MODIFIED ANTIBODY CONSTANT REGION

Technical Field

The present invention relates to antibody constant regions that have improved physicochemical properties (stability and homogeneity), immunogenicity (antigenicity), and safety, and/or half-life in plasma; and antibodies comprising the constant regions.

Background Art

Antibodies are drawing attention as pharmaceuticals as they are highly stable in plasma (blood) and have 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).

Almost all antibody pharmaceuticals currently available on the market are of the IgG1 subclass. IgG1 type antibodies are expected be useful as anti-cancer antibody pharmaceuticals since they can bind to Fcγ receptor and exert ADCC activity. However, binding of the Fc domain to Fcγ receptor, which is important for effector function such as ADCC, can cause unnecessary adverse effects, and thus it is preferable to eliminate such binding activity from antibody pharmaceuticals intended for neutralizing biological activity (Non-patent Document 3). Furthermore, since Fcγ receptor is expressed in antigen-presenting cells, molecules that bind to Fcγ receptor tend to be presented as antigens. It has been reported that immunogenicity is and can be enhanced by linking a protein or peptide to the Fc domain of IgG1 (Non-patent Document 4 and Patent Document 1). Interaction between the antibody Fc domain and Fcγ receptor is thought to be a cause of the serious adverse effects encountered in phase-I clinical trials of TGN1412 (Non-patent Document 5). Thus, binding to Fcγ receptor is considered unfavorable in antibody pharmaceuticals intended for neutralizing the biological activity of an antigen from the perspective of adverse effect and immunogenicity.

A method for impairing the binding to Fcγ receptor is to alter the subtype of the IgG antibody from IgG1 to IgG2 or IgG4; however, this method cannot completely inhibit the binding (Non-patent Document 6). One of the methods reported for completely inhibiting the binding to Fcγ receptor is to artificially alter the Fc domain. For example, the effector functions of anti-CD3 antibodies and anti-CD4 antibodies cause adverse effects. Thus, amino acids that are not present in the wild type sequence were introduced into the Fcγ-receptor-binding domain of Fc (Non-patent Documents 3 and 7), and clinical trials are currently being conducted to assess anti-CD3 antibodies that do not bind to Fcγ receptor and anti-CD4 antibodies that have a mutated Fc domain (Non-patent Documents 5 and 8). Alternatively, Fcγ receptor-nonbinding antibodies

can be prepared by altering the FcγR-binding domain of IgG1 (at positions 233, 234, 235, 236, 327, 330, and 331 in the EU numbering system) to an IgG2 or IgG4 sequence (Non-patent Document 9 and Patent Document 2). However, these molecules contain novel non-natural peptide sequences of nine to twelve amino acids, which may constitute a T-cell epitope peptide and thus pose immunogenicity risk. There is no previous report on Fcγ receptor-nonbinding antibodies that have overcome these problems.

Meanwhile, physicochemical properties of antibody proteins, in particular, homogeneity and stability, are very crucial in the development of antibody pharmaceuticals. For the IgG2 subtype, heterogeneity originated from disulfide bonds in the hinge region has been reported (Non-patent Document 10 and Patent Document 3). It is not easy to manufacture them as a pharmaceutical in large-scale while maintaining the objective substances/related substances related heterogeneity between productions. Thus, single substances are desirable as much as possible for antibody molecules developed as pharmaceuticals.

IgG2 and IgG4 are unstable under acidic conditions. IgG type antibodies are in general exposed to acidic conditions in the purification process using Protein A and the virus inactivation process. Thus, attention is needed regarding the stability of IgG2 and IgG4 during these processes, and it is preferable that antibody molecules developed as pharmaceuticals are also stable under acidic conditions. Natural IgG2 and IgG4, and Fcγ receptor-nonbinding antibodies derived from IgG2 or IgG4 (Non-patent Documents 6 and 7 and Patent Document 2) have such problems. It is desirable to solve these problems when developing antibodies into pharmaceuticals.

IgG1-type antibodies are relatively stable under acidic conditions, and the degree of heterogeneity originated from disulfide bonds in the hinge region is also lower in this type of antibodies. However, IgG1-type antibodies are reported to undergo non-enzymatic peptide bond cleavage in the hinge region in solutions when they are stored as formulations, and Fab fragments are generated as impurities as a result (Non-patent Document 11). It is desirable to overcome the generation of impurity when developing antibodies into pharmaceuticals.

Furthermore, for heterogeneity of the C-terminal sequence of an antibody, deletion of C-terminal amino acid lysine residue, and amidation of the C-terminal amino group due to deletion of both of the two C-terminal amino acids, glycine and lysine, have been reported (Non-patent Document 12). It is preferable to eliminate such heterogeneity when developing antibodies into pharmaceuticals.

The constant region of an antibody pharmaceutical aimed for neutralizing an antigen preferably has a sequence that overcomes all the problems described above. However, a constant region that meets all the requirements has not been reported.

A preferred form of antibody pharmaceutical administration is thought to be

subcutaneous formulation in chronic autoimmune diseases and such. Low-cost, convenient antibody pharmaceuticals 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, and by conferring the antibody with high stability so that high concentration formulations can be prepared.

In general, it is necessary that subcutaneous formulations are high-concentration formulations. From the perspective of stability or such, the concentration limit of IgG-type antibody formulations is in general thought to be about 100 mg/ml (Non-patent Document 13). Thus, it is a challenge to secure stability at high concentration. However, there is no report published on the improvement of the stability of IgG at high concentrations by introducing amino acid substitutions into its constant region. A method for prolonging the antibody half-life in plasma has been reported and it substitutes amino acids in the constant region (Non-patent Documents 14 and 15); however, introduction of non-natural sequences into the constant region is not unpreferable from the perspective of immunogenicity risk.

As described above, when the purpose of an antibody pharmaceutical is to neutralize an antigen, it is preferable that all the problems described above have been overcome with regard to its constant-region sequence. However, a constant region that meets all the requirements has not been reported. Thus, there are demands for antibody constant regions that have overcome the problems described above.

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] Reddy MP, Kinney CA, Chaikin MA, Payne A, Fishman-Lobell J, Tsui P, Dal Monte PR, Doyle ML, Brigham-Burke MR, Anderson D, Reff M, Newman R, Hanna N, Sweet RW, Truneh A. Elimination of Fc receptor-dependent effector functions of a modified IgG4 monoclonal antibody to human CD4. J. Immunol. 2000 Feb 15;164(4):1925-33

[Non-patent Document 4] Guyre PM, Graziano RF, Goldstein J, Wallace PK, Morganelli PM, Wardwell K, Howell AL. Increased potency of Fc-receptor-targeted antigens. Cancer Immunol. Immunother. 1997 Nov-Dec;45(3-4):146-8

[Non-patent Document 5] Strand V, Kimberly R, Isaacs JD. Biologic therapies in rheumatology: lessons learned, future directions. Nat. Rev. Drug Discov. 2007 Jan;6(1):75-92

[Non-patent Document 6] Gessner JE, Heiken H, Tamm A, Schmidt RE. The IgG Fc receptor family. Ann. Hematol. 1998 Jun;76(6):231-48

[Non-patent Document 7] Cole MS, Anasetti C, Tso JY. Human IgG2 variants of chimeric anti-CD3 are nonmitogenic to T cells. J. Immunol. 1997 Oct 1;159(7):3613-21
[Non-patent Document 8] Chau LA, Tso JY, Melrose J, Madrenas J. HuM291(Nuvion), a humanized Fc receptor-nonbinding antibody against CD3, anergizes peripheral blood T cells as partial agonist of the T cell receptor. Transplantation 2001 Apr 15;71(7):941-50
[Non-patent Document 9] Armour KL, Clark MR, Hadley AG, Williamson LM. Recombinant human IgG molecules lacking Fcgamma receptor I binding and monocyte triggering activities. Eur. J. Immunol. 1999 Aug;29(8):2613-24
[Non-patent Document 10] Chu GC, Chelius D, Xiao G, Khor HK, Coulibaly S, Bondarenko PV. Accumulation of Succinimide in a Recombinant Monoclonal Antibody in Mildly Acidic Buffers Under Elevated Temperatures. Pharm. Res. 2007 Mar 24;24(6):1145-56
[Non-patent Document 11] AJ Cordoba, BJ Shyong, D Breen, RJ Harris. Nonenzymatic hinge region fragmentation of antibodies in solution. J. Chromatogr. B. Anal. Technol. Biomed. Life Sci. (2005) 818, 115-121
[Non-patent Document 12] Johnson KA, Paisley-Flango K, Tangarone BS, Porter TJ, Rouse JC. Cation exchange-HPLC and mass spectrometry reveal C-terminal amidation of an IgG1 heavy chain. Anal. Biochem. 2007 Jan 1;360(1):75-83
[Non-patent Document 13] 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 14] Hinton PR, Xiong JM, Johlfs MG, Tang MT, Keller S, Tsurushita N. An engineered human IgG1 antibody with longer serum half-life. J. Immunol. 2006 Jan 1;176(1):346-56
[Non-patent Document 15] 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
[Patent Document 1] US 20050261229A1
[Patent Document 2] WO 99/58572
[Patent Document 3] US 2006/0194280

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 antibody constant regions that have improved physicochemical properties (stability and homogeneity), immunogenicity, safety, and pharmacokinetics (retention in plasma (blood)) by amino acid alteration.

[Means for Solving the Problems]

The present inventors conducted dedicated studies to generate antibody constant regions that are improved through alternation of their amino acid sequences and have improved physicochemical properties (stability and homogeneity), immunogenicity, and safety, and pharmacokinetics. As a result, the present inventors successfully improved antibody constant region to have increased stability under acid conditions, reduced heterogeneity originated from disulfide bonds in the hinge region, reduced heterogeneity originated from the H-chain C terminus, and increased stability at high concentrations, as well as discovered novel constant region sequences having reduced Fcγ receptor-binding activity, while minimizing the generation of novel T-cell epitope peptides.

The present invention relates to antibody constant regions that are superior in terms of safety, immunogenicity risk, physicochemical properties (stability and homogeneity), and pharmacokinetics a through improvement by amino acid alteration; antibodies comprising such antibody constant region; pharmaceutical compositions comprising such antibody; and methods for producing them. More specifically, the present invention provides:

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

(a) a human antibody constant region that comprises deletions of both Gly at position 329 (position 446 in the EU numbering system, see sequences of proteins of immunological interest, NIH Publication No.91-3242) and Lys at position 330 (position 447 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 1;

(b) a human antibody constant region that comprises deletions of both Gly at position 325 (position 446 in the EU numbering system) and Lys at position 326 (position 447 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2; and

(c) a human antibody constant region that comprises deletions of both Gly at position 326 (position 446 in the EU numbering system) and Lys at position 327 (position 447 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 3;

[2] an IgG2 constant region in which the amino acids at positions 209 (position 330 in the EU numbering system), 210 (position 331 in the EU numbering system), and 218 (position 339 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 have been substituted with other amino acids;

[3] an IgG2 constant region in which the amino acid at position 276 (position 397 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 has been substituted with another amino acid;

[4] an IgG2 constant region in which the amino acids at positions 14 (position 131 in the EU numbering system), 102 (position 219 in the EU numbering system), and/or 16 (position 133 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 have been substituted

with another amino acid;

[5] the IgG2 constant region of [4], in which the amino acids at positions 20 (position 137 in the EU numbering system) and 21 (position 138 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 have been substituted with other amino acids;

[6] an IgG2 constant region 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/or Gln at position 298 (position 419 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 have been substituted with other amino acids;

[7] an IgG2 constant region in which the amino acids at positions 209 (position 330 in the EU numbering system), 210 (position 331 in the EU numbering system), 218 (position 339 in the EU numbering system), 276 (position 397 in the EU numbering system), 14 (position 131 in the EU numbering system), 16 (position 133 in the EU numbering system), 102 (position 219 in the EU numbering system), 20 (position 137 in the EU numbering system), and 21 (position 138 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 have been substituted with other amino acids;

[8] the IgG2 constant region of [7], which further comprises deletions of both Gly at position 325 (position 446 in the EU numbering system) and Lys at position 326 (position 447 in the EU numbering system);

[9] an IgG2 constant region in which the amino acids at positions 276 (position 397 in the EU numbering system), 14 (position 131 in the EU numbering system), 16 (position 133 in the EU numbering system), 102 (position 219 in the EU numbering system), 20 (position 137 in the EU numbering system), and 21 (position 138 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 have been substituted with other amino acids;

[10] the IgG2 constant region of [9], which further comprises deletions of both Gly at position 325 (position 446 in the EU numbering system) and Lys at position 326 (position 447 in the EU numbering system);

[11] an IgG2 constant region 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) in the amino acid sequence of SEQ ID NO: 2 have been substituted with other amino acids;

[12] the IgG2 constant region of [11], which further comprises deletions of both Gly at position 325 (position 446 in the EU numbering system) and Lys at position 326 (position 447 in the EU numbering system);

[13] an IgG2 constant region 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) in the amino acid sequence of SEQ ID NO: 2 have been substituted with other amino acids;

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

[15] an IgG4 constant region in which the amino acid at position 289 (position 409 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 3 has been substituted with another amino acid;

[16] an IgG4 constant region in which the amino acids at position 289 (position 409 in the EU numbering system), positions 14, 16, 20, 21, 97, 100, 102, 103, 104, and 105 (positions 131, 133, 137, 138, 214, 217, 219, 220, 221, and 222 in the EU numbering system, respectively), and positions 113, 114, and 115 (positions 233, 234, and 235 in the EU numbering system, respectively), have been substituted with other amino acids, and the amino acid at position 116 (position 236 in the EU numbering system) has been deleted from the amino acid sequence of SEQ ID NO: 3;

[17] the IgG4 constant region of [16], which further comprises deletions of both Gly at position 326 (position 446 in the EU numbering system) and Lys at position 327 (position 447 in the EU numbering system);

[18] an IgG1 constant region in which Asn at position 317 (position 434 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 1 has been substituted with another amino acid;

[19] the IgG1 constant region of [18], which further comprises deletions of both Gly at position 329 (position 446 in the EU numbering system) and Lys at position 330 (position 447 in the EU numbering system);

[20] an IgG2 constant region 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), 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: 2 have been substituted with other amino acids;
[21] the IgG2 constant region of [20], which further comprises deletions of both Gly at position 325 (position 446 in the EU numbering system) and Lys at position 326 (position 447 in the EU numbering system);
[22] an IgG2 constant region 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), and Ser at position 21 (position 138 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 have been substituted with other amino acids;
[23] the IgG2 constant region of [22], which further comprises deletions of both Gly at position 325 (position 446 in the EU numbering system) and Lys at position 326 (position 447 in the EU numbering system);
[24] a human antibody constant region comprising the amino acid sequence of SEQ ID NO: 5;
[25] a human antibody constant region comprising the amino acid sequence of SEQ ID NO: 7;
[26] a human antibody constant region comprising the amino acid sequence of SEQ ID NO: 9;
[27] a human antibody constant region comprising the amino acid sequence of SEQ ID NO: 35;
[28] a human antibody constant region comprising the amino acid sequence of SEQ ID NO: 36;
[29] a human antibody constant region comprising the amino acid sequence of SEQ ID NO: 37;
[30] a human antibody constant region comprising the amino acid sequence of SEQ ID NO: 43;
[31] a human antibody constant region comprising the amino acid sequence of SEQ ID NO: 57 (M40ΔGK);
[32] a human antibody constant region comprising the amino acid sequence of SEQ ID NO: 55 (M86ΔGK);
[33] an antibody comprising the constant region of any one of [1] to [32];
[34] an anti-IL-6 receptor antibody comprising the constant region of any one of [1] to [32]; and
[35] a pharmaceutical composition comprising the constant region of any one of [1] to [32].

Brief Description of the Drawings

Fig. 1 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. 2 is a diagram showing the result of cation exchange chromatography (IEC) analysis of WT-IgG1, WT-IgG2, and WT-IgG4.

Fig. 3 is a diagram showing predicted disulfide bonding in the hinge region of WT-IgG2.

Fig. 4 is a diagram showing predicted disulfide bonding in the hinge region of

IgG2-SKSC.

Fig. 5 is a diagram showing the result of cation exchange chromatography (IEC) analysis of WT-IgG2 and IgG2-SKSC.

Fig. 6 is a diagram showing the result of cation exchange chromatography (IEC) analysis of humanized PM-1 antibody, H chain C-terminal ΔK antibody, and H chain C-terminal ΔGK antibody.

Fig. 7 shows comparison of the amounts WT-IgG1, WT-IgG2, WT-IgG4, WT-M14ΔGK, WT-M17ΔGK, and WT-M11ΔGK bound to FcγRI.

Fig. 8 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. 9 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. 10 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. 11 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. 12 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. 13 is a diagram showing the result of cation exchange chromatography (IEC) analysis of WT-IgG2, WT-M14ΔGK, and WT-M31ΔGK.

Fig. 14 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. 15 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. 16 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. 17 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. 18 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 and F2H/L39.

Fig. 19 is a graph showing the activities of TOCILIZUMAB, the control, and Fv5-M83 to neutralize BaF/g130.

Fig. 20 is a graph showing the activities of TOCILIZUMAB, Fv3-M73, and Fv4-M73 to

neutralize BaF/gp130.

Fig. 21 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. 22 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. 23 is a graph showing the time courses of concentration of free soluble IL-6 receptor in cynomolgus monkeys after intravenous administration of TOCILIZUMAB, the control, Fv3-M73, Fv4-M73, or Fv5-M83.

Fig. 24 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.

Mode for Carrying Out the Invention

The present invention provides antibody constant regions whose physicochemical properties (stability and homogeneity), immunogenicity, safety, and/or pharmacokinetics have been improved by altering the amino acid sequence of an antibody constant region; antibodies comprising such constant region; pharmaceutical compositions comprising such antibody; and methods for producing them.

Herein, the constant region refers to IgG1, IgG2, or IgG4 type constant region. The antibody constant region is preferably a human antibody constant region. The amino acid sequences of human IgG1, IgG2, and IgG4 constant regions are known (human IgG1 constant region, SEQ ID NO: 1; human IgG2 constant region, SEQ ID NO: 2; and human IgG4 constant region, SEQ ID NO: 3). 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 substitutions of the present invention. 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: 2 include IgG2 constant regions that comprise one or more amino acid substitutions and/or modifications in the amino acid sequence of SEQ ID NO: 2 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: 1 and IgG4 constant regions comprising the amino acid sequence of SEQ ID NO: 3. The sequence of human IgG4 constant region has been altered to improve the stability of the hinge region (Mol. Immunol. 1993 Jan;30(1):105-8). Furthermore, the sugar chain at position 297 in the EU

numbering system may be of any sugar-chain structure, or there may not be any sugar chain linked at this site (for example, can be produced with *E. coli*).

<IgG2 having altered amino acids>

The present invention provides IgG2 constant regions with an improved stability under acid conditions.

More specifically, the present invention provides 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: 2 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: 2 with another amino acid.

The IgG2 constant regions provided by the present invention, which have an improved stability under acid conditions, may also have other amino acid substitutions, deletions, additions, and/or insertions, as long as they have at least the amino acid substitution described above.

The present invention provides IgG2 constant regions with reduced heterogeneity of hinge region.

More specifically, the present invention provides 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/or Cys at position 102 (position 219 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 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.

The IgG2 constant regions provided by the present invention, which have reduced heterogeneity, may also have other amino acid substitutions, deletions, additions, and/or insertions, as long as they have at least the amino acid substitution described above.

For example, mutating Cys at position 14 and Arg at position 16 in an IgG2 constant region comprising the amino acid sequence of SEQ ID NO: 2 may generate non-natural, novel peptide sequences of nine to twelve amino acids, which can become T-cell epitope peptides, and

thus generate immunogenicity risk. Even with the introduction of the amino acid substitutions described above, the generation of non-natural T-cell epitope peptides can be avoided by substituting Glu at position 20 (position 137 in the EU numbering system) and Ser at position 21 (position 138 in the EU numbering system) with other amino acids. The type of amino acid after substitution is not particularly limited; however, substitutions of Gly for Glu at position 20 and Gly for Ser at position 21 are preferred.

The present invention also provides IgG2 constant regions with reduced Fcγ receptor-binding activity.

More specifically, 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: 2 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 alterations are not preferred because they result in generation of non-human 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: 2 have been substituted with Ser, Ser, and Ala, respectively.

The IgG2 constant regions provided by the present invention, which have reduced Fcγ receptor-binding activity, may also have other amino acid substitutions, deletions, additions, and/or insertions, as long as they have at least the amino acid substitution described above.

The present invention provides IgG2 constant regions with reduced C-terminal heterogeneity.

More specifically, 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: 2. The heterogeneity originated from the C terminus of

antibody H chain can be reduced only when both of the amino acids are deleted.

The IgG2 constant regions provided by the present invention, which have reduced C-terminal heterogeneity, may also have other amino acid substitutions, deletions, additions, and/or insertions, as long as they have at least the amino acid substitution described above.

The present invention further provides IgG2 constant regions with improved pharmacokinetics.

Specifically, the present invention provides 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: 2 have been substituted with other amino acids. These amino acid substitutions enable to improve antibody pharmacokinetics. 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.

Below is a preferred embodiment of IgG2 of the present invention, which has improved stability under acidic conditions, 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, Met at position 276, 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: 2 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), Val for Met at position 276 (position 397 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: 4 (M14).

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: 5 (M14ΔGK).

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: 2 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: 54 (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: 55 (M86ΔGK).

Below is another preferred embodiment of the IgG2 constant regions of the present invention, which have improved stability under acidic conditions and reduced heterogeneity in the hinge region.

IgG2 constant regions comprising an amino acid sequence in which Met at position 276, 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: 2 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 (position 397 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: 6 (M31).

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: 7 (M31ΔGK).

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: 2 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: 56 (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: 57 (M40ΔGK).

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: 2.

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.

Specifically, the present invention provides an antibody constant region comprising the amino acid sequence of SEQ ID NO: 35 (M58).

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: 2.

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.

Specifically, the present invention provides an antibody constant region comprising the amino acid sequence of SEQ ID NO: 37 (M73).

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 pharmacokinetics, and/or higher stability in preparations in comparison with the IgG1 constant region.

<IgG4 having altered amino acids>

The present invention provides IgG4 constant regions that are stable at acidic conditions.

More specifically, 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: 3 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 277 (position 409 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 3 with another amino acid.

The IgG4 constant regions provided by the present invention, which have an improved stability under acidic conditions, may also have other amino acid substitutions, deletions, additions, and/or insertions, as long as they have at least the amino acid substitution described above.

The present invention provides IgG4 constant regions with reduced C-terminal heterogeneity.

The present invention provides IgG4 constant regions 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 IgG4 constant region comprising the amino acid sequence of SEQ ID NO: 3. The heterogeneity originated from the C terminus of antibody H chain can be reduced only when both of the amino acids are deleted.

The IgG4 constant regions provided by the present invention, which have reduced C-terminal heterogeneity, may also have other amino acid substitutions, deletions, additions, and/or insertions, as long as they have at least the amino acid substitution described above.

Another preferred embodiment of IgG4 of the present invention, which has improved stability under acidic conditions, reduced heterogeneity in the hinge region, and/or reduced Fcγ receptor-binding activity, includes IgG4 comprising the constant region described below.

IgG4 constant regions comprising an amino acid sequence in which 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, Pro at position 105, Glu at position 113, Phe at position 114, Leu at position 115, and Arg at position 289 have been substituted with other amino acids, and simultaneously Gly at position 116 has been deleted in the amino acid sequence of SEQ ID NO: 3.

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.

Such IgG4 constant regions include, for example, IgG4 constant regions comprising the amino acid sequence of SEQ ID NO: 8 (M11).

In another preferred embodiment, the IgG4 constant regions of the present invention include IgG4 constant regions further comprising the deletion of Gly at position 325 (position 446 in the EU numbering system) and Lys at position 326 (position 447 in the EU numbering system) in the above-described IgG4 constant region. Such antibodies include, for example, IgG4 constant regions comprising the amino acid sequence of SEQ ID NO: 9 (M11ΔGK).

<IgG1 having altered amino acids>

The present invention provides IgG1 constant regions with reduced C-terminal heterogeneity.

More specifically, the present invention provides IgG1 constant regions having the deletion of Gly at position 329 (position 446 in the EU numbering system) and Lys at position 330 (position 447 in the EU numbering system) in the IgG1 constant region comprising the amino acid sequence of SEQ ID NO: 1. The heterogeneity originated from the H-chain C terminus of an antibody can be reduced only when both of the amino acids are deleted.

The present invention provides IgG1 constant regions with improved pharmacokinetics.

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: 1 has been substituted with another amino acid. The type of amino acid after substitution is not particularly limited; however, substitution to Ala is preferred.

The present invention provides a constant region having the deletion of Gly at position 329 and Lys at position 330 in the amino acid sequence of SEQ ID NO: 36. More specifically, the present invention provides an antibody constant region comprising the amino acid sequence of SEQ ID NO: 43 (M83).

The IgG1 constant regions provided by the present invention, which have reduced C-terminal heterogeneity, may also have other amino acid substitutions, deletions, additions, and/or insertions, as long as they have at least the amino acid deletions described above.

The present invention also provides antibodies comprising any one of the antibody constant regions described above. The type and origin of antibodies of the present invention are not particularly limited, as long as they comprise the antibody constant region described above, and can be any antibodies.

The antibodies of the present invention also include modified products of antibodies comprising any of the amino acid substitutions described above. 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, fully humanized antibodies, or

such. In a preferred embodiment, the antibodies of the present invention are humanized antibodies.

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 also include modification products of an antibody comprising any one of the constant regions described above.

Such antibody modification products include, for example, antibodies linked with various molecules such as polyethylene glycol (PEG) and cytotoxic substances. Such antibody modification products can be obtained by chemically modifying antibodies of the present invention. Methods for modifying antibodies are already established in this field.

The antibodies of the present invention may also be bispecific antibodies. "Bispecific antibody" refers to an antibody that has in a single molecule variable regions that recognize different epitopes. The epitopes may be present in a single molecule or in separate molecules.

The antibody constant regions described above can be used as a constant region in an antibody against an arbitrary antigen. The antigen is not particularly limited.

The antibodies of the present invention can also be obtained by, for example, the following methods. In one embodiment to obtain antibodies of the present invention, one or more amino acid residues are first deleted or substituted with amino acids of interest in the constant region. Methods for substituting one or more amino acid residues with amino acids of interest 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 the constant region of an antibody with amino acids of interest.

In another embodiment to obtain antibodies, an antibody that binds to an antigen of interest 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. The binding activity of the

antibody can be determined by known methods. Next, one or more amino acid residues in the constant region of the antibody are deleted or substituted with amino acids of interest.

More specifically, the present invention relates to methods for producing antibodies, which comprise the steps of:

(a) expressing a DNA encoding an H chain in which one or more amino acid residues in the constant region are deleted or substituted with amino acids of interest, and a DNA encoding an L chain; 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 an antibody H chain in which one or more amino acid residues in the constant region are deleted or substituted with amino acids of interest, and a DNA encoding an antibody L chain. A DNA encoding an H chain in which one or more amino acid residues in the constant region are deleted or substituted with amino acids of interest can be prepared, for example, by obtaining a DNA encoding the constant region of a wild type H chain, and introducing an appropriate substitution so that a codon encoding a particular amino acid in the constant region encodes an amino acid of interest.

Alternatively, a DNA encoding an H chain in which one or more amino acid residues in the constant region are deleted or 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 constant region of the wild type H chain are deleted or 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 an H chain in which one or more amino acid residues in the constant region are deleted or 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 region, but are not limited thereto. A DNA encoding an L 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, an H chain expression vector is constructed by inserting a DNA encoding an H chain variable region into an expression vector along with a DNA encoding an H chain constant region. Likewise, an L chain expression vector is constructed by inserting a DNA encoding an L chain variable region into an expression vector along with a DNA encoding an L chain constant region. Alternatively, these H and L 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.

<Methods for improving the IgG2 constant region 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: 2 (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: 2 (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.

<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: 2 (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: 2 (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.

<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: 2. 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: 2. 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 pharmacokinetics by substituting amino acids of IgG2 constant region>

The present invention also relates to methods for improving the pharmacokinetics of an antibody, which comprise the step of substituting His at position 14 (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: 2. The methods of the present invention for improving the pharmacokinetics 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 pharmacokinetics 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: 2 or 35 (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 pharmacokinetics of an antibody may comprise other steps of amino acid substitution, as long as they comprise the above-described step.

<Methods for improving the pharmacokinetics by substituting amino acids of IgG1 constant region>

The present invention also relates to methods for improving the pharmacokinetics of an antibody, 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: 1. 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 pharmacokinetics of an antibody 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 pharmacokinetics of an antibody and reducing the heterogeneity originated from deletion of C-terminal amino acids, which comprise the step of substituting Asn at position 317 (EU434) and deleting Gly at position 329 (EU446) and Lys at position 330 (EU447) in an IgG1 constant region comprising the amino acid sequence of SEQ ID NO: 1. 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 pharmacokinetics of an antibody may comprise other steps of amino acid substitution, as long as they comprise the above-described step.

<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: 2. 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: 2. 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 also relates to methods for reducing the 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: 2 (M14ΔGK), 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: 2 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: 2 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: 2 with another amino acid;

(d) substituting Met at position 276 (position 397 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 with another amino acid;

(e) substituting Cys at position 14 (position 131 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 with another amino acid;

(f) substituting Arg at position 16 (position 133 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 with another amino acid;

(g) substituting Cys at position 102 (position 219 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 with another amino acid;

(h) substituting Glu at position 20 (position 137 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 with another amino acid;

(i) substituting Ser at position 21 (position 138 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 with another amino acid; 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: 2.

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), Val for Met at position 276 (position 397 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 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: 2 (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: 2 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: 2 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: 2 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: 2 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: 2 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: 2 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: 2 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: 2 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: 2.

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 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 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: 2

(M31ΔGK), the steps of:

(a) substituting Met at position 276 (position 397 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 with another amino acid;

(b) substituting Cys at position 14 (position 131 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 with another amino acid;

(c) substituting Arg at position 16 (position 133 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 with another amino acid;

(d) substituting Cys at position 102 (position 219 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 with another amino acid;

(e) substituting Glu at position 20 (position 137 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 with another amino acid;

(f) substituting Ser at position 21 (position 138 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 with another amino acid; 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: 2.

The type of amino acid after substitution is not particularly limited; however, substitutions of Val for Met at position 276 (position 397 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, all of which comprise in an IgG2 constant region comprising the amino acid sequence of SEQ ID NO: 2 (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: 2 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: 2 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: 2 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: 2 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: 2 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: 2.

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 present invention also relates to methods for reducing antibody heterogeneity originated from the hinge region of IgG2, methods for improving pharmacokinetics, 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: 2 (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: 2;

(b) substituting Lys for Arg at position 16 (position 133 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2;

(c) substituting Ser for Cys at position 102 (position 219 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2;

(d) substituting Gly for Glu at position 20 (position 137 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2;

(e) substituting Gly for Ser at position 21 (position 138 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2;

(f) substituting Gln for His at position 147 (position 268 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2;

(g) substituting Gln for Arg at position 234 (position 355 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2;

(h) substituting Glu for Gln at position 298 (position 419 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2; 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: 2.

The present invention also relates to methods for reducing antibody heterogeneity originated from the hinge region of IgG2, methods for improving pharmacokinetics, 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: 2 (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: 2;
(b) substituting Lys for Arg at position 16 (position 133 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2;
(c) substituting Ser for Cys at position 102 (position 219 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2;
(d) substituting Gly for Glu at position 20 (position 137 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2;
(e) substituting Gly for Ser at position 21 (position 138 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2;
(f) substituting Gln for His at position 147 (position 268 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2;
(g) substituting Gln for Arg at position 234 (position 355 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2;
(h) substituting Glu for Gln at position 298 (position 419 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2;
(i) substituting Ala for Asn at position 313 (position 434 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2; 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: 2.

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.

<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: 3 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: 3 (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.

<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: 3 (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: 3. 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 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: 3 (M11ΔGK), 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: 3 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: 3 with another amino acid;

(c) substituting Glu at position 20 (position 137 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 3 with another amino acid;

(d) substituting Ser at position 21 (position 138 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 3 with another amino acid;

(e) substituting Arg at position 97 (position 214 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 3 with another amino acid;

(f) substituting Ser at position 100 (position 217 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 3 with another amino acid;

(g) substituting Tyr at position 102 (position 219 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 3 with another amino acid;

(h) substituting Gly at position 103 (position 220 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 3 with another amino acid;

(i) substituting Pro at position 104 (position 221 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 3 with another amino acid;

(j) substituting Pro at position 105 (position 222 in the EU numbering system) in the amino acid

sequence of SEQ ID NO: 3 with another amino acid;
(k) substituting Glu at position 113 (position 233 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 3 with another amino acid;
(l) substituting Phe at position 114 (position 234 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 3 with another amino acid;
(m) substituting Leu at position 115 (position 235 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 3 with another amino acid;
(n) deleting Gly at position 116 (position 236 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 3;
(o) substituting Arg at position 289 (position 409 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 3 with another amino acid; 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: 3.

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.

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.

<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: 1. 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: 1. 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 antibody constant regions described above are not particularly limited, and may be used for any antibodies. Examples of antibodies which use the constant region of the present invention include:

(a) a heavy chain that comprises the amino acid sequence of SEQ ID NO: 48 (VH4-M73);
(b) a heavy chain that comprises the amino acid sequence of SEQ ID NO: 46 (VH3-M73);
(c) a heavy chain that comprises the amino acid sequence of SEQ ID NO: 44 (VH5-M83);
(d) a light chain that comprises the amino acid sequence of SEQ ID NO: 49 (VL1-kappa);
(e) a light chain that comprises the amino acid sequence of SEQ ID NO: 47 (VL3-kappa);
(f) a light chain that comprises the amino acid sequence of SEQ ID NO: 45 (VL5-kappa);
(g) an antibody that comprises the heavy chain of (a) and the light chain of (d) (FV3-M73);
(h) an antibody that comprises the heavy chain of (b) and the light chain of (e) (FV4-M73); and
(i) an antibody that comprises the heavy chain of (c) and the light chain of (f) (FV5-M83).

<Pharmaceutical compositions comprising antibodies>

The present invention provides pharmaceutical compositions comprising an antibody of the present invention.

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

Hereinbelow, the present invention is further specifically described with reference to the Examples, but it is not to be construed as being limited thereto.

[Example 1] 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 a humanized anti-human IL-6 receptor antibody, 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: 13) and WT-IgG4 (SEQ ID NO: 14). 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 Reference 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 L chain (SEQ ID NO: 15), WT-IgG1, WT-IgG2, and WT-IgG4 were expressed by the method described below. Human embryonic kidney cancer-derived HEK293H cells (Invitrogen) were suspended in DMEM (Invitrogen) supplemented with 10% Fetal Bovine Serum (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 4 to 5 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. 2000 g, 5 min, 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.

(1) Humanized PM-1 antibody (PM-1 VH + IgG1) H chain, SEQ ID NO: 12 (amino acid sequence)

(2) Humanized PM-1 VH + IgG2 H chain, SEQ ID NO: 13 (amino acid sequence)

(3) Humanized PM-1 VH + IgG4 H chain, SEQ ID NO: 14 (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. 1. 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 an altered CH3 domain

The stability of IgG2 and IgG4 molecules under acidic condition was demonstrated to be lower than that of IgG1. Thus, altered 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. 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. Since positions 397 and 409 of IgG1 in the EU numbering system are valine and lysine, respectively, an altered IgG2 antibody that comprises the substitution of valine for methionine at position 397 in the EU numbering system (IgG2-M397V, SEQ ID NO: 16 (amino acid sequence)) and an altered IgG4 antibody that comprises the substitution of lysine for arginine at position 409 in the EU numbering system (IgG4-R409K, SEQ ID NO: 17 (amino acid sequence)) are prepared.

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. 1. 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 altered 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. The purified antibodies of were dialyzed against a solution of 20 mM sodium acetate, 150 mM NaCl, pH 6.0 (EasySEP, TOMY). DSC measurement (measurements of midpoint temperature and Tm value) was carried out at a heating rate of 1°C/min from 40 to 100°C at a protein concentration of about 0.1 mg/ml. Furthermore, the midpoint temperatures of thermal denaturation of WT-IgG2, WT-IgG4, IgG2-M397V, and IgG4-R409K were determined. The result showed that the Tm value for the altered 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 alterations 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 2] 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 1, 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
GradientB: 50%-75% (75 min) in the analysis of WT-IgG1
B: 30%-55% (75 min) in the analysis of WT-IgG2 and WT-IgG4

The result is shown in Fig. 2. 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 (Non-patent Document 10). Thus, the hetero-peaks of IgG2 shown in Fig. 2 are also assumed to be objective substance/related substances derived from the disulfide bonds. It is not easy to manufacture them as a pharmaceutical in large-scale while maintaining the objective substances/related substances related heterogeneity between productions. Thus, homogeneous (less heterogeneous) substances are desirable as much as possible for antibody molecules developed as pharmaceuticals. 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.

<u>Preparation and assessment of altered WT-IgG2 CH1 domain and hinge region</u>

As shown in Fig. 3, 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 H chain CH1 domain and L chain C-terminal cysteine, and two corresponding cysteines in the H 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 altered 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 altered 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 H chain CH1 domain, and substituting serine for cysteine at position 219, EU numbering, in the upper hinge of H chain of the wild type IgG2 constant region sequence (hereinafter IgG2-SKSC) (IgG2-SKSC, SEQ ID NO: 18). These substitutions would enable IgG2-SKSC to form a homogenous covalent bond between H and L chains, which is a disulfide bond between the C-terminal cysteine of the L chain and cysteine at position 220 in the EU numbering system (Fig. 4).

The methods described in Reference 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 min)

The result is shown in Fig. 5. 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 alterations such as those used to generate IgG2-SKSC, which allow formation of a single disulfide bond between the C-terminal cysteine of the L 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 1. 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 3] Improvement of C-terminal heterogeneity in IgG molecules

Construction of an expression vector for H chain C-terminal ΔGK antibody from WT-IgG1

For heterogeneity of the C-terminal sequences of an antibody, deletion of C-terminal amino acid lysine residue, and amidation of the C-terminal amino group due to deletion of both of the two C-terminal amino acids, glycine and lysine, have been reported (Non-patent Document 12). 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 altered to reduce the C-terminal heterogeneity. Specifically, the present inventors altered the nucleotide sequence of wild type IgG1 to delete the C-terminal lysine and glycine from the H 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 H chain using pB-CH vector encoding the humanized PM-1 antibody (WT) obtained in Reference 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. H chain C-terminal ΔK and ΔGK antibodies were obtained by expressing the engineered H chains and the L chain of the humanized PM-1 antibody. The antibodies were expressed and purified by the method described in Reference Example 1.

Purified H 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 H 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, H chain C-terminal ΔK antibody, and H chain C-terminal ΔGK antibody were compared.

Column: ProPac WCX-10 (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 min) -> (105 min) -> 67% B -> (1 min) -> 100% B (5 min)
Detection: 280 nm

The analysis result for the non-altered humanized PM-1 antibody, H chain C-terminal ΔK antibody, and H chain C-terminal ΔGK antibody is shown in Fig. 6. According to Non-patent Document 10, a basic peak with more prolonged retention time than that of the main peak contains an H chain C terminus with Lys at position 449 and an H chain C terminus with amidated Pro at position 447. The intensity of the basic peak was significantly reduced in the H chain C-terminal ΔGK antibody, while no such significant reduction was observed in the H chain C-terminal ΔK antibody. This suggests that the C-terminal heterogeneity of the H chain can be reduced only when the two C-terminal amino acids are deleted from the H chain.

The temperature of thermal denaturation of the H chain C-terminal ΔGK antibody was determined by DSC to assess the effect of the deletion of the two residues at the H 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 H 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 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 H 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.

[Example 4] 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 (Non-patent Documents 5 and 6). 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, M11ΔGK, and M17ΔGK, Fcγ receptor-nonbinding, optimized constant regions

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 alteration 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 (Non-patent Documents 3 and 7), and the resulting Fcγ receptor-nonbinding anti-CD3 and anti-CD4 antibodies are currently under clinical trials (Non-patent Documents 5 and 8). According to another report (Patent Document 3), 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, alterations 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 alter 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

alteration 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 alteration 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 1 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 2 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 H chain to reduce the C-terminal heterogeneity. The constant region sequence having all of the mutations introduced was named M14ΔGK (M14ΔGK, SEQ ID NO: 5). 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 H chain sequence whose variable region was WT and constant region was M14ΔGK (M14ΔGK, SEQ ID NO: 5; WT-M14ΔGK, SEQ ID NO: 19) was constructed by the method described in Reference Example 1. An antibody having WT-M14ΔGK as H chain and WT as L chain was expressed and purified by the method described in Reference Example 1.

Furthermore, in WT-M11ΔGK (M11ΔGK, SEQ ID NO: 8; WT-M11ΔGK, SEQ ID NO: 21), mutations were introduced with the same method 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 alteration newly generates non-human sequence and thus increases the

immunogenicity risk) to reduce the Fcγ receptor binding. In addition to the above alteration, 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 1) to improve the stability under acidic condition; and the amino acids at positions 446 and 447 in the EU numbering system were deleted (Example 3) to reduce the C-terminal heterogeneity.

Furthermore, WT-M17ΔGK (M17ΔGK, SEQ ID NO: 10; WT-M17ΔGK, SEQ ID NO: 20) was constructed 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 3).

WT-M17ΔGK or WT-M11ΔGK was used as the H chain, and WT was used as the L 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

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 13000 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. 7. 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 3300 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 altered 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. 8. 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 4300 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+ and the flow rate was 20 μl/min. The measurement temperature was 25°C. The concentration of each IgG or altered 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. 9. 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. 10. 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. 11. 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. 12, 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 5] Preparation and assessment of M31ΔGK

M14ΔGK prepared in Example 4 was altered 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: 7). An expression vector for a sequence of antibody H chain whose variable region is WT and constant region sequence is M31ΔGK (WT-M31ΔGK, SEQ ID NO: 22) was constructed by the method described in Reference Example 1. Using WT-M31ΔGK H chain and WT L chain, WT-M31ΔGK was expressed and purified by the method described in Reference Example 1.

In addition to WT-M31ΔGK, 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 (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 min) -> (65 min) -> 100% B -> (1 min)
Detection: 280 nm

The analysis result for WT-IgG2, WT-M14ΔGK, and WT-M31ΔGK is shown in Fig. 13. 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 6] Assessment of the plasma retention of WT-M14

<u>Method for estimating the retention in human plasma</u>

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 taken up 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 improving the pharmacokinetics of these IgG antibodies include methods for improving the above-described binding to human FcRn, and this is achieved by altering 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 an altered 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: 24). 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: 25).

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% Fetal Bovine Serum (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 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 bindings of WT-IgG1 and WT-M14 to human FcRn were assessed by BIAcore. As shown in Table 1, the result indicated that the binding of WT-M14 was slightly greater than that of WT-IgG1.

Table 1

	KD(μM)
WT-IgG1	2.07
WT-M14	1.85

As shown in Fig. 14, 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 7] Preparation of WT-M44, WT-M58, and WT-M73 which have improved pharmacokinetics

Preparation of the WT-M58 molecule

As described in Example 6, the plasma retention of WT-M14 in human FcRn transgenic mice was comparable to that of WT-IgG1. Known methods to improve pharmacokinetics include those to lower the isoelectric point of an antibody and those to enhance the binding to FcRn. Here, the modifications described below were introduced to improve the pharmacokinetics 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: 26). Expression vectors were prepared by the same method described in Example 1. WT-M58 and L(WT) were used as H chain and L 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: 27) 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: 58) was also generated by deletions of glycine at position 446, EU numbering and lysine at position 447, EU numbering to reduce H chain C-terminal heterogeneity. Furthermore, WT-M73 (amino acid sequence of SEQ ID NO: 28) 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 H chain, while L (WT) was used as L 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 bindings of WT-IgG1, WT-M44, WT-M58, and WT-M73 to human FcRn were assessed by BIAcore. As shown in Table 2, the result indicates that the bindings 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 2

	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. 24, 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. 15, all of WT-M44, WT-M58, and WT-M73 were confirmed to have improved pharmacokinetics relative to WT-IgG1. The pharmacokinetics-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 pharmacokinetics of antibodies with the M73 constant region in human is also significantly enhanced when compared to antibodies with the IgG1 constant region.

[Example 8] Effect of the novel constant regions M14 and M58 in reducing heterogeneity in various antibodies

As described in Example 4, 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 VL as set forth in

SEQ ID NOs: 29 and 30, respectively); anti-IL-31 receptor antibody H0L0 (the amino acid sequences of H0L0_VH and H0L0_VL as set forth in SEQ ID NOs: 31 and 32, respectively); and anti-RANKL antibody DNS (the amino acid sequences of DNS_VH and DNS_VL as set forth in SEQ ID NOs: 33 and 34, respectively). For each of these antibodies, antibodies with IgG1 constant region (SEQ ID NO: 1), IgG2 constant region (SEQ ID NO: 2), or M14 (SEQ ID NO: 5) or M58 (SEQ ID NO: 35) 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. 16.

As shown in Fig. 16, 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 H-chain CH1 domain and at position 219, EU numbering, in the upper hinge of H chain.

[Example 9] Effect of the novel constant region M58 to improve the pharmacokinetics in various antibodies

As described in Example 7, 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 to human FcRn and pharmacokinetics in human FcRn transgenic mice. So, IgG1 type antibodies other than the humanized PM1 antibody were also tested to assess whether their pharmacokinetics 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: 31 and 32, respectively) and anti-RANKL antibody DNS (the amino acid sequences of DNS_VH and DNS_VL as set forth in SEQ ID NOs: 33 and 34, respectively). For each of these antibodies, antibodies with IgG1 constant region (SEQ ID NO: 1) or M58 (SEQ ID NO: 35) were generated and assessed for their binding to human FcRn by the method described in Example 6. The result is shown in Table 3.

Table 3

	KD (μM)		
	WT	H0L0	DNS
IgG1	1.42	1.07	1.36
M58	1.03	0.91	1.03

As shown in Table 3, 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 bindings 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 pharmacokinetics in human is improved by converting the constant region from the IgG1 type to M58.

[Example 10] Effect of cysteine in the CH1 domain on heterogeneity and stability

As described in Example 2, cysteines in the hinge region and CH1 domain of IgG2 were substituted to decrease the heterogeneity of natural IgG2. Assessment of various altered antibodies revealed that heterogeneity could be reduced without decreasing stability by using SKSC (SEQ ID NO: 38). SKSC (SEQ ID NO: 38) is an altered constant region obtained by substituting serine for cysteine at position 131 and lysine for arginine at position 133, EU numbering, in the H-chain CH1 domain, and serine for cysteine at position 219, EU numbering, in the H-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 H-chain upper hinge. The altered IgG2 constant region SC (SEQ ID NO: 39) was prepared by substituting serine for cysteine at position 219 and CS (SEQ ID NO: 40) was prepared by substituting serine for cysteine at position 220, EU numbering, in IgG2. WT-SC (SEQ ID NO: 41) and WT-CS (SEQ ID NO: 42) 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: 1), IgG2 (SEQ ID NO: 2), SC (SEQ ID NO: 39), CS (SEQ ID NO: 40), SKSC (SEQ ID NO: 38), or M14 (SEQ ID NO: 5), 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: 29 and 30, respectively), which is an anti IL-6 receptor antibody different from WT. The antibodies were compared with regard to heterogeneity.

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. 17.

As shown in Fig. 17, 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 differential scanning calorimetry (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 to 100°C, and at a protein concentration of about 0.1 mg/ml. The denaturation curves obtained by DSC are shown in Fig. 18. The Tm values of the Fab domains are listed in Table 4 below.

Table 4

	Tm/℃
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 alter 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 pharmacokinetics, and therefore are expected to be very useful as constant regions for antibody pharmaceuticals.

[Example 11] 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 altering TOCILIZUMAB (H chain, WT-IgG1 (SEQ ID NO: 12); L chain, WT (SEQ ID NO: 15). The following fully humanized IL-6 receptor antibodies were prepared which use as constant region M73 or M83 prepared in Example 7: Fv3-M73 (H chain, VH4-M73, SEQ ID NO: 48; L chain, VL1-kappa, SEQ ID NO: 49), Fv4-M73 (H chain, VH3-M73, SEQ ID NO: 46; L chain, VL3-kappa, SEQ ID NO: 47), and

Fv5-M83 (H chain, VH5-M83, SEQ ID NO: 44; L chain, VL5-kappa, SEQ ID NO: 45).

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 5 (see Reference Example for method). 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) (see Reference Example for method). The results obtained by determining the biological activities of these antibodies using BaF/gp130 are shown in Fig. 19 (TOCILIZUMAB, the control, and Fv5-M83 with a final IL-6 concentration of 300 ng/ml) and Fig. 20 (TOCILIZUMAB, Fv3-M73, and Fv4-M73 with a final IL-6 concentration of 30 ng/ml). As shown in Table 5, 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. 20, Fv3-M73 and Fv4-M73 exhibit slightly stronger activities than TOCILIZUMAB. As shown in Fig. 19, 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 10 times higher neutralizing activity in terms of 50% inhibitory concentration than the control (the known high-affinity anti-IL-6 receptor antibody).

Table 5

	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 pharmacokinetics 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 12] 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. 21. The result showed that each of Fv3-M73, Fv4-M73, and Fv5-M83 exhibited significantly improved pharmacokinetics in cynomolgus monkeys when compared to TOCILIZUMAB and the control. Of them, Fv3-M73 and Fv4-M73 exhibited substantially improved pharmacokinetics 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. 22. 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. 23.

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]

<u>Preparation of soluble recombinant cynomolgus monkey IL-6 receptor (cIL-6R)</u>

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 H chain and L 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 H chain and L 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.

Assessment for the biological activity by human gp130-expressing BaF3 cells (BaF/gp130)

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 600 ng/ml or 60 ng/ml human interleukin-6 (TORAY) (final concentration of 300 ng/ml or 30 ng/ml, respectively), appropriate amount of 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.

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 pH7.4, and then running IL-6 receptor SR344 adjusted to be various concentrations at pH7.4 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.

$$\frac{\text{Free soluble IL-6 receptor concentration after antibody administration}}{\text{Soluble IL-6 receptor concentration before antibody administration}} \times 100$$

Industrial Applicability

The present invention provides antibody constant regions suitable for pharmaceuticals, whose physicochemical properties (stability and homogeneity), immunogenicity, safety, and pharmacokinetics have been improved by amino acid alteration.

CLAIMS

1. An IgG2 constant region in which Met at position 276 (position 397 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 has been substituted with another amino acid.

2. The IgG2 constant region of claim 1, wherein a stability of an antibody comprising the IgG2 constant region of claim 1 is improved compared with an antibody comprising the IgG2 constant region comprising the amino acid sequence of SEQ ID NO: 2 under acidic condition.

3. The IgG2 constant region of claim 1 or 2, wherein the acidic condition is the acidic condition in the purification process using Protein A and in virus inactivation process.

4. The IgG2 constant region of any one of claims 1 to 3, wherein an antibody comprising the IgG2 constant region of claim 1 has the stability comparable to an antibody comprising the IgG2 constant region comprising the amino acid sequence of SEQ ID NO: 2.

5. The IgG2 constant region of any one of claims 1 to 4, in which Met at position 276 (position 397 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 has been substituted with Val.

6. The IgG2 constant region in which at least Met at position 276 (position 397 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 has been substituted with Val.

7. The IgG4 constant region in which Arg at position 289 (position 409 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 3 has been substituted with another amino acid.

8. The IgG4 constant region of claim 7, wherein a stability of an antibody comprising the IgG4 constant region of claim 7 is improved compared with an antibody comprising the IgG4 constant region comprising the amino acid sequence of SEQ ID NO: 3 under acidic condition.

9. The IgG4 constant region of claim 7 or 8, wherein the acidic condition is the acidic condition in the purification process using Protein A and in virus inactivation process.

10. The IgG4 constant region of any one of claims 7 to 9, wherein an antibody comprising the IgG4 constant region of claim 7 has the stability comparable to an antibody comprising the IgG4 constant region comprising the amino acid sequence of SEQ ID NO: 3.

11. The IgG4 constant region of any one of claims 7 to 10, in which Arg at position 289 (position 409 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 3 has been substituted with Lys.

12. The IgG4 constant region in which at least Arg at position 289 (position 409 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 3 has been substituted with Lys.

13. An antibody comprising the constant region of any one of claims 1 to 12.

14. The antibody of claim 13, which is a chimeric antibody, a humanized antibody, a fully humanized antibody or a human antibody.

15. The antibody of claim 13 or 14, which is a bispecific antibody, or anti IL-6 receptor antibody, anti-IL-31 receptor antibody or anti-RANKL antibody.

16. The method for producing an antibody comprising the constant region of the following (a) or (b), comprising the step of culturing a host cell into which DNA encoding the constant region of the following (a) or (b) is introduced,

(a) the IgG2 constant region in which at least Met at position 276 (position 397 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 has been substituted with another amino acid, or

(b) the IgG4 constant region in which at least Arg at position 289 (position 409 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 3 has been substituted with another amino acid,

wherein the antibody has an improved stability compared with an antibody comprising a wild-type constant region under acidic condition.

17. The method of claim 16, wherein, in case that the antibody comprises the IgG2 constant region of (a), Met at position 276 (position 397 in the EU numbering system) has been substituted with Val, and in case that the antibody comprises the IgG4 constant region of (b), Arg at position 289 (position 409 in the EU numbering system) has been substituted with Lys.

18. The method for producing an antibody whose stability under acidic condition is improved, comprising the step of substituting Met at position 276 (position 397 in the EU numbering system) in the IgG2 constant region comprising amino acid sequence of SEQ ID NO: 2 with Val.

19. The method of claim 18, further comprising the step of linking the IgG2 constant region comprising the substitution of Met at position 276 (position 397 in the EU numbering system) with Val to an antibody variable region, wherein an antibody comprising the IgG2 constant region has a low content of aggregate in gel filtration chromatography analysis, compared to an antibody comprising the constant region comprising the amino acid sequence of SEQ ID NO: 2.

20. The method for producing an antibody whose stability under acidic condition is improved, comprising the step of substituting Arg at position 289 (position 409 in the EU numbering system) in the IgG4 constant region comprising the amino acid sequence of SEQ ID NO: 3 with Lys.

21. The method of claim 20, further comprising the step of linking the IgG4 constant region comprising the substitution of Arg at position 289 (position 409 in the EU numbering system) with Lys to an antibody variable region, wherein an antibody comprising the IgG4 constant region has a low content of aggregate in gel filtration chromatography analysis, compared to an antibody comprising the constant region comprising the amino acid sequence of SEQ ID NO: 4.

22. The IgG2 constant region in which at least Met at position 276 (position 397 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 2 has been substituted with Val, wherein an antibody comprising the IgG2 constant region has an improved stability under acidic condition in gel filtration chromatography analysis, compared to an antibody comprising the constant region comprising the amino acid sequence of SEQ ID NO: 2.

23. The IgG4 constant region in which at least Arg at position 289 (position 409 in the EU numbering system) in the amino acid sequence of SEQ ID NO: 3 has been substituted with Lys, wherein an antibody comprising the IgG4 constant region has an improved stability under acidic condition in gel filtration chromatography analysis, compared to an antibody comprising the constant region comprising the amino acid sequence of SEQ ID NO: 3.