plasma half-life of a polypeptide comprising an antibody variable region could be regulated by controlling the isoelectric point of the polypeptide, and that heteromultimers of a polypeptide comprising an antibody variable region could be efficiently produced by utilizing differences in the isoelectric point. Specifically, the present inventors identified specific amino acid positions in a CDR sequence constituting an antibody variable region, that allow one to control the charge on the surface of an antibody molecule without affecting the antibody structure and function such as the antigen-binding activity of the antibody variable region. In addition, the present inventors demonstrated that the plasma half-life of a polypeptide comprising an antibody variable region could be regulated by controlling the charge on antibody surface to modify the isoelectric point, and that antibodies with controlled plasma half-lives indeed retained their antigen-binding activities. Furthermore, the present inventors demonstrated that the tumor growth-suppressing effect of antibodies that exhibit cytotoxicity in cancer cells could be enhanced by controlling the plasma half-life of the antibodies, and thereby completed the present invention. In addition, the present inventors demonstrated that heterodimers comprising antibodies that bind to two or more different types of antigens could be isolated and purified by modifying their isoelectric points by controlling the CDR charge.

Furthermore, the present inventors conducted dedicated studies to produce second-generation molecules that are more superior than the first-generation humanized anti-IL-6 receptor IgG1 antibody TOCILIZUMAB, and have been improved to exhibit enhanced drug efficacy and retention in plasma, and thus produce a prolonged therapeutic effect even when the frequency of administration is reduced. They have also been improved to have reduced immunogenicity and improved safety and physical properties (stability and homogeneity), by modifying amino acid sequences of the variable and constant regions of TOCILIZUMAB. As a result, the present inventors discovered multiple CDR mutations in the variable regions of TOCILIZUMAB that enable to improve the antigen-binding activity (affinity). The present inventors thus successfully improved the affinity significantly using a

combination of such mutations. The present inventors also successfully improved plasma retention by modifying the variable region sequence to lower the isoelectric point of an antibody. Furthermore, the present inventors successfully reduced immunogenicity risk by removing some of the *in silico*-predicted T-cell epitope peptides in the variable regions and the mouse sequences that remain in the framework of TOCILIZUMAB. In addition, the present inventors successfully increased the stability at higher concentrations. Furthermore, the present inventors also successfully discovered novel constant region sequences that do not bind to Fcγ receptor and that improve the stability under acidic conditions, heterogeneity originated from disulfide bonds in the hinge region, heterogeneity originated from the heavy chain C terminus, and stability in high concentration formulations, while minimizing the generation of new T-cell epitope peptides in the constant region of TOCILIZUMAB. The present inventors successfully discovered second-generation molecules that are more superior to TOCILIZUMAB by combining amino acid sequence modifications in the CDR, variable, and constant regions.

More specifically, the present invention provides:

[1] a method for modifying the isoelectric point of a polypeptide comprising an antibody variable region while retaining the antigen-binding activity of the variable region, which comprises modifying the charge of at least one exposable amino acid residue on the surface of complementarity determining region (CDR) of the polypeptide;

[2] the method of [1], wherein the polypeptide comprising an antibody variable region further comprises an FcRn-binding domain;

[3] the method of [1], wherein the polypeptide comprising an antibody variable region is an IgG antibody;

[4] the method of [1], wherein the polypeptide comprising an antibody variable region is a chimeric antibody, humanized antibody, or human antibody;

[5] the method of [1], wherein the polypeptide comprising an antibody variable region is a multispecific polypeptide that binds to at least two types of antigens;

[6] the method of [1], wherein the charge of amino acid residue is modified by amino acid substitution;

[7] the method of [1], wherein the modification in the charge of amino acid residue results in a change of 1.0 or more in the theoretical isoelectric point;

[8] the method of [1], wherein the exposable amino acid residue on the surface of the CDR region is at least one amino acid residue selected from amino acid residues at positions 31, 61, 62, 64, and 65 in the heavy chain variable region and positions 24, 27, 53, 54, and 55 in the light chain variable region according to Kabat's numbering system;

[9] a polypeptide comprising an antibody variable region with a modified isoelectric point, which is obtained by the method of any one of [1] to [8];

[10] a method for controlling the plasma pharmacokinetics of a polypeptide comprising an antibody variable region, which comprises modifying the isoelectric point of the polypeptide by the method of any one of [1] to [8];

[11] the method of [10], wherein the control of pharmacokinetics refers to increase or decrease of any one of the parameters of clearance (CL) in plasma, area under the concentration curve (AUC), mean retention time in plasma, and half-life in plasma (t1/2);

[12] a polypeptide comprising an antibody variable region whose pharmacokinetics in plasma is controlled, which is obtained by the method of [10];

[13] a method for producing a polypeptide comprising an antibody variable region with a modified isoelectric point, which comprises:

(a) modifying a nucleic acid encoding a polypeptide so as to modify the charge of at least one exposable amino acid residue on the surface of the CDR region of the polypeptide;

(b) culturing a host cell to express the nucleic acid; and

(c) collecting the polypeptide comprising an antibody variable region from the host cell culture;

[14] the method of [13], wherein the polypeptide comprising an antibody variable region further comprises an FcRn-binding domain;

[15] the method of [13], wherein the polypeptide comprising an antibody variable region is an IgG antibody;

[16] the method of [13], wherein the polypeptide comprising an antibody variable region is a chimeric antibody, humanized antibody, or human antibody;

[17] the method of [13], wherein the polypeptide comprising an antibody variable region is a multispecific polypeptide that binds to at least two types of antigens;

[18] the method of [13], wherein the charge of amino acid residue is modified by amino acid substitution;

[19] the method of [13], wherein the modification in the charge of amino acid residue results in a change of 1.0 or more in the theoretical isoelectric point;

[20] the method of [13], wherein the exposable amino acid residue on the surface of the CDR region is at least one amino acid residue selected from amino acid residues at positions 31, 61, 62, 64, and 65 in the heavy chain variable region and positions 24, 27, 53, 54, and 55 in the light chain variable region according to Kabat's numbering system;

[21] a polypeptide comprising an antibody variable region with a modified isoelectric point, which is obtained by the method of any one of [13] to [20];

[22] a method for producing a polypeptide comprising an antibody variable region whose pharmacokinetics in plasma is controlled, which comprises modifying the isoelectric point of the polypeptide comprising an antibody variable region by the method of any one of [13] to [20];

[23] the method [22], wherein the control of pharmacokinetics refers to increase or decrease of

any one of the parameters of clearance (CL) in plasma, area under the concentration curve (AUC), mean retention time in plasma, and half-life in plasma (t1/2);

[24] a polypeptide comprising an antibody variable region whose pharmacokinetics in plasma is controlled, which is produced by the method of 22;

[25] a method for producing a multispecific polypeptide comprising a first polypeptide and a second polypeptide each of which comprises an antibody variable region, which comprises:

(a) modifying a nucleic acid encoding a polypeptide so as to modify the charge of at least one exposable amino acid residue on the surface of the CDR region of the first polypeptide and second polypeptide, specifically modifying both or either one of a nucleic acid encoding the amino acid residues of the first polypeptide and a nucleic acid encoding the amino acid residues of the second polypeptide, so as to increase the difference between the isoelectric points of the first polypeptide and second polypeptide when compared to before modification;

(b) culturing a host cell to express the nucleic acids; and

(c) collecting a multispecific antibody from the host cell culture;

[26] the method of [25], wherein the step of collecting the multispecific polypeptide comprising the first polypeptide and second polypeptide from the host cell culture is achieved by a standard chromatography;

[27] the method of [25], wherein the nucleic acid is modified so that the peaks for homomultimer of the first polypeptide, homomultimer of the second polypeptide, and heteromultimer of the first polypeptide and second polypeptide are more clearly separated in a standard chromatographic analysis when compared to those before modification;

[28] the method of [25], wherein the multispecific polypeptide is a multispecific antibody;

[29] a multispecific antibody that is produced by the method of [27];

[30] the multispecific antibody of [29], which is a bispecific antibody;

[31] an antibody whose isoelectric point is modified as compared to the antibody before modification while retaining the antigen-binding activity, which comprises a human-derived framework region (FR), a human constant region, and a CDR selected from the group consisting of human-derived CDRs, nonhuman animal-derived CDRs, and synthetic CDRs, wherein at least one exposable amino acid residue on the surface of the CDR region is different in the charge from the amino acid residue at the corresponding position in the wild type CDR;

[32] the antibody of [31], wherein the human constant region comprises a human Fc domain;

[33] the antibody of [31], whose pharmacokinetics in plasma is controlled by modifying the isoelectric point;

[34] an IgG antibody whose isoelectric point is modified when compared to that before amino acid modification, wherein the charge of at least one amino acid residue selected from amino acid residues at positions 31, 61, 62, 64, and 65 in the heavy chain variable region and positions

24, 27, 53, 54, and 55 in the light chain variable region according to Kabat's numbering system;
[35] the antibody of [34], wherein the modified amino acid is selected from the amino acid residues in either of groups (a) and (b) below:
(a) glutamic acid (E) and aspartic acid (D); and
(b) lysine (K), arginine (R), and histidine (H);
[36] a multispecific antibody comprising a first polypeptide and a second polypeptide, whose isoelectric points are different from each other, and at least one amino acid residue of the first polypeptide selected from amino acid residues at positions 31, 61, 62, 64, and 65 in the heavy chain variable region and positions 24, 27, 53, 54, and 55 in the light chain variable region according to Kabat's numbering system is charged;
[37] the antibody of [36], wherein at least one amino acid residue of the second polypeptide selected from amino acid residues at positions 31, 61, 62, 64, and 65 in the heavy chain variable region and positions 24, 27, 53, 54, and 55 in the light chain variable region according to Kabat's numbering system has no charge or has a charge opposite to the charge of the selected amino acid residue of the first polypeptide;
[38] the antibody of [36], wherein the amino acid residue having a charge and the amino acid residue having an opposite charge as a combination are each selected from the different group of:
(a) glutamic acid (E) and aspartic acid (D); and
(b) lysine (K), arginine (R), and histidine (H);
[39] the multispecific antibody comprising a first polypeptide and a second polypeptide of [36], which gives separated peaks for the homomultimer of the first polypeptide and the homomultimer of the second polypeptide in a standard chromatographic analysis;
[40] a composition comprising a pharmaceutically acceptable carrier and the antibody of any one of [31] to [39];
[41] a nucleic acid encoding a polypeptide that constitutes the antibody of any one of [31] to [39];
[42] a host cell comprising the nucleic acid of [41];
[43] a method for producing the antibody of any one of [31] to [39], which comprises the steps of culturing the host cell of [42] and collecting the polypeptide from the cell culture; and
[44] a method for substituting an exposable amino acid residue on the surface of the complementarity determining region (CDR) of a polypeptide comprising an antibody variable region while retaining the antigen-binding activity of the polypeptide, which comprises substituting at least one amino acid residue selected from amino acid residues at positions 31, 61, 62, 64, and 65 in the heavy chain variable region and positions 24, 27, 53, 54, and 55 in the light chain variable region according to Kabat's numbering system.

The present invention also provides:

[1] a method for producing a glypican 3 antibody with controlled blood pharmacokinetics, which comprises the steps of:
(a) modifying a nucleic acid encoding at least one amino acid residue so as to modify the charge of at least one exposable amino acid residue on the surface of the glypican 3 antibody;
(b) culturing a host cell comprising the nucleic acid so as to express the nucleic acid; and
(c) collecting the glypican 3 antibody from the host cell culture;
[2] the method of [1], wherein the control of blood pharmacokinetics refers to increase or decrease of any one of the parameters of half-life in blood, mean retention time in blood, and clearance in blood;
[3] the method of [1], wherein the charge of the amino acid residue is modified by amino acid substitution in step (a);
[4] the method of [1], wherein the exposable amino acid residue on the surface of the glypican 3 antibody is located in a region other than the FcRn-binding domain of the glypican 3 antibody;
[5] the method of [4], wherein the FcRn-binding domain comprises an Fc domain;
[6] the method of [1], wherein the glypican 3 antibody is an IgG antibody;
[7] the method of [6], wherein the amino acid residue whose charge is to be modified is an amino acid residue in the heavy chain variable region or light chain variable region of the IgG antibody;
[8] the method of [7], wherein the glypican 3 antibody is a glypican 3 antibody comprising a complementarity determining region (CDR), human-derived framework region (FR), and human constant region, and wherein the modification of charge of the amino acid residue in step (a) is modification of at least one exposable amino acid residue on the surface of CDR or FR of the antibody to be modified to an amino acid residue having a different charge;
[9] the method of [8], wherein the glypican 3 antibody is an antibody with reduced content of fucose linked to its Fc domain;
[10] a glypican 3 antibody, which is produced by the method of any one of [1] to [9];
[11] a method for stabilizing an glypican 3 antibody that comprises a complementarity determining region (CDR), human-derived framework region (FR), and human constant region, which comprises modifying at least one amino acid residue constituting the glypican 3 antibody to increase the Tm value, and which comprises the steps of:
(a) modifying a nucleic acid encoding at least one amino acid residue to increase the Tm value of the glypican 3 antibody to be modified;
(b) culturing a host cell comprising the nucleic acid so as to express the nucleic acid; and
(c) collecting the antibody from the host cell culture;
[12] the method of [11], wherein the amino acid residue in step (a) is located within the heavy or light chain FR1 and/or FR2 region;
[13] the method of [12], wherein the amino acid residue of the heavy chain FR2 region of [12] is

substituted with an amino acid residue of an FR2 region of the VH4 subclass;
[14] the method of [12], wherein the amino acid residue of the light chain FR2 region of [12] is substituted with an amino acid residue of an FR2 region of the VK3 subclass;
[15] a method for controlling the cytotoxicity of an antibody, which comprises the steps of;
(a) modifying a nucleic acid encoding at least one amino acid so as to modify the charge of at least one exposable amino acid on the surface of an antibody that has cytotoxicity;
(b) culturing a host cell comprising the nucleic acid so as to express the nucleic acid; and
(c) collecting the antibody from the host cell culture;
[16] the method of [15], wherein the control of blood pharmacokinetics refers to control of any one of the parameters of half-life in blood, mean retention time in blood, and clearance in blood;
[17] the method of [15], wherein the charge of the amino acid residue is modified by amino acid substitution in step (a);
[18] the method of [15], wherein the exposable amino acid residue on the antibody surface is located in a region other than the FcRn-binding domain of the antibody;
[19] the method of [18], wherein the FcRn-binding domain comprises an Fc domain;
[20] the method of [15], wherein the glypican 3 antibody is an IgG antibody;
[21] the method of [20], wherein the amino acid residue whose charge is to be modified is an amino acid residue in the heavy chain variable region or light chain variable region of the IgG antibody;
[22] the method of [21], wherein the antibody comprises a complementarity determining region (CDR) derived from a nonhuman animal, human-derived framework region (FR), and human constant region, and wherein the modification of charge of the amino acid residue in step (a) is modification of at least one exposable amino acid residue on the surface of CDR or FR of the antibody to be modified to an amino acid residue having a different charge;
[23] the method of [22], wherein the antibody is an antibody with reduced content of fucose linked to its Fc domain;
[24] an antibody which is produced by the method of any one of [15] to [23];
[25] the method of [24], wherein the antibody is a glypican 3 antibody;
[26] an antibody which comprises a heavy chain variable region comprising one or more of:
(a) substitution of T for K at amino acid position 19;
(b) substitution of E for Q at amino acid position 43;
(c) substitution of S for K at amino acid position 63;
(d) substitution of Q for K at amino acid position 65; and
(e) substitution of D for G at amino acid position 66;
in the heavy chain variable region of SEQ ID NO: 195; and
a light chain variable region comprising one or more of:

(f) substitution of E for Q at amino acid position 27;
(g) substitution of T for K at amino acid position 79; and
(h) substitution of S for R at amino acid position 82;
in the light chain variable region of SEQ ID NO: 201;
[27] the antibody of [26], which comprises the heavy chain of SEQ ID NO: 197 and the light chain of SEQ ID NO: 203;
[28] the antibody of [26], which comprises the heavy chain of SEQ ID NO: 198 and the light chain of SEQ ID NO: 204;
[29] an antibody which comprises a heavy chain variable region comprising one or more of:
(a) substitution of K for Q at amino acid position 43;
(b) substitution of N for D at amino acid position 52; and
(c) substitution of R for Q at amino acid position 107;
in the heavy chain variable region of SEQ ID NO: 195; and
a light chain variable region comprising one or more of:
(d) substitution of Q for E at amino acid position 17;
(e) substitution of R for Q at amino acid position 27; and
(f) substitution of R for Q at amino acid position 105;
in the light chain variable region of SEQ ID NO: 201;
[30] the antibody of [29], which comprises the heavy chain variable region of SEQ ID NO: 198 and the light chain variable region of SEQ ID NO: 204;
[31] the antibody of [29], which comprises the heavy chain variable region of SEQ ID NO: 199 and the light chain variable region of SEQ ID NO: 205;
[32] the antibody of any one of [26] to [31], which comprises a human antibody constant region;
[33] a composition comprising the antibody of [32] and a pharmaceutically acceptable carrier;
[34] a therapeutic agent for cancer, which comprises the antibody of [32] as an active ingredient;
[35] the therapeutic agent for cancer of [34], wherein the cancer is liver cancer;
[36] a nucleic acid encoding a polypeptide constituting the antibody of any one of [26] to [31];
[37] a host cell comprising the nucleic acid of [36]; and
[38] a method for producing the antibody of any one of [26] to [31], which comprises the steps of culturing the host cell of [37] and collecting the polypeptide from the cell culture.

Furthermore, the present invention provides:
[1] an anti-IL-6 receptor antibody of any one of:
(a) an antibody that comprises a heavy chain variable region comprising CDR1 in which Ser at position 1 in the amino acid sequence of SEQ ID NO: 1 has been substituted with another amino acid;
(b) an antibody that comprises a heavy chain variable region comprising CDR1 in which Trp at

position 5 in the amino acid sequence of SEQ ID NO: 1 has been substituted with another amino acid;

(c) an antibody that comprises a heavy chain variable region comprising CDR2 in which Tyr at position 1 in the amino acid sequence of SEQ ID NO: 2 has been substituted with another amino acid;

(d) an antibody that comprises a heavy chain variable region comprising CDR2 in which Thr at position 8 in the amino acid sequence of SEQ ID NO: 2 has been substituted with another amino acid;

(e) an antibody that comprises a heavy chain variable region comprising CDR2 in which Thr at position 9 in the amino acid sequence of SEQ ID NO: 2 has been substituted with another amino acid;

(f) an antibody that comprises a heavy chain variable region comprising CDR3 in which Ser at position 1 in the amino acid sequence of SEQ ID NO: 3 has been substituted with another amino acid;

(g) an antibody that comprises a heavy chain variable region comprising CDR3 in which Leu at position 2 in the amino acid sequence of SEQ ID NO: 3 has been substituted with another amino acid;

(h) an antibody that comprises a heavy chain variable region comprising CDR3 in which Thr at position 5 in the amino acid sequence of SEQ ID NO: 3 has been substituted with another amino acid;

(i) an antibody that comprises a heavy chain variable region comprising CDR3 in which Ala at position 7 in the amino acid sequence of SEQ ID NO: 3 has been substituted with another amino acid;

(j) an antibody that comprises a heavy chain variable region comprising CDR3 in which Met at position 8 in the amino acid sequence of SEQ ID NO: 3 has been substituted with another amino acid;

(k) an antibody that comprises a heavy chain variable region comprising CDR3 in which Ser at position 1 and Thr at position 5 in the amino acid sequence of SEQ ID NO: 3 have been substituted with other amino acids;

(l) an antibody that comprises a heavy chain variable region comprising CDR3 in which Leu at position 2, Ala at position 7, and Met at position 8 in the amino acid sequence of SEQ ID NO: 3 have been substituted with other amino acids;

(m) an antibody that comprises a light chain variable region comprising CDR1 in which Arg at position 1 in the amino acid sequence of SEQ ID NO: 4 has been substituted with another amino acid;

(n) an antibody that comprises a light chain variable region comprising CDR1 in which Gln at

position 4 in the amino acid sequence of SEQ ID NO: 4 has been substituted with another amino acid;

(o) an antibody that comprises a light chain variable region comprising CDR1 in which Tyr at position 9 in the amino acid sequence of SEQ ID NO: 4 has been substituted with another amino acid;

(p) an antibody that comprises a light chain variable region comprising CDR1 in which Asn at position 11 in the amino acid sequence of SEQ ID NO: 4 has been substituted with another amino acid;

(q) an antibody that comprises a light chain variable region comprising CDR2 in which Thr at position 2 in the amino acid sequence of SEQ ID NO: 5 has been substituted with another amino acid;

(r) an antibody that comprises a light chain variable region comprising CDR3 in which Gln at position 1 in the amino acid sequence of SEQ ID NO: 6 has been substituted with another amino acid;

(s) an antibody that comprises a light chain variable region comprising CDR3 in which Gly at position 3 in the amino acid sequence of SEQ ID NO: 6 has been substituted with another amino acid;

(t) an antibody that comprises a light chain variable region comprising CDR1 in which Tyr at position 9 in the amino acid sequence of SEQ ID NO: 4 has been substituted with another amino acid, and CDR3 in which Gly at position 3 in the amino acid sequence of SEQ ID NO: 6 has been substituted with another amino acid;

(u) an antibody that comprises a light chain variable region comprising CDR3 in which Thr at position 5 in the amino acid sequence of SEQ ID NO: 6 has been substituted with another amino acid;

(v) an antibody that comprises a light chain variable region comprising CDR3 in which Gln at position 1 and Thr at position 5 in the amino acid sequence of SEQ ID NO: 6 have been substituted with other amino acids;

(w) an antibody that comprises a heavy chain variable region comprising CDR2 in which Thr at position 9 in the amino acid sequence of SEQ ID NO: 2 has been substituted with another amino acid, and CDR3 in which Ser at position 1 and Thr at position 5 in the amino acid sequence of SEQ ID NO: 3 have been substituted with other amino acids;

(x) an antibody that comprises the heavy chain variable region of (k) and the light chain variable region of (v); and

(y) the antibody of (x) that further comprises the CDR2 of (e);

[2] an anti-IL-6 receptor antibody that comprises a light chain variable region comprising CDR2 in which Thr at position 2 in the amino acid sequence of SEQ ID NO: 5 has been substituted

with another amino acid;

[3] an anti-IL-6 receptor antibody of any one of:

(a) an antibody that comprises a heavy chain variable region comprising FR1 in which Arg at position 13 in the amino acid sequence of SEQ ID NO: 7 has been substituted with another amino acid;

(b) an antibody that comprises a heavy chain variable region comprising FR1 in which Gln at position 16 in the amino acid sequence of SEQ ID NO: 7 has been substituted with another amino acid;

(c) an antibody that comprises a heavy chain variable region comprising FR1 in which Thr at position 23 in the amino acid sequence of SEQ ID NO: 7 has been substituted with another amino acid;

(d) an antibody that comprises a heavy chain variable region comprising FR1 in which Thr at position 30 in the amino acid sequence of SEQ ID NO: 7 has been substituted with another amino acid;

(e) an antibody that comprises a heavy chain variable region comprising FR1 in which Arg at position 13, Gln at position 16, Thr at position 23, and Thr at position 30 in the amino acid sequence of SEQ ID NO: 7 have been substituted with other amino acids;

(f) an antibody that comprises a heavy chain variable region comprising FR2 in which Arg at position 8 in the amino acid sequence of SEQ ID NO: 8 has been substituted with another amino acid;

(g) an antibody that comprises a heavy chain variable region comprising FR3 in which Met at position 4 in the amino acid sequence of SEQ ID NO: 9 has been substituted with another amino acid;

(h) an antibody that comprises a heavy chain variable region comprising FR3 in which Leu at position 5 in the amino acid sequence of SEQ ID NO: 9 has been substituted with another amino acid;

(i) an antibody that comprises a heavy chain variable region comprising FR3 in which Arg at position 16 in the amino acid sequence of SEQ ID NO: 9 has been substituted with another amino acid;

(j) an antibody that comprises a heavy chain variable region comprising FR3 in which Val at position 27 in the amino acid sequence of SEQ ID NO: 9 has been substituted with another amino acid;

(k) an antibody that comprises a heavy chain variable region comprising FR3 in which Met at position 4, Leu at position 5, Arg at position 16, and Val at position 27 in the amino acid sequence of SEQ ID NO: 9 have been substituted with other amino acids;

(l) an antibody that comprises a heavy chain variable region comprising FR4 in which Gln at

position 3 in the amino acid sequence of SEQ ID NO: 10 has been substituted with another amino acid;

(m) an antibody that comprises a light chain variable region comprising FR1 in which Arg at position 18 in the amino acid sequence of SEQ ID NO: 11 has been substituted with another amino acid;

(n) an antibody that comprises a light chain variable region comprising FR2 in which Lys at position 11 in the amino acid sequence of SEQ ID NO: 12 has been substituted with another amino acid;

(o) an antibody that comprises a light chain variable region comprising FR3 in which Gln at position 23 in the amino acid sequence of SEQ ID NO: 13 has been substituted with another amino acid;

(p) an antibody that comprises a light chain variable region comprising FR3 in which Pro at position 24 in the amino acid sequence of SEQ ID NO: 13 has been substituted with another amino acid;

(q) an antibody that comprises a light chain variable region comprising FR3 in which Ile at position 27 in the amino acid sequence of SEQ ID NO: 13 has been substituted with another amino acid;

(r) an antibody that comprises a light chain variable region comprising FR3 in which Gln at position 23, Pro at position 24, and Ile at position 27 in the amino acid sequence of SEQ ID NO: 13 have been substituted with other amino acids;

(s) an antibody that comprises a light chain variable region comprising FR4 in which Lys at position 10 in the amino acid sequence of SEQ ID NO: 14 has been substituted with another amino acid;

(t) an antibody that comprises a heavy chain variable region comprising FR4 in which Ser at position 5 in the amino acid sequence of SEQ ID NO: 10 has been substituted with another amino acid;

(u) an antibody that comprises a heavy chain variable region comprising FR4 in which Gln at position 3 and Ser at position 5 in the amino acid sequence of SEQ ID NO: 10 have been substituted with other amino acids;

(v) an antibody that comprises a heavy chain variable region comprising FR3 comprising the amino acid sequence of SEQ ID NO: 184;

(w) an antibody that comprises a heavy chain variable region comprising the FR1 of (e), FR2 of (f), FR3 of (k), and FR4 of (l) or (u);

(x) an antibody that comprises a light chain variable region comprising the FR1 of (m), FR2 of (n), FR3 of (r), and FR4 of (s); and

(y) an antibody that comprises the heavy chain variable region of (w) and the light chain variable

region of (x);

[4] an anti-IL-6 receptor antibody of any one of:

(a) an antibody that comprises a heavy chain variable region comprising CDR1 in which Ser at position 1 in the amino acid sequence of SEQ ID NO: 1 has been substituted with another amino acid;

(b) an antibody that comprises a heavy chain variable region comprising CDR2 in which Thr at position 9 in the amino acid sequence of SEQ ID NO: 2 has been substituted with another amino acid;

(c) an antibody that comprises a heavy chain variable region comprising CDR2 in which Ser at position 16 in the amino acid sequence of SEQ ID NO: 2 has been substituted with another amino acid;

(d) an antibody that comprises a heavy chain variable region comprising CDR2 in which Thr at position 9 and Ser at position 16 in the amino acid sequence of SEQ ID NO: 2 have been substituted with other amino acids;

(e) an antibody that comprises a light chain variable region comprising CDR1 in which Arg at position 1 in the amino acid sequence of SEQ ID NO: 4 has been substituted with another amino acid;

(f) an antibody that comprises a light chain variable region comprising CDR2 in which Thr at position 2 in the amino acid sequence of SEQ ID NO: 5 has been substituted with another amino acid;

(g) an antibody that comprises a light chain variable region comprising CDR2 in which Arg at position 4 in the amino acid sequence of SEQ ID NO: 5 has been substituted with another amino acid;

(h) an antibody that comprises a light chain variable region comprising CDR2 in which Thr at position 2 and Arg at position 4 in the amino acid sequence of SEQ ID NO: 5 have been substituted with other amino acids;

(i) an antibody that comprises a light chain variable region comprising CDR3 in which Thr at position 5 in the amino acid sequence of SEQ ID NO: 6 has been substituted with another amino acid;

(j) an antibody that comprises a heavy chain variable region comprising the CDR1 of (a), CDR2 of (d), and CDR3 comprising the amino acid sequence of SEQ ID NO: 3;

(k) an antibody that comprises a light chain variable region comprising the CDR1 of (e), CDR2 of (h), and CDR3 of (i); and

(l) an antibody that comprises the heavy chain variable region of (j) and the light chain variable region of (k);

[5] an anti-IL-6 receptor antibody of any one of:

(a) an antibody that comprises a heavy chain variable region comprising CDR1 in which Ser at position 1 in the amino acid sequence of SEQ ID NO:1 has been substituted with another amino acid, CDR2 in which Thr at position 9 and Ser at position 16 in the amino acid sequence of SEQ ID NO: 2 have been substituted with other amino acids, and CDR3 in which Ser at position 1 and Thr at position 5 in the amino acid sequence of SEQ ID NO: 3 have been substituted with other amino acids;

(b) an antibody that comprises a light chain variable region comprising CDR1 in which Arg at position 1 in the amino acid sequence of SEQ ID NO: 4 has been substituted with another amino acid, CDR2 in which Thr at position 2 and Arg at position 4 in the amino acid sequence of SEQ ID NO:5 have been substituted with other amino acids, and CDR3 in which Gln at position 1 and Thr at position 5 in the amino acid sequence of SEQ ID NO:6 have been substituted with other amino acids;

(c) an antibody that comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 22;

(d) an antibody that comprises a light chain variable region comprising the amino acid sequence of SEQ ID NO: 23;

(e) an antibody that comprises the heavy chain variable region of (a) and the light chain variable region of (b); and

(f) an antibody that comprises the heavy chain variable region of (c) and the light chain variable region of (d);

[6] a human antibody constant region of any one of:

(a) a human antibody constant region that comprises deletions of both Gly at position 329 (446 in the EU numbering system) and Lys at position 330 (447 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 19;

(b) a human antibody constant region that comprises deletions of both Gly at position 325 (446 in the EU numbering system) and Lys at position 326 (447 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20; and

(c) a human antibody constant region that comprises deletions of both Gly at position 326 (446 in the EU numbering system) and Lys at position 327 (447 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 21;

[7] an IgG2 constant region in which the amino acids at positions 209 (330 in the EU numbering system), 210 (331 in the EU numbering system), and 218 (339 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 have been substituted with other amino acids;

[8] an IgG2 constant region in which the amino acid at position 276 (397 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 has been substituted with another amino acid;

[9] an IgG2 constant region in which the amino acid at position 14 (131 in the EU numbering system), 102 (219 in the EU numbering system), and/or 16 (133 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 has been substituted with another amino acid;

[10] the IgG2 constant region of [9], wherein the amino acids at positions 20 (137 in the EU numbering system) and 21 (138 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 have been substituted with other amino acids;

[11] an IgG2 constant region in which His at position 147 (268 in the EU numbering system), Arg at position234 (355 in the EU numbering system), and/or Gln at position 298 (419 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 has been substituted with another amino acid;

[12] an IgG2 constant region in which the amino acids at positions 209 (330 in the EU numbering system), 210 (331 in the EU numbering system), 218 (339 in the EU numbering system), 276 (397 in the EU numbering system), 14 (131 in the EU numbering system), 16 (133 in the EU numbering system), 102 (219 in the EU numbering system), 20 (137 in the EU numbering system), and 21 (138 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 have been substituted with other amino acids;

[13] the IgG2 constant region of [12], which further comprises deletions of both Gly at position 325 (446 in the EU numbering system) and Lys at position 326 (447 in the EU numbering system);

[14] an IgG2 constant region in which the amino acids at positions 276 (397 in the EU numbering system), 14 (131 in the EU numbering system), 16 (133 in the EU numbering system), 102 (219 in the EU numbering system), 20 (137 in the EU numbering system), and 21 (138 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 have been substituted with other amino acids;

[15] the IgG2 constant region of [14], which further comprises deletions of both Gly at position 325 (446 in the EU numbering system) and Lys at position 326 (447 in the EU numbering system);

[16] an IgG2 constant region in which the Cys at position 14 (131 in the EU numbering system), Arg at position 16 (133 in the EU numbering system), Cys at position 102 (219 in the EU numbering system), Glu at position 20 (137 in the EU numbering system), Ser at position 21 (138 in the EU numbering system), His at position 147 (268 in the EU numbering system), Arg at position 234 (355 in the EU numbering system), and Gln at position 298 (419 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 have been substituted with other amino acids;

[17] the IgG2 constant region of [16], which further comprises deletions of both Gly at position 325 (446 in the EU numbering system) and Lys at position 326 (447 in the EU numbering

system);

[18] an IgG2 constant region in which the Cys at position 14 (131 in the EU numbering system), Arg at position 16 (133 in the EU numbering system), Cys at position 102 (219 in the EU numbering system), Glu at position 20 (137 in the EU numbering system), Ser at position 21 (138 in the EU numbering system), His at position 147 (268 in the EU numbering system), Arg at position 234 (355 in the EU numbering system), Gln at position 298 (419 in the EU numbering system), and Asn at position 313 (434 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 have been substituted with other amino acids;

[19] the IgG2 constant region of [18], which further comprises deletions of both Gly at position 325 (446 in the EU numbering system) and Lys at position 326 (447 in the EU numbering system);

[20] an IgG4 constant region in which the amino acid at position 289 (409 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 21 has been substituted with another amino acid;

[21] an IgG4 constant region in which the amino acids at position 289 (409 in the EU numbering system), positions 14, 16, 20, 21, 97, 100, 102, 103, 104, and 105 (131, 133, 137, 138, 214, 217, 219, 220, 221, and 222 in the EU numbering system, respectively), and positions 113, 114, and 115 (233, 234, and 235 in the EU numbering system, respectively), have been substituted with other amino acids, and the amino acid at position 116 (236 in the EU numbering system) has been deleted from the amino acid sequence of SEQ ID NO: 21;

[22] the IgG4 constant region of [21], which further comprises deletions of both Gly at position 326 (446 in the EU numbering system) and Lys at position 327 (447 in the EU numbering system);

[23] an IgG2 constant region in which Ala at position 209 (330 in the EU numbering system), Pro at position 210 (331 in the EU numbering system), Thr at position 218 (339 in the EU numbering system), Cys at position 14 (131 in the EU numbering system), Arg at position 16 (133 in the EU numbering system), Cys at position 102 (219 in the EU numbering system), Glu at position 20 (137 in the EU numbering system), and Ser at position 21 (138 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 have been substituted with other amino acids;

[24] the IgG2 constant region of [23], which further comprises deletions of both Gly at position 325 (446 in the EU numbering system) and Lys at position 326 (447 in the EU numbering system);

[25] an IgG2 constant region in which Cys at position 14 (131 in the EU numbering system), Arg at position 16 (133 in the EU numbering system), Cys at position 102 (219 in the EU numbering system), Glu at position 20 (137 in the EU numbering system), and Ser at position 21 (138 in the

EU numbering system) in the amino acid sequence of SEQ ID NO: 20 have been substituted with other amino acids;

[26] the IgG2 constant region of [25], which further comprises deletions of both Gly at position 325 (446 in the EU numbering system) and Lys at position 326 (447 in the EU numbering system);

[27] a constant region comprising the amino acid sequence of SEQ ID NO: 24;

[28] a constant region comprising the amino acid sequence of SEQ ID NO: 118;

[29] a constant region comprising the amino acid sequence of SEQ ID NO: 25;

[30] a constant region comprising the amino acid sequence of SEQ ID NO: 151;

[31] a constant region comprising the amino acid sequence of SEQ ID NO: 152;

[32] a constant region comprising the amino acid sequence of SEQ ID NO: 153;

[33] a constant region comprising the amino acid sequence of SEQ ID NO: 164;

[34] a human antibody constant region comprising the amino acid sequence of SEQ ID NO: 194 (M40ΔGK);

[35] a human antibody constant region comprising the amino acid sequence of SEQ ID NO: 192 (M86ΔGK);

[36] an antibody comprising the constant region of any one of [6] to [35];

[37] the antibody of [36], which binds to an IL-6 receptor;

[38] an anti-IL-6 receptor antibody whose binding activity to an IL-6 receptor is 1 nM or less;

[39] an anti-IL-6 receptor antibody, wherein the measured isoelectric point of the full-length antibody is 7.0 or lower or the theoretical isoelectric point of the variable region is 5.0 or lower;

[40] an anti-IL-6 receptor antibody, wherein the increase in the ratio of antibody aggregate after one month at 25°C in a buffer containing 20 mM Histidine-HCl and 150 mM NaCl at pH 6.5 to 7.0 is 0.3% or less when the concentration of the antibody is 100 mg/ml; and

[41] a pharmaceutical composition comprising the antibody of any one of [36] to [40].

Brief Description of the Drawings

Fig. 1 is a graph showing the BaF/gp130-neutralizing activities of WT and RD_6.

Fig. 2 is a graph showing a sensorgram for the interaction between rhIL-s6R (R&D systems) and WT.

Fig. 3 is a graph showing a sensorgram for the interaction between rhIL-s6R (R&D systems) and RD_6.

Fig. 4-1 is a diagram showing a list of CDR mutations that improve the affinity or neutralizing activity in comparison with WT.

Fig. 4-2 is the continuation of Fig. 4-1.

Fig. 5 is a diagram showing a list of CDR mutations that in combination improve the

affinity or neutralizing activity.

Fig. 6 is a graph showing the BaF/gp130-neutralizing activities of WT and RDC23.

Fig. 7 is a graph showing a sensorgram for the interaction between rhIL-s6R (R&D systems) and RDC23.

Fig. 8 is a graph showing a sensorgram for the interaction between rhsIL-6R and WT.

Fig. 9 is a graph showing a sensorgram for the interaction between rhsIL-6R and RDC23.

Fig. 10 is a graph showing a sensorgram for the interaction between SR344 and WT.

Fig. 11 is a graph showing a sensorgram for the interaction between SR344 and RDC23.

Fig. 12 is a graph showing the BaF/gp130-neutralizing activities of WT and H53L28.

Fig. 13 is a graph showing a sensorgram for the interaction between SR344 and H53/L28.

Fig. 14 is a graph showing transitions in the plasma concentrations of WT and H53/L28 after intravenous administration to mice.

Fig. 15 is a graph showing transitions in the plasma concentrations of WT and H53/L28 after subcutaneous administration to mice.

Fig. 16 is a graph showing the BaF/gp130-neutralizing activities of WT and PF1.

Fig. 17 is a graph showing a sensorgram for the interaction between SR344 and PF1.

Fig. 18 is a graph showing the result of testing the stability of WT and PF1 at high concentrations.

Fig. 19 is a graph showing transitions in the plasma concentrations of WT and PF1 after intravenous administration to human IL-6 receptor transgenic mice.

Fig. 20 is a graph showing transitions in the plasma concentrations of free human soluble IL-6 receptor after intravenous administration of WT or PF1 to human IL-6 receptor transgenic mice.

Fig. 21 is a graph showing the result of using gel filtration chromatography to analyze the content of aggregates in WT-IgG1, WT-IgG2, WT-IgG4, IgG2-M397V, and IgG4-R409K purified by hydrochloric acid elution.

Fig. 22 is a diagram showing the result of cation exchange chromatography (IEC) analysis of WT-IgG1, WT-IgG2, and WT-IgG4.

Fig. 23 is a diagram showing predicted disulfide bonding in the hinge region of WT-IgG2.

Fig. 24 is a diagram showing predicted disulfide bonding in the hinge region of WT-IgG2-SKSC.

Fig. 25 is a diagram showing the result of cation exchange chromatography (IEC) analysis of WT-IgG2 and IgG2-SKSC.

Fig. 26 is a diagram showing the result of cation exchange chromatography (IEC) analysis of humanized PM-1 antibody, heavy chain C-terminal ΔK antibody, and heavy chain C-terminal ΔGK antibody.

Fig. 27 shows comparison of the amounts WT-IgG1, WT-IgG2, WT-IgG4, WT-M14ΔGK, WT-M17ΔGK, and WT-M11ΔGK bound to FcγRI.

Fig. 28 is a graph showing comparison of the amounts WT-IgG1, WT-IgG2, WT-IgG4, WT-M14ΔGK, WT-M17ΔGK, and WT-M11ΔGK bound to FcγRIIa.

Fig. 29 is a graph showing comparison of the amounts WT-IgG1, WT-IgG2, WT-IgG4, WT-M14ΔGK, WT-M17ΔGK, and WT-M11ΔGK bound to FcγRIIb.

Fig. 30 is a graph showing comparison of the amounts WT-IgG1, WT-IgG2, WT-IgG4, WT-M14ΔGK, WT-M17ΔGK, and WT-M11ΔGK bound to FcγRIIIa (Val).

Fig. 31 is a graph showing the increase of aggregation in a stability test for WT-IgG1, WT-M14ΔGK, WT-M17ΔGK, and WT-M11ΔGK at high concentrations.

Fig. 32 is a graph showing the increase of Fab fragments in a stability test for WT-IgG1, WT-M14ΔGK, WT-M17ΔGK, and WT-M11ΔGK at high concentrations.

Fig. 33 is a diagram showing the result of cation exchange chromatography (IEC) analysis of WT-IgG2, WT-M14ΔGK, and WT-M31ΔGK.

Fig. 34 is a graph showing the BaF/gp130-neutralizing activities of WT and F2H/L39-IgG1.

Fig. 35 is a graph showing the plasma concentration time courses of antibodies after subcutaneous administration of WT, PF1, or F2H/L39-IgG1 at 1.0 mg/kg to cynomolgus monkeys.

Fig. 36 is a graph showing the time courses of CRP concentration in the groups of cynomolgus monkeys administered with WT or F2H/L39-IgG1.

Fig. 37 is a graph showing the time courses of free cynomolgus monkey IL-6 receptor concentration in the groups of cynomolgus monkeys administered with WT or F2H/L39-IgG1.

Fig. 38 is a graph showing the time courses of plasma concentrations of WT-IgG1 and WT-M14 after intravenous administration to human FcRn transgenic mice.

Fig. 39 is a graph showing the time courses of plasma concentrations of WT-IgG1, WT-M14, and WT-M58 after intravenous administration to human FcRn transgenic mice.

Fig. 40 is a graph showing the time courses of plasma concentrations of WT-IgG1, WT-M44, WT-M58, and WT-M73 after intravenous administration to human FcRn transgenic mice.

Fig. 41 is a diagram showing a cation exchange chromatography-based assessment of the effect on heterogeneity by the constant region of anti IL-6 receptor antibodies WT and F2H/L39, anti-IL-31 receptor antibody H0L0, and anti-RANKL antibody DNS.

Fig. 42 is a diagram showing a cation exchange chromatography-based assessment of the effect on heterogeneity by the CH1 domain cysteine of anti IL-6 receptor antibodies WT and F2H/L39.

Fig. 43 is a diagram showing a DSC-based assessment of the effect on denaturation peak by the CH1 domain cysteine of anti IL-6 receptor antibody WT.

Fig. 44 is a graph showing the activities of TOCILIZUMAB, the control, and Fv5-M83 to neutralize BaF/g130.

Fig. 45 is a graph showing the activities of TOCILIZUMAB, Fv3-M73, and Fv4-M73 to neutralize BaF/gp130.

Fig. 46 is a graph showing the plasma concentration time courses of TOCILIZUMAB, the control, Fv3-M73, Fv4-M73, and Fv5-M83 in cynomolgus monkeys after intravenous administration.

Fig. 47 is a graph showing the time courses of CRP concentration in cynomolgus monkeys after intravenous administration of TOCILIZUMAB, the control, Fv3-M73, Fv4-M73, or Fv5-M83.

Fig. 48 is a graph showing the time courses of percentage of soluble IL-6 receptor neutralization in cynomolgus monkeys after intravenous administration of TOCILIZUMAB, the control, Fv3-M73, Fv4-M73, or Fv5-M83.

Fig. 49 is a chart obtained by DSC measurement of the Hspu2.2Lspu2.2 (Hu2.2Lu2.2) antibody.

Fig. 50 is an electrophoretic image of the H0L0 and Hspu2.2Lspu2.2 (Hu2.2Lu2.2) antibodies by high-pI isoelectric focusing.

Fig. 51 is an electrophoretic image of the H0L0 and Hspd1.8Lspd1.6 (Hd1.8Ld1.6) antibodies by low-pI isoelectric focusing.

Fig. 52 is a graph showing the glypican 3 (antigen)-binding activities of the H15L4 and H0L0 antibodies determined by competitive ELISA.

Fig. 53 is a graph showing the glypican 3 (antigen)-binding activities of the Hspu2.2Lspu2.2 (Hu2.2Lu2.2) and H0L0 antibodies determined by competitive ELISA.

Fig. 54 is a graph showing the glypican 3 (antigen)-binding activities of the Hspd1.8Lspd1.6 (Hd1.8Ld1.6) and H0L0 antibodies determined by competitive ELISA.

Fig. 55 shows the antitumor effects of the H0L0, Hspu2.2Lspu2.2 (Hu2.2Lu2.2), and Hspd1.8Lspd1.6 (Hd1.8Ld1.6) antibodies in the human hepatocarcinoma-grafted mouse model.

Fig. 56 shows the plasma concentrations of the H0L0, Hspu2.2Lspu2.2 (Hu2.2Lu2.2), and Hspd1.8Lspd1.6 (Hd1.8Ld1.6) antibodies in the human hepatocarcinoma-grafted model mice.

Fig. 57 shows ADCC of each test antibody against cells of the human hepatocarcinoma

line Hep G2.

Fig. 58 is a graph showing the IL-6 receptor-neutralizing activities of 6R_b_H1L1, 6R_b_H2L2, 6R_b_H2L3, and 6R_b_H2L4 in BaF/6R.

Fig. 59 is a graph showing the glypican 3 (antigen)-binding activities of the GPC_H1L1 and GPC_H2L2 antibodies determined by competitive ELISA.

Fig. 60 is a graph showing the glypican 3 (antigen)-binding activities of the GPC_H2L2 and GPC_H3L3 antibodies determined by competitive ELISA.

Fig. 61 is a diagram showing peak separation for A chain-B chain heterodimer, A chain homodimer, and B chain homodimer in cation exchange chromatography of 6R_a_H1H3L3, GPC3_H2H3L3, and 31R_H1aH2aL2.

Mode for Carrying Out the Invention

The present invention provides methods for modifying the isoelectric point of a polypeptide comprising an antibody variable region while retaining the antigen-binding activity of the variable region, which comprise modifying the charge of at least one exposable amino acid residue on the polypeptide's CDR surface. The present invention also provides polypeptides comprising an antibody variable region with a modified isoelectric point obtained by the above methods; for example, antibodies that comprise a human-derived framework region (FR), human constant region, and CDR selected from the group consisting of human-derived CDRs, nonhuman animal-derived CDRs, and synthetic CDRs, in which at least one exposable amino acid residue on the CDR surface is an amino acid residue having a different charge from that of the amino acid residue at the corresponding position in the wild-type CDR, and have a modified isoelectric point compared to before modification while retaining their antigen-binding activity.

In a preferred embodiment, the methods of the present invention comprise modifying the charge of at least one exposable amino acid residue on the antibody surface. Specifically, the pharmacokinetics of an antibody in plasma (pharmacokinetics in blood) can be controlled by modifying the charges of amino acid residues in the antibody to change the antibody's isoelectric point. As a result of modification, for example, the antibody with controlled pharmacokinetics in plasma can exert superior antitumor activity against cancer cells than the original antibody.

In the methods of the present invention, "retaining the antigen-binding activity" means having at least 80% or more, preferably 85% or more, and more preferably 90% or more of the binding activity of the peptide before modification. As long as sufficient binding activity for binding to the antigen can be retained for the antibody to exert its function, the affinity determined at 37°C under physiological conditions may be, for example, 100 nM or less, preferably 50 nM or less, more preferably 10 nM or less, and still more preferably 1 nM or less.

Whether a polypeptide comprising an antibody variable region with a modified isoelectric point obtained by the methods of the present invention retains the antigen-binding activity can be tested by known methods such as Biacore (intermolecular interaction analysis), cell proliferation assay, ELISA (enzyme-linked immunosorbent assay), EIA (enzyme immunoassay), RIA (radioimmunoassay), and fluorescence immunoassay.

"Polypeptides of the present invention comprising an antibody variable region" include, but are not limited to, for example, antibodies, minibodies (low molecular weight antibodies), and scaffold proteins.

In the present invention, any scaffold protein is acceptable as long as it is a peptide that has a stable three-dimensional structure and is capable of binding to at least an antigen. Such peptides include, for example, fragments of antibody variable regions, fibronectin, protein A domain, LDL receptor A domain, lipocalin, and other molecules described in Nygren *et al.* (Current Opinion in Structural Biology, (1997) 7:463-469; Journal of Immunol Methods, (2004) 290:3-28), Binz *et al.* (Nature Biotech. (2005) 23:1257-1266), and Hosse *et al.* (Protein Science, (2006) 15:14-27).

Herein, the term "antibody" is used in the broadest sense, and includes monoclonal antibodies, polyclonal antibodies, and mutant antibodies (such as chimeric antibodies, humanized antibodies, minibodies (including antibody fragments), and multispecific antibodies) as long as they display a desired biological activity. In the present invention, the methods of antibody modification of the present invention can be used favorably on these antibodies when they are obtained (produced).

The "antibodies" of the present invention include antibodies in which the charge of amino acid residues has been modified as described above, and whose amino acid sequences have been further modified by amino acid substitutions, deletions, additions, and/or insertions. The "antibodies" also include antibodies whose amino acid sequences have been modified by amino acid substitutions, deletions, additions, and/or insertions, or chimerization, humanization, or such, and in which the charge of amino acid residues has been further modified. Modifications may be performed at the same time when mouse antibodies are humanized, or further modifications may be performed on humanized antibodies.

Amino acid sequence modifications, such as amino acid substitutions, deletions, additions, and/or insertions, and humanization and chimerization, can be achieved by methods known to those skilled in the art. When the antibodies of the present invention are prepared as recombinant antibodies, likewise, the amino acid sequences of the antibody variable and constant regions may also be modified by amino acid substitutions, deletions, additions, and/or insertions, or chimerization, humanization and the like.

The antibodies of the present invention may be derived from any animal, such as a

mouse, human, rat, rabbit, goat, or camel. Furthermore, the antibodies may be modified, for example, chimeric antibodies, and in particular, modified antibodies that include amino acid substitutions in their sequence, such as humanized antibodies. The antibodies may be any kind of antibody, such as antibody modification products linked with various molecules, antibody fragments, and minibodies.

"Chimeric antibodies" are antibodies prepared by combining sequences derived from different animals. An example is an antibody having heavy and light chain variable (V) regions from a mouse antibody and heavy and light chain constant (C) regions from a human antibody. Chimeric antibodies can be prepared by known methods. To obtain such chimeric antibodies, for example, a DNA encoding an antibody variable region may be ligated with a DNA encoding a human antibody constant region; the resulting ligation product is inserted into an expression vector; and the construct is introduced into a host to produce the chimeric antibody.

The minibodies of the present invention are not particularly limited by their structure nor their method of production, so long as they have antigen-binding activity. Some minibodies have an activity greater than that of a whole antibody (Orita *et al.*, Blood, (2005) 105:562-566). Herein, the "minibodies" are not particularly limited, so long as they are a portion of a whole antibody (for example, whole IgG). However, the minibodies preferably include a heavy chain variable region (VH) or a light chain variable region (VL). Examples of preferred antibody fragments are Fab, $F(ab')_2$, Fab', and Fv. The amino acid sequence of a heavy chain variable region or light chain variable region in an antibody fragment may be modified by substitutions, deletions, additions, and/or insertions. Furthermore, some portions of a heavy chain variable region and light chain variable region may be deleted, so long as the resulting fragments retain their antigen-binding ability. For example, of the antibody fragments described above, "Fv" is a minimal antibody fragment composed of the complete antigen-recognition and binding sites. "Fv" is a dimer (VH-VL dimer) composed of one unit of heavy chain variable region and one unit of light chain variable region bound very strongly by non-covalent bonding. An antigen-binding site is formed on the surface of the VH-VL dimer by the three CDRs of each variable region. Six CDRs confer an antigen-binding site to the antibody. However, even one variable region (or half of an Fv composed of only three antigen-specific CDRs) has the ability to recognize and bind to an antigen, although its affinity is lower than that of the complete binding site. Thus, molecules smaller than Fv are also included in the context of minibodies of the present invention. The variable regions of a minibody may also be chimerized or humanized.

The minibodies preferably include both a heavy chain variable region and a light chain variable region. Examples of suitable minibodies include antibody fragments such as Fab, Fab', F(ab')2, and Fv, and scFv (single-chain Fv), which can be prepared using antibody fragments

(Huston *et al.*, Proc. Natl. Acad. Sci. USA (1988) 85:5879-83; Pluckthun "The Pharmacology of Monoclonal Antibodies" Vol. 113, Resenburg and Moore (eds.), Springer Verlag, New York, pp. 269-315, (1994)), diabodies (Holliger *et al.*, Proc. Natl. Acad. Sci. USA (1993) 90:6444-8; EP 404097; WO93/11161; Johnson *et al.*, Method in Enzymology (1991) 203:88-98; Holliger *et al.*, Protein Engineering (1996) 9:299-305; Perisic *et al.*, Structure (1994) 2:1217-26; John *et al.*, Protein Engineering (1999) 12(7):597-604; Atwell *et al.*, Mol. Immunol. (1996) 33:1301-12), sc(Fv)2 (Hudson *et al.*, J Immunol. Methods (1999) 231:177-89; Orita *et al.*, Blood (2005) 105:562-566), triabodies (Journal of Immunological Methods (1999) 231:177-89), and tandem diabodies (Cancer Research (2000) 60:4336-41).

An antibody fragment can be prepared by treating an antibody with an enzyme, for example, a protease such as papain or pepsin (see Morimoto *et al.*, J. Biochem. Biophys. Methods (1992) 24:107-17; Brennan *et al.*, Science (1985) 229:81). Alternatively, antibody fragments can also be produced by genetic recombination based on its amino acid sequence.

A minibody having a structure that results from modification of an antibody fragment can be prepared using antibody fragments obtained by enzyme treatment or genetic recombination. Alternatively, after constructing a gene which encodes a whole minibody, and introducing the construct into an expression vector, the minibody may be expressed in appropriate host cells (see, for example, Co *et al.*, J. Immunol. (1994) 152:2968-76; Better and Horwitz, Methods Enzymol. (1989) 178:476-96; Pluckthun and Skerra, Methods Enzymol. (1989) 178:497-515; Lamoyi, Methods Enzymol. (1986) 121:652-63; Rousseaux *et al.*, Methods Enzymol. (1986) 121:663-9; Bird and Walker, Trends Biotechnol. (1991) 9:132-7).

The above described "scFVs" are single-chain polypeptides that include two variable regions linked together *via* a linker or such, as required. The two variable regions in an scFv are typically one heavy chain variable region and one light chain variable region, but an scFv may include two heavy chain variable regions or two light chain variable regions. In general, scFv polypeptides include a linker between the heavy chain variable region and light chain variable region, thereby forming a paired portion of heavy chain variable region and light chain variable region required for antigen binding. A peptide linker composed of ten or more amino acids is typically used as the linker between heavy chain variable region and light chain variable region when forming an intramolecular paired portion between heavy chain variable region and light chain variable region. However, the linkers of the scFv of the present invention are not limited to such peptide linkers, so long as they do not inhibit the formation of an scFv. To review scFv, see Pluckthun "The Pharmacology of Monoclonal Antibody", Vol. 113 (Rosenburg and Moore ed., Springer Verlag, NY, pp.269-315 (1994)).

The term "diabodies (Db)" refers to bivalent antibody fragments constructed by gene fusion (P. Holliger *et al.*, Proc. Natl. Acad. Sci. USA 90: 6444-6448 (1993); EP 404,097;

WO93/11161 and such). Diabodies are dimers composed of two polypeptide chains, wherein each polypeptide chain includes within the same chain a light chain variable region and a heavy chain variable region connected with a linker short enough to disable interaction of these two regions, for example a linker of about five amino acid residues. Light chain variable region and heavy chain variable region encoded on the same polypeptide chain will form a dimer because the linker between light chain variable region and heavy chain variable region is too short to form a single chain variable region fragment. Therefore, the resulting diabody has two antigen-binding sites. Herein, when light chain variable region and heavy chain variable region directed against two different epitopes (a and b) are expressed simultaneously as combinations of VLa-VHb and VLb-VHa connected with a linker of about five residues, they are secreted as bispecific Db.

Since diabodies include two molecules of scFvs, they thus composed of four variable regions, and as a result have two antigen-binding sites. When the objective is to form a diabody, unlike as in the case with scFvs that do not form dimers, ordinarily, linkers forming a connection between heavy chain variable region and light chain variable region in each scFv molecules are linkers of about five amino acids when used as peptide linkers. However, scFv linkers for diabody formation are not limited to such peptide linkers so long as they do not interfere with scFv expression and diabody formation.

Of the several antibody isotypes, IgG antibody has a significantly larger molecular weight, and its major metabolic pathway is not renal excretion. IgG antibody, which comprises an Fc domain as part of the molecule, is known to be recycled through a salvage pathway *via* fetal Fc receptor (FcRn) expressed in endothelial cells of blood vessels or such, and thus has a longer *in vivo* half-life. IgG antibody is thought to be mainly metabolized *via* a metabolic pathway in endothelial cells (He XY, Xu Z, Melrose J, Mullowney A, Vasquez M, Queen C, Vexler V, Klingbeil C, Co MS, Berg EL. Humanization and pharmacokinetics of a monoclonal antibody with specificity for both E- and P-selectin. J Immunol. (1998) 160 (2):1029-35). Specifically, it is thought that when nonspecifically incorporated into endothelial cells, IgG antibody is recycled *via* binding to FcRn while free IgG antibody is metabolized. The plasma half-life of IgG antibody is shortened when its Fc domain has been modified to reduce its FcRn-binding activity. In contrast, the plasma half-life of IgG antibody can be prolonged by modifying amino acid residues that constitute the Fc domain to increase the FcRn-binding activity (J Immunol. (1998) 160 (2):1029-35). As described above, conventional methods for controlling the plasma pharmacokinetics of IgG antibody are based on modifying the FcRn-binding activity through modification of amino acid residues that constitute the Fc domain. However, as described in the Examples below, the present invention revealed that the plasma half-life of an antibody depends on its isoelectric point with a high correlation. Specifically, the

present invention demonstrated that the plasma half-life of antibody could be controlled without modifying the amino acid sequence that constitutes the Fc, whose modification potentially results in acquisition of immunogenicity.

Without intending to adhere to a particular theory, the present inventors currently believe the following theory. The rate of non-specific IgG antibody uptake by endothelial cells is thought to depend on the physicochemical Coulomb interaction between IgG antibody and the negatively charged cell surface. Thus, a decrease (increase) of the isoelectric point of IgG antibody reduces (enhances) the Coulomb interaction, which decreases (increases) the non-specific uptake by endothelial cells, and as a result, the metabolism in endothelial cells is reduced (enhanced). This enables to control the pharmacokinetics in plasma. Since the Coulomb interaction between endothelial cells and the negative charge on cell surface is a physicochemical interaction, it is thought that the interaction does not exclusively depend on the amino acid sequence that constitutes the antibody. Thus, the methods of the present invention for controlling the pharmacokinetics in plasma are applicable not only to specific antibodies but also to any polypeptides comprising an antibody variable region. Preferred peptides include peptides with a molecular weight of 50,000 or more, more preferably 100,000 or more, and still more preferably 140,000 or more. Since the major metabolic pathway of such peptides is not renal excretion, it is amply possible to attain the effect of controlling plasma pharmacokinetics in the present invention. Herein, the impairment (enhancement) of the Coulomb interaction means a increase (decrease) in the Coulomb force, which is a repulsive force.

The polypeptides of the present invention comprising the FcRn-binding domain are not limited to IgG antibodies. The polypeptides may be any proteins as long as they can bind to (have the binding activity or affinity to) Fc receptor (FcRn). Preferably, the polypeptides of the present invention comprising the FcRn-binding domain are proteins comprising an antibody Fc domain or an Fc-like domain, but are not limited thereto. The Fc domain may be a modified Fc domain, for example, an Fc domain described in J Immunol. (1998) 160 (2):1029-35 cited above. The polypeptides of the present invention comprising the FcRn-binding domain include, for example, IgG antibodies. Furthermore, modified forms of the antibodies (proteins) are also included in the polypeptides of the present invention comprising an FcRn-binding domain, as long as they can bind to FcRn. The most preferred polypeptides of the present invention comprising an FcRn-binding domain include, for example, IgG antibodies.

When an IgG antibody is used as the antibody of the present invention, it may be of any subtype as long as it is an antibody molecule of the IgG type. The antibody may be a multispecific (for example, bispecific) IgG antibody. Such a bispecific antibody is an antibody that has specificities to two types of different epitopes, and includes antibodies that recognize different antigens and those recognize different epitopes in a single antigen. When antibody

molecules are minibodies such as scFv and Fab whose major metabolic pathway is renal excretion, their pharmacokinetics in plasma cannot be regulated by controlling the isoelectric points as described above. However, the present invention is applicable to any kinds of antibody molecules as long as they are polypeptides comprising an antibody variable region whose major metabolic pathway is not renal excretion. Such polypeptides include, for example, scFv-Fc, dAb-Fc, and Fc fusion proteins. Since the major metabolic pathway of these molecules is not renal excretion, their pharmacokinetics in plasma can be controlled by modifying isoelectric point using the methods of the present invention. Antibody molecules to which the present invention is applicable also include antibody-like molecules. "Antibody-like molecules" refers to molecules that function *via* binding to their target molecules (Binz HK, Amstutz P, Pluckthun A. Engineering novel binding proteins from nonimmunoglobulin domains. Nat Biotechnol. 2005 Oct;23(10):1257-68), and include, for example, DARPins, affibodies, and avimers.

When an antibody of the present invention is, for example, a bispecific anti-glypican 3 antibody, it can bind specifically not only to glypican 3 but also to an epitope of an antigen other than glypican 3. Such non-glypican 3 antigens preferably include, for example, surface antigens that allow for specific binding to NK cells, cytotoxic T cells, LAK cells, and other cells to recruit these cells. It was reported that in the presence of a bispecific antibody prepared from antibody MUSE11 which recognizes an adenocarcinoma-related antigen MUC1 and antibody OKT3 which recognizes a LAK cell surface antigen, LAK cells exerted cytotoxic activity against bile duct carcinoma (Katayose Y, Kudo T, Suzuki M, Shinoda M, Saijyo S, Sakurai N, Saeki H, Fukuhara K, Imai K, Matsuno S. MUC1-specific targeting immunotherapy with bispecific antibodies: inhibition of xenografted human bile duct carcinoma growth. Cancer Res. (1996) 56(18):4205-12). Glypican 3 antibodies with improved plasma pharmacokinetics, which are provided by the present invention, can be preferably used instead of the MUSE11 antibody which recognizes MUC1. Furthermore, bispecific glypican 3 antibodies that recognize different epitopes on a glypican 3 molecule can also be used as preferred antibodies of the present invention.

The above-mentioned "bispecific antibody" may be, for example, an antibody having a structure in which a heavy chain variable region and a light chain variable region are linked in a single chain (for example, sc(Fv)2). The bispecific antibody may also be an antibody-like molecule (for example, scFv-Fc) produced by fusing an scFv (or sc(Fv)2), in which a heavy chain variable region and a light chain variable region are linked, to an Fc domain (a constant region lacking the CH1 domain). A multispecific antibody consisting of scFv-Fc has an (scFv)2-Fc type structure with VH1-linker-VL1-Fc as the first polypeptide and VH2-linker-VL2-Fc as the second polypeptide. Alternatively, the bispecific antibody may be

an antibody-like molecule in which a single domain antibody is linked with an Fc domain (Curr. Opin. Drug Discov. Devel. (2006) 9(2):184-93).

In the present invention, the charge of amino acid residues can be modified through amino acid substitution. Amino acid substitution can be achieved by the methods described below.

In order to retain antigen-binding activity, as the target of substitution in the present invention, the exposable amino acid residue on the surface of the CDR region is preferably at least one amino acid residue selected from amino acid residues at positions 31, 61, 62, 64, and 65 in the heavy chain variable region and at positions 24, 27, 53, 54, and 55, Kabat's numbering, in the light chain variable region. Such amino acid substitutions are advantageous in that the original function (antigen-binding activity or such) of the polypeptides comprising an antibody variable region before amino acid substitution is retained and that the substitutions can be achieved regardless of antibody specificity.

Furthermore, the present invention provides methods for controlling pharmacokinetics of polypeptides comprising an antibody variable region by modifying their isoelectric points. Polypeptides comprising an antibody variable region with controlled pharmacokinetics obtained by such methods are also included in the present invention.

Herein, "controlled plasma pharmacokinetics" means that when the antibody pharmacokinetics in plasma is compared before and after modification of amino acids constituting an antibody, the pharmacokinetics in plasma has been changed in a desired direction. Specifically, when one desires to prolong the half-life (in plasma) of an antibody as a drug, "controlled plasma pharmacokinetics" means prolongation of the antibody half-life in plasma. Alternatively, when one desires to shorten the antibody half-life in plasma, "controlled plasma pharmacokinetics" means shortening of the antibody half-life in plasma.

In the present invention, whether the antibody pharmacokinetics in plasma has been changed in a desired direction, that is, whether the pharmacokinetics in plasma has been controlled as intended can be appropriately assessed by kinetic tests using, for example, mice, rats, rabbits, dogs, monkeys, or others. In the present invention, "prolongation of the half-life in plasma" or "shortening of the half-life in plasma" can also be assessed using instead of half-life in plasma (t1/2), any one of the parameters: mean retention time in plasma, clearance (CL) in plasma, area under the concentration curve (AUC), and half-life in plasma (Pharmacokinetics: Enshuniyoru Rikai (Understanding through practice). Nanzando). The "controlled plasma kinetics" achieved according the present invention can be appropriately assessed using the parameters, for example, by carrying out noncompartmental analysis according to the protocol appended to the *in vivo* kinetics analysis software WinNonlin (Pharsight).

The antibody function can be sustained by controlling the pharmacokinetics in plasma. For example, the methods of the present invention can be applied to sustain the function of antibodies having cytotoxicity, and regulate the duration of the functions that the polypeptides have before modification, such as cytotoxic effect, antagonistic activity, and agonistic activity.

Herein, "exposable amino acid residue on the surface" typically refers to an amino acid residue located on the surface of a polypeptide constituting an antibody. "Amino acid residue located on the surface of a polypeptide" refers to an amino acid residue whose side chain can be in contact with solvent molecules (which are in general water molecules). However, the whole side chain is not necessarily in contact with solvent molecules. When at least a portion of the side chain is in contact with solvent molecules, the amino acid residue is defined as an "amino acid located on the surface". Those skilled in the art can prepare a homology model for a polypeptide or antibody by homology modeling or such using commercially available softwares. Based on the homology model, amino acid residues on the surface of a polypeptide that constitutes an appropriate antibody can be selected as "amino acid residues on the polypeptide surface".

Herein, the "exposable amino acid residues on the surface" are not particularly limited; however, the amino acid residues are preferably located in an antibody domain other than the FcRn-binding domain. Such preferred FcRn-binding domain includes, for example, Fc domain.

In the present invention, amino acid residues whose charge is to be modified are preferably amino acid residues that constitute an antibody heavy or light chain variable region. Specifically, the variable region preferably includes CDR and FR.

Those skilled in the art can suitably select surface amino acid residues in the antibody variable region using homology models produced by homology modeling and such. For example, surface amino acid residues in the antibody variable region are preferably selected from amino acid residues of heavy chain variable regions H1, H3, H5, H8, H10, H12, H13, H15, H16, H19, H23, H25, H26, H31, H39, H42, H43, H44, H46, H61, H62, H64, H65, H68, H71, H72, H73, H75, H76, H81, H82b, H83, H85, H86, H105, H108, H110, and H112, Kabat's numbering. For example, in the heavy chain FR region of the humanized glypican 3 antibody of SEQ ID NO: 195, examples of surface amino acids are amino acid residues at positions 1, 3, 5, 8, 10, 12, 13, 15, 16, 19, 23, 25, 26, 39, 42, 43, 44, 46, 69, 72, 73, 74, 76, 77, 82, 85, 87, 89, 90, 107, 110, 112, and 114, without being limited thereto. For the heavy chain CDR region, surface amino acids can be selected using similar homology models. Specifically, the amino acid residue H97, Kabat's numbering, is exposed on the surface of most antibodies, and for example, Ser at position 101 in the heavy chain CDR of the humanized glypican 3 antibody of SEQ ID NO: 195 corresponds to that amino acid residue. Other amino acid residues in the heavy chain CDR of the humanized glypican 3 antibody of SEQ ID NO: 195 preferably include

amino acid residues at positions 52, 54, 62, 63, 65, and 66.

In the light chain variable region, surface amino acid residues in the antibody variable region are preferably selected from amino acid residues L1, L3, L7, L8, L9, L11, L12, L16, L17, L18, L20, L22, L24, L27, L38, L39, L41, L42, L43, L45, L46, L49, L53, L54, L55, L57, L60, L63, L65, L66, L68, L69, L70, L74, L76, L77, L79, L80, L81, L85, L100, L103, L105, L106, and L107, Kabat's numbering. Amino acid residues at positions 1, 3, 7, 8, 9, 11, 12, 16, 17, 18, 20, 22, 43, 44, 45, 46, 48, 49, 50, 54, 62, 65, 68, 70, 71, 73, 74, 75, 79, 81, 82, 84, 85, 86, 90, 105, 108, 110, 111, and 112 in the humanized glypican 3 antibody of SEQ ID NO: 195 are examples of surface amino acids. However, the surface amino acids of the present invention are not limited thereto. Furthermore, for the light chain CDR region, surface amino acid residues can be selected using homology models similar to those used for determining surface amino acid residues in the heavy chain CDR. Amino acid residues in light chain CDR of the humanized glypican 3 antibody of SEQ ID NO: 201 preferably include amino acid residues at positions 24, 27, 33, 55, and 59.

Specifically, in the methods of the present invention, "modification" of an amino acid residue refers to substitution of a different amino acid residue for an original amino acid residue, deletion of an original amino acid residue, addition of an extra amino acid residue, and so on. The "modification" preferably refers to substitution of a different amino acid residue for an original amino acid residue. Specifically, in the present invention, "modification of the charge of an amino acid residue" preferably refers to amino acid substitutions.

Such "modification of the charge of an amino acid residue" in a glypican 3 antibody of the present invention is preferably achieved, for example, by modifying the charge of at least one amino acid residue selected from the amino acid residues at positions 19, 43, 52, 54, 62, 63, 65, 66, and 107 in the heavy chain variable region constituting the humanized glypican 3 antibody of SEQ ID NO: 195. Alternatively, the modification is preferably achieved, for example, by modifying the charge of at least one amino acid residue selected from the amino acid residues at positions 17, 24, 27, 33, 55, 59, 79, 82, and 105 in the light chain variable region constituting the humanized glypican 3 antibody of SEQ ID NO: 201. Of the amino acid residues mentioned above, it is not necessary to modify amino acid residues other than the ones whose charge has already been modified, as long as the modification has achieved the intended effect of controlling the pharmacokinetics in plasma. However, these amino acid residues can be appropriately modified to be electrically neutral or to have the same type of charge as the modified amino acid residues.

The above-described "modification of the charge of an amino acid residue" in the CDR of an anti-human IL-6 receptor antibody (6R_a_H1L1) of the present invention is preferably achieved while retaining its antigen-binding activity, for example, by modifying at least one

amino acid residue selected from the amino acid residues at positions 31, 64, and 65, Kabat's numbering, in the heavy chain variable region constituting anti-human IL-6 receptor antibody of SEQ ID NO: 221. Alternatively, the modification is preferably achieved, for example, by modifying the charge of at least one amino acid residue selected from the amino acid residues at positions 24, 27, 53, and 55, Kabat's numbering, in the light chain variable region constituting the anti-human IL-6 receptor antibody of SEQ ID NO: 224. Among the amino acid residues mentioned above, it is not necessary to modify amino acid residues other than the ones whose charge has already been modified, as long as the modification has achieved the intended effect of controlling the pharmacokinetics in plasma. However, these amino acid residues can be appropriately modified to be electrically neutral or to have the same type of charge as the modified amino acid residues.

The above-described "modification of the charge of an amino acid residue" in the CDR of an anti-human IL-6 receptor antibody (6R_b_H1L1) of the present invention is preferably achieved while retaining the antigen-binding activity, for example, by modifying the charge of at least one amino acid residue selected from the amino acid residues in the heavy chain variable region constituting the anti-human IL-6 receptor antibody of SEQ ID NO: 227, for example, the amino acid residue at position 31, Kabat's numbering. Alternatively, the modification is preferably achieved, for example, by modifying the charge of at least one amino acid residue selected from the amino acid residues at positions 24, 53, 54, and 55, Kabat's numbering, in the light chain variable region constituting the anti-human IL-6 receptor antibody of SEQ ID NO: 229. Among the amino acid residues mentioned above, it is not necessary to modify amino acid residues other than the ones whose charge has already been modified, as long as the modification has achieved the intended effect of controlling the pharmacokinetics in plasma. However, these amino acid residues can be appropriately modified to be electrically neutral, or to have the same type of charge as the modified amino acid residues.

The above-described "modification of the charge of an amino acid residue" in the CDR of an anti-human GPC3 antibody of the present invention is preferably achieved while retaining the antigen-binding activity, for example, by modifying the charge of at least one amino acid residue selected from the amino acid residues at positions 61, 62, 64, and 65, Kabat's numbering, in the heavy chain variable region constituting the anti-human GPC3 antibody of SEQ ID NO: 233. Alternatively, the modification is preferably achieved, for example, by modifying the charge of at least one amino acid residue selected from the amino acid residues at positions 24 and 27, Kabat's numbering, in the light chain variable region constituting the anti-human GPC3 antibody of SEQ ID NO: 236. Among the amino acid residues mentioned above, it is not necessary to modify amino acid residues other than the ones whose charge has already been modified, as long as the modification has achieved the intended effect of controlling the

pharmacokinetics in plasma. However, these amino acid residues can be appropriately modified to be electrically neutral, or to have the same type of charge as the modified amino acid residues.

The above-described "modification of the charge of an amino acid residue" in the CDR of an anti-human IL-31 receptor antibody of the present invention is preferably achieved while retaining the antigen-binding activity, for example, by modifying the charge of at least one amino acid residue selected from the amino acid residues at positions 61, 62, 64, and 65, Kabat's numbering, in the heavy chain variable region constituting the anti-human IL-31 receptor antibody of SEQ ID NO: 239. Alternatively, the modification is preferably achieved, for example, by modifying the charge of at least one amino acid residue selected from the amino acid residues at positions 24 and 54, Kabat's numbering, in the light chain variable region constituting the anti-human IL-31 receptor antibody of SEQ ID NO: 242. Among the amino acid residues mentioned above, it is not necessary to modify amino acid residues other than the ones whose charge has already been modified, as long as the modification has achieved the intended effect of controlling the pharmacokinetics in plasma. However, these amino acid residues can be appropriately modified to be electrically neutral, or to have the same type of charge as the modified amino acid residues.

Amino acids are known to include charged amino acids. Generally known amino acids having positive charge (positively charged amino acids) are lysine (K), arginine (R), and histidine (H). Known amino acids having negative charge (negatively charged amino acids) include aspartic acid (D) and glutamic acid (E). Others are known to be non-charged amino acids.

Preferably, the above-described "modified amino acid residues" are appropriately selected from the amino acid residues in either of groups (a) and (b) below:

(a) glutamic acid (E) and aspartic acid (D); and

(b) lysine (K), arginine (R), and histidine (H).

However, the amino acid residues are not limited to these examples.

In a preferred embodiment, amino acid residues are substituted by non-charged amino acid residues when the original amino acid residues (before modification) already have charge. Specifically, the modification of the present invention includes: (1) substitution of a non-charged amino acid for a charged amino acid; (2) substitution of an amino acid having opposite charge for a charged amino acid; and (3) substitution of a charged amino acid for a non-charged amino acid.

In the present invention, amino acid residues constituting an antibody are preferably modified so as to change the isoelectric point of the antibody. When there are multiple amino acid residues to be modified, they may include a few non-charged amino acid residues.

Examples of preferred "modification of the charge of an amino acid residue" in a glypican 3 antibody of the present invention are described below. Modifications to increase the isoelectric point value include, for example, introduction of at least one substitution selected from Q43K, D52N, and Q107R in the heavy chain variable region constituting the humanized glypican 3 antibody of SEQ ID NO: 195. More preferably, the sequence is substituted with the amino acid sequence of SEQ ID NO: 198. Modifications to increase the isoelectric point value also include, for example, introduction of at least one substitution selected from E17Q, Q27R, and Q105R in the light chain variable region constituting the humanized glypican 3 antibody of SEQ ID NO: 201. More preferably, the sequence is substituted with the amino acid sequence of SEQ ID NO: 204. Meanwhile, modifications to decrease the isoelectric point value include, for example, introduction of at least one substitution selected from K19T, Q43E, K63S, K65Q, and G66D in the heavy chain variable region constituting the humanized glypican 3 antibody of SEQ ID NO: 195. More preferably, the sequence is substituted with the amino acid sequence of SEQ ID NO: 197. Modifications to decrease the isoelectric point value also include, for example, introduction of at least one substitution selected from Q27E, K79T, and R82S in the light chain variable region constituting the humanized glypican 3 antibody of SEQ ID NO: 201. More preferably, the sequence is substituted with the amino acid sequence of SEQ ID NO: 203.

Examples of preferred "modification of the charge of an amino acid residue" in an anti-human IL-6 receptor antibody (6R_a_H1L1) provided by the present invention include substitutions of at least one amino acid selected from the amino acid substitutions listed in Table 20.

Examples of preferred "modification of the charge of an amino acid residue" in an anti-human IL-6 receptor antibody (6R_b_H1L1) provided by the present invention include substitutions of at least one amino acid selected from the amino acid substitutions listed in Table 22.

Examples of preferred "modification of the charge of an amino acid residue" in an anti-human GPC3 antibody provided by the present invention include substitutions of at least one amino acid selected from the amino acid substitutions listed in Table 24.

Examples of preferred "modification of the charge of an amino acid residue" in an anti-human IL-31 receptor antibody provided by the present invention include substitutions of at least one amino acid selected from the amino acid substitutions listed in Table 27.

In the present invention, the number of amino acid residues to be modified is not particularly limited. For example, when modifying an antibody variable region, it is preferable to modify a sufficient but minimal number of amino acid residues for achieving controlled plasma pharmacokinetics as intended to avoid loss of the antigen-binding activity and to prevent an increase in immunogenicity. Alternatively, amino acid modifications for increasing the

antigen-binding activity may be appropriately combined with amino acid modifications to decrease immunogenicity.

The antigen-binding activity of an antibody can be determined using known methods, for example, enzyme-linked immunosorbent assay (ELISA), enzyme immunoassay (EIA), radioimmunoassay (RIA), and fluorescence immunoassay. The methods are described in a standard text, Antibodies A Laboratory Manual (Ed Harlow, David Lane, Cold Spring Harbor Laboratory, 1988).

Methods for determining the cell-binding activity of an antibody include, for example, the methods described on pages 359 to 420 in Antibodies A Laboratory Manual (Ed Harlow, David Lane, Cold Spring Harbor Laboratory, 1988). Specifically, the activity can be assessed using cells as an antigen based on the principle of Biacore, cell proliferation assay, ELISA, or FACS (fluorescence activated cell sorting). When ELISA is used, the cell-binding activity of an antibody is quantitatively assessed by comparing the levels of signals generated in the enzyme reaction. Specifically, a test antibody is added to each ELISA plate immobilized with forced expression cells, and cell-bound test antibody is detected using an enzyme-labeled antibody that recognizes the test antibody. Alternatively, when FACS is used, the cell-binding activity of antibodies can be compared by preparing a dilution series of a test antibody and determining the titer of binding to forced expression cells for each of the antibodies.

When an antigen is not immobilized on a carrier such as an ELISA plate but is expressed on the surface of cells suspended in buffer or such, the binding of an antibody to the antigen can be assayed by using FACS. Flow cytometers that are used in this assay include, for example, FACSCanto™ II, FACSAria™, FACSArray™, FACSVantage™ SE, and FACSCalibur™ (all of which are from BD Biosciences); and EPICS ALTRA HyPerSort, Cytomics FC 500, EPICS XL-MCL ADC, EPICS XL ADC, and Cell Lab Quanta / Cell Lab Quanta SC (all of which are from Beckman Coulter).

Preferred methods for determining the antigen-binding activity of an antibody include, for example, analytical methods which comprise: reacting a test antibody with cells expressing the antigen, staining the cells with an FITC-labeled secondary antibody that recognizes the test antibody, assaying the cells using FACSCalibur (BD), and then determining the fluorescence intensity using CellQuest Software (BD). When FACSCalibur is used for the measurement, after staining the cells with an FITC-labeled secondary antibody that specifically recognizes the test antibody bound to the antigen on the surface of the antigen-expressing cells in the methods described above, the binding can be assessed by comparing the geometric mean value (test Geo-Mean value) with a control Geo-Mean value obtained using a control antibody. The geometric mean values are obtained by a method that analyzes fluorescence intensity using CellQuest Software. A formula to determine the Geo-Mean values (geometric means) is

described in CellQuest Software User's Guide (BD Biosciences).

In order to not increase the *in vivo* immunogenicity in humans administered with an antibody, the amino acid sequences after modification in the present invention are preferably human sequences (sequences of a human-derived natural antibody), but are not limited thereto. Furthermore, in order to turn each of the modified FRs (FR1, FR2, FR3, and FR4) into a human sequence, mutations are preferably introduced into positions other than those that have been modified for modification of isoelectric point. The method of replacing each FR with a human sequence in this manner has been reported in a non-patent document (Ono K, Ohtomo T, Yoshida K, Yoshimura Y, Kawai S, Koishihara Y, Ozaki S, Kosaka M, Tsuchiya M. The humanized anti-HM1.24 antibody effectively kills multiple myeloma cells by human effector cell-mediated cytotoxicity. Mol. Immunol. (1999) 36(6):387-395). Furthermore, to modify the isoelectric point of an antibody, each FR can be modified into another human FR with a modified isoelectric point (for example, FR3 can be replaced with another human FR for a lower isoelectric point). Such a humanization method has been reported in a non-patent document (Dall'Acqua WF, Damschroder MM, Zhang J, Woods RM, Widjaja L, Yu J, Wu H. Antibody humanization by framework shuffling. Methods. (2005) 36(1):43-60).

Furthermore, when a polypeptide of interest with controlled pharmacokinetics in plasma cannot be produced by slight modifications to the surface charge, the desired antibody with controlled pharmacokinetics in plasma can be preferably obtained by repeating modification of surface charge and evaluation of pharmacokinetics in plasma.

In a non-patent document (J Immunol. (1998) 160(2):1029-35), chimeric EP5C7.g4, a chimeric anti-E, P-selectin antibody (IgG4), and HuEP5C7.g4, a humanized anti-E, P-selectin antibody (IgG4) were compared, and their pharmacokinetics in Rhesus monkey plasma were shown to be comparable to each other. In another non-patent document (Gobburu JV, Tenhoor C, Rogge MC, Frazier DE Jr, Thomas D, Benjamin C, Hess DM, Jusko WJ. Pharmacokinetics/dynamics of 5c8, a monoclonal antibody to CD154 (CD40 ligand) suppression of an immune response in monkeys. J Pharmacol Exp Ther. (1998) 286(2):925-30), a chimeric anti-CD154 antibody, ch5d8, and a humanized anti-CD154 antibody, Hu5c8 were compared, and their pharmacokinetics in cynomolgus monkey plasma were revealed to be comparable. Furthermore, another non-patent document (Kashmiri SV, Shu L, Padlan EA, Milenic DE, Schlom J, Hand PH., Generation, characterization, and *in vivo* studies of humanized anticarcinoma antibody CC49. Hybridoma. (1995) 14 (5):461-73) showed that a chimeric antibody cCC49 and a humanized antibody HuCC49 had comparable pharmacokinetics in mouse plasma. In addition, non-patent documents (Graves SS, Goshorn SC, Stone DM, Axworthy DB, Reno JM, Bottino B, Searle S, Henry A, Pedersen J, Rees AR, Libby RT. Molecular modeling and preclinical evaluation of the humanized NR-LU-13 antibody. Clin Cancer Res. (1999)

5(4):899-908; Couto JR, Blank EW, Peterson JA, Ceriani RL. Anti-BA46 monoclonal antibody Mc3: humanization using a novel positional consensus and *in vivo* and *in vitro* characterization. Cancer Res. (1995) 55(8):1717-22) showed that mouse and humanized antibodies exhibited the same pharmacokinetic characteristics and distribution in mouse plasma. This suggests that the pharmacokinetics and distribution in plasma of the chimeric antibody and humanized antibody are comparable because both mouse and human Fcs are cross-reactive to mouse FcRn. As seen from these examples, a chimeric antibody and a humanized antibody sharing the same CDR exhibit the same pharmacokinetic characteristics in plasma. Specifically, when an antibody is humanized by known methods such as that described in a non-patent document (Nat Biotechnol. (1997) 15(7):637-40), the pharmacokinetics of the humanized antibody in plasma is comparable to that of the chimeric antibody; thus, humanized antibodies with controlled pharmacokinetics in plasma cannot be produced by known methods.

However, with the methods of the present invention, a humanized antibody whose pharmacokinetics in plasma is controlled (specifically, whose half-life in plasma is prolonged or shortened) as compared to the chimeric antibody can be produced by modifying exposable amino acid residues on the surface of the chimeric antibody in the process of humanization to modify the isoelectric point of the antibody. Exposable amino acids on the surface of a humanized antibody may be modified to control its pharmacokinetics in plasma at the time of antibody humanization. Alternatively, the isoelectric point of a humanized antibody may further be modified by using a humanized antibody as a starting material and modifying the exposable amino acid residues on its surface.

In the present invention, the isoelectric point can be determined by isoelectric focusing, which is known to those skilled in the art. The theoretical isoelectric point can be determined using gene and amino acid sequence analysis software (GENETYX and the like). This is useful for the present invention when considerable modification of the isoelectric point is necessary, for example, for sufficient control of plasma pharmacokinetics or other purposes. It is particularly preferred when it is necessary to modify the theoretical isoelectric point by 1.0 or more, and is more preferred when the isoelectric point needs to be modified by 3.0 or more.

In a non-patent document (Adams CW, Allison DE, Flagella K, Presta L, Clarke J, Dybdal N, McKeever K, Sliwkowski MX. Humanization of a recombinant monoclonal antibody to produce a therapeutic HER dimerization inhibitor, pertuzumab. Cancer Immunol Immunother. (2006) 55(6):717-27), three kinds of humanized antibodies, trastuzumab, bevacizumab, and pertuzumab, which were produced *via* humanization using a same human antibody FR sequence, showed nearly comparable pharmacokinetics in plasma. Specifically, when produced *via* humanization using a same FR sequence, antibodies exhibit nearly comparable pharmacokinetics in plasma. In addition to the process of humanization described above, the methods of the

present invention enable to control the concentration of an antibody (in plasma) as a drug by modifying the isoelectric point of the antibody through modification of exposable amino acid residues on the surface of the antibody.

The methods of the present invention are also applicable to human antibodies. Human antibodies whose plasma pharmacokinetics is controlled (specifically, half-life in plasma is prolonged or shortened) as compared to the original human antibodies prepared in the first step can be produced by modifying their isoelectric points through modification of exposable amino acid residues on the surface of human antibodies prepared from human antibody libraries, human antibody-producing mice, or such.

The antibody half-life in plasma is prolonged when its isoelectric point value is decreased. Conversely, the antibody half-life in plasma is shortened when its isoelectric point value is increased. Higher isoelectric points are known to improve the transfer of antibodies into tissues (Vaisitti T, Deaglio S, Malavasi F. Cationization of monoclonal antibodies: another step towards the "magic bullet"?, J Biol Regul HomeostAgents. (2005) 19(3-4):105-12; Pardridge WM, Buciak J, Yang J, Wu D. Enhanced endocytosis in cultured human breast carcinoma cells and *in vivo* biodistribution in rats of a humanized monoclonal antibody after cationization of the protein. (1998) 286(1):548-54). However, such antibodies exhibit increased immunogenicity and cell internalization activity, and hence further improvement is needed to yield effective antibodies for cancer therapies that are based on mechanisms such as cytotoxic activities, ADCC and CDC, which are inhibited by cell internalization activity. Specifically, it is not understood whether an increase or decrease of the isoelectric point value enhances the antitumor effect of antibodies effective for cancer therapies that are based on mechanisms such as cytotoxic activities, ADCC and CDC, which are inhibited by cell internalization activity. In the present invention, modified antibodies with decreased or increased isoelectric point were produced from humanized antibodies and their antitumor effects were compared to see which modification gives a stronger antitumor effect. Surprisingly, the result showed that humanized antibodies with reduced isoelectric point exerted a more superior effect on liver cancer.

Antibodies produced by further modification of the above-described antibodies with modified charge of amino acid residues as a starting material by substitution, deletion, addition, and/or insertion of amino acid residues are included in the "antibodies" of the present invention. Antibodies produced by further modification of the charge of the amino acid residues of antibodies whose amino acid sequence has been modified by amino acid substitution, deletion, addition and/or insertion of amino acid residues, or chimerization, humanization, or such are also included in the "antibodies" of the present invention.

Preferred modifications for improving the characteristics of antibodies provided by the

present invention include, for example, modifications to improve antibody stability (hereinafter referred to as "modification of stability"). In an aqueous solution, an antibody exists in equilibrium between two states, namely, native state and inactive denaturation state. As seen from the second law of thermodynamics ($\Delta G = \Delta H - T\Delta S$), the stability of the native state depends on the Gibbs free energy change ΔG in the system, as well as the balance between enthalpy change ΔH (reflecting changes in hydrophobic interaction, hydrogen bonding, and the like in the polypeptide chain) and entropy change ΔS (reflecting changes in solvation and degree of conformational freedom), both of which contribute to Gibbs free energy change. Positive ΔG values imply that a protein is more stable in the native state than in the denaturation state. The greater the positive value of ΔG is, the more stable the protein is in the native state. In order to denature a protein, it is necessary to remove forces that contribute to this stability. For example, when a protein solution is exposed to high temperature, conformational freedom is increased, resulting in impairment of factors that contribute to protein stability. This leads to protein thermal denaturation. The term $-T\Delta S$ is dominant in such denaturation. The ΔH for protein unfolding caused by thermal denaturation can be directly determined by differential scanning calorimetry (DSC), as specifically described in the Examples herein. A DSC curve for the protein thermal denaturation process gives an endothermic peak at a temperature called denaturation midpoint (Tm), which is intrinsic to individual test proteins. The denaturation enthalpy is determined by integrating the peak. The Tm value generally serves as an indicator for thermal stability. The thermal capacity change (ΔCp) in protein denaturation can also be determined by DSC. The thermal capacity change associated with thermal denaturation is primarily caused by hydration of amino acid residues not exposed on the molecular surface in the native state but exposed to solvent molecules as a result of protein denaturation.

As described above, the "modification" of amino acid residues in the methods provided by the present invention specifically means substitution of a different amino acid residue for an original amino acid residue, deletion of an original amino acid residue, addition of an extra amino acid residue, and the like. The preferred modification is substitution of a different amino acid residue for an original amino acid residue. Specifically, in the present invention, modification by amino acid substitution is preferred for modification of antibody stability. Stability modification achieved by modifying amino acid residues of an antibody increases the Tm value of the antibody. Specifically, the Tm value is preferably used as an indicator for modification of antibody stability.

For a glypican 3 antibody provided by the present invention, "stability modification" is preferably achieved, for example, by modifying at least one amino acid residue selected from the amino acid residues at positions 37, 40, 48, and 51 in the heavy chain variable region constituting the humanized glypican 3 antibody of SEQ ID NO: 195. Alternatively, "stability

modification" is preferably achieved, for example, by modifying at least one amino acid residue selected from the amino acid residues at positions 2, 25, 42, 48, 50, 83, and 84 in the light chain variable region constituting the humanized glypican 3 antibody of SEQ ID NO: 201. Of the above-mentioned amino acid residues, it is not necessary to modify amino acid residues other than those already underwent stability modification, as long as the desired Tm is achieved. However, these amino acid residues can be appropriately modified to have a comparable or higher Tm than the humanized glypican 3 antibody before modification.

Stability modification can be carried out by randomly modifying each amino acid residue constituting the humanized antibody to be modified. Alternatively, stability modification can be carried out by substituting a portion of the amino acid sequence constituting a humanized antibody to be modified with the amino acid sequence of a known antibody with high Tm that structurally corresponds to the portion of the amino acid sequence of the humanized antibody to be modified. Positions of amino acid residues to be modified are not particularly limited; however, amino acid residues in the FR region can be preferably modified. Alternatively, amino acid residues in the CDR region can also be appropriately modified as long as the modification does not impair the antigen-binding activity. Furthermore, the number of amino acid residues to be modified is not particularly limited, and a particular segment within the FR region may be substituted with a desired segment. All of the segments in the FR region, FR1, FR2, FR3, and FR4, or a combination of one or more of the segments may be modified.

Preferred FR region segments for modification include, for example, FR2 regions of the heavy chain and light chain. Specifically, the preferred modification includes, for example, modification of amino acid residues to modify the FR2 of the heavy chain of a humanized glypican 3 antibody of the VH1b subclass, which is shown in SEQ ID NO: 195, to an FR2 of the VH4 subclass, namely, V37I which is substitution of isoleucine for valine at position 37, and similarly modifications of A40P, M48I, and L51I. Alternatively, the preferred modification includes, for example, modification of the light chain FR2 region of a humanized glypican 3 antibody of the VK2 subclass, which is shown in SEQ ID NO: 201, to an FR2 of the VK3 subclass, namely, modifications of L42Q, S48A, and Q50R, as well as modification of V2I which corresponds to modification of FR1 to a germ-line sequence.

Amino acid sequence modifications such as amino acid substitutions, deletions, additions, and/or insertions, and humanization and chimerization can be preferably achieved by methods known to those skilled in the art. When the antibodies of the present invention are prepared as recombinant antibodies, likewise, the amino acid sequences of the antibody variable and constant regions may also be preferably modified by amino acid substitutions, deletions, additions, and/or insertions.

Antibodies derived from any animal, such as mouse, human, rat, rabbit, goat, or camel

antibodies, are preferably used in the present invention. Furthermore, modified antibodies that include amino acid substitutions in their sequence, such as chimeric antibodies and in particular humanized antibodies can be preferably used. Antibody modification products linked with various molecules can also be preferably used.

"Chimeric antibodies" are antibodies prepared by combining sequences derived from different animals. A preferred example is an antibody having heavy and light chain variable regions from a mouse antibody and heavy and light chain constant regions from a human antibody. Chimeric antibodies can be prepared by known methods. For example, a DNA encoding an antibody variable region and a DNA encoding a human antibody constant region are fused in frame, the resulting recombinant DNA is inserted into a commonly used expression vector, a host introduced with the vector is cultured, and a chimeric antibody is appropriately obtained or isolated from the cell culture.

"Humanized antibodies" are also referred to as reshaped human antibodies, and can be obtained by linking the CDR of a nonhuman mammalian antibody, for example mouse antibody, and the FR of a human antibody. A DNA sequence encoding a humanized antibody can be synthesized by overlap PCR, using several oligonucleotides as templates. Materials and methods for overlap PCR is described in WO98/13388 or the like. A DNA encoding the variable region of a humanized antibody of the present invention can be obtained by overlap PCR using several oligonucleotides designed to include oligonucleotide sequences that overlap with each other, and they are ligated in frame with a DNA encoding the human antibody constant region to form a codon sequence. The DNA thus ligated is then inserted into an expression vector in an expressible manner, and introduced into a host.

Methods for identifying CDRs are known (Kabat *et al.*, Sequence of Proteins of Immunological Interest (1987), National Institute of Health, Bethesda, Md.; Chothia *et al.*; Nature (1989) 342:877). General genetic recombination techniques suitable for this purpose are also known (see European Patent Application Publication EP 125023; and WO96/02576). For example, the CDR of a nonhuman animal antibody such as a mouse antibody can be determined, and a DNA is prepared such that it encodes an antibody in which the CDR is ligated with the FR of a human antibody. Human antibody FRs linked *via* CDRs are selected such that the CDRs form a suitable antigen binding site. If required, amino acid residues in the FRs of an antibody variable region may be modified so that the CDRs of the reshaped human antibody can form a suitable antigen binding site (Sato, K. *et al.*, Cancer Res. (1993) 53:851-856). Modifiable amino acid residues in the FRs include residues that directly bind to an antigen *via* non-covalent bonds (Amit *et al.*, Science (1986) 233:747-53), residues that have some impact or effect on the CDR structure (Chothia *et al.*, J. Mol. Biol. (1987) 196:901-17), and residues involved in the interaction between heavy chain variable region and light chain variable region (Patent

Publication EP 239400).

A commonly used expression vector inserted with the DNA is transformed or transduced into a host cell, and the humanized antibody encoded by the DNA is produced and isolated from the cell culture by culturing the host cell.

When the antibodies of the present invention are humanized or human antibodies, the constant regions of these antibodies are preferably derived from human antibodies. For example, Cγ1, Cγ2, Cγ3, and Cγ4 can be used for the heavy chain constant region, while Cκ and Cλ can be preferably used for the light chain constant region. The human antibody constant region may be modified as required to improve antibody or its production stability. A chimeric antibody of the present invention preferably includes a variable region of an antibody derived from a nonhuman mammal and a constant region of a human antibody. A humanized antibody preferably includes CDRs of an antibody derived from a nonhuman mammal and FRs and constant regions of a human antibody. A human antibody preferably includes CDRs of an antibody derived from human and FRs and constant regions of a human antibody. The constant regions of the human antibodies include specific amino acid sequences that correspond to the isotype of IgG (IgG1, IgG2, IgG3, and IgG4), IgM, IgA, IgD, and IgE. The constant regions of the humanized antibodies provided by the present invention may be the constant regions of antibodies of any isotype. Without being limited thereto, a constant region of human IgG is preferably used. The FRs of a human antibody to be used as FRs of the humanized and human antibodies are not particularly limited, and may be derived from an antibody of any isotype.

In order to reduce immunogenicity, a germ-line sequence can be substituted for all or some of the amino acid residues constituting the FR region using a method similar to the one described in a non-patent document (Mol Immunol. (1999) 36(6):387-395). This is based on the rational prediction that germ-line sequences have lower immunogenicity. The amino acid sequence constituting the FR region of a humanized antibody is aligned and compared with germ-line amino acid sequences (Abhinandan K. R. and Martin C. R., J. Mol. Biol. (2007) 369:852-862). Amino acid residues constituting an FR region of a humanized antibody that are found to be different in the above comparison can be substituted with germ-line amino acid residues, as long as the substitution does not result in the loss of antigen-binding activity. Specifically, such substitutions include, for example, substitutions of I for L at position 70, R for T at position 87, and A for T at position 97, which are the amino acid residues that constitute the heavy chain variable region of SEQ ID NO: 195. Furthermore, the substitutions also include substitution of A for S at position 25, in which is the amino acid residue that constitutes the light chain variable region of SEQ ID NO: 201.

One or more of the amino acids constituting the variable and constant regions of modified chimeric, human, or humanized antibodies of the present invention may be modified by

deletion, substitution, insertion, and/or addition, as long as the antibodies exhibit binding specificity to an antigen.

Since the immunogenicity of chimeric, humanized, and human antibodies comprising human-derived sequences in the human body has been attenuated, they are expected to be useful when administered to humans for therapeutic purposes or such.

Known sequences can be used for the genes encoding the heavy chain or light chain of antibodies before introduction of mutations by methods of the present invention. Alternatively, new sequences for antibody genes can be obtained by methods known to those skilled in the art. For example, they may be preferably obtained from an antibody library. The genes can also be cloned from monoclonal antibody-producing hybridomas by a known method such as RT-PCR using their mRNA as template.

Regarding antibody libraries, many antibody libraries are already known. Since methods for producing antibody libraries are also known, those skilled in the art can appropriately obtain or produce antibody libraries. Examples include antibody phage libraries disclosed by Clackson *et al.*, Nature (1991) 352:624-8; Marks *et al.*, J. Mol. Biol. (1991) 222:581-97; Waterhouses *et al.*, Nucleic Acids Res. (1993) 21:2265-6; Griffiths *et al.*, EMBO J. (1994) 13:3245-60; Vaughan *et al.*, Nature Biotechnology (1996) 14:309-14; and Japanese Patent Kohyo Publication No. (JP-A) H20-504970 (unexamined Japanese national phase publication corresponding to a non-Japanese international publication). In addition, known methods such as methods that use eukaryotic cells in preparing libraries (WO95/15393 pamphlet) and ribosome display methods may be preferably used. Furthermore, techniques for obtaining human antibodies by panning using human antibody libraries are also known. For example, single chain antibodies (scFvs) obtained by fusing human antibody heavy and light chain variable regions in frame are expressed on the surface of phages using phage display methods. Then, phages that bind to antigens are selected to isolate genes encoding antibody-binding scFv from the phages. The DNA sequences encoding the variable regions of heavy and light chains of antibodies that bind to the antigens can be determined by sequencing the genes. A human antibody can be appropriately obtained by inserting an antibody gene comprising the sequences into suitable expression vectors, and expressing the gene in suitable host cells as described later. These methods are already well known, and one can refer to WO92/01047, WO92/20791, WO93/06213, WO93/11236, WO93/19172, WO95/01438, and WO95/15388.

Basically, known techniques are used for methods for obtaining genes encoding antibodies from monoclonal antibody-producing hybridomas. The details will be described later; briefly, antibody genes are preferably obtained by immunizing an animal with a desired sensitizing antigen according to conventional immunization methods, fusing the immune cells

obtained from the animal with known parent cells by common cell fusion methods, screening monoclonal antibody-producing cells (hybridomas) by common screening methods, synthesizing cDNAs of antibody variable regions from mRNAs of the obtained hybridomas as template using reverse transcriptase, and linking them with DNAs encoding the desired antibody constant regions in inflame.

More specifically, preferable examples are shown below, but are not particularly limited thereto. Sensitizing antigens for obtaining the antibodies provided by the present invention include both complete antigens with immunogenicity and incomplete antigens composed of haptens and such that do not show immunogenicity. For example, full length proteins, and their partial polypeptides and peptides may be preferably used. The soluble GPC3 core protein of SEQ ID NO: 207 is a suitable example. In addition, it is known that substances composed of polysaccharides, nucleic acids, lipids, and such may act as antigens. Thus, there are no particular limitations on antigens of the antibodies of the present invention. Antigens can be prepared by methods known to those skilled in the art, and they can be prepared, for example, by the following methods using baculoviruses (for example, WO98/46777). When the immunogenicity of an antigen is low, it can be preferably linked to a macromolecule that has immunogenicity, such as albumin, and then used to immunize animals. When transmembrane molecules are used as antigens, extracellular polypeptide fragments of the molecules can be used as a preferable sensitizing antigen. Alternatively, cells expressing the molecules on their surface may also be used as a sensitizing antigen. When sensitizing antigens are insoluble molecules, the molecules may be solubilized by linking with water-soluble molecules, and the solubilized binding molecules are preferably used as a sensitizing antigen.

Antibody-producing cells can be preferably obtained by immunizing animals using suitable sensitizing antigens described above. Alternatively, antibody-producing cells can be prepared by *in vitro* immunization of lymphocytes that can produce antibodies. Various vertebrate animals and mammals can be used as the animals for immunization. In particular, rodents, lagomorphas, and primates are generally used. Examples of such animals include mice, rats, and hamsters for rodents, rabbits for lagomorphas, and monkeys including the cynomolgus monkey, rhesus monkey, hamadryas, and chimpanzees for primates. In addition, transgenic animals carrying human antibody gene repertoires are also known, and human antibodies can be preferably obtained by using these animals (see WO96/34096; Mendez *et al.*, Nat. Genet. (1997) 15:146-56). Instead of using such transgenic animals, desired human antibodies having binding activity against antigens can be obtained by, for example, *in vitro* sensitization of human lymphocytes with desired antigens or cells expressing the desired antigens, and then fusing the sensitized lymphocytes with human myeloma cells such as U266 (see Japanese Patent Application Kokoku Publication No. (JP-B) H1-59878 (examined, approved Japanese patent

application published for opposition)). Furthermore, desired human antibodies can be preferably obtained by immunizing transgenic animals carrying on their genomes a complete repertoire of human antibody genes with desired antigens (see WO93/12227, WO92/03918, WO94/02602, WO96/34096, and WO96/33735).

Animal immunization can be carried out by appropriately diluting and suspending a sensitizing antigen in Phosphate-Buffered Saline (PBS), physiological saline, or such, and forming an emulsion by mixing an adjuvant if necessary, and then intraperitoneally or subcutaneously injecting the sensitizing antigen into animals. After that, the sensitizing antigen mixed with Freund's incomplete adjuvant is preferably administered several times every 4 to 21 days. Production of antibodies against the sensitizing antigen in the immunized animals can be confirmed by measuring the antibody titer in animal sera using conventional methods, for example, known methods such as enzyme-linked immunosorbent assay (ELISA) and flow cytometry (FACS).

Antibody-producing cells obtained from lymphocytes or animals immunized with a desired antigen can be fused with myeloma cells to generate hybridomas using conventional fusing agents (for example, polyethylene glycol) (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, 1986, 59-103). Hybridomas can be preferably produced, for example, by the methods of Milstein *et al.* (G. Kohler and C. Milstein, Methods Enzymol. (1981) 73:3-46). Monoclonal antibodies that specifically bind to an antigen protein produced by the hybridomas can be obtained by culturing and growing the hybridomas thus obtained. The binding specificity of the monoclonal antibodies to the antigen proteins can be appropriately measured using known analysis methods, such as immunoprecipitation, radioimmunoassay (RIA), and enzyme-linked immunosorbent assay (ELISA), and flow cytometry (FACS). Thereafter, hybridomas that produce antibodies of interest whose specificity, affinity, or activity has been determined can be subcloned by methods such as limiting dilution if necessary. Finally, the monoclonal antibodies produced by the hybridomas can be isolated.

Next, genes encoding the selected antibodies can be cloned from hybridomas or antibody-producing cells (sensitized lymphocytes and such) using probes that may specifically bind to the genes (for example, oligonucleotides complementary to sequences encoding the antibody constant regions). Cloning by RT-PCR is also possible by using the mRNA obtained from hybridomas or antibody-producing cells (sensitized lymphocytes and such) as template. Immunoglobulins are classified into five different classes, IgA, IgD, IgE, IgG, and IgM according to their structures and functions. These classes are further divided into several isotypes (for example, IgG1, IgG2, IgG3, and IgG4; IgA1 and IgA2; and such). The class and subclass of antibodies provided by the present invention are not particularly limited and may be any of these classes or subclasses; however, IgG is a particularly preferred class.

It is possible to modify genes encoding amino acid sequences constituting heavy chain and light chain using genetic engineering techniques. Genetically modified antibodies such as chimeric antibodies and humanized antibodies that have been artificially modified for the purpose of decreasing heterologous antigenicity against humans and such can be appropriately produced for antibodies such as mouse antibodies, rat antibodies, rabbit antibodies, hamster antibodies, sheep antibodies, and camel antibodies by modifying nucleic acid residues that encode the amino acid sequences constituting the antibodies. Chimeric antibodies are antibodies composed of the heavy chain and light chain variable regions derived from a nonhuman mammalian antibody, for example, mouse antibody, and the heavy chain and light chain constant regions of a human antibody. They can be obtained by ligating the DNA encoding a variable region of a mouse antibody to the DNA encoding a constant region of a human antibody, incorporating them into an expression vector, and introducing the vector into a host for production of the antibody. A humanized antibody, which is also called a reshaped human antibody, is an antibody in which a human antibody FR is ligated in frame with the CDR of a nonhuman mammalian antibody, for example, mouse antibody, to form a codon sequence. A DNA sequence encoding this humanized antibody can be obtained by overlap PCR using several oligonucleotides as templates. The materials and methods for overlap PCR are described in WO98/13388 or the like.

A DNA encoding the variable region of a recombinant antibody of the present invention can be obtained by overlap PCR using several oligonucleotides designed to include oligonucleotide sequences that overlap with each other, and they are ligated in frame with a DNA encoding the human antibody constant region to form a codon sequence. The DNA thus ligated can be incorporated into an expression vector in an expressible manner, and the vector can be introduced into a host. An antibody encoded by the DNA is expressed by culturing the host. Expressed antibodies are obtained by suitably purifying the culture solution of the host or such (see EP239400 and WO96/02576). Human antibody FRs to be ligated *via* the CDR are selected when the CDR forms a favorable antigen-binding site against the antigen. If necessary, amino acid residues in the FR of an antibody variable region may be substituted such that the CDR of the reshaped human antibody forms an appropriate antigen-binding site against the antigen (K. Sato *et al.*, Cancer Res. (1993) 53:851-856).

In addition to the humanization described above, antibodies may be modified to improve their biological properties such as binding activity to an antigen recognized by the antibody. In the present invention, such modifications can be carried out using methods such as site-directed mutagenesis (see for example, Kunkel Proc. Natl. Acad. Sci. USA (1985) 82:488), PCR mutagenesis, and cassette mutagenesis. In general, mutant antibodies whose biological properties have been improved show amino acid sequence identity and/or similarity of 70% or

higher, more preferably 80% or higher, and even more preferably 90% or higher (for example, 95% or higher, 97%, 98%, 99%, etc.), when compared to the amino acid sequence of the antibody to be modified (namely, an antibody from which the modified antibody is prepared). Herein, sequence identity and/or similarity is defined as the ratio of amino acid residues that are homologous (same residues) or similar (amino acid residues classified into the same group based on the general properties of amino acid side chains) to the amino acid residues of an antibody from which the modified antibody is prepared, after the sequence identity value has been maximized by sequence alignment and gap introduction, if necessary. Generally, naturally-occurring amino acid residues are classified into groups based on the characteristics of their side chains: (1) hydrophobic: alanine, isoleucine, valine, methionine, and leucine; (2) neutral hydrophilic: asparagine, glutamine, cysteine, threonine, and serine; (3) acidic: aspartic acid and glutamic acid; (4) basic: arginine, histidine, and lysine; (5) residues that affect the orientation of the chain: glycine and proline; and (6) aromatic: tyrosine, tryptophan, and phenylalanine.

In a preferred embodiment, modifications that are aimed at enhancing antibody functions preferably include, for example, enhancement of the cytotoxic activity of antibodies including humanized antibodies. Such preferred cytotoxic activities include, for example, ADCC and CDC. Herein, CDC refers to cytotoxic activity of the complement system. When a specific antibody binds to an antigen on the target cell surface, cells carrying Fcγ receptor (immune cells and others) bind to the Fc *via* Fcγ receptor, and the cytotoxic activity exerted against target cells is referred to as ADCC. Whether a test antibody has ADCC or CDC can be assessed by known methods (for example, Current protocols in Immunology, Chapter 7. Immunologic studies in humans, Editor, John E, Coligan *et al.*, John Wiley & Sons, Inc., (1993)).

Specifically, first, effector cells, complement solutions, and target cells are prepared.

(1) Preparation of effector cells

Spleens are excised from CBA/N mice or the like, and then spleen cells are separated in RPMI1640 medium (Invitrogen). Effector cells can be prepared by washing the cells with the same medium containing 10% fetal bovine serum (FBS, HyClone) and then adjusting the cell concentration to 5×10^6 cells/ml.

(2) Preparation of complement solution

Complement solutions can be prepared by 10x dilution of Baby Rabbit Complement (CEDARLANE) in a medium (Invitrogen) containing 10% FBS.

(3) Preparation of target cells

Target cells expressing the antigen protein to which a test antibody binds can be radio-labeled by incubating them with 0.2 mCi of [^{51}Cr] sodium chromate (GE Healthcare

Bioscience) in DMEM supplemented with 10% FBS at 37°C for one hour. Cells expressing the antigen protein to which a test antibody binds include cells transformed with the gene encoding the antigen protein to which a test antibody binds, ovary cancer cells, prostate cancer cells, breast cancer cells, uterine cancer cells, liver cancer cells, lung cancer cells, pancreatic cancer cells, stomach cancer cells, urinary bladder cancer cells, and colon cancer cells. The target cells can be prepared by washing the radio-labeled cells three times with RPMI1640 medium supplemented with 10% FBS and adjusting the cell concentration to 2×10^5 cells/ml.

ADCC and CDC can be determined by the method described below. ADCC assay is carried out by adding 50 µl/well each of target cells and test antibody into a 96-well round-bottomed plate (Becton Dickinson) and incubating it on ice for 15 minutes. Then, 100 µl of the effector cells is added, and the resulting reaction mixture is incubated in a carbon dioxide gas incubator for four hours. The test antibody can be appropriately used at a final concentration in a range of 0 to 10 µg/ml. After incubation, 100 µl of supernatant is sampled and its radioactivity is determined using a gamma counter (COBRAII AUTO-GAMMA, MODEL D5005, Packard Instrument Company). The cytotoxic activity (%) can be calculated from the obtained radioactivity value according to the following formula:

(A-C) / (B-C) x 100

where A represents the radioactivity (cpm) of each test antibody sample, B represents the radioactivity (cpm) of a sample containing 1% NP-40 (Nacalai Tesque), and C represents the radioactivity (cpm) of a sample containing target cells alone.

CDC assay is carried out by adding 50 µl/well each of target cells and test antibody into a 96-well flat-bottomed plate (Becton Dickinson) and incubating it on ice for 15 minutes. Then, 100 µl of the complement solution is added, and the resulting reaction mixture is incubated in a carbon dioxide gas incubator for four hours. The test antibody can be appropriately used at a final concentration in a range of 0 to 3 µg/ml. After incubation, 100 µl of supernatant is sampled and its radioactivity is determined using a gamma counter. The cytotoxic activity can be calculated by the same method used for ADCC determination.

The cytotoxic activity of the antibody conjugate is determined by adding 50 µl/well each of target cells and test antibody conjugate in a 96-well flat-bottomed plate (Becton Dickinson) and incubating it on ice for 15 minutes. The plate is incubated in a carbon dioxide gas incubator for one to four hours. The antibody can be appropriately used at a final concentration in a range of 0 to 3 µg/ml. After incubation, 100 µl of supernatant is sampled and its radioactivity is determined using a gamma counter. The cytotoxic activity can be calculated by the same method used for ADCC determination.

As described above, the heavy chain and light chain variable regions of an antibody generally consist of three CDRs and four FRs. In a preferred embodiment of the present

invention, amino acid residues to be subjected to "modification" can be appropriately selected, for example, from amino acid residues constituting a CDR or FR.

By using public databases such as Kabat, those skilled in the art can readily obtain an amino acid sequence constituting an antibody variable region FR that actually exists in an organism such as human or mouse.

In a preferred embodiment, the present invention provides humanized antibodies whose pharmacokinetics in plasma is controlled by the methods of the present invention. Such humanized antibodies include, for example, humanized antibodies comprising nonhuman animal-derived CDR, human-derived FR, and human constant region, and whose pharmacokinetics in plasma is controlled relative to a chimeric antibody sharing the same constant region, in which at least one exposable amino acid residue on the surface of the antibody CDR or FR has opposite charge to the amino acid residue at the corresponding position in the CDR or FR of the original antibody.

In another preferred embodiment, the present invention provides human antibodies whose pharmacokinetics in plasma is controlled by the methods of the present invention. Such human antibodies include, for example, human antibodies comprising the human-derived CDR, human-derived FR, and human constant region, and whose pharmacokinetics in plasma is controlled relative to a chimeric antibody sharing the same constant region, in which at least one exposable amino acid residue on the surface of the antibody CDR or FR has opposite charge to the amino acid residue at the corresponding position in the CDR or FR of the original antibody.

The human constant region preferably refers to a region comprising the wild-type human Fc domain; however, modified Fc can also be preferably used. The "modified Fc" includes Fc in which amino acid residues constituting the Fc are modified, and Fc in which modification of the Fc domain is altered. Specifically, such alteration of modification preferably includes, for example, modification of the type of glycosylation in the Fc domain. A specific preferred example is the "antibody with reduced content of fucose linked to the antibody Fc domain" specifically disclosed in the Reference Experimental Examples herein.

The "antibody with reduced content of fucose linked to the antibody Fc domain" refers to an antibody whose fucose content is significantly reduced relative to a control antibody, preferably one with undetectable fucose. In general, fucose is added to the N-glycoside linkage sugar chains linked at two sites in the Fc domains of two molecules of heavy chain constituting a single antibody molecule. Herein, the "antibody with reduced content of fucose linked to the antibody Fc domain" refers to an antibody, which when compared to such a common antibody as control, has a fucose content of 50% or less, preferably 25% or less, more preferably 10% or less, still more preferably 0% of the total sugar chain content in the control antibody. Fucose content can be determined by the specific analytical methods described below in the Reference

Experimental Examples. Methods for preparing such antibodies with reduced fucose content are described in the Reference Experimental Examples herein. Such methods also preferably include, for example, the preparation methods using animal cells that are deficient in fucosyl transferase (Biotechnol Bioeng. (2004) 87(5):614-22) and preparation methods using animal cells with altered complex-type branched sugar chain modification (Biotechnol Bioeng. (2006) 93(5):851-61). Furthermore, the preparation methods also preferably include those that use non-animal cells such as plant cells (Nature Biotechnology (2006) 24:1591-7) or yeast cells (Nature Biotechnology (2006) 24:210-5) as host cells.

In a preferred embodiment, the present invention relates to a method for producing a polypeptide comprising an antibody variable region with a modified isoelectric point, which comprises:

(a) modifying a nucleic acid encoding a polypeptide so as to modify the charge of at least one exposable amino acid residue on the surface of the CDR region of the polypeptide;

(b) culturing a host cell to express the nucleic acid; and

(c) collecting the polypeptide comprising an antibody variable region from the host cell culture.

In another preferred embodiment, the present invention relates to a method for producing a polypeptide comprising an antibody variable region with controlled pharmacokinetics in plasma, which comprises:

(a) modifying a nucleic acid encoding a polypeptide so as to modify the charge of at least one exposable amino acid residue on the surface of the CDR region of the polypeptide;

(b) culturing a host cell to express the nucleic acid; and

(c) collecting the polypeptide comprising an antibody variable region from the host cell culture.

Furthermore, the polypeptides comprising an antibody variable region with controlled plasma pharmacokinetics produced by the methods are also included in the present invention.

The present invention provides methods for producing multispecific polypeptides comprising a first polypeptide and a second polypeptide each comprising an antibody variable region. In addition, the present invention provides multispecific polypeptides produced by the methods. A preferred embodiment of the production methods of the present invention is a method comprising modifying both or either one of a nucleic acid encoding the amino acid residues of a first polypeptide and a nucleic acid encoding the amino acid residues of a second polypeptide, so as to increase the difference between the isoelectric points of the first polypeptide and second polypeptide. That is, multispecific antibodies can be produced based on difference in isoelectric points, and the difference can be increased by modifying the charges of the amino acid residues in the first polypeptide and second polypeptide. More specifically, a preferred production method comprises the following steps of:

(a) modifying a nucleic acid encoding a polypeptide so as to modify the charge of at least one

exposable amino acid residue on the surface of the CDR region of the first polypeptide and second polypeptide, specifically modifying both or either one of a nucleic acid encoding the amino acid residues of a first polypeptide and a nucleic acid encoding the amino acid residues of a second polypeptide, so as to increase the difference between the isoelectric points of the first polypeptide and second polypeptide when compared to before modification;

(b) culturing host cells to express the nucleic acids; and

(c) collecting a multispecific antibody from the host cell culture.

In the present invention, "polypeptides" generally refers to peptides and proteins whose length is approximately ten amino acids or longer. Polypeptides are generally derived from organisms, but are not particularly limited thereto, and for example, they may be composed of an artificially designed sequence. They may also be naturally derived polypeptides, synthetic polypeptides, recombinant polypeptides, or such. Additionally, fragments of the above-mentioned polypeptides are also included in the polypeptides of the present invention.

In the present invention, "multispecific polypeptides comprising a first polypeptide and a second polypeptide each comprising an antibody variable region" refers to a polypeptide comprising a variable region of an antibody that binds to two or more types of different epitopes, or different epitopes in a single antigen. Polypeptides comprising an antibody variable region include, for example, the antibodies, minibodies, and scaffold proteins mentioned above.

In the present invention, the phrase "the difference between the isoelectric points of the polypeptides is increased" means that the isoelectric points of two or more polypeptides are made unequal by modifying the charges of the amino acids on the surface of each polypeptide, or increasing the difference between the isoelectric points of two or more polypeptides. The difference in the isoelectric points can be observed, for example, by using a technique such as isoelectric focusing. In the present invention, the isoelectric points are preferably changed without altering the structure and function (activity) of the polypeptides.

That is, the present invention provides a method for producing a multispecific polypeptide comprising a first polypeptide and a second polypeptide, wherein the method comprises the steps of:

(a) modifying both or either one of a nucleic acid encoding the amino acid residues of the first polypeptide and a nucleic acid encoding the amino acid residues of the second polypeptide, so that the difference between the isoelectric point of the first polypeptide and that of the second polypeptide will be 1.0 or more, preferably 1.2 or more, and more preferably 1.5 or more;

(b) culturing host cells to express the nucleic acids; and

(c) collecting the multispecific antibody from the host cell culture.

Furthermore, the present invention provides a method of modifying multispecific polypeptides for purification of multispecific antibodies comprising the first polypeptide and

second polypeptide. A preferred embodiment of the purification method of the present invention is a method comprising the step of modifying both or either one of a nucleic acid encoding the amino acid residues of a first polypeptide and a nucleic acid encoding the amino acid residues of a second polypeptide, so as to increase the difference between the isoelectric points of the first polypeptide and second polypeptide. That is, the difference in isoelectric points is introduced into the polypeptides by modifying the charges of the amino acid residues of the first polypeptide and second polypeptide. Multispecific antibodies can be purified using this difference in isoelectric points. More specifically, a purification method comprises the following steps of:

(a) modifying a nucleic acid encoding a polypeptide so as to modify the charge of at least one exposable amino acid residue on the surface of the CDR region of the first polypeptide and second polypeptide, specifically modifying both or either one of a nucleic acid encoding the amino acid residues of the first polypeptide and a nucleic acid encoding the amino acid residues of the second polypeptide, so as to increase the difference between the isoelectric points of the first polypeptide and second polypeptide when compared to before modification;

(b) culturing host cells to express the nucleic acids; and

(c) purifying said multispecific antibody from the host cell culture by standard chromatography.

Methods for producing multispecific antibodies which comprise the purification steps of the above-mentioned purification methods are also included in the present invention.

In the methods of the present invention, the phrase "modification of nucleic acids" refers to modifying nucleic acid sequences to form codons corresponding to the amino acid residues that are introduced by "modification" of the present invention. More specifically, the phrase refers to modifying nucleic acids constituting codons to be modified to codons encoding amino acid residues introduced by the modification. Usually, the phrase means gene manipulation or mutagenesis that modifies at least one nucleotide of a codon to produce a codon that encodes an amino acid residue of interest. More specifically, a codon encoding the original amino acid residue is replaced by a codon encoding the amino acid residue to be introduced by the modification. Such nucleic acid modifications can be carried out appropriately by those skilled in the art using known techniques, for example, site-directed mutagenesis or PCR mutagenesis.

The nucleic acids of the present invention are generally cloned (inserted) into suitable vectors and then introduced into host cells. These vectors are not particularly limited as long as the inserted nucleic acids are stably maintained. For example, when *Escherichia coli* (*E. coli*) is used as a host, the cloning vectors are preferably pBluescript vectors (Stratagene) and such, while various commercially available vectors may be used. When vectors are used for the purpose of producing the polypeptides of the present invention, expression vectors are

particularly useful. There is no particular limitation on expression vectors, so long as they can express polypeptides in test tubes, *E. coli*, cultured cells, or individual organisms. For example, preferred vectors include pBEST vector (Promega) for expression in test tubes, pET vector (Invitrogen) in *E. coli*, the pME18S-FL3 vector (GenBank Accession No. AB009864) in cultured cells, and the pME18S vector (Mol. Cell Biol. (1998) 8:466-472) in individual organisms. Insertion of the DNAs of the present invention into vectors can be performed, for example, by standard methods such as ligase reactions using restriction enzyme sites (Current protocols in Molecular Biology edit. Ausubel *et al.*, (1987) Publish. John Wiley & Sons. Section 11.4-11.11).

There is no particular limitation on the above-mentioned host cells, and various host cells are used depending on the purpose. Cells used for expressing polypeptides include bacterial cells (for example, *Streptococcus*, *Staphylococcus*, *E. coli*, *Streptomyces*, and *Bacillus subtilis*), fungal cells (for example, yeast and *Aspergillus*), insect cells (for example, *Drosophila* S2 and *Spodoptera* SF9), animal cells (for example, CHO, COS, HeLa, C127, 3T3, BHK, HEK293, Bowes melanoma cell), and plant cells. Vectors can be introduced into host cells using known methods, such as the calcium phosphate precipitation method, electroporation method (Current protocols in Molecular Biology edit. Ausubel *et al.*, (1987) Publish. John Wiley & Sons. Section 9.1-9.9), lipofection method, and microinjection method.

For secreting host cell-expressed polypeptides (antibodies) into the lumen of the endoplasmic reticulum, periplasmic space, or extracellular environment, suitable secretion signals can be incorporated into the antibodies of interest. These signals may be intrinsic or foreign to the polypeptides (antibodies) of interest.

When the polypeptides (antibodies) of the present invention are secreted into culture media, the polypeptides (antibodies) produced by the above-mentioned methods can be harvested by collecting the media. When the antibodies of the present invention are produced inside cells, the cells first are lysed, and then these antibodies are collected.

The antibodies of the present invention can be preferably collected and purified from recombinant cell cultures using known methods, including ammonium sulfate or ethanol precipitation, acidic extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxyapatite chromatography, and lectin chromatography.

In the present invention, polypeptides with nucleic acid modification are preferably a homomultimer of a first polypeptide, a homomultimer of a second polypeptide, and a heteromultimer of the first polypeptide and second polypeptide. Examples of the homomultimer of a first polypeptide, the homomultimer of a second polypeptide, and the heteromultimer of the first polypeptide and second polypeptide include those described in Examples, but are not limited thereto.

Examples of standard chromatography in the present invention include cation exchange chromatography, anion exchange chromatography, hydrophobic chromatography, hydroxyapatite chromatography, hydrophobic charge interaction chromatography, and chromatofocusing, but are not limited thereto.

In the above-mentioned methods of the present invention, a first polypeptide and a second polypeptide preferably comprise a heavy chain variable region. The variable region may comprise, for example, a CDR and an FR.

Furthermore, in the above-mentioned methods of the present invention, a variable region of a multispecific antibody preferably comprises a light chain variable region.

Additionally, in the above-mentioned methods of the present invention, a first polypeptide and a second polypeptide preferably comprise heavy chain constant regions. Such heavy chain constant regions preferably generate difference between the isoelectric points of the first polypeptide and second polypeptide. Examples of such heavy chain constant regions include heavy chain constant regions of antibodies having different isoelectric points. The isoelectric point difference can be introduced into the first polypeptide and the second polypeptide using the heavy chain constant regions of IgG1, IgG2, IgG3, or IgG4 which have isoelectric points that are originally different from each other. Alternatively, the amino acids in the heavy chain constant regions of the first polypeptide and the second polypeptide that cause differences in isoelectric point among these subclasses can be modified alone, or in combination with adjacent amino acids that do not have any effect on the isoelectric points to generate non-wild-type human constant regions, and isoelectric point difference can be introduced into the two constant regions. Examples of positions to be modified for introducing isoelectric point difference into the constant regions include, for example, positions 137, 196, 203, 214, 217, 233, 268, 274, 276, 297, 355, 392, 419, and 435, EU numbering, in the heavy chain constant region.

Furthermore, since removal of sugar chains from a heavy chain constant region generates isoelectric point difference, position 297, which is a glycosylated site, is another example of a position to be modified for introducing isoelectric point difference.

For methods that comprise the above-mentioned first polypeptide and second polypeptide comprising a heavy chain constant region, methods that combine with the method in which the above-mentioned first polypeptide and second polypeptide comprise a heavy chain variable region, and/or the method in which the multispecific antibody comprises a third polypeptide comprising a light chain variable region, and a first polypeptide and a second polypeptide that each forms a multimer with the third polypeptide, are included in the present invention.

Multispecific polypeptides produced by the above-mentioned methods are also included in the present invention.

Furthermore, in an embodiment, when the first polypeptide in the multispecific antibody provided by the present invention comprises a heavy chain variable region, at least one amino acid residue at positions 31, 61, 62, 64, and 65, Kabat's numbering, in the heavy chain variable region is made to carry a charge so that "the difference of isoelectric points will be increased". In another embodiment, when the polypeptide comprises a light chain variable region, at least one amino acid residue at positions 24, 27, 53, 54, and 55, Kabat's numbering, in the light chain variable region is made to carry a charge so that "the difference of isoelectric points will be increased". Of the amino acid residues of the first polypeptide indicated by the above-mentioned numbering, amino acid residues other than the charged amino acid residue may have the same type of charge as that of the charged amino acid residue, or may be uncharged, or may have the opposite charge of that of the charged amino acid residue, as long as the isoelectric point of the first polypeptide and that of the second polypeptide are different.

The above-mentioned multispecific antibodies of the present invention comprise a second polypeptide that preferably has the opposite charge of that of the charged amino acid residue in the first polypeptide, or is uncharged. More specifically, the second polypeptide in the multispecific antibodies comprises a heavy chain variable region, and at least one amino acid residue at positions 31, 61, 62, 64, and 65, Kabat's numbering, in the region is uncharged or has the opposite charge of that of the amino acid residue selected to carry a charge in the variable region in the first polypeptide. In addition, when the second polypeptide comprises a light chain variable region, at least one amino acid residue at positions 24, 27, 53, 54, and 55, Kabat's numbering, in the light chain variable region is uncharged or has the opposite charge of that of the amino acid residue selected to carry a charge in the variable region in the first polypeptide. Of the amino acid residues of the second polypeptide indicated by the above-mentioned numbering, amino acid residues other than the charged amino acid residue may have the same type of charge as that of the charged amino acid residue, or may be uncharged, or may have the opposite charge of that of the charged amino acid residue, as long as the isoelectric point of the first polypeptide and that of the second polypeptide are different.

To lower isoelectric points in multispecific antibodies comprising an antibody constant region, it is desirable to apply, for example, an IgG2 or IgG4 sequence to position 137, an IgG1, IgG2, or IgG4 sequence to position 196, an IgG2 or IgG4 sequence to position 203, an IgG2 sequence to position 214, an IgG1, IgG3, or IgG4 sequence to position 217, an IgG1, IgG3, or IgG4 sequence to position 233, an IgG4 sequence to position 268, an IgG2, IgG3, or IgG4 sequence to position 274, an IgG1, IgG2, or IgG4 sequence to position 276, an IgG4 sequence to position 355, an IgG3 sequence to position 392, an IgG4 sequence to position 419, and an IgG1, IgG2, or IgG4 sequence to position 435. To increase isoelectric points, it is desirable to apply, for example, an IgG1 or IgG3 sequence to position 137, an IgG3 sequence to position 196, the

IgG1 or IgG3 sequence to position 203, an IgG1, IgG3, or IgG4 sequence to position 214, an IgG2 sequence to position 217, an IgG2 sequence to position 233, an IgG1, IgG2, or IgG3 sequence to position 268, an IgG1 sequence to position 274, an IgG3 sequence to position 276, an IgG1, IgG2, or IgG3 sequence to position 355, an IgG1, IgG2, or IgG4 sequence to position 392, an IgG1, IgG2, or IgG3 sequence to position 419, and an IgG3 sequence to position 435.

It is not necessary to apply all of these sequences, as long as there is sufficient difference between the isoelectric points of the two heavy chains.

Regarding the above-mentioned antibodies, the phrase "having the same type of charge" means, for example, that the above-mentioned amino acid residue in the heavy chain variable region according to Kabat's numbering and the above-mentioned amino acid residue in the heavy chain constant region according to EU numbering both carry an amino acid residue included in either of the groups (a) and (b) below.

(a) glutamic acid (E) and aspartic acid (D); and

(b) lysine (K), arginine (R), and histidine (H).

The phrase, "having the opposite charge" means that, for example, at least one of the above-mentioned amino acid residues, by Kabat's numbering or EU numbering, in the second polypeptide comprising a heavy chain variable region and/or a heavy chain constant region is included in either one of the above-mentioned groups (a) or (b), and its corresponding amino acid residue at a position in the heavy chain variable region and/or heavy chain constant region comprised in the first polypeptide is included in the other group.

More specifically, the present invention provides multispecific antibodies, in which the above-mentioned amino acid residues having the same type of charge are selected from the amino acid residues included in either one of the above-mentioned group (a) or (b).

In a preferred embodiment of the present invention, if the original amino acid residue (before modification) is already charged, it may be modified to be an uncharged amino acid residue.

In the present invention, an amino acid residue is preferably modified such that the difference between the isoelectric points of the first polypeptide and that of the second polypeptide will be increased. Furthermore, when multiple amino acid residues are introduced by modification, a few uncharged amino acid residues may be included in these amino acid residues.

Furthermore, the present invention relates to compositions (agents) comprising a polypeptide with controlled plasma pharmacokinetics in the present invention (for example, an IgG antibody) and a pharmaceutically acceptable carrier.

In the present invention, "pharmaceutical compositions" generally refers to agents for treating or preventing, or testing and diagnosing diseases.

The pharmaceutical compositions of the present invention can be preferably formulated by methods known to those skilled in the art. For example, such pharmaceutical compositions can be used parenterally in the form of injections, which are sterile solutions or suspensions prepared with water or another pharmaceutically acceptable liquid. For example, such compositions may be formulated by appropriately combining with a pharmaceutically acceptable carrier or medium, specifically, sterile water, physiological saline, vegetable oil, emulsifier, suspension, surfactant, stabilizer, flavoring agent, excipient, vehicle, preservative, binder, or such, and mixed in a unit dose form that meets the generally accepted requirements for preparation of pharmaceuticals. In such preparations, the amount of active ingredient is adjusted such that a suitable amount within a specified range is obtained.

Sterile compositions for injection can be formulated using vehicles such as distilled water for injection, according to standard protocols for formulation.

Aqueous solutions for injection include, for example, physiological saline and isotonic solutions containing glucose or other adjuvants (for example, D-sorbitol, D-mannose, D-mannitol, and sodium chloride). Appropriate solubilizers, for example, alcohols (ethanol and such), polyalcohols (propylene glycol, polyethylene glycol, and such), and non-ionic surfactants (polysorbate 80™, HCO-50, and such) may be used in combination.

Oils include sesame and soybean oils. Benzyl benzoate and/or benzyl alcohol can be used as solubilizers in combination. Buffers (for example, phosphate buffer and sodium acetate buffer), soothing agents (for example, procaine hydrochloride), stabilizers (for example, benzyl alcohol and phenol), and/or antioxidants can also be combined. Prepared injections are generally filled into appropriate ampules.

The pharmaceutical compositions of the present invention are preferably administered parenterally. For example, the compositions may be in the form of injections, transnasal agents, transpulmonary agents, or transdermal agents. For example, such compositions can be administered systemically or locally by intravenous injection, intramuscular injection, intraperitoneal injection, subcutaneous injection, or such.

The administration methods can be appropriately selected in consideration of a patient's age and symptoms. The dosage of a pharmaceutical composition comprising an antibody or a polynucleotide encoding an antibody may be set, for example, within the range of 0.0001 to 1,000 mg/kg weight for each administration. Alternatively, the dosage may be, for example, from 0.001 to 100,000 mg per patient. However, in the present invention, the dosage is not necessarily limited to the ranges described above. Although the dosage and administration method vary depending on a patient's weight, age, symptoms, and such, those skilled in the art can select appropriate dosage and administration methods in consideration of the factors described above.

The present invention also provides nucleic acids encoding antibodies with controlled pharmacokinetics in plasma (for example, humanized glypican 3 antibodies). Furthermore, vectors that carry these nucleic acids are also included in the present invention.

The present invention also provides host cells carrying the above-described nucleic acids. The host cells are not particularly limited and include, for example, bacterial cells such as *E. coli* and various animal cells. The host cells may be preferably used, for example, as a production system to produce and express the antibodies of the present invention. More specifically, the present invention provides a production system for the production of antibodies using the host cells. *In vitro* and *in vivo* systems for production of polypeptides are preferably used. Eukaryotic cells or prokaryotic cells are preferable examples used in an *in vitro* production system.

Eukaryotic cells that are used as host cells include, for example, animal cells, plant cells, and fungal cells. Animal cells include: mammalian cells, for example, CHO (J. Exp. Med. (1995) 108:945), COS, HEK293, 3T3, myeloma, BHK (baby hamster kidney), HeLa, and Vero; amphibian cells such as *Xenopus laevis* oocytes (Valle, *et al.*, Nature (1981) 291:338-340); and insect cells such as Sf9, Sf21, and Tn5. For expressing the antibodies of the present invention, CHO-DG44, CHO-DX11B, COS7 cells, HEK293 cells, and BHK cells can be suitably used. Of the animal cells, CHO cells are particularly preferable for large-scale expression. Vectors can be introduced into a host cell by, for example, calcium phosphate methods, DEAE-dextran methods, methods using cationic liposome DOTAP (Boehringer-Mannheim), electroporation methods, or lipofection methods.

It is known that plant cells such as *Nicotiana tabacum*-derived cells and *Lemna minor* cells are protein production systems, and these cells can be used to produce antibodies of the present invention by methods that culture calluses from these cells. Protein expression systems that use fungal cells including yeast cells, for example, cells of the genus *Saccharomyces* (*Saccharomyces cerevisiae*, *Saccharomyces pombe*, etc.), and cells of filamentous fungi, for example, the genus *Aspergillus* (*Aspergillus niger*, etc.) are known, and these cells can be used as a host to produce antibodies of the present invention.

When prokaryotic cells are used, production systems that use bacterial cells are preferably used. Production systems that use bacterial cells including *Bacillus subtilis* as well as *E. coli* described above are known, and they can preferably be used to produce antibodies of the present invention.

When an antibody is produced using a host cell of the present invention, a polynucleotide encoding an antibody of the present invention may be expressed by culturing the host cell transformed with an expression vector comprising the polynucleotide. Culturing can be preferably performed according to known methods. For example, when animal cells are

used as a host, DMEM, MEM, RPMI 1640, or IMDM may be preferably used as the culture medium. The culture medium may be preferably used with serum supplement solutions such as FBS or fetal calf serum (FCS). Alternatively, cells can be cultured in serum-free cultures. The preferred pH is about 6 to 8 during the course of culturing, although it depends on the host cell. Incubation is carried out typically at about 30°C to 40°C for about 15 to 200 hours. Medium is exchanged, aerated, or agitated, as necessary.

Meanwhile, as systems for producing antibodies *in vivo*, for example, those using animals and those using plants may be preferably used. A polynucleotide encoding an antibody of the present invention is introduced into an animal or plant to produce a glypican 3 antibody in the body of the animal or the plant, and then the antibody is collected. The "host" of the present invention includes such animals and plants.

When animals are used as a host, production systems that use mammals or insects are available. Mammals such as goat, pig, sheep, mouse, and cattle may be preferably used (Vicki Glaser, SPECTRUM Biotechnology Applications (1993)). When mammals are used, transgenic animals may be used.

For example, a polynucleotide encoding an antibody of the present invention may be prepared as a fusion gene with a gene encoding a polypeptide specifically produced in milk, such as goat β-casein. Next, polynucleotide fragments containing this fusion gene are injected into goat embryos, which are then introduced back into female goats. The antibody of interest can be obtained from milk produced by the transgenic goats, which are born from the goats that received the embryos, or by their offspring. Appropriate hormones may be administered to the transgenic goats to increase the volume of milk containing the antibody produced by the transgenic goats (Ebert *et al.*, Bio/Technology (1994) 12:699-702).

Insects such as silkworms may be used for producing antibodies of the present invention. When silkworms are used, baculoviruses carrying a polynucleotide encoding an antibody of interest can be used to infect silkworms, so that a glypican 3 antibody of interest can be obtained from the body fluids of these silkworms (Susumu *et al.*, Nature (1985) 315:592-594).

Plants used for producing antibodies of the present invention include, for example, tobacco. When tobacco is used, a polynucleotide encoding an antibody of interest is inserted into a plant expression vector, for example, pMON 530, and then the vector is introduced into a bacterium such as *Agrobacterium tumefaciens*. The bacteria are then used to infect tobacco such as *Nicotiana tabacum*, and the desired glypican 3 antibody can be obtained from the infected leaves of the tobacco (Ma *et al.*, Eur. J. Immunol. (1994) 24:131-138). Alternatively, the same bacteria can be used to infect *Lemna minor*, and after cloning, the desired glypican 3 antibody can be obtained from the infected cells of *Lemna minor* (Cox K.M. *et al.*, Nat. Biotechnol. 2006 Dec;24(12):1591-1597).

The antibody thus obtained may be isolated from the inside or outside (such as the medium and milk) of host cells, and purified as a substantially pure and homogenous antibody. Methods used for separating and purifying an antibody are not limited, and methods used in standard polypeptide purification may be applied. Antibodies may be isolated and purified by appropriately selecting or combining, for example, chromatographic columns, filtration, ultrafiltration, salting-out, solvent precipitation, solvent extraction, distillation, immunoprecipitation, SDS-polyacrylamide gel electrophoresis, isoelectric focusing, dialysis, recrystallization, and such.

Chromatographies include, for example, affinity chromatography, ion exchange chromatography, hydrophobic chromatography, gel filtration chromatography, reverse-phase chromatography, and adsorption chromatography (Strategies for Protein Purification and Characterization: A Laboratory Course Manual. Ed Daniel R. Marshak *et al.*, (1996) Cold Spring Harbor Laboratory Press). These chromatographies can be carried out using liquid phase chromatography such as HPLC and FPLC. Examples of columns for affinity chromatography include protein A columns and protein G columns. Examples of the columns that use protein A include Hyper D, POROS, and Sepharose F. F. (Pharmacia).

Another preferred embodiment of the present invention includes a method for producing an antibody with controlled plasma pharmacokinetics in the present invention, wherein the method comprises the steps of culturing the host cells of the present invention as described above and collecting the glypican 3 antibody from the cell culture.

The present invention provides pharmaceutical compositions comprising second-generation molecules that are more superior to the humanized anti-IL-6 receptor IgG1 antibody TOCILIZUMAB, and have been improved to exhibit enhanced drug efficacy and retention in plasma, and thus produce a prolonged therapeutic effect even when the frequency of administration is reduced. They have also been improved to have reduced immunogenicity and improved safety and physical properties, by modifying amino acid sequences of the variable and constant regions of TOCILIZUMAB; and methods for producing such pharmaceutical compositions. The present invention also provides antibody constant regions that are suitable for pharmaceuticals.

The present invention relates to anti-IL-6 receptor antibodies exhibiting superior antigen-binding activity, neutralizing activity, retention in plasma, stability, and/or homogeneity, and reduced immunogenicity risk.

Preferably, the anti-IL-6 receptor antibody is a humanized PM-1 antibody (TOCILIZUMAB). More specifically, the present invention provides humanized PM-1 antibodies with enhanced antigen-binding activity, humanized PM-1 antibodies with enhanced neutralizing activity, humanized PM-1 antibodies showing improved retention in plasma,

humanized PM-1 antibodies with reduced immunogenicity risk, humanized PM-1 antibodies with improved stability, and humanized PM-1 antibodies with improved homogeneity, all of which have been achieved through amino acid substitution.

Humanized PM-1 antibodies bind to the human IL-6 receptor, and thus inhibit the binding between human IL-6 and the human IL-6 receptor. Herein, SEQ IDs in the Sequence Listing correspond to the amino acid sequences of humanized PM-1 antibodies shown below.

Heavy chain amino acid sequence: SEQ ID NO: 15

Light chain amino acid sequence: SEQ ID NO: 16

Heavy chain variable region amino acid sequence: SEQ ID NO: 17

Light chain variable region amino acid sequence: SEQ ID NO: 18

Heavy chain CDR1 (HCDR1) amino acid sequence: SEQ ID NO: 1

Heavy chain CDR2 (HCDR2) amino acid sequence: SEQ ID NO: 2

Heavy chain CDR3 (HCDR3) amino acid sequence: SEQ ID NO: 3

Heavy chain FR1 (HFR1) amino acid sequence: SEQ ID NO: 7

Heavy chain FR2 (HFR2) amino acid sequence: SEQ ID NO: 8

Heavy chain FR3 (HFR3) amino acid sequence: SEQ ID NO: 9

Heavy chain FR4 (HFR4) amino acid sequence: SEQ ID NO: 10

Light chain CDR1 (LCDR1) amino acid sequence: SEQ ID NO: 4

Light chain CDR2 (LCDR2) amino acid sequence: SEQ ID NO: 5

Light chain CDR3 (LCDR3) amino acid sequence: SEQ ID NO: 6

Light chain FR1 (LFR1) amino acid sequence: SEQ ID NO: 11

Light chain FR2 (LFR2) amino acid sequence: SEQ ID NO: 12

Light chain FR3 (LFR3) amino acid sequence: SEQ ID NO: 13

Light chain FR4 (LFR4) amino acid sequence: SEQ ID NO: 14

<Antibodies with enhanced affinity and neutralizing activity>

The present invention provides anti-human IL-6 receptor antibodies exhibiting strong human IL-6 receptor-binding and/or neutralizing activity. More specifically, the present invention provides the following antibodies of (a) to (y), and methods for producing the antibodies:

(a) An anti-human IL-6 receptor antibody comprising a heavy chain CDR1 in which Ser at position 1 in the amino acid sequence of SEQ ID NO: 1 (HCDR1) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Trp (RD_68), Thr (RD_37), Asp (RD_8), Asn (RD_11), Arg (RD_31), Val (RD_32), Phe (RD_33), Ala (RD_34), Gln (RD_35), Tyr (RD_36), Leu (RD_38), His (RD_42), Glu (RD_45), or Cys (RD_46) is preferred.

A sequence resulting from the substitution of Trp for Ser at position 1 in the amino acid sequence of SEQ ID NO: 1 is shown in SEQ ID NO: 26.

A sequence resulting from the substitution of Thr for Ser at position 1 in the amino acid sequence of SEQ ID NO: 1 is shown in SEQ ID NO: 27.

A sequence resulting from the substitution of Asp for Ser at position 1 in the amino acid sequence of SEQ ID NO: 1 is shown in SEQ ID NO: 28.

A sequence resulting from the substitution of Asn for Ser at position 1 in the amino acid sequence of SEQ ID NO: 1 is shown in SEQ ID NO: 29.

A sequence resulting from the substitution of Arg for Ser at position 1 in the amino acid sequence of SEQ ID NO: 1 is shown in SEQ ID NO: 30.

A sequence resulting from the substitution of Val for Ser at position 1 in the amino acid sequence of SEQ ID NO: 1 is shown in SEQ ID NO: 31.

A sequence resulting from the substitution of Phe for Ser at position 1 in the amino acid sequence of SEQ ID NO: 1 is shown in SEQ ID NO: 32.

A sequence resulting from the substitution of Ala for Ser at position 1 in the amino acid sequence of SEQ ID NO: 1 is shown in SEQ ID NO: 33.

A sequence resulting from the substitution of Gln for Ser at position 1 in the amino acid sequence of SEQ ID NO: 1 is shown in SEQ ID NO: 34.

A sequence resulting from the substitution of Tyr for Ser at position 1 in the amino acid sequence of SEQ ID NO: 1 is shown in SEQ ID NO: 35.

A sequence resulting from the substitution of Leu for Ser at position 1 in the amino acid sequence of SEQ ID NO: 1 is shown in SEQ ID NO: 36.

A sequence resulting from the substitution of His for Ser at position 1 in the amino acid sequence of SEQ ID NO: 1 is shown in SEQ ID NO: 37.

A sequence resulting from the substitution of Glu for Ser at position 1 in the amino acid sequence of SEQ ID NO: 1 is shown in SEQ ID NO: 38.

A sequence resulting from the substitution of Cys for Ser at position 1 in the amino acid sequence of SEQ ID NO: 1 is shown in SEQ ID NO: 39.

(b) An anti-human IL-6 receptor antibody comprising a heavy chain CDR1 in which Trp at position 5 in the amino acid sequence of SEQ ID NO: 1 (HCDR1) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Ile (RD_9) or Val (RD_30) is preferred.

A sequence resulting from the substitution of Ile for Trp at position 5 in the amino acid sequence of SEQ ID NO: 1 is shown in SEQ ID NO: 40.

A sequence resulting from the substitution of Val for Trp at position 5 in the amino acid

sequence of SEQ ID NO: 1 is shown in SEQ ID NO: 41.

(c) An anti-human IL-6 receptor antibody comprising a heavy chain CDR2 in which Tyr at position 1 in the amino acid sequence of SEQ ID NO: 2 (HCDR2) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Phe (RD_82) is preferred.

A sequence resulting from the substitution of Phe for Tyr at position 1 in the amino acid sequence of SEQ ID NO: 2 is shown in SEQ ID NO: 42.

(d) An anti-human IL-6 receptor antibody comprising a heavy chain CDR2 in which Thr at position 8 in the amino acid sequence of SEQ ID NO: 2 (HCDR2) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Arg (RD_79) is preferred.

A sequence resulting from the substitution of Arg for Thr at position 8 in the amino acid sequence of SEQ ID NO: 2 is shown in SEQ ID NO: 43.

(e) An anti-human IL-6 receptor antibody comprising a heavy chain CDR2 in which Thr at position 9 in the amino acid sequence of SEQ ID NO: 2 (HCDR2) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Ser (RD_12) or Asn (RD_61) is preferred.

A sequence resulting from the substitution of Ser for Thr at position 9 in the amino acid sequence of SEQ ID NO: 2 is shown in SEQ ID NO: 44.

A sequence resulting from the substitution of Asn for Thr at position 9 in the amino acid sequence of SEQ ID NO: 2 is shown in SEQ ID NO: 45.

(f) An anti-human IL-6 receptor antibody comprising a heavy chain CDR3 in which Ser at position 1 in the amino acid sequence of SEQ ID NO: 3 (HCDR3) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Ile (RD_2), Val (RD_4), Thr (RD_80), or Leu (RD_5) is preferred.

A sequence resulting from the substitution of Ile for Ser at position 1 in the amino acid sequence of SEQ ID NO: 3 is shown in SEQ ID NO: 46.

A sequence resulting from the substitution of Val for Ser at position 1 in the amino acid sequence of SEQ ID NO: 3 is shown in SEQ ID NO: 47.

A sequence resulting from the substitution of Thr for Ser at position 1 in the amino acid sequence of SEQ ID NO: 3 is shown in SEQ ID NO: 48.

A sequence resulting from the substitution of Leu for Ser at position 1 in the amino acid

sequence of SEQ ID NO: 3 is shown in SEQ ID NO: 49.

(g) An anti-human IL-6 receptor antibody comprising a heavy chain CDR3 in which Leu at position 2 in the amino acid sequence of SEQ ID NO: 3 (HCDR3) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Thr (RD_84) is preferred.

A sequence resulting from the substitution of Thr for Leu at position 2 in the amino acid sequence of SEQ ID NO: 3 is shown in SEQ ID NO: 50.

(h) An anti-human IL-6 receptor antibody comprising a heavy chain CDR3 in which Thr at position 5 in the amino acid sequence of SEQ ID NO: 3 (HCDR3) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Ala (RD_3) or Ile (RD_83) is preferred. In addition, the substitution of Ser (RDC_14H) for Thr at position 5 is also preferred.

A sequence resulting from the substitution of Ala for Thr at position 5 in the amino acid sequence of SEQ ID NO: 3 is shown in SEQ ID NO: 51.

A sequence resulting from the substitution of Ile for Thr at position 5 in the amino acid sequence of SEQ ID NO: 3 is shown in SEQ ID NO: 52.

A sequence resulting from the substitution of Ser for Thr at position 5 in the amino acid sequence of SEQ ID NO: 3 is shown in SEQ ID NO: 53.

(i) An anti-human IL-6 receptor antibody comprising a heavy chain CDR3 in which Ala at position 7 in the amino acid sequence of SEQ ID NO: 3 (HCDR3) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Ser (RD_81) or Val (PF_3H) is preferred.

A sequence resulting from the substitution of Ser for Ala at position 7 in the amino acid sequence of SEQ ID NO: 3 is shown in SEQ ID NO: 54.

A sequence resulting from the substitution of Val for Ala at position 7 in the amino acid sequence of SEQ ID NO: 3 is shown in SEQ ID NO: 55.

(j) An anti-human IL-6 receptor antibody comprising a heavy chain CDR3 in which Met at position 8 in the amino acid sequence of SEQ ID NO: 3 (HCDR3) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Leu (PF_4H) is preferred.

A sequence resulting from the substitution of Leu for Met at position 8 in the amino acid sequence of SEQ ID NO: 3 is shown in SEQ ID NO: 56.

(k) An anti-human IL-6 receptor antibody comprising a heavy chain CDR3 in which Ser at position 1 and Thr at position 5 in the amino acid sequence of SEQ ID NO: 3 (HCDR3) have been substituted with other amino acids.

The type of amino acid after substitution is not particularly limited; however, substitutions of Leu for Ser at position 1 and Ala for Thr at position 5 (RD_6) are preferred. Other preferred substitutions include: substitutions of Val for Ser at position 1 and Ala for Thr at position 5 (RDC_2H); substitutions of Ile for Ser at position 1 and Ala for Thr at position 5 (RDC_3H); substitutions of Thr for Ser at position 1 and Ala for Thr at position 5 (RDC_4H); substitutions of Val for Ser at position 1 and Ile for Thr at position 5 (RDC_5H); substitutions of Ile for Ser at position 1 and Ile for Thr at position 5 (RDC_6H); substitutions of Thr for Ser at position 1 and Ile for Thr at position 5 (RDC_7H); and substitutions of Leu for Ser at position 1 and Ile for Thr at position 5 (RDC_8H).

A sequence resulting from the substitutions of Leu for Ser at position 1 and Ala for Thr at position 5 in the amino acid sequence of SEQ ID NO: 3 is shown in SEQ ID NO: 57.

A sequence resulting from the substitutions of Val for Ser at position 1 and Ala for Thr at position 5 in the amino acid sequence of SEQ ID NO: 3 is shown in SEQ ID NO: 58.

A sequence resulting from the substitutions of Ile for Ser at position 1 and Ala for Thr at position 5 in the amino acid sequence of SEQ ID NO: 3 is shown in SEQ ID NO: 59.

A sequence resulting from the substitutions of Thr for Ser at position 1 and Ala for Thr at position 5 in the amino acid sequence of SEQ ID NO: 3 is shown in SEQ ID NO: 60.

A sequence resulting from the substitutions of Val for Ser at position 1 and Ile for Thr at position 5 in the amino acid sequence of SEQ ID NO: 3 is shown in SEQ ID NO: 61.

A sequence resulting from the substitutions of Ile for Ser at position 1 and Ile for Thr at position 5 in the amino acid sequence of SEQ ID NO: 3 is shown in SEQ ID NO: 62.

A sequence resulting from the substitutions of Thr for Ser at position 1 and Ile for Thr at position 5 in the amino acid sequence of SEQ ID NO: 3 is shown in SEQ ID NO: 63.

A sequence resulting from the substitutions of Leu for Ser at position 1 and Ile for Thr at position 5 in the amino acid sequence of SEQ ID NO: 3 is shown in SEQ ID NO: 64.

(l) An anti-human IL-6 receptor antibody comprising a heavy chain CDR3 in which Leu at position 2, Ala at position 7, and Met at position 8 in the amino acid sequence of SEQ ID NO: 3 (HCDR3) have been substituted with other amino acids.

The type of amino acid after substitution is not particularly limited; however, substitutions of Thr for Leu at position 2, Val for Ala at position 7, and Leu for Met at position 8 (RD_78) are preferred.

A sequence resulting from the substitutions of Thr for Leu at position 2, Val for Ala at position 7, and Leu for Met at position 8 in the amino acid sequence of SEQ ID NO: 3 is shown

in SEQ ID NO: 65.

(m) An anti-human IL-6 receptor antibody comprising a light chain CDR1 in which Arg at position 1 in the amino acid sequence of SEQ ID NO: 4 (LCDR1) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Phe (RD_18) is preferred.

A sequence resulting from the substitution of Phe for Arg at position 1 in the amino acid sequence of SEQ ID NO: 4 is shown in SEQ ID NO: 66.

(n) An anti-human IL-6 receptor antibody comprising a light chain CDR1 in which Gln at position 4 in the amino acid sequence of SEQ ID NO: 4 (LCDR1) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Arg (RD_26) or Thr (RD_20) is preferred.

A sequence resulting from the substitution of Arg for Gln at position 4 in the amino acid sequence of SEQ ID NO: 4 is shown in SEQ ID NO: 67.

A sequence resulting from the substitution of Thr for Gln at position 4 in the amino acid sequence of SEQ ID NO: 4 is shown in SEQ ID NO: 68.

(o) An anti-human IL-6 receptor antibody comprising a light chain CDR1 in which Tyr at position 9 in the amino acid sequence of SEQ ID NO: 4 (LCDR1) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Phe (RD_73) is preferred.

A sequence resulting from the substitution of Phe for Tyr at position 9 in the amino acid sequence of SEQ ID NO: 4 is shown in SEQ ID NO: 69.

(p) An anti-human IL-6 receptor antibody comprising a light chain CDR1 in which Asn at position 11 in the amino acid sequence of SEQ ID NO: 4 (LCDR1) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Ser (RD_27) is preferred.

A sequence resulting from the substitution of Ser for Asn at position 11 in the amino acid sequence of SEQ ID NO: 4 is shown in SEQ ID NO: 70.

(q) An anti-human IL-6 receptor antibody comprising a light chain CDR2 in which Thr at position 2 in the amino acid sequence of SEQ ID NO: 5 (LCDR2) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Gly is preferred.

A sequence resulting from the substitution of Gly for Thr at position 2 in the amino acid sequence of SEQ ID NO: 5 is shown in SEQ ID NO: 71.

(r) An anti-human IL-6 receptor antibody comprising a light chain CDR3 in which Gln at position 1 in the amino acid sequence of SEQ ID NO: 6 (LCDR3) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however substitution to Gly (RD_28), Asn (RD_29), or Ser (RDC_15L) is preferred.

A sequence resulting from the substitution of Gly for Gln at position 1 in the amino acid sequence of SEQ ID NO: 6 is shown in SEQ ID NO: 72.

A sequence resulting from the substitution of Asn for Gln at position 1 in the amino acid sequence of SEQ ID NO: 6 is shown in SEQ ID NO: 73.

A sequence resulting from the substitution of Ser for Gln at position 1 in the amino acid sequence of SEQ ID NO: 6 is shown in SEQ ID NO: 74.

(s) An anti-human IL-6 receptor antibody comprising a light chain CDR3 in which Gly at position 3 in the amino acid sequence of SEQ ID NO: 6 has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Ser is preferred.

A sequence resulting from the substitution of Ser for Gly at position 3 in the amino acid sequence of SEQ ID NO: 6 is shown in SEQ ID NO: 75.

(t) An anti-human IL-6 receptor antibody comprising a light chain CDR1 in which Tyr at position 9 in the amino acid sequence of SEQ ID NO: 4 (LCDR1) has been substituted with another amino acid, and a light chain CDR3 in which Gly at position 3 in the amino acid sequence of SEQ ID NO: 6 (LCDR3) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, Tyr at position 9 in the amino acid sequence of SEQ ID NO: 4 (LCDR1) is preferably substituted with Phe, while Gly at position 3 in the amino acid sequence of SEQ ID NO: 6 (LCDR3) is preferably substituted with Ser (RD_72).

(u) An anti-human IL-6 receptor antibody comprising a light chain CDR3 in which Thr at position 5 in the amino acid sequence of SEQ ID NO: 6 (LCDR3) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Arg (RD_23) or Ser is preferred.

A sequence resulting from the substitution of Arg for Thr at position 5 in the amino acid sequence of SEQ ID NO: 6 is shown in SEQ ID NO: 76.

A sequence resulting from the substitution of Ser for Thr at position 5 in the amino acid

sequence of SEQ ID NO: 6 is shown in SEQ ID NO: 77.

(v) An anti-human IL-6 receptor antibody comprising a light chain CDR3 in which Gln at position 1 and Thr at position 5 in the amino acid sequence of SEQ ID NO: 6 (LCDR3) have been substituted with other amino acids.

The type of amino acid after substitution is not particularly limited; however, substitutions of Gly for Gln at position 1 and Ser for Thr at position 5 (RD_22) are preferred. Other preferred substitutions include substitutions of Gly for Gln at position 1 and Arg for Thr at position 5 (RDC_11L).

A sequence resulting from the substitutions of Gly for Gln at position 1 and Ser for Thr at position 5 in the amino acid sequence of SEQ ID NO: 6 is shown in SEQ ID NO: 78.

A sequence resulting from the substitutions of Gly for Gln at position 1 and Arg for Thr at position 5 in the amino acid sequence of SEQ ID NO: 6 is shown in SEQ ID NO: 79.

(w) An anti-human IL-6 receptor antibody comprising a heavy chain CDR2 in which Thr at position 9 in the amino acid sequence of SEQ ID NO: 2 (HCDR2) has been substituted with another amino acid, and a heavy chain CDR3 in which Ser at position 1 and Thr at position 5 in the amino acid sequence of SEQ ID NO: 3 (HCDR3) have been substituted with other amino acids.

Thr at position 9 in the amino acid sequence of SEQ ID NO: 2 (HCDR2) is preferably replaced with Asn. Furthermore, preferred combinations of amino acids for substitutions of Ser at position 1 and Thr at position 5 in the amino acid sequence of SEQ ID NO: 3 (HCDR3) include: Leu and Ala (RDC_27H); Val and Ala (RDC_28H); Ile and Ala (RDC_30H); Thr and Ala (RDC_4H); Val and Ile (RDC_29H); Ile and Ile (RDC_32H); Thr and Ile (RDC_7H); and Leu and Ile (RDC_8H).

(x) An antibody that comprises a variable region comprising the heavy chain CDR3 of (k) and a variable region comprising the light chain CDR3 of (v).

(y) The antibody of (x), which further comprises the heavy chain CDR2 of (e).

The present invention provides antibodies comprising at least the amino acid substitution of any one of (a) to (y) described above and methods for producing the antibodies. Thus, the antibodies of the present invention can also comprise other amino acid substitutions in addition to the amino acid substitution of any one of (a) to (y) described above. Furthermore, the antibodies of the present invention also include antibodies comprising a combination of any amino acid substitutions of (a) to (y) described above. The amino acid substitutions of (a) to (y) described above include substitutions of the CDR amino acid sequences described above to other amino acids. Amino acid substitutions other than those of (a) to (y) described above include, for example, amino acid sequence substitutions, deletions, additions, and/or insertions in other CDR regions. Such substitutions also include amino acid sequence substitutions,

deletions, additions, and/or insertions in the FR regions. Such substitutions further include substitutions, deletions, additions, and/or insertions in the constant regions.

Furthermore, the antibodies of the present invention also include antibodies in which a high affinity CDR discovered in the present invention is grafted into any framework other than a humanized PM-1 antibody. The antibodies of the present invention also include antibodies in which the loss of affinity as a result of grafting a high affinity CDR discovered in the present invention into any framework other than a humanized PM-1 antibody has been compensated by mutations introduced into the FR to restore the original affinity (see, for example, Curr. Opin. Biotechnol. 1994 Aug;5(4):428-33), and antibodies in which the loss has been compensated by mutations introduced into the CDR region to restore the original affinity (see, for example, US 2006/0122377).

In the present invention, the amino acid substitution of any one of (a) to (y) described above is preferably introduced into a humanized PM-1 antibody. Humanized PM-1 antibodies introduced with the amino acid substitution of any one of (a) to (y) described above have strong IL-6 receptor-neutralizing activity. Humanized PM-1 antibodies introduced with the amino acid substitution of any one of (a) to (y) described above are effective as therapeutic agents for IL-6-associated inflammatory diseases such as rheumatoid arthritis.

Antibodies comprising the amino acid substitution of any one of (a) to (y) described above can also be referred to as, for example, (1) or (2) described below. An example of antibody comprising the substitution of (a) is described here; other antibodies comprising the substitution of any one of (b) to (y) can also be referred to in the same way.

(1) An antibody that comprises a heavy chain variable region comprising CDR1 comprising an amino acid sequence in which Ser at position 1 in the amino acid sequence of SEQ ID NO: 1 has been substituted with another amino acid

(2) An antibody that comprises a heavy chain comprising CDR1 comprising an amino acid sequence in which Ser at position 1 in the amino acid sequence of SEQ ID NO: 1 has been substituted with another amino acid

<Antibodies with enhanced binding activity>

The present invention further provides anti-IL-6 receptor antibodies with strong IL-6 receptor-binding activity. Herein, "anti-IL-6 receptor antibodies with strong IL-6 receptor-binding activity" typically refers to antibodies whose affinity is measured to be 1 nM or less at 37°C under physiological conditions, preferably 0.1 nM or less, and more preferably 0.04 nM or less. Such anti-IL-6 receptor antibodies with strong IL-6 receptor binding activity are assumed to have an enhanced activity of neutralizing the biological activity of the antigen.

There is no limitation on the type of amino acid substitutions introduced to the present invention's anti-IL-6 receptor antibodies with strong IL-6 receptor binding activity. Such

amino acid substitutions include, for example, the above-described amino acid substitutions.

The type of IL-6 receptor is not particularly limited; however, human IL-6 receptor is preferred.

The binding activity can be determined by methods known to those skilled in the art, for example, using Biacore or such, based on surface plasmon resonance (SPR).

<Antibodies having a CDR sequence with reduced immunogenicity risk>

The present invention also provides anti-IL-6 receptor antibodies with reduced immunogenicity, in particular, humanized PM-1 antibodies. The immunogenicity is assumed to be enhanced when the sequence of an antibody contains a T-cell epitope that binds to HLA. Thus, the immunogenicity risk for an antibody can be reduced by removing the T-cell epitope from the antibody sequence through sequence substitution.

The present invention provides light chain variable regions of humanized anti-human IL-6 receptor antibodies with reduced immunogenicity, in particular, those of humanized PM-1 antibodies, from which T-cell epitopes have been removed through substituting other amino acids in the antibody amino acid sequences, in particular, CDR sequences. The present invention also provides antibodies comprising such light chain variable regions.

More specifically, the present invention provides light chain CDR2 in which Thr at position 2 in the amino acid sequence of SEQ ID NO: 5 (LCDR2) has been substituted with another amino acid. The present invention also provides light chain variable regions comprising such light chain CDR2. The present invention also provides anti-IL-6 receptor antibodies comprising such light chain variable region. The amino acid sequence after substitution is not particularly limited; however, substitution to Gly is preferred. A sequence comprising the substitution of Gly for Thr at position 2 in the amino acid sequence of SEQ ID NO: 5 is shown in SEQ ID NO: 71. The amino acid substitution is preferably introduced into a light chain variable region of a humanized PM-1 antibody.

<FR and CDR of H53/L28>

The present invention also provides anti-human IL-6 receptor antibodies with improved plasma pharmacokinetic, increased stability, and/or reduced immunogenicity. The half-lives of IgGs sharing the same Fc domain in plasma have been found to be correlated to isoelectric points with a high correlation coefficient. Then, the present inventors tried modifying the isoelectric points of the variable regions of two antibodies against different antigens, and successfully controlled their half-lives in plasma without modifying their Fc domains irrespective of the antigen specificity. The rate of non-specific antibody uptake by endothelial cells is assumed to depend on the physicochemical Coulomb interaction between IgG and negatively charged cell surface. Lowering the isoelectric point of IgG impairs the Coulomb interaction, which reduces the non-specific uptake by endothelial cells, and as a result, the metabolism in endothelial cells is

reduced. This can prolong the retention in plasma.

Specifically, the present invention provides anti-human IL-6 receptor antibodies with reduced isoelectric point and improved retention in plasma, by substituting amino acids in the amino acid sequence of an anti-IL-6 receptor antibody, in particular, a humanized PM-1 antibody. Specifically, the humanized PM-1 antibody is modified to reduce its isoelectric point by substituting other amino acids at H13 (amino acid at position 13 in SEQ ID NO: 7), H16 (amino acid at position 16 in SEQ ID NO: 7), H43 (amino acid at position 8 in SEQ ID NO: 8), H81 (amino acid at position 16 in SEQ ID NO: 9), H105 (amino acid at position 3 in SEQ ID NO: 10), L18 (amino acid at position 18 in SEQ ID NO: 11), L45 (amino acid at position 11 in SEQ ID NO: 12), L79 (amino acid at position 23 in SEQ ID NO: 13), L107 (amino acid at position 10 in SEQ ID NO: 14), H31 (amino acid at position 1 in SEQ ID NO: 1), L24 (amino acid at position 1 in SEQ ID NO: 4), and/or L53 (amino acid at position 4 in SEQ ID NO: 5), Kabat's numbering (Kabat EA *et al.*, 1991 Sequences of Proteins of Immunological Interest. NIH). These substitutions can lower the isoelectric point of a humanized PM-1 antibody without affecting its binding activity and stability. Some amino acid residues originated from the mouse sequence remain unsubstituted in the humanized PM-1 antibody to maintain its binding activity even after humanization of the mouse sequence. More specifically, amino acids at H27 (amino acid at position 27 in SEQ ID NO: 7), H28 (amino acid at position 28 in SEQ ID NO: 7), H29 (amino acid at position 29 in SEQ ID NO: 7), H30 (amino acid at position 30 in SEQ ID NO: 7), and H71 in the humanized PM-1 antibody (positions are numbered according to Kabat's numbering system described above) are of the mouse sequence. HFR1 can be converted into a human sequence by substituting H13, H16, H23, and H30, which enables to produce an antibody whose immunogenicity risk is lower than that of the humanized PM-1 antibody. Furthermore, since the humanized PM-1 antibody is an antibody humanized by CDR grafting, its stability may be further improved. Antibodies can be stabilized, for example, by substituting hydrophilic amino acids for amino acid residues exposed on the surface of the antibody variable region. Alternatively, antibodies can also be stabilized by modifying the CDR sequence to a consensus sequence. The humanized PM-1 antibody can be stabilized by a substitution of Ile for Met at H69 (amino acid position 4 in SEQ ID NO: 9) (stabilization of the hydrophobic core), Ser for Leu at H70 (amino acid at position 5 in SEQ ID NO: 9) (conversion of the surface-exposed residue to a hydrophilic residue), Asn for Thr at H58 (amino acid at position 9 in SEQ ID NO: 2) (modification of the heavy chain CDR2 to a consensus sequence), Gly for Ser at H65 (amino acid at position 16 in SEQ ID NO: 2) (substitution of Gly in the β turn region and modification of the heavy chain CDR2 to a consensus sequence), or Ser for Thr at L93 (amino acid at position 5 in SEQ ID NO: 6) (conversion of the surface-exposed residue to a hydrophilic residue) (positions are numbered according to Kabat's numbering system described above).

Alternatively, *in silico*-predicted T-cell epitopes can be removed by substituting Gly for Thr at L51 at position 2 in LCDR2 (SEQ ID NO: 5) described above, and this can reduce the immunogenicity risk without affecting the binding activity and stability. Anti-IL-6 receptor antibodies with improved stability and antibody pharmacokinetics in plasma, as well as reduced immunogenicity can be obtained by using these amino acid substitutions in combination.

Such antibodies include, for example, the antibodies of (1) to (37) below.

(1) An antibody that comprises a heavy chain variable region comprising FR1 in which Arg at position 13 in the amino acid sequence of SEQ ID NO: 7 has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Lys is preferred.

A sequence resulting from the substitution of Lys for Arg at position 13 in the amino acid sequence of SEQ ID NO: 7 is shown in SEQ ID NO: 80.

(2) An antibody that comprises a heavy chain variable region comprising FR1 in which Gln at position 16 in the amino acid sequence of SEQ ID NO: 7 has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution of Glu is preferred.

A sequence resulting from the substitution of Glu for Gln at position 16 in the amino acid sequence of SEQ ID NO: 7 is shown in SEQ ID NO: 81.

(3) An antibody that comprises a heavy chain variable region comprising FR1 in which Thr at position 23 in the amino acid sequence of SEQ ID NO: 7 has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Ala is preferred.

A sequence resulting from the substitution of Ala for Thr at position 23 in the amino acid sequence of SEQ ID NO: 7 is shown in SEQ ID NO: 82.

(4) An antibody that comprises a heavy chain variable region comprising FR1 in which Thr at position 30 in the amino acid sequence of SEQ ID NO: 7 has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Ser is preferred.

A sequence resulting from the substitution of Ser for Thr at position 30 in the amino acid sequence of SEQ ID NO: 7 is shown in SEQ ID NO: 83.

(5) An antibody that comprises a heavy chain variable region comprising FR1 in which Arg at position 13, Gln at position 16, Thr at position 23, and Thr at position 30 in the amino acid

sequence of SEQ ID NO: 7 have been substituted with other amino acids.

The type of amino acid after substitution is not particularly limited; however, substitutions of Lys for Arg at position 13, Glu for Gln at position 16, Ala for Thr at position 23, and Ser for Thr at position 30 are preferred.

A sequence resulting from the substitutions of Lys for Arg at position 13, Glu for Gln at position 16, Ala for Thr at position 23, and Ser for Thr at position 30 in the amino acid sequence of SEQ ID NO: 7 is shown in SEQ ID NO: 84.

(6) An antibody that comprises a heavy chain variable region comprising FR2 in which Arg at position 8 in the amino acid sequence of SEQ ID NO: 8 has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Glu is preferred.

A sequence resulting from the substitution of Glu for Arg at position 8 in the amino acid sequence of SEQ ID NO: 8 is shown in SEQ ID NO: 85.

(7) An antibody that comprises a heavy chain variable region comprising FR3 in which Met at position 4 in the amino acid sequence of SEQ ID NO: 9 has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Ile is preferred.

A sequence resulting from the substitution of Ile for Met at position 4 in the amino acid sequence of SEQ ID NO: 9 is shown in SEQ ID NO: 86.

(8) An antibody that comprises a heavy chain variable region comprising FR3 in which Leu at position 5 in the amino acid sequence of SEQ ID NO: 9 has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Ser is preferred.

A sequence resulting from the substitution of Ser for Leu at position 5 in the amino acid sequence of SEQ ID NO: 9 is shown in SEQ ID NO: 87.

(9) An antibody that comprises a heavy chain variable region comprising FR3 in which Arg at position 16 in the amino acid sequence of SEQ ID NO: 9 has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Lys is preferred.

A sequence resulting from the substitution of Lys for Arg at position 16 in the amino acid sequence of SEQ ID NO: 9 is shown in SEQ ID NO: 88.

(10) An antibody that comprises a heavy chain variable region comprising FR3 in which Val at

position 27 in the amino acid sequence of SEQ ID NO: 9 has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Ala is preferred.

A sequence resulting from the substitution of Ala for Val at position 27 in the amino acid sequence of SEQ ID NO: 9 is shown in SEQ ID NO: 89.

(11) An antibody that comprises a heavy chain variable region comprising FR3 in which Met at position 4, Leu at position 5, Arg at position 16, and Val at position 27 in the amino acid sequence of SEQ ID NO: 9 (HFR3) have been substituted with other amino acids.

The type of amino acid after substitution is not particularly limited; however, substitutions of Ile for Met at position 4, Ser for Leu at position 5, Lys for Arg at position 16, and Ala for Val at position 27 are preferred.

A sequence resulting from the substitutions of Ile for Met at position 4, Ser for Leu at position 5, Lys for Arg at position 16, and Ala for Val at position 27 in the amino acid sequence of SEQ ID NO: 9 is shown in SEQ ID NO: 90.

(12) An antibody that comprises a heavy chain variable region comprising FR4 in which Gln at position 3 in the amino acid sequence of SEQ ID NO: 10 (HFR4) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Glu is preferred.

A sequence resulting from the substitution of Glu for Gln at position 3 in the amino acid sequence of SEQ ID NO: 10 is shown in SEQ ID NO: 91.

(13) An antibody that comprises a light chain variable region comprising FR1 in which Arg at position 18 in the amino acid sequence of SEQ ID NO: 11 (LFR1) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Ser is preferred.

A sequence resulting from the substitution of Ser for Arg at position 18 in the amino acid sequence of SEQ ID NO: 11 is shown in SEQ ID NO: 92.

(14) An antibody that comprises a light chain variable region comprising FR2 in which Lys at position 11 in the amino acid sequence of SEQ ID NO: 12 (LFR2) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Glu is preferred.

A sequence resulting from the substitution of Glu for Lys at position 11 in the amino acid sequence of SEQ ID NO: 12 is shown in SEQ ID NO: 93.

(15) An antibody that comprises a light chain variable region comprising FR3 in which Gln at position 23 in the amino acid sequence of SEQ ID NO: 13 has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Glu is preferred.

A sequence resulting from the substitution of Glu for Gln at position 23 in the amino acid sequence of SEQ ID NO: 13 is shown in SEQ ID NO: 94.

(16) An antibody that comprises a light chain variable region comprising FR3 in which Pro at position 24 in the amino acid sequence of SEQ ID NO: 13 has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Ala is preferred.

A sequence resulting from the substitution of Ala for Pro at position 24 in the amino acid sequence of SEQ ID NO: 13 is shown in SEQ ID NO: 95.

(17) An antibody that comprises a light chain variable region comprising FR3 in which Ile at position 27 in the amino acid sequence of SEQ ID NO: 13 has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Ala is preferred.

A sequence resulting from the substitution of Ala for Ile at position 27 in the amino acid sequence of SEQ ID NO: 13 is shown in SEQ ID NO: 96.

(18) An antibody that comprises a light chain variable region comprising FR3 in which Gln at position 23, Pro at position 24, and Ile at position 27 in the amino acid sequence of SEQ ID NO: 13 (LFR3) have been substituted with other amino acids.

The type of amino acid after substitution is not particularly limited; however, substitutions of Glu for Gln at position 23, Ala for Pro at position 24, and Ala for Ile at position 27 are preferred.

A sequence resulting from the substitutions of Glu for Gln at position 23, Ala for Pro at position 24, and Ala for Ile at position 27 in the amino acid sequence of SEQ ID NO: 13 is shown in SEQ ID NO: 97.

(19) An antibody that comprises a light chain variable region comprising FR4 in which Lys at position 10 in the amino acid sequence of SEQ ID NO: 14 (LFR4) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Glu is preferred.

A sequence resulting from the substitution of Glu for Lys at position 10 in the amino

acid sequence of SEQ ID NO: 14 is shown in SEQ ID NO: 98.

(20) An antibody that comprises a heavy chain variable region comprising FR4 in which Ser at position 5 in the amino acid sequence of SEQ ID NO: 10 (HFR4) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Thr is preferred.

A sequence resulting from the substitution of Thr for Ser at position 5 in the amino acid sequence of SEQ ID NO: 10 is shown in SEQ ID NO: 132.

(21) An antibody that comprises a heavy chain variable region comprising FR4 in which Gln at position 3 and Ser at position 5 in the amino acid sequence of SEQ ID NO: 10 (HFR4) have been substituted with other amino acids.

The type of amino acid after substitution is not particularly limited; however, substitutions of Glu for Gln at position 3 and Thr for Ser at position 5 are preferred.

A sequence resulting from the substitutions of Glu for Gln at position 3 and Thr for Ser at position 5 in the amino acid sequence of SEQ ID NO: 10 is shown in SEQ ID NO: 133.

(22) An antibody that comprises a heavy chain variable region of a humanized PM-1 antibody comprising the amino acid substitutions of (5), (6), (11), and (21).

(23) An antibody that comprises a light chain variable region of a humanized PM-1 antibody comprising the amino acid substitutions of (13), (14), (18), and (19).

(24) An antibody that comprises the heavy chain variable region of (22) and the light chain variable region of (23).

(25) An antibody that comprises a heavy chain variable region comprising CDR1 in which Ser at position 1 in the amino acid sequence of SEQ ID NO: 1 (HCDR1) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution of Asp is preferred.

A sequence resulting from the substitution of Asp for Ser at position 1 in the amino acid sequence of SEQ ID NO: 1 is shown in SEQ ID NO: 28.

(26) An antibody that comprises a heavy chain variable region comprising CDR2 in which Ser at position 16 in the amino acid sequence of SEQ ID NO: 2 has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution of Gly is preferred.

A sequence resulting from the substitution of Gly for Ser at position 16 in the amino acid sequence of SEQ ID NO: 2 is shown in SEQ ID NO: 99.

(27) An antibody that comprises a heavy chain variable region comprising CDR2 in which Thr at

position 9 and Ser at position 16 in the amino acid sequence of SEQ ID NO: 2 (HCDR2) have been substituted with other amino acids.

The type of amino acid after substitution is not particularly limited; however, substitutions of Asn for Thr at position 9 and Gly for Ser at position 16 are preferred.

A sequence resulting from the substitutions of Asn for Thr at position 9 and Gly for Ser at position 16 in the amino acid sequence of SEQ ID NO: 2 is shown in SEQ ID NO: 100.

(28) An antibody that comprises a light chain variable region comprising CDR1 in which Arg at position 1 in the amino acid sequence of SEQ ID NO: 4 (LCDR1) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution of Gln is preferred.

A sequence resulting from the substitution of Gln for Arg at position 1 in the amino acid sequence of SEQ ID NO: 4 is shown in SEQ ID NO: 101.

(29) An antibody that comprises a light chain variable region comprising CDR2 in which Arg at position 4 in the amino acid sequence of SEQ ID NO: 5 has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Glu is preferred.

A sequence resulting from the substitution of Glu for Arg at position 4 in the amino acid sequence of SEQ ID NO: 5 is shown in SEQ ID NO: 102.

(30) An antibody that comprises a light chain variable region comprising CDR2 in which Thr at position 2 and Arg at position 4 in the amino acid sequence of SEQ ID NO: 5 (LCDR2) have been substituted with other amino acids.

The type of amino acid after substitution is not particularly limited; however, substitutions of Gly for Thr at position 2 and Glu for Arg at position 4 are preferred.

A sequence resulting from the substitutions of Gly for Thr at position 2 and Glu for Arg at position 4 in the amino acid sequence of SEQ ID NO: 5 is shown in SEQ ID NO: 103.

(31) An antibody that comprises a light chain variable region comprising CDR3 in which Thr at position 5 in the amino acid sequence of SEQ ID NO: 6 (LCDR3) has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Ser is preferred.

A sequence resulting from the substitution of Ser for Thr at position 5 in the amino acid sequence of SEQ ID NO: 6 is shown in SEQ ID NO: 77.

(32) An antibody that comprises a heavy chain variable region comprising the amino acid substitutions of (25) and (27).

(33) An antibody that comprises a light chain variable region comprising the amino acid substitutions of (28), (30), and (31).

(34) An antibody that comprises the heavy chain variable region of (32) and the light chain variable region of (33).

(35) An antibody that comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 104 (heavy chain variable region of H53/L28).

(36) An antibody that comprises a light chain variable region comprising the amino acid sequence of SEQ ID NO: 105 (light chain variable region of H53/L28).

(37) An antibody that comprises the heavy chain variable region of (35) and the light chain variable region of (36).

Any amino acid substitutions of (1) to (37) described above are preferably introduced into a humanized PM-1 antibody. The present invention provides antibodies comprising at least the amino acid substitution of any one of (1) to (37) described above and methods for producing those antibodies. Thus, the antibodies of the present invention also include antibodies comprising other amino acid substitutions in addition to the amino acid substitution of any one of (1) to (37) described above. The antibodies of the present invention also include antibodies comprising combinations of multiple amino acid substitutions of (1) to (37) described above. The amino acid substitutions of (1) to (37) described above include, for example, substitutions in the amino acid sequences of FR and CDR described above. Amino acid substitutions other than those of (1) to (37) described above include other substitutions, deletions, additions, and/or insertions in FR and CDR sequences than those described above. The amino acid substitutions also include substitutions, deletions, additions, and/or insertions in the amino acid sequences of constant regions.

Furthermore, in addition to those described above, amino acid modifications that result in a lower isoelectric point without loss of the activity of anti-IL-6 receptor antibody, include, for example, substitutions of Lys at position 15 and/or Ser at position 16 in the amino acid sequence of SEQ ID NO: 2 with other amino acids. The type of amino acid after substitution is not particularly limited; however, substitutions of Gln for Lys at position 15 and Asp for Ser at position 16 are preferred. A sequence comprising the substitutions of Gln for Lys at position 15 and Asp for Ser at position 16 in the amino acid sequence of SEQ ID NO: 2 is shown in SEQ ID NO: 121. Alternatively, such amino acid substitutions may also be introduced into the amino acid sequence of SEQ ID NO: 100. A sequence comprising the substitutions of Gln for Lys at position 15 and Asp for Gly at position 16 in the amino acid sequence of SEQ ID NO: 100 is shown in SEQ ID NO: 122. Thus, the present invention provides antibodies that comprise a heavy chain variable region comprising CDR2 in which Lys at position 15 and/or Ser at position 16 in the amino acid sequence of SEQ ID NO: 2 or 100 have been substituted with other amino

acids.

Other modifications that result in a lower isoelectric point include substitution of Gln at position 4 in the amino acid sequence of SEQ ID NO: 4 has been substituted with another amino acid. The type of amino acid after substitution is not particularly limited; however, substitution to Glu is preferred. An amino acid sequence comprising the substitution of Glu for Gln at position 4 in the amino acid sequence of SEQ ID NO: 4 is shown in SEQ ID NO: 123. Alternatively, this amino acid substitution may also be introduced into the amino acid sequence of SEQ ID NO: 101. An amino acid sequence comprising the substitution of Glu for Gln at position 4 in the amino acid sequence of SEQ ID NO: 101 is shown in SEQ ID NO: 124. Thus, the present invention provides antibodies that comprise a light chain variable region comprising CDR1 in which Gln at position 4 in the amino acid sequence of SEQ ID NO: 4 or 101 has been substituted with another amino acid.

Other modifications that result in a lower isoelectric point include substitution of His at position 6 in the amino acid sequence of SEQ ID NO: 5 with another amino acid. The type of amino acid after substitution is not particularly limited; however, substitution to Glu is preferred. An amino acid sequence comprising the substitution of Glu for His at position 6 in the amino acid sequence of SEQ ID NO: 5 is shown in SEQ ID NO: 125. Alternatively, this amino acid substitution may also be introduced into the amino acid sequence of SEQ ID NO: 103. An amino acid sequence comprising the substitution of Glu for His at position 6 in the amino acid sequence of SEQ ID NO: 103 is shown in SEQ ID NO: 126. Thus, the present invention provides antibodies that comprise a light chain variable region comprising CDR2 in which His at position 6 in the amino acid sequence of SEQ ID NO: 5 or 103 has been substituted with another amino acid.

Furthermore, modifications that result in reduced immunogenicity risk include substitution of Val for Ala at position 27 (H89, Kabat's numbering) in the amino acid sequence of heavy chain FR3 of SEQ ID NO: 90. An amino acid sequence comprising the substitution of Val for Ala at position 27 in the amino acid sequence of SEQ ID NO: 90 is shown in SEQ ID NO: 127. Thus, the present invention provides antibodies that comprise a heavy chain variable region comprising FR3 in which Val has been substituted for Ala at position 27 in the amino acid sequence of SEQ ID NO: 90.

The only mouse sequence that remains in the amino acid sequences of heavy chain FR3 of SEQ ID NO: 9 and 90 is Arg at position 6 (H71, Kabat's numbering). Anti-human IL-6 receptor antibodies having a framework consisting entirely of human sequences can be produced by using as a FR3 sequence, the human sequence of human VH1 subclass (SEQ ID NO: 128) or human VH3 subclass (SEQ ID NO: 129) where Arg is conserved at H71. Thus, the present invention provides antibodies that comprise a heavy chain variable region comprising the FR3 of

SEQ ID NO: 128 or 129.

Furthermore, modifications that improve stability include substitution of Ile for Ser at position 5 (H107, Kabat's numbering) in the amino acid sequence of heavy chain FR4 of SEQ ID NO: 10. An amino acid sequence comprising the substitution of Ile for Ser at position 5 in the amino acid sequence of SEQ ID NO: 10 is shown in SEQ ID NO: 130. Alternatively, this amino acid sequence may also be introduced into the amino acid sequence of SEQ ID NO: 91. An amino acid sequence comprising the substitution of Ile for Ser at position 5 in the amino acid sequence of SEQ ID NO: 91 is shown in SEQ ID NO: 131. Thus, the present invention provides antibodies that comprise a heavy chain variable region comprising FR4 in which Ile has been substituted for Ser at position 5 in the amino acid sequence of SEQ ID NO: 10 or 91.

Such amino acid substitutions are preferably introduced into the humanized PM-1 antibody, H53/L28 (an antibody comprising the heavy chain variable region of SEQ ID NO: 104 and the light chain variable region of SEQ ID NO: 105), or PF1 antibody (an antibody comprising the heavy chain variable region of SEQ ID NO: 22 and the light chain variable region of SEQ ID NO: 23). The present invention provides antibodies comprising at least such amino acid substitutions and methods for producing the antibodies. Thus, the antibodies of the present invention include antibodies comprising, in addition to such amino acid substitutions, the amino acid substitution of any one of (1) to (37) described above and/or other amino acid substitutions than those of (1) to (37) described above. Amino acid substitutions other than those of (1) to (37) described above include other substitutions, deletions, additions, and/or insertions in FR and CDR sequences than those described above. The amino acid substitutions also include substitutions, deletions, additions, and/or insertions in the amino acid sequences of constant regions.

<Anti-human IL-6 receptor antibodies with low isoelectric point>

The present invention also provides anti-IL-6 receptor antibodies with a low isoelectric point. The antibodies of the present invention with low isoelectric point include antibodies in which the measured isoelectric point of the whole antibody is low and antibodies in which the theoretical isoelectric point of the variable region (VH/VL) is low.

Herein, "anti-IL-6 receptor antibodies in which the measured isoelectric point of the whole antibody is low" typically refers to antibodies in which the measured isoelectric point is 7.5 or less, preferably 7.0 or less, and more preferably 6.0 or less. The measured isoelectric point can be determined by methods known to those skilled in the art, for example, non-denaturation gel isoelectric focusing or capillary isoelectric focusing.

Herein, "anti-IL-6 receptor antibodies in which the theoretical isoelectric point of the variable region is low" typically refers to antibodies in which the theoretical isoelectric point is 5.5 or less, preferably 5.0 or less, and more preferably 4.0 or less. The theoretical isoelectric

point can be determined by methods known to those skilled in the art. For example, the theoretical isoelectric points of heavy chain variable region and light chain variable region of a variable region can be computed by using software such as GENETYX (GENETYX CORPORATION).

There is no limitation on the type of amino acid substitution to be introduced to obtain anti-IL-6 receptor antibodies of the present invention with low isoelectric point. Such amino acid substitutions include, for example, the amino acid substitutions described above. Such anti-IL-6 receptor antibodies with low isoelectric point are assumed to show prolonged retention in plasma.

The type of IL-6 receptor is not particularly limited; however, human IL-6 receptor is preferred.

<Anti-human IL-6 receptor antibodies that are stable at high concentrations>

Furthermore, the present invention provides anti-IL-6 receptor antibodies that are stable at high concentrations.

Herein, "stable at high concentrations" means that the increase in the proportion of aggregates of anti-IL-6 receptor antibody ([peak area for aggregate in gel filtration chromatogram]/[total peak area in gel filtration chromatogram] x 100) generated in a high-concentration antibody solution (100 mg/ml) at 25°C in one month is 0.3% or less, preferably 0.2% or less, and more preferably 0.1% or less when the antibody is in a buffer of pH 6.5 to 7.0 properly selected for subcutaneous administration, for example, 20 mM histidine-HCl, 150 mM NaCl. The concentration of anti-IL-6 receptor antibody may be 100 mg/ml or higher, for example, 200 or 300 mg/ml.

There is no limitation on the anti-IL-6 receptor antibodies of the present invention that are stable at high concentrations. The antibodies can be prepared, for example, with the above-described amino acid substitutions or such.

The type of IL-6 receptor is not particularly limited; however, human IL-6 receptor is preferred.

The present invention also provides humanized PM-1 antibodies comprising any one of the amino acid substitutions of (1) to (37) described above and further comprising any of the amino acid substitutions of (a) to (y) described above to improve their binding activity and/or neutralizing activity. In an embodiment, such antibodies include those comprising a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 22 (PF1_H) and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 23 (PF1_L) (PF1), but are not limited thereto.

Furthermore, the present invention provides anti-IL-6 receptor antibodies of any of the following:

(A) a heavy chain variable region that comprises CDR1 comprising the amino acid sequence of SEQ ID NO: 165 (CDR1 of VH5-M83), CDR2 comprising the amino acid sequence of SEQ ID NO: 166 (CDR2 of VH5-M83), and CDR3 comprising the amino acid sequence of SEQ ID NO: 167 (CDR3 of VH5-M83);

(B) a light chain variable region that comprises CDR1 comprising the amino acid sequence of SEQ ID NO: 101 (CDR1 of VL5), CDR2 comprising the amino acid sequence of SEQ ID NO: 168 (CDR2 of VL5), and CDR3 comprising the amino acid sequence of SEQ ID NO: 79 (CDR3 of VL5);

(C) an antibody that comprises the heavy chain variable region of (A) and the light chain variable region of (B);

(D) a heavy chain variable region that comprises CDR1 comprising the amino acid sequence of SEQ ID NO: 169 (CDR1 of VH3-M73), CDR2 comprising the amino acid sequence of SEQ ID NO: 170 (CDR2 of VH3-M73), and CDR3 comprising the amino acid sequence of SEQ ID NO: 171 (CDR3 of VH3-M73);

(E) a light chain variable region that comprises CDR1 comprising the amino acid sequence of SEQ ID NO: 172 (CDR1 of VL3), CDR2 comprising the amino acid sequence of SEQ ID NO: 173 (CDR2 of VL3), and CDR3 comprising the amino acid sequence of SEQ ID NO: 79 (CDR3 of VL3);

(F) an antibody that comprises the heavy chain variable region of (D) and the light chain variable region of (E);

(G) a heavy chain variable region that comprises CDR1 comprising the amino acid sequence of SEQ ID NO: 169 (CDR1 of VH4-M73), CDR2 comprising the amino acid sequence of SEQ ID NO: 174 (CDR2 of VH4-M73), and CDR3 comprising the amino acid sequence of SEQ ID NO: 171 (CDR3 of VH4-M73);

(H) a light chain variable region that comprises CDR1 comprising the amino acid sequence of SEQ ID NO: 175 (CDR1 of VL1), CDR2 comprising the amino acid sequence of SEQ ID NO: 173 (CDR2 of VL1), and CDR3 comprising the amino acid sequence of SEQ ID NO: 79 (CDR3 of VL1); and

(I) an antibody that comprises the heavy chain variable region of (G) and the light chain variable region of (H).

Furthermore, the present invention provides anti-IL-6 receptor antibodies of any of the following:

(a) an antibody that comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 159 (H96-IgG1 variable region);

(b) an antibody that comprises a heavy chain variable region in which at least one of amino acids of Trp at position 35, Tyr at position 51, Ser at position 63, Lys at position 65, Gly at position 66,

Val at position 99, Ile at position 103, Tyr at position 108, Glu at position 111, and Thr at position 113 in the amino acid sequence of SEQ ID NO: 159 (H96-IgG1 variable region) has been substituted with another amino acid;

(c) an antibody that comprises a heavy chain variable region comprising an amino acid sequence in which Lys at position 65, Gly at position 66, Val at position 99, Ile at position 103, Glu at position 111, and Thr at position 113 in the amino acid sequence of SEQ ID NO: 159 (H96-IgG1 variable region) have been substituted with other amino acids;

(d) an antibody that comprises a heavy chain variable region comprising an amino acid sequence in which Trp at position 35, Tyr at position 51, Ser at position 63, Lys at position 65, Gly at position 66, Val at position 99, Ile at position 103, and Tyr at position 108 in the amino acid sequence of SEQ ID NO: 159 (H96-IgG1 variable region) have been substituted with other amino acids;

(e) an antibody that comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 160 (F2H-IgG1 variable region);

(f) an antibody that comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 161 (VH5-M83 variable region);

(g) an antibody that comprises a light chain variable region comprising an amino acid sequence in which Gln at position 27 and/or His at position 55 in the amino acid sequence of SEQ ID NO: 23 (PF1L) have been substituted with other amino acids;

(h) an antibody that comprises a light chain variable region comprising the amino acid sequence of SEQ ID NO: 162 (L39 variable region);

(i) an antibody that comprises a light chain variable region comprising the amino acid sequence of SEQ ID NO: 163 (VL5-kappa variable region);

(j) an antibody that comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 176 (VH3-M73 variable region);

(k) an antibody that comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 178 (VH4-M73 variable region);

(l) an antibody that comprises a light chain variable region comprising the amino acid sequence of SEQ ID NO: 177 (VL3-kappa variable region);

(m) an antibody that comprises a light chain variable region comprising the amino acid sequence of SEQ ID NO: 179 (VL1-kappa variable region);

(n) an antibody that comprises the heavy chain variable region of (e) and the light chain variable region of (h);

(o) an antibody that comprises the heavy chain variable region of (f) and the light chain variable region of (i) (combination of FV5-M83 variable regions);

(p) an antibody that comprises the heavy chain variable region of (j) and the light chain variable

region of (l) (combination of FV4-M73 variable regions); and
(q) an antibody that comprises the heavy chain variable region of (k) and the light chain variable region of (m) (combination of FV3-M73 variable regions).

The type of amino acid after substitution is not particularly limited in the amino acid substitution of the heavy chain variable regions of (a) to (d) above; however, substitutions of Val for Trp at position 35, Phe for Tyr at position 51, Thr for Ser at position 63, Gln for Lys at position 65, Asp for Gly at position 66, Leu for Val at position 99, Ala for Ile at position 103, Val for Tyr at position 108, Gln for Glu at position 111, Ile for Thr at position 113 are preferred. Alternatively, the type of amino acid after substitution is not particularly limited in the amino acid substitution of the light chain variable region of (g) above; however, substitutions of Glu for Gln at position 27 and Glu for His at position 55 are preferred. Amino acid substitutions, deletions, insertions, and/or additions other than the amino acid substitution described above may be included.

The antibody constant regions of the present invention are not particularly limited, and any constant regions may be used. For example, constant regions comprising a natural sequence such as IgG1, IgG2, and IgG4 and modified constant regions prepared by introducing amino acid substitutions, deletions, additions, and/or insertions into a constant region comprising a natural sequence can be used. The examples of such modified constant regions include the constant regions described below.

The examples of antibodies using the variable regions of the present invention mentioned above include:
(1) an antibody that comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 134 (H96-IgG1);
(2) an antibody that comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 135 (F2H-IgG1);
(3) an antibody that comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 137 (VH5-IgG1);
(4) an antibody that comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 139 (VH5-M83);
(5) an antibody that comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 136 (L39);
(6) an antibody that comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 138 (VL5-kappa);
(7) an antibody that comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 180 (VH3-M73);
(8) an antibody that comprises a heavy chain comprising the amino acid sequence of SEQ ID

NO: 182 (VH4-M73);

(9) an antibody that comprises a light chain comprising the amino acid sequence of SEQ ID NO: 181 (VL3-kappa);

(10) an antibody that comprises a light chain comprising the amino acid sequence of SEQ ID NO: 183 (VL1-kappa);

(11) an antibody that comprises the heavy chain of (2) and the light chain of (5);

(12) an antibody that comprises the heavy chain of (3) and the light chain of (6);

(13) an antibody that comprises the heavy chain of (4) and the light chain of (6) (FV5-M83);

(14) an antibody that comprises the heavy chain of (7) and the light chain of (9) (FV4-M73);

(15) an antibody that comprises the heavy chain of (8) and the light chain of (10) (FV3-M73); and

(16) an antibody having an activity equivalent to that of any of the antibodies of (1) to (15).

Herein, "having equivalent activity" means that the antigen-binding activity and/or neutralizing activity are equivalent. "Equivalent activity" in the present invention does not necessarily mean completely identical activity, but may be, for example, 50% or more of the activity, preferably 70% or more, and more preferably 90% or more.

Furthermore, the present invention provides CDR and FR of any of the following:

(i) a heavy chain FR1 that comprises the amino acid sequence of SEQ ID NO: 84 (heavy chain FR1 of VH5);

(ii) a heavy chain FR1 that comprises the amino acid sequence of SEQ ID NO: 186 (heavy chain FR1 of VH3 and VH4);

(iii) a heavy chain FR2 that comprises the amino acid sequence of SEQ ID NO: 85 (heavy chain FR2 of VH3, VH4, and VH5);

(iv) a heavy chain FR3 that comprises the amino acid sequence of SEQ ID NO: 184 (heavy chain FR3 of VH3, VH4, and VH5);

(v) a heavy chain FR4 that comprises the amino acid sequence of SEQ ID NO: 133 (heavy chain FR4 of VH3, VH4, and VH5);

(vi) a light chain FR1 that comprises the amino acid sequence of SEQ ID NO: 92 (light chain FR1 of VL1, VL3, and VL5);

(vii) a light chain FR2 that comprises the amino acid sequence of SEQ ID NO: 93 (light chain FR2 of VL1, VL3, and VL5);

(viii) a light chain FR3 that comprises the amino acid sequence of SEQ ID NO: 97 (light chain FR3 of VL1, VL3, and VL5);

(ix) a light chain FR4 that comprises the amino acid sequence of SEQ ID NO: 98 (light chain FR4 of VL1, VL3, and VL5);

(x) a heavy chain CDR1 that comprises the amino acid sequence of SEQ ID NO: 169 (heavy

chain CDR1 of VH3 and VH4);
(xi) a heavy chain CDR1 that comprises the amino acid sequence of SEQ ID NO: 165 (heavy chain CDR1 of VH5);
(xii) a heavy chain CDR2 that comprises the amino acid sequence of SEQ ID NO: 170 (heavy chain CDR2 of VH3);
(xiii) a heavy chain CDR2 that comprises the amino acid sequence of SEQ ID NO: 174 (heavy chain CDR2 of VH4);
(xiv) a heavy chain CDR2 that comprises the amino acid sequence of SEQ ID NO: 166 (heavy chain CDR2 of VH5);
(xv) a heavy chain CDR3 that comprises the amino acid sequence of SEQ ID NO: 171 (heavy chain CDR3 of VH3 and VH4);
(xvi) a heavy chain CDR3 that comprises the amino acid sequence of SEQ ID NO: 167 (heavy chain CDR3 of VH5);
(xvii) a light chain CDR1 that comprises the amino acid sequence of SEQ ID NO: 175 (light chain CDR1 of VL1);
(xviii) a light chain CDR1 that comprises the amino acid sequence of SEQ ID NO: 172 (light chain CDR1 of VL3);
(xix) a light chain CDR1 that comprises the amino acid sequence of SEQ ID NO: 101 (light chain CDR1 of VL5);
(xx) a light chain CDR2 that comprises the amino acid sequence of SEQ ID NO: 173 (light chain CDR2 of VL1 and VL3);
(xxi) a light chain CDR2 that comprises the amino acid sequence of SEQ ID NO: 168 (light chain CDR2 of VL5); and
(xxii) a light chain CDR3 that comprises the amino acid sequence of SEQ ID NO: 79 (light chain CDR3 of VL1, VL3, and VL5).

The antibodies of the present invention also include fragments and processed products of antibodies comprising any of the amino acid substitutions described above. Such antibody fragments include, for example, Fab, F(ab')2, Fv, single chain Fv (scFv) in which heavy and light chains are linked together *via* an appropriate linker, single domain heavy chain and single domain light chain (for example, Nat. Biotechnol. 2005 Sep;23(9):1126-36), Unibody (WO2007/059782 A1), and SMIP (WO2007/014278 A2). The origin of antibodies is not particularly limited. The antibodies include human, mouse, rat, and rabbit antibodies. The antibodies of the present invention may be chimeric, humanized, completely humanized antibodies, or such.

Specifically, such antibody fragments are obtained by treating antibodies with an enzyme, for example, papain or pepsin, or by constructing genes to encode such antibody

fragments, inserting them into expression vectors, and then expressing them in appropriate host cells (see, for example, Co, M. S. *et al.*, J. Immunol. (1994) 152:2968-2976; Better, M. and Horwitz, A. H. Methods in Enzymology (1989) 178:476-496; Plückthun, A.; Skerra, A., Methods in Enzymology (1989) 178:497-515; Lamoyi, E., Methods in Enzymology (1989) 121:652-663; Rousseaux, J. *et al.*, Methods in Enzymology (1989) 121:663-66; Bird, R. E. *et al.*, TIBTECH (1991) 9:132-137).

scFv is obtained by linking variable regions of antibody heavy and light chains. In such scFv, the heavy chain variable region is linked to the light chain variable region *via* a linker, preferably a peptide linker (Huston, J. S. *et al.*, Proc. Natl. Acad. Sci. USA (1988) 85:5879-5883). The heavy chain and light chain variable regions in an scFv may be derived from any of the antibodies described above. The peptide linker to link the variable regions includes, for example, arbitrary single chain peptides of 12 to 19 amino acid residues.

<Antibody constant regions>

The present invention also provides the antibody constant regions of (i) to (xxi) described below, which have been improved through amino acid substitution. The constant region refers to IgG1, IgG2, or IgG4 type constant region. The amino acid sequences of human IgG1, IgG2, and IgG4 constant regions are known (human IgG1 constant region, SEQ ID NO: 19; human IgG2 constant region, SEQ ID NO: 20; and human IgG4 constant region, SEQ ID NO: 21). The sequence of the human IgG4 constant region has been modified to improve the stability of the hinge region (Mol. Immunol. 1993 Jan;30(1):105-8). The present invention also provides antibodies that comprise such an amino acid substitution-containing antibody constant region. The antibody constant regions are preferably human antibody constant regions.

The amino acid substitution-containing antibody constant regions of the present invention may comprise other amino acid substitutions or modifications as long as they comprise the amino acid substitution of any one of (i) to (xxi) described below. Therefore, IgG2 constant regions comprising the amino acid substitutions of the present invention in the IgG2 constant region comprising the amino acid sequence of SEQ ID NO: 20 include IgG2 constant regions that comprise one or more amino acid substitutions and/or modifications in the amino acid sequence of SEQ ID NO: 20 and further comprise the amino acid substitutions of the present invention, as well as IgG2 constant regions that comprise the amino acid substitutions of the present invention and further comprise one or more amino acid substitutions and/or modifications. The same applies to IgG1 constant regions comprising the amino acid sequence of SEQ ID NO: 19 and IgG4 constant regions comprising the amino acid sequence of SEQ ID NO: 21.

Furthermore, the sugar chain at position 297 in the EU numbering system (see sequences of proteins of immunological interest, NIH Publication No.91-3242) may be of any

sugar-chain structure, or there may not be any sugar chain linked at this site (for example, constant regions produced in host cells where glycosylation does not occur, such as *E. coli*).

(i) Improvement of the stability of IgG2 constant region at acidic conditions

In an embodiment, the IgG2 constant region of the present invention comprising amino acid substitutions includes IgG2 constant regions in which Met at position 276 (position 397 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 has been substituted with another amino acid. The type of amino acid after substitution is not particularly limited; however, substitution to Val is preferred. The antibody stability under acidic conditions can be improved by substituting Met at position 276 (position 397 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 with another amino acid.

(ii) Improvement of the heterogeneity of IgG2 constant region

In an embodiment, the IgG2 constant region of the present invention comprising amino acid substitutions includes IgG2 constant regions in which Cys at position 14 (position 131 in the EU numbering system), Arg at position 16 (position 133 in the EU numbering system), and Cys at position 102 (position 219 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 have been substituted with other amino acids. The type of amino acid after substitution is not particularly limited; however, substitutions of Ser for Cys at position 14 (position 131 in the EU numbering system), Lys for Arg at position 16 (position 133 in the EU numbering system), and Ser for Cys at position 102 (position 219 in the EU numbering system) (IgG2-SKSC) are preferred.

These substitutions can reduce the heterogeneity originated from the hinge region of IgG2. The IgG2 constant regions of the present invention comprising amino acid substitutions include IgG2 constant regions comprising at least one of the three types of amino acid substitutions described above; however, the IgG2 constant regions preferably comprise substitutions of Cys at position 14 and Cys at position 102 with other amino acids or all three types of the amino acid substitutions described above.

(iii) Impairment of the binding of IgG2 constant region to FcγR

In an embodiment, the present invention also provides IgG2 constant regions comprising an amino acid sequence in which Ala at position 209 (EU330), Pro at position 210 (EU331), and/or Thr at position 218 (EU339) of the amino acid sequence of SEQ ID NO: 20 have been substituted with Ser, Ser, and Ala, respectively. The substitutions for Ala at position 209 (EU330) and for Pro at position 210 (EU331) have already been reported to enable the impairment of the Fcγ receptor binding (Eur. J. Immunol. 1999 Aug;29(8):2613-24). From the perspective of immunogenicity risk, however, these modifications are not preferred because they result in generation of nonhuman derived peptides that can become T-cell epitopes. However, the Fcγ receptor binding of IgG2 can be reduced by substituting Ala for Thr at position 218

(EU339) at the same time, and the 9-12 amino acid peptides which can become T-cell epitopes are derived from human only.

The IgG2 constant regions of the present invention comprising amino acid substitutions comprise at least one of the three types of amino acid substitutions described above; however, the IgG2 constant regions preferably comprise all three types of the amino acid substitutions described above. In a preferred embodiment, the IgG2 constant regions of the present invention comprising amino acid substitutions include IgG2 constant regions comprising an amino acid sequence in which Ala at position 209 (EU330), Pro at position 210 (EU331), and Thr at position 218 (EU339) in the amino acid sequence of SEQ ID NO: 20 have been substituted with Ser, Ser, and Ala, respectively.

(iv) Improvement of the C-terminal heterogeneity of IgG2 constant region

The present invention provides IgG2 constant regions comprising an amino acid sequence in which Gly at position 325 (position 446 in the EU numbering system) and Lys at position 326 (position 447 in the EU numbering system) have been deleted in the amino acid sequence of SEQ ID NO: 20. The heterogeneity originated from the C terminus of antibody heavy chain can be reduced only when both of the amino acids are deleted.

(v) Improvement of the retention in plasma by modifying IgG2 constant region

An embodiment of the IgG2 constant regions with amino acid substitutions of the present invention includes IgG2 constant regions in which His at position 147 (position 268 in the EU numbering system), Arg at position 234 (position 355 in the EU numbering system), and Gln at position 298 (position 419 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 have been substituted with other amino acids. These amino acid substitutions enable to improve antibody retention in plasma. The type of amino acid after substitution is not particularly limited; however, substitutions of Gln for His at position 147 (position 268 in the EU numbering system), Gln for Arg at position 234 (position 355 in the EU numbering system), and Glu for Gln at position 298 (position 419 in the EU numbering system) are preferred. The IgG2 constant regions with amino acid substitutions of the present invention include IgG2 constant regions comprising at least one of the three types of the amino acid substitutions described above; however, the IgG2 constant regions preferably comprise all three types of the amino acid substitutions described above.

(vi) Improvement of the stability of IgG4 constant region at acidic conditions

The present invention provides IgG4 constant regions comprising an amino acid sequence in which Arg at position 289 (position 409 in the EU numbering system) of the amino acid sequence of SEQ ID NO: 21 has been substituted with another amino acid. The type of amino acid after substitution is not particularly limited; however, substitution to Lys is preferred. The antibody stability under acidic conditions can be improved by substituting Arg at position

289 (position 409 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 21 with another amino acid.

(vii) Improvement of the C-terminal heterogeneity of IgG4 constant region

The present invention provides IgG4 constant regions comprising an amino acid sequence in which Gly at position 326 (position 446 in the EU numbering system) and Lys at position 327 (position 447 in the EU numbering system) have been deleted in the amino acid sequence of SEQ ID NO: 21. The heterogeneity originated from the C terminus of antibody heavy chain can be reduced only when both of the amino acids are deleted.

(viii) Improvement of the C-terminal heterogeneity of IgG1 constant region

The present invention provides IgG1 constant regions comprising an amino acid sequence in which Gly at position 329 (position 446 in the EU numbering system) and Lys at position 330 (position 447 in the EU numbering system) have been deleted in the amino acid sequence of SEQ ID NO: 19. The heterogeneity originated from the C terminus of antibody heavy chain can be reduced only when both of the amino acids are deleted.

(ix)

The present invention provides IgG1 constant regions comprising an amino acid sequence in which Asn at position 317 (position 434 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 19 has been substituted with another amino acid.

The type of amino acid after substitution is not particularly limited; however, substitution to Ala is preferred.

(x)

The present invention provides IgG2 constant regions comprising an amino acid sequence in which Ala at position 209 (position 330 in the EU numbering system), Pro at position 210 (position 331 in the EU numbering system), Thr at position 218 (position 339 in the EU numbering system), Met at position 276 (position 397 in the EU numbering system), Cys at position 14 (position 131 in the EU numbering system), Arg at position 16 (position 133 in the EU numbering system), Cys at position 102 (position 219 in the EU numbering system), Glu at position 20 (position 137 in the EU numbering system), and Ser at position 21 (position 138 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 have been substituted with other amino acids.

The type of amino acid after substitution is not particularly limited; however, substitutions of Ser for Ala at position 209, Ser for Pro at position 210, Ala for Thr at position 218, Val for Met at position 276, Ser for Cys at position 14, Lys for Arg at position 16, Ser for Cys at position 102, Gly for Glu at position 20, and Gly for Ser at position 21 are preferred.

(xi)

The present invention provides IgG2 constant regions comprising an amino acid

sequence in which Ala at position 209 (position 330 in the EU numbering system), Pro at position 210 (position 331 in the EU numbering system), Thr at position 218 (position 339 in the EU numbering system), Met at position 276 (position 397 in the EU numbering system), Cys at position 14 (position 131 in the EU numbering system), Arg at position 16 (position 133 in the EU numbering system), Cys at position 102 (position 219 in the EU numbering system), Glu at position 20 (position 137 in the EU numbering system), and Ser at position 21 (position 138 in the EU numbering system) have been substituted with other amino acids, and simultaneously Gly at position 325 (position 446 in the EU numbering system) and Lys at position 326 (position 447 in the EU numbering system) have been deleted in the amino acid sequence of SEQ ID NO: 20.

The type of amino acid after substitution is not particularly limited; however, substitutions of Ser for Ala at position 209, Ser for Pro at position 210, Ala for Thr at position 218, Val for Met at position 276, Ser for Cys at position 14, Lys for Arg at position 16, Ser for Cys at position 102, Gly for Glu at position 20, and Gly for Ser at position 21 are preferred.

(xii)

The present invention provides IgG2 constant regions comprising an amino acid sequence in which Met at position 276 (position 397 in the EU numbering system), Cys at position 14 (position 131 in the EU numbering system), Arg at position 16 (position 133 in the EU numbering system), Cys at position 102 (position 219 in the EU numbering system), Glu at position 20 (position 137 in the EU numbering system), and Ser at position 21 (position 138 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 have been substituted with other amino acids.

The type of amino acid after substitution is not particularly limited; however, substitutions of Val for Met at position 276, Ser for Cys at position 14, Lys for Arg at position 16, Ser for Cys at position 102, Gly for Glu at position 20, and Gly for Ser at position 21 are preferred.

(xiii)

The present invention provides IgG2 constant regions comprising an amino acid sequence in which Met at position 276 (position 397 in the EU numbering system), Cys at position 14 (position 131 in the EU numbering system), Arg at position 16 (position 133 in the EU numbering system), Cys at position 102 (position 219 in the EU numbering system), Glu at position 20 (position 137 in the EU numbering system), and Ser at position 21 (position 138 in the EU numbering system) have been substituted with other amino acids, and simultaneously Gly at position 325 (position 446 in the EU numbering system) and Lys at position 326 (position 447 in the EU numbering system) have been deleted in the amino acid sequence of SEQ ID NO: 20.

The type of amino acid after substitution is not particularly limited; however, substitutions of Val for Met at position 276, Ser for Cys at position 14, Lys for Arg at position 16, Ser for Cys at position 102, Gly for Glu at position 20, and Gly for Ser at position 21 are preferred.

(xiv)

The present invention provides IgG2 constant regions comprising an amino acid sequence in which Cys at position 14 (position 131 in the EU numbering system), Arg at position 16 (position 133 in the EU numbering system), Cys at position 102 (position 219 in the EU numbering system), Glu at position 20 (position 137 in the EU numbering system), Ser at position 21 (position 138 in the EU numbering system), His at position 147 (position 268 in the EU numbering system), Arg at position 234 (position 355 in the EU numbering system), and Gln at position 298 (position 419 in the EU numbering system) have been substituted with other amino acids, and simultaneously Gly at position 325 (position 446 in the EU numbering system) and Lys at position 326 (position 447 in the EU numbering system) have been deleted in the amino acid sequence of SEQ ID NO: 20.

The type of amino acid after substitution is not particularly limited; however, substitutions of Ser for Cys at position 14, Lys for Arg at position 16, Ser for Cys at position 102, Gly for Glu at position 20, Gly for Ser at position 21, Gln for His at position 147, Gln for Arg at position 234, and Glu for Gln at position 298 are preferred.

(xv)

The present invention provides IgG2 constant regions comprising an amino acid sequence in which Cys at position 14 (position 131 in the EU numbering system), Arg at position 16 (position 133 in the EU numbering system), Cys at position 102 (position 219 in the EU numbering system), Glu at position 20 (position 137 in the EU numbering system), Ser at position 21 (position 138 in the EU numbering system), His at position 147 (position 268 in the EU numbering system), Arg at position 234 (position 355 in the EU numbering system), Gln at position 298 (position 419 in the EU numbering system), and Asn at position 313 (position 434 in the EU numbering system) have been substituted with other amino acids, and simultaneously Gly at position 325 (position 446 in the EU numbering system) and Lys at position 326 (position 447 in the EU numbering system) have been deleted in the amino acid sequence of SEQ ID NO: 20.

The type of amino acid after substitution is not particularly limited; however, substitutions of Ser for Cys at position 14, Lys for Arg at position 16, Ser for Cys at position 102, Gly for Glu at position 20, Gly for Ser at position 21, Gln for His at position 147, Gln for Arg at position 234, Glu for Gln at position 298, and Ala for Asn at position 313 are preferred.

(xvi)

The present invention provides IgG4 constant regions comprising an amino acid sequence in which Arg at position 289 (position 409 in the EU numbering system), Cys at position 14, Arg at position 16, Glu at position 20, Ser at position 21, Arg at position 97, Ser at position 100, Tyr at position 102, Gly at position 103, Pro at position 104, and Pro at position 105 (positions 131, 133, 137, 138, 214, 217, 219, 220, 221, and 222 in the EU numbering system, respectively), Glu at position 113, Phe at position 114, and Leu at position 115 (positions 233, 234, and 235 in the EU numbering system, respectively) have been substituted with other amino acids, and simultaneously Gly at position 116 (position 236 in the EU numbering system) has been deleted in the amino acid sequence of SEQ ID NO: 21.

The type of amino acid after substitution is not particularly limited; however, substitutions of Ser for Cys at position 14 (position 131 in the EU numbering system), Lys for Arg at position 16 (position 133 in the EU numbering system), Gly for Glu at position 20 (position 137 in the EU numbering system), Gly for Ser at position 21 (position 138 in the EU numbering system), Thr for Arg at position 97 (position 214 in the EU numbering system), Arg for Ser at position 100 (position 217 in the EU numbering system), Ser for Tyr at position 102 (position 219 in the EU numbering system), Cys for Gly at position 103 (position 220 in the EU numbering system), Val for Pro at position 104 (position 221 in the EU numbering system), Glu for Pro at position 105 (position 222 in the EU numbering system), Pro for Glu at position 113 (position 233 in the EU numbering system), Val for Phe at position 114 (position 234 in the EU numbering system), Ala for Leu at position 115 (position 235 in the EU numbering system), and Lys for Arg at position 289 (position 409 in the EU numbering system) are preferred.

(xvii)

The present invention provides IgG4 constant regions comprising an amino acid sequence in which Arg at position 289 (position 409 in the EU numbering system), Cys at position 14, Arg at position 16, Glu at position 20, Ser at position 21, Arg at position 97, Ser at position 100, Tyr at position 102, Gly at position 103, Pro at position 104, and Pro at position 105 (positions 131, 133, 137, 138, 214, 217, 219, 220, 221, and 222 in the EU numbering system, respectively), Glu at position 113, Phe at position 114, and Leu at position 115 (positions 233, 234, and 235 in the EU numbering system, respectively) have been substituted with other amino acids, and simultaneously Gly at position 116 (position 236 in the EU numbering system), Gly at position 326 (position 446 in the EU numbering system), and Lys at position 327 (position 447 in the EU numbering system) have been deleted in the amino acid sequence of SEQ ID NO: 21.

The type of amino acid after substitution is not particularly limited; however, substitutions of Ser for Cys at position 14 (position 131 in the EU numbering system), Lys for Arg at position 16 (position 133 in the EU numbering system), Gly for Glu at position 20 (position 137 in the EU numbering system), Gly for Ser at position 21 (position 138 in the EU

numbering system), Thr for Arg at position 97 (position 214 in the EU numbering system), Arg for Ser at position 100 (position 217 in the EU numbering system), Ser for Tyr at position 102 (position 219 in the EU numbering system), Cys for Gly at position 103 (position 220 in the EU numbering system), Val for Pro at position 104 (position 221 in the EU numbering system), Glu for Pro at position 105 (position 222 in the EU numbering system), Pro for Glu at position 113 (position 233 in the EU numbering system), Val for Phe at position 114 (position 234 in the EU numbering system), Ala for Leu at position 115 (position 235 in the EU numbering system), and Lys for Arg at position 289 (position 409 in the EU numbering system) are preferred.

(xviii)

The present invention provides IgG1 constant regions comprising an amino acid sequence in which Asn at position 317 (position 434 in the EU numbering system) has been substituted with another amino acid, and simultaneously Gly at position 329 (position 446 in the EU numbering system) and Lys at position 330 (position 447 in the EU numbering system) have been deleted in the amino acid sequence of SEQ ID NO: 19.

The type of amino acid after substitution of Asn at position 317 (position 434 in the EU numbering system) is not particularly limited; however, substitution to Ala is preferred.

(xix)

Below is a preferred embodiment of IgG2 of the present invention, which has reduced heterogeneity in the hinge region and/or reduced Fcγ receptor-binding activity.

Antibodies comprising an IgG2 constant region comprising an amino acid sequence in which Ala at position 209, Pro at position 210, Thr at position 218, Cys at position 14, Arg at position 16, Cys at position 102, Glu at position 20, and Ser at position 21 in the amino acid sequence of SEQ ID NO: 20 have been substituted with other amino acids.

The type of amino acid after substitution is not particularly limited; however, substitutions of Ser for Ala at position 209 (position 330 in the EU numbering system), Ser for Pro at position 210 (position 331 in the EU numbering system), Ala for Thr at position 218 (position 339 in the EU numbering system), Ser for Cys at position 14 (position 131 in the EU numbering system), Lys for Arg at position 16 (position 133 in the EU numbering system), Ser for Cys at position 102 (position 219 in the EU numbering system), Gly for Glu at position 20 (position 137 in the EU numbering system), and Gly for Ser at position 21 (position 138 in the EU numbering system) are preferred.

Such IgG2 constant regions include, for example, IgG2 constant regions comprising the amino acid sequence of SEQ ID NO: 191 (M86).

In another preferred embodiment, IgG2 constant regions of the present invention include IgG2 constant regions resulting from the deletion of Gly at position 325 and Lys at position 326 in the above-described IgG2 constant regions to reduce C-terminal heterogeneity.

Such antibodies include, for example, IgG2 that comprises a constant region comprising the amino acid sequence of SEQ ID NO: 192 (M86ΔGK).

(xx)

Below is another preferred embodiment of the IgG2 constant regions of the present invention, which have reduced heterogeneity in the hinge region.

IgG2 constant regions comprising an amino acid sequence in which Cys at position 14, Arg at position 16, Cys at position 102, Glu at position 20, and Ser at position 21 in the amino acid sequence of SEQ ID NO: 20 have been substituted with other amino acids.

The type of amino acid after substitution is not particularly limited; however, substitutions of Ser for Cys at position 14 (position 131 in the EU numbering system), Lys for Arg at position 16 (position 133 in the EU numbering system), Ser for Cys at position 102 (position 219 in the EU numbering system), Gly for Glu at position 20 (position 137 in the EU numbering system), and Gly for Ser at position 21 (position 138 in the EU numbering system) are preferred.

Such IgG2 constant regions include, for example, IgG2 constant regions comprising the amino acid sequence of SEQ ID NO: 193 (M40).

In another preferred embodiment, the IgG2 constant regions of the present invention include IgG2 constant regions further comprising the deletion of Gly at position 325 and Lys at position 326 in the above-described IgG2 constant regions. Such antibodies include, for example, IgG2 constant regions comprising the amino acid sequence of SEQ ID NO: 194 (M40ΔGK).

(xxi) M14ΔGK, M17ΔGK, M11ΔGK, M31ΔGK, M58, M73, M86ΔGK, and M40ΔGK

The present invention also provides an antibody constant region comprising the amino acid sequence of SEQ ID NO: 24 (M14ΔGK). The present invention also provides an antibody constant region comprising the amino acid sequence of SEQ ID NO: 116 (M17ΔGK). The present invention also provides an antibody constant region comprising the amino acid sequence of SEQ ID NO: 25 (M11ΔGK). The present invention further provides an antibody constant region comprising the amino acid sequence of SEQ ID NO: 118 (M31ΔGK). The present invention further provides an antibody constant region comprising the amino acid sequence of SEQ ID NO: 151 (M58). The present invention further provides an antibody constant region comprising the amino acid sequence of SEQ ID NO: 153 (M73). The present invention further provides an antibody constant region comprising the amino acid sequence of SEQ ID NO: 164 (M83). The present invention further provides an antibody constant region comprising the amino acid sequence of SEQ ID NO: 192 (M86ΔGK). The present invention further provides an antibody constant region comprising the amino acid sequence of SEQ ID NO: 194 (M40ΔGK). These antibody constant regions have been optimized to have reduced Fcγ

receptor binding activity, reduced immunogenicity risk, improved stability under acidic conditions, reduced heterogeneity, improved retention in plasma, and/or higher stability in preparations in comparison with the IgG1 constant region.

The present invention provides antibodies comprising the antibody constant region of any one of (i) to (xxi) described above. There is no limitation on the type of antigen and origin of antibody, as long as the antibodies comprise an antibody constant region described above. The preferred antibodies include, for example, antibodies that bind to IL-6 receptor. Alternatively, the preferred antibodies include, for example, humanized antibodies. Such antibodies include, for example, antibodies comprising the variable region of humanized PM-1 antibody. Such a variable region of humanized PM-1 antibody may comprise any of the above-described amino acid substitutions, or other amino acid substitutions, deletions, additions, and/or insertions. Specifically, the substitutions include, for example, modifications that improve the affinity of (a) to (y) described above; modifications that lower the isoelectric point of (i) to (viii) described above, modifications that improve the stability of (α) to (ζ) described below; and modifications that reduce immunogenicity, but are not limited thereto.

In one embodiment, such antibodies include antibodies that comprise a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 113 (PF_1+M14ΔGK) and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 23 (PF1_L) (the light chain constant region may be kappa or lambda, or a modified form thereof) (PF1), but are not limited thereto.

Alternatively, the antibody constant regions described above and/or antibody molecules comprising an antibody constant region described above can be linked as a form of Fc fusion molecule to antibody-like binding molecule (scaffold molecules), bioactive peptides, binding peptides, or such.

The antibodies of the present invention can also be obtained by, for example, the following methods in addition to those described in the Examples. In one embodiment to obtain antibodies of the present invention, one or more amino acid residues are first substituted with amino acids of interest in at least one region selected from the group consisting of CDR, FR, and constant regions of an anti-IL-6 receptor antibody known to those skilled in the art. Methods for obtaining anti-IL-6 receptor antibodies known to those skilled in the art are not limited. Methods for substituting one or more amino acid residues with amino acids of interest in at least one region selected from the group consisting of the CDR, FR, and constant regions include, for example, site-directed mutagenesis (Hashimoto-Gotoh, T., Mizuno, T., Ogasahara, Y., and Nakagawa, M. An oligodeoxyribonucleotide-directed dual amber method for site-directed mutagenesis. Gene (1995) 152:271-275; Zoller, M. J., and Smith, M. Oligonucleotide-directed mutagenesis of DNA fragments cloned into M13 vectors. Methods

Enzymol. (1983) 100:468-500; Kramer, W., Drutsa, V., Jansen, H. W., Kramer, B., Pflugfelder, M., and Fritz, H. J. The gapped duplex DNA approach to oligonucleotide-directed mutation construction. Nucleic Acids Res. (1984) 12:9441-9456; Kramer W., and Fritz H. J. Oligonucleotide-directed construction of mutations *via* gapped duplex DNA Methods. Enzymol. (1987) 154:350-367; Kunkel, T. A. Rapid and efficient site-specific mutagenesis without phenotypic selection. Proc. Natl. Acad. Sci. USA (1985) 82:488-492). These methods can be used to substitute target amino acids in antibodies with amino acids of interest. Methods for substituting amino acids include library technologies such as framework shuffling (Mol. Immunol. 2007 Apr;44(11):3049-60) and CDR repair (US2006/0122377). Using these methods, amino acids can be substituted into appropriate frameworks and CDRs.

In another embodiment to obtain antibodies, an antibody that binds to IL-6 receptor is first prepared by methods known to those skilled in the art. When the prepared antibody is derived from a nonhuman animal, it can be humanized. Then, the prepared antibody is tested to assess whether it has neutralizing activity by using methods known to those skilled in the art. The binding activity and neutralizing activity of antibodies can be determined, for example, by the methods described in the Examples; however, such methods are not limited thereto. Next, one or more amino acid residues in at least one selected from the group consisting of CDR, FR, and constant regions of antibody are substituted with amino acids of interest.

More specifically, the present invention relates to methods for producing antibodies with improved neutralizing activity, binding activity, or stability, or reduced immunogenicity, which comprise the steps of:

(a) expressing a DNA encoding a heavy chain in which one or more amino acid residues in at least one region selected from the group consisting of CDR, FR, and constant regions are substituted with amino acids of interest, and a DNA encoding a light chain in which one or more amino acid residues in at least one region selected from the group consisting of CDR and FR regions are substituted with amino acids of interest; and

(b) collecting the expression products of step (a).

The first step of the production methods of the present invention is expressing a DNA encoding a mutant anti-IL-6 receptor antibody heavy chain in which one or more amino acid residues in at least one region selected from the group consisting of CDR, FR, and constant regions are substituted with amino acids of interest, and a DNA encoding an anti-IL-6 receptor antibody light chain in which one or more amino acid residues in at least one region selected from the group consisting of CDR and FR regions are substituted with amino acids of interest. A DNA encoding a heavy chain in which one or more amino acid residues in at least one region selected from the group consisting of CDR, FR, and constant regions are substituted with amino acids of interest can be prepared, for example, by obtaining a DNA encoding the CDR, FR, or

constant region of a wild type heavy chain, and introducing an appropriate substitution so that a codon encoding a particular amino acid in at least one selected from the group consisting of the CDR, FR, and constant regions encodes an amino acid of interest. Furthermore, a DNA encoding a light chain in which one or more amino acid residues in at least one selected from the group consisting of CDR and FR regions are substituted with amino acids of interest can be prepared, for example, by obtaining a DNA encoding the CDR and/or FR regions of a wild type light chain and introducing an appropriate substitution so that a codon encoding a particular amino acid in the CDR and/or FR regions encodes an amino acid of interest.

Alternatively, a DNA encoding a heavy chain in which one or more amino acid residues in at least one selected from the group consisting of CDR, FR, and constant regions are substituted with amino acids of interest can also be prepared by designing and then chemically synthesizing a DNA encoding a protein in which one or more amino acid residues in at least one selected from the group consisting of CDR, FR, and constant regions of the wild type heavy chain are substituted with amino acids of interest. Furthermore, a DNA encoding a light chain in which one or more amino acid residues in the CDR and/or FR regions are substituted with amino acids of interest can also be prepared by designing and then chemically synthesizing a DNA encoding a protein in which one or more amino acid residues in the CDR and/or FR regions of a wild type light chain are substituted with amino acids of interest.

The type of amino acid substitution includes the substitutions described herein, but is not limited thereto.

Alternatively, a DNA encoding a heavy chain in which one or more amino acid residues in at least one region selected from the group consisting of CDR, FR, and constant regions are substituted with amino acids of interest can also be prepared as a combination of partial DNAs. Such combinations of partial DNAs include, for example, the combination of a DNA encoding a variable region and a DNA encoding a constant region, and the combination of a DNA encoding an Fab region and a DNA encoding an Fc domain, but are not limited thereto. A DNA encoding a light chain can also be prepared as a combination of partial DNAs.

Methods for expressing the above-described DNAs include the methods described below. For example, a heavy chain expression vector is constructed by inserting a DNA encoding a heavy chain variable region into an expression vector along with a DNA encoding a heavy chain constant region. Likewise, a light chain expression vector is constructed by inserting a DNA encoding a light chain variable region into an expression vector along with a DNA encoding a light chain constant region. Alternatively, these heavy and light chain genes may be inserted into a single vector. Expression vectors include, for example, SV40 virus-based vectors, EB virus-based vectors, and BPV (papilloma virus)-based vectors, but are not limited thereto.

Host cells are co-transformed with an antibody expression vector constructed by the methods described above. Such host cells include the above-described cells such as CHO (Chinese hamster ovary) cells as well as microorganisms such as *E. coli*, yeast, and *Bacillus subtilis*, and plants and animals (Nature Biotechnology (2007) 25:563-565; Nature Biotechnology (1998) 16:773-777; Biochemical and Biophysical Research Communications (1999) 255:444-450; Nature Biotechnology (2005) 23:1159-1169; Journal of Virology (2001) 75:2803-2809; Biochemical and Biophysical Research Communications (2003) 308:94-100). The transformation can be preferably achieved by using electroporation, the lipofectin method (R. W. Malone *et al.*, Proc. Natl. Acad. Sci. USA (1989) 86:6077; P. L. Felgner *et al.*, Proc. Natl. Acad. Sci. USA (1987) 84:7413), calcium phosphate method (F. L. Graham & A. J. van der Eb, Virology (1973) 52:456-467), DEAE-Dextran method, and the like.

In the next step of antibody production, the expression products obtained in step (a) are collected. The expression products can be collected, for example, by culturing the transformants and then separating the products from the transformed cells or culture media. Separation and purification of antibodies can be achieved by an appropriate combination of methods such as centrifugation, ammonium sulfate fractionation, salting out, ultrafiltration, columns of 1q, FcRn, Protein A, and Protein G, affinity chromatography, ion exchange chromatography, and gel filtration chromatography.

Those skilled in the art can appropriately prepare the constant regions of the present invention according to the methods for preparing antibodies.

The present invention further relates to methods for enhancing the activity of an anti-IL-6 receptor antibody to bind or neutralize an IL-6 receptor, which comprise at least one step selected from the group consisting of:

(A) substituting Ser at position 1 in the amino acid sequence of SEQ ID NO: 1 (HCDR1) with another amino acid;

(B) substituting Trp at position 5 in the amino acid sequence of SEQ ID NO: 1 (HCDR1) with another amino acid;

(C) substituting Tyr at position 1 in the amino acid sequence of SEQ ID NO: 2 (HCDR2) with another amino acid;

(D) substituting Thr at position 8 in the amino acid sequence of SEQ ID NO: 2 (HCDR2) with another amino acid;

(E) substituting Thr at position 9 in the amino acid sequence of SEQ ID NO: 2 (HCDR2) with another amino acid;

(F) substituting Ser at position 1 in the amino acid sequence of SEQ ID NO: 3 (HCDR3) with another amino acid;

(G) substituting Leu at position 2 in the amino acid sequence of SEQ ID NO: 3 (HCDR3) with

another amino acid;
(H) substituting Thr at position 5 in the amino acid sequence of SEQ ID NO: 3 (HCDR3) with another amino acid;
(I) substituting Ala at position 7 in the amino acid sequence of SEQ ID NO: 3 (HCDR3) with another amino acid;
(J) substituting Met at position 8 in the amino acid sequence of SEQ ID NO: 3 (HCDR3) with another amino acid;
(K) substituting Ser at position 1 and Thr at position 5 in the amino acid sequence of SEQ ID NO: 3 (HCDR3) with other amino acids;
(L) substituting Leu at position 2, Ala at position 7, and Met at position 8 in the amino acid sequence of SEQ ID NO: 3 (HCDR3) with other amino acids;
(M) substituting Arg at position 1 in the amino acid sequence of SEQ ID NO: 4 (LCDR1) with another amino acid;
(N) substituting Gln at position 4 in the amino acid sequence of SEQ ID NO: 4 (LCDR1) with another amino acid;
(O) substituting Tyr at position 9 in the amino acid sequence of SEQ ID NO: 4 (LCDR1) with another amino acid;
(P) substituting Asn at position 11 in the amino acid sequence of SEQ ID NO: 4 (LCDR1) with another amino acid;
(Q) substituting Thr at position 2 in the amino acid sequence of SEQ ID NO: 5 (LCDR2) with another amino acid;
(R) substituting Gln at position 1 in the amino acid sequence of SEQ ID NO: 6 (LCDR3) with another amino acid;
(S) substituting Gly at position 3 in the amino acid sequence of SEQ ID NO: 6 (LCDR3) with another amino acid;
(T) substituting Tyr at position 9 in the amino acid sequence of SEQ ID NO: 4 (LCDR1) and Gly at position 3 in the amino acid sequence of SEQ ID NO: 6 (LCDR3) with other amino acids;
(U) substituting Thr at position 5 in the amino acid sequence of SEQ ID NO: 6 (LCDR3) with another amino acid;
(V) substituting Gln at position 1 and Thr at position 5 in the amino acid sequence of SEQ ID NO: 6 (LCDR3) with other amino acids; and
(W) substituting Thr at position 9 in the amino acid sequence of SEQ ID NO: 2 (HCDR2), and Ser at position 1 and Thr at position 5 in the amino acid sequence of SEQ ID NO: 3 (HCDR3) with other amino acids; or
(X) a step comprising (V) and (W).

In (A) described above, the type of amino acid after substitution is not particularly

limited as long as the affinity is improved; however, substitution to Trp, Thr, Asp, Asn, Arg, Val, Phe, Ala, Gln, Tyr, Leu, His, Glu, or Cys is preferred.

In (B) described above, the type of amino acid after substitution is not particularly limited as long as the affinity is improved; however, substitution to Ile or Val is preferred.

In (C) described above, the type of amino acid after substitution is not particularly limited as long as the affinity is improved; however, substitution to Phe is preferred.

In (D) described above, the type of amino acid after substitution is not particularly limited as long as the affinity is improved; however, substitution to Arg is preferred.

In (E) described above, the type of amino acid after substitution is not particularly limited as long as the affinity is improved; however, substitution to Ser or Asn is preferred.

In (F) described above, the type of amino acid after substitution is not particularly limited as long as the affinity is improved; however, substitution to Ile, Val, Thr, or Leu is preferred.

In (G) described above, the type of amino acid after substitution is not particularly limited as long as the affinity is improved; however, substitution to Thr is preferred.

In (H) described above, the type of amino acid after substitution is not particularly limited as long as the affinity is improved; however, substitution to Ala, Ile, or Ser is preferred. Other preferred substitutions include substitution of Ser for Thr at position 5.

In (I) described above, the type of amino acid after substitution is not particularly limited as long as the affinity is improved; however, substitution to Ser or Val is preferred.

In (J) described above, the type of amino acid after substitution is not particularly limited as long as the affinity is improved; however, substitution to Leu is preferred.

In (K) described above, the type of amino acid after substitution is not particularly limited as long as the affinity is improved; however, substitutions of Leu for Ser at position 1 and Ala for Thr at position 5 are preferred. Other preferred substitutions include those of Val for Ser at position 1 and Ala for Thr at position 5; Ile for Ser at position 1 and Ala for Thr at position 5; Thr for Ser at position 1 and Ala for Thr at position 5; Val for Ser at position 1 and Ile for Thr at position 5; Ile for Ser at position 1 and Ile for Thr at position 5; Thr for Ser at position 1 and Ile for Thr at position 5; and Leu for Ser at position 1 and Ile for Thr at position 5.

In (L) described above, the type of amino acid after substitution is not particularly limited as long as the affinity is improved; however, substitution of Thr for Leu at position 2, Val for Ala at position 7, and Leu for Met at position 8 are preferred.

In (M) described above, the type of amino acid after substitution is not particularly limited as long as the affinity is improved; however, substitution to Phe is preferred.

In (N) described above, the type of amino acid after substitution is not particularly limited as long as the affinity is improved; however, substitution to Arg or Thr is preferred.

In (O) described above, the type of amino acid after substitution is not particularly limited as long as the affinity is improved; however, substitution to Phe is preferred.

In (P) described above, the type of amino acid after substitution is not particularly limited as long as the affinity is improved; however, substitution to Ser is preferred.

In (Q) described above, the type of amino acid after substitution is not particularly limited as long as the affinity is improved; however, substitution to Gly is preferred.

In (R) described above, the type of amino acid after substitution is not particularly limited as long as the affinity is improved; however, substitution to Gly, Asn, or Ser is preferred.

In (S) described above, the type of amino acid after substitution is not particularly limited as long as the affinity is improved; however, substitution to Ser is preferred.

In (T) described above, the type of amino acid after substitution is not particularly limited as long as the affinity is improved; however, substitutions of Phe for Tyr in the amino acid sequence of SEQ ID NO: 4 (LCDR1) and Ser for Gly in the amino acid sequence of SEQ ID NO: 6 (LCDR3) are preferred.

In (U) described above, the type of amino acid after substitution is not particularly limited as long as the affinity is improved; however, substitution to Arg or Ser is preferred.

In (V) described above, the type of amino acid after substitution is not particularly limited as long as the affinity is improved; however, substitutions of Gly for Gln at position 1 and Ser for Thr at position 5 are preferred. Other preferred substitutions include those of Gly for Gln at position 1 and Arg for Thr at position 5.

In (W) described above, substitution of Asn for Thr at position 9 in the amino acid sequence of SEQ ID NO: 2 (HCDR2) is preferred. The preferred combinations of amino acids after substitution for Ser at position 1 and Thr at position 5 in the amino acid sequence of SEQ ID NO: 3 (HCDR3) include Leu and Ala, Val and Ala, Ile and Ala, Thr and Ala, Val and Ile, Ile and Ile, Thr and Ile, and Leu and Ile.

In the steps of (A) to (X) above, the method for amino acid substitution is not particularly limited. The substitution can be achieved, for example, by site-directed mutagenesis described above or a method described in the Examples. When an amino acid is substituted in a heavy chain variable region, the original amino acid sequence of the heavy chain variable region before substitution is preferably an amino acid sequence of the heavy chain variable region of a humanized PM-1 antibody. Alternatively, when an amino acid is substituted in a light chain variable region, the original amino acid sequence of the light chain variable region before substitution is preferably an amino acid sequence of the light chain variable region of a humanized PM-1 antibody. Furthermore, it is preferable to introduce the amino acid substitutions of steps (A) to (X) described above into the humanized PM-1 antibody.

The methods of the present invention for enhancing the binding or neutralizing activity

of an anti-IL-6 receptor antibody comprise at least any one of the steps of (A) to (X) described above. Specifically, the methods of the present invention may comprise two or more of the steps of (A) to (X) described above. Furthermore, the methods of the present invention may comprise other steps (for example, amino acid substitutions, deletions, additions and/or insertions other than those of (A) to (X) described above) as long as they comprise any one of the steps of (A) to (X) described above. Furthermore, for example, FR may comprise amino acid substitutions, deletions, additions and/or insertions, and the constant region may comprise amino acid substitutions, deletions, additions and/or insertions. It is preferable to introduce the amino acid substitutions described above into the humanized PM-1 antibody.

<Methods for reducing the immunogenicity risk of an anti-IL-6 receptor antibody>

The present invention also relates to methods for reducing the immunogenicity of an anti-IL-6 receptor antibody, which comprise the step of substituting Gly for Thr at position 2 in the amino acid sequence of SEQ ID NO: 5 (LCDR2). The methods of the present invention for reducing the immunogenicity of an anti-IL-6 receptor antibody may comprise other steps of amino acid substitution, as long as they comprise the step of substituting Gly for Thr at position 2 in the amino acid sequence of SEQ ID NO: 5 (LCDR2). The method for amino acid substitution is not particularly limited. The substitution can be achieved, for example, by site-directed mutagenesis described above or a method described in the Examples.

It is preferable to introduce the amino acid substitutions described above into the humanized PM-1 antibody or a variant thereof comprising substitutions, deletions, and/or insertions.

<Methods for lowering the isoelectric point of an anti-IL-6 receptor antibody>

The present invention also relates to methods for lowering the isoelectric point of an anti-IL-6 receptor antibody, which comprise at least one step selected from the group consisting of:

(i) substituting Gln at position 16 in the amino acid sequence of SEQ ID NO: 7 (HFR1) with another amino acid;

(ii) substituting Arg at position 8 in the amino acid sequence of SEQ ID NO: 8 (HFR2) with another amino acid;

(iii) substituting Arg at position 16 in the amino acid sequence of SEQ ID NO: 9 (HFR3) with another amino acid;

(iv) substituting Gln at position 3 in the amino acid sequence of SEQ ID NO: 10 (HFR4) with another amino acid;

(v) substituting Arg at position 18 in the amino acid sequence of SEQ ID NO: 11 (LFR1) with another amino acid;

(vi) substituting Lys at position 11 in the amino acid sequence of SEQ ID NO: 12 (LFR2) with

another amino acid;
(vii) substituting Gln at position 23 in the amino acid sequence of SEQ ID NO: 13 (LFR3) with another amino acid;
(viii) substituting Lys at position 10 in the amino acid sequence of SEQ ID NO: 14 (LFR4) with another amino acid;
(ix) substituting Ser at position 1 in the amino acid sequence of SEQ ID NO: 1 (HCDR1) with another amino acid;
(x) substituting Arg at position 1 in the amino acid sequence of SEQ ID NO: 4 (LCDR1) with another amino acid;
(xi) substituting Arg at position 4 in the amino acid sequence of SEQ ID NO: 5 (LCDR2) with another amino acid;
(xii) substituting Arg at position 13 in the amino acid sequence of SEQ ID NO: 7 (HFR1) with another amino acid;
(xiii) substituting Lys at position 15 and/or Ser at position 16 in the amino acid sequence of SEQ ID NO: 2 (HFR1) or 100 with other amino acids;
(xiv) substituting Gln at position 4 in the amino acid sequence of SEQ ID NO: 4 (LCDR1) or 101 with another amino acid; and
(xv) substituting His at position 6 in the amino acid sequence of SEQ ID NO: 5 (LCDR2) or 103 with another amino acid.

In (i) described above, the type of amino acid after substitution is not particularly limited as long as the isoelectric point is lowered; however, substitution to Glu is preferred.

In (ii) described above, the type of amino acid after substitution is not particularly limited as long as the isoelectric point is lowered; however, substitution to Glu is preferred.

In (iii) described above, the type of amino acid after substitution is not particularly limited as long as the isoelectric point is lowered; however, substitution to Lys is preferred.

In (iv) described above, the type of amino acid after substitution is not particularly limited as long as the isoelectric point is lowered; however, substitution to Glu is preferred.

In (v) described above, the type of amino acid after substitution is not particularly limited as long as the isoelectric point is lowered; however, substitution to Ser is preferred.

In (vi) described above, the type of amino acid after substitution is not particularly limited as long as the isoelectric point is lowered; however, substitution to Glu is preferred.

In (vii) described above, the type of amino acid after substitution is not particularly limited as long as the isoelectric point is lowered; however, substitution to Glu is preferred.

In (viii) described above, the type of amino acid after substitution is not particularly limited as long as the isoelectric point is lowered; however, substitution to Glu is preferred.

In (ix) described above, the type of amino acid after substitution is not particularly

limited as long as the isoelectric point is lowered; however, substitution to Asp is preferred.

In (x) described above, the type of amino acid after substitution is not particularly limited as long as the isoelectric point is lowered; however, substitution to Gln is preferred.

In (xi) described above, the type of amino acid after substitution is not particularly limited as long as the isoelectric point is lowered; however, substitution to Glu is preferred.

In (xii) described above, the type of amino acid after substitution is not particularly limited as long as the isoelectric point is lowered; however, substitution to Lys is preferred.

In (xiii) described above, the type of amino acid after substitution is not particularly limited as long as the isoelectric point is lowered; however, substitutions to Gln for Lys at position 15 and Asp for Ser at position 16 are preferred.

In (xiv) described above, the type of amino acid after substitution is not particularly limited as long as the isoelectric point is lowered; however, substitution to Glu is preferred.

In (xv) described above, the type of amino acid after substitution is not particularly limited as long as the isoelectric point is lowered; however, substitution to Glu is preferred.

In the steps of (i) to (xv) described above, the method for amino acid substitution is not particularly limited. The substitution can be achieved, for example, by site-directed mutagenesis described above or a method described in the Examples. When an amino acid is substituted in a heavy chain variable region, the original amino acid sequence of the heavy chain variable region before substitution is preferably an amino acid sequence of the heavy chain variable region of a humanized PM-1 antibody. Alternatively, when an amino acid is substituted in a light chain variable region, the original amino acid sequence of the light chain variable region before substitution is preferably an amino acid sequence of the light chain variable region of a humanized PM-1 antibody. Furthermore, it is preferable to introduce the amino acid substitutions of the steps of (i) to (xv) described above into the humanized PM-1 antibody.

The methods of the present invention for lowering the isoelectric point of an anti-IL-6 receptor antibody comprise at least any one of the steps of (i) to (xv) described above. Specifically, the methods of the present invention may comprise two or more of the steps of (i) to (xv) described above. Furthermore, the methods of the present invention may comprise other steps (for example, amino acid substitutions, deletions, additions and/or insertions other than those of (i) to (xv) described above) as long as they comprise any one of the steps of (i) to (xv) described above. Furthermore, for example, the constant region may comprise amino acid substitutions, deletions, additions and/or insertions.

<Methods for improving the stability of an anti-IL-6 receptor antibody>

The present invention also relates to methods for increasing the stability of an anti-IL-6 receptor antibody, which comprise at least one step selected from the group consisting of:

(α) substituting Met at position 4 in the amino acid sequence of SEQ ID NO: 9 (HFR3) with another amino acid;

(β) substituting Leu at position 5 in the amino acid sequence of SEQ ID NO: 9 (HFR3) with another amino acid;

(γ) substituting Thr at position 9 in the amino acid sequence of SEQ ID NO: 2 (HCDR2) with another amino acid;

(δ) substituting Thr at position 5 in the amino acid sequence of SEQ ID NO: 6 (LCDR3) with another amino acid;

(ε) substituting Ser at position 16 in the amino acid sequence of SEQ ID NO: 2 (HCDR2) with another amino acid; and

(ζ) substituting Ser at position 5 in the amino acid sequence of SEQ ID NO: 10 (FR4) with another amino acid.

In (α) described above, the type of amino acid after substitution is not particularly limited as long as the stability is improved; however, substitution to Ile is preferred.

In (β) described above, the type of amino acid after substitution is not particularly limited as long as the stability is improved; however, substitution to Ser is preferred.

In (γ) described above, the type of amino acid after substitution is not particularly limited as long as the stability is improved; however, substitution to Asn is preferred.

In (δ) described above, the type of amino acid after substitution is not particularly limited as long as the stability is improved; however, substitution to Ser is preferred.

In (ε) described above, the type of amino acid after substitution is not particularly limited as long as the stability is improved; however, substitution to Gly is preferred.

In (ζ) described above, the type of amino acid after substitution is not particularly limited as long as the stability is improved; however, substitution to Ile is preferred.

In the steps of (α) to (ζ) described above, the method for amino acid substitution is not particularly limited. The substitution can be achieved, for example, by site-directed mutagenesis described above or a method described in the Examples. When an amino acid is substituted in a heavy chain variable region, the original amino acid sequence of the heavy chain variable region before substitution is preferably an amino acid sequence of the heavy chain variable region of a humanized PM-1 antibody. Alternatively, when an amino acid is substituted in a light chain variable region, the original amino acid sequence of the light chain variable region before substitution is preferably an amino acid sequence of the light chain variable region of a humanized PM-1 antibody. Furthermore, it is preferable to introduce the amino acid substitutions of (α) to (ζ) described above into the humanized PM-1 antibody.

The methods of the present invention for improving the stability of an anti-IL-6 receptor antibody comprise at least any one of the steps of (α) to (ζ) described above. Specifically, the

methods of the present invention may comprise two or more of the steps of (α) to (ζ) described above. Furthermore, the methods of the present invention may comprise other steps (for example, amino acid substitutions, deletions, additions and/or insertions other than those of (α) to (ζ) described above) as long as they comprise any one of the steps of (α) to (ζ) described above. Furthermore, for example, the constant region may comprise amino acid substitutions, deletions, additions and/or insertions.

<Methods for reducing the immunogenicity of an anti-IL-6 receptor antibody>

The present invention also relates to methods for reducing the immunogenicity of an anti-IL-6 receptor antibody, in particular, a humanized PM-1 antibody, which comprise the step of substituting Lys for Arg at position 13, Glu for Gln at position 16, Ala for Thr at position 23, and/or Ser for Thr at position 30 in the amino acid sequence of SEQ ID NO: 7 (HFR1). The methods of the present invention for reducing the immunogenicity of an anti-IL-6 receptor antibody may comprise other steps of amino acid substitution, as long as they comprise the step of substituting Ser for Thr at position 30 in the amino acid sequence of SEQ ID NO: 7 (HFR1).

The present invention further relates to methods for reducing the immunogenicity of an anti-IL-6 receptor antibody, in particular, a humanized PM-1 antibody, which comprise the step of substituting Val for Ala at position 27 in the amino acid sequence of SEQ ID NO: 90 (HFR3). The methods of the present invention for reducing the immunogenicity of an anti-IL-6 receptor antibody may comprise other steps of amino acid substitution, as long as they comprise the step of substituting Val for Ala at position 27 in the amino acid sequence of SEQ ID NO: 90 (HFR3).

The method for amino acid substitution is not particularly limited. The substitution can be achieved, for example, by site-directed mutagenesis described above or a method described in the Examples.

The present invention further relates to methods for reducing antibody immunogenicity, which comprise converting the FR3 of an anti-IL-6 receptor antibody, in particular, a humanized PM-1 antibody, H53/L28, or PF1 antibody, into an FR3 comprising the amino acid sequence of SEQ ID NO: 128 or 129.

<Methods for improving antibody stability under acidic conditions>

The present invention also relates to methods for improving antibody stability under acidic conditions, which comprise the step of substituting Met at position 276 (position 397 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 (IgG2) with another amino acid. The methods of the present invention for improving antibody stability under acidic conditions may comprise other steps of amino acid substitution, as long as they comprise the step of substituting Met at position 276 (position 397 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 (IgG2) with another amino acid. The type of amino acid after substitution is not particularly limited; however, substitution to Val is preferred. The method

for amino acid substitution is not particularly limited. The substitution can be achieved, for example, by site-directed mutagenesis described above or a method described in the Examples.

The kind of target antibody is not particularly limited; however, the antibody is preferably an anti-human IL-6 receptor antibody, more preferably a humanized PM-1 antibody or a variant thereof comprising substitutions, deletions, and/or insertions.

<Methods for reducing the heterogeneity originated from the hinge region of IgG2 constant region>

The present invention also relates to methods for reducing antibody heterogeneity, which comprise the step of substituting Cys at position 14 (position 131 in the EU numbering system), Arg at position 16 (position 133 in the EU numbering system), and/or Cys at position 102 (position 219 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 (IgG2) with other amino acids. The type of amino acid after substitution is not particularly limited; however, substitutions of Ser for Cys at position 14, Lys for Arg at position 16, and Ser for Cys at position 102 are preferred. The methods of the present invention for reducing antibody heterogeneity may comprise other steps of amino acid substitution, as long as they comprise the step of substituting Cys at position 14 (position 131 in the EU numbering system), Arg at position 16 (position 133 in the EU numbering system), and/or Cys at position 102 (position 219 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 (IgG2). The method for amino acid substitution is not particularly limited. The substitutions can be achieved, for example, by site-directed mutagenesis described above or a method described in the Examples. In the amino acid substitution, all of the three amino acids described above may be substituted or one or two (for example, positions 14 and 102) of them may be substituted.

The kind of target antibody is not particularly limited; however, the antibody is preferably an anti-human IL-6 receptor antibody, more preferably a humanized PM-1 antibody or a variant thereof comprising substitutions, deletions, and/or insertions.

<Methods for reducing the heterogeneity originated from deletion of C-terminal amino acids in an IgG2 constant region>

The present invention also relates to methods for reducing antibody heterogeneity, which comprise the step of deleting Gly at position 325 (position 446 in the EU numbering system) and Lys at position 326 (position 447 in the EU numbering system) in an IgG2 constant region comprising the amino acid sequence of SEQ ID NO: 20. The methods of the present invention for reducing antibody heterogeneity may comprise other steps of amino acid substitution, as long as they comprise the step of deleting Gly at position 325 (position 446 in the EU numbering system) and Lys at position 326 (position 447 in the EU numbering system) in an IgG2 constant region comprising the amino acid sequence of SEQ ID NO: 20. The method for

amino acid substitution is not particularly limited. The substitution can be achieved, for example, by site-directed mutagenesis described above or a method described in the Examples.

The kind of target antibody is not particularly limited; however, the antibody is preferably an anti-human IL-6 receptor antibody, more preferably a humanized PM-1 antibody or a variant thereof comprising substitutions, deletions, and/or insertions.

<Methods for reducing the FcγR binding while maintaining the human sequence in the IgG2 constant region>

The present invention also relates to methods for reducing the FcγR binding of an antibody, which comprise the step of substituting Ser for Ala at position 209 (EU330), Ser for Pro at position 210 (EU331), and Ala for Thr at position 218 (EU339) in an IgG2 constant region comprising the amino acid sequence of SEQ ID NO: 20. The methods of the present invention for reducing the FcγR binding of an antibody may comprise other steps of amino acid substitution, as long as they comprise the step of substituting Ser for Ala at position 209 (EU330), Ser for Pro at position 210 (EU331), and Ala for Thr at position 218 (EU339) in an IgG2 constant region comprising the amino acid sequence of SEQ ID NO: 20. The method for amino acid substitution is not particularly limited. The substitution can be achieved, for example, by site-directed mutagenesis described above or a method described in the Examples.

<Methods for improving the retention in plasma by substituting amino acids of IgG2 constant region>

The present invention also relates to methods for improving the retention in plasma of an antibody, which comprise the step of substituting His at position 147 (EU268), Arg at position 234 (EU355), and/or Gln at position 298 (EU419) in an IgG2 constant region comprising the amino acid sequence of SEQ ID NO: 20. The methods of the present invention for improving the retention in plasma of an antibody may comprise other steps of amino acid substitution, as long as they comprise the above-described step. The type of amino acid after substitution is not particularly limited; however, substitutions of Gln for His at position 147 (EU268), Gln for Arg at position 234 (EU355), and Glu for Gln at position 298 (EU419) are preferred.

The present invention also relates to methods for improving the retention in plasma of an antibody, which comprise the step of substituting Asn at position 313 (EU434) in an IgG2 constant region comprising the amino acid sequence of SEQ ID NO: 20 or 151 (M58). The type of amino acid after substitution is not particularly limited; however, substitution to Ala is preferred. The methods of the present invention for improving the retention in plasma of an antibody may comprise other steps of amino acid substitution, as long as they comprise the above-described step.

The kind of target antibody is not particularly limited; however, the antibody is preferably an anti-human IL-6 receptor antibody, more preferably a humanized PM-1 antibody

or a variant thereof comprising substitutions, deletions, and/or insertions.

The present invention also relates to methods for reducing antibody heterogeneity originated from the hinge region of IgG2, methods for improving antibody stability under acidic conditions, methods for reducing antibody heterogeneity originated from C-terminus, and/or methods for reducing the FcγR binding of an antibody, all of which comprise in an IgG2 constant region comprising the amino acid sequence of SEQ ID NO: 20 (M14ΔGK), the steps of:

(a) substituting Ser for Ala at position 209 (position 330 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(b) substituting Ser for Pro at position 210 (position 331 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(c) substituting Ala for Thr at position 218 (position 339 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(d) substituting Val for Met at position 276 (position 397 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(e) substituting Ser for Cys at position 14 (position 131 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(f) substituting Lys for Arg at position 16 (position 133 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(g) substituting Ser for Cys at position 102 (position 219 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(h) substituting Gly for Glu at position 20 (position 137 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(i) substituting Gly for Ser at position 21 (position 138 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20; and

(j) deleting Gly at position 325 and Lys at position 326 (positions 446 and 447 in the EU numbering system, respectively) in the amino acid sequence of SEQ ID NO: 20.

The methods of the present invention may comprise other steps such as amino acid substitution and deletion, as long as they comprise the steps described above. The methods for amino acid substitution and deletion are not particularly limited. The substitution and deletion can be achieved, for example, by site-directed mutagenesis described above or a method described in the Examples.

The kind of target antibody is not particularly limited; however, it is preferably an anti-human IL-6 receptor antibody, more preferably a humanized PM-1 antibody or a variant thereof comprising substitutions, deletions, and/or insertions.

The present invention also relates to methods for reducing the heterogeneity originated from the hinge region of IgG2, methods for improving antibody stability under acidic conditions,

and/or methods for reducing antibody heterogeneity originated from C-terminus, all of which comprise in an IgG2 constant region comprising the amino acid sequence of SEQ ID NO: 20 (M31ΔGK), the steps of:

(a) substituting Val for Met at position 276 (position 397 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(b) substituting Ser for Cys at position 14 (position 131 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(c) substituting Lys for Arg at position 16 (position 133 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(d) substituting Ser for Cys at position 102 (position 219 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(e) substituting Gly for Glu at position 20 (position 137 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(f) substituting Gly for Ser at position 21 (position 138 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20; and

(g) deleting Gly at position 325 and Lys at position 326 (positions 446 and 447 in the EU numbering system, respectively) in the amino acid sequence of SEQ ID NO: 20.

The present invention also relates to methods for reducing antibody heterogeneity originated from the hinge region of IgG2, methods for improving antibody retention in plasma, and/or methods for reducing antibody heterogeneity originated from C-terminus, all of which comprise in an IgG2 constant region comprising the amino acid sequence of SEQ ID NO: 20 (M58), the steps of:

(a) substituting Ser for Cys at position 14 (position 131 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(b) substituting Lys for Arg at position 16 (position 133 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(c) substituting Ser for Cys at position 102 (position 219 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(d) substituting Gly for Glu at position 20 (position 137 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(e) substituting Gly for Ser at position 21 (position 138 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(f) substituting Gln for His at position 147 (position 268 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(g) substituting Gln for Arg at position 234 (position 355 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(h) substituting Glu for Gln at position 298 (position 419 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20; and

(i) deleting Gly at position 325 and Lys at position 326 (positions 446 and 447 in the EU numbering system, respectively) in the amino acid sequence of SEQ ID NO: 20.

The present invention also relates to methods for reducing antibody heterogeneity originated from the hinge region of IgG2, methods for improving antibody retention in plasma, and/or methods for reducing antibody heterogeneity originated from C-terminus, all of which comprise in an IgG2 constant region comprising the amino acid sequence of SEQ ID NO: 20 (M73), the steps of:

(a) substituting Ser for Cys at position 14 (position 131 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(b) substituting Lys for Arg at position 16 (position 133 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(c) substituting Ser for Cys at position 102 (position 219 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(d) substituting Gly for Glu at position 20 (position 137 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(e) substituting Gly for Ser at position 21 (position 138 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(f) substituting Gln for His at position 147 (position 268 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(g) substituting Gln for Arg at position 234 (position 355 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(h) substituting Glu for Gln at position 298 (position 419 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20;

(i) substituting Ala for Asn at position 313 (position 434 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20; and

(j) deleting Gly at position 325 and Lys at position 326 (positions 446 and 447 in the EU numbering system, respectively) in the amino acid sequence of SEQ ID NO: 20.

The present invention also relates to methods for reducing the heterogeneity originated from the hinge region of IgG2, methods for reducing antibody heterogeneity originated from C-terminus, and/or methods for reducing the FcγR binding of an antibody, all of which comprise, in an IgG2 constant region comprising the amino acid sequence of SEQ ID NO: 20 (M86ΔGK), the steps of:

(a) substituting Ala at position 209 (position 330 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 with another amino acid;

(b) substituting Pro at position 210 (position 331 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 with another amino acid;
(c) substituting Thr at position 218 (position 339 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 with another amino acid;
(d) substituting Cys at position 14 (position 131 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 with another amino acid;
(e) substituting Arg at position 16 (position 133 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 with another amino acid;
(f) substituting Cys at position 102 (position 219 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 with another amino acid;
(g) substituting Glu at position 20 (position 137 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 with another amino acid;
(h) substituting Ser at position 21 (position 138 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 with another amino acid; and
(i) deleting Gly at position 325 and Lys at position 326 (positions 446 and 447 in the EU numbering system, respectively) in the amino acid sequence of SEQ ID NO: 20.

The type of amino acid after substitution is not particularly limited; however, substitutions of Ser for Ala at position 209 (position 330 in the EU numbering system), Ser for Pro at position 210 (position 331 in the EU numbering system), Ala for Thr at position 218 (position 339 in the EU numbering system), Ser for Cys at position 14 (position 131 in the EU numbering system), Lys for Arg at position 16 (position 133 in the EU numbering system), Ser for Cys at position 102 (position 219 in the EU numbering system), Gly for Glu at position 20 (position 137 in the EU numbering system), and Gly for Ser at position 21 (position 138 in the EU numbering system) are preferred.

The present invention further relates to methods for reducing the heterogeneity originated from the hinge region of IgG2 and/or methods for reducing antibody heterogeneity originated from C-terminus, which comprise in an IgG2 constant region comprising the amino acid sequence of SEQ ID NO: 20 (M40ΔGK), the steps of:
(a) substituting Cys at position 14 (position 131 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 with another amino acid;
(b) substituting Arg at position 16 (position 133 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 with another amino acid;
(c) substituting Cys at position 102 (position 219 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 with another amino acid;
(d) substituting Glu at position 20 (position 137 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 with another amino acid;

(e) substituting Ser at position 21 (position 138 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 20 with another amino acid; and
(f) deleting Gly at position 325 and Lys at position 326 (positions 446 and 447 in the EU numbering system, respectively) in the amino acid sequence of SEQ ID NO: 20.

The type of amino acid after substitution is not particularly limited; however, substitutions of Ser for Cys at position 14 (position 131 in the EU numbering system), Lys for Arg at position 16 (position 133 in the EU numbering system), Ser for Cys at position 102 (position 219 in the EU numbering system), Gly for Glu at position 20 (position 137 in the EU numbering system), and Gly for Ser at position 21 (position 138 in the EU numbering system) are preferred.

The methods of the present invention may comprise other steps such as amino acid substitution and deletion, as long as they comprise the steps described above. The methods for amino acid substitution and deletion are not particularly limited. The substitution and deletion can be achieved, for example, by site-directed mutagenesis described above or a method described in the Examples.

The kind of target antibody is not particularly limited; however, it is preferably an anti-human IL-6 receptor antibody, more preferably a humanized PM-1 antibody or a variant thereof comprising substitutions, deletions, and/or insertions.

<Methods for improving the stability of an IgG4 constant region under acidic conditions>

The present invention also relates to methods for improving antibody stability under acidic conditions, which comprise the step of substituting Arg at position 289 (position 409 in the EU numbering system) of an IgG4 constant region comprising the amino acid sequence of SEQ ID NO: 21 (Mol. Immunol. 1993 Jan;30(1):105-8) with another amino acid. The methods of the present invention for improving antibody stability under acidic conditions may comprise other steps of amino acid substitution, as long as they comprise the step of substituting Arg at position 289 (position 409 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 21 (human IgG4 constant region) with another amino acid. The type of amino acid after substitution is not particularly limited; however, substitution to Lys is preferred. The method for amino acid substitution is not particularly limited. The substitution can be achieved, for example, by site-directed mutagenesis described above or a method described in the Examples.

The kind of target antibody is not particularly limited; however, the antibody is preferably an anti-human IL-6 receptor antibody, more preferably a humanized PM-1 antibody or a variant thereof comprising substitutions, deletions, and/or insertions.

<Methods for reducing the heterogeneity originated from deletion of C-terminal amino acids in an IgG4 constant region>

The present invention also relates to methods for reducing the heterogeneity of an

antibody, which comprise the step of deleting Gly at position 326 (position 446 in the EU numbering system) and Lys at position 327 (position 447 in the EU numbering system) in an IgG4 constant region comprising the amino acid sequence of SEQ ID NO: 21 (Mol. Immunol. 1993 Jan;30(1):105-8). The methods of the present invention for reducing the heterogeneity may comprise other steps of amino acid substitution, as long as they comprise the step of deleting Lys at position 327 (position 447 in the EU numbering system) and/or Gly at position 326 (position 446 in the EU numbering system) in an IgG4 constant region comprising the amino acid sequence of SEQ ID NO: 21 (Mol. Immunol. 1993 Jan;30(1):105-8). The method for amino acid substitution is not particularly limited. The substitution can be achieved, for example, by site-directed mutagenesis described above or a method described in the Examples.

The kind of target antibody is not particularly limited; however, the antibody is preferably an anti-human IL-6 receptor antibody, more preferably a humanized PM-1 antibody or a variant thereof comprising substitutions, deletions, and/or insertions.

The present invention also relates to methods for improving the stability under acidic conditions, methods for reducing the heterogeneity originated from C-terminus, and/or methods for reducing the FcγR binding of an antibody, all of which comprise in an IgG4 constant region comprising the amino acid sequence of SEQ ID NO: 21 (Mol. Immunol. 1993 Jan;30(1):105-8) (M11ΔGK), the steps of:

(a) substituting Ser for Cys at position 14 (position 131 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 21;

(b) substituting Lys for Arg at position 16 (position 133 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 21;

(c) substituting Gly for Glu at position 20 (position 137 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 21;

(d) substituting Gly for Ser at position 21 (position 138 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 21;

(e) substituting Thr for Arg at position 97 (position 214 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 21;

(f) substituting Arg for Ser at position 100 (position 217 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 21;

(g) substituting Ser for Tyr at position 102 (position 219 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 21;

(h) substituting Cys for Gly at position 103 (position 220 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 21;

(i) substituting Val for Pro at position 104 (position 221 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 21;

(j) substituting Glu for Pro at position 105 (position 222 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 21;
(k) substituting Pro for Glu at position 113 (position 233 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 21;
(l) substituting Val for Phe at position 114 (position 234 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 21;
(m) substituting Ala for Leu at position 115 (position 235 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 21;
(n) deleting Gly at position 116 (position 236 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 21;
(o) substituting Lys for Arg at position 289 (position 409 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 21; and
(p) deleting Gly at position 236 and Lys at position 237 (positions 446 and 447 in the EU numbering system, respectively) in the amino acid sequence of SEQ ID NO: 21.

The methods of the present invention may comprise other steps, such as amino acid substitution and deletion, as long as they comprise the steps described above. The method for amino acid substitution and deletion are not particularly limited. The substitution and deletion can be achieved, for example, by site-directed mutagenesis described above or a method described in the Examples.

The kind of target antibody is not particularly limited; however, the antibody is preferably an anti-human IL-6 receptor antibody, more preferably a humanized PM-1 antibody or a variant thereof comprising substitutions, deletions, and/or insertions.

<Methods for reducing the heterogeneity originated from deletion of C-terminal amino acids in an IgG1 constant region>

The present invention also relates to methods for reducing antibody heterogeneity, which comprise the step of deleting Gly at position 329 (position 446 in the EU numbering system) and Lys at position 330 (position 447 in the EU numbering system) in an IgG1 constant region comprising the amino acid sequence of SEQ ID NO: 19. The methods of the present invention for reducing antibody heterogeneity may comprise other steps of amino acid substitutions, as long as they comprise the step of deleting Lys at position 330 (position 447 in the EU numbering system) and Gly at position 329 (position 446 in the EU numbering system) in an IgG1 constant region comprising the amino acid sequence of SEQ ID NO: 19. The method for amino acid substitution is not particularly limited. The substitution can be achieved, for example, by site-directed mutagenesis described above or a method described in the Examples.

<Methods for improving the retention in plasma by substituting amino acids of IgG1 constant

region>

The present invention relates to methods for improving the antibody retention in plasma, which comprise the step of substituting Asn at position 317 (EU434) in an IgG1 constant region comprising the amino acid sequence of SEQ ID NO: 19 with another amino acid. The type of amino acid after substitution is not particularly limited; however, substitution to Ala is preferred. The methods of the present invention for improving the retention in plasma may comprise other steps of amino acid substitution, as long as they comprise the above-described step.

The present invention also relates to methods for improving the retention in plasma and/or methods for reducing the heterogeneity originated from C-terminus, both of which comprise, in an IgG1 constant region comprising the amino acid sequence of SEQ ID NO: 19 (M83), the steps of:

(a) substituting Ala for Asn at position 317 (EU 434) in the amino acid sequence of SEQ ID NO: 19; and

(b) deleting Lys at position 330 (position 447 in the EU numbering system) and Gly at position 329 (position 446 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 19.

The kind of target antibody is not particularly limited; however, the antibody is preferably an anti-human IL-6 receptor antibody, more preferably a humanized PM-1 antibody or a variant thereof comprising substitutions, deletions, and/or insertions.

The constant regions of the present invention described above can be combined with any antibody variable regions, and preferably with variable regions derived from antibodies against human IL-6 receptor. Variable regions of antibodies against human IL-6 receptor include, for example, variable regions of a humanized PM-1 antibody. The variable regions of a humanized PM-1 antibody may not comprise any amino acid substitutions or may comprise substitutions such as those described above.

The present invention provides pharmaceutical compositions comprising an antibody of the present invention. The pharmaceutical compositions of the present invention are useful in treating diseases associated with IL-6, such as rheumatoid arthritis.

The pharmaceutical compositions of the present invention can be formulated, in addition to the antibodies, with pharmaceutically acceptable carriers by known methods. For example, the compositions can be used parenterally, when the antibodies are formulated in a sterile solution or suspension for injection using water or any other pharmaceutically acceptable liquid. For example, the compositions can be formulated by appropriately combining the antibodies with pharmaceutically acceptable carriers or media, specifically, sterile water or physiological saline, vegetable oils, emulsifiers, suspending agents, surfactants, stabilizers, flavoring agents, excipients, vehicles, preservatives, binding agents, and such, by mixing them at a unit dose and form required by generally accepted pharmaceutical implementations. The

content of the active ingredient in such a formulation is adjusted so that an appropriate dose within the required range can be obtained.

Sterile compositions for injection can be formulated using vehicles such as distilled water for injection, according to standard protocols.

Aqueous solutions used for injection include, for example, physiological saline and isotonic solutions containing glucose or other adjuvants such as D-sorbitol, D-mannose, D-mannitol, and sodium chloride. These can be used in conjunction with suitable solubilizers such as alcohol, specifically ethanol, polyalcohols such as propylene glycol and polyethylene glycol, and non-ionic surfactants such as Polysorbate 80™ and HCO-50.

Oils include sesame oils and soybean oils, and can be combined with solubilizers such as benzyl benzoate or benzyl alcohol. These may also be formulated with buffers, for example, phosphate buffers or sodium acetate buffers; analgesics, for example, procaine hydrochloride; stabilizers, for example, benzyl alcohol or phenol; or antioxidants. The prepared injections are typically aliquoted into appropriate ampules.

The administration is preferably carried out parenterally, and specifically includes injection, intranasal administration, intrapulmonary administration, and percutaneous administration. For example, injections can be administered systemically or locally by intravenous injection, intramuscular injection, intraperitoneal injection, or subcutaneous injection.

Furthermore, the method of administration can be appropriately selected according to the age and symptoms of the patient. A single dose of the pharmaceutical composition containing an antibody or a polynucleotide encoding an antibody can be selected, for example, from the range of 0.0001 to 1,000 mg per kg of body weight. Alternatively, the dose may be, for example, in the range of 0.001 to 100,000 mg/person. However, the dose is not limited to these values. The dose and method of administration vary depending on the patient's body weight, age, and symptoms, and can be appropriately selected by those skilled in the art.

As used herein, the three-letter and single-letter codes for respective amino acids are as follows:

Alanine: Ala (A)
Arginine: Arg (R)
Asparagine: Asn (N)
Aspartic acid: Asp (D)
Cysteine: Cys (C)
Glutamine: Gln (Q)
Glutamic acid: Glu (E)
Glycine: Gly (G)

Histidine: His (H)
Isoleucine: Ile (I)
Leucine: Leu (L)
Lysine: Lys (K)
Methionine: Met (M)
Phenylalanine: Phe (F)
Proline: Pro (P)
Serine: Ser (S)
Threonine: Thr (T)
Tryptophan: Trp (W)
Tyrosine: Tyr (Y)
Valine: Val (V)

All prior art documents cited herein are incorporated by reference in their entirety.

Examples

Herein below, the present invention is specifically described with reference to the Examples, but it is not to be construed as being limited thereto.

[Example 1] Improvement of antigen-binding activity through CDR modification using affinity maturation technology

Preparation of SR344

A CHO cell line constitutively expressing a sequence of N-terminal 1st to 344th amino acids of soluble human IL-6R (hereinafter "SR344") reported in J. Biochem. (1990) 108:673-676 (Yamasaki *et al.*, Science (1988) 241:825-828 (GenBank #X12830)) was prepared.

SR344 was purified from the culture supernatant of SR344-expresssing CHO cells using three types of column chromatography: Blue Sepharose 6 FF column chromatography, affinity chromatography with an SR344-specific antibody-immobilized column, and gel filtration column chromatography.

The culture supernatant was directly loaded onto a Blue Sepharose 6 FF column (GE Healthcare Bio-Sciences) equilibrated with 20 mM Tris-HCl buffer (pH 8.0), and the non-adsorbed fraction was thoroughly washed off using the same buffer. Then, the column was washed with the same buffer containing 300 mM KCl. The adsorbed protein was then eluted using the same buffer in the presence of 300 mM KCl with a linear concentration gradient of 0 to 0.5 M KSCN. Fractions eluted with the KSCN concentration gradient were analyzed by Western blotting using an SR344-specific antibody, and fractions containing SR344 were

collected.

The SR344-specific antibody-immobilized column was pre-equilibrated with Tris-buffered saline (TBS). The SR344 fraction obtained in the first step was concentrated by ultrafiltration using Amicon Ultra-15 (Millipore; molecular weight cut-off of 10 kDa), and diluted two fold with TBS before it was loaded onto the column. After the column was washed with TBS, the adsorbed protein was eluted with 100 mM glycine-HCl buffer (pH 2.5). The eluted fractions were neutralized by adding 1 M Tris (pH 8.1). The obtained fractions were analyzed by SDS-PAGE to collect SR344-containing fractions.

The fraction obtained in the second step was concentrated using Amicon Ultra-15 (molecular weight cut-off of 10 kDa) and loaded onto a Superdex 200 column (GE Healthcare Bio-Sciences) equilibrated with PBS. The fraction eluted as the major peak was used as the final purified sample of SR344.

Establishment of a human gp130-expressing BaF3 cell line

A BaF3 cell line expressing human gp130 was established by the procedure described below, to obtain a cell line that proliferates in an IL-6-dependent manner.

A full-length human gp130 cDNA (Hibi *et al.*, Cell (1990) 63:1149-1157 (GenBank #NM_002184)) was amplified by PCR and cloned into the expression vector pCOS2Zeo to construct pCOS2Zeo/gp130. pCOS2Zeo is an expression vector constructed by removing the DHFR gene expression region from pCHOI (Hirata *et al.*, FEBS Letter (1994) 356:244-248) and inserting the expression region of the Zeocin resistance gene. The full-length human IL-6R cDNA was amplified by PCR and cloned into pcDNA3.1(+) (Invitrogen) to construct hIL-6R/pcDNA3.1(+).

10 μg of pCOS2Zeo/gp130 was mixed with BaF3 cells (0.8×10^7 cells) suspended in PBS, and then pulsed at 0.33 kV and 950 μFD using Gene Pulser (Bio-Rad). The BaF3 cells having the gene introduced by electroporation were cultured for one whole day and night in RPMI 1640 medium (Invitrogen) supplemented with 0.2 ng/ml mouse interleukin-3 (Peprotech) and 10% FBS (HyClone), and selected by adding RPMI 1640 medium supplemented with 100 ng/ml human interleukin-6 (R&D systems), 100 ng/ml human interleukin-6 soluble receptor (R&D systems), and 10% FBS to establish a human gp130-expressing BaF3 cell line (hereinafter "BaF3/gp130"). This BaF/gp130 proliferates in the presence of human interleukin-6 (R&D systems) and SR344, and thus can be used to assess the growth inhibition activity (or IL-6 receptor neutralizing activity) of an anti-IL-6 receptor antibody.

Construction of a library of modified CDRs

First, a humanized PM-1 antibody (Cancer Res. 1993 Feb 15;53(4):851-6) was

converted into scFv. The heavy chain variable region and light chain variable region regions were amplified by PCR to prepare a humanized PM-1 HL scFv having the linker sequence GGGGSGGGGSGGGGS (SEQ ID NO: 106) between heavy chain variable region and light chain variable region.

Two types of libraries were constructed by PCR using the prepared humanized PM-1 HL scFv-encoding DNA as a template. One was a target library where one of the amino acids in a CDR is designed as X, and the other was a library where only the hot spot sequences in a CDR are substituted with random sequences. The target library where one of the amino acids in each CDR is designed as X was constructed as follows. The library portion was constructed by PCR using a primer containing NNS for the amino acids to be incorporated into the library, while the remaining was prepared by standard PCR. The two were linked together by assembly PCR. In this construction, only one CDR was diversified as a library (see J. Mol. Biol. (1996) 256:77-88). Likewise, the library where only the hot spot sequences were substituted with random sequences was constructed by PCR using a primer containing NNS for all hot spot amino acids. In this construction, two libraries were constructed: one was a library where only the hot spot in heavy chain variable region was diversified, and the other was a library where only the hot spot in light chain variable region was diversified (see Nature Biotechnology 1999 June;17:568-572).

A ribosome display library was constructed using the above-described libraries according to J. Immunological Methods (1999) 231:119-135. To perform *in vitro* translation based on the cell-free *E. coli* system, an SDA sequence (ribosome binding site) and T7 promoter were attached to the 5' end and a partial gene3 sequence was ligated as a ribosome display linker to the 3' end using *Sfi*I.

Selection of high affinity scFv by ribosome display

Ribosome display-based panning was carried out (Nature Biotechnology 2000 Dec;18:1287-1292). The prepared SR344 was biotinylated using NHS-PEO4-Biotin (Pierce) and then used as an antigen. Off-rate selection was performed to obtain high affinity scFv with high efficiency (JBC (2004) 279(18):18870-18877). The concentrations of biotinylated antigen and competitor antigen were 1 nM and 1 μM, respectively. The time of competition in the fourth round was 10 O/N.

scFv: insertion into phagemid, antigen-binding activity and sequence analysis

PCR was performed to reconstruct HL scFv using the template DNA pool obtained in the fourth round and specific primers. After digestion with *Sfi*I, the fragment was inserted into the phagemid vector pELBG lacI predigested with *Sfi*I. XL1-Blue (Stratagene) was

transformed with the resulting construct. Using the yielded colonies, antigen-binding activity was assessed by phage ELISA and the HL scFv sequence was analyzed. The phage ELISA was carried out using plates coated with SR344 at 1 μg/ml (J. Mol. Biol. (1992) 227:381-388). Clones exhibiting SR344 binding activity were analyzed for their sequences using specific primers.

Conversion of scFv into IgG, and expression and purification of IgG

IgG expression was conducted using animal cell expression vectors. Clones enriched with a particular mutation were subjected to PCR to amplify their light chain variable regions and heavy chain variable regions. After *Xho*I/*Nhe*I digestion and *Eco*RI digestion, the amplified DNAs were inserted into an animal cell expression vector. The nucleotide sequence of each DNA fragment was determined using a DNA sequencer (ABI PRISM 3730xL DNA Sequencer or ABI PRISM 3700 DNA Sequencer (Applied Biosystems)) using the BigDye Terminator Cycle Sequencing Kit (Applied Biosystems) according to the method described in the attached instruction manual.

Expression of IgG-converted antibodies

Antibody expression was performed by the method described below. Human embryonic kidney cancer-derived HEK293H cells (Invitrogen) were suspended in DMEM (Invitrogen) supplemented with 10% FBS (Invitrogen). The cells (10-ml/plate; cell density of 5 to 6 x 10^5 cells/ml) were plated on dishes for adherent cells (10 cm in diameter; CORNING) and cultured in a CO_2 incubator (37°C, 5% CO_2) for one whole day and night. Then, the medium was removed by aspiration, and 6.9 ml of CHO-S-SFM-II medium (Invitrogen) was added. The prepared plasmid DNA mixture (13.8 μg in total) was combined with 20.7 μl of 1 μg/ml Polyethylenimine (Polysciences Inc.) and 690 μl of CHO-S-SFMII medium. The resulting mixture was incubated at room temperature for 10 minutes, and then added to the cells in each dish. The cells were incubated in a CO_2 incubator (at 37°C under 5% CO_2) for four to five hours. Then, 6.9 ml of CHO-S-SFM-II medium (Invitrogen) was added to the dishes, and the cells were incubated in a CO_2 incubator for three days. The culture supernatants were collected and centrifuged (approx. 2,000 g, five minutes, room temperature) to remove the cells, and sterilized through 0.22-μm filter MILLEX$^{(R)}$-GV (Millipore). The samples were stored at 4°C until use.

Purification of IgG-converted antibodies

50 μl of rProtein A Sepharose^{TM} Fast Flow (Amersham Biosciences) suspended in TBS was added to the obtained culture supernatants, and the combined solutions were mixed by

inversion at 4°C for four hours or more. The solutions were transferred into 0.22-μm filter cups of Ultrafree(R)-MC (Millipore). After washing three times with 500 μl of TBS, the rProtein A Sepharose™ resin was suspended in 100 μl of 50 mM sodium acetate (pH 3.3) aqueous solution, and the mixture was incubated for two minutes to elute the antibody. Immediately, the eluate was neutralized by adding 6.7 μl of 1.5 M Tris-HCl (pH 7.8). Elution was carried out twice, yielding 200 μl of purified antibody. The absorbance at 280 nm was determined using ND-1000 Spectrophotometer (NanoDrop) or spectrophotometer DU-600 (Beckman) using 2 or 50 μl of the antibody solution, respectively. The antibody concentration was calculated from the obtained value according to the following formula:

[Antibody concentration (mg/ml)] = (absorbance x dilution fold) / 14.6 x 10

Assessment of the IgG-converted clones for human IL-6 receptor-neutralizing activity

The IL-6 receptor neutralizing activity was assessed using BaF3/gp130 which proliferates in an IL-6/IL-6 receptor-dependent manner. After three washes with RPMI1640 supplemented with 10% FBS, BaF3/gp130 cells were suspended at 5 x 10^4 cells/ml in RPMI1640 supplemented with 60 ng/ml human interleukin-6 (TORAY), 60 ng/ml recombinant soluble human IL-6 receptor (SR344), and 10% FBS. The cell suspensions were dispensed (50 μl/well) into 96-well plates (Corning). Then, the purified antibodies were diluted with RPMI1640 containing 10% FBS, and added to each well (50 μl/well). The cells were cultured at 37°C under 5% CO_2 for three days. WST-8 Reagent (Cell Counting Kit-8; Dojindo Laboratories) was diluted two-fold with PBS. Immediately after 20 μl of the reagent was added to each well, the absorbance at 450 nm (reference wavelength: 620 nm) was measured using SUNRISE CLASSIC (TECAN). After culturing for two hours, the absorbance at 450 nm (reference wavelength: 620 nm) was measured again. The IL-6 receptor neutralizing activity was assessed using the change of absorbance during two hours as an indicator.

As a result, a number of antibodies whose activities were higher than that of the humanized PM-1 antibody (wild type (WT)) were obtained. Mutations in the antibodies whose activities were higher than that of WT are shown in Fig. 4. For example, as shown in Fig. 1, the neutralizing activity of RD_6 was about 50 times higher than WT in terms of 100% inhibitory concentration.

Biacore-based affinity analysis of the IgG-converted clones

The clones whose activities were higher than that of the wild type were analyzed for antigen-antibody reaction kinetics using Biacore T100 (Biacore). The antigen-antibody interaction was measured by immobilizing 1,800 to 2,600 RU (resonance units) of rec-Protein A (Zymed) (hereinafter "Protein A") onto a sensor chip, binding various antibodies onto the chip,

and then flowing the antigen over the chip as an analyte. Various concentrations of recombinant human IL-6R sR (R&D systems) (hereinafter "rhIL-6sR") were used as the antigen. All measurements were carried out at 25°C. The kinetic parameters, association rate constant k_a (1/Ms) and dissociation rate constant k_d (1/s) were calculated from the sensorgrams obtained by measurement. Then, K_D (M) was determined based on the rate constants. The respective parameters were determined using Biacore T100 Evaluation Software (Biacore).

As a result, a number of antibodies exhibiting higher affinity than the humanized PM-1 antibody (wild type (WT)) were obtained. As an example, sensorgrams of the wild type (WT) and RD_6 are shown in Figs. 2 and 3, respectively. The result of kinetic parameter analysis revealed that RD_6 had about 50 times higher affinity than WT (Table 1). In addition to RD_6, antibodies exhibiting affinity dozens of times higher than WT were also obtained. Mutations that result in higher affinity than WT are shown in Fig. 4.

Table 1

SAMPLE	k_a (1/Ms)	k_d (1/s)	K_D (M)
WT	2.8E+6	1.8E-3	6.5E-10
RD_6	2.3E+6	2.8E-5	1.2E-11

[Example 2] Improvement of antigen-binding activity through various combinations of CDR modifications

Mutations associated with strong activity or high affinity were combined to create antibodies with stronger activity and higher affinity.

Production, expression, and purification of modified antibodies

Amino acids at selected sites were modified to produce modified antibodies. Specifically, mutations were introduced into the prepared H(WT) variable region (H(WT), SEQ ID NO: 107) and L(WT) variable region (L(WT), SEQ ID NO: 108) using the QuikChange Site-Directed Mutagenesis Kit (Stratagene) by the method described in the attached instruction manual. After it was confirmed that the antibody heavy chain gene fragment inserted into a plasmid was the humanized antibody variable region gene sequence of interest, the plasmid was digested with *Xho*I and *Not*I. A plasmid containing the antibody light chain gene fragment as an insert was digested with *Eco*RI. Then, the reaction mixtures were subjected to electrophoresis in 1% agarose gel. A DNA fragment of the expected size (about 400 bp) was purified using the QIAquick Gel Extraction Kit (QIAGEN) by the method described in the attached instruction manual. The DNA was eluted with 30 μl of sterile water. Then, the

antibody heavy chain gene fragment was inserted into an animal cell expression vector to construct the heavy chain expression vector of interest. An expression vector for the light chain was also constructed in the same way. Ligation was carried out using the Rapid DNA Ligation Kit (Roche Diagnostics). The *E. coli* strain DH5α (Toyobo) was transformed with the plasmids. The nucleotide sequence of each DNA fragment was determined with a DNA sequencer (ABI PRISM 3730xL DNA Sequencer or ABI PRISM 3700 DNA Sequencer (Applied Biosystems)) using the BigDye Terminator Cycle Sequencing Kit (Applied Biosystems) according to the method described in the attached instruction manual. The antibodies were expressed using the constructed expression vectors and purified by the method described in Example 1.

Assessment for the activity of neutralizing human IL-6 receptor

The purified antibodies were assessed for their neutralizing activity by the method described in Example 1. The neutralizing activity was assessed using 600 ng/ml human interleukin-6 (TORAY). A number of novel antibodies with stronger activity than WT were obtained. The CDR sequences of the antibodies are shown in Fig. 5. Of them, the antibody with the strongest activity (referred to as RDC_23) has RDC_5H as a heavy chain and RDC_11L as a light chain. The neutralizing activity of RDC_23 is shown in Fig. 6. The activity of RDC_23 was demonstrated to be about 100 times higher than WT in terms of 100% inhibitory concentration. Improved neutralizing activity was observed not only in RDC_23, which is an antibody having RDC_5H as a heavy chain and RDC_11L as a light chain, but also in antibodies RDC_2, RDC_3, RDC_4, RDC_5, RDC_6, RDC_7, RDC_8, RDC_27, RDC_28, RDC_29, RDC_30, and RDC_32, which all have L(WT) as a light chain, and RDC_2H, RDC_3H, RDC_4H, RDC_5H, RDC_6H, RDC_7H, RDC_8H, RDC_27H, RDC_28H, RDC_29H, RDC_30H, and RDC_32H as a heavy chain, respectively, as well as in an antibody referred to as RDC_11, which has H(WT) and RDC_11L as heavy and light chains, respectively. It was thus shown that antibodies having stronger neutralizing activity could be obtained by combining mutations discovered by affinity maturation. Furthermore, since antibodies containing such a combination of mutations had improved neutralizing activity, they were also expected to have improved affinity.

Biacore-based affinity analysis using Protein A

Thus, of the antibodies with improved neutralizing activity, RDC_2, RDC_3, RDC_4, RDC_5, RDC_6, RDC_7, RDC_8, RDC_11, and RDC_23 were analyzed for antigen-antibody reaction kinetics using Biacore T100 (Biacore). The antigen-antibody interaction was measured by immobilizing 4,400 to 5,000 RU of rec-Protein A (Zymed) immobilized onto a sensor chip by the amine coupling method, binding various antibodies onto the chip, and then

flowing the antigen over the chip as an analyte. For the antigen, various concentrations of rhIL-6sR were used. All measurements were carried out at 25°C. The kinetic parameters, association rate constant k_a (1/Ms) and dissociation rate constant k_d (1/s) were calculated from the sensorgrams obtained by measurement. Then, K_D (M) was determined based on the rate constants. The respective parameters were determined using Biacore T100 Evaluation Software (Biacore). The result showed that RDC_2, RDC_3, RDC_4, RDC_5, RDC_6, RDC_7, RDC_8, RDC_11, and RDC_23, all of which contained a combination of mutations, had a smaller K_D value than RD_28 which contains a single mutation (Table 2). The sensorgram for RDC_23 which has a higher affinity than others is shown in Fig. 7.

Table 2

SAMPLE	ka (1/Ms)	kd (1/s)	KD (M)
RD_28	9.4E+05	1.1E-04	1.2E-10
RDC_2	1.1E+06	2.5E-05	2.2E-11
RDC_3	1.0E+06	3.7E-05	3.7E-11
RDC_4	1.1E+06	2.9E-05	2.7E-11
RDC_5	1.2E+06	2.8E-05	2.2E-11
RDC_6	1.2E+06	3.5E-05	2.9E-11
RDC_7	1.1E+06	4.2E-05	3.8E-11
RDC_8	1.4E+06	3.6E-05	2.5E-11
RDC_11	1.1E+06	7.0E-05	6.5E-11
RDC_23	1.2E+06	3.1E-05	2.5E-11

This finding suggests that these antibodies have higher affinities than the parental antibodies that do not have the combinations of mutations. As in the case of the neutralizing activity, this indicates that antibodies having greater affinity can be obtained by combining mutations discovered by affinity maturation. The amino acid sequences of variants having higher activity or affinity than WT are shown below (mutations relative to WT are underlined).

(HCDR2)

SEQ ID NO: 45 YISYSGITNYNPSLKS

(HCDR3)

SEQ ID NO: 57 LLARATAMDY

SEQ ID NO: 58 VLARATAMDY

SEQ ID NO: 59 ILARATAMDY

SEQ ID NO: 60 TLARATAMDY

SEQ ID NO: 61 VLARITAMDY

SEQ ID NO: 62 ILARITAMDY

SEQ ID NO: 63 TLARITAMDY

SEQ ID NO: 64 LLARITAMDY
(LCDR3)
SEQ ID NO: 79 GQGNRLPYT

Specifically, an anti-IL-6 receptor antibody with markedly improved affinity and neutralizing activity as compared to WT can be produced by designing the antibody to have Asn at amino acid position 9 in HCDR2, Leu, Val, Ile, or Thr at amino acid position 1 in HCDR3, Ala or Ile at amino acid position 5 in HCDR3, Gly at amino acid position 1 in LCDR3, and Arg at amino acid position 5 in LCDR3.

Biacore-based affinity analysis using Protein A/G

WT and RDC_23 were analyzed for antigen-antibody reaction kinetics using Biacore T100 (Biacore). The antigen-antibody interaction was measured by immobilizing purified Recomb Protein A/G (Pierce) (hereinafter "Protein A/G") onto a sensor chip, binding various antibodies onto the chip, and then flowing the antigen as an analyte over the chip. Various concentrations of rhIL-6sR (R&D systems) and recombinant soluble IL-6 receptor (SR344 prepared in Example 1) were used as the antigen. The sugar chain structure of rhIL-6sR produced by baculovirus-infected insect cells is of high-mannose type. On the other hand, the sugar chain structure of SR344 produced by CHO cells is assumed to be of the complex sugar chain type with sialic acid at its end. Since the sugar chain structure of soluble IL-6 receptor in an actual human body is assumed to be of the complex sugar chain type with sialic acid at its end, SR344 is expected to have a structure closer to that of soluble IL-6 receptor in the human body. Thus, a comparison test between rhIL-6sR and SR344 was carried out in this experiment.

The kinetic parameters, association rate constant k_a (1/Ms) and dissociation rate constant k_d (1/s) were calculated from the sensorgrams obtained by measurement. Then, K_D (M) was determined based on the rate constants. The respective parameters were determined using Biacore T100 Evaluation Software (Biacore).

A sensor chip was prepared by immobilizing about 3,000 RU of Protein A/G onto CM5 (Biacore) with the amine coupling method. The kinetics of the interaction between the two types of soluble IL-6 receptors (rhIL-6sR and SR344) and the antibodies (WT and RDC_23) bound to Protein A/G was analyzed using the prepared sensor chip. The running buffer used was HBS-EP+, and the flow rate was 20 μl/min. Each antibody was prepared so that about 100 RU of the antibody was bound to Protein A/G. For the analyte, rhIL-6sR was prepared at 0, 0.156, 0.313, and 0.625 μg/ml using HBS-EP+, while SR344 was adjusted to 0, 0.0654, 0.131, and 0.261 μg/ml. In the first step of the measurement, the antibodies of interest, WT and RDC_23, were bound to Protein A/G, and an analyte solution was added thereto. After three minutes of interaction, the solution was switched with HBS-EP+ (Biacore), and the dissociation

phase was monitored for ten minutes. After measurement of the dissociation phase, the sensor chip was regenerated by washing with 10 μl of 10 mM glycine-HCl (pH 1.5). The association, dissociation, and regeneration constituted one analytic cycle. All experiments were carried out at 37°C.

WT and RDC_23 were measured according to the above cycle. The resulting sensorgrams for the two types of soluble IL-6 receptors, rhIL-6sR and SR344, are shown in Figs. 8, 9, 10, and 11. The obtained sensorgrams were kinetically analyzed using Biacore T100 Evaluation Software, which is a data analysis software specific for Biacore (Table 3). The result showed that when comparing rhIL-6sR and SR344, the affinities of both WT and RDC_23 for SR344 were two- to three-fold weaker For both rhIL-6sR and SR344, RDC_23 had affinities that are about 40 to 60 times improved as compared to WT. Thus, it was demonstrated that because of the combination of respective CDR modifications obtained by affinity maturation, RDC_23 also had a markedly higher affinity than WT for SR344 whose structure is presumably close to that of soluble IL-6 receptor in the human body. All measurements described hereinafter in the Examples were carried out at 37°C to kinetically analyze the antigen-antibody reaction using SR344 and protein A/G.

Table 3

SAMPLE	ANALYTE	k_a (1/Ms)	k_d (1/s)	K_D (M)
WT	rhIL-6sR	1.3E+6	1.5E-3	1.2E-9
	SR344	4.9E+5	2.0E-3	4.0E-9
RDC_23	rhIL-6sR	1.6E+6	4.5E-5	2.8E-11
	SR344	6.4E+5	4.3E-5	6.7E-11

[Example 3] Generation of H53/L28 with improved plasma retention and reduced immunogenicity risk through modifications of CDR and framework

The antibody obtained by humanizing a mouse PM-1 antibody (hereinafter referred to as "wild type" or "WT"; the WT heavy and light chains are referred to as "H(WT)" and "L(WT)", respectively) as described in Cancer Res. 1993 Feb 15;53(4):851-6, was modified to improve the retention in plasma, reduce the immunogenicity risk, and increase the stability. The modifications are described below. For the purpose of improving the retention in plasma, the heavy and light chain variable region sequences of WT were modified to lower the isoelectric point.

Creation of a three-dimensional structure model for the humanized PM-1 antibody

First, to identify amino acid residues exposed on the surface of the variable regions of the humanized PM-1 antibody (H(WT)/L(WT)), a model for the Fv domain of the antibody obtained by humanizing a mouse PM-1 antibody was created by homology modeling using the MOE software (Chemical Computing Group Inc.).

Selection of modification sites to reduce the isoelectric point of the humanized PM-1 antibody

A detailed analysis of the model created suggested that of the surface exposed amino acids in the FR sequence, H16, H43, H81, H105, L18, L45, L79, and L107 (Kabat's numbering; Kabat EA *et al.*, 1991, Sequences of Proteins of Immunological Interest, NIH), and of those in the CDR sequence, H31, H64, H65, L24, L27, L53, and L55, were potential candidates for the sites of modification to reduce the isoelectric point without decreasing the activity or stability.

Removal of remaining mouse sequences from the humanized PM-1 antibody

The humanized PM-1 antibody is an antibody whose sequence was obtained by humanizing the mouse PM-1 antibody (Cancer Res. 1993 Feb 15;53(4):851-6). The heavy chain of the humanized PM-1 antibody was obtained by grafting CDR onto the NEW framework which is a human antibody variable region. However, mouse sequences remain at H27, H28, H29, H30, and H71 in the heavy chain to maintain the activity. From the perspective of immunogenicity risk, the best result is expected when the number of mouse sequences is minimized. Thus, the present inventors searched for sequences for converting H27, H28, H29, and H30 into human sequences.

Selection of modification sites to improve the stability of the humanized PM-1 antibody

The present inventors speculated that it might be possible to improve the stability of the humanized PM-1 antibody (H(WT)/L(WT)) by substituting glycine for serine at H65 (stabilization of the turn structure; stabilization through conversion into an HCDR2 consensus sequence), isoleucine for methionine at H69 (stabilization of the hydrophobic core structure), serine for leucine at H70 (stabilization through replacement of the surface exposed residue with a hydrophilic residue), asparagine for threonine at H58 (stabilization through conversion into an HCDR2 consensus sequence), serine for threonine at L93 (stabilization through replacement of the surface exposed residue with a hydrophilic residue), and isoleucine for serine at H107 (stabilization of the β sheet) in its variable regions, and considered these modifications as candidates for increasing stability.

Removal of *in silico* predicted T-cell epitopes from the humanized PM-1 antibody

First, the variable regions of the humanized PM-1 antibody (H(WT)/L(WT)) were

analyzed using TEPITOPE (Methods 2004 Dec;34(4):468-75). The result showed that the light chain CDR2 contained many T-cell epitopes that bind to HLA. Thus, TEPITOPE analysis was carried out to find modifications that would reduce the immunogenicity risk of the light chain CDR2 without decreasing the stability, binding activity, or neutralizing activity. The result demonstrated that HLA-binding T-cell epitopes can be removed without decreasing the stability, binding activity, or neutralizing activity by substituting glycine for threonine at L51 in the light chain CDR2.

Selection of respective framework sequences

Homology search can be performed for the individual frames by using a database constructed with the data of human antibody amino acid sequences available from the public databases: Kabat Database (ftp://ftp.ebi.ac.uk/pub/databases/kabat/) and IMGT Database (http://imgt.cines.fr/). From the perspectives of reducing the isoelectric point, removing remaining mouse sequences, and improving the stability, human frameworks were selected by searching the database for human framework sequences containing the modifications described above. The result showed that the modified antibody H53/L28 met the requirements described above without decreasing the binding activity or neutralizing activity when its respective frameworks were constituted of the sequences indicated below. SOURCE indicates origins of the human sequences. Underlined amino acid residues in each sequence represent modified amino acids relative to WT.

Table 4

H53	SOURCE	SEQUENCE
FR1	Germline : IMGT_hVH_4_b	QVQLQESGPGLVKPSETLSLTCAVSGYSIS
FR2	Blood 1996 88: 4620-4629	WVRQPPGEGLEWIG
FR3	Germline : IMGT_hVH_4_b (EXCEPT BOLD-INDICATED H71 & H89)	RVTISRDTSKNQFSLKLSSVTAADTAAYYCAR
FR4	J IMMUNOL 142: 4027-4033 (1989)	WGEGTLVTVSS

L28	SOURCE	SEQUENCE
FR1	Immunology. 1988 Aug;64(4):573-9	DIQMTQSPSSLSASVGDSVTITC
FR2	Germline : IMGT_hVk_1D_8	WYQQKPGKAPELLIY
FR3	Germline : IMGT_hVk_6D_41	GVPSRFSGSGSGTDFTFTISSLEAEDAATYYC
FR4	J. Exp. Med. 1997 185: 1435-1446	FGQGTKVEIE

Furthermore, the above-described FR3 of H53 contains a nonhuman sequence; thus, it is preferable to further reduce the immunogenicity risk. A possible modification for reducing the

immunogenicity risk is a sequence substitution resulting in an exchange of Ala at H89 to Val (SEQ ID NO: 127). Moreover, since Arg at H71 in FR3 of H53 is important for the binding activity (Cancer Res. 1993 Feb 15;53(4):851-6), anti-human IL-6 receptor antibodies containing heavy and light chains whose frameworks consist of a fully human sequence may be produced by using an FR3 sequence of the human VH1 subclass (SEQ ID NO: 128) or the human VH3 subclass (SEQ ID NO: 129) where Arg at H71 is conserved.

Selection of respective CDR sequences

The respective CDR sequences of H53/L28 were selected as shown below, from the perspectives of reducing the isoelectric point, improving the stability, and removing T-cell epitopes, and most importantly, not decreasing the binding activity or neutralizing activity.

Table 5

H53	SEQUENCE
CDR1	DDHAWS
CDR2	YISYSGITNYNPSLKG
CDR3	SLARTTAMDY

L28	SEQUENCE
CDR1	QASQDISSYLN
CDR2	YGSELHS
CDR3	QQGNSLPYT

Construction of expression vector for modified antibody, expression and purification of the antibody

An expression vector for modified antibody was constructed, and the antibody was expressed and purified by the method described in Example 1. The humanized mouse PM-1 antibody was successively modified to have the framework and CDR sequences selected for mutagenesis vectors for H(WT) and L(WT) of the antibody. Using the finally obtained H53/L28-encoding animal cell expression vector (antibody amino acid sequences: H53, SEQ ID NO: 104; and L28, SEQ ID NO: 105) having the selected framework and CDR sequences, H53/L28 was expressed and purified, and then used in the assessment described below.

Assessment of modified antibody H53/L28 for the isoelectric point by isoelectric focusing

WT and the modified antibody H53/L28 were analyzed by isoelectric focusing to assess

the change in the isoelectric point of the whole antibody caused by the amino acid modifications in the variable regions. The procedure of isoelectric focusing is described below. Using Phastsystem Cassette (Amersham Biosciences), Phast-Gel Dry IEF gel (Amersham Biosciences) was rehydrated for about 30 minutes in the rehydration solution indicated below.

Milli-Q water	1.5 ml
Pharmalyte 5-8 for IEF (Amersham Biosciences)	50 µl
Pharmalyte 8-10.5 for IEF (Amersham Biosciences)	50 µl

Electrophoresis was carried out in PhastSystem (Amersham Biosciences) using the rehydrated gel according to the program indicated below. The samples were loaded onto the gel in Step 2. Calibration Kit for pI (Amersham Biosciences) was used as the pI markers.

Step 1:	2000 V	2.5 mA	3.5 W	15°C	75 Vh
Step 2:	200 V	2.5 mA	3.5 W	15°C	15 Vh
Step 3:	2,000 V	2.5 mA	3.5 W	15°C	410 Vh

After electrophoresis, the gel was fixed with 20% TCA, and then silver-stained using the Silver Staining Kit, protein (Amersham Biosciences), according to the protocol attached to the kit. After staining, the isoelectric point of the sample (the whole antibody) was calculated from the known isoelectric points of pI markers. The result showed that the isoelectric point of WT was about 9.3, and the isoelectric point of the modified antibody H53/L28 was about 6.5 to 6.7. The amino acid substitution in WT yielded H53/L28 whose isoelectric point is about 2.7 lowered. The theoretical isoelectric point of the variable regions of H53/L28 (heavy chain variable region and light chain variable region sequences) was calculated by GENETYX (GENETYX CORPORATION). The determined theoretical isoelectric point was 4.52. Meanwhile, the theoretical isoelectric point of WT was 9.20. Thus, the amino acid substitution in WT yielded H53/L28 having a variable region whose theoretical isoelectric point is about 4.7 lowered.

Assessment of H53/L28 for the human IL-6 receptor-neutralizing activity

WT and H53/L28 were assessed by the method described in Example 1. The result is shown in Fig. 12. The activity of modified antibody H53/L28 to neutralize BaF/gp130 improved several fold in comparison to WT. Specifically, the comparison of H53/L28 with WT revealed that the isoelectric point could be reduced while improving the neutralizing activity.

Biacore-based analysis of H53/L28 for the affinity for human IL-6 receptor

The affinities of WT and H53/L28 for human IL-6 receptor were assessed by kinetic analysis using Biacore T100 (Biacore). The antigen-antibody interaction was measured by

immobilizing purified Recomb Protein A/G (Pierce) (hereinafter "Protein A/G") onto a sensor chip, binding various antibodies onto the chip, and then flowing the antigen over the chip as an analyte. Various concentrations of recombinant soluble IL-6 receptor (SR344) were used as the antigen. The measurement conditions were the same as described in Example 2.

The sensorgrams obtained for WT and H53/L28 are shown in Fig. 13. Kinetic analysis was carried out using Biacore-specific data analysis software Biacore T100 Evaluation Software. The result is shown in Table 6. The result showed that K_D in H53/L28 was reduced about six-fold compared to WT, and this means the affinity was improved about six-fold. Specifically, the comparison of H53/L28 with WT revealed that the affinity could be improved six-fold while reducing the isoelectric point at the same time. A detailed analysis suggested that the amino acid mutation that contributed to the affinity improvement was the substitution of glycine for threonine at L51. In other words, it is thought that the affinity can be improved by substituting glycine for threonine at L51.

Table 6

SAMPLE	k_a (1/Ms)	k_d (1/s)	K_D (M)
WT	4.9E+5	2.0E-3	4.0E-9
H53/L28	7.6E+5	5.2E-4	6.8E-10

Prediction of T-cell epitopes in H53/L28 using TEPITOPE

H53/L28 was analyzed by TEPITOPE (Methods. 2004 Dec;34(4):468-75). The result showed that the number of potential HLA-binding peptides was significantly reduced in H53/L28 as compared to WT. This suggests reduction of the immunogenicity risk in human.

[Example 4] Assessment of the plasma retention of H53/L28

Assessment of the modified antibody H53/L28 for its plasma pharmacokinetics in normal mice

To assess the retention in plasma of the modified antibody H53/L28 with reduced isoelectric point, the plasma pharmacokinetics was compared between WT and the modified antibody H53/L28 using normal mice.

A single dose of WT or H53/L28 was intravenously or subcutaneously administered at 1 mg/kg to mice (C57BL/6J; Charles River Japan, Inc.). The blood was collected before administration and 15 minutes, 2 hours, 8 hours, 1 day, 2 days, 5 days, 7 days, 14 days, 21 days, and 28 days after administration. Note that the blood was collected at 15 minutes after administration only from the intravenous administration groups. The collected blood was

immediately centrifuged at 4°C and 15,000 rpm for 15 minutes to obtain plasma. The separated blood plasma was stored until use in a freezer at -20°C or below.

The concentration in the mouse plasma was determined by ELISA. First, Recombinant Human IL-6 sR (R&D Systems) was biotinylated using EZ-Link™ Sulfo-NFS-Biotinylation Kit (PIERCE). The biotinylated human-sIL-6R was dispensed into Reacti-Bind Streptavidin High Binding Capacity (HBC) Coated Plates (PIERCE), and then incubated at room temperature for one hour or more. Thus, human-sIL-6R-immobilized plates were prepared as described above. Mouse plasma samples and standard samples (plasma concentrations: 3.2, 1.6, 0.8, 0.4, 0.2, 0.1, and 0.05 μg/ml) were prepared and dispensed into the human-sIL-6R-immobilized plates. The samples were incubated at room temperature for one hour, and then anti-human IgG-AP (Sigma) was added for reaction. After color development using the BluePhos Microwell Phosphatase Substrates System (Kirkegaard & Perry Laboratories) as a substrate, the absorbance at 650 nm was measured with a microplate reader. The plasma concentrations in the mice were determined based on the absorbance of the calibration curve using the analytical software SoftMax Pro (Molecular Devices). The time courses for the plasma concentrations of WT and H53/L28 after intravenous administration and subcutaneous administration are shown in Figs. 14 and 15, respectively.

The obtained plasma concentration-time data were evaluated by a model-independent analysis using the pharmacokinetic analysis software WinNonlin (Pharsight) to estimate pharmacokinetic parameters (AUC, clearance (CL), and half-life (T1/2)). T1/2 was estimated from the plasma concentrations at the last three points or those in the terminal phase automatically selected by WinNonlin. BA was calculated from the ratio of AUC after subcutaneous administration versus AUC after intravenous administration. The determined pharmacokinetic parameters are shown in Table 7.

Table 7

	iv		sc		
	CL mL/h/kg	T1/2 day	CL/F mL/h/kg	T1/2 day	BA %
WT	0.177	18.5	0.180	14.7	113
H53/L28	0.102	23.5	0.086	29.7	121

The half-life (T1/2) of H53/L28 in plasma after intravenous administration was prolonged to about 1.3 times that of WT, while the clearance was reduced about 1.7 times. T1/2 of H53/L28 after subcutaneous administration was prolonged to about twice that of WT, while the clearance was reduced about 2.1 times. Thus, the retention of H53/L28 in plasma could be significantly improved by lowering the isoelectric point of WT.

H53/L28 is a humanized anti-IL-6 receptor antibody with improved binding activity and neutralizing activity, reduced immunogenicity risk, and significantly improved retention in plasma as compared to the humanized PM-1 antibody (WT). Therefore, the modifications used to create H53/L28 may be very useful in the development of pharmaceuticals.

[Example 5] Preparation of the PF1 antibody

Construction of expression and mutagenesis vectors for the humanized PM-1 antibody

A total of four CDR mutations discovered in Example 2 which improved the affinity of RDC_23 (two each in the heavy and light chains) were introduced into H53/L28 created in Example 4. The heavy and light chains obtained by introducing the mutations of RDC_23 into H53/L28 were named PF1_H and PF1_L, respectively. The modified antibody was prepared, expressed, and purified by the method described in Example 1. The amino acid sequences of PF1_H and PF1_L are shown in SEQ ID NOs: 22 and 23, respectively.

Assessment for the human IL-6 receptor-neutralizing activity

The neutralizing activity of the purified PF1 antibody was assessed by the method described in Example 1. The neutralizing activity assessment was carried out using 600 ng/ml human interleukin-6 (TORAY). The neutralizing activities of WT and PF1 are shown in Fig. 16. PF1 was demonstrated to have an activity about 100 to 1,000 times higher than WT in terms of 100% inhibitory concentration.

Biacore-based analysis of the PF1 antibody for the affinity for human IL-6 receptor

This measurement was carried out under the same conditions described in Example 2. The running buffer used was HBS-EP+, and the flow rate was 20 μl/min. Each antibody was prepared so that about 100 RU of the antibody was bound to Protein A/G. SR344 was prepared at 0, 0.065, 0.131, and 0.261 μg/ml using HBS-EP+ and used as an analyte. In the first step of the measurement, the antibody in solution was bound to Protein A/G, and the analyte solution was allowed to interact therewith. After three minutes of interaction, the solution was switched to HBS-EP+, and the dissociation phase was monitored for 10 or 15 minutes. After measurement of the dissociation phase, the sensor chip was regenerated by washing with 10 μl of 10 mM glycine-HCl (pH 1.5). The association, dissociation, and regeneration constitute one analysis cycle. Each antibody was measured according to this cycle.

The obtained sensorgram for PF1 is shown in Fig. 17. The sensorgram was kinetically analyzed using the Biacore-specific data analysis software, Biacore T100 Evaluation Software. The result is shown along with those for WT and H53/L28 in Table 8. The result showed that

the affinity of PF1 was about 150 times improved as compared to WT. RDC_23 has a high affinity as a result of combination through affinity maturation, and H53/L28 has a prolonged retention in plasma and improved affinity. Through combination of both, PF1 obtained a higher affinity than RDC_23 or H53/L28 by an additive effect.

Table 8

SAMPLE	k_a (1/Ms)	k_d (1/s)	K_D (M)
WT	4.9E+05	2.0E-03	4.0E-09
RDC_23	6.4E+05	4.3E-05	6.7E-11
H53/L28	7.6E+05	5.2E-04	6.8E-10
PF1	1.3E+06	3.5E-05	2.7E-11

Assessment of the PF1 antibody for thermal stability by DSC

To assess the thermal stability of the PF1 antibody, the midpoint of thermal denaturation (Tm value) was determined by DSC. The purified antibodies of WT and PF1 were dialyzed against a solution of 20 mM sodium acetate, 150 mM NaCl, pH 6.0 (EasySEP, TOMY). DSC measurement was carried out at a heating rate of 1°C/min from 40°C to 100°C at a protein concentration of about 0.1 mg/ml. The result showed that the Tm of the WT Fab domain was about 94°C and that of the PF1 Fab domain was 91°C. The Tm of the Fab domain of an IgG1 type antibody molecule is generally within the range of about 60°C to 85°C (Biochem. Biophys. Res. Commun. 2007 Apr 13;355(3):751-7; Mol Immunol. 2007 Apr;44(11):3049-60). Thus, the observed thermal stability of the PF1 antibody was extremely high as compared to those of typical IgG1 molecules.

Assessment of the PF1 antibody for stability at high concentrations

The PF1 antibody was assessed for stability in high concentration formulations. Purified WT and PF1 antibodies were dialyzed against a solution of 20 mM histidine chloride, 150 mM NaCl, pH 6.5 (EasySEP, TOMY), and then concentrated by ultrafilters. The antibodies were tested for stability at high concentrations. The conditions were as follows.

Antibodies: WT and PF1

Buffer: 20 mM histidine chloride, 150 mM NaCl, pH 6.0

Concentration: 145 mg/ml

Storage temperature and time period: 25°C for two weeks, 25°C for four weeks, or 25°C for seven weeks

Aggregation assessment method:

System: Waters Alliance
Column: G3000SWxl (TOSOH)
Mobile phase: 50 mM sodium phosphate, 300 mM KCl, pH 7.0
Flow rate, wavelength: 0.5 ml/min, 220 nm
100 times diluted samples were analyzed

The contents of aggregate in the initial formulations (immediately after preparation) and formulations stored under various conditions were evaluated by the gel filtration chromatography described above. Differences (amounts increased) in the content of aggregate relative to the initial formulations are shown in Fig. 18. As a result, the following findings were obtained: (1) both WT and PF1 were very stable; (2) the amount of aggregate increased during seven weeks at 25°C was about 0.7% for WT and about 0.3% for PF1, which means that the amount of aggregate increased per month at 25°C was about 0.4% and about 0.17%, respectively; and (3) PF1 was markedly stable at high concentrations. WO 2003/039485 has disclosed data on the stability of Daclizumab, which is available as a high concentration IgG formulation on the market, at 25°C in a 100 mg/ml preparation. The amount of aggregate increased per month at 25°C is about 0.3% in the formulation of 100 mg/ml Daclizumab. Even when compared to Daclizumab, PF1 exhibits an excellent stability at high concentrations. The increase of the number of aggregates is very problematic in developing high-concentration liquid formulations as pharmaceuticals. The increase of PF1 antibody aggregate was demonstrated to be very small even when the concentration of the PF1 antibody was high.

PF1 is a molecule resulting from modification of WT. The purposes of the modification include improvement of the antigen-binding activity, improvement of the retention in plasma by lowering its isoelectric point, reduction of the immunogenicity risk by removing T-cell epitopes and remaining mouse sequences, and improvement of the stability. Indeed, the stability of PF1 in 100 mg/ml or higher concentration preparations was demonstrated to be very high even when compared to WT. Stable and highly convenient high-concentration formulations for subcutaneous administration can be provided by using such molecules.

[Example 6] PK/PD test of the PF1 antibody using human IL-6 receptor transgenic mice

Test for pharmacokinetics (*in vivo* kinetics) using human IL-6 receptor transgenic mice

WT and PF1 prepared in Example 5 were assessed for their pharmacokinetics (*in vivo* kinetics) in human IL-6 receptor transgenic mice (hIL-6R tg mice; Proc. Natl. Acad. Sci. U S A. 1995 May 23;92(11):4862-6) and their human soluble IL-6 receptor-neutralizing activity *in vivo*. WT and PF1 were intravenously administered once at 10 mg/kg into hIL-6R tg mice. Blood was collected before administration and 15 minutes, two, four, and eight hours, one day, two,

four, and seven days after administration. The blood collected was immediately centrifuged at 4°C and 15,000 rpm for 15 minutes to obtain blood plasma. The separated plasma was stored in a freezer at -20°C or below until use.

The concentrations in the mouse plasma were determined by ELISA. Standard samples were prepared at 6.4, 3.2, 1.6, 0.8, 0.4, 0.2, and 0.1 μg/ml as concentrations in plasma. Mouse plasma samples and standard samples were dispensed into immunoplates (Nunc-Immuno Plate, MaxiSorp (Nalge Nunc International)) immobilized with Anti-human IgG (γ-chain specific) F(ab')2 (Sigma). The samples were incubated at room temperature for one hour, and then Goat Anti-Human IgG-BIOT (Southern Biotechnology Associates) and Streptavidin-alkaline phosphatase conjugate (Roche Diagnostics) were subsequently added for reaction. After color development using the BluePhos Microwell Phosphatase Substrates System (Kirkegaard & Perry Laboratories) as a substrate, the absorbance at 650 nm was measured with a microplate reader. The concentrations in the mouse plasma were determined based on the absorbance of the calibration curve using the analytical software SoftMax Pro (Molecular Devices). The time courses for the plasma concentrations of WT and PF1 are shown in Fig. 19. The plasma PF1 concentration four days after administration was about five times higher than WT. This suggests that the retention of PF1 in the plasma of human IL-6 receptor transgenic mice is improved as compared to WT.

The human IL-6 receptor transgenic mice have been demonstrated to produce plasma circulating human soluble IL-6 receptor. Thus, the human soluble IL-6 receptor-neutralizing efficacy in plasma can be assessed by administering anti-human IL-6 receptor antibodies to human IL-6 receptor transgenic mice.

The concentration of free human soluble IL-6 receptor in mouse plasma was determined to assess the degree of neutralization of human soluble IL-6 receptor by administration of WT or PF1. 6 μl of the mouse plasma was diluted two-fold with a dilution buffer containing BSA. The diluted plasma was loaded onto an appropriate amount of rProtein A Sepharose Fast Flow resin (GE Healthcare) dried in 0.22-μm filter cup (Millipore), and all IgG type antibodies (mouse IgG, anti-human IL-6 receptor antibody, and anti-human IL-6 receptor antibody-human soluble IL-6 receptor complex) in the plasma were adsorbed by Protein A. Then, the solution in the cup was spinned down using a high-speed centrifuge to collect the solution that passed through. Since the solution that passed through does not contain Protein A-bound anti-human IL-6 receptor antibody-human soluble IL-6 receptor complex, the concentration of free soluble IL-6 receptor can be determined by measuring the concentration of human soluble IL-6 receptor in the passed solution. The concentration of soluble IL-6 receptor was determined using Quantikine Human IL-6 sR (R&D Systems). The concentration of free soluble IL-6 receptor in mice was measured 4, 8, 24, 48, 96, and 168 hours after administration of WT or PF1 according to the

attached instruction manual.

The result is shown in Fig. 20. In both cases of WT and PF1, the concentration of free soluble IL-6 receptor was 10 ng/ml or less, four hours and up to eight hours after intravenous administration of a single dose of WT or PF1 at 10 mg/kg, indicating that the human soluble IL-6 receptor was neutralized. However, while the concentration of free soluble IL-6 receptor was about 500 ng/ml 24 hours after WT administration, it was 10 ng/ml or less after PF1 administration. This indicates that PF1 neutralizes human soluble IL-6 receptor in a more sustainable way than WT.

PF1 was created by combining RDC_23 discovered through affinity maturation and H53/L28 exhibiting improved properties such as prolonged retention in plasma, and thus predicted to be able to exhibit prolonged retention in plasma and high neutralizing activity *in vivo*. Indeed, as compared to WT, PF1 was demonstrated to be more sustainable in plasma and to exhibit a prolonged neutralizing effect in human IL-6 receptor transgenic mice producing human soluble IL-6 receptor.

PF1 is more superior than WT (humanized PM-1 antibody) in terms of immunogenicity risk and stability in high concentration preparations, as well as retention in plasma and IL-6 receptor-neutralizing effect in human IL-6 receptor transgenic mice. Thus, the modifications made to create PF1 may be very useful in the development of pharmaceuticals.

[Example 7] Improvement of the stability of IgG2 and IgG4 under acidic condition

Construction of expression vectors for IgG2- or IgG4-converted humanized IL-6 receptor antibodies and expression of the antibodies

To reduce the Fcγ receptor-binding activity, the constant region of humanized PM-1 antibody (Cancer Res. 1993 Feb 15;53(4):851-6), which is of the IgG1 isotype, was substituted with IgG2 or IgG4 (Mol. Immunol. 1993 Jan;30(1):105-8) to generate molecules WT-IgG2 (SEQ ID NO: 109) and WT-IgG4 (SEQ ID NO: 110). An animal cell expression vector was used to express the IgGs. An expression vector, in which the constant region of humanized PM-1 antibody (IgG1) used in Example 1 was digested with *Nhe*I/*Not*I and then substituted with the IgG2 or IgG4 constant region by ligation, was constructed. The nucleotide sequence of each DNA fragment was determined with a DNA sequencer (ABI PRISM 3730xL DNA Sequencer or ABI PRISM 3700 DNA Sequencer (Applied Biosystems)) using the BigDye Terminator Cycle Sequencing Kit (Applied Biosystems) according to the attached instruction manual. Using the WT light chain, WT-IgG1, WT-IgG2, and WT-IgG4 were expressed by the method described in Example 1.

(1) Humanized PM-1 antibody (WT-IgG1) heavy chain, SEQ ID NO: 15 (amino acid sequence)

(2) WT-IgG2 heavy chain, SEQ ID NO: 109 (amino acid sequence)
(3) WT-IgG4 heavy chain, SEQ ID NO: 110 (amino acid sequence)

Purification of WT-IgG1, WT-IgG2, and WT-IgG4 through elution from Protein A using hydrochloric acid

50 μl of rProtein A Sepharose™ Fast Flow (Amersham Biosciences) suspended in TBS was added to the obtained culture supernatants, and the combined solutions were mixed by inversion at 4°C for four hours or more. The solutions were transferred into 0.22-μm filter cups of Ultrafree(R)-MC (Millipore). After washing three times with 500 μl of TBS, the rProtein A Sepharose™ resins were suspended in 100 μl of 10 mM HCl/150 mM NaCl (pH 2.0) and the mixtures were incubated for two minutes to elute the antibodies (hydrochloric acid elution). Immediately, the eluates were neutralized by adding 6.7 μl of 1.5 M Tris-HCl (pH 7.8). The elution was carried out twice, yielding 200 μl of purified antibodies.

Gel filtration chromatography analysis of WT-IgG1, WT-IgG2, and WT-IgG4 purified by hydrochloric acid elution

The contents of aggregate in the purified samples obtained by hydrochloric acid elution were assessed by gel filtration chromatography analysis.
Aggregation assessment method:

System: Waters Alliance
Column: G3000SWxl (TOSOH)
Mobile phase: 50 mM sodium phosphate, 300 mM KCl, pH 7.0
Flow rate, wavelength: 0.5 ml/min, 220 nm

The result is shown in Fig. 21. While the content of aggregate in WT-IgG1 after purification was about 2%, those of WT-IgG2 and WT-IgG4 after purification were about 25%. This suggests that IgG1 is stable to acid during hydrochloric acid elution, and by contrast, IgG2 and IgG4 are unstable and underwent denaturation/aggregation. Thus, the stability of IgG2 and IgG4 under acidic condition was demonstrated to be lower than that of IgG1. Protein A has been frequently used to purify IgG molecules, and the IgG molecules are eluted from Protein A under acidic condition. In addition, virus inactivation, which is required when developing IgG molecules as pharmaceuticals, is generally carried out under acidic condition. It is thus desirable that the stability of IgG molecules under acidic condition is higher. However, the stability of IgG2 and IgG4 molecules under acidic condition was found to be lower than that of IgG1, and suggests for the first time that there is a problem of denaturation/aggregation under acidic condition in developing IgG2 and IgG4 molecules as pharmaceuticals. It is desirable that this problem of denaturation/aggregation be overcome when developing them as pharmaceuticals.

To date, however, no report has been published on a method for solving this problem through amino acid substitution.

Preparation and assessment of WT-IgG2 and WT-IgG4 having a modified CH3 domain

The stability of IgG2 and IgG4 molecules under acidic condition was demonstrated to be lower than that of IgG1. Thus, modified forms of IgG2 and IgG4 molecules were tested to improve the stability under acidic condition. According to models for the constant regions of IgG2 and IgG4 molecules, one of the potential destabilizing factors under acidic condition was thought to be the instability at the CH3-CH3 domain interface. As a result of various examinations, methionine at position 397 in the EU numbering system in IgG2, or arginine at position 409 in the EU numbering system in IgG4 was thought to destabilize the CH3/CH3 interface. Then, modified IgG2 and IgG4 antibodies were prepared. A modified IgG2 antibody comprises the substitution of valine for methionine at position 397 in the EU numbering system (IgG2-M397V, SEQ ID NO: 111 (amino acid sequence)) and a modified IgG4 antibody comprises the substitution of lysine for arginine at position 409 in the EU numbering system (IgG4-R409K, SEQ ID NO: 112 (amino acid sequence)).

The methods used for constructing expression vectors for the antibodies of interest, and expressing and purifying the antibodies, were the same as those used for the hydrochloric acid elution described above. Gel filtration chromatography analysis was carried out to estimate the contents of aggregate in the purified samples obtained by hydrochloric acid elution from Protein A.

Aggregation assessment method:

System: Waters Alliance
Column: G3000SWxl (TOSOH)
Mobile phase: 50 mM sodium phosphate, 300 mM KCl, pH 7.0
Flow rate, wavelength: 0.5 ml/min, 220 nm

The result is shown in Fig. 21. While the content of aggregate in WT-IgG1 after purification was about 2%, those in WT-IgG2 and WT-IgG4 after purification were about 25%. By contrast, the contents of aggregate in variants with modified CH3 domain, IgG2-M397V and IgG4-R409K, were comparable (approx. 2%) to that in IgG1. This finding demonstrates that the stability of an IgG2 or IgG4 antibody under acidic condition can be improved by substituting valine for methionine of IgG2 at position 397 in the EU numbering system or lysine for arginine of IgG4 at position 409 in the EU numbering system, respectively. Furthermore, the midpoint temperatures of thermal denaturation of WT-IgG2, WT-IgG4, IgG2-M397V, and IgG4-R409K were determined by the same method as described in Example 5. The result showed that the Tm value for the modified CH3 domain was higher in IgG2-M397V and IgG4-R409K as

compared to WT-IgG2 and WT-IgG4, respectively. This suggests that IgG2-M397V and IgG4-R409K are also superior in terms of thermal stability as compared to WT-IgG2 and WT-IgG4, respectively.

IgG2 and IgG4 are exposed to acidic condition in virus inactivation process and in the purification process using Protein A. Thus, denaturation/aggregation in the above processes was problematic. However, it was discovered that the problem could be solved by using IgG2-M397V and IgG4-R409K for the sequences of IgG2 and IgG4 constant regions. Thus, these modifications were revealed to be very useful in developing IgG2 and IgG4 antibody pharmaceuticals. Furthermore, the usefulness of IgG2-M397V and IgG4-R409K was also demonstrated by the finding that they are superior in thermal stability.

[Example 8] Improvement of heterogeneity derived from disulfide bonds in IgG2

Purification of WT-IgG1, WT-IgG2, and WT-IgG4 through acetic acid elution from Protein A

50 μl of rProtein A Sepharose™ Fast Flow (Amersham Biosciences) suspended in TBS was added to the culture supernatants obtained in Example 7, and the combined solutions were mixed by inversion at 4°C for four hours or more. The solutions were transferred into 0.22-μm filter cups of Ultrafree®-MC (Millipore). After washing three times with 500 μl of TBS, the rProtein A Sepharose™ resins were suspended in 100 μl of aqueous solution of 50 mM sodium acetate (pH 3.3) and the mixtures were incubated for two minutes to elute the antibodies. Immediately, the eluates were neutralized by adding 6.7 μl of 1.5 M Tris-HCl (pH 7.8). The elution was carried out twice, yielding 200 μl of purified antibodies.

Analysis of WT-IgG1, WT-IgG2, and WT-IgG4 by cation exchange chromatography (IEC)

Purified WT-IgG1, WT-IgG2, and WT-IgG4 were analyzed for homogeneity by cation exchange chromatography.

Assessment method using IEC:

System: Waters Alliance

Column: ProPac WCX-10 (Dionex)

Mobile phase A: 25 mM MES-NaOH, pH 6.1

B: 25 mM MES-NaOH, 250 mM Na-Acetate, pH 6.1

Flow rate, wavelength: 0.5 ml/min, 280 nm

Gradient B: 50%-75% (75 minutes) in the analysis of WT-IgG1

B: 30%-55% (75 minutes) in the analysis of WT-IgG2 and WT-IgG4

The result is shown in Fig. 22. WT-IgG2 showed more than one peak in the ion exchange analysis while WT-IgG1 and WT-IgG4 exhibited a single peak. This suggests that

the IgG2 molecule is more heterogeneous as compared to IgG1 and IgG4. Indeed, IgG2 isotypes have been reported to have heterogeneity derived from disulfide bonds in the hinge region (Chu GC *et al.*, Pharm. Res. 2007 Mar 24;24(6):1145-56). Thus, the hetero-peaks of IgG2 shown in Fig. 22 are also assumed to be desired substance/related substances derived from the disulfide bonds. It is difficult to produce antibody pharmaceuticals on a large scale while maintaining the difference in the heterogeneity of a desired substance/related substances between productions, and thus, antibody molecules to be developed as pharmaceuticals are desirably substances that are as homogeneous (less heterogeneous) as possible. For wild type IgG2, there is a problem of homogeneity which is important in developing antibody pharmaceuticals. Indeed, US20060194280 (A1) has shown that natural IgG2 gives various hetero-peaks as a result of the disulfide bonds in ion exchange chromatography analysis, and that the biological activity varies among these peaks. US20060194280 (A1) reports refolding in the purification process as a method for combining the hetero-peaks into a single one, but use of such a process in the production is costly and complicated. Thus, a preferred method for combining the hetero-peaks into a single one is based on amino acid substitution. Although the heterogeneity originated from disulfide bonds in the hinge region should be overcome to develop IgG2 as pharmaceuticals, no report has been published to date on a method for solving this problem through amino acid substitution.

Preparation and assessment of modified WT-IgG2 CH1 domain and hinge region

As shown in Fig. 23, there are various potential disulfide bond patterns for an IgG2 molecule. Possible causes of the heterogeneity derived from the hinge region of IgG2 were differential pattern of disulfide bonding and free cysteines. IgG2 has two cysteines (at positions 219 and 220 in the EU numbering system) in the upper hinge region, and cysteines adjacent to the two upper-hinge cysteines include cysteine at position 131 in the EU numbering system in the heavy chain CH1 domain and light chain C-terminal cysteine, and two corresponding cysteines in the heavy chain upper hinge of the dimerization partner. Specifically, there are eight cysteines in total in the vicinity of the upper hinge region of IgG2 when the antibody is in the associated form of H2L2. This may be the reason for the various heterogeneous patterns due to wrong disulfide bonding and free cysteines.

The hinge region sequence and CH1 domain of IgG2 were modified to reduce the heterogeneity originated from the IgG2 hinge region. Examinations were conducted to avoid the heterogeneity of IgG2 due to differential pattern of disulfide bonding and free cysteines. The result of examining various modified antibodies suggested that the heterogeneity could be avoided without decreasing the thermal stability by substituting serine and lysine for cysteine and arginine at positions 131 and 133 in the EU numbering system, respectively, in the heavy

chain CH1 domain, and substituting serine for cysteine at position 219, EU numbering, in the upper hinge of heavy chain of the wild type IgG2 constant region sequence (hereinafter "IgG2-SKSC") (IgG2-SKSC, SEQ ID NO: 120). These substitutions would enable IgG2-SKSC to form a homogenous covalent bond between heavy and light chains, which is a disulfide bond between the C-terminal cysteine of the light chain and cysteine at position 220 in the EU numbering system (Fig. 24).

The methods described in Example 1 were used to construct an expression vector for IgG2-SKSC and to express and purify IgG2-SKSC. The purified IgG2-SKSC and wild type IgG2 (WT-IgG2) were analyzed for homogeneity by cation exchange chromatography.

Assessment method using IEC:

System: Waters Alliance
Column: ProPac WCX-10 (Dionex)
Mobile phase A: 25 mM MES-NaOH, pH 5.6
B: 25 mM MES-NaOH, 250 mM Na-Acetate, pH 5.6
Flow rate, wavelength: 0.5 ml/min, 280 nm
Gradient B: 50%-100% (75 minutes)

The result is shown in Fig. 25. As expected above, IgG2-SKSC was shown to be eluted at a single peak while WT-IgG2 gave multiple peaks. This suggests that the heterogeneity derived from disulfide bonds in the hinge region of IgG2 can be avoided by using modifications such as those used to generate IgG2-SKSC, which allow formation of a single disulfide bond between the C-terminal cysteine of the light chain and cysteine at position 220 in the EU numbering system. The midpoint temperatures of thermal denaturation of WT-IgG1, WT-IgG2, and IgG2-SKSC were determined by the same methods as described in Example 5. The result showed that WT-IgG2 gave a peak for Fab domain which has a lower Tm value than WT-IgG1, while IgG2-SKSC did not give such a peak. This suggests that IgG2-SKSC is also superior in thermal stability as compared to WT-IgG2.

Although wild type IgG2 was thought to have a homogeneity problem which is important in developing antibody pharmaceuticals, it was found that this problem could be solved by using IgG2-SKSC for the constant region sequence of IgG2. Thus, IgG2-SKSC is very useful in developing IgG2 antibody pharmaceuticals. Furthermore, the usefulness of IgG2-SKSC was also demonstrated by the finding that it is superior in thermal stability.

[Example 9] Improvement of C-terminal heterogeneity in IgG molecules

Construction of an expression vector for heavy chain C-terminal ΔGK antibody from WT-IgG1

There is a report on the heterogeneity of antibody C-terminal sequence, which results

from the deletion of C-terminal amino acid lysine residue and the amidation of the C-terminal amino group due to deletion of the two C-terminal amino acids glycine and lysine (Johnson KA *et al.*, Anal. Biochem. 2007 Jan 1;360(1):75-83). The absence of such heterogeneity is preferred when developing antibody pharmaceuticals. Actually, in humanized PM-1 antibody TOCILIZUMAB, the major component is the sequence that lacks the C-terminal amino acid lysine, which is encoded by the nucleotide sequence but deleted in post-translational modification, and the minor component having the lysine also coexists as heterogeneity. Thus, the C-terminal amino acid sequence was modified to reduce the C-terminal heterogeneity. Specifically, the present inventors modified the nucleotide sequence of wild type IgG1 to delete the C-terminal lysine and glycine from the heavy chain constant region of the IgG1, and assessed whether the amidation of the C-terminal amino group could be suppressed by deleting the two C-terminal amino acids glycine and lysine.

Mutations were introduced into the C-terminal sequence of the heavy chain using pB-CH vector encoding the humanized PM-1 antibody (WT) obtained in Example 1. The nucleotide sequence encoding Lys at position 447 and/or Gly at position 446 in the EU numbering system was converted into a stop codon by introducing a mutation using the QuikChange Site-Directed Mutagenesis Kit (Stratagene) according to the method described in the attached instruction manual. Thus, expression vectors for antibody engineered to lack the C-terminal amino acid lysine (position 447 in the EU numbering system) and antibody engineered to lack the two C-terminal amino acids glycine and lysine (positions 446 and 447 in the EU numbering system, respectively) were constructed. Heavy chain C-terminal ΔK and ΔGK antibodies were obtained by expressing the engineered heavy chains and the light chain of the humanized PM-1 antibody. The antibodies were expressed and purified by the method described in Example 1.

Purified heavy chain C-terminal ΔGK antibody was analyzed by cation exchange chromatography according to the following procedure. The effect of the C-terminal deletion on heterogeneity was assessed by cation exchange chromatography analysis using the purified heavy chain C-terminal ΔGK antibody according to the method described below. The conditions of cation exchange chromatography analysis are described below. Chromatograms for humanized PM-1 antibody, heavy chain C-terminal ΔK antibody, and heavy chain C-terminal ΔGK antibody were compared.

Column: ProPac WCX-10, 4 x 250 mm (Dionex)
Mobile phase A: 25 mmol/l MES/NaOH, pH 6.1
B: 25 mmol/l MES/NaOH, 250 mmol/l NaCl, pH 6.1
Flow rate: 0.5 ml/min
Gradient: 25% B (5 minutes) → (105 minutes) → 67% B → (1 minute)

→ 100% B (5 minutes)

Detection: 280 nm

The analysis result for the non-modified humanized PM-1 antibody, heavy chain C-terminal ΔK antibody, and heavy chain C-terminal ΔGK antibody is shown in Fig. 26. According to Chu GC *et al.*, Pharm Res. 2007 Mar 24;24(6):1145-56, a basic peak with more prolonged retention time than that of the main peak contains a heavy chain C terminus with Lys at position 449 and a heavy chain C terminus with amidated Pro at position 447. The intensity of the basic peak was significantly reduced in the heavy chain C-terminal ΔGK antibody, while no such significant reduction was observed in the heavy chain C-terminal ΔK antibody. This suggests that the C-terminal heterogeneity of the heavy chain can be reduced only when the two C-terminal amino acids are deleted from the heavy chain.

The temperature of thermal denaturation of the heavy chain C-terminal ΔGK antibody was determined by DSC to assess the effect of the deletion of the two residues at the heavy chain C terminus on thermal stability. For the DSC measurement, the antibody was dialyzed against 20 mM acetic acid buffer (pH 6.0) containing 150 mM NaCl to change the buffer. After thorough deaeration, the humanized PM-1 antibody and heavy chain C-terminal ΔGK antibody solutions, and the reference solution (outer dialysate) were enclosed in calorimetric cells, and thoroughly thermally equilibrated at 40°C. Then, the samples were scanned at from 40°C to 100°C with a rate of about 1K/min. The resulting denaturation peaks were assigned (Rodolfo *et al.*, Immunology Letters, 1999, p 47-52). The result showed that the C-terminal deletion had no effect on the thermal denaturation temperature of CH3 domain.

Thus, the heterogeneity originated from the C-terminal amino acid can be reduced without affecting the thermal stability of antibody by deleting the C-terminal lysine and glycine from the heavy chain constant region at the nucleotide sequence level. Since all of the constant regions of human antibodies IgG1, IgG2, and IgG4 contain Gly and Lys at positions 446 and 447 in the EU numbering system in their C-terminal sequences, the method for reducing the C-terminal amino acid heterogeneity discovered in this example and others is also expected to be applicable to IgG2 and IgG4 constant regions and variants thereof.

[Example 10] Construction of M14ΔGK with a novel optimized constant region sequence

When an antibody pharmaceutical is aimed at neutralizing an antigen, effector functions such as ADCC of Fc domain are unnecessary and therefore the binding to Fcγ receptor is unnecessary. The binding to Fcγ receptor is assumed to be unfavorable from the perspectives of immunogenicity and adverse effect (Strand V *et al.*, Nat. Rev. Drug Discov. 2007 Jan;6(1):75-92; Gessner JE *et al.*, Ann. Hematol. 1998 Jun;76(6):231-48). The humanized anti-IL-6 receptor IgG1 antibody TOCILIZUMAB does not need to bind to Fcγ receptor,

because it only needs to specifically bind to IL-6 receptor and neutralize its biological activity in order to be used as a therapeutic agent for diseases associated with IL-6, such as rheumatoid arthritis.

Construction and assessment of M14ΔGK, a Fcγ receptor-nonbinding, optimized constant region

A possible method for impairing the Fcγ receptor binding is to convert the IgG antibody from IgG1 isotype to IgG2 or IgG4 isotype (Ann. Hematol. 1998 Jun;76(6):231-48). As a method for completely eliminating the binding to Fcγ receptor, a method of introducing an artificial modification into Fc domain has been reported. For example, since the effector functions of anti-CD3 antibody and anti-CD4 antibody cause adverse effects, amino acid mutations that are not present in the wild type sequence have been introduced into the Fcγ receptor-binding region of Fc domain (Cole MS *et al.*, J. Immunol. 1997 Oct 1;159(7):3613-21; Reddy MP *et al.*, J. Immunol. 2000 Feb 15;164(4):1925-33), and the resulting Fcγ receptor-nonbinding anti-CD3 and anti-CD4 antibodies are under clinical trials (Strand V *et al.*, Nat. Rev. Drug Discov. 2007 Jan;6(1):75-92; Chau LA *et al.*, Transplantation 2001 Apr 15;71(7):941-50). According to another report (Kim SJ *et al.*, Mol Cells. 2005 Aug 31;20(1):17-29 Review), Fcγ receptor-nonbinding antibodies can be prepared by converting the FcγR-binding domain of IgG1 (at positions 233, 234, 235, 236, 327, 330, and 331 in the EU numbering system) into the sequence of IgG2 (at positions 233, 234, 235, and 236 in the EU numbering system) or IgG4 (at positions 327, 330, and 331 in the EU numbering system). However, if all of the above mutations are introduced into IgG1, novel peptide sequences of nine amino acids, which potentially serve as non-natural T-cell epitope peptides, will be generated, and this increases the immunogenicity risk. The immunogenicity risk should be minimized in developing antibody pharmaceuticals.

To overcome the above problem, modifications in the IgG2 constant region were considered. In the FcγR-binding domain of IgG2 constant region, residues at positions 327, 330, and 331 in the EU numbering system are different from the nonbinding sequence of IgG4 while those at positions 233, 234, 235, and 236 in the EU numbering system are amino acids of nonbinding type. Thus, it is necessary to modify the amino acids at positions 327, 330, and 331 in the EU numbering system to the sequence of IgG4 (G2Δa described in Eur. J. Immunol. 1999 Aug;29(8):2613-24). However, since the amino acid at position 339 in the EU numbering system in IgG4 is alanine while the corresponding residue in IgG2 is threonine, a simple modification of the amino acids at positions 327, 330, and 331 in the EU numbering system to the sequence of IgG4 unfavorably generates a novel peptide sequence of 9 amino acids, potentially serving as a non-natural T-cell epitope peptide, and thus increases the immunogenicity risk. Then, the present inventors found that the generation of novel peptide

sequence could be prevented by introducing the substitution of alanine for threonine at position 339 in the EU numbering system in IgG2, in addition to the modification described above.

In addition to the mutations described above, other mutations were introduced, and they were the substitution of valine for methionine at position 397 in the EU numbering system in IgG2, which was discovered in Example 7 to improve the stability of IgG2 under acidic condition; and the substitution of serine for cysteine at position 131 in the EU numbering system, the substitution of lysine for arginine at position 133 in the EU numbering system, and the substitution of serine for cysteine at position 219 in the EU numbering system, which were discovered in Example 8 to improve the heterogeneity originated from disulfide bonds in the hinge region. Furthermore, since the mutations at positions 131 and 133 generate a novel peptide sequence of 9 amino acids, potentially serving as a non-natural T-cell epitope peptide, and thus generate the immunogenicity risk, the peptide sequence around positions 131 to 139 was converted into a natural human sequence by introducing the substitution of glycine for glutamic acid at position 137 in the EU numbering system and the substitution of glycine for serine at position 138 in the EU numbering system. Furthermore, glycine and lysine at positions 446 and 447 in the EU numbering system were deleted from the C terminus of heavy chain to reduce the C-terminal heterogeneity. The constant region sequence having all of the mutations introduced was named M14ΔGK (M14ΔGK, SEQ ID NO: 24). Although there is a mutation of cysteine at position 219 to serine in M14ΔGK as a novel 9-amino acid peptide sequence which potentially serves as a T-cell epitope peptide, the immunogenicity risk was considered very low since the amino acid property of serine is similar to that of cysteine. The immunogenicity prediction by TEPITOPE also suggested that there was no difference in immunogenicity.

An expression vector for the antibody heavy chain sequence whose variable region was WT and constant region was M14ΔGK (M14ΔGK, SEQ ID NO: 24; WT-M14ΔGK, SEQ ID NO: 113) was constructed by the method described in Example 1. An antibody having WT-M14ΔGK as heavy chain and WT as light chain was expressed and purified by the method described in Example 1.

Furthermore, WT-M17ΔGK (M17ΔGK, SEQ ID NO: 116; WT-M17ΔGK, SEQ ID NO: 115) was constructed with the same method by introducing mutations into the IgG1 constant region at positions 233, 234, 235, 236, 327, 330, 331, and 339 in the EU numbering system (G1Δab described in Eur. J. Immunol. 1999 Aug;29(8):2613-24) to impair the Fcγ receptor binding and by deleting the amino acids at positions 446 and 447 in the EU numbering system to reduce the C-terminal heterogeneity (Example 9). An expression vector for WT-M11ΔGK (M11ΔGK, SEQ ID NO: 25; WT-M11ΔGK, SEQ ID NO: 114) was constructed. In WT-M11ΔGK, mutations were introduced into the IgG4 constant region at positions 233, 234,

235, and 236 in the EU numbering system (G4Δb described in Eur. J. Immunol. 1999 Aug;29(8):2613-24; this modification newly generates nonhuman sequence and thus increases the immunogenicity risk) to reduce the Fcγ receptor binding. In addition to the above modification, to reduce the immunogenicity risk, mutations were introduced at positions 131, 133, 137, 138, 214, 217, 219, 220, 221, and 222 in the EU numbering system so that the pattern of disulfide bonding in the hinge region was the same as that of M14ΔGK; a mutation was introduced at position 409 in the EU numbering system (Example 7) to improve the stability under acidic condition; and the amino acids at positions 446 and 447 in the EU numbering system were deleted (Example 9) to reduce the C-terminal heterogeneity. WT-M17ΔGK or WT-M11ΔGK was used as the heavy chain, and WT was used as the light chain. These antibodies were expressed and purified by the method described in Example 1.

Assessment of WT-M14ΔGK, WT-M17ΔGK, and WT-M11ΔGK for Fcγ receptor-binding activity

The FcγRI binding was assessed by the procedure described below. Using Biacore T100, human-derived Fcγ receptor I (hereinafter "FcγRI") immobilized onto a sensor chip was allowed to interact with IgG1, IgG2, IgG4, M11ΔGK, M14ΔGK, or M1ΔGK 7 as an analyte. The amounts of bound antibody were compared. The measurement was conducted using Recombinant Human FcRIA/CD64 (R&D systems) as human-derived FcγRI, and IgG1, IgG2, IgG4, M11ΔGK, M14ΔGK, and M17ΔGK as samples. FcγRI was immobilized onto the sensor chip CM5 (Biacore) by the amine coupling method. The final amount of immobilized hFcγRI was about 13,000 RU. The running buffer used was HBS-EP+, and the flow rate was 20 μl/min. The sample concentration was adjusted to 100 μg/ml using HBS-EP+. The analysis included two steps: two minutes of association phase where 10 μl of an antibody solution was injected and the subsequent four minutes of dissociation phase where the injection was switched with HBS-EP+. After the dissociation phase, the sensor chip was regenerated by injecting 20 μl of 5 mM sodium hydroxide. The association, dissociation, and regeneration constitute one analysis cycle. Various antibody solutions were injected to obtain sensorgrams. As analytes, IgG4, IgG2, IgG1, M11, M14, and M17 were injected in this order. This series of injection was repeated twice. The result of comparison of data on the determined amounts of bound antibody is shown in Fig. 27. The comparison shows that the amount of bound antibody is reduced in the order of: IgG1 > IgG4 >> IgG2 = M11ΔGK = M14ΔGK = M17ΔGK. Thus, it was revealed that the FcγRI binding of wild type IgG2, M11ΔGK, M14ΔGK, and M17ΔGK was weaker than that of wild type IgG1 and IgG4.

The FcγRIIa binding was assessed by the procedure described below. Using Biacore T100, human-derived Fcγ receptor IIa (hereinafter "FcγRIIa") immobilized onto a sensor chip

was allowed to interact with IgG1, IgG2, IgG4, M11ΔGK, M14ΔGK, or M17ΔGK as an analyte. The amounts of bound antibody were compared. The measurement was conducted using Recombinant Human FcRIIA/CD32a (R&D systems) as human-derived FcγRIIa, and IgG1, IgG2, IgG4, M11ΔGK, M14ΔGK, and M17ΔGK as samples. FcγRIIa was immobilized onto the sensor chip CM5 (Biacore) by the amine coupling method. The final amount of immobilized FcγRIIa was about 3,300 RU. The running buffer used was HBS-EP+, and the flow rate was 20 μl/min. Then, the running buffer was injected until the baseline was stabilized. The measurement was carried out after the baseline was stabilized. The immobilized FcγRIIa was allowed to interact with an antibody of each IgG isotype (IgG1, IgG2, or IgG4) or antibody introduced with mutations (M11ΔGK, M14ΔGK, or M17ΔGK) as an analyte. The amount of bound antibody was observed. The running buffer used was HBS-EP+, and the flow rate was 20 μl/min. The measurement temperature was 25°C. The concentration of each IgG or modified form thereof was adjusted to 100 μg/ml. 20 μl of an analyte was injected and allowed to interact with the immobilized FcγRIIa. After interaction, the analyte was dissociated from FcγRIIa and the sensor chip was regenerated by injecting 200 μl of the running buffer. As analytes, IgG4, IgG2, IgG1, M11ΔGK, M14ΔGK, and M17ΔGK were injected in this order. This series of injection was repeated twice. The result of comparison of data on the amounts of bound antibody determined is shown in Fig. 28. The comparison shows that the amount of bound antibody is reduced in the order of: IgG1 > IgG2 = IgG4 > M11ΔGK = M14ΔGK = M17ΔGK. Thus, it was revealed that the FcγRIIa binding of M11ΔGK, M14ΔGK, and M17ΔGK was weaker than that of wild type IgG1, IgG2, and IgG4.

The FcγRIIb binding was assessed by the procedure described below. Using Biacore T100, human-derived Fcγ receptor IIb (hereinafter "FcγRIIb") immobilized onto a sensor chip was allowed to interact with IgG1, IgG2, IgG4, M11ΔGK, M14ΔGK, or M17ΔGK as an analyte. The amounts of bound antibody were compared. The measurement was conducted using Recombinant Human FcRIIB/C (R&D systems) as human-derived FcγRIIb, and IgG1, IgG2, IgG4, M11ΔGK, M14ΔGK, and M17ΔGK as samples. FcγRIIb was immobilized onto the sensor chip CM5 (Biacore) by the amine coupling method. The final amount of immobilized FcγRIIb was about 4,300 RU. Then, the running buffer was injected until the baseline was stabilized. The measurement was carried out after the baseline was stabilized. The immobilized FcγRIIb was allowed to interact with an antibody of each IgG isotype (IgG1, IgG2, or IgG4) or antibody introduced with mutations (M11ΔGK, M14ΔGK, or M17ΔGK) as an analyte. The amount of bound antibody was observed. The running buffer used was HBS-EP+ (10 mM HEPES, 0.15 M NaCl, 3 mM EDTA, 0.05% v/v Surfactant P20), and the flow rate was 20 μl/min. The measurement temperature was 25°C. The concentration of each IgG or modified form thereof was adjusted to 200 μg/ml. 20 μl of an analyte was injected and

allowed to interact with the immobilized FcγRIIb. After interaction, the analyte was dissociated from FcγRIIb and the sensor chip was regenerated by injecting 200 μl of the running buffer. As analytes, IgG4, IgG2, IgG1, M11ΔGK, M14ΔGK, and M17ΔGK were injected in this order. This series of injection was repeated twice. The result of comparison of data on the amounts of bound antibody determined is shown in Fig. 29. The comparison shows that the amount of bound antibody is reduced in the order of: IgG4 > IgG1 > IgG2 > M11ΔGK = M14ΔGK = M17ΔGK. Thus, it was revealed that the FcγRIIb binding of M11ΔGK, M14ΔGK, and M17ΔGK was weaker than that of wild type IgG1, IgG2, and IgG4.

The FcγRIIIa binding was assessed by the procedure described below. Using Biacore T100, human-derived Fcγ receptor IIIa (hereinafter "FcγRIIIa") immobilized onto a sensor chip was allowed to interact with IgG1, IgG2, IgG4, M11ΔGK, M14ΔGK, or M17ΔGK as an analyte. The amounts of bound antibody were compared. The measurement was conducted using hFcγRIIIaV-His6 (recombinant hFcγRIIIaV-His6 prepared in the applicants' company) as human-derived FcγRIIIa, and IgG1, IgG2, IgG4, M11ΔGK, M14ΔGK, and M17ΔGK as samples. FcγRIIIa was immobilized onto the sensor chip CM5 (Biacore) by the amine coupling method. The final amount of immobilized hFcγRIIIaV-His6 was about 8200 RU. The running buffer used was HBS-EP+, and the flow rate was 5 μl/min. The sample concentration was adjusted to 250 μg/ml using HBS-EP+. The analysis included two steps: two minutes of association phase where 10 μl of an antibody solution was injected and the subsequent four minutes of dissociation phase where the injection was switched with HBS-EP+. After the dissociation phase, the sensor chip was regenerated by injecting 20 μl of 5 mM hydrochloric acid. The association, dissociation, and regeneration constitute one analysis cycle. Various antibody solutions were injected to obtain sensorgrams. As analytes, IgG4, IgG2, IgG1, M11ΔGK, M14ΔGK, and M17ΔGK were injected in this order. The result of comparison of data on the determined amounts of bound antibody is shown in Fig. 30. The comparison shows that the amount of bound antibody is reduced in the order of: IgG1 >> IgG4 > IgG2 > M17ΔGK > M11ΔGK = M14ΔGK. Thus, it was revealed that the FcγRIIIa binding of M11ΔGK, M14ΔGK, and M17ΔGK was weaker than that of wild type IgG1, IgG2, and IgG4. Furthermore, the FcγRIIIa binding of M11ΔGK and M14ΔGK was found to be weaker than that of M17ΔGK containing the mutation G1Δab reported in Eur. J. Immunol. 1999 Aug;29(8):2613-24.

The finding described above demonstrates that the Fcγ receptor binding of WT-M14ΔGK, WT-M17ΔGK, and WT-M11ΔGK is markedly reduced as compared to wild type IgG1. The immunogenicity risk due to Fcγ receptor-mediated internalization into APC and adverse effects caused by the effector function such as ADCC can be avoided by using WT-M14ΔGK, WT-M17ΔGK, or WT-M11ΔGK as a constant region. Thus, WT-M14ΔGK, WT-M17ΔGK, and WT-M11ΔGK are useful as constant region sequence of antibody

pharmaceuticals aimed at neutralizing antigens.

Assessment of WT-M14ΔGK, WT-M17ΔGK, and WT-M11ΔGK for stability at high concentrations

WT-M14ΔGK, WT-M17ΔGK, and WT-M11ΔGK were assessed for stability at high concentrations. The purified antibodies of WT-IgG1, WT-M14ΔGK, WT-M17ΔGK, and WT-M11ΔGK were dialyzed against a solution of 20 mM histidine chloride, 150 mM NaCl, pH 6.5 (EasySEP, TOMY), and then concentrated by ultrafilters. The antibodies were tested for stability at high concentrations. The conditions were as follows.

Antibodies: WT-IgG1, WT-M14ΔGK, WT-M17ΔGK, and WT-M11ΔGK

Buffer: 20 mM histidine chloride, 150 mM NaCl, pH 6.5

Concentration: 61 mg/ml

Storage temperature and time period: 40°C for two weeks, 40°C for one month, 40°C for two months

Aggregation assessment method:

System: Waters Alliance

Column: G3000SWxl (TOSOH)

Mobile phase: 50 mM sodium phosphate, 300 mM KCl, pH 7.0

Flow rate, wavelength: 0.5 ml/min, 220 nm

100 times diluted samples were analyzed

The contents of aggregate in the initial formulations (immediately after preparation) and formulations stored under various conditions were estimated by gel filtration chromatography described above. Differences (amounts increased) in the content of aggregate relative to the initial formulations are shown in Fig. 31. The result showed that the amounts of aggregate in WT-M14ΔGK, WT-M17ΔGK, and WT-M11ΔGK increased only slightly as compared to WT-IgG1 and were about half of the content in WT. Furthermore, as shown in Fig. 32, the amount of increased Fab fragment was comparable between WT-IgG1 and WT-M17ΔGK, while the amounts increased in WT-M14ΔGK and WT-M11ΔGK were about one quarter of the amount in WT. Degeneration pathways of IgG type antibody formulations include formation of aggregate and generation of Fab degradate as described in WO 2003/039485. Based on the two criteria, aggregation and Fab fragment generation, WT-M14ΔGK and WT-M11ΔGK were demonstrated to have a superior stability in formulations as compared to WT-IgG1. Thus, even for antibodies that have an IgG1 constant region with poor stability and could not be prepared as antibody pharmaceuticals in high-concentration liquid formulations, the use of WT-M14ΔGK, WT-M17ΔGK, or WT-M11ΔGK as a constant region was expected to allow production of more stable high-concentration liquid formulations.

In particular, M14ΔGK was expected to be very useful as a novel constant region sequence that would (1) overcome the instability of the original IgG2 molecule under acidic condition; (2) improve the heterogeneity originated from disulfide bonds in the hinge region; (3) not bind to Fcγ receptor; (4) have a minimized number of novel peptide sequences of 9 amino acids which potentially serve as T-cell epitope peptides; and (5) have a better stability than IgG1 in high-concentration formulations.

[Example 11] Preparation of PF1-M14ΔGK antibody

The variable region of PF1 (whose constant region is IgG1) constructed in Example 5 was excised using *Xho*I and *Nhe*I. The constant region of M14ΔGK (whose variable region is WT) constructed in Example 7 was excised using *Nhe*I and *Not*I. The two antibody heavy chain gene fragments were inserted into an animal cell expression vector to construct an expression vector for the heavy chain of interest, PF1-M14ΔGK (PF1_H-M14ΔGK, SEQ ID NO: 117). The light chain used was PF1_L. The antibody PF1-M14ΔGK was expressed and purified by the method described in Example 1.

The antibody PF1-M14ΔGK was superior in various aspects as compared to WT (humanized PM-1 antibody) and thus expected to be very useful as anti-IL-6 receptor antibody pharmaceuticals.

[Example 12] Preparation and assessment of M31ΔGK

M14ΔGK prepared in Example 10 was modified by substituting the IgG2 sequence for the amino acids at positions 330, 331, and 339 in the EU numbering system to construct M31ΔGK (M31ΔGK, SEQ ID NO: 118). An expression vector for a sequence of antibody heavy chain whose variable region is WT and constant region sequence is M31ΔGK (WT-M31ΔGK, SEQ ID NO: 119) was constructed by the method described in Example 1. Using WT-M31ΔGK heavy chain and WT light chain, WT-M31 was expressed and purified by the method described in Example 1.

In addition to WT-M31, WT-IgG2 and WT-M14ΔGK were expressed and purified at the same time, and analyzed by cation exchange chromatography by the procedure described below. The conditions used in the cation exchange chromatography analysis were as follows. Chromatograms for WT-IgG2, WT-M14ΔGK, and WT-M31ΔGK were compared.

Column: ProPac WCX-10, 4 x 250 mm (Dionex)
Mobile phase A: 25 mmol/l MES/NaOH, pH 6.1
B: 25 mmol/l MES/NaOH, 250 mmol/l NaCl, pH 6.1
Flow rate: 0.5 ml/min
Gradient: 0% B (5 minutes) → (65 minutes) → 100% B → (1 minute)

Detection: 280 nm

The analysis result for WT-IgG2, WT-M14ΔGK, and WT-M31ΔGK is shown in Fig. 33. Like WT-M14ΔGK, WT-M31ΔGK was demonstrated to be eluted as a single peak, while WT-IgG2 gave multiple peaks. This indicates that the heterogeneity derived from disulfide bonds in the hinge region of IgG2 can also be avoided in WT-M31ΔGK.

[Example 13] Preparation of a fully humanized antibody F2H/L39-IgG1

Complete humanization of the framework sequence of the PF1 antibody

Arginine at position 71 (Kabat's numbering; Kabat EA *et al.*, 1991. Sequences of Proteins of Immunological Interest. NIH) is the only mouse sequence that remains in PF1_H prepared in Example 5. This is unpreferable from the perspective of immunogenicity. In general, the residue at position 71 in the heavy chain is an important sequence for the conformation of HCDR2. In fact, it has been reported that during generation of the humanized PM1 antibody, the residue at position 71 is essential for the binding activity of mouse PM1 antibody. The binding activity was demonstrated to be significantly reduced by substituting valine at position 71 (Cancer Research (1993) 53:851-856). Meanwhile, PF1_H is classified into the VH4 family of human germ-line genes, and valine at position 71 is highly conserved in the VH4 family. The neutralizing activity was also demonstrated to be significantly reduced by substituting valine for arginine at position 71.

Thus, to completely remove the mouse sequence while maintaining the arginine at position 71, the present inventors searched among sequences of human germ-line genes and reported human antibodies for sequences that have arginine at position 71 and share conserved residues important for the maintenance of antibody tertiary structure. As a result, the inventors discovered a candidate sequence which contains important conserved residues although its homology to PF1_H is low as shown in Table 9.

Table 9

KABAT NUMBERING	66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 82a 82b 82c 83 84 85 86 87 88 89 90 91 92 93 94	source
PF1_H CANDIDATE SEQUENCE	R V T I S R D T S K N Q F S L K L S S V T A A D T A A Y Y C A R	Germline: IMGT_hVH_4_b (EXCEPT H71&H89)
	R V T I S R D N S K N T L Y L Q M N S L R A E D T A V Y Y C A R	Mol. Immunol. 44(4):412-422 (2007)

H96-IgG1 (amino acid sequence of SEQ ID NO: 134) was designed by substituting the above-described candidate sequence for the region of positions 66 to 94 in PF1_H-IgG1, Kabat's numbering. The antibody variable region was prepared by PCR (assembly PCR) using a combination of synthetic oligo-DNAs. The constant region was amplified from an expression vector for IgG1 by PCR. The antibody variable region and constant region were linked

together by assembly PCR, and then inserted into an animal cell expression vector. H96/PF1L-IgG1 was expressed and purified by the method described in Example 1.

Assessment of H96/PF1L-IgG1, an antibody with fully humanized framework

The Tm of purified H96/PF1L-IgG1 was determined by the method described in Example 5. The affinity measurement was carried out under essentially the same conditions used in Example 5. Note that the concentration of SR344 was adjusted to 0, 0.36, and 1.4 μg/ml, and the dissociation phase was monitored for 15 minutes. The result showed that the Tm and affinity of H96/PF1L-IgG1 were almost the same as those of PF1-IgG1 (Table 10).

Table 10

	Tm (°C)	k_a (1/Ms)	k_d (1/s)	KD (M)
PF1 ANTIBODY	91.3	1.4E+06	4.2E-05	3.1E-11
H96/PF1L-IgG1	89.8	1.2E+06	4.8E-05	3.9E-11

As described above, the present inventors generated an antibody with a completely humanized PF1 antibody framework, using H96 for the PF1 antibody heavy chain to completely remove the remaining mouse sequence from the PF1 antibody while maintaining its Tm and affinity. Since the framework sequence of H96/PF1L-IgG1 has no mouse-derived sequence, H96/PF1L-IgG1 is expected to be superior, especially from the perspective of immunogenicity.

Construction of F2H/L39-IgG1 with lowered isoelectric point and attenuated immunogenicity risk

As demonstrated in Example 4, the retention in plasma can be prolonged by lowering isoelectric point through modification of amino acids in the antibody variable region. Thus, the amino acid substitutions shown below were further introduced into H96-IgG1 constructed above. To lower isoelectric point, glutamine was substituted for lysine at position 64, and aspartic acid was substituted for glycine at position 65. Furthermore, to reduce the immunogenicity risk, glutamine was substituted for glutamic acid at position 105 and isoleucine was substituted for threonine at position 107. In addition, to achieve affinity enhancement such as that in Example 2, modification was introduced where leucine was substituted for valine at position 95 and alanine was substituted for isoleucine at position 99. To prepare F2H-IgG1 (amino acid sequence of SEQ ID NO: 135), these amino acid substitutions were introduced into H96-IgG1 by the method described in Example 1.

Furthermore, the following amino acid substitutions were introduced into PF1L. To lower isoelectric point, glutamic acid was substituted for glutamine at position 27 and glutamic

acid was substituted for leucine at position 55. To prepare L39 (amino acid sequence of SEQ ID NO: 136), these amino acid substitutions were introduced into PF1L by the method described in Example 1. Using F2H-IgG1 as heavy chain and L39 as light chain, F2H/L39-IgG1 was expressed and purified by the method described in Example 1.

Biacore-based analysis of F2H/L39-IgG1 for the affinity for human IL-6 receptor

Humanized PM1 antibody (wild type (WT)), PF1 antibody (constructed in Example 5), and F2H/L39-IgG1 were analyzed for affinity. This measurement was carried out under essentially the same conditions used in Example 4. Note that the concentration of SR344 was adjusted to 0, 0.36, and 1.4 μg/ml, and the dissociation phase was monitored for 15 minutes (Table 11).

Table 11

SAMPLE	k_a (1/Ms)	k_d (1/s)	KD (M)
PF1-IgG1	1.5E+06	4.4E-05	3.0E-11
F2H/L39-IgG1	7.7E+05	4.0E-05	5.2E-11

The result showed that F2H/L39-IgG1 had very strong affinity (maintaining a KD in the order of 10^{-11}) but its k_a was decreased to about half of that of PF1-IgG1.

Assessment of F2H/L39-IgG1 for its human IL-6 receptor-neutralizing activity

The neutralizing activities of humanized PM1 antibody (wild type (WT)) and F2H/L39-IgG1 were assessed by the method described in Example 1. The assessment of neutralizing activity was carried out using 600 ng/ml human interleukin-6 (TORAY). As shown in Fig. 34, F2H/L39-IgG1 was demonstrated to have a very strong activity, 100 or more times higher than WT in terms of 100% inhibitory concentration.

Assessment of F2H/L39-IgG1 for its isoelectric point by isoelectric focusing

The isoelectric point of F2H/L39-IgG1 was determined by the method described in Example 3. The isoelectric point of F2H/L39-IgG1 was 5.5, suggesting that its retention in plasma was prolonged due to a lower isoelectric point relative to the PF1 antibody prepared in Example 5.

The theoretical isoelectric point of the variable regions of F2H/L39 (heavy chain variable region and light chain variable region sequences) was calculated to be 4.3 by using GENETYX (GENETYX CORPORATION). Meanwhile, the theoretical isoelectric point of WT was 9.20. Thus, WT has been converted through amino acid substitution into F2H/L39

which has a variable region with a theoretical isoelectric point decreased by about 4.9.

PK/PD test of F2H/L39-IgG1 using cynomolgus monkeys

The humanized PM1 antibody (wild type (WT)), PF1 antibody, and F2H/L39-IgG1 were assessed for their pharmacokinetics (PK) and pharmacodynamics (PD) in cynomolgus monkeys. WT, PF1, and F2H/L39-IgG1 were subcutaneously administered once at 1.0 mg/kg, and blood was collected before administration and over the time course. The concentration of each antibody in plasma was determined in the same way as described in Example 6. The plasma concentration time courses of WT, PF1, and F2H/L39-IgG1 are shown in Fig. 35. The efficacy of each antibody to neutralize membrane-bound cynomolgus monkey IL-6 receptor was assessed. Cynomolgus monkey IL-6 was administered subcutaneously in the lower back at 5 μg/kg every day from Day 3 to Day 10 after antibody administration, and the CRP concentration in each animal was determined 24 hours later. The time courses of CRP concentration after administration of WT or F2H/L39 are shown in Fig. 36. To assess the efficacy of each antibody to neutralize soluble cynomolgus monkey IL-6 receptor, the concentration of free soluble cynomolgus monkey IL-6 receptor in the plasma of cynomolgus monkeys was determined. The time courses of free soluble cynomolgus monkey IL-6 receptor concentration after administration of WT or F2H/L39 are shown in Fig. 37.

These results showed that the plasma concentration time courses of WT and PF1 were comparable to each other; however, the plasma concentration of F2H/L39-IgG1, which has a reduced isoelectric point, was maintained higher than that of these two antibodies. Meanwhile, when compared to WT, F2H/L39-IgG1 which has a high affinity for IL-6 receptor was found to maintain lower concentrations of CRP and free soluble cynomolgus monkey IL-6 receptor.

[Example 14] Assessment of the plasma retention of WT-M14

Method for estimating the retention in human plasma

The prolonged retention (slow elimination) of IgG molecule in plasma is known to be due to the function of FcRn which is known as a salvage receptor of IgG molecule (Nat. Rev. Immunol. 2007 Sep;7(9):715-25). When incorporated into endosomes *via* pinocytosis, under the acidic conditions within endosome (approx. pH 6.0), IgG molecules bind to FcRn expressed in endosomes. While IgG molecules that do not bind to FcRn are transferred and degraded in lysosomes, those bound to FcRn are translocated to the cell surface and then released from FcRn back into plasma again under the neutral conditions in plasma (approx. pH 7.4).

Known IgG-type antibodies include the IgG1, IgG2, IgG3, and IgG4 isotypes. The plasma half-lives of these isotypes in human are reported to be about 36 days for IgG1 and IgG2;

about 29 days for IgG3; and 16 days for IgG4 (Nat. Biotechnol. 2007 Dec;25(12):1369-72). Thus, the retention of IgG1 and IgG2 in plasma is believed to be the longest. In general, the isotypes of antibodies used as pharmaceutical agents are IgG1, IgG2, and IgG4. Methods reported for further prolonging the retention of these IgG antibodies in plasma include methods for improving the above-described binding activity to human FcRn, and this is achieved by modifying the sequence of IgG constant region (J. Biol. Chem. 2007 Jan 19;282(3):1709-17; J. Immunol. 2006 Jan 1;176(1):346-56).

There are species-specific differences between mouse FcRn and human FcRn (Proc. Natl. Acad. Sci. USA. 2006 Dec 5;103(49):18709-14). Therefore, to predict the plasma retention of IgG antibodies that have a modified constant region sequence in human, it is desirable to assess the binding to human FcRn and retention in plasma in human FcRn transgenic mice (Int. Immunol. 2006 Dec;18(12):1759-69).

Assessment of the binding to human FcRn

FcRn is a complex of FcRn and β2-microglobulin. Oligo-DNA primers were prepared based on the human FcRn gene sequence disclosed (J. Exp. Med. (1994) 180(6):2377-2381). A DNA fragment encoding the whole gene was prepared by PCR using human cDNA (Human Placenta Marathon-Ready cDNA, Clontech) as a template and the prepared primers. Using the obtained DNA fragment as a template, a DNA fragment encoding the extracellular domain containing the signal region (Met1-Leu290) was amplified by PCR, and inserted into an animal cell expression vector (the amino acid sequence of human FcRn as set forth in SEQ ID NO: 140). Likewise, oligo-DNA primers were prepared based on the human β2-microglobulin gene sequence disclosed (Proc. Natl. Acad. Sci. USA. (2002) 99(26):16899-16903). A DNA fragment encoding the whole gene was prepared by PCR using human cDNA (Hu-Placenta Marathon-Ready cDNA, CLONTECH) as a template and the prepared primers. Using the obtained DNA fragment as a template, a DNA fragment encoding the whole β2-microglobulin containing the signal region (Met1-Met119) was amplified by PCR and inserted into an animal cell expression vector (the amino acid sequence of human β2-microglobulin as set forth in SEQ ID NO: 141).

Soluble human FcRn was expressed by the following procedure. The plasmids constructed for human FcRn and β2-microglobulin were introduced into cells of the human embryonic kidney cancer-derived cell line HEK293H (Invitrogen) using 10% FBS (Invitrogen) by lipofection. The resulting culture supernatant was collected, and FcRn was purified using IgG Sepharose 6 Fast Flow (Amersham Biosciences) by the method described in J. Immunol. 2002 Nov 1;169(9):5171-80, followed by further purification using HiTrap Q HP (GE Healthcare).

The binding to human FcRn was assessed using Biacore 3000. An antibody was bound to Protein L or rabbit anti-human IgG Kappa chain antibody immobilized onto a sensor chip, human FcRn was added as an analyte for interaction with the antibody, and the affinity (KD) was calculated from the amount of bound human FcRn. Specifically, Protein L or rabbit anti-human IgG Kappa chain antibody was immobilized onto sensor chip CM5 (Biacore) by the amine coupling method using 50 mM Na-phosphate buffer (pH 6.0) containing 150 mM NaCl as the running buffer. Then, an antibody was diluted with a running buffer containing 0.02% Tween20, and injected to be bound to the chip. Human FcRn was then injected and the binding activity of the human FcRn to antibody was assessed.

The affinity was computed using BIAevaluation Software. The obtained sensorgram was used to calculate the amount of hFcRn bound to the antibody immediately before the end of human FcRn injection. The affinity of the antibody for human FcRn was calculated by fitting with the steady state affinity method.

Assessment for the plasma retention in human FcRn transgenic mice

The pharmacokinetics in human FcRn transgenic mice (B6.mFcRn-/-.hFcRn Tg line 276 +/+ mice; Jackson Laboratories) was assessed by the following procedure. An antibody was intravenously administered once at a dose of 1 mg/kg to mice, and blood was collected at appropriate time points. The collected blood was immediately centrifuged at 15,000 rpm and 4°C for 15 minutes to obtain blood plasma. The separated plasma was stored in a freezer at -20°C or below until use. The plasma concentration was determined by ELISA.

Predictive assessment of the plasma retention of WT-M14 in human

The activities of WT-IgG1 and WT-M14 to bind to human FcRn were assessed by Biacore. As shown in Table 12, the result indicated that the binding activity of WT-M14 was slightly greater than that of WT-IgG1.

Table 12

	KD(μM)
WT-IgG1	2.07
WT-M14	1.85

As shown in Fig. 38, however, the retention in plasma was comparable between WT-IgG1 and WT-M14 when assessed using human FcRn transgenic mice. This finding suggests that the plasma retention of the M14 constant region in human is comparable to that of the IgG1 constant region.

[Example 15] Preparation of WT-M44, WT-M58, and WT-M73 which have improved retention in plasma

Preparation of the WT-M58 molecule

As described in Example 14, the plasma retention of WT-M14 in human FcRn transgenic mice was comparable to that of WT-IgG1. Known methods to improve plasma retention include those to lower the isoelectric point of an antibody and those to enhance the binding activity to FcRn. Here, the modifications described below were introduced to improve the plasma retention of WT-M14. Specifically, the following substitutions were introduced into WT-M31ΔGK, which was prepared from WT-M14 as described in Example 4: substitution of methionine for valine at position 397; substitution of glutamine for histidine at position 268; substitution of glutamine for arginine at position 355; and substitution of glutamic acid for glutamine at position 419 in the EU numbering system. These four substitutions were introduced into WT-M31ΔGK to generate WT-M58 (amino acid sequence of SEQ ID NO: 142). Expression vectors were prepared by the same method described in Example 1. WT-M58 and L(WT) were used as heavy chain and light chain, respectively. WT-M58 was expressed and purified by the method described in Example 1.

Construction of the WT-M73 molecule

On the other hand, WT-M44 (amino acid sequence of SEQ ID NO: 143) was generated by introducing into IgG1 a substitution of alanine for the amino acid at position 434, EU numbering. WT-M83 (amino acid sequence of SEQ ID NO: 185) was also generated by deletions of glycine at position 446, EU numbering and lysine at position 447, EU numbering to reduce heavy chain C-terminal heterogeneity. Furthermore, WT-M73 (amino acid sequence of SEQ ID NO: 144) was generated by introducing into WT-M58 a substitution of alanine at position 434, EU numbering.

Expression vectors for the above antibodies were constructed by the method described in Example 1. WT-M44, WT-M58, or WT-M73 was used as heavy chain, while L (WT) was used as light chain. WT-M44, WT-M58, and WT-M73 were expressed and purified by the method described in Example 1.

Predictive assessment of the plasma retention of WT-M44, WT-M58, and WT-M73 in human

The binding activities of WT-IgG1, WT-M44, WT-M58, and WT-M73 to human FcRn were assessed by Biacore. As shown in Table 13, the result indicates that the binding activities of WT-M44, WT-M58, and WT-M73 are greater than WT-IgG1, and about 2.7, 1.4, and 3.8 times of that of WT-IgG1, respectively.

Table 13

	KD(μM)
WT-IgG1	1.62
WT-M44	0.59
WT-M58	1.17
WT-M73	0.42

As a result of assessing WT-IgG1, WT-M14, and WT-M58 for their plasma retention in human FcRn transgenic mice, as shown in Fig. 39, WT-M58 was confirmed to have increased retention in plasma relative to WT-IgG1 and WT-M14. Furthermore, WT-IgG1, WT-M44, WT-M58, and WT-M73 were assessed for their plasma retention in human FcRn transgenic mice. As shown in Fig. 40, all of WT-M44, WT-M58, and WT-M73 were confirmed to have improved retention in plasma relative to WT-IgG1. The plasma retention-improving effect correlated with the binding activity to human FcRn. In particular, the plasma level of WT-M73 at Day 28 was improved to about 16 times of that of WT-IgG1. This finding suggests that the plasma retention of antibodies with the M73 constant region in human is also significantly increased when compared to antibodies with the IgG1 constant region.

[Example 16] Effect of the novel constant regions M14 and M58 in reducing heterogeneity in various antibodies

As described in Example 8, it was demonstrated that the heterogeneity originated from the hinge region of IgG2 could be reduced by converting the IgG2 constant region to M14 in the humanized anti-IL-6 receptor PM1 antibody (WT). IgG2 type antibodies other than the humanized PM1 antibody were also tested to assess whether the heterogeneity can be reduced by converting their constant regions into M14 or M58.

Antibodies other than the humanized PM1 antibody were: the anti IL-6 receptor antibody F2H/L39 (the amino acid sequences of F2H/L39_VH and F2H/L39 light chain variable region as set forth in SEQ ID NOs: 145 and 146, respectively); anti-IL-31 receptor antibody H0L0 (the amino acid sequences of H0L0_VH and H0L0_VL as set forth in SEQ ID NOs: 147 and 148, respectively); and anti-RANKL antibody DNS (the amino acid sequences of DNS_VH and DNS_VL as set forth in SEQ ID NOs: 149 and 150, respectively). For each of these antibodies, antibodies with IgG1 constant region (SEQ ID NO: 19), IgG2 constant region (SEQ ID NO: 20), or M14 (SEQ ID NO: 24) or M58 (SEQ ID NO: 151) were generated.

The generated antibodies were assessed for heterogeneity by cation exchange chromatography using an adequate gradient and an appropriate flow rate on a ProPac WCX-10 (Dionex) column (mobile phase A: 20 mM sodium acetate (pH 5.0), mobile phase B: 20 mM

sodium acetate/1M NaCl (pH 5.0)). The assessment result obtained by cation exchange chromatography (IEC) is shown in Fig. 41.

As shown in Fig. 41, conversion of the constant region from an IgG1 type into an IgG2 type was demonstrated to increase heterogeneity not only in the humanized anti-IL-6 receptor PM1 antibody (WT), but also in the anti-IL-6 receptor antibody F2H/L39, anti-IL-31 receptor antibody H0L0, and anti-RANKL antibody DNS. In contrast, heterogeneity could be decreased in all of these antibodies by converting their constant region into M14 or M58. Thus, it was demonstrated that, regardless of the type of antigen or antibody variable region sequence, the heterogeneity originated from natural IgG2 could be reduced by substituting serines for cysteines at position 131, EU numbering, in the heavy-chain CH1 domain and at position 219, EU numbering, in the upper hinge of heavy chain.

[Example 17] Effect of the novel constant region M58 to improve the plasma retention in various antibodies

As described in Example 15, it was demonstrated that conversion of the constant region from IgG1 into M58 in the humanized anti-IL-6 receptor PM1 antibody (WT) improved the binding activity to human FcRn and plasma retention in human FcRn transgenic mice. So, IgG1 type antibodies other than the humanized PM1 antibody were also tested to assess whether their retention in plasma can be improved by converting their constant region into M58.

Antibodies other than the humanized PM1 antibody (WT) were the anti-IL-31 receptor antibody H0L0 (the amino acid sequences of H0L0_VH and H0L0_VL as set forth in SEQ ID NOs: 147 and 148, respectively) and anti-RANKL antibody DNS (the amino acid sequences of DNS_VH and DNS_VL as set forth in SEQ ID NOs: 149 and 150, respectively). For each of these antibodies, antibodies with IgG1 constant region (SEQ ID NO: 19) or M58 (SEQ ID NO: 151) were generated, and assessed for their binding activity to human FcRn by the method described in Example 14. The result is shown in Table 14.

Table 14

	KD (μM)		
	WT	H0L0	DNS
IgG1	1.42	1.07	1.36
M58	1.03	0.91	1.03

As shown in Table 14, it was demonstrated that as a result of conversion of the constant region from the IgG1 type to M58, as with anti-IL-6 receptor antibody WT, the binding activities of both the anti-IL-31 receptor antibody H0L0 and anti-RANKL antibody DNS to human FcRn

were improved. This suggests the possibility that regardless of the type of antigen or sequence of antibody variable region, the plasma retention in human is improved by converting the constant region from the IgG1 type to M58.

[Example 18] Effect of cysteine in the CH1 domain on heterogeneity and stability

As described in Example 8, cysteines in the hinge region and CH1 domain of IgG2 were substituted to decrease the heterogeneity of natural IgG2. Assessment of various modified antibodies revealed that heterogeneity could be reduced without decreasing stability by using SKSC (SEQ ID NO: 154). SKSC (SEQ ID NO: 154) is a modified constant region obtained by substituting serine for cysteine at position 131 and lysine for arginine at position 133, EU numbering, in the heavy-chain CH1 domain, and serine for cysteine at position 219, EU numbering, in the heavy-chain upper hinge of the wild type IgG2 constant region sequence.

Meanwhile, another possible method for decreasing heterogeneity is a single substitution of serine for cysteine at position 219, or serine for cysteine at position 220, EU numbering, in the heavy-chain upper hinge. The modified IgG2 constant region SC (SEQ ID NO: 155) was prepared by substituting serine for cysteine at position 219 and CS (SEQ ID NO: 156) was prepared by substituting serine for cysteine at position 220, EU numbering, in IgG2. WT-SC (SEQ ID NO: 157) and WT-CS (SEQ ID NO: 158) were prepared to have SC and CS, respectively, and compared with WT-IgG1, WT-IgG2, WT-SKSC, and WT-M58 in terms of heterogeneity and thermal stability. Furthermore, F2H/L39-IgG1, F2H/L39-IgG2, F2H/L39-SC, F2H/L39-CS, F2H/L39-SKSC, and F2H/L39-M14, which have the constant region of IgG1 (SEQ ID NO: 19), IgG2 (SEQ ID NO: 20), SC (SEQ ID NO: 155), CS (SEQ ID NO: 156), SKSC (SEQ ID NO: 154), or M14 (SEQ ID NO: 24), respectively, were prepared from F2H/L39 (the amino acid sequences of F2H/L39_VH and F2H/L39_VL as set forth in SEQ ID NOs: 145 and 146, respectively), which is an anti IL-6 receptor antibody different from WT. The antibodies were compared with regard to heterogeneity and stability.

WT-IgG1, WT-IgG2, WT-SC, WT-CS, WT-SKSC, WT-M58, F2H/L39-IgG1, F2H/L39-IgG2, F2H/L39-SC, F2H/L39-CS, F2H/L39-SKSC, and F2H/L39-M14 were assessed for heterogeneity by cation exchange chromatography using an adequate gradient and an appropriate flow rate on a ProPac WCX-10 (Dionex) column (mobile phase A: 20 mM sodium acetate (pH 5.0), mobile phase B: 20 mM sodium acetate/1M NaCl (pH 5.0)). The assessment result obtained by cation exchange chromatography is shown in Fig. 42.

As shown in Fig.42, conversion of the constant region from an IgG1 type to an IgG2 type was demonstrated to increase heterogeneity in both WT and F2H/L39. In contrast, heterogeneity was significantly decreased by converting the constant region into SKSC and M14 or M58. Meanwhile, conversion of the constant region into SC significantly decreased

heterogeneity, as in the case of SKSC. However, conversion into CS did not sufficiently improve heterogeneity.

In addition to low heterogeneity, high stability is generally desired when preparing stable formulations in development of antibody pharmaceuticals. Thus, to assess stability, the midpoint temperature of thermal denaturation (Tm value) was determined by DSC (VP-DSC; Microcal). The midpoint temperature of thermal denaturation (Tm value) serves as an indicator of stability. In order to prepare stable formulations as pharmaceutical agents, a higher midpoint temperature of thermal denaturation (Tm value) is preferred (J. Pharm. Sci. 2008 Apr;97(4):1414-26). WT-IgG1, WT-IgG2, WT-SC, WT-CS, WT-SKSC, and WT-M58 were dialyzed (EasySEP; TOMY) against a solution of 20 mM sodium acetate, 150 mM NaCl, pH 6.0. DSC measurement was carried out at a heating rate of 1°C/min in a range of 40°C to 100°C, and at a protein concentration of about 0.1 mg/ml. The denaturation curves obtained by DSC are shown in Fig. 43. The Tm values of the Fab domains are listed in Table 15 below.

Table 15

	Tm/°C
WT-IgG1	94.8
WT-IgG2	93.9
WT-SC	86.7
WT-CS	86.4
WT-SKSC	93.7
WT-M58	93.7

The Tm values of WT-IgG1 and WT-IgG2 were almost the same (about 94°C; Tm of IgG2 was about 1°C lower). Meawhile, the Tm values of WT-SC and WT-CS were about 86°C, and thus significantly lower than those of WT-IgG1 and WT-IgG2. On the other hand, the Tm values of WT-M58 and WT-SKSC were about 94°C, and comparable to those of WT-IgG1 and WT-IgG2. This suggests that WT-SC and WT-CS are markedly unstable as compared to IgG2, and thus, WT-SKSC and WT-M58, both of which also comprise substituion of serine for cysteine in the CH1 domain, are preferred in the development of antibody pharmaceuticals. The reason for the significant decrease of Tm in WT-SC and WT-CS relative to IgG2 is thought to be differences in the disulfide-bonding pattern between WT-SC or WT-CS and IgG2.

Furthermore, comparison of DSC denaturation curves showed that WT-IgG1, WT-SKSC, and WT-M58 each gave a sharp and single denaturation peak for the Fab domain. In contrast, WT-SC and WT-CS each gave a broader denaturation peak for the Fab domain. WT-IgG2 also gave a shoulder peak on the lower temperature side of the Fab domain denaturation peak. In general, it is considered that a single component gives a sharp DSC denaturation peak, and when two or more components with different Tm values (namely,

heterogeneity) are present, the denaturation peak becomes broader. Specifically, the above-described result suggests the possibility that each of WT-IgG2, WT-SC, and WT-CS contains two or more components, and thus the natural-IgG2 heterogeneity has not been sufficiently reduced in WT-SC and WT-CS. This finding suggests that not only cysteines in the hinge region but also those in the CH1 domain are involved in the wild type-IgG2 heterogeneity , and it is necessary to modify not only cysteines in the hinge region but also those in the CH1 domain to decrease the DSC heterogeneity. Furthermore, as described above, stability comparable to that of wild type IgG2 can be acheived only when cysteines in both the hinge region and CH1 domain are substituted.

The above finding suggests that from the perspective of heterogeneity and stability, SC and CS, which are constant regions introduced with serine substitution for only the hinge region cysteine, are insufficient as constant regions to decrease heterogeneity originated from the hinge region of IgG2. It was thus discovered that the heterogeneity could be significantly decreased while maintaining an IgG2-equivalent stability, only when the cysteine at position 131, EU numbering, in the CH1 domain was substituted with serine in addition to cysteine at hinge region. Such constant regions include M14, M31, M58, and M73 described above. In particular, M58 and M73 are stable and less heterogeneous, and exhibit improved retention in plasma, and therefore are expected to be very useful as constant regions for antibody pharmaceuticals.

[Example 19] Generation of fully humanized anti-IL-6 receptor antibodies with improved PK/PD

To generate a fully humanized anti-IL-6 receptor antibody with improved PK/PD, the molecules described below were created by modifying TOCILIZUMAB (heavy chain, WT-IgG1 (SEQ ID NO: 15); light chain, WT (SEQ ID NO: 105).

To improve the ka of F2H-IgG1, substitutions of valine for tryptophan at position 35, phenylalanine for tyrosine at position 50, and threonine for serine at position 62, which are the affinity enhancing substitution obtained in Example 2, were carried out. Furthermore, to lower isoelectric point without increasing immunogenicity risk, substitutions of valine for tyrosine at position 102, glutamic acid for glutamine at position 105, and threonine for isoleucine at position 107 were carried out, and conversion of the constant region from an IgG1 type to an M83 type was carried out and generated VH5-M83 (amino acid sequence of SEQ ID NO: 139). In addition, to improve the ka of L39, VL5-kappa (amino acid sequence of SEQ ID NO: 181) was prepared and it comprises a substitution of glutamine for glutamic acid at position 27. Furthermore, TOCILIZUMAB variants were prepared by combining two or more of the mutations in variable and constant regions described in the above examples and newly discovered mutations. The following fully humanized IL-6 receptor antibodies were discovered using various screening tests: Fv3-M73 (heavy chain, VH4-M73, SEQ ID NO: 182; light chain,

VL1-kappa, SEQ ID NO: 183), Fv4-M73 (heavy chain, VH3-M73, SEQ ID NO: 180; light chain, VL3-kappa, SEQ ID NO: 181), and Fv5-M83 (heavy chain, VH5-M83, SEQ ID NO: 139; light chain, VL5-kappa, SEQ ID NO: 138).

The affinities of prepared Fv3-M73, Fv4-M73, and Fv5-M83 against IL-6 receptor were compared to that of TOCILIZUMAB. The affinities of these anti- IL-6 receptor antibodies determined are shown in Table 16. Furthermore, their BaF/gp130-neutralizing activities were compared to those of TOCILIZUMAB and the control (the known high affinity anti-IL-6 receptor antibody described in Reference Example, and VQ8F11-21 hIgG1 described in US 2007/0280945). The results obtained by determining the biological activities of these antibodies using BaF/gp130 are shown in Fig. 44 (TOCILIZUMAB, the control, and Fv5-M83 with a final IL-6 concentration of 300 ng/ml) and Fig. 45 (TOCILIZUMAB, Fv3-M73, and Fv4-M73 with a final IL-6 concentration of 30 ng/ml). As shown in Table 16, Fv3-M73 and Fv4-M73 have about two to three times higher affinity than TOCILIZUMAB, while Fv5-M83 exhibits about 100 times higher affinity than TOCILIZUMAB (since it was difficult to measure the affinity of Fv5-M83, instead the affinity was determined using Fv5-IgG1, which has an IgG1-type constant region; the constant region is generally thought to have no effect on affinity). As shown in Fig. 45, Fv3-M73 and Fv4-M73 exhibit slightly stronger activities than TOCILIZUMAB. As shown in Fig. 44, Fv5-M83 has a very strong activity, which is more than 100 times greater than that of TOCILIZUMAB in terms of 50% inhibitory concentration. Fv5-M83 also exhibits about ten times higher neutralizing activity in terms of 50% inhibitory concentration than the control (the known high-affinity anti-IL-6 receptor antibody).

Table 16

	k_a(1/Ms)	k_d(1/s)	KD (M)
TOCILIZUMAB	4.0E+05	1.1E-03	2.7E-09
Fv3-M73	8.5E+05	8.7E-04	1.0E-09
Fv4-M73	7.5E+05	1.0E-03	1.4E-09
Fv5-M83	1.1E+06	2.8E-05	2.5E-11

The isoelectric points of TOCILIZUMAB, the control, Fv3-M73, Fv4-M73, and Fv5-M83 were determined by isoelectric focusing using a method known to those skilled in the art. The result showed that the isoelectric point was about 9.3 for TOCILIZUMAB; about 8.4 to 8.5 for the control; about 5.7 to 5.8 for Fv3-M73; about 5.6 to 5.7 for Fv4-M73; and 5.4 to 5.5 for Fv5-M83. Thus, each antibody had a significantly lowered isoelectric point when compared to TOCILIZUMAB and the control. Furthermore, the theoretical isoelectric point of the variable regions VH/VL was calculated by GENETYX (GENETYX CORPORATION). The result showed that the theoretical isoelectric point was 9.20 for TOCILIZUMAB; 7.79 for the

control; 5.49 for Fv3-M73; 5.01 for Fv4-M73; and 4.27 for Fv5-M83. Thus, each antibody had a significantly lowered isoelectric point when compared to TOCILIZUMAB and the control. Accordingly, the plasma retention of Fv3-M73, Fv4-M73, and Fv5-M83 was thought to be improved when compared to TOCILIZUMAB and the control.

T-cell epitopes in the variable region sequence of TOCILIZUMAB, Fv3-M73, Fv4-M73, or Fv5-M83 were analyzed using TEPITOPE (Methods. 2004 Dec;34(4):468-75). As a result, TOCILIZUMAB was predicted to have T-cell epitopes, of which many could bind to HLA. In contrast, the number of sequences that were predicted to bind to T-cell epitopes was significantly reduced in Fv3-M73, Fv4-M73, and Fv5-M83. In addition, the framework of Fv3-M73, Fv4-M73, or Fv5-M83 has no mouse sequence and is thus fully humanized. These suggest the possibility that immunogenicity risk is significantly reduced in Fv3-M73, Fv4-M73, and Fv5-M83 when compared to TOCILIZUMAB.

[Example 20] PK/PD test of fully humanized anti-IL-6 receptor antibodies in monkeys

Each of TOCILIZUMAB, the control, Fv3-M73, Fv4-M73, and Fv5-M83 was intravenously administered once at a dose of 1 mg/kg to cynomolgus monkeys to assess the time courses of their plasma concentrations (see Reference Example for method). The plasma concentration time courses of TOCILIZUMAB, Fv3-M73, Fv4-M73, and Fv5-M83 after intravenous administration are shown in Fig. 46. The result showed that each of Fv3-M73, Fv4-M73, and Fv5-M83 exhibited significantly improved plasma retention in cynomolgus monkeys when compared to TOCILIZUMAB and the control. Of them, Fv3-M73 and Fv4-M73 exhibited substantially improved plasma retention when compared to TOCILIZUMAB.

The efficacy of each antibody to neutralize membrane-bound cynomolgus monkey IL-6 receptor was assessed. Cynomolgus monkey IL-6 was administered subcutaneously in the lower back at 5 μg/kg every day from Day 6 to Day 18 after antibody administration (Day 3 to Day 10 for TOCILIZUMAB), and the CRP concentration in each animal was determined 24 hours later (see Reference Example for method). The time course of CRP concentration after administration of each antibody is shown in Fig. 47. To assess the efficacy of each antibody to neutralize soluble cynomolgus monkey IL-6 receptor, the plasma concentration of free soluble cynomolgus monkey IL-6 receptor in the cynomolgus monkeys was determined and percentage of soluble IL-6 receptor neutralization were calculated (see Reference Example for method). The time course of percentage of soluble IL-6 receptor neutralization after administration of each antibody is shown in Fig. 48.

Each of Fv3-M73, Fv4-M73, and Fv5-M83 neutralized membrane-bound cynomolgus monkey IL-6 receptor in a more sustainable way, and suppressed the increase of CRP over a

longer period when compared to TOCILIZUMAB and the control (the known high-affinity anti-IL-6 receptor antibody). Furthermore, each of Fv3-M73, Fv4-M73, and Fv5-M83 neutralized soluble cynomolgus monkey IL-6 receptor in a more sustainable way, and suppressed the increase of free soluble cynomolgus monkey IL-6 receptor over a longer period when compared to TOCILIZUMAB and the control. These findings demonstrate that all of Fv3-M73, Fv4-M73, and Fv5-M83 are superior in sustaining the neutralization of membrane-bound and soluble IL-6 receptors than TOCILIZUMAB and the control. Of them, Fv3-M73 and Fv4-M73 are remarkably superior in sustaining the neutralization. Meanwhile, Fv5-M83 suppressed CRP and free soluble cynomolgus monkey IL-6 receptor more strongly than Fv3-M73 and Fv4-M73. Thus, Fv5-M83 is considered to be stronger than Fv3-M73, Fv4-M73, and the control (the known high-affinity anti-IL-6 receptor antibody) in neutralizing membrane-bound and soluble IL-6 receptors. It was considered that results in *in vivo* of cynomolgus monkeys reflect the stronger affinity of Fv5-M83 for IL-6 receptor and stronger biological activity of Fv5-M83 in the BaF/gp130 assay system relative to the control.

These findings suggest that Fv3-M73 and Fv4-M73 are highly superior in sustaining their activities as an anti-IL-6 receptor-neutralizing antibody when compared to TOCILIZUMAB and the control, and thus enable to significantly reduce the dosage and frequency of administration. Furthermore, Fv5-M83 was demonstrated to be remarkably superior in terms of the strength of activity as an anti-IL-6 receptor-neutralizing antibody as well as sustaining their activity. Thus, Fv3-M73, Fv4-M73, and Fv5-M83 are expected to be useful as pharmaceutical IL-6 antagonists.

[Reference Example]

Preparation of soluble recombinant cynomolgus monkey IL-6 receptor (cIL-6R)

Oligo-DNA primers were prepared based on the disclosed gene sequence for Rhesus monkey IL-6 receptor (Birney *et al.*, Ensembl 2006, Nucleic Acids Res. 2006 Jan 1;34 (Database issue):D556-61). A DNA fragment encoding the whole cynomolgus monkey IL-6 receptor gene was prepared by PCR using the primers, and as a template, cDNA prepared from the pancreas of cynomolgus monkey. The resulting DNA fragment was inserted into an animal cell expression vector, and a stable expression CHO line (cyno.sIL-6R-producing CHO cell line) was prepared using the vector. The culture medium of cyno.sIL-6R-producing CHO cells was purified using a HisTrap column (GE Healthcare Bioscience) and then concentrated with Amicon Ultra-15 Ultracel-10k (Millipore). A final purified sample of soluble cynomolgus monkey IL-6 receptor (hereinafter "cIL-6R") was obtained through further purification on a Superdex200pg16/60 gel filtration column (GE Healthcare Bioscience).

Preparation of recombinant cynomolgus monkey IL-6 (cIL-6)

Cynomolgus monkey IL-6 was prepared by the procedure described below. The nucleotide sequence encoding 212 amino acids deposited under SWISSPROT Accession No. P79341 was prepared and cloned into an animal cell expression vector. The resulting vector was introduced into CHO cells to prepare a stable expression cell line (cyno.IL-6-producing CHO cell line). The culture medium of cyno.IL-6-producing CHO cells was purified using a SP-Sepharose/FF column (GE Healthcare Bioscience) and then concentrated with Amicon Ultra-15 Ultracel-5k (Millipore). A final purified sample of cynomolgus monkey IL-6 (hereinafter "cIL-6") was obtained through further purification on a Superdex75pg26/60 gel filtration column (GE Healthcare Bioscience), followed by concentration with Amicon Ultra-15 Ultracel-5k (Millipore).

Preparation of a known high-affinity anti-IL-6 receptor antibody

An animal cell expression vector was constructed to express VQ8F11-21 hIgG1, a known high-affinity anti-IL-6 receptor antibody. VQ8F11-21 hIgG1 is described in US 2007/0280945 A1 (US 2007/0280945 A1; the amino acid sequences of heavy chain and light chain as set forth in SEQ ID NOs: 19 and 27, respectively). The antibody variable region was constructed by PCR using a combination of synthetic oligo DNAs (assembly PCR). IgG1 was used as the constant region. The antibody variable and constant regions were combined together by assembly PCR, and then inserted into an animal cell expression vector to construct expression vectors for the heavy chain and light chain of interest. The nucleotide sequences of the resulting expression vectors were determined by a method known to those skilled in the art. The high-affinity anti-IL-6 receptor antibody (hereinafter abbreviated as "control") was expressed and purified using the constructed expression vectors by the method described in Example 1.

Biacore-based analysis of binding to IL-6 receptor

Antigen-antibody reaction kinetics was analyzed using Biacore T100 (GE Healthcare). The SR344-antibody interaction was measured by immobilizing appropriate amounts of anti-IgG (γ-chain specific) $F(ab')_2$ onto a sensor chip by amine coupling method, binding antibodies of interest onto the chip at pH 7.4, and then flowing IL-6 receptor SR344 adjusted to be various concentrations at pH 7.4 over the chip as an analyte. All measurements were carried out at 37°C. The kinetic parameters, association rate constant k_a (1/Ms) and dissociation rate constant k_d (1/s) were calculated from the sensorgrams obtained by measurement. Then, K_D (M) was determined based on the rate constants. The respective parameters were determined using

Biacore T100 Evaluation Software (GE Healthcare).

PK/PD test to determine the plasma concentrations of antibodies, CRP, and free soluble IL-6 receptor in monkeys

The plasma concentrations in cynomolgus monkeys were determined by ELISA using a method known to those skilled in the art. The concentration of CRP was determined with an automated analyzer (TBA-120FR; Toshiba Medical Systems Co.) using Cias R CRP (KANTO CHEMICAL CO., INC.).

The plasma concentration of free soluble cynomolgus monkey IL-6 receptor in cynomolgus monkeys was determined by the procedure described below. All IgG antibodies (cynomolgus monkey IgG, anti-human IL-6 receptor antibody, and anti-human IL-6 receptor antibody-soluble cynomolgus monkey IL-6 receptor complex) in the plasma were adsorbed onto Protein A by loading 30 μl of cynomolgus monkey plasma onto an appropriate amount of rProtein A Sepharose Fast Flow resin (GE Healthcare) dried in a 0.22-μm filter cup (Millipore). Then, the solution in cup was spinned down using a high-speed centrifuge to collect the solution that passed through. The solution that passed through does not contain Protein A-bound anti-human IL-6 receptor antibody-soluble cynomolgus monkey IL-6 receptor complex. Therefore, the concentration of free soluble IL-6 receptor can be determined by measuring the concentration of soluble cynomolgus monkey IL-6 receptor in the solution that passed through Protein A. The concentration of soluble cynomolgus monkey IL-6 receptor was determined using a method known to those skilled in the art for measuring the concentrations of soluble human IL-6 receptor. Soluble cynomolgus monkey IL-6 receptor (cIL-6R) prepared as described above was used as a standard.

Then the percentage of soluble IL-6 receptor neutralization was calculated by following formula.

[(Free soluble IL-6 receptor concentration after antibody administration) / (soluble IL-6 receptor concentration before antibody administration)] x 100

[Example 21]

(1) Preparation of point mutant genes of humanized antibody H0L0

Various point mutant genes were constructed using as a starting material the gene encoding a glypican 3 antibody comprising the CDR of humanized antibody GC33 disclosed in WO2006/046751. Oligo DNAs were designed and synthesized based on forward and reverse sequences containing a mutation site. A number of point mutant genes were prepared using QuikChange Site-Directed Mutagenesis Kit (Stratagene) available on the market. The genes comprising point mutations were prepared by PCR under the conditions below. A reaction

mixture consisting of 10 ng of template plasmid, 10 pmol each of forward and reverse synthetic oligo DNAs, 10x Buffer appended to the kit, dNTP mix, and Pfu turbo DNA polymerase was treated by heating at 95°C for 30 seconds, followed by PCR of 18 cycles consisting of: 95°C for 30 seconds, 55°C for one minute, and 68°C for four minutes. *Dpn*I included in the kit was added to the reaction mixture, followed by one hour of restriction enzyme digestion at 37°C. As a result of transforming DH5α competent cells (TOYOBO) with the reaction mixture, transformants were obtained. Plasmid DNAs were isolated from the transformants and then sequenced. The point mutant genes, which were confirmed to have introduced point mutations based on the determined nucleotide sequences of the plasmid DNAs, were cloned into expression vectors that enabled the expression of insert genes in animal cells. The modified genes were obtained by modifications described below.

Humanized antibody H0L0 and its point mutants were transiently expressed using polyethyleneimine (Polysciences Inc.). HEK293 cells were detached using Trypsin EDTA (Invitrogen) and plated at 6 x 10^6 cells/10 ml in 10-cm^2 culture dishes. On the next day, 4.6 μg and 9.2 μg of the heavy chain and light chain expression plasmid DNAs, respectively, were combined with 690 μl of SFMII medium and 20.8 μg of polyethyleneimine. After mixing the combined materials, the mixture was incubated at room temperature for ten minutes. The whole mixture was added dropwise to each of the culture dishes where HEK293 cells had been plated as described above, and the culture supernatant was collected after about 72 hours. The expressed humanized antibody H0L0 and its point mutants were purified from the culture supernatants using rProteinA Sepharose™ Fast Flow (GE Healthcare) according to the appended protocol.

(1-1) Modification of Tm value of humanized antibody H0L0

Thermal denaturation midpoint temperature (Tm) is defined as the top of denaturation peak in thermograms (Cp vs T) obtained as a result of heating a test sample solution at a constant programmed heating rate. To determine the Tm value of humanized antibody H0L0, a sample solution for DSC assay was prepared by the following procedure. First, a solution containing 50 to 100 μg of an antibody was placed into a dialysis membrane and dialyzed for one whole day and night against 20 mol/l sodium acetate buffer (pH 6.0) containing 150 mmol/l sodium chloride as the outer dialysate. Then, a sample solution was prepared by adjusting the antibody concentration to 50 to 100 μg/ml using the outer dialysate, and used as a test sample solution for DSC assay.

An appropriate DSC device, for example, DSC-II (Calorimetry Sciences Corporation) is preferably used in this experiment. After thorough deaeration, the sample solution prepared by the method described above and the reference solution (outer dialysate) were enclosed in

calorimetric cells, and thoroughly thermally equilibrated at 40°C. Then, the solutions were scanned from 40°C to 100°C with a scanning rate of about 1 K/min. The assay result was displayed as the top of denaturation peak which is a function of temperature. The peaks for the Fab domain were assigned to determine the thermal denaturation midpoint temperature for humanized antibody H0L0, based on a non-patent document (Rodolfo *et al.*, Immunology Letters (1999) 47-52). As a specific example, a DSC chart obtained for the Hspu2.2Lspu2.2 (Hu2.2Lu2.2) antibody is shown in Fig. 49.

According to calculation by the method described above, the Tm value of humanized antibody H0L0 comprising the heavy chain of SEQ ID NO: 195 and the light chain of SEQ ID NO: 201 was 76.6°C. As examples of known antibodies, the Tm values of Synagis and Herceptin were calculated to be 85.4°C and 81.8°C, respectively. This suggests that the Tm value of humanized antibody H0L0 is lower than those of known antibodies.

In order to increase the Tm value of humanized antibody H0L0, a modified antibody was prepared. H15 (SEQ ID NO: 196) was prepared by modifying FR2 of the H0L0 antibody heavy chain (SEQ ID NO: 195) with modifications V37I, A40P, M48I, and L51I which converted the subclass from VH1b to VH4. The Tm value was improved to 79.1°C. L4 (SEQ ID NO: 202) was prepared by modifying FR2 of the H0L0 antibody light chain (SEQ ID NO: 201) with modifications L42Q, S48A, and Q50R which converted the subclass from VK2 to VK3, and by substituting V2 of FR1 with a germ-line sequence, I (V2I modification). The Tm value was improved to 77.2°C. Antibody H15L4 was prepared by combining these two modified antibodies, and as a result, the Tm value was improved to 80.5°C.

(1-2) Modification of isoelectric point value of humanized antibody H0L0

The blood half-life of an antibody is prolonged as the isoelectric point value of the antibody decreases. Conversely, an increase in the antibody isoelectric point value improves the transfer of the antibody into tissues. It is still remains unknown whether the tumor-suppressing effect of antibodies that are effective in cancer therapy is potentiated by an increase or a decrease in the antibody isoelectric point value. Thus, modified antibodies were prepared from humanized antibody H0L0, one of which had a decreased isoelectric point and the other had an increased isoelectric point. The tumor-suppressing effect was compared between the two antibodies to test which modification results in a stronger tumor-suppressing effect.

The isoelectric point value of each antibody was calculated based on the isoelectric focusing analysis according to the following procedure. Phast-Gel Dry IEF gel (Amercham Bioscience) was swollen for about 60 minutes in Phastsystem Cassette (Amercham Bioscience) using a swelling solution with either of the following compositions.

(a) Composition of high isoelectric point swelling solution:

1.5 ml of 10% glycerol

100 µl Pharmalyte 8-10.5 for IEF (Amercham Bioscience)

(b) Composition of low isoelectric point swelling solution:

1.5 ml of purified water

20 µl of Pharmalyte 8-10.5 for IEF (Amercham Bioscience)

80 µl of Pharmalyte 5-8 for IEF (Amercham Bioscience)

About 0.5 µg of antibody was loaded onto the swollen gel, and isoelectric focusing was carried out using programmed PhastSystem (Amercham Bioscience). The samples were added to the gel at Step 2 in the program indicated below. pI Calibration Kit was used as pI markers (Amercham Bioscience).

Step 1: 2,000 V, 2.5 mA, 3.5 W, 15°C, 75 Vh

Step 2: 200 V, 2.5 mA, 3.5 W, 15°C, 15 Vh

Step 3: 2,000 V, 2.5 mA, 3.5 W, 15°C, 410 Vh

After electrophoresis, the gel was fixed with 20% TCA, and then sliver-stained using Silver Staining Kit, protein (Amercham Bioscience) according to the appended protocol. After staining, the isoelectric point of each antibody as a test sample was calculated based on the known isoelectric points of the pI markers. Electrophoretic patterns of high pI and low pI isoelectric focusing are shown in Figs. 50 and 51, respectively.

(a) Modifications resulting in an increase of isoelectric point

Hspu2.2 (Hu2.2) (SEQ ID NO: 200) was prepared by further modifying H15 by Q43K, D52N, and Q107R. Lspu2.2 (Lu2.2) (SEQ ID NO: 206) was prepared by further modifying L4 by E17Q, Q27R, and Q105R, as well as S25A (substitution of S25 in CDR2 by A which is highly frequent in the germ line). The Tm value and isoelectric point value of the Hspu2.2Lspu2.2 antibody (Hu2.2Lu2.2) consisting of Hspu2.2 (Hu2.2) and Lspu2.2 (Lu2.2) were determined to be 76.8°C and 9.6, respectively. The isoelectric point value of the H0L0 antibody is 8.9. Thus, the isoelectric point value has been increased by 0.7 in the Hspu2.2Lspu2.2 antibody (Hu2.2Lu2.2).

(b) Modifications resulting in a decrease of isoelectric point

Hspd1.8 (Hd1.8) (SEQ ID NO: 199) was prepared by further modifying H15 by K19T, Q43E, K63S, K65Q, and G66D. Lspd1.6 (Ld1.6) (SEQ ID NO: 205) was prepared by further modifying L4 by Q27E, substitution of TISSLQ for KISRVE at positions 79 to 84 in FR3 of L4, and the same modification S25A as in Lspu2.2 (Lu2.2). The Tm value and isoelectric point value of the Hspd1.8Lspd1.6 antibody (Hd1.8Ld1.6) consisting of Hspd1.8 (Hd1.8) and Lspd1.6 (Ld1.6) were determined to be 72.6°C and 7.4, respectively. The isoelectric point value of the H0L0 antibody is 8.9. Thus, the isoelectric point value has been decreased by 1.5 in the Hspd1.8Lspd1.6 antibody (Hd1.8Ld1.6).

(2) Assessment of antibody H0L0 point mutants for binding activity by competitive ELISA

The H0L0 antibody and its point mutants were purified as described in (1) and assessed by competitive ELISA. The concentration of soluble GPC3 core polypeptide (SEQ ID NO: 207) was adjusted to 1 μg/ml. 100 μl of the polypeptide solution was added to each well of a 96-well plate. The plate was incubated overnight at 4°C to immobilize the soluble GPC3 core polypeptide onto the plate. The plate immobilized with the soluble GPC3 core polypeptide was washed three times with washing buffer using SkanWasher 400 (Molecular Devices). After 200 μl of blocking buffer was added, the plate was blocked at 4°C overnight or longer. Then, the plate immobilized with the soluble GPC3 core polypeptide was washed three times with washing buffer using SkanWasher 400. Next, various concentrations of the H0L0 antibody or its point mutants were mixed with a final concentration of 0.3 μg/ml biotinylated H0L0 antibody, and each mixture was added to the plate at 100 μl/well. The H0L0 antibody was biotinylated using Biotin Labeling Kit (Roche) according to the appended protocol. The plate was incubated at room temperature for one hour, and then washed five times with washing buffer using SkanWasher 400 (Molecular Devices). Goat anti-streptavidin alkaline phosphatase (Zymed) was 20,000-times diluted with substrate buffer and added to the plate at 100 μl/well. The plate was incubated at room temperature for one hour, and then washed five times with washing buffer using SkanWasher 400. The concentration of phosphatase substrate (Sigma) was adjusted to 1 mg/ml using the substrate buffer, and the solution was added to the plate at 100 μl/well. The plate was incubated for one hour. The absorbance of reaction mixture at 405 nm in each well was determined using Benchmark Plus (Bio-Rad). The wavelength of reference absorbance used was 655 nm.

As shown in Fig. 52, the antigen-binding activity of antibody H15L4 was comparable to that of the H0L0 antibody which was subjected to modification. Furthermore, as shown in Fig. 53, the antigen-binding activity of the Hspu2.2Lspu2.2 antibody (Hu2.2Lu2.2) was comparable to that of the H0L0 antibody which was subjected to modification. In addition, as shown in Fig. 54, the antigen-binding activity of the Hspd1.8Lspd1.6 antibody (Hd1.8Ld1.6) was comparable to that of the H0L0 antibody which was subjected to modification.

[Reference Experimental Example 22] Disruption of fucose transporter gene in CHO cells

(1) Construction of targeting vectors

(1-1) Construction of KO1 vector

A *Bam*HI site and a TGCGC sequence were added to the 5' end of the start codon of hygromycin resistance gene (*Hygr*) by PCR using pcDNA3.1/Hygro (Invitrogen) and the

Hyg5-BH and Hyg3-NT primers to make the same as the sequence adjacent to the 5' end of the start codon of fucose transporter gene. A *Not*I site was added to the 3' end of the region containing up to the SV40 polyA addition signal. The resulting *Hygr* was excised.

Forward primer

Hyg5-BH: 5'-GGATCCTGCGCATGAAAAAGCCTGAACTCACC-3' (SEQ ID NO: 208)

Reverse primer

Hyg3-NT: 5'-GCGGCCGCCTATTCCTTTGCCCTCGGACG-3' (SEQ ID NO: 209)

The fucose transporter targeting vector ver.1 (herein referred to as "KO1 vector") was constructed by inserting into pMC1DT-A vector (Yagi T, Proc. Natl. Acad. Sci. USA (1990) 87:9918-22) the 5' (*Sma*I at position 2780 to *Bam*HI at position 4232 in the nucleotide sequence of SEQ ID NO: 210) and 3' (from position 4284 to *Sac*I at position 10934) segments of fucose transporter, and an *Hygr* fragment. The characteristic of the KO1 vector is that *Hygr* is expressed from the fucose transporter promoter when homologous recombination occurs because no promoter is attached to the *Hygr* fragment. However, *Hygr* is not always expressed sufficiently to acquire resistance to hygromycin B when only a single copy of the vector is introduced into a cell by homologous recombination. The KO1 vector was introduced into cells after *Not*I digestion. The fucose transporter was expected to lose 41 base pairs of exon 1 including the start codon from introduction of the KO1 vector, which would result in the loss of its function.

(1-2) Construction of pBSK-pgk-1-Hygr

The mouse pgk-1 gene promoter was excised from a pKJ2 vector (Popo H, Biochemical Genetics (1990) 28:299-308) with *Eco*RI and *Pst*I, and cloned into pBluescript (Stratagene) at the site between *Eco*RI and *Pst*I to prepare pBSK-pgk-1. An *Eco*T22I site and a Kozak sequence were added to the 5' end of *Hygr* by PCR using pcDNA3.1/Hygro and the Hyg5-AV and Hyg3-BH primers. A *Bam*HI site was added to the 3' end of the region containing up to the SV40 polyA addition signal. The resulting *Hygr* was excised.

Forward primer

Hyg5-AV: 5'-ATGCATGCCACCATGAAAAAGCCTGAACTCACC-3' (SEQ ID NO: 211)

Reverse primer

Hyg3-BH: 5'-GGATCCCAGGCTTTACACTTTATGCTTC-3' (SEQ ID NO: 212)

The *Hygr* (*Eco*T22I-*Bam*HI) fragment was inserted into pBSK-pgk-1 at *Pst*I-*Bam*HI site to prepare pBSK-pgk-1-Hygr.

(1-3) Construction of KO2 vector

The fucose transporter targeting vector ver.2 (herein referred to as "KO2 vector") was

constructed by inserting into a pMC1DT-A vector the 5' (*Sma*I at position 2780 to *Bam*HI at position 4232 in the nucleotide sequence of SEQ ID NO: 210) and 3' (from position 4284 to *Sac*I at position 10934) segments of fucose transporter, and a pgk-1-Hygr fragment. Unlike the KO1 vector, the KO2 vector carries *Hygr* linked to the promoter of pgk-1 gene. Therefore, once a single copy of the vector is introduced into cells *via* homologous recombination, the cells acquire hygromycin B resistance. The KO2 vector was introduced into cells after *Not*I digestion. The fucose transporter was expected to lose 46 base pairs of exon 1 including the start codon by introduction of the KO2 vector, which would result in the loss of its function.

(1-4) Construction of pBSK-pgk-1-Puror

A pPUR vector (BD Biosciences) was digested with *Pst*I and *Bam*HI. The excised fragment (Puror) was inserted into pBSK-pgk-1 at the *Pst*I-*Bam*HI site to prepare pBSK-pgk-1-Puror.

(1-5) Construction of KO3 vector

The fucose transporter targeting vector ver.3 (herein referred to as "KO3 vector") was constructed by inserting into a pMC1DT-A vector the 5' (*Sma*I at position 2780 to *Bam*HI at position 4232 in the nucleotide sequence of SEQ ID NO: 210) and 3' (from position 4284 to *Sac*I at position 10934) segments of fucose transporter, and a pgk-1-Puror fragment. A sequence for annealing with the screening primer indicated below was attached to the 3' end of pgk-1-Puror in advance. The KO3 vector was introduced into cells after *Not*I digestion. The fucose transporter was expected to lose 46 base pairs of exon 1 including the start codon from introduction of the KO3 vector, which would result in the loss of its function.

Reverse primer

RSGR-A: 5'-GCTGTCTGGAGTACTGTGCATCTGC-3' (SEQ ID NO: 213)

The fucose transporter gene was knocked out using the three types of targeting vectors described above.

(2) Introduction of vectors into CHO cells

CHO-S-SFMII HT- (Invitrogen) was supplemented with 1/100 volume of HT Supplement (100x) (Invitrogen) and penicillin-streptomycin (Invitrogen), and used as a culture medium (hereinafter referred to as "SFMII(+)"). A CHO cell line DXB11 was passaged using the medium. SFMII(+) was also used to culture the cells after gene transfer. 8×10^6 CHO cells were suspended in 0.8 ml of Dulbecco's phosphate buffered saline (hereinafter abbreviated as "PBS"; Invitrogen). The cell suspension was combined with 30 μg of a targeting vector, and transferred into Gene Pulser Cuvette (4 mm) (Bio-Rad). After ten minutes of incubation on ice,

the vector was introduced into the cells by electroporation under the conditions of 1.5 kV and 25 μFD using Gene-Pulser II (Bio-Rad). After vector transfer, the cells were suspended in 200 ml of SFMII(+) medium and plated in twenty 96-well round-bottomed plates (Iwaki) at 100 μl/well. The plates were incubated in a CO_2 incubator at 37°C for 24 hours, and then a drug was added thereto.

(3) First knockout

The KO1 or KO2 vector was introduced into CHO cells. Selection was carried out 24 hours after gene transfer using hygromycin B (Invitrogen). Hygromycin B was dissolved at a concentration of 0.3 mg/ml in SFMII(+), and a 100-μl aliquot was added to each well.

(4) PCR screening for homologous recombinants

(4-1) Preparation of PCR samples

Homologous recombinants were screened by PCR. CHO cells used in the screening were cultured in 96-well flat-bottomed plates. After removing the culture supernatants, 50 μl of cell lysis buffer was added to each well and the plates were incubated at 55°C for two hours. Then, proteinase K was inactivated by heating at 95°C for 15 minutes. The resulting samples were used as PCR templates. The composition of cell lysis buffer per well was: 5 μl of 10x LA buffer II (appended to Takara LATaq), 2.5 μl of 10% NP-40 (Roche), 4 μl of proteinase K (20 mg/ml; Takara), and 38.5 μl of distilled water (Nacalai Tesque).

(4-2) PCR conditions

The PCR mixtures consisted of 1 μl of a PCR sample described above, 5 μl of 10x LA buffer II, 5 μl of $MgCl_2$ (25 mM), 5 μl of dNTP (2.5 mM), 2 μl of primers each (10 μM each), 0.5 μl of LA Taq (5 IU/μl), and 29.5 μl of distilled water (50 μl in total). TP-F4 and THygro-R1 were used as PCR primers in the screening for cells introduced with the KO1 vector, and TP-F4 and THygro-F1 were used in the screening for cells introduced with the KO2 vector .

The PCR conditions used to assess cells introduced with the KO1 vector were: pre-heating at 95°C for one minute, and 40 amplification cycles of 95°C for 30 seconds, 60°C for 30 seconds, and 60°C for two minutes, followed by heating at 72°C for seven minutes. The PCR conditions used to assess cells introduced with KO2 vector were: pre-heating at 95°C for one minute, and 40 amplification cycles of 95°C for 30 seconds and 70°C for three minutes, followed by heating at 70°C for seven minutes.

The primers are shown below. In cell samples where homologous recombination is mediated by the KO1 vector, the size of the amplified DNA is about 1.6 kb. In cell samples where homologous recombination is mediated by the KO2 vector, the size of the amplified DNA

is about 2.0 kb. The TP-F4 primer has been designed to be placed outside the vector and within the 5' genomic region of fucose transporter. The THygro-F1 and THygro-R1 primers have been designed to be placed within *Hygr* of the vector.

Forward primers (KO1 and KO2)

TP-F4: 5'-GGAATGCAGCTTCCTCAAGGGACTCGC-3' (SEQ ID NO: 214)

Reverse primer (KO1)

THygro-R1: 5'-TGCATCAGGTCGGAGACGCTGTCGAAC-3' (SEQ ID NO: 215)

Reverse primer (KO2)

THygro-F1: 5'-GCACTCGTCCGAGGGCAAAGGAATAGC-3' (SEQ ID NO: 216)

(5) PCR screening results

918 cells introduced with KO1 vector were analyzed, and only one was assessed to be a homologous recombinant cell (the frequency of homologous recombination was about 0.1%). 537 cells introduced with the KO2 vector were analyzed, and 17 cells were assessed to be homologous recombinant cells (the frequency of homologous recombination was about 3.2%).

(6) Southern blot analysis

Furthermore, Southern blotting was also used to confirm the recombinant cells. 10 μg of genomic DNA was prepared from cultured cells according to a conventional method and analyzed by Southern blotting. A 387-bp probe was prepared from the region of positions 2113 to 2500 in the nucleotide sequence of SEQ ID NO: 210 by PCR using the pair of primers shown below, and used in Southern blotting to confirm the recombinant cells. The genomic DNAs were digested with *Bgl*II.

Forward primer

Bgl-F: 5'-TGTGCTGGGAATTGAACCCAGGAC-3' (SEQ ID NO: 217)

Reverse primer

Bgl-R: 5'-CTACTTGTCTGTGCTTTCTTCC-3' (SEQ ID NO: 218)

*Bgl*II digestion yielded an approximately 3.0-kb band of chromosomal fucose transporter, and approximately 4.6-kb and 5.0-kb bands from chromosomes that have undergone homologous recombination mediated by the KO1 and KO2 vectors, respectively. One and seven cells that had undergone homologous recombination mediated by the KO1 and KO2 vectors, respectively, were used in the experiments. The only cell line obtained using the KO1 vector was named 5C1. In fact, subsequent analyses revealed that the cell line included different cell populations. Thus, the cell line was recloned by limiting dilution and then used in subsequent experiments. One of the cell lines obtained using the KO2 vector was named 6E2.

(7) Second knockout

A cell line completely deficient in the fucose transporter gene was established using three types of vectors from a cell line in which the KO1 and KO2 vectors successfully mediated homologous recombination. The combinations of vector and cell line were as follows. Method 1, KO2 vector and cell line 5C1 (KO1); Method 2, KO2 vector and cell line 6E2 (KO2); and Method 3, KO3 vector and cell line 6E2 (KO2). The vectors were introduced into cells of the respective cell lines. Selection was carried out 24 hours after vector transfer using hygromycin B and puromycin (Nacalai Tesques). The final concentration of hygromycin B was 1 mg/ml in Method 1 and 7 mg/ml in Method 2. In Method 3, hygromycin B and puromycin were added at final concentrations of 0.15 mg/ml and 8 μg/ml, respectively.

(8) PCR screening for homologous recombinants

Samples were prepared by the same method described above. For the screening in Method 1, both of the PCR methods described above were used to detect cells that had undergone homologous recombination mediated with the KO1 and KO2 vectors. TPS-F1 and SHygro-R1 were placed in the regions of positions 3924 to 3950 and 4248 to 4274 in the nucleotide sequence of SEQ ID NO: 210. These PCR primers were designed for Method 2, and used to amplify a 350-bp region of the fucose transporter gene that is deficient in the KO2 vector. Accordingly, when the 350-bp region was not amplified in the PCR screening of Method 2, the cells were considered to be completely deficient in the fucose transporter gene. The PCR conditions used were: pre-heating at 95°C for one minute, and 35 amplification cycles of 95°C for 30 seconds and 70°C for one minute, followed by heating at 70°C for seven minutes.

Forward primer

TPS-F1: 5'-CTCGACTCGTCCCTATTAGGCAACAGC-3' (SEQ ID NO: 219)

Reverse primer

SHygro-R1: 5'-TCAGAGGCAGTGGAGCCTCCAGTCAGC-3' (SEQ ID NO: 220)

The forward and reverse primers used in Method 3 were TP-F4 and RSGR-A, respectively. The PCR conditions used were: pre-heating at 95°C for one minute, and 35 amplification cycles of 95°C for 30 seconds, 60°C for 30 seconds, and 72°C for two minutes, followed by heating at 72°C for seven minutes. An approximately 1.6-kb DNA is amplified when the sample is cells that have undergone homologous recombination mediated by the KO3 vector. The PCR was carried out to detect cells that had undergone homologous recombination mediated by the KO3 vector, as well as to confirm that the homologous recombination mediated by the KO2 vector remained.

(9) PCR screening results

616 cells were analyzed by Method 1, and 18 were assessed to be homologous recombinants (the frequency of homologous recombination was about 2.9%). 524 cells were analyzed by Method 2, and two were assessed to be homologous recombinants (the frequency of homologous recombination was about 0.4%). Furthermore, 382 cells were analyzed by Method 3, and seven were assssed to be homologous recombinants (the frequency of homologous recombination was about 1.8%).

(10) Southern blot analysis

As a result of analysis according to the method described above, one of the analyzed cell lines was found to be completely deficient in the fucose transporter gene. In the first knockout, the results of PCR and Southern blot analyses were consistent with each other. However, the PCR result was not consistent with Southern blotting in the second knockout.

(11) Analysis of fucose expression

Furthermore, 26 cell lines that had been assessed to be homologous recombinants by PCR were analyzed for fucose expression. 1×10^6 cells were stained using 100 μl of PBS containing 5 μg/ml Lens *culinaris Agglutinin*, FITC Conjugate (Vector Laboratories), 2.5% FBS, and 0.02% sodium azide (hereinafter referred to as "FACS lysis solution") on ice for one hour. Then, the cells were washed three times with FACS lysis solution, and assayed using FACSCalibur (Becton Dickinson). The result of Southern blot analysis showed that the expression level of fucose was reduced only in the FTP-KO cell line which had been assessed to be completely deficient in the fucose transporter gene.

[Reference Experimental Example 23] Establishment of antibody-producing cells derived from the FTP-KO line and purification of antibody produced by the cells

Hygromycin B was prepared at a final concentration of 1 mg/ml in SFMII(+) medium. The fucose transporter-deficient cell line (FT-KO cell; clone name, 3F2) obtained as described in Example 21 was cultured in this medium. 8×10^6 cells of 3F2 were suspended in 0.8 ml of Dulbecco's phosphate buffered saline. The cell suspension was combined with 25 μg of the expression vector for humanized glypican 3 antibody, and transferred into a Gene Pulser Cuvette. After ten minutes of incubation on ice, the vector was introduced into the cells by electroporation under the conditions of 1.5 kV and 25 μFD using Gene Pulser II. After vector transfer, the cells were suspended in 40 ml of SFMII(+) medium, and plated onto a 96-well flat-bottomed plate (Iwaki) in an amount of 100 μl/well. The plate was incubated at 37°C in a CO_2 incubator for 24 hours, and then Geneticin (Invitrogen) was added thereto at a final concentration of 0.5 mg/ml. The levels of antibody produced by the drug-resistant cells were determined to establish

humanized glypican 3 antibody-producing cell lines.

Supernatants were collected from cultures of the antibody-producing cells, and loaded onto a Hitrap rProtein A (Pharmacia) column using a P-1 pump (Pharmacia). After the column was washed with binding buffer (20 mM sodium phosphate (pH 7.0)), bound antibody was eluted with elution buffer (0.1 M glycine-HCl (pH 2.7)). Immediately, the eluates were neutralized with neutralization buffer (1M Tris-HCl (pH 9.0)). The eluted antibody fractions were selected by DC Protein Assay (Bio-Rad), and the pooled fractions were concentrated up to about 2 ml using Centriprep YM 10 (Millipore). Next, the concentrated solutions were subjected to gel filtration using Superdex 200 26/60 (Pharmacia) equilibrated with 20 mM acetic acid buffer (pH 6.0) containing 150 mM NaCl. Peak monomer fractions of the eluates were collected, and concentrated using Centriprep YM 10. After filtration with MILLEX-GW 0.22-μm Filter Unit (Millipore), the concentrated solutions were stored at 4°C. The concentrations of purified antibodies were determined by calculation using the molar extinction coefficient and absorbance at a wavelength of 280 nm.

[Reference Experimental Example 24] Analysis of sugar chains linked to humanized anti-glypican 3 antibody produced by FT-KO cells

(1) Preparation of 2-aminobenzamide-labeled sugar chains (2-AB-labeled sugar chains)

The antibodies produced by the FT-KO cells of the present invention and antibodies produced by CHO cells as a control sample were treated with N-glycosidase F (Roche Diagnostics) to release the sugar chains from the protein (Weitzhandler M. *et al.*, Journal of Pharmaceutical Sciences (1994) 83(12):1670-1675). After deproteination using ethanol (Schenk B. *et al.*, The Journal of Clinical Investigation (2001) 108(11):1687-1695), the free sugar chains were concentrated to dryness, and fluorescently labeled with 2-aminopyridine (Bigge J. C. *et al.*, Analytical Biochemistry (1995) 230(2):229-238). The reagent was removed from the 2-AB-labeled sugar chains by solid phase extraction using a cellulose cartridge. After concentration by centrifugation, purified 2-AB-labeled sugar chains were obtained for use in the analyses. Next, the purified 2-AB-labeled sugar chains were treated with β-galactosidase (Seikagaku Co.) to obtain agalactosyl 2-AB-labeled sugar chains.

(2) Analysis of agalactosyl 2-AB-labeled sugar chains by normal phase HPLC

Agalactosyl 2-AB-labeled sugar chains were prepared by the above method, using as the starting materials sugar chains freed from antibodies produced by the FT-KO cells of the present invention or antibodies produced by CHO cells (control). The sugar chains were analyzed by normal phase HPLC using an amide column TSKgel Amide-80 (Tosoh Co.), and the chromatograms were compared to each other. In the antibodies produced by CHO cells, the

main component of sugar chain was G(0), and G(0)-Fuc which had no fucose was estimated to account for about 4% of total sugar chains based on the calculation of the peak area ratio. On the other hand, in the antibodies produced by the FT-KO cells, G(0)-Fuc was the main component, and based on the calculation of the peak area ratio, 90% or more of total sugar chains had no fucose in the antibodies produced by any of the antibody-producing cell lines.

Table 17

RELATIVE RATIO OF AGALACTOSYL 2-AB-LABELED SUGAR CHAIN ESTIMATED BY NORMAL PHASE HPLC

SUGAR CHAIN	CHO	FT-KO-a	FT-KO-b	FT-KO-c
G(0)-Fuc	4.0%	92.4%	92.5%	93.2%
G(0)	96.0%	7.6%	7.5%	6.8%

[Example 25] Establishment of cell lines stably expressing humanized antibody H0L0 or its point mutants

The genes encoding antibodies were cloned into expression vectors. The antibodies were: Hspu2.2Lspu2.2 (Hu2.2Lu2.2) and Hspd1.8Lspd1.6 (Hd1.8Ld1.6), which were prepared as modified antibodies from the H0L0 antibody by the method described in Example 21; and the H0L0 antibody, which was used for such modifications. The respective genes encoding the heavy chain and light chain of each antibody were cloned into different expression vectors to express the genes. Two types of expression vectors were selected to carry a desired combination of genes encoding the heavy chain and light chain as described above, and after digestion with *PvuI*, they were introduced by electroporation into cells of FTP-KO line produced as described in Reference Experimental Example 22.

The transformed cell lines stably producing the H0L0 antibody or its modified antibodies were produced by electroporation using Gene Pulser II (Bio-Rad). 10 μg each of the expression plasmid DNAs for the heavy and light chains, which provided a desired combination of heavy and light chains, were mixed with 0.75 ml of suspension of CHO cells (1×10^7 cells/ml) in PBS. The mixture was incubated on ice for ten minutes, transferred into a Gene Pulser II Cuvette, and then electrically pulsed at 1.5 kV and 25 μFD. The pulsed mixture was incubated at room temperature for ten minutes, and then suspended in CHO-S-SFMII/1% HT/1% PS medium. The same medium as used to prepare 5x, 10x, and 50x dilutions, and the suspensions were aliquoted (100 μl) into each well of 96-well culture plates. The plates were incubated under 5% CO_2 in a CO_2 incubator for 24 hours. Then, Geneticin (GIBCO) and Zeocin (Invitrogen) were added at final concentrations of 500 and 600 μg/ml to each well, respectively. The plates were further incubated for two weeks. Colonies of transformed cells resistant to both Geneticin and Zeocin were selected by culturing in the same medium

supplemented with 500 μg/ml Geneticin (GIBCO) and 600 μg/ml Zeocin (Invitrogen). The antibody concentrations in culture supernatants of transformed cells thus selected were assessed using BiacoreQ (Biacore). Accordingly, transformant lines highly expressing a desired antibody were established. The antibody concentrations in culture supernatants were determined according to the protocol appended to BiacoreQ (Biacore).

[Example 26] Drug efficacy test of humanized antibody H0L0 and its point mutants by *in vivo* model

(1) Maintenance of cell lines that are subjected to transplantation in an *in vivo* model

The Hep G2 cell line (ATCC) was used and maintained by culturing in Minimum Essential Eagle Medium (Sigma) supplemented with 10% FBS, 1 mmol/l MEM Sodium Pyruvate (Invitrogen), and 1 mmol/l MEM Non-Essential Amino Acids (Invitrogen) (hereinafter referred to as "passaging medium").

(2) Preparation of Hep G2-grafted mouse model

A Hep G2 cell suspension was prepared at 5×10^7 cells/ml using a solution containing 1:1 ratio of the passaging medium and Matrigel Matrix (BD Bioscience). 100 μl of the cell suspension (5×10^6 cells/head) was transplanted subcutaneously at an abdominal site into SCID mice (male, five weeks old) (CLEA Japan Inc.). On the day before cell transplantation, 100 μl of an anti-asialo GM1 antibody (Wako Pure Chemical Industries; the content of one vial was dissolved in 5 ml of the solution) was administered into the peritoneal cavities of the mice. The tumor volume was calculated based on the formula:

(Tumor volume) = (major axis) x (minor axis) x (minor axis) / 2.

When the mean tumor volume reached 130 to 330 mm^3, the mouse was assessed to be acceptable for the model.

(3) Preparation of samples containing each test antibody for administration

On the day of administration, samples for administration were prepared using physiological saline so that each contained one of antibodies H0L0, Hu2.2Lu2.2, and Hd1.8Ld1.6 at 0.5 mg/ml (group administrated with an antibody at 5 mg/kg) or 0.1 mg/ml (group administrated with an antibody at 1 mg/kg).

(4) Administration of antibody-containing samples for administration

27 days after transplantation of Hep G2 cells to the mouse model prepared as described above in (2), the samples prepared as described above in (3) were administered at a dose of 10 ml/kg into the caudal vein once a week for three weeks. As a negative control, physiological

saline was administered in the same way at a dose of 10 ml/kg into the caudal vein once a week for three weeks. Each group included five mice, and was administered with a sample containing any one of the respective test antibodies. Almost simultaneously with administration, venous blood was collected from three mice in each of the respective groups as test samples to determine the concentration of each antibody in mouse blood. Specifically, blood was collected from the dorsal metatarsal vein at two time points: half an hour after the first administration and immediately before the second administration. 20 μl of collected blood was heparinated, and plasma was obtained by centrifugation.

(5) Assessment of test antibodies for antitumor effect

The antitumor effect of each test antibody in a model mouse transplanted with human liver cancer was assessed by measuring the tumor volume one week after the final administration of the samples. The result shown in Fig. 55 demonstrates the trendency that the effect is enhanced with the Hspd1.8Lspd1.6 antibody (Hd1.8Ld1.6), and the effect is impaired with the Hspu2.2Lspu2.2 antibody (Hu2.2Lu2.2).

(6) Concentration of each test antibody in blood

The concentrations of test antibodies in mouse plasma were determined according to the ELISA method described in Example 21. Samples with a plasma concentration of 12.8, 6.4, 3.2, 1.6, 0.8, 0.4, or 0.2 μg/ml were prepared as calibration standards. The standard samples and test samples of mouse plasma appropriately diluted at a desired concentration were aliquoted into immunoplates (Nunc-Immuno Plate, MaxiSoup (Nalge Nunc International)) immobilized with soluble glypican-3 core (Chugai Pharmaceutical Co. Ltd.). The plates were incubated at room temperature for one hour. Then, goat anti-human IgG-BIOT (Southern Biotechnology Associates) and streptavidin-alkaline phosphatase conjugate (Roche Diagnostics) were sequentially aliquoted, and color development was achieved using as the substrate BluePhos Microwell Phosphatase Substrates System (Kirkegaard & Perry Laboratories). The degree of color development of the reaction mixture in each well was calculated by measuring the absorbance of the reaction mixture at 650 nm on a microplate reader. The antibody concentrations in mouse plasma were calculated using analysis software SoftMax Pro (Molecular Devices) based on the calibration curves prepared from absorbance of the standard samples.

The concentrations in mouse plasma 30 minutes and seven days after administration are shown in Fig. 56. It was demonstrated that with any antibody dosage, the lower the isoelectric point of a test antibody, the higher the antibody concentration in plasma seven days after administration.

[Example 27] ADCC of each test antibody when human peripheral blood mononuclear cells are used as effector cells

ADCC of each test antibody was assayed using human peripheral blood mononuclear cells (hereinafter referred to as "human PBMC") as effector cells by the procedure described below.

(1) Preparation of human PBMC solutions

Using syringes pre-filled with 200 μl of 1,000 units/ml heparin solution (Novo-Heparin 5000 units for Injection; Novo Nordisk), 50 ml of peripheral blood was collected from healthy volunteers (male adult) affiliated with Chugai Pharmaceutical Co. Ltd. The peripheral blood was diluted two-fold with PBS(-), and divided into four equal parts, each of which was transferred into a pre-centrifuged leukocyte separation tube Leucosep (Greiner Bio-One) containing 15 ml of Ficoll-Paque PLUS. The separation tubes containing an aliquot of the peripheral blood were centrifuged at 2,150 rpm and room temperature for ten minutes. Then, the resulting mononuclear cell fractions were collected. The cells in each fraction was washed once with Dulbecco's Modified Eagle's Medium (Sigma) containing 10% FBS (hereinafter referred to as "10% FBS/D-MEM"), and then suspended at a density of 5×10^6 cells/ml in 10% FBS/D-MEM. The cell suspensions were used as human PBMC solutions in the subsequent experiments.

(2) Preparation of target cells

Hep G2 cells were detached from dishes, and then plated at 1×10^4 cells/well on 96-well round-bottomed plates. The plates were incubated under 5% carbon dioxide gas in a CO_2 incubator at 37°C overnight. On the next day, 5.55 MBq of Cr-51 was added to each well of the plates. Then, the plates were incubated under 5% carbon dioxide gas in a CO_2 incubator at 37°C for three hours. The Hep G2 cells in the plates were used as target cells in the subsequent ADCC assay.

(3) Chrome release assay (ADCC)

ADCC is assessed based on specific chrome release rate determined by chrome release assay. The target cells prepared as described in (2) were washed with medium. 100 μl of the H0L0, Hu2.2Lu2.2, or Hd1.8Ld1.6 antibodies was added to the cells at various concentrations (0, 0.004, 0.04, 0.4, 4, and 40 μg/ml). After the plates were incubated at room temperature for 15 minutes, the antibody solutions were removed. Then, 100 μl of culture medium was added to each well. The plates were incubated under 5% carbon dioxide gas in a CO_2 incubator at 37°C for one hour. 100 μl of human PBMC solution prepared as described in (1) was added to each

well (5 x 10^5 cells/well). The plates were incubated under 5% carbon dioxide gas in a CO_2 incubator at 37°C for four hours, and then centrifuged. 100 µl of culture supernatant in each well of the plates was measured for radioactivity using a gamma counter. The specific chrome release rate was determined by the following formula:

[Specific chrome release rate (%)] = (A-C) x 100 / (B-C).

In this formula, "A" represents mean radioactivity (cpm) of 100 µl of culture supernatant in each well. "B" represents mean radioactivity (cpm) of 100 µl of culture supernatant in a well containing target cells, 100 µl of 2% NP-40 aqueous solution (Nonidet P-40; Nacalai Tesques), and 50 µl of 10% FBS/D-MEM. Furthermore, "C" represents mean radioactivity (cpm) of 100 µl of culture supernatant in a well containing target cells and 150 µl of 10% FBS/D-MEM. The test was conducted in triplicate. The mean and standard deviation of the specific chrome release rate (%) which reflects the ADCC of each test antibody were calculated based on the assay described above.

(4) Assessment of ADCC of each test antibody

The test antibody-mediated ADCC of human PBMC was assessed. The result showed that all the antibodies tested exhibited ADCC. The result is shown in Fig. 57. A significance test was performed on the specific chrome release rates determined for various concentrations of each test antibody. The result showed that the specific chrome release rate was not significantly different among the respective test antibodies at any antibody concentration. SAS preclinical package (SAS Institute Inc.) was used for statistical analysis. These results showed that there was no difference in ADCC among the respective test antibodies with a modified isoelectric point.

[Example 28] Preparation of anti-human IL-6 receptor antibody, anti-human GPC3 antibody, and anti-human IL-31 receptor antibody

1. Preparation of anti-human IL-6 receptor antibody

Two types of anti-human IL-6 receptor antibodies were prepared: 6R_a_H1L1 consisting of 6R_a_H1 (SEQ ID NO: 221) as the heavy chain and 6R_a_L1 (SEQ ID NO: 224) as the light chain, and 6R_b_H1L1 consisting of 6R_b_H1 (SEQ ID NO: 227) as the heavy chain and 6R_b_L1 (SEQ ID NO: 229) as the light chain. Animal cell expression vectors encoding each amino acid sequence were prepared, and the antibodies were expressed and purified by the methods described in Reference Examples 1 and 2.

2. Preparation of anti-human GPC3 antibody

An anti-human GPC3 antibody, GPC3_H1L1, which consists of GPC3_H1 (SEQ ID

NO: 233) as the heavy chain and GPC3_L1 (SEQ ID NO: 236) as the light chain was prepared. Animal cell expression vectors encoding each amino acid sequence were prepared, and the antibody was expressed and purified by the methods described in Reference Examples 1 and 2.

3. Anti-human IL-31 receptor antibody

An anti-human IL-31 receptor antibody 31R_H1L1 consisting of 31R_H1 (SEQ ID NO: 239) as the heavy chain and 31R_L1 (SEQ ID NO: 242) as the light chain was prepared. Animal cell expression vectors encoding each amino acid sequence were prepared, and the antibody was expressed and purified by the methods described in Reference Examples 1 and 2.

[Example 29] Reduction of the isoelectric point of anti-human IL-6 receptor antibody, anti-human GPC3 antibody, or anti-human IL-31 receptor antibody via amino acid substitution

1. Search for CDR sequences that reduce the isoelectric point without reduction of antigen-binding activity

WO/2007/114319 describes examples of controlling the isoelectric point by substitution of amino acids in CDR, where amino acid substitutions were introduced into heavy chain CDR3. Heavy chain CDR3 is closely associated with antibody-antigen-binding activity; thus, it is anticipated that for some kinds of antibodies, the isoelectric point could not be reduced by substituting amino acids at same positions without reducing antigen-binding activity. Therefore, the present inventors searched for candidate CDR sequences that allow reduction of isoelectric point without reducing antigen-binding activity regardless of antibody specificity. Such candidate CDR sequences that allow reduction of isoelectric point without reducing antigen-binding activity were found to include H31, H52, H61, H62, H64, and H65 in the heavy chain variable region, and L24, L27, L27a, L53, L54, L55, and L56 in the light chain variable region (Kabat numbering). Then, some of the candidate CDR sequences were introduced into the anti-human IL-6 receptor antibody, anti-human GPC3 antibody, and anti-human IL-31 receptor antibody mentioned below by amino acid substitution, and the resulting antibodies were tested to assess whether their isoelectric points can be reduced without reducing the antigen-binding activity.

2. Preparation of anti-human IL-6 receptor antibodies with a reduced isoelectric point, binding activity assessment, and isoelectric point determination

To construct 6R_a_H2 (SEQ ID NO: 222) and 6R_a_L2 (SEQ ID NO: 225), amino acid substitutions for reducing the isoelectric point and other amino acid substitutions were introduced into each of 6R_a_H1 (SEQ ID NO: 221) and 6R_a_L1 (SEQ ID NO: 224)

constituting the anti-human IL-6 receptor antibody 6R_a_H1L1. After vector construction, 6R_a_H2L2 was expressed and purified by the methods described in Reference Examples 1 and 2. Furthermore, to construct 6R_a_H3 (SEQ ID NO: 223) and 6R_a_L3 (SEQ ID NO: 226), amino acid substitutions for isoelectric point reduction and other amino acid substitutions were introduced into 6R_a_H2L2. Vectors were constructed by the method described in Reference Example 1, and then 6R_a_H3L3 was expressed and purified.

The dissociation constants (KD) of 6R_a_H1L1, 6R_a_H2L2, and 6R_a_H3L3 from their antigen, human IL-6 receptor, were determined by the Biacore T100-based method described in Reference Example 3. The dissociation constants (KD) of 6R_a_H1L1, 6R_a_H2L2, and 6R_a_H3L3 for IL-6 receptor were comparable to each other as shown in Table 18 below, and the introduced amino acid substitutions did not significantly reduce the antigen-binding activity.

Table 18

	DISSOCIATION CONSTANT (KD)
6R_a_H1L1	6.70E-11
6R_a_H2L2	3.00E-11
6R_a_H3L3	5.20E-11

The isoelectric point was determined by isoelectric focusing known to those skilled in the art. The isoelectric point of 6R_a_H1L1 was about 9.2, while the isoelectric points of 6R_a_H2L2 and 6R_a_H3L3 comprising amino acid substitutions for isoelectric point reduction were about 6.1 and 5.4, respectively. The isoelectric points were reduced by about 3.1 and 3.8 relative to 6R_a_H1L1, respectively. Furthermore, the theoretical isoelectric point of the variable region VH/VL was calculated using GENETYX (GENETYX CORPORATION). The theoretical isoelectric point of 6R_a_H1L1 was 9.37, while those of 6R_a_H2L2 and 6R_a_H3L3 were 4.63 and about 4.27, respectively. The theoretical isoelectric point was reduced by 4.74 and 5.10 in 6R_a_H2L2 and 6R_a_H3L3 relative to 6R_a_H1L1, respectively. These results are summarized in Table 19.

Table 19

	ANTI-HUMAN IL-6 RECEPTOR ANTIBODY		
	6R_a_H1L1	6R_a_H2L2	6R_a_H3L3
ACTUAL pI	9.24	6.06	5.44
THEORETICAL pI	9.37	4.63	4.27

The amino acid substitutions introduced into the CDR sequence of 6R_a_H1L1 are summarized in Table 20 below. It was revealed that these CDR amino acid substitutions could reduce the isoelectric point of the 6R_a_H1L1 molecule, which is an anti-human IL-6 receptor antibody, without significantly reducing its antigen-binding activity.

Table 20

CLASSIFICATION	MODIFIED POSITION (KABAT NO)	H1 SEQUENCE	AMINO ACID AFTER MODIFICATION
CDR1	31	S	D
CDR2	64	K	Q
CDR2	65	S	D

CLASSIFICATION	MODIFIED POSITION (KABAT NO)	L1 SEQUENCE	AMINO ACID AFTER MODIFICATION
CDR1	24	R	Q
CDR2	53	R	E
CDR2	55	R	E

Next, to construct 6R_b_H2 (SEQ ID NO: 228) and 6R_b_L2 (SEQ ID NO: 230), amino acid substitutions for isoelectric point reduction and other amino acid substitutions were introduced into 6R_b_H1 (SEQ ID NO: 227) and 6R_b_L1 (SEQ ID NO: 229) constituting 6R_b_H1L1, which is another anti-human IL-6 receptor antibody. After vector construction, 6R_b_H2L2 was expressed and purified by the methods described in Reference Examples 1 and 2. Furthermore, to construct 6R_b_L3 (SEQ ID NO: 231) and 6R_b_L4 (SEQ ID NO: 232), amino acid substitutions for isoelectric point reduction and other amino acid substitutions were introduced into 6R_b_H2L2. Vectors were constructed by the method described in Reference Example 1, and then 6R_b_H2L3 and 6R_b_H2L4 were expressed and purified.

6R_b_H1L1, 6R_b_H2L2, 6R_a_H2L3, and 6R_b_H2L4 were assayed using the method described in Reference Example 4 for their activity to neutralize the antigen, human IL-6 receptor. As shown in Fig. 58, the neutralizing activities of 6R_b_H1L1, 6R_b_H2L2, 6R_a_H2L3, and 6R_b_H2L4 were comparable to each other. The amino acid substitutions did

not significantly reduce the antigen-binding activity.

The isoelectric point was determined by isoelectric focusing known to those skilled in the art. The isoelectric point of 6R_b_H1L1 was about 9.3, while the isoelectric point of 6R_b_H2L2 comprising amino acid substitutions for isoelectric point reduction was about 5.9. The isoelectric point of 6R_b_H2L2 was reduced by about 3.4 relative to 6R_b_H1L1. Furthermore, the theoretical isoelectric point of the variable region VH/VL was calculated using GENETYX (GENETYX CORPORATION). The theoretical isoelectric point of 6R_b_H1L1 was 9.20, while those of 6R_b_H2L2, 6R_b_H2L3, and 6R_b_H2L4 were 4.52, about 4.46, and about 4.37, respectively. The theoretical isoelectric point was reduced by 4.68, 4.74, and 4.83 in 6R_b_H2L2, 6R_b_H2L3, and 6R_b_H2L4 relative to 6R_b_H1L1, respectively. These results are summarized in Table 21.

Table 21

	ANTI-HUMAN IL-6 RECEPTOR ANTIBODY			
	6R_b_H1L1	6R_b_H2L2	6R_b_H2L3	6R_b_H2L4
ACTUAL pI	9.20	5.94	N.T.	N.T.
THEORETICAL pI	9.20	4.52	4.46	4.37

N.T.: Not tested

The amino acid substitutions introduced into the CDR sequence of 6R_b_H1L1 are summarized in Table 22 below. It was revealed that these CDR amino acid substitutions could reduce the isoelectric point of the 6R_b_H1L1 molecule, which is an anti-human IL-6 receptor antibody, without significantly reducing its antigen-binding activity.

Table 22

CLASSIFICATION	MODIFIED POSITION (KABAT NO)	H1 SEQUENCE	AMINO ACID AFTER MODIFICATION
CDR1	31	S	D

CLASSIFICATION	MODIFIED POSITION (KABAT NO)	L1 SEQUENCE	AMINO ACID AFTER MODIFICATION
CDR1	24	R	Q
CDR2	53	R	E
CDR2	54	L	E
CDR2	55	R	E

3. Preparation of anti-human GPC3 antibodies with a reduced isoelectric point, binding activity assessment, and isoelectric point determination

To construct GPC3_H2 (SEQ ID NO: 234) and GPC3_L2 (SEQ ID NO: 237), amino acid substitutions for isoelectric point reduction and other amino acid substitutions were introduced into GPC3_H1 (SEQ ID NO: 233) and GPC3_L1 (SEQ ID NO: 236) constituting the anti-human GPC3 antibody GPC3_H1L1. After vector construction, GPC3_H2L2 was expressed and purified by the methods described in Reference Examples 1 and 2. Furthermore, to construct GPC3_H3 (SEQ ID NO: 235) and GPC3_L3 (SEQ ID NO: 238), amino acid substitutions for isoelectric point reduction and other amino acid substitutions were introduced into GPC3_H2L2. Vectors were constructed by the method described in Reference Example 1, and then GPC3_H3L3 was expressed and purified.

GPC3_H1L1, GPC3_H2L2, and GPC3_H3L3 were assessed by the competitive ELISA method described in Reference Example 5 for their binding activity to the antigen, human GPC3. The result is shown in Figs. 59 and 60. The glypican 3 binding activity was comparable between GPC3-H1L1 and GPC3-H2L2 and between GPC3-H2L2 and GPC3-H3L3. The amino acid substitutions did not significantly reduce the antigen-binding activity.

The isoelectric point was determined by isoelectric focusing known to those skilled in the art. The isoelectric point of GPC3_H1L1 was about 9.6, while the isoelectric point of GPC3_H2L2 comprising amino acid substitutions for isoelectric point reduction was about 8.9. The isoelectric point of GPC3_H2L2 was reduced by 0.7 relative to GPC3_H1L1. Furthermore, the isoelectric point of GPC3_H2L2 was about 8.7, while the isoelectric point of GPC3_H3L3 comprising amino acid substitutions for isoelectric point reduction was about 6.5. The

isoelectric point of GPC3_H3L3 was reduced by 2.2 relative to GPC3_H2L2. In addition, the theoretical isoelectric point of GPC3_H1L1 was 9.65, while that of GPC3_H2L2 was 8.47. Thus, the theoretical isoelectric point of GPC3_H2L2 was reduced by 1.18 relative to GPC3_H1L1. Likewise, the theoretical isoelectric point of GPC3_H2L2 was 8.47, while that of GPC3_H3L3 was 4.93. The theoretical isoelectric point of GPC3_H2L2 was reduced by 3.54 relative to GPC3_H1L1. These results are summarized in Table 23.

Table 23

	ANTI-HUMAN GPC3 ANTIBODY	
	H1L1	H2L2
ACTUAL pI	9.6	8.9
THEORETICAL pI	9.65	8.47

	ANTI-HUMAN GPC3 ANTIBODY	
	H2L2	H3L3
ACTUAL pI	8.7	6.5
THEORETICAL pI	8.47	4.93

The amino acid substitutions introduced into the CDR sequence of GPC3_H1L1 are summarized in Table 24 below. It was revealed that these CDR amino acid substitutions could reduce the isoelectric point of the GPC3_H1L1 molecule, which is an anti-human GPC3 antibody, without significantly reducing its antigen-binding activity.

Table 24

CLASSIFICATION	MODIFIED POSITION (KABAT NO)	H1 SEQUENCE	AMINO ACID AFTER MODIFICATION
CDR2	61	Q	E
CDR2	62	K	S
CDR2	64	K	Q
CDR2	65	G	D

CLASSIFICATION	MODIFIED POSITION (KABAT NO)	L1 SEQUENCE	AMINO ACID AFTER MODIFICATION
CDR1	24	R	Q
CDR1	27	R	Q
CDR1	27	R	E

4. Preparation of anti-human IL-31 receptor antibodies with a reduced isoelectric point, binding activity assessment, and isoelectric point determination

To construct 31R_H2 (SEQ ID NO: 240) and 31R_L2 (SEQ ID NO: 243), amino acid substitutions for isoelectric point reduction and other amino acid substitutions were introduced into 31R_H1 (SEQ ID NO: 239) and 31R_L1 (SEQ ID NO: 242) constituting 31R_H1L1. After vector construction, 31R_H2L2 was expressed and purified by the methods described in Reference Examples 1 and 2. Furthermore, to construct 31R_H3 (SEQ ID NO: 241), amino acid substitutions for isoelectric point reduction and other amino acid substitutions were introduced into 31R_H2L2. Vectors were constructed by the method described in Reference Example 1, and then 31R_H3L2 was expressed and purified.

31R_H2L2 and 31R_H3L2 were assessed for their IL-31-binding affinity by the Biacore-based method described in Reference Example 6. The result is summarized in Table 25. As shown in Table 25, the NR10-binding activities of 31R_H2L2 and 31R_H3L2 were comparable to that of 31R_H1L1. Thus, the amino acid substitutions did not significantly reduce the antigen-binding activity.

Table 25

	ka (1/Ms)	kd (1/s)	KD (M)
31R_H1L1	3.7E+05	1.2E-03	3.3E-09
31R_H2L2	4.2E+05	1.6E-03	3.9E-09
31R_H3L2	4.4E+05	1.6E-03	3.6E-09

The isoelectric point was determined by isoelectric focusing known to those skilled in the art. The isoelectric point of 31R_H1L1 was about 7.76, while the isoelectric points of 31R_H2L2 and 31R_H3L2 comprising amino acid substitutions for isoelectric point reduction were about 5.49 and about 5.43, respectively. The isoelectric point was reduced by about 2.27 and about 2.33 relative to 31R_H1L1, respectively. Furthermore, the theoretical isoelectric point of 31R_H1L1 was about 7.76, while the theoretical isoelectric points of 31R_H2L2 and 31R_H3L2 were 4.63 and about 4.54, respectively. The theoretical isoelectric points were reduced by about 3.13 and about 3.22 relative to 31R_H1L1. These results are summarized in Table 26.

Table 26

	ANTI-HUMAN IL-31 RECEPTOR ANTIBODY		
	H1L1	H2L2	H3L2
ACTUAL pI	7.76	5.49	5.43
THEORETICAL pI	7.76	4.63	4.54

The amino acid substitutions introduced into the CDR sequence of 31R_H1L1 are summarized in Table 27 below. It was revealed that these CDR amino acid substitutions could reduce the isoelectric point of the 31R_H1L1 molecule, which is an anti-human IL-31 receptor antibody, without significantly reducing the antigen-binding activity.

Table 27

CLASSIFICATION	MODIFIED POSITION (KABAT NO)	H1 SEQUENCE	AMINO ACID AFTER MODIFICATION
CDR2	61	Q	D
CDR2	62	K	Q
CDR2	64	K	Q
CDR2	65	G	D

CLASSIFICATION	MODIFIED POSITION (KABAT NO)	L1 SEQUENCE	AMINO ACID AFTER MODIFICATION
CDR1	24	R	Q
CDR2	54	L	E

5. CDR sequences that allow reduction of the isoelectric point of anti-human IL-6 receptor antibodies, anti-human GPC3 antibody, or anti-human IL-31 receptor antibody without reducing their antigen-binding activity

The heavy chain and light chain CDR sequences of the two types of anti-human IL-6 receptor antibodies (6R_a and 6R_b), anti-human GPC3 antibody (GPC3), and anti-human IL-31 receptor antibody (31R) prepared as described in the above assessment sections are shown in Tables 28 and 29, respectively. Amino acid substitutions that reduced the isoelectric point without reducing the antigen-binding activity are marked.

Table 28

CDR	HCDR1						HCDR2															HCDR3											
Number	31	32	32a	33	34	35	50	51	52	52a	53	54	55	56	57	58	59	60	61	62	63	64	65	95	96	97	98	99	100	100a	100b	100c	100d	101	102
6R_a_H1	S	D	H	A	W	S	Y	I	S	-	Y	S	G	I	T	T	Y	N	P	S	L	K	S	V	L	A	R	I	T	A	-	-	M	D	Y
6R_a_H2	D	D	H	A	W	S	Y	I	S	-	Y	S	G	I	T	N	Y	N	P	S	L	K	G	V	L	A	R	I	T	A	-	-	M	D	Y
6R_a_H3	D	D	H	A	W	S	Y	I	S	-	Y	S	G	I	T	N	Y	N	P	S	L	Q	D	L	L	A	R	A	T	A	-	-	M	D	Y
6R_b_H1	S	D	H	A	W	S	Y	I	S	-	Y	S	G	I	T	T	Y	N	P	S	L	K	G	S	L	A	R	T	T	A	-	-	M	D	Y
6R_b_H2	D	D	H	A	W	S	Y	I	S	-	Y	S	G	I	T	N	Y	N	P	S	L	K	G	S	L	A	R	T	T	A	-	-	M	D	Y
GPC3_H1	D	Y	-	E	M	H	A	I	N	P	K	T	G	D	T	A	Y	S	Q	K	F	K	G	F	Y	S	Y	-	-	-	-	-	-	T	Y
GPC3_H2	D	Y	-	E	M	H	A	L	D	P	K	T	G	D	T	A	Y	S	Q	K	F	K	G	F	Y	S	Y	-	-	-	-	-	-	T	Y
GPC3_H3	D	Y	-	E	M	H	A	I	D	P	K	T	G	D	T	A	Y	S	E	S	F	Q	D	F	Y	S	Y	-	-	-	-	-	-	T	Y
31R_H1	G	Y	-	I	M	N	L	I	N	P	Y	N	G	G	T	S	Y	N	Q	K	F	K	G	D	G	Y	D	D	G	P	Y	T	M	D	Y
31R_H2	G	Y	-	I	M	N	L	I	N	P	Y	N	G	G	T	S	Y	N	Q	Q	F	Q	D	D	G	Y	D	D	G	P	Y	T	M	D	Y
31R_H3	G	Y	-	I	M	N	L	I	N	P	Y	N	G	G	T	S	Y	N	D	Q	F	Q	D	D	G	Y	D	D	G	P	Y	T	M	D	Y
POSITION EFFECTIVE IN MULTIPLE ANTIBODIES	O																		O	O		O	O											

Table 29

CDR	LCDR1															LCDR2							LCDR3								
Number	24	25	26	27	27a	27b	27c	27d	27e	28	29	30	31	32	33	34	50	51	52	53	54	55	56	89	90	91	92	93	94	95	96	97
6R_a_L1	R	A	S	Q	D	-	-	-	-	-	I	S	S	Y	L	N	Y	T	S	R	L	H	S	G	Q	G	N	R	L	P	Y	T
6R_a_L2	Q	A	S	Q	D	-	-	-	-	-	I	S	S	Y	L	N	Y	G	S	E	L	H	S	G	Q	G	N	R	L	P	Y	T
6R_a_L3	Q	A	S	E	D	-	-	-	-	-	I	S	S	Y	L	N	Y	G	S	E	L	E	S	G	Q	G	N	R	L	P	Y	T
6R_b_L1	R	A	S	Q	D	-	-	-	-	-	I	S	S	Y	L	N	Y	T	S	R	L	H	S	Q	Q	G	N	T	L	P	Y	T
6R_b_L2	Q	A	S	Q	D	-	-	-	-	-	I	S	S	Y	L	N	Y	G	S	E	L	H	S	Q	Q	G	N	S	L	P	Y	T
6R_b_L3	Q	A	S	Q	D	-	-	-	-	-	I	S	S	Y	L	N	Y	G	S	E	E	H	S	Q	Q	G	N	S	L	P	Y	T
6R_b_L4	Q	A	S	Q	D	-	-	-	-	-	I	S	S	Y	L	N	Y	G	S	E	L	E	S	Q	Q	G	N	S	L	P	Y	T
GPC3_L1	R	A	S	R	S	L	V	H	S	N	R	N	T	Y	L	H	K	V	S	N	R	F	S	S	Q	N	T	H	V	P	P	T
GPC3_L2	R	S	S	Q	S	L	V	H	S	N	R	N	T	Y	L	H	K	V	S	N	R	F	S	S	Q	N	T	H	V	P	P	T
GPC3_L3	Q	A	S	E	S	L	V	H	S	N	R	N	T	Y	L	H	K	V	S	N	R	F	S	S	Q	N	T	H	V	P	P	T
31R_L1	R	T	S	E	N	-	-	-	-	-	I	Y	S	F	L	A	N	A	K	T	L	A	K	Q	H	H	Y	E	S	P	L	T
31R_L2	Q	T	S	E	D	-	-	-	-	-	I	Y	S	F	L	A	N	A	Q	T	E	A	Q	Q	H	H	Y	E	S	P	L	T
POSITION EFFECTIVE IN MULTIPLE ANTIBODIES	O			O																O	O	O										

The above result demonstrates that positions H31, H61, H62, H64, and H65 in the heavy chain variable region and positions L24, L27, L53, L54, and L55 in the light chain variable region (Kabat numbering) are common CDR position, regardless of antibody specificity, where amino acid substitutions for reducing isoelectric point of antibody can be introduced without significantly reducing antigen-binding activity.

WO/2007/114319 describes that IgG pharmacokinetics can be improved by reducing the antibody isoelectric point. In WO/2007/114319, amino acids were substituted mainly in the

antibody framework of antibody variable region to avoid reduction of antigen-binding activity. The changes in the measured and theoretical isoelectric points of anti-Factor IXa antibody were about 0.9 and 1.0, respectively. The changes in the measured and theoretical isoelectric points of anti-Factor X antibody were about 0.5 and 0.1, respectively. The isoelectric point changes were small.

In the present invention, CDR sequences that do not result in reduction of antibody-antigen binding activity were discovered, and amino acid substitutions can be introduced not only into the variable region framework but also into the antibody CDR to reduce isoelectric point. As a result, the measured and theoretical isoelectric points were reduced by about 3.8 and about 5.1, respectively, in the anti-human IL-6 receptor antibody described above; the measured and theoretical isoelectric points were reduced by about 3.1 and about 4.7, respectively, in the anti-human GPC3 antibody; and the measured and theoretical isoelectric points were reduced by about 3.2 and about 2.3, respectively, in the anti-human IL-31 receptor antibody. The present invention revealed that amino acid substitutions in the CDR could result in significant reduction of the isoelectric point as compared to amino acid substitutions in the framework alone.

[Example 30] Assessment of pharmacokinetics of anti-human IL-6 receptor antibodies, anti-human GPC3 antibodies, and anti-human IL-31 receptor antibodies with a reduced isoelectric point

1. Assessment of anti-human IL-6 receptor antibodies for their pharmacokinetics in cynomolgus monkeys and mice

6R_a_H1L1, an anti-human IL-6 receptor antibody, and 6R_a_H2L2 and 6R_a_H3L3, anti-human IL-6 receptor antibodies with a decreased isoelectric point, were assessed for their pharmacokinetics in cynomolgus monkeys. 6R_a_H1L1 or 6R_a_H2L2 was intravenously administered once at 1.0 mg/kg. Blood was collected over time before and after administration. Furthermore, 6R_a_H2L2 or 6R_a_H3L3 was subcutaneously administered once at 1.0 mg/kg. Blood was collected over time before and after administration.

The plasma concentrations were measured by ELISA. Appropriate concentrations of standard samples and test plasma samples were aliquoted into wells of immunoplates (Nunc-Immuno Plate, MaxiSorp (Nalge Nunc International)) coated with anti-human IgG (γ-chain specific) F(ab')2 (Sigma). The samples were incubated at room temperature for one hour, and then Goat Anti-Human IgG-BIOT (Southern Biotechnology Associates) and streptavidin-alkaline phosphatase conjugate (Roche Diagnostics) were subsequently reacted. After color development using the BluePhos Microwell Phosphatase Substrates System

(Kirkegaard & Perry Laboratories) as a substrate, the absorbance at 650 nm was measured with a microplate reader. The plasma concentrations were determined based on the absorbance of the calibration curve using the analytical software SoftMax Pro (Molecular Devices). The obtained plasma concentration-time data were evaluated by model-free analysis using the pharmacokinetic analysis software WinNonlin (Pharsight) to estimate clearance (CL). The result is shown in Table 30. When administered intravenously, 6R_a_H2L2, which has a reduced isoelectric point, exhibited slower clearance than 6R_a_H1L1. This suggests that the pharmacokinetics is improved by reducing the isoelectric point. Furthermore, when administered subcutaneously, 6R_a_H3L3, which has a reduced isoelectric point, exhibited slower clearance than 6R_a_H2L2. This suggests that the pharmacokinetics is improved by reducing the isoelectric point.

Table 30

	CL (mL/h/kg)
6R_a_H1L1 iv	1.82
6R_a_H2L2 iv	0.91
6R_a_H2L2 sc	1.43
6R_a_H3L3 sc	0.93

Next, 6R_b_H1L1, which is another anti-human IL-6 receptor antibody, and 6R_b_H2L2, an anti-human IL-6 receptor antibody with a reduced isoelectric point, were assessed for their pharmacokinetics in mice (C57BL/6J; Charles River Japan, Inc.). 6R_b_H1L1 or 6R_b_H2L2 was intravenously administered once at 1.0 mg/kg. Blood was collected over time before and after administration. Furthermore, 6R_b_H1L1 or 6R_b_H2L2 was subcutaneously administered once at 1.0 mg/kg. Blood was collected over time before and after administration.

The plasma concentrations were measured by ELISA. First, Recombinant Human IL-6 sR (R&D Systems) was biotinylated using EZ-Link™ Sulfo-NFS-Biotinylation Kit (Pierce). The biotinylated human-sIL-6R was aliquoted into wells of Reacti-Bind Streptavidin High Binding Capacity (HBC) Coated Plates (Pierce), and incubated at room temperature for one hour or more to prepare human-sIL-6R-immobilized plates. Appropriate concentrations of standard samples and mouse test plasma samples were prepared and aliquoted into wells of the human-sIL-6R-immobilized plates. The samples were incubated at room temperature for one hour, and then reacted with Anti-human IgG-AP (Sigma). After color development using the BluePhos Microwell Phosphatase Substrates System (Kirkegaard & Perry Laboratories) as a substrate, the absorbance at 650 nm was measured with a microplate reader. The plasma

concentrations were determined based on the absorbance of the calibration curve using the analytical software SoftMax Pro (Molecular Devices). The obtained plasma concentration-time data were evaluated by model-free analysis using the pharmacokinetic analysis software WinNonlin (Pharsight) to estimate the clearance (CL). The result is shown in Table 31. In every case of the intravenous administration and subcutaneous administration, 6R_a_H2L2, which has a reduced isoelectric point, exhibited slower clearance than 6R_a_H1L1. This suggests that the pharmacokinetics can be improved by reducing the isoelectric point.

Table 31

	CL (mL/h/kg)
6R_b_H1L1 iv	0.18
6R_b_H2L2 iv	0.10
6R_b_H1L1 sc	0.18
6R_b_H2L2 sc	0.09

2. Assessment of anti-human GPC3 antibodies for their pharmacokinetics in mice

GPC3_H1L1, an anti-human GPC3 antibody, and GPC3_H2L2 and GPC3_H3L3, anti-human GPC3 antibodies with a reduced isoelectric point, were assessed for their pharmacokinetics in C.B-17/Icr scid mice. GPC3_H1L1, GPC3_H2L2, or GPC3_H3L3 was intravenously administered once at 5.0 mg/kg. Blood was collected over time before and after administration.

The plasma concentrations were measured by ELISA. Appropriate concentrations of standard samples, and test samples of mouse plasma appropriately diluted to desired concentrations were aliquoted into wells of immunoplates (Nunc-Immuno Plate, MaxiSoup (Nalge Nunc International)) immobilized with the antigen GPC3 (Chugai Pharmaceutical Co. Ltd.). The plates were incubated at room temperature for one hour, and then Goat Anti-Human IgG-BIOT (Southern Biotechnology Associates) and streptavidin-alkaline phosphatase conjugate (Roche Diagnostics) were aliquoted in succession. After color development using the BluePhos Microwell Phosphatase Substrates System (Kirkegaard & Perry Laboratories) as a substrate, the absorbance at 650 nm was measured with a microplate reader. The plasma concentrations were determined based on the absorbance of the calibration curve using the analytical software SoftMax Pro (Molecular Devices). The obtained plasma concentration-time data were evaluated by model-free analysis using the pharmacokinetic analysis software WinNonlin (Pharsight) to estimate clearance (CL). The result is shown in Table 32. GPC3_H2L2, which has a reduced isoelectric point, exhibited slower clearance than GPC3_H1L1. Furthermore,

GPC3_H3L3, which has a further reduced isoelectric point, exhibited slower clearance than GPC3_H2L2. This suggests that the pharmacokinetics can be improved by reducing isoelectric point.

Table 32

	CL(mL/h/kg)
GPC3_H1 L1	2.34
GPC3_H2L2	0.38
GPC3_H3L3	0.22

3. Assessment of anti-human IL-31 receptor antibodies for their pharmacokinetics in mice

31R_H1L1, an anti-human IL-31 receptor antibody, and 31R_H2L2, an anti-human IL-31 receptor antibody with a reduced isoelectric point, were assessed for their pharmacokinetics in mice (C57BL/6J; Charles River Japan, Inc.). 31R_H1L1 or 31R_H2L2 was intravenously administered once at 1.0 mg/kg. Blood was collected over time before and after administration.

The plasma concentrations were measured by ELISA. Appropriate concentrations of standard samples and test plasma samples were aliquoted into wells of immunoplates (Nunc-Immuno Plate, MaxiSorp (Nalge Nunc International)) immobilized with anti-human IgG (Fc-specific) antibody (Sigma). The samples were incubated at room temperature for one hour. Goat Anti-Human IgG-ALP (Sigma) was reacted at room temperature for one hour. After color development using the BluePhos Microwell Phosphatase Substrates System (Kirkegaard & Perry Laboratories) as a substrate, the absorbance at 650 nm was measured with a microplate reader. The plasma concentrations were determined based on the absorbance of the calibration curve using the analytical software SoftMax Pro (Molecular Devices).

The obtained plasma concentration-time data were evaluated by model-free analysis using the pharmacokinetic analysis software WinNonlin (Pharsight) to estimate clearance (CL). The result is shown in Table 33. 31R_H2L2, which has a reduced isoelectric point, exhibited slower clearance than 31R_H1L1. This suggests that the clearance rate is decreased by reducing the isoelectric point.

Table 33

	CL(mL/h/kg)
31 R_H1 L1	0.15
31 R_H2L2	0.13

3. Conclusions

The present invention revealed that the pharmacokinetics of various antibodies against different antigens can be improved by reducing their isoelectric points without reducing the antibody-antigen binding activity through substitution of amino acids in the CDR sequence. It was shown that among amino acid substitutions in the CDR sequence, those at positions H31, H61, H62, H64, and H65 in the heavy chain variable region, and those at positions L24, L27, L53, L54, and L55 in the light chain variable region (Kabat numbering) are amino acid substitutions that can be introduced to reduce antibody isoelectric point without significantly reducing the antigen-binding activity, and can thus improve antibody pharmacokinetics regardless of the antibody specificity. These mutation positions in the CDR sequence are considered useful as positions for amino acid substitution to improve antibody pharmacokinetics regardless of the antibody specificity, since amino acid substitutions at these positions can reduce antibody isoelectric point without significantly reducing the antibody-antigen binding activity.

[Example 31] Separation of homodimer and heterodimer peaks of anti-human IL-6 receptor antibody, anti-human GPC3 antibody, or anti-human IL-31 receptor antibody with a decreased isoelectric point by conventional chromatography

1. Expression of heterodimer of anti-Factor IX antibody/anti-Factor X antibody

The patent document WO/2007/114325 has reported methods for purifying IgG-type bispecific antibodies having a common L chain. To express IgG-type bispecific antibodies having a common L chain, it is necessary to express two types of heavy chains (A chain and B chain) and a common light chain. In this case, not only A chain-B chain heterodimer, which is the bispecific antibody of interest, but also A chain homodimer and B chain homodimer are expressed; thus, the bispecific antibody of interest, A chain-B chain heterodimer, has to be purified from the mixture of three kinds of antibodies. This patent document also describes that conventional methods were not able to purify A chain-B chain heterodimer by separating the A chain-B chain heterodimer peak from the peaks of A chain and B chain homodimers by conventional chromatography, but the A chain-B chain heterodimer can be purified by separating

the peaks of A chain-B chain heterodimer, and A chain and B chain homodimers by conventional cation exchange chromatography when the difference between the isoelectric points of A chain and B chain homodimers was increased by substituting amino acids in the variable regions of the two kinds of heavy chains, namely A chain and B chain. In this patent, amino acids were substituted in the framework alone, because amino acid substitutions in the variable region CDR were considered to affect the antibody-antigen binding activity. However, as described above, amino acid substitutions in the framework do not cause significant changes in isoelectric point. Thus, to achieve efficient purification of A chain-B chain heterodimer, it is preferred to further increase the difference between the isoelectric points of A chain and B chain homodimers. In this context, it was tested whether the peaks of A chain-B chain heterodimer, A chain homodimer, and B chain homodimer could be separated by introducing the CDR amino acid substitutions in Example 28 that reduce antibody isoelectric point without significantly reducing antibody-antigen binding activity.

2. Expression of heterodimer of anti-human IL-6 receptor antibody/anti-human IL-6 receptor antibody with a reduced isoelectric point

6R_a_H1H3L3 (mixture of A chain-B chain heterodimer (6R_a_H1/H3/L3), A chain homodimer (6R_a_H1/L3), and B chain homodimer (6R_a_H3/L3)) was expressed and purified by the method described in Reference Example 2 using 6R_a_L3 (SEQ ID NO: 226) as a common light chain, 6R_a_H1 (SEQ ID NO: 221) as an A chain, and 6R_a_H3 (SEQ ID NO: 223) as a B chain whose isoelectric point had been reduced without reducing the antigen-binding activity to increase the difference in isoelectric point when compared to the A chain.

3. Expression of heterodimer anti-human GPC3 antibody/anti-human GPC3 antibody with a reduced isoelectric point

GPC3_H2H3L3 (mixture of A chain-B chain heterodimer (GPC3_H2/H3/L3), A chain homodimer (GPC3_H2/L3), and B chain homodimer (GPC3_H3/L3)) was expressed and purified by the method described in Reference Example 2 using GPC3_L3 (SEQ ID NO: 238) as a common light chain, GPC3_H2 (SEQ ID NO: 234) as an A chain, and GPC3_H3 (SEQ ID NO: 235) as a B chain whose isoelectric point had been reduced without reduction of the antigen-binding activity to increase the difference in isoelectric point when compared to the A chain.

4. Expression of heterodimer of anti-human IL-31 receptor antibody/anti-human IL-31 receptor antibody with a reduced isoelectric point

31R_H1aH2aL2 (mixture of A chain-B chain heterodimer (31R_H1a/H2a/L2), A chain

homodimer (31R_H1a/L2), and B chain homodimer (31R_H2a/L2)) was expressed and purified by the method described in Reference Example 2 using 31R_L2 (SEQ ID NO: 243) as a common light chain, and as a A chain 31R_H1a (SEQ ID NO: 244) which was obtained by modifying the constant region of 31R_H1, and 31R_H2a (SEQ ID NO: 245) as a B chain which was obtained by modifying the constant region of 31R_H2 whose isoelectric point had been reduced without reduction of the antigen-binding activity to increase the difference in isoelectric point when compared to the A chain.

5. Assessment of expressed antibody by cation exchange chromatography

The differences in the theoretical VH/VL isoelectric point between antibody A chain and B chain homodimers prepared as described above are summarized in Table 34. By introducing into not only the heavy-chain framework but also the heavy-chain CDR sequence, amino acid substitutions that reduce the isoelectric point without loss of binding activity, the difference in the theoretical isoelectric point can be increased up to 1.56 between A chain and B chain homodimers. The patent document WO/2007/114325 has reported that the difference in the theoretical VH/VL isoelectric point between A chain and B chain homodimers can be increased up to 1.13 by reducing the isoelectric point of the A chain homodimer by amino acid substitution in its framework alone and simultaneously increasing the isoelectric point of the B chain homodimer by amino acid substitution in its framework alone. The result of assessment described herein shows that the difference in the theoretical isoelectric point can be increased up to 1.56 by introducing amino acid substitutions into not only the framework but also the CDR sequence even when amino acid substitutions are only introduced into one chain (i.e., only the isoelectric point of one chain is reduced). Specifically, the present invention demonstrated that in order to separate A chain and B chain homodimers, the difference in the isoelectric point between the two kinds of homodimers could be further increased by introducing amino acid substitutions into not only the framework but also the CDR sequence without loss of binding activity. In general, the separation by conventional ion exchange chromatography depends on the difference in the isoelectric point between the two components to be separated. Thus, the substitutions described above enable easy separation of the two components.

Table 34

MOLECULE NAME		THEORETICAL pI OF VH/VL	THEORETICAL pI DIFFERENCE
A CHAIN HOMODIMER	6a_H1_L3	4.86	0.59
B CHAIN HOMODIMER	6a_H3_L3	4.27	
A CHAIN HOMODIMER	GPC3_H2_L3	6.49	1.56
B CHAIN HOMODIMER	GPC3_H3_L3	4.93	
A CHAIN HOMODIMER	31R_H1_L2	5.06	0.43
B CHAIN HOMODIMER	31R_H2_L2	4.63	

6R_a_H1H3L3, GPC3_H2H3L3, and 31R_H1aH2aL2 were tested to assess whether they can be separated individually as peaks of A chain-B chain heterodimer, A chain homodimer, and B chain homodimer by cation exchange chromatography. ProPac WCX-10 (Dionex) was used as a column of conventional cation exchange chromatography. The chromatography was carried out with an appropriate flow rate and gradient using 25 MES (pH 5.0) as mobile phase A and 25 mM MES containing 1 M NaCl (pH 5.0) as mobile phase B. The result of assessment by cation exchange chromatography is shown in Fig. 61. All of 6R_a_H1H3L3, GPC3_H2H3L3, and 31R_H1aH2aL2 were demonstrated to be separated into peaks of A chain-B chain heterodimer, A chain homodimer, and B chain homodimer.

Regardless of the antibody specificity, amino acid substitutions at positions of H31, H61, H62, H64, and H65 (Kabat numbering) in the heavy chain variable region can reduce antibody isoelectric point without significantly reducing antibody-antigen binding activity. It was thus revealed that the amino acid substitutions enabled separation of the heterodimer and homodimers by cation exchange chromatography. Mutations at these positions in the CDR sequence can reduce antibody isoelectric point without significantly reducing the antibody-antigen binding activity regardless of the antibody specificity. Thus, the positions are useful as positions for amino acid substitution to increase the difference in isoelectric point between the bispecific antibody heterodimer and homodimers.

[Reference Example 1] Construction of genes for antibody-expression vectors

Each mutant was constructed using the QuikChange Site-Directed Mutagenesis Kit (Stratagene) or by assemble PCR. When the QuikChange Site-Directed Mutagenesis Kit (Stratagene) was used, mutants were constructed by the method described in the appended protocol. Alternatively, assemble PCR was carried out using either of the methods described below. In the first method, oligo DNAs were synthesized based on forward and reverse

sequences including modification sites. Two fragments, namely 5' and 3' fragments, including modification sites were constructed by PCR using PrimeSTAR (Takara), and combinations of forward oligo DNA including modification site and reverse oligo DNA that bound to the vector carrying the gene to be modified, and reverse oligo DNA including modification site and forward oligo DNA that bound to the vector carrying the gene to be modified. Each mutant was constructed by linking the two fragments by assemble PCR. In the second method, an appropriate number of oligo DNAs were prepared so as to cover the entire variable region. The complete variable region was constructed by linking the oligo DNAs by assemble PCR. Mutants constructed by the methods described above were inserted into expression vectors capable of expressing insert genes in animal cells. The nucleotide sequences of the obtained expression vectors were determined by a method known to those skilled in the art.

[Reference Example 2] Expression and purification of antibodies

Antibodies were expressed by the method described below. Cells of human fetal renal carcinoma line HEK293H (Invitrogen) were suspended at a density of 5×10^5 to 6×10^5 cells/ml in DMEM (Invitrogen) supplemented with 10% FBS (Invitrogen), and plated into adhesion cell dishes (10-cm diameter; Corning) at 10 ml/dish. The cells were cultured in a CO_2 incubator (37°C, 5% CO_2) for one whole day and night. Then, the medium was removed by aspiration, and 6.9 ml of CHO-S-SFM-II medium (Invitrogen) was added to the dish. The prepared plasmids were introduced into cells by lipofection. The supernatants obtained after culturing were collected, and then the cells were removed by centrifugation (at room temperature and about 2,000 g for five minutes). The culture supernatants were sterilized by filtration with 0.22-μm filter MILLEX (R)-GV (Millipore). Antibodies were purified from the resulting culture supernatants using rProtein A Sepharose™ Fast Flow (Amersham Biosciences) by a method known to those skilled in the art. The concentrations of the purified antibodies were determined from the absorbance at 280 nm measured with a spectrophotometer. The antibody concentrations were calculated from the determined values using extinction coefficient determined by the PACE method (Protein Science (1995) 4:2411-2423).

[Reference Example 3] Biacore-based method for assessing the affinity of anti-human IL-6 receptor antibody for IL-6 receptor

1. Preparation of soluble human IL-6 receptor

Recombinant human IL-6 receptor, which is the antigen, was prepared by the method described below. A CHO cell line constitutively expressing the sequence of N-terminal amino acids 1 to 344 of soluble human IL-6 receptor (Yamasaki *et al.*, Science (1988) 241:825-828

(GenBank # X12830)) reported in J. Biochem. (1990) 108:673-676 was prepared. The soluble human IL-6 receptor was purified from the culture supernatant of soluble human IL-6 receptor-expressing CHO cells using three types of column chromatography: Blue Sepharose 6 FF column chromatography, affinity chromatography on a column immobilized with a soluble human IL-6 receptor specific antibody, and gel filtration column chromatography. The fraction eluted as the major peak was used as the final purified sample.

2. Biacore-based assessment of affinity for soluble human IL-6 receptor

The antigen-antibody reaction kinetics between anti-human IL-6 receptor antibody and soluble human IL-6 receptor was analyzed using Biacore T100 (GE Healthcare Biosciences). The antigen-antibody interaction was measured by immobilizing rec-Protein A (Zymed) (hereinafter "Protein A") onto a sensor chip, capturing an antibody with the immobilized Protein A, and then reacting the antibody with the antigen as an analyte using a method known to those skilled in the art. The running buffer used was HBS-EP+, and the flow rate was 20 μl/min. Each antibody was prepared so that about 100 RU of the antibody was bound to Protein A/G. Soluble human IL-6 receptor was prepared at 0, 0.065, 0.131, and 0.261 μg/ml using HBS-EP+ and used as an analyte. In the first step of the measurement, the antibody in solution was bound to Protein A/G, and the analyte solution was allowed to interact with the antibody. After three minutes of interaction, the solution was switched to HBS-EP+, and the dissociation phase was monitored for 10 or 15 minutes. After measurement of the dissociation phase, the sensor chip was regenerated by washing with 10 μl of 10 mM glycine-HCl (pH 1.5). The association, dissociation, and regeneration constitute one analysis cycle. Each antibody was measured according to this cycle. The obtained sensorgrams were kinetically analyzed using the Biacore-specific data analysis software, Biacore T100 Evaluation Software (GE Healthcare Biosciences).

[Reference Example 4] Method for assessing the IL-6 receptor-neutralizing activity of anti-human IL-6 receptor antibody using BaF/6R cells

To obtain a cell line that proliferates in an IL-6-dependent manner, a BaF3 cell line expressing human gp130 and human IL-6R was established by the procedure described below. The full-length human IL-6R cDNA was amplified by PCR and cloned into pcDNA3.1(+) (Invitrogen) to construct hIL-6R/pcDNA3.1(+). pCOS2Zeo/gp130 was introduced into BaF3 cells by electroporation. A BaF3 cell line expressing human gp130 (hereinafter "BaF/gp130") was established by selection in the presence of human interleukin-6 (R&D systems) and 100 ng/ml human interleukin-6 soluble receptor (R&D systems). Next, the full-length human IL-6R cDNA was amplified by PCR and cloned into pcDNA3.1(+) (Invitrogen) to construct

hIL-6R/pcDNA3.1(+). By electroporation, pcDNA3.1(+)/hIL-6R was introduced into the BaF/gp130 cell prepared described above. A BaF3 cell line expressing human IL-6R (hereinafter "BaF/6R") was established by selection in the presence of human interleukin-6 (R&D systems). Since BaF/6R proliferates in the presence of human interleukin-6 (R&D systems), it can be used to assess the growth inhibition activity of an anti-human IL-6 receptor antibody (namely, the human IL-6 receptor-neutralizing activity).

The anti-human IL-6 receptor antibody was assessed for its human IL-6 receptor-neutralizing activity using BaF/6R. After washing three times with RPMI1640 supplemented with 10% FBS, BaF/6R was suspended at 2.5 x 10^4 to 5.0 x 10^4 cells/ml in RPMI1640 containing 10% FBS and 20 ng/ml human interleukin-6 (Toray) (at a final concentration of 10 ng/ml), and aliquoted (50 μl) into each well of 96 well-plates (Corning). Then, the anti-human IL-6 receptor antibody was diluted with RPMI1640 containing 10% FBS and added to each well (50 μl/well). The cells were cultured at 37°C under 5% CO_2 for three days. WST-8 Reagent (Cell Counting Kit-8; Dojindo Laboratories) was diluted two-fold with PBS. Immediately after 20 μl of the reagent was added to each well, the absorbance at 450 nm (reference wavelength: 620 nm) was measured using SUNRISE CLASSIC (TECAN). After culturing for two hours, the absorbance at 450 nm (reference wavelength: 620 nm) was measured again. The human IL-6 receptor-neutralizing activity was assessed using the change of absorbance during two to four hours as an indicator.

[Reference Example 5] Assessment of modified anti-human GPC3 antibodies for their binding activity by competitive ELISA

The binding activities of prepared antibodies were determined by competitive ELISA. The soluble GPC3 core polypeptide (SEQ ID NO: 207) prepared at 1 μg/ml was added to 96-well plates (100 μl/well). The plates were incubated at 4°C overnight to immobilize the soluble GPC3 core polypeptide onto the plates. After washing the plates immobilized with the soluble GPC3 core polypeptide three times with washing buffer using SkanWasher 400 (Molecular Devices), 200 μl of blocking buffer was added thereto. The plates were incubated at 4°C for 30 minutes or more for blocking. The plates immobilized with the soluble GPC3 core polypeptide and blocked were washed three times with washing buffer using SkanWasher 400. Then, 100 μl of various concentrations of antibody GPC3-H2L2 or a different antibody were combined with 100 μl of biotinylated antibody GPC3-H2L2 at a final concentration of 0.3 μg/ml, and the resulting mixtures were added to the wells (200 μl/well). The GPC3-H2L2 antibody was biotinylated using a Biotin Labeling kit (Roche) according to the appended protocol. The plates were incubated at room temperature for one hour, and then washed five times with washing buffer using SkanWasher 400 (Molecular Devices). 100 μl of goat anti

streptavidin alkaline phosphatase (Zymed) 20,000-times diluted with substrate buffer was added to each well. The plates were incubated at room temperature for one hour, and then washed five times with washing buffer using SkanWasher 400. Phosphatase Substrate (Sigma) was prepared at 1 mg/ml using substrate buffer, and added to each well (100 μl). The plates were incubated for one hour. The absorbance of the reaction mixture in each well was measured at 405 nm with reference absorbance at 655 nm using Benchmark Plus (Bio-Rad).

[Reference Example 6] Biacore-based method for assessing the affinity of anti-human IL-31 receptor antibody for IL-31 receptor

1. Preparation of soluble human IL-31 receptor

The extracellular domain of human IL-31 receptor was amplified by PCR using human IL-31 receptor cDNA as a template. After attaching a FLAG tag sequence to the C-terminal end, the PCR product was inserted into a mammalian cell expression vector. 10 μg of the linearized vector was introduced into Chinese hamster ovary cell line DG44 by electroporation (Bio-Rad Gene Pulser II; 25 μF, 1.5 kV). A cell line showing high level expression was obtained. The cell line was cultured on a large scale. Soluble NR10 was purified from the culture supernatant using anti-FLAG antibody column (Sigma) and gel filtration. The amino acid sequence of soluble human IL-31 receptor is shown in SEQ ID NO: 246.

2. Biacore-based assessment of the affinity for soluble human IL-31 receptor

The antigen-antibody reaction kinetics between anti-human IL-31 receptor antibody and soluble human IL-31 receptor was analyzed using Biacore T100 (GE Healthcare Biosciences). The antigen-antibody interaction was measured by immobilizing rec-Protein A (Zymed) (hereinafter "Protein A") onto a sensor chip, capturing an antibody with the immobilized Protein A, and then reacting the antibody with the antigen as an analyte using a method known to those skilled in the art. Each antibody was prepared so that an appropriate amount of the antibody was bound to Protein A/G. Soluble human IL-31 receptor was prepared at 0, 38.5, 77.0, and 154 nM using HBS-EP+ and used as an analyte. In the first step of the measurement, the antibody in solution was bound to Protein A/G, and the analyte solution was allowed to interact with the antibody. After three minutes of interaction, the solution was switched to HBS-EP+, and the dissociation phase was monitored for five minutes. After measurement of the dissociation phase, the sensor chip was regenerated by washing with 10 μl of 10 mM glycine-HCl (pH 1.5). The association, dissociation, and regeneration constitute one analysis cycle. Each antibody was measured according to this cycle. The obtained sensorgrams were kinetically analyzed using the Biacore-specific data analysis software, Biacore T100

Evaluation Software (GE Healthcare Biosciences).

Industrial Applicability

The present invention provides methods for modifying the isoelectric points of antibodies, methods for purifying multispecific antibodies, and methods for improving antibody pharmacokinetics in plasma, all of which are based on modification of the charge of at least one exposable amino acid residue on the surface of the complementarity determining region (CDR) while retaining antigen-binding activity; pharmaceutical compositions comprising as an active ingredient an antibody with a modified isoelectric point; and methods for producing the compositions. Multispecific antibodies can be efficiently purified to high purity by modifying antibody isoelectric point. Furthermore, antibody pharmacokinetics in plasma can be improved by modifying antibody isoelectric point. Such antibodies can produce a prolonged therapeutic effect even when the administration frequency is reduced. It should be noted that antibodies obtained by the methods of the present invention retain antigen-binding activity.

CLAIMS

1. A method for modifying the isoelectric point of a polypeptide comprising an antibody variable region while retaining the antigen-binding activity of the variable region, which comprises modifying the charge of at least one exposable amino acid residue on the surface of complementarity determining region (CDR) of the polypeptide.

2. The method of claim 1, wherein the polypeptide comprising an antibody variable region further comprises an FcRn-binding domain.

3. The method of claim 1, wherein the polypeptide comprising an antibody variable region is an IgG antibody.

4. The method of claim 1, wherein the polypeptide comprising an antibody variable region is a chimeric antibody, humanized antibody, or human antibody.

5. The method of claim 1, wherein the polypeptide comprising an antibody variable region is a multispecific polypeptide that binds to at least two types of antigens.

6. The method of claim 1, wherein the charge of amino acid residue is modified by amino acid substitution.

7. The method of claim 1, wherein the modification in the charge of amino acid residue results in a change of 1.0 or more in the theoretical isoelectric point.

8. The method of claim 1, wherein the exposable amino acid residue on the surface of the CDR region is at least one amino acid residue selected from amino acid residues at positions 31, 61, 62, 64, and 65 in the heavy chain variable region and positions 24, 27, 53, 54, and 55 in the light chain variable region according to Kabat's numbering system.

9. A polypeptide comprising an antibody variable region with a modified isoelectric point, which is obtained by the method of any one of claims 1 to 8.

10. A method for controlling the plasma pharmacokinetics of a polypeptide comprising an antibody variable region, which comprises modifying the isoelectric point of the polypeptide by

the method of any one of claims 1 to 8.

11. The method of claim 10, wherein the control of pharmacokinetics refers to increase or decrease of any one of the parameters of clearance (CL) in plasma, area under the concentration curve (AUC), mean retention time in plasma, and half-life in plasma (t1/2).

12. A polypeptide comprising an antibody variable region whose pharmacokinetics in plasma is controlled, which is obtained by the method of claim 10.

13. A method for producing a polypeptide comprising an antibody variable region with a modified isoelectric point, which comprises:
(a) modifying a nucleic acid encoding a polypeptide so as to modify the charge of at least one exposable amino acid residue on the surface of the CDR region of the polypeptide;
(b) culturing a host cell to express the nucleic acid; and
(c) collecting the polypeptide comprising an antibody variable region from the host cell culture.

14. The method of claim 13, wherein the polypeptide comprising an antibody variable region further comprises an FcRn-binding domain.

15. The method of claim 13, wherein the polypeptide comprising an antibody variable region is an IgG antibody.

16. The method of claim 13, wherein the polypeptide comprising an antibody variable region is a chimeric antibody, humanized antibody, or human antibody.

17. The method of claim 13, wherein the polypeptide comprising an antibody variable region is a multispecific polypeptide that binds to at least two types of antigens.

18. The method of claim 13, wherein the charge of amino acid residue is modified by amino acid substitution.

19. The method of claim 13, wherein the modification in the charge of amino acid residue results in a change of 1.0 or more in the theoretical isoelectric point.

20. The method of claim 13, wherein the exposable amino acid residue on the surface of the CDR region is at least one amino acid residue selected from amino acid residues at positions 31,

61, 62, 64, and 65 in the heavy chain variable region and positions 24, 27, 53, 54, and 55 in the light chain variable region according to Kabat's numbering system.

21. A polypeptide comprising an antibody variable region with a modified isoelectric point, which is obtained by the method of any one of claims 13 to 20.

22. A method for producing a polypeptide comprising an antibody variable region whose pharmacokinetics in plasma is controlled, which comprises modifying the isoelectric point of the polypeptide comprising an antibody variable region by the method of any one of claims 13 to 20.

23. The method claim 22, wherein the control of pharmacokinetics refers to increase or decrease of any one of the parameters of clearance (CL) in plasma, area under the concentration curve (AUC), mean retention time in plasma, and half-life in plasma (t1/2).

24. A polypeptide comprising an antibody variable region whose pharmacokinetics in plasma is controlled, which is produced by the method of 22.

25. A method for producing a multispecific polypeptide comprising a first polypeptide and a second polypeptide each of which comprises an antibody variable region, which comprises:
(a) modifying a nucleic acid encoding a polypeptide so as to modify the charge of at least one exposable amino acid residue on the surface of the CDR region of the first polypeptide and second polypeptide, specifically modifying both or either one of a nucleic acid encoding the amino acid residues of the first polypeptide and a nucleic acid encoding the amino acid residues of the second polypeptide, so as to increase the difference between the isoelectric points of the first polypeptide and second polypeptide when compared to before modification;
(b) culturing a host cell to express the nucleic acids; and
(c) collecting a multispecific antibody from the host cell culture.

26. The method of claim 25, wherein the step of collecting the multispecific polypeptide comprising the first polypeptide and second polypeptide from the host cell culture is achieved by a standard chromatography.

27. The method of claim 25, wherein the nucleic acid is modified so that the peaks for homomultimer of the first polypeptide, homomultimer of the second polypeptide, and heteromultimer of the first polypeptide and second polypeptide are more clearly separated in a standard chromatographic analysis when compared to those before modification.

28. The method of claim 25, wherein the multispecific polypeptide is a multispecific antibody.

29. A multispecific antibody that is produced by the method of claim 27.

30. The multispecific antibody of claim 29, which is a bispecific antibody.

31. An antibody whose isoelectric point is modified as compared to the antibody before modification while retaining the antigen-binding activity, which comprises a human-derived framework region (FR), a human constant region, and a CDR selected from the group consisting of human-derived CDRs, nonhuman animal-derived CDRs, and synthetic CDRs, wherein at least one exposable amino acid residue on the surface of the CDR region is different in the charge from the amino acid residue at the corresponding position in the wild type CDR.

32. The antibody of claim 31, wherein the human constant region comprises a human Fc domain.

33. The antibody of claim 31, whose pharmacokinetics in plasma is controlled by modifying the isoelectric point.

34. An IgG antibody whose isoelectric point is modified when compared to that before amino acid modification, wherein the charge of at least one amino acid residue selected from amino acid residues at positions 31, 61, 62, 64, and 65 in the heavy chain variable region and positions 24, 27, 53, 54, and 55 in the light chain variable region according to Kabat's numbering system.

35. The antibody of claim 34, wherein the modified amino acid is selected from the amino acid residues in either of groups (a) and (b) below:
(a) glutamic acid (E) and aspartic acid (D); and
(b) lysine (K), arginine (R), and histidine (H).

36. A multispecific antibody comprising a first polypeptide and a second polypeptide, whose isoelectric points are different from each other, and at least one amino acid residue of the first polypeptide selected from amino acid residues at positions 31, 61, 62, 64, and 65 in the heavy chain variable region and positions 24, 27, 53, 54, and 55 in the light chain variable region according to Kabat's numbering system is charged.

37. The antibody of claim 36, wherein at least one amino acid residue of the second polypeptide

selected from amino acid residues at positions 31, 61, 62, 64, and 65 in the heavy chain variable region and positions 24, 27, 53, 54, and 55 in the light chain variable region according to Kabat's numbering system has no charge or has a charge opposite to the charge of the selected amino acid residue of the first polypeptide.

38. The antibody of claim 36, wherein the amino acid residue having a charge and the amino acid residue having an opposite charge as a combination are each selected from the different group of:
(a) glutamic acid (E) and aspartic acid (D); and
(b) lysine (K), arginine (R), and histidine (H).

39. The multispecific antibody comprising a first polypeptide and a second polypeptide of claim 36, which gives separated peaks for the homomultimer of the first polypeptide and the homomultimer of the second polypeptide in a standard chromatographic analysis.

40. A composition comprising a pharmaceutically acceptable carrier and the antibody of any one of claims 31 to 39.

41. A nucleic acid encoding a polypeptide that constitutes the antibody of any one of claims 31 to 39.

42. A host cell comprising the nucleic acid of claim 41.

43. A method for producing the antibody of any one of claims 31 to 39, which comprises the steps of culturing the host cell of claim 42 and collecting the polypeptide from the cell culture.

44. A method for substituting an exposable amino acid residue on the surface of the complementarity determining region (CDR) of a polypeptide comprising an antibody variable region while retaining the antigen-binding activity of the polypeptide, which comprises substituting at least one amino acid residue selected from amino acid residues at positions 31, 61, 62, 64, and 65 in the heavy chain variable region and positions 24, 27, 53, 54, and 55 in the light chain variable region according to Kabat's numbering system.