AGLYCOSYLATED Fc-CONTAINING POLYPEPTIDES

Cross-Reference to Related Applications

This application claims the benefit of U.S. Provisional Application Serial No. 61/784,669, filed March 14, 2013. The above-identified application is incorporated herein by reference.

Reference to the Sequence Listing

The present application is being filed along with a Sequence Listing in electronic format. The Sequence Listing is provided as a text file entitled A-1892-WO-PCT_ST25.txt created March 13, 2014, which is 57,344 bytes in size. The information in the electronic format of the Sequence Listing is incorporated herein by reference in its entirety.

Background

IL-2 binds three transmembrane receptor subunits: IL-2Rβ and IL-2Rγ which together activate intracellular signaling events upon IL-2 binding, and CD25 (IL-2Rα) which serves to stabilize the interaction between IL-2 and IL-2Rβγ. The signals delivered by IL-2Rβγ include those of the PI3-kinase, Ras-MAP-kinase, and STAT5 pathways.

T cells require expression of CD25 to respond to the low concentrations of IL-2 that typically exist in tissues. T cells that express CD25 include both FOXP3+ regulatory T cells (Treg cells), which are essential for suppressing autoimmune inflammation, and FOXP3- T cells that have been activated to express CD25. FOXP3- CD25+ T effector cells (Teff) may be either CD4+ or CD8+ cells, both of which may contribute to inflammation, autoimmunity, organ graft rejection, or graft-versus-host disease. IL-2-stimulated STAT5 signaling is crucial for normal T-reg cell growth and survival and for high FOXP3 expression.

In co-owned WO 2010/085495, we describe the use of IL-2 muteins to preferentially expand or stimulate Treg cells. When administered to a subject, the effect on Treg cells is useful for treating inflammatory and autoimmune diseases. Although the IL-2 muteins described therein are useful for expanding Treg over Teff cells *in vivo*, it was desirable to create IL-2 muteins that had optimal attributes for a human therapeutic.

Summary

Described herein are IL-2 muteins that are amenable to high-yield manufacturability and have optimized pharmacological activity. In the effort to produce an exemplary IL-2 mutein-based human therapeutic, a number of unexpected and unpredictable observations occurred. The IL-2 muteins described herein are the result of that effort.

The IL-2 muteins described herein have a minimal numbers of alterations to IL-2, thereby decreasing the likelihood of creating an immune response against the IL-2 mutein and/or endogenous

IL-2, yet maintain Treg preferential expansion and activation. In one aspect, the present invention refers to a polypeptide comprising a Fc region of a human IgG1 antibody wherein said Fc region comprises a N77G mutation wherein the numbering is as provided in SEQ ID NO: 3 or 4, and said Fc region of a human IgG1 comprises at least 90% identity to the amino acid sequence set forth in SEQ ID NO:3, and wherein said Fc region comprises an A67C and L86C, or an V39C and L86C, or an R72C and V82C, or an V103C and I112C substitution within the amino acid sequence set forth in SEQ ID NO:3 or SEQ ID NO:4. In another aspect, the present invention refers to an antibody comprising a Fc region of the present invention. In another aspect, the present invention refers to a Fc-fusion protein comprising the Fc region of the present invention. In another aspect, the present invention refers to a nucleic acid encoding a polypeptide of the present invention. In another aspect, the present invention refers to an expression vector comprising the nucleic acid of the present invention. In another aspect, the present invention refers to a host cell comprising the nucleic acid of the present invention. In another aspect, the present invention refers to a host cell comprising the expression vector of the present invention. In another aspect, the present invention refers to a method of making an aglycosylated IgG1 Fc-containing molecule, said method comprising: a) expressing a nucleic acid encoding a polypeptide of the present invention in a mammalian cell culture; and b) harvesting the aglycosylated IgG1 Fc-containing molecule from said culture.

Moreover, also described herein are in certain examples, that the IL-2 mutein is fused to a molecule, e.g. an antibody Fc, that increases the serum half-life when administered to a subject. IL-2 muteins have a short serum half-life (3 to 5 hrs for sub-cutaneous injection). Exemplary IL-2 mutein Fc fusions described herein have a half-life in humans of at least 1 day, at least 3 days, at least 5 days, at least 10 days, at least 15 days, at least 20 days, or at least 25 days. This effect on the pharmacokinetics of the IL-2 muteins allows for decreased or less frequent dosing of the IL-2 mutein therapeutic.

Moreover, when creating a pharmaceutical large molecule, consideration must be made for the ability to produce the large molecule in large quantities, while minimizing aggregation and maximizing the stability of the molecule. The IL-2 mutein Fc-fusion molecules demonstrate such attributes.

Additionally, in certain embodiments, the IL-2 mutein Fc-fusion protein contains an IgG1 Fc region. When it is desirable to abolish the effector functions of IgG1 (e.g., ADCC activity), it was found that mutation of the asparagine at position 297 to glycine (N297G; EU numbering scheme) provided greatly improved purification efficiency and biophysical properties over other mutations that lead to an aglycosylation IgG1 Fc. In preferred examples, cysteines are engineered into the Fc to allow disulfide bonds, which increased stability of the aglycosylated Fc-containing molecule. The usefulness of the aglycosylated Fc goes beyond the IL-2 mutein Fc-fusion context. Thus, provided herein are Fc-containing molecules, Fc-fusions and antibodies, comprising a N297G substitution and optionally substitution of one or more additional residues to cysteine.

Another example includes glycosylated peptide linkers. Preferred linker peptides that are amenable to N-glycosylation include GGNGT (SEQ ID NO:6) or YGNGT (SEQ ID NO:7).

Brief Description of the Figures

FIG. 1 In a short term stimulation assay, homodimerization by fusion to the C-terminus of IgG-Fc does not alter the activity of IL-2 muteins with reduced potency and with high affinity for CD25.

FIG. 2A and FIG. 2B IL-2 muteins with the indicated mutations and fused to the C-terminus of one side of an Fc-heterodimer were tested for their ability to stimulate STAT5 phosphorylation in T cells. These muteins also contained three mutations conferring high affinity for CD25 (V69A, N71R, Q74P). Their activity was compared to three forms of IL-2 without Fc fusion (open symbols): WT IL-2, HaWT (high affinity for CD25) (N29S, Y31H, K35R, T37A, K48E, V69A, N71R, Q74P), and HaD (high affinity for CD25 and reduced signaling activity) (N29S, Y31H, K35R, T37A, K48E, V69A, N71R, Q74P, N88D). Phospho-STAT5 responses are shown for gated FOXP3+CD4+ and FOXP3-CD4+ T cells.

FIG. 3 Proliferation of T cell subsets in response to titrations of IL-2 muteins fused to Fc-heterodimer. Activity of fusion proteins was compared to three forms of IL-2 without Fc fusion (open symbols): WT IL-2, HaWT (high affinity for CD25) (N29S, Y31H, K35R, T37A, K48E, V69A, N71R, Q74P), and HaD (high affinity for CD25 and reduced signaling activity) (N29S, Y31H, K35R, T37A, K48E, V69A, N71R, Q74P, N88D)

FIG. 4 Proliferation of NK cells in response to titrations of IL-2 muteins fused to Fc-heterodimer. Activity of fusion proteins was compared to three forms of IL-2 without Fc fusion (open symbols): WT IL-2, HaWT (high affinity for CD25) (N29S, Y31H, K35R, T37A, K48E, V69A, N71R, Q74P), and HaD (high affinity for CD25 and reduced signaling activity) (N29S, Y31H, K35R, T37A, K48E, V69A, N71R, Q74P, N88D)

FIG. 5 Proliferation of T cell subsets in response to titrations of IL-2 muteins fused to Fc-homodimer N297G. Activity of Fc.muteins was compared to WT IL-2 (open circles) and Fc.WT (closed circles). Mutations that confer high affinity for CD25 (HaMut1) were V69A and Q74P.

FIG. 6 Proliferation of NK cells in response to titrations of IL-2 muteins fused to Fc-homodimer N297G. Activity of Fc.muteins was compared to WT IL-2 (open circles) and Fc.WT (closed circles).

FIG. 7A and FIG. 7B Fc.IL-2 muteins without mutations that confer high affinity for CD25 promote Treg expansion and FOXP3 upregulation in humanized mice.

FIG. 8 Low weekly doses (0.5 μg per animal) of Fc.IL-2 muteins promote Treg expansion and FOXP3 upregulation in humanized mice, with better activity observed for Fc.V91K relative to Fc.N88D and Fc.WT.

FIG. 9 Fc.V91K and Fc.N88D persist on the surface of activated T cells through association with CD25.

Detailed Description of Preferred Embodiments

The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described. All references cited within the body of this specification are expressly incorporated by reference in their entirety.

Standard techniques may be used for recombinant DNA, oligonucleotide synthesis, tissue culture and transformation, protein purification, etc. Enzymatic reactions and purification techniques may be performed according to the manufacturer's specifications or as commonly accomplished in the art or as described herein. The following procedures and techniques may be generally performed according to conventional methods well known in the art and as described in various general and more specific references that are cited and discussed throughout the specification. *See, e.g.,* Sambrook *et al.*, 2001, *Molecular Cloning: A Laboratory Manuel*, 3rd ed., Cold Spring Harbor Laboratory Press, cold Spring Harbor, N.Y., which is incorporated herein by reference for any purpose. Unless specific definitions are provided, the nomenclature used in connection with, and the laboratory procedures and techniques of, analytic chemistry, organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well known and commonly used in the art. Standard techniques may be used for chemical synthesis, chemical analyses, pharmaceutical preparation, formulation, and delivery and treatment of patients.

IL-2

The IL-2 muteins described herein are variants of wild-type human IL-2. As used herein, "wild-type human IL-2," "wild-type IL-2," or "WT IL-2" shall mean the polypeptide having the following amino acid sequence:

APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLR PRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFXQSIISTLT

Wherein X is C, S, V, or A (SEQ ID NO:2).

Variants may contain one or more substitutions, deletions, or insertions within the wild-type IL-2 amino acid sequence. Residues are designated herein by the one letter amino acid code followed by the IL-2 amino acid position, e.g., K35 is the lysine residue at position 35 of SEQ ID NO:2. Substitutions are designated herein by the one letter amino acid code followed by the IL-2 amino acid position followed by the substituting one letter amino acid code., e.g., K35A is a substitution of the lysine residue at position 35 of SEQ ID NO:2 with an alanine residue.

IL-2 Muteins

Provided herein are human IL-2 muteins that preferentially stimulate T regulatory (Treg) cells. As used herein "preferentially stimulates T regulatory cells" means the mutein promotes the proliferation, survival, activation and/or function of CD3+FoxP3+ T cells over CD3+FoxP3- T cells. Methods of measuring the ability to preferentially stimulate Tregs can be measured by flow cytometry of peripheral blood leukocytes, in which there is an observed increase in the percentage of FOXP3+CD4+ T cells among total CD4+ T cells, an increase in percentage of FOXP3+CD8+ T cells among total CD8+ T cells, an increase in percentage of FOXP3+ T cells relative to NK cells, and/or a greater increase in the expression level of CD25 on the surface of FOXP3+ T cells relative to the increase of CD25 expression on other T cells. Preferential growth of Treg cells can also be detected as increased representation of demethylated FOXP3 promoter DNA (i.e. the Treg-specific demethylated region, or TSDR) relative to demethylated CD3 genes in DNA extracted from whole blood, as detected by sequencing of polymerase chain reaction (PCR) products from bisulfite-treated genomic DNA (J. Sehouli, et al. 2011. Epigenetics 6:2, 236-246).

IL-2 muteins that preferentially stimulate Treg cells increase the ratio of CD3+FoxP3+ T cells over CD3+FoxP3- T cells in a subject or a peripheral blood sample at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, at least 150%, at least 200%, at least 300%, at least 400%, at least 500%, at least 600%, at least 700%, at least 800%, at least 900%, or at least 1000%.

Preferred IL-2 muteins include, but are not limited to, IL-2 muteins comprising V91K or N88D substitution in the amino acid sequence set forth in SEQ ID NO:2. An exemplary IL-2 mutein is set forth in SEQ ID NO:1. Particularly preferred is the amino acid sequence set forth in SEQ ID NO:1 comprising a C125A substitution. Although it may be advantageous to reduce the number of further mutations to the

wild-type IL-2 sequence, the invention includes IL-2 muteins having truncations or additional insertions, deletions, or substitutions in addition to the V91K or N88D substitution, provided that said muteins maintain the activity of preferentially simulating Tregs. Thus, embodiments include IL-2 muteins that preferentially stimulate Treg cells and comprise an amino acid sequence having a V91K or N88D that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence set forth in SEQ ID NO:2. In particularly preferred embodiments, such IL-2 muteins comprises an amino acid sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence set forth in SEQ ID NO:2.

For amino acid sequences, sequence identity and/or similarity is determined by using standard techniques known in the art, including, but not limited to, the local sequence identity algorithm of Smith and Waterman, 1981, *Adv. Appl. Math.* 2:482, the sequence identity alignment algorithm of Needleman and Wunsch, 1970, *J. Mol. Biol.* 48:443, the search for similarity method of Pearson and Lipman, 1988, *Proc. Nat. Acad. Sci. U.S.A.* 85:2444, computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, Wis.), the Best Fit sequence program described by Devereux *et al.*, 1984, *Nucl. Acid Res.* 12:387-395, preferably using the default settings, or by inspection. Preferably, percent identity is calculated by FastDB based upon the following parameters: mismatch penalty of 1; gap penalty of 1; gap size penalty of 0.33; and joining penalty of 30, "Current Methods in Sequence Comparison and Analysis," Macromolecule Sequencing and Synthesis, Selected Methods and Applications, pp 127-149 (1988), Alan R. Liss, Inc.

An example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. It can also plot a tree showing the clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, 1987, *J. Mol. Evol.* 35:351-360; the method is similar to that described by Higgins and Sharp, 1989, *CABIOS* 5:151-153. Useful PILEUP parameters including a default gap weight of 3.00, a default gap length weight of 0.10, and weighted end gaps.

Another example of a useful algorithm is the BLAST algorithm, described in: Altschul *et al.*, 1990, *J. Mol. Biol.* 215:403-410; Altschul *et al.*, 1997, *Nucleic Acids Res.* 25:3389-3402; and Karin *et al.*, 1993, *Proc. Natl. Acad. Sci. U.S.A.* 90:5873-5787. A particularly useful BLAST program is the WU-BLAST-2 program which was obtained from Altschul *et al.*, 1996, *Methods in Enzymology* 266:460-480. WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span=1, overlap fraction=0.125, word threshold (T)=II. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity.

An additional useful algorithm is gapped BLAST as reported by Altschul *et al.*, 1993, *Nucl. Acids Res.* 25:3389-3402. Gapped BLAST uses BLOSUM-62 substitution scores; threshold T parameter set to 9;

the two-hit method to trigger ungapped extensions, charges gap lengths of k a cost of 10+k; X_u set to 16, and X_g set to 40 for database search stage and to 67 for the output stage of the algorithms. Gapped alignments are triggered by a score corresponding to about 22 bits.

While the site or region for introducing an amino acid sequence variation may be predetermined, the mutation *per se* need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed IL-2 mutein screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants may be done using assays described herein, for example.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about one (1) to about twenty (20) amino acid residues, although considerably larger insertions may be tolerated. Deletions range from about one (1) to about twenty (20) amino acid residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative or variant. Generally these changes are done on a few amino acids to minimize the alteration of the molecule, particularly the immunogenicity and specificity of the antigen binding protein. However, larger changes may be tolerated in certain circumstances. Conservative substitutions are generally made in accordance with the following chart depicted as TABLE 1.

Table 1

Original Residue	Exemplary Substitutions
Ala	Ser
Arg	Lys
Asn	Gln, His
Asp	Glu
Cys	Ser, Ala
Gln	Asn
Glu	Asp
Gly	Pro
His	Asn, Gln
Ile	Leu, Val
Leu	Ile, Val
Lys	Arg, Gln, Glu
Met	Leu, Ile
Phe	Met, Leu, Tyr, Trp
Ser	Thr
Thr	Ser
Trp	Tyr, Phe
Tyr	Trp, Phe
Val	Ile, Leu

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those shown in TABLE 1. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, *e.g.*, seryl or threonyl, is substituted for (or by) a hydrophobic residue, *e.g.*, leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, *e.g.*, lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, *e.g.*, glutamyl or aspartyl; or (d) a residue having a bulky side chain, *e.g.*, phenylalanine, is substituted for (or by) one not having a side chain, *e.g.*, glycine.

The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analogue, although variants also are selected to modify the characteristics of the IL-2 mutein as needed. Alternatively, the variant may be designed such that the biological activity of the IL-2 mutein is altered. For example, glycosylation sites may be altered or removed as discussed herein.

IL-2 Muteins having extended serum half-life

Because the IL-2 muteins provided herein preferentially expand Tregs over, for example Teff or NK cells, it is expected that the safety profile when administered to a patient will differ from that of wild-type IL-2 or PROLEUKIN. Side-effects associated with wild-type IL-2 or PROLEUKIN include flu-like symptoms, chills/rigor, arthralgia, fever, rash, pruritus, injection site reactions, hypotension, diarrhea, nausea, anxiety, confusion, and depression. The IL-2 muteins provided herein may be altered to include or fused to molecules that extend the serum half-life of the mutein without increasing the risk that such half-life extension would increase the likelihood or the intensity of a side-effect or adverse event in a patient. Subcutaneous dosing of such an extended serum half-life mutein may allow for prolonged target coverage with lower systemic maximal exposure (C_{max}). Extended serum half-life may allow a lower or less frequent dosing regimen of the mutein.

The serum half-life of the IL-2 muteins provided herein may be extended by essentially any method known in the art. Such methods include altering the sequence of the IL-2 mutein to include a peptide that binds to the neonatal Fcγ receptor or bind to a protein having extended serum half-life, e.g., IgG or human serum albumin. In other embodiments, the IL-2 mutein is fused to a polypeptide that confers extended half-life on the fusion molecule. Such polypeptides include an IgG Fc or other polypeptides that bind to the neonatal Fcγ receptor, human serum albumin, or polypeptides that bind to a protein having extended serum half-life. In preferred embodiments, the IL-2 mutein is fused to an IgG Fc molecule.

The IL-2 mutein may be fused to the N-terminus or the C-terminus of the IgG Fc region. As shown in the Examples, fusion to the C-terminus of the IgG Fc region maintains the IL-2 mutein activity to a greater extent than when fused to the N-terminus of the IgG Fc.

One embodiment of the present invention is directed to a dimer comprising two Fc-fusion polypeptides created by fusing an IL-2 mutein to the Fc region of an antibody. The dimer can be made by, for example, inserting a gene fusion encoding the fusion protein into an appropriate expression vector, expressing the gene fusion in host cells transformed with the recombinant expression vector, and allowing the expressed fusion protein to assemble much like antibody molecules, whereupon interchain bonds form between the Fc moieties to yield the dimer.

The term "Fc polypeptide"or "Fc region" as used herein includes native and mutein forms of polypeptides derived from the Fc region of an antibody. Truncated forms of such polypeptides containing the hinge region that promotes dimerization also are included. In certain embodiments, the Fc region comprises an antibody CH2 and CH3 domain. Along with extended serum half-life, fusion proteins comprising Fc moieties (and oligomers formed therefrom) offer the advantage of facile purification by affinity chromatography over Protein A or Protein G columns. Preferred Fc regions are derived from human IgG, which includes IgG1, IgG2, IgG3, and IgG4. Herein, specific residues within the Fc are identified by position. All Fc positions are based on the EU numbering scheme.

One of the functions of the Fc portion of an antibody is to communicate to the immune system when the antibody binds its target. This is considered "effector function." Communication leads to

antibody-dependent cellular cytotoxicity (ADCC), antibody-dependent cellular phagocytosis (ADCP), and/or complement dependent cytotoxicity (CDC). ADCC and ADCP are mediated through the binding of the Fc to Fc receptors on the surface of cells of the immune system. CDC is mediated through the binding of the Fc with proteins of the complement system, e.g., C1q.

The IgG subclasses vary in their ability to mediate effector functions. For example, IgG1 is much superior to IgG2 and IgG4 at mediating ADCC and CDC. Thus, in embodiments wherein effector function is undesirable, an IgG2 Fc would be preferred. IgG2 Fc-containing molecules, however, are known to be more difficult to manufacture and have less attractive biophysical properties, such as a shorter half-life, as compared to IgG1 Fc-containing molecules.

The effector function of an antibody can be increased, or decreased, by introducing one or more mutations into the Fc. Embodiments of the invention include IL-2 mutein Fc fusion proteins having an Fc engineered to increase effector function (U.S. 7,317,091 and Strohl, *Curr. Opin. Biotech.*, 20:685-691, 2009; both incorporated herein by reference in its entirety). Exemplary IgG1 Fc molecules having increased effector function include those having the following substitutions:

S239D/I332E

S239D/A330S/I332E

S239D/A330L/I332E

S298A/D333A/K334A

P247I/A339D

P247I/A339Q

D280H/K290S

D280H/K290S/S298D

D280H/K290S/S298V

F243L/R292P/Y300L

F243L/R292P/Y300L/P396L

F243L/R292P/Y300L/V305I/P396L

G236A/S239D/I332E

K326A/E333A

K326W/E333S

K290E/S298G/T299A

K290N/S298G/T299A

K290E/S298G/T299A/K326E

K290N/S298G/T299A/K326E

Another method of increasing effector function of IgG Fc-containing proteins is by reducing the fucosylation of the Fc. Removal of the core fucose from the biantennary complex-type oligosachharides attached to the Fc greatly increased ADCC effector function without altering antigen binding or CDC effector function. Several ways are known for reducing or abolishing fucosylation of Fc-containing molecules, e.g., antibodies. These include recombinant expression in certain mammalian cell lines including a FUT8 knockout cell line, variant CHO line Lec13, rat hybridoma cell line YB2/0, a cell line comprising a small interfering RNA specifically against the FUT8 gene, and a cell line coexpressing β-1,4-*N*-acetylglucosaminyltransferase III and Golgi α-mannosidase II. Alternatively, the Fc-containing molecule may be expressed in a non-mammalian cell such as a plant cell, yeast, or prokaryotic cell, e.g., E. coli.

In preferred embodiments of the invention, IL-2 mutein Fc-fusion proteins comprise an Fc engineered to decrease effector function. Exemplary Fc molecules having decreased effector function include those having the following substitutions:

N297A or N297Q (IgG1)

L234A/L235A (IgG1)

V234A/G237A (IgG2)

L235A/G237A/E318A (IgG4)

H268Q/V309L/A330S/A331S (IgG2)

C220S/C226S/C229S/P238S (IgG1)

C226S/C229S/E233P/L234V/L235A (IgG1)

L234F/L235E/P331S (IgG1)

S267E/L328F (IgG1)

It is known that human IgG1 has a glycosylation site at N297 (EU numbering system) and glycosylation contributes to the effector function of IgG1 antibodies. An exemplary IgG1 sequence is provided in SEQ ID NO:3. Groups have mutated N297 in an effort to make aglycosylated antibodies. The mutations have focuses on substituting N297 with amino acids that resemble asparagine in physiochemical nature such as glutamine (N297Q) or with alanine (N297A) which mimics asparagines without polar groups.

As used herein, "aglycosylated antibody" or "aglycosylated fc" refers to the glycosylation status of the residue at position 297 of the Fc. An antibody or other molecule may contain glycosylation at one or more other locations but may still be considered an aglycosylated antibody or aglcosylated Fc-fusion protein.

In our effort to make an effector functionless IgG1 Fc, it was discovered that mutation of amino acid N297 of human IgG1 to glycine, i.e., N297G, provides far superior purification efficiency and biophysical properties over other amino acid substitutions at that residue. See Example 8. Thus, in preferred embodiments, the IL-2 mutein Fc-fusion protein comprises a human IgG1 Fc having a N297G substitution. The Fc comprising the N297G substitution is useful in any context wherein a molecule comprises a human IgG1 Fc, and is not limited to use in the context of an IL-2 mutein Fc-fusion. In certain embodiments, an antibody comprises the Fc having a N297G substitution.

An Fc comprising a human IgG1 Fc having the N297G mutation may also comprise further insertions, deletions, and substitutions. In certain embodiments the human IgG1 Fc comprises the N297G substitution and is at least 90% identical, at least 91% identical, at least 92% identical, at least 93% identical, at least 94% identical, at least 95% identical, at least 96% identical, at least 97% identical, at least 98% identical, or at least 99% identical to the amino acid sequence set forth in SEQ ID NO:3. In a particularly preferred embodiment, the C-terminal lysine residue is substituted or deleted. The amino acid sequence of human IgG1 comprising the N297G substitution and deletion of the C-terminal lysine is set forth in SEQ ID NO:4.

A glycosylated IgG1 Fc-containing molecules were shown to be less stable than glycosylated IgG1 Fc-containing molecules. The Fc region may be further engineered to increase the stability of the aglycosylated molecule. In some embodiments, one or more amino acids are substituted to cysteine so to form di-sulfide bonds in the dimeric state. Residues V259, A287, R292, V302, L306, V323, or I332 of the amino acid sequence set forth in SEQ ID NO:3 may be substituted with cysteine. In preferred embodiments, specific pairs of residues are substitution such that they preferentially form a di-sulfide bond with each other, thus limiting or preventing di-sulfide bond scrambling. Preferred pairs include, but are not limited to, A287C and L306C, V259C and L306C, R292C and V302C, and V323C and I332C.

Provided herein are Fc-containing molecules wherein one or more of residues V259, A287, R292, V302, L306, V323, or I332 are substituted with cysteine. Preferred Fc-containing molecules include those comprising A287C and L306C, V259C and L306C, R292C and V302C, or V323C and I332C substitutions.

Exemplary Fc-containing molecules comprise:

Human IgG1 Fc with N297G, A287C, L306C substitutions and deletion of C-terminal K

DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNCKTKPREEQY**G**ST YRVVSVCTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO:39)

Human IgG1 Fc with N297G, V259C, L306C substitutions and deletion of C-terminal K

DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPECTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGST
YRVVSVCTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV
EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO:40)

Human IgG1 Fc with N297G, R292C, V302C substitutions and deletion of C-terminal K

DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGST
YRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV
EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO:41)

Human IgG1 Fc with N297G, A287C, L306C substitutions

DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNCKTKPREEQYGST
YRVVSVCTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV
EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:42)

Human IgG1 Fc with N297G, V259C, L306C substitutions

DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPECTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGST
YRVVSVCTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV
EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:43)

Human IgG1 Fc with N297G, R292C, V302C substitutions

DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGST
YRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV
EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:44)

Additional mutations that may be made to the IgG1 Fc include those facilitate heterodimer formation amongst Fc-containing polypeptides. In some embodiments, Fc region is engineering to create "knobs" and "holes" which facilitate heterodimer formation of two different Fc-containing polypeptide chains when co-expressed in a cell. U.S. 7,695,963. In other embodiments, the Fc region is altered to use electrostatic steering to encourage heterodimer formation while discouraging homodimer formation of two different Fc-containing polypeptide when co-expressed in a cell. WO 09/089,004, which is incorporated herein by reference in its entirety. Preferred heterodimeric Fc include those wherein one chain of the Fc comprises D399K and E356K substitutions and the other chain of the Fc

comprises K409D and K392D substitutions. In other embodiments, one chain of the Fc comprises D399K, E356K, and E357K substitutions and the other chain of the Fc comprises K409D, K392D, and K370D substitutions.

In certain embodiments, it may be advantageous for the IL-2 mutein Fc-fusion protein to be monomeric, i.e., contain only a single IL-2 mutein molecule. In such embodiments, the Fc-region of the fusion protein may contain one or more mutations that facilitate heterodimer formation. The fusion protein is co-expressed with an Fc-region having reciprocal mutations to those in the IL-2 mutein Fc-fusion polypeptide but lacking an IL-2 mutein. When the heterodimer of the two Fc-containing polypeptides forms, the resulting protein comprises only a single IL-2 mutein.

Another method of creating a monomeric IL-2 mutein Fc-fusion protein is fusing the IL-2 mutein to a monomeric Fc, i.e., an Fc region that does not dimerize. Stable monomeric Fcs comprise mutations that discourage dimerization and that stabilize the molecule in the monomeric form. Preferred monomeric Fcs are disclosed in WO 2011/063348, which is incorporated herein by reference in its entirety. In certain embodiments, IL-2 mutein Fc fusion proteins comprise an Fc comprising negatively charged amino acids at positions 392 and 409 along with a threonine substitution at Y349, L351, L368, V397, L398, F405, or Y407.

In certain embodiments, the IL-2 mutein Fc-fusion protein comprises a linker between the Fc and the IL-2 mutein. Many different linker polypeptides are known in the art and may be used in the context of an IL-2 mutein Fc-fusion protein. In preferred embodiments, the IL-2 mutein Fc-fusion protein comprises one or more copies of a peptide consisting of GGGGS (SEQ ID NO:5), GGNGT (SEQ ID NO:6), or YGNGT (SEQ ID NO:7) between the Fc and the IL-2 mutein. In some embodiments, the polypeptide region between the Fc region and the IL-2 mutein region comprises a single copy of GGGGS (SEQ ID NO:5), GGNGT (SEQ ID NO:6), or YGNGT (SEQ ID NO:7). As shown herein, the linkers GGNGT (SEQ ID NO:6) or YGNGT (SEQ ID NO:7) are glycosylated when expressed in the appropriate cells and such glycosylation may help stabilize the protein in solution and/or when administered *in vivo*. Thus, in certain embodiments, an IL-2 mutein fusion protein comprises a glycosylated linker between the Fc region and the IL-2 mutein region.

It is contemplated that the glycosylated linker may be useful when placed in the context of a polypeptide. Provided herein are polypeptides comprising GGNGT (SEQ ID NO:6) or YGNGT (SEQ ID NO:7) inserted into the amino acid sequence of the polypeptide or replacing one or more amino acids within the amino acid sequence of the polypeptide. In preferred embodiments, GGNGT (SEQ ID NO:6) or YGNGT (SEQ ID NO:7) is inserted into a loop of the polypeptides tertiary structure. In other embodiments, one or more amino acids of a loop are replaced with GGNGT (SEQ ID NO:6) or YGNGT (SEQ ID NO:7).

The C-terminal portion of the Fc and/or the amino terminal portion of the IL-2 mutein may contain one or more mutations that alter the glycosylation profile f the IL-2 mutein Fc-fusion protein when expressed in mammalian cells. In certain embodiments, the IL-2 mutein further comprises a T3 substitution, e.g., T3N or T3A. The IL-2 mutein may further comprise an S5 substitution, such as S5T

Covalent modifications of IL-2 mutein and IL-2 mutein Fc-fusion proteins are included within the scope of this invention, and are generally, but not always, done post-translationally. For example, several types of covalent modifications of the IL-2 mutein or IL-2 mutein Fc-fusion protein are introduced into the molecule by reacting specific amino acid residues of the IL-2 mutein or IL-2 mutein Fc-fusion protein with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues.

Cysteinyl residues most commonly are reacted with α-haloacetates (and corresponding amines), such as chloroacetic acid or chloroacetamide, to give carboxymethyl or carboxyamidomethyl derivatives. Cysteinyl residues also are derivatized by reaction with bromotrifluoroacetone, α-bromo-β-(5-imidozoyl)propionic acid, chloroacetyl phosphate, N-alkylmaleimides, 3-nitro-2-pyridyl disulfide, methyl 2-pyridyl disulfide, p-chloromercuribenzoate, 2-chloromercuri-4-nitrophenol, or chloro-7-nitrobenzo-2-oxa-1,3-diazole.

Histidyl residues are derivatized by reaction with diethylpyrocarbonate at pH 5.5-7.0 because this agent is relatively specific for the histidyl side chain. Para-bromophenacyl bromide also is useful; the reaction is preferably performed in 0.1M sodium cacodylate at pH 6.0.

Lysinyl and amino terminal residues are reacted with succinic or other carboxylic acid anhydrides. Derivatization with these agents has the effect of reversing the charge of the lysinyl residues. Other suitable reagents for derivatizing alpha-amino-containing residues include imidoesters such as methyl picolinimidate; pyridoxal phosphate; pyridoxal; chloroborohydride; trinitrobenzenesulfonic acid; O-methylisourea; 2,4-pentanedione; and transaminase-catalyzed reaction with glyoxylate.

Arginyl residues are modified by reaction with one or several conventional reagents, among them phenylglyoxal, 2,3-butanedione, 1,2-cyclohexanedione, and ninhydrin. Derivatization of arginine residues requires that the reaction be performed in alkaline conditions because of the high pK_a of the guanidine functional group. Furthermore, these reagents may react with the groups of lysine as well as the arginine epsilon-amino group.

The specific modification of tyrosyl residues may be made, with particular interest in introducing spectral labels into tyrosyl residues by reaction with aromatic diazonium compounds or tetranitromethane. Most commonly, N-acetylimidizole and tetranitromethane are used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively. Tyrosyl residues are iodinated using ^{125}I or ^{131}I to prepare labeled proteins for use in radioimmunoassay, the chloramine T method described above being suitable.

Carboxyl side groups (aspartyl or glutamyl) are selectively modified by reaction with carbodiimides (R'—N=C=N--R'), where R and R' are optionally different alkyl groups, such as 1-cyclohexyl-3-(2-morpholinyl-4-ethyl) carbodiimide or 1-ethyl-3-(4-azonia-4,4-dimethylpentyl) carbodiimide. Furthermore, aspartyl and glutamyl residues are converted to asparaginyl and glutaminyl residues by reaction with ammonium ions.

Derivatization with bifunctional agents is useful for crosslinking antigen binding proteins to a water-insoluble support matrix or surface for use in a variety of methods. Commonly used crosslinking agents include, *e.g.*, 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), and bifunctional maleimides such as bis-N-maleimido-1,8-octane. Derivatizing agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate yield photoactivatable intermediates that are capable of forming crosslinks in the presence of light. Alternatively, reactive water-insoluble matrices such as cyanogen bromide-activated carbohydrates and the reactive substrates described in U.S. Pat. Nos. 3,969,287; 3,691,016; 4,195,128; 4,247,642; 4,229,537; and 4,330,440 are employed for protein immobilization.

Glutaminyl and asparaginyl residues are frequently deamidated to the corresponding glutamyl and aspartyl residues, respectively. Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues falls within the scope of this invention.

Other modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α-amino groups of lysine, arginine, and histidine side chains (T. E. Creighton, Proteins: Structure and Molecular Properties, W. H. Freeman & Co., San Francisco, 1983, pp. 79-86), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the IL-2 mutein or IL-2 mutein Fc-fusion protein included within the scope of this invention comprises altering the glycosylation pattern of the protein. As is known in the art, glycosylation patterns can depend on both the sequence of the protein (*e.g.*, the presence or absence of particular glycosylation amino acid residues, discussed below), or the host cell or organism in which the protein is produced. Particular expression systems are discussed below.

Glycosylation of polypeptides is typically either N-linked or O-linked. N-linked refers to the attachment of the carbohydrate moiety to the side chain of an asparagine residue. The tri-peptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tri-peptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-acetylgalactosamine, galactose, or xylose, to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

Addition of glycosylation sites to the IL-2 mutein or IL-2 mutein Fc-fusion protein may be conveniently accomplished by altering the amino acid sequence such that it contains one or more of the above-described tri-peptide sequences (for N-linked glycosylation sites). The alteration may also be made by the addition of, or substitution by, one or more serine or threonine residues to the starting sequence (for O-linked glycosylation sites). For ease, the IL-2 mutein or IL-2 mutein Fc-fusion protein amino acid sequence is preferably altered through changes at the DNA level, particularly by mutating

the DNA encoding the target polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the IL-2 mutein or IL-2 mutein Fc-fusion protein is by chemical or enzymatic coupling of glycosides to the protein. These procedures are advantageous in that they do not require production of the protein in a host cell that has glycosylation capabilities for N- and O-linked glycosylation. Depending on the coupling mode used, the sugar(s) may be attached to (a) arginine and histidine, (b) free carboxyl groups, (c) free sulfhydryl groups such as those of cysteine, (d) free hydroxyl groups such as those of serine, threonine, or hydroxyproline, (e) aromatic residues such as those of phenylalanine, tyrosine, or tryptophan, or (f) the amide group of glutamine. These methods are described in WO 87/05330 published Sep. 11, 1987, and in Aplin and Wriston, 1981, *CRC Crit. Rev. Biochem.*, pp. 259-306.

Removal of carbohydrate moieties present on the starting IL-2 mutein or IL-2 mutein Fc-fusion protein may be accomplished chemically or enzymatically. Chemical deglycosylation requires exposure of the protein to the compound trifluoromethanesulfonic acid, or an equivalent compound. This treatment results in the cleavage of most or all sugars except the linking sugar (N-acetylglucosamine or N-acetylgalactosamine), while leaving the polypeptide intact. Chemical deglycosylation is described by Hakimuddin *et al.*, 1987, *Arch. Biochem. Biophys.* 259:52 and by Edge *et al.*, 1981, *Anal. Biochem.* 118:131. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura *et al.*, 1987, *Meth. Enzymol.* 138:350. Glycosylation at potential glycosylation sites may be prevented by the use of the compound tunicamycin as described by Duskin *et al.*, 1982, *J. Biol. Chem.* 257:3105. Tunicamycin blocks the formation of protein-N-glycoside linkages.

Another type of covalent modification of the IL-2 mutein or IL-2 mutein Fc-fusion protein comprises linking the IL-2 mutein or IL-2 mutein Fc-fusion protein to various nonproteinaceous polymers, including, but not limited to, various polyols such as polyethylene glycol, polypropylene glycol or polyoxyalkylenes, in the manner set forth in U.S. Pat. Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337. In addition, amino acid substitutions may be made in various positions within the IL-2 mutein or IL-2 mutein Fc-fusion protein to facilitate the addition of polymers such as PEG. Thus, embodiments of the invention include PEGylated IL-2 muteins and IL-2 mutein Fc-fusion proteins. Such PEGylated proteins may have increase increased half-life and/or reduced immunogenicity over the non-PEGylated proteins.

Polynucleotides Encoding IL-2 Muteins and IL-2 Mutein Fc-fusion Proteins

Encompassed within the invention are nucleic acids encoding IL-2 muteins and IL-2 mutein Fc-fusion proteins. Aspects of the invention include polynucleotide variants (*e.g.*, due to degeneracy) that encode the amino acid sequences described herein. In preferred embodiments, the polypeptide encoded by the isolated nucleic acid is a component of an IL-2 mutein Fc-fusion protein.

Nucleotide sequences corresponding to the amino acid sequences described herein, to be used as probes or primers for the isolation of nucleic acids or as query sequences for database searches, can

be obtained by "back-translation" from the amino acid sequences. The well-known polymerase chain reaction (PCR) procedure can be employed to isolate and amplify a DNA sequence encoding IL-2 muteins and IL-2 mutein Fc-fusion protein. Oligonucleotides that define the desired termini of the combination of DNA fragments are employed as 5' and 3' primers. The oligonucleotides can additionally contain recognition sites for restriction endonucleases, to facilitate insertion of the amplified combination of DNA fragments into an expression vector. PCR techniques are described in Saiki et al., *Science* 239:487 (1988); *Recombinant DNA Methodology*, Wu et al., eds., Academic Press, Inc., San Diego (1989), pp. 189-196; and *PCR Protocols: A Guide to Methods and Applications*, Innis *et. al.*, eds., Academic Press, Inc. (1990).

Nucleic acid molecules of the invention include DNA and RNA in both single-stranded and double-stranded form, as well as the corresponding complementary sequences. An "isolated nucleic acid" is a nucleic acid that has been separated from adjacent genetic sequences present in the genome of the organism from which the nucleic acid was isolated, in the case of nucleic acids isolated from naturally-occurring sources. In the case of nucleic acids synthesized enzymatically from a template or chemically, such as PCR products, cDNA molecules, or oligonucleotides for example, it is understood that the nucleic acids resulting from such processes are isolated nucleic acids. An isolated nucleic acid molecule refers to a nucleic acid molecule in the form of a separate fragment or as a component of a larger nucleic acid construct. In one preferred embodiment, the nucleic acids are substantially free from contaminating endogenous material. The nucleic acid molecule has preferably been derived from DNA or RNA isolated at least once in substantially pure form and in a quantity or concentration enabling identification, manipulation, and recovery of its component nucleotide sequences by standard biochemical methods (such as those outlined in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1989)). Such sequences are preferably provided and/or constructed in the form of an open reading frame uninterrupted by internal non-translated sequences, or introns, that are typically present in eukaryotic genes. Sequences of non-translated DNA can be present 5' or 3' from an open reading frame, where the same do not interfere with manipulation or expression of the coding region.

The variants according to the invention are ordinarily prepared by site specific mutagenesis of nucleotides in the DNA encoding the IL-2 mutein or IL-2 mutein Fc-fusion protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the recombinant DNA in cell culture as outlined herein. However, IL-2 muteins and IL-2 mutein Fc-fusion may be prepared by *in vitro* synthesis using established techniques. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, *e.g.*, Treg expansion, although variants can also be selected which have modified characteristics as will be more fully outlined below.

As will be appreciated by those in the art, due to the degeneracy of the genetic code, an extremely large number of nucleic acids may be made, all of which encode IL-2 muteins and IL-2 mutein Fc-fusion proteins of the present invention. Thus, having identified a particular amino acid sequence, those skilled in the art could make any number of different nucleic acids, by simply modifying the

sequence of one or more codons in a way which does not change the amino acid sequence of the encoded protein.

The present invention also provides expression systems and constructs in the form of plasmids, expression vectors, transcription or expression cassettes which comprise at least one polynucleotide as above. In addition, the invention provides host cells comprising such expression systems or constructs.

Typically, expression vectors used in any of the host cells will contain sequences for plasmid maintenance and for cloning and expression of exogenous nucleotide sequences. Such sequences, collectively referred to as "flanking sequences" in certain embodiments will typically include one or more of the following nucleotide sequences: a promoter, one or more enhancer sequences, an origin of replication, a transcriptional termination sequence, a complete intron sequence containing a donor and acceptor splice site, a sequence encoding a leader sequence for polypeptide secretion, a ribosome binding site, a polyadenylation sequence, a polylinker region for inserting the nucleic acid encoding the polypeptide to be expressed, and a selectable marker element. Each of these sequences is discussed below.

Optionally, the vector may contain a "tag"-encoding sequence, *i.e.*, an oligonucleotide molecule located at the 5' or 3' end of the IL-2 muteins or IL-2 mutein Fc-fusion protein coding sequence; the oligonucleotide sequence encodes polyHis (such as hexaHis (SEQ ID NO:21)), or another "tag" such as FLAG, HA (hemaglutinin influenza virus), or *myc*, for which commercially available antibodies exist. This tag is typically fused to the polypeptide upon expression of the polypeptide, and can serve as a means for affinity purification or detection of the IL-2 mutein from the host cell. Affinity purification can be accomplished, for example, by column chromatography using antibodies against the tag as an affinity matrix. Optionally, the tag can subsequently be removed from the purified IL-2 muteins and IL-2 mutein Fc-fusion proteins by various means such as using certain peptidases for cleavage.

Flanking sequences may be homologous (*i.e.*, from the same species and/or strain as the host cell), heterologous (*i.e.*, from a species other than the host cell species or strain), hybrid (*i.e.*, a combination of flanking sequences from more than one source), synthetic or native. As such, the source of a flanking sequence may be any prokaryotic or eukaryotic organism, any vertebrate or invertebrate organism, or any plant, provided that the flanking sequence is functional in, and can be activated by, the host cell machinery.

Flanking sequences useful in the vectors of this invention may be obtained by any of several methods well known in the art. Typically, flanking sequences useful herein will have been previously identified by mapping and/or by restriction endonuclease digestion and can thus be isolated from the proper tissue source using the appropriate restriction endonucleases. In some cases, the full nucleotide sequence of a flanking sequence may be known. Here, the flanking sequence may be synthesized using the methods described herein for nucleic acid synthesis or cloning.

Whether all or only a portion of the flanking sequence is known, it may be obtained using polymerase chain reaction (PCR) and/or by screening a genomic library with a suitable probe such as an oligonucleotide and/or flanking sequence fragment from the same or another species. Where the

flanking sequence is not known, a fragment of DNA containing a flanking sequence may be isolated from a larger piece of DNA that may contain, for example, a coding sequence or even another gene or genes. Isolation may be accomplished by restriction endonuclease digestion to produce the proper DNA fragment followed by isolation using agarose gel purification, Qiagen® column chromatography (Chatsworth, CA), or other methods known to the skilled artisan. The selection of suitable enzymes to accomplish this purpose will be readily apparent to one of ordinary skill in the art.

An origin of replication is typically a part of those prokaryotic expression vectors purchased commercially, and the origin aids in the amplification of the vector in a host cell. If the vector of choice does not contain an origin of replication site, one may be chemically synthesized based on a known sequence, and ligated into the vector. For example, the origin of replication from the plasmid pBR322 (New England Biolabs, Beverly, MA) is suitable for most gram-negative bacteria, and various viral origins (*e.g.*, SV40, polyoma, adenovirus, vesicular stomatitus virus (VSV), or papillomaviruses such as HPV or BPV) are useful for cloning vectors in mammalian cells. Generally, the origin of replication component is not needed for mammalian expression vectors (for example, the SV40 origin is often used only because it also contains the virus early promoter).

A transcription termination sequence is typically located 3' to the end of a polypeptide coding region and serves to terminate transcription. Usually, a transcription termination sequence in prokaryotic cells is a G-C rich fragment followed by a poly-T sequence. While the sequence is easily cloned from a library or even purchased commercially as part of a vector, it can also be readily synthesized using methods for nucleic acid synthesis such as those described herein.

A selectable marker gene encodes a protein necessary for the survival and growth of a host cell grown in a selective culture medium. Typical selection marker genes encode proteins that (a) confer resistance to antibiotics or other toxins, *e.g.*, ampicillin, tetracycline, or kanamycin for prokaryotic host cells; (b) complement auxotrophic deficiencies of the cell; or (c) supply critical nutrients not available from complex or defined media. Specific selectable markers are the kanamycin resistance gene, the ampicillin resistance gene, and the tetracycline resistance gene. Advantageously, a neomycin resistance gene may also be used for selection in both prokaryotic and eukaryotic host cells.

Other selectable genes may be used to amplify the gene that will be expressed. Amplification is the process wherein genes that are required for production of a protein critical for growth or cell survival are reiterated in tandem within the chromosomes of successive generations of recombinant cells. Examples of suitable selectable markers for mammalian cells include dihydrofolate reductase (DHFR) and promoterless thyrnidine kinase genes. Mammalian cell transformants are placed under selection pressure wherein only the transformants are uniquely adapted to survive by virtue of the selectable gene present in the vector. Selection pressure is imposed by culturing the transformed cells under conditions in which the concentration of selection agent in the medium is successively increased, thereby leading to the amplification of both the selectable gene and the DNA that encodes another gene, such as an IL-2 mutein or IL-2 mutein Fc-fusion protein. As a result, increased quantities of a polypeptide such as an IL-2 mutein or IL-2 mutein Fc-fusion protein are synthesized from the amplified DNA.

A ribosome-binding site is usually necessary for translation initiation of mRNA and is characterized by a Shine-Dalgarno sequence (prokaryotes) or a Kozak sequence (eukaryotes). The element is typically located 3' to the promoter and 5' to the coding sequence of the polypeptide to be expressed. In certain embodiments, one or more coding regions may be operably linked to an internal ribosome binding site (IRES), allowing translation of two open reading frames from a single RNA transcript.

In some cases, such as where glycosylation is desired in a eukaryotic host cell expression system, one may manipulate the various pre- or prosequences to improve glycosylation or yield. For example, one may alter the peptidase cleavage site of a particular signal peptide, or add prosequences, which also may affect glycosylation. The final protein product may have, in the -1 position (relative to the first amino acid of the mature protein) one or more additional amino acids incident to expression, which may not have been totally removed. For example, the final protein product may have one or two amino acid residues found in the peptidase cleavage site, attached to the amino-terminus. Alternatively, use of some enzyme cleavage sites may result in a slightly truncated form of the desired polypeptide, if the enzyme cuts at such area within the mature polypeptide.

Expression and cloning vectors of the invention will typically contain a promoter that is recognized by the host organism and operably linked to the molecule encoding the IL-2 mutein or IL-2 mutein Fc-fusion protein. Promoters are untranscribed sequences located upstream (*i.e.*, 5') to the start codon of a structural gene (generally within about 100 to 1000 bp) that control transcription of the structural gene. Promoters are conventionally grouped into one of two classes: inducible promoters and constitutive promoters. Inducible promoters initiate increased levels of transcription from DNA under their control in response to some change in culture conditions, such as the presence or absence of a nutrient or a change in temperature. Constitutive promoters, on the other hand, uniformly transcribe gene to which they are operably linked, that is, with little or no control over gene expression. A large number of promoters, recognized by a variety of potential host cells, are well known.

Suitable promoters for use with yeast hosts are also well known in the art. Yeast enhancers are advantageously used with yeast promoters. Suitable promoters for use with mammalian host cells are well known and include, but are not limited to, those obtained from the genomes of viruses such as polyoma virus, fowlpox virus, adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, retroviruses, hepatitis-B virus and most preferably Simian Virus 40 (SV40). Other suitable mammalian promoters include heterologous mammalian promoters, for example, heat-shock promoters and the actin promoter.

Additional promoters which may be of interest include, but are not limited to: SV40 early promoter (Benoist and Chambon, 1981, *Nature* 290:304-310); CMV promoter (Thornsen *et al.*, 1984, *Proc. Natl. Acad. U.S.A.* 81:659-663); the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto *et al.*, 1980, *Cell* 22:787-797); herpes thymidine kinase promoter (Wagner *et al.*, 1981, *Proc. Natl. Acad. Sci. U.S.A.* 78:1444-1445); promoter and regulatory sequences from the metallothionine gene Prinster *et al.*, 1982, *Nature* 296:39-42); and prokaryotic promoters such as the beta-lactamase promoter (Villa-Kamaroff *et al.*, 1978, *Proc. Natl. Acad. Sci. U.S.A.* 75:3727-3731); or the

tac promoter (DeBoer *et al.*, 1983, *Proc. Natl. Acad. Sci. U.S.A.* 80:21-25). Also of interest are the following animal transcriptional control regions, which exhibit tissue specificity and have been utilized in transgenic animals: the elastase I gene control region that is active in pancreatic acinar cells (Swift *et al.*, 1984, *Cell* 38:639-646; Ornitz *et al.*, 1986, *Cold Spring Harbor Symp. Quant. Biol.* 50:399-409; MacDonald, 1987, *Hepatology* 7:425-515); the insulin gene control region that is active in pancreatic beta cells (Hanahan, 1985, *Nature* 315:115-122); the immunoglobulin gene control region that is active in lymphoid cells (Grosschedl *et al.*, 1984, *Cell* 38:647-658; Adames *et al.*, 1985, *Nature* 318:533-538; Alexander *et al.*, 1987, *Mol. Cell. Biol.* 7:1436-1444); the mouse mammary tumor virus control region that is active in testicular, breast, lymphoid and mast cells (Leder *et al.*, 1986, *Cell* 45:485-495); the albumin gene control region that is active in liver (Pinkert *et al.*, 1987, *Genes and Devel.* 1 :268-276); the alpha-feto-protein gene control region that is active in liver (Krumlauf *et al.*, 1985, *Mol. Cell. Biol.* 5:1639-1648; Hammer *et al.*, 1987, *Science* 253:53-58); the alpha 1-antitrypsin gene control region that is active in liver (Kelsey *et al.*, 1987, *Genes and Devel.* 1:161-171); the beta-globin gene control region that is active in myeloid cells (Mogram *et al.*, 1985, *Nature* 315:338-340; Kollias *et al.*, 1986, *Cell* 46:89-94); the myelin basic protein gene control region that is active in oligodendrocyte cells in the brain (Readhead *et al.*, 1987, *Cell* 48:703-712); the myosin light chain-2 gene control region that is active in skeletal muscle (Sani, 1985, *Nature* 314:283-286); and the gonadotropic releasing hormone gene control region that is active in the hypothalamus (Mason *et al.*, 1986, *Science* 234:1372-1378).

An enhancer sequence may be inserted into the vector to increase transcription by higher eukaryotes. Enhancers are cis-acting elements of DNA, usually about 10-300 bp in length, that act on the promoter to increase transcription. Enhancers are relatively orientation and position independent, having been found at positions both 5' and 3' to the transcription unit. Several enhancer sequences available from mammalian genes are known (*e.g.*, globin, elastase, albumin, alpha-feto-protein and insulin). Typically, however, an enhancer from a virus is used. The SV40 enhancer, the cytomegalovirus early promoter enhancer, the polyoma enhancer, and adenovirus enhancers known in the art are exemplary enhancing elements for the activation of eukaryotic promoters. While an enhancer may be positioned in the vector either 5' or 3' to a coding sequence, it is typically located at a site 5' from the promoter. A sequence encoding an appropriate native or heterologous signal sequence (leader sequence or signal peptide) can be incorporated into an expression vector, to promote extracellular secretion of the IL-2 mutein or IL-2 mutein Fc-fusion protein. The choice of signal peptide or leader depends on the type of host cells in which the protein is to be produced, and a heterologous signal sequence can replace the native signal sequence. Examples of signal peptides that are functional in mammalian host cells include the following: the signal sequence for interleukin-7 (IL-7) described in US Patent No. 4,965,195; the signal sequence for interleukin-2 receptor described in Cosman *et al.*,1984, *Nature* 312:768; the interleukin-4 receptor signal peptide described in EP Patent No. 0367 566; the type I interleukin-1 receptor signal peptide described in U.S. Patent No. 4,968,607; the type II interleukin-1 receptor signal peptide described in EP Patent No. 0 460 846.

The vector may contain one or more elements that facilitate expression when the vector is integrated into the host cell genome. Examples include an EASE element (Aldrich et al. 2003 *Biotechnol Prog.* 19:1433-38) and a matrix attachment region (MAR). MARs mediate structural organization of the

chromatin and may insulate the integrated vector from "position" effect. Thus, MARs are particularly useful when the vector is used to create stable transfectants. A number of natural and synthetic MAR-containing nucleic acids are known in the art, *e.g.*, U.S. Pat. Nos. 6,239,328; 7,326,567; 6,177,612; 6,388,066; 6,245,974; 7,259,010; 6,037,525; 7,422,874; 7,129,062.

Expression vectors of the invention may be constructed from a starting vector such as a commercially available vector. Such vectors may or may not contain all of the desired flanking sequences. Where one or more of the flanking sequences described herein are not already present in the vector, they may be individually obtained and ligated into the vector. Methods used for obtaining each of the flanking sequences are well known to one skilled in the art.

After the vector has been constructed and a nucleic acid molecule encoding an IL-2 mutein or IL-2 mutein Fc-fusion protein has been inserted into the proper site of the vector, the completed vector may be inserted into a suitable host cell for amplification and/or polypeptide expression. The transformation of an expression vector into a selected host cell may be accomplished by well known methods including transfection, infection, calcium phosphate co-precipitation, electroporation, microinjection, lipofection, DEAE-dextran mediated transfection, or other known techniques. The method selected will in part be a function of the type of host cell to be used. These methods and other suitable methods are well known to the skilled artisan, and are set forth, for example, in Sambrook *et al.*, 2001, *supra*.

A host cell, when cultured under appropriate conditions, synthesizes an IL-2 mutein or IL-2 mutein Fc-fusion protein that can subsequently be collected from the culture medium (if the host cell secretes it into the medium) or directly from the host cell producing it (if it is not secreted). The selection of an appropriate host cell will depend upon various factors, such as desired expression levels, polypeptide modifications that are desirable or necessary for activity (such as glycosylation or phosphorylation) and ease of folding into a biologically active molecule. A host cell may be eukaryotic or prokaryotic.

Mammalian cell lines available as hosts for expression are well known in the art and include, but are not limited to, immortalized cell lines available from the American Type Culture Collection (ATCC) and any cell lines used in an expression system known in the art can be used to make the recombinant polypeptides of the invention. In general, host cells are transformed with a recombinant expression vector that comprises DNA encoding a desired IL-2 mutein or IL-2 mutein Fc-fusion. Among the host cells that may be employed are prokaryotes, yeast or higher eukaryotic cells. Prokaryotes include gram negative or gram positive organisms, for example *E. coli* or bacilli. Higher eukaryotic cells include insect cells and established cell lines of mammalian origin. Examples of suitable mammalian host cell lines include the COS-7 line of monkey kidney cells (ATCC CRL 1651) (Gluzman *et al.*, 1981, Cell 23:175), L cells, 293 cells, C127 cells, 3T3 cells (ATCC CCL 163), Chinese hamster ovary (CHO) cells, or their derivatives such as Veggie CHO and related cell lines which grow in serum-free media (Rasmussen *et al.*, 1998, *Cytotechnology* 28: 31), HeLa cells, BHK (ATCC CRL 10) cell lines, and the CVI/EBNA cell line derived from the African green monkey kidney cell line CVI (ATCC CCL 70) as described by McMahan *et al.*, 1991, EMBO J. 10: 2821, human embryonic kidney cells such as 293, 293 EBNA or MSR 293, human

epidermal A431 cells, human Colo205 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HL-60, U937, HaK or Jurkat cells. Optionally, mammalian cell lines such as HepG2/3B, KB, NIH 3T3 or S49, for example, can be used for expression of the polypeptide when it is desirable to use the polypeptide in various signal transduction or reporter assays.

Alternatively, it is possible to produce the polypeptide in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Suitable yeasts include Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces strains, Candida, or any yeast strain capable of expressing heterologous polypeptides. Suitable bacterial strains include Escherichia coli, Bacillus subtilis, Salmonella typhimurium, or any bacterial strain capable of expressing heterologous polypeptides. If the polypeptide is made in yeast or bacteria, it may be desirable to modify the polypeptide produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional polypeptide. Such covalent attachments can be accomplished using known chemical or enzymatic methods.

The polypeptide can also be produced by operably linking the isolated nucleic acid of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, Calif., U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), and Luckow and Summers, *Bio/Technology* 6:47 (1988). Cell-free translation systems could also be employed to produce polypeptides using RNAs derived from nucleic acid constructs disclosed herein. Appropriate cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts are described by Pouwels *et al.* (*Cloning Vectors: A Laboratory Manual*, Elsevier, New York, 1985). A host cell that comprises an isolated nucleic acid of the invention, preferably operably linked to at least one expression control sequence, is a "recombinant host cell".

In certain aspects, the invention includes an isolated nucleic acidic acid encoding a human IL-2 mutein that preferentially stimulates T regulatory cells and comprises a V91K substitution and an amino acid sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence set forth in SEQ ID NO:1. The isolated nucleic acid may encode any of the exemplary IL-2 muteins provided herein.

Also included are isolated nucleic acids encoding any of the exemplary IL-2 mutein Fc-fusion proteins described herein. In preferred embodiments, the Fc portion of an antibody and the human IL-2 mutein are encoded within a single open-reading frame, optionally with a linker encoded between the Fc region and the IL-2 mutein.

In another aspect, provided herein are expression vectors comprising the above IL-2 mutein- or IL-2 mutein Fc-fusion protein-encoding nucleic acids operably linked to a promoter.

In another aspect, provided herein are host cells comprising the isolated nucleic acids encoding the above IL-2 muteins or IL-2 mutein Fc-fusion proteins. The host cell may be a prokaryotic cell, such as *E. coli*, or may be a eukaryotic cell, such as a mammalian cell. In certain embodiments, the host cell is a Chinese hamster ovary (CHO) cell line.

In another aspect, provided herein are methods of making a human IL-2 mutein. The methods comprising culturing a host cell under conditions in which a promoter operably linked to a human IL-2 mutein is expressed. Subsequently, the human IL-2 mutein is harvested from said culture. The IL-2 mutein may be harvested from the culture media and/or host cell lysates.

In another aspect, provided herein are methods of making a human IL-2 mutein Fc-fusion protein. The methods comprising culturing a host cell under conditions in which a promoter operably linked to a human IL-2 mutein Fc-fusion protein is expressed. Subsequently, the human IL-2 mutein Fc-fusion protein is harvested from said culture. The human IL-2 mutein Fc-fusion protein may be harvested from the culture media and/or host cell lysates.

Pharmaceutical Compositions

In some embodiments, the invention provides a pharmaceutical composition comprising a therapeutically effective amount of an IL-2 mutein together with a pharmaceutically effective diluents, carrier, solubilizer, emulsifier, preservative, and/or adjuvant. In certain embodiments, the IL-2 mutein is within the context of an IL-2 mutein Fc-fusion protein. Pharmaceutical compositions of the invention include, but are not limited to, liquid, frozen, and lyophilized compositions.

Preferably, formulation materials are nontoxic to recipients at the dosages and concentrations employed. In specific embodiments, pharmaceutical compositions comprising a therapeutically effective amount of an IL-2 mutein containing therapeutic molecule, e.g, an IL-2 mutein Fc-fusion, are provided.

In certain embodiments, the pharmaceutical composition may contain formulation materials for modifying, maintaining or preserving, for example, the pH, osmolarity, viscosity, clarity, color, isotonicity, odor, sterility, stability, rate of dissolution or release, adsorption or penetration of the composition. In such embodiments, suitable formulation materials include, but are not limited to, amino acids (such as glycine, glutamine, asparagine, arginine, proline, or lysine); antimicrobials; antioxidants (such as ascorbic acid, sodium sulfite or sodium hydrogen-sulfite); buffers (such as borate, bicarbonate, Tris-HCl, citrates, phosphates or other organic acids); bulking agents (such as mannitol or glycine); chelating agents (such as ethylenediamine tetraacetic acid (EDTA)); complexing agents (such as caffeine, polyvinylpyrrolidone, beta-cyclodextrin or hydroxypropyl-beta-cyclodextrin); fillers; monosaccharides; disaccharides; and other carbohydrates (such as glucose, mannose or dextrins); proteins (such as serum albumin, gelatin or immunoglobulins); coloring, flavoring and diluting agents; emulsifying agents; hydrophilic polymers (such as polyvinylpyrrolidone); low molecular weight polypeptides; salt-forming counterions (such as sodium); preservatives (such as benzalkonium chloride, benzoic acid, salicylic acid, thimerosal, phenethyl alcohol, methylparaben, propylparaben, chlorhexidine, sorbic acid or hydrogen peroxide); solvents (such as glycerin, propylene glycol or polyethylene glycol);

sugar alcohols (such as mannitol or sorbitol); suspending agents; surfactants or wetting agents (such as pluronics, PEG, sorbitan esters, polysorbates such as polysorbate 20, polysorbate, triton, tromethamine, lecithin, cholesterol, tyloxapal); stability enhancing agents (such as sucrose or sorbitol); tonicity enhancing agents (such as alkali metal halides, preferably sodium or potassium chloride, mannitol sorbitol); delivery vehicles; diluents; excipients and/or pharmaceutical adjuvants. See, REMINGTON'S PHARMACEUTICAL SCIENCES, 18" Edition, (A. R. Genrmo, ed.), 1990, Mack Publishing Company.

In certain embodiments, the optimal pharmaceutical composition will be determined by one skilled in the art depending upon, for example, the intended route of administration, delivery format and desired dosage. See, for example, REMINGTON'S PHARMACEUTICAL SCIENCES, supra. In certain embodiments, such compositions may influence the physical state, stability, rate of *in vivo* release and rate of *in vivo* clearance of the antigen binding proteins of the invention. In certain embodiments, the primary vehicle or carrier in a pharmaceutical composition may be either aqueous or non-aqueous in nature. For example, a suitable vehicle or carrier may be water for injection, physiological saline solution or artificial cerebrospinal fluid, possibly supplemented with other materials common in compositions for parenteral administration. Neutral buffered saline or saline mixed with serum albumin are further exemplary vehicles. In specific embodiments, pharmaceutical compositions comprise Tris buffer of about pH 7.0-8.5, or acetate buffer of about pH 4.0-5.5, and may further include sorbitol or a suitable substitute therefor. In certain embodiments of the invention, Il-2 mutein compositions may be prepared for storage by mixing the selected composition having the desired degree of purity with optional formulation agents (REMINGTON'S PHARMACEUTICAL SCIENCES, supra) in the form of a lyophilized cake or an aqueous solution. Further, in certain embodiments, the IL-2 mutein product may be formulated as a lyophilizate using appropriate excipients such as sucrose.

The pharmaceutical compositions of the invention can be selected for parenteral delivery. Alternatively, the compositions may be selected for inhalation or for delivery through the digestive tract, such as orally. Preparation of such pharmaceutically acceptable compositions is within the skill of the art. The formulation components are present preferably in concentrations that are acceptable to the site of administration. In certain embodiments, buffers are used to maintain the composition at physiological pH or at a slightly lower pH, typically within a pH range of from about 5 to about 8.

When parenteral administration is contemplated, the therapeutic compositions for use in this invention may be provided in the form of a pyrogen-free, parenterally acceptable aqueous solution comprising the desired IL-2 mutein composition in a pharmaceutically acceptable vehicle. A particularly suitable vehicle for parenteral injection is sterile distilled water in which the IL-2 mutein composition is formulated as a sterile, isotonic solution, properly preserved. In certain embodiments, the preparation can involve the formulation of the desired molecule with an agent, such as injectable microspheres, bio-erodible particles, polymeric compounds (such as polylactic acid or polyglycolic acid), beads or liposomes, that may provide controlled or sustained release of the product which can be delivered via depot injection. In certain embodiments, hyaluronic acid may also be used, having the effect of promoting sustained duration in the circulation. In certain embodiments, implantable drug delivery devices may be used to introduce the IL-2 mutein composition.

Additional pharmaceutical compositions will be evident to those skilled in the art, including formulations involving IL-2 mutein compositions in sustained- or controlled-delivery formulations. Techniques for formulating a variety of other sustained- or controlled-delivery means, such as liposome carriers, bio-erodible microparticles or porous beads and depot injections, are also known to those skilled in the art. See, for example, International Patent Application No. PCT/US93/00829, which is incorporated by reference and describes controlled release of porous polymeric microparticles for delivery of pharmaceutical compositions. Sustained-release preparations may include semipermeable polymer matrices in the form of shaped articles, e.g., films, or microcapsules. Sustained release matrices may include polyesters, hydrogels, polylactides (as disclosed in U.S. Pat. No. 3,773,919 and European Patent Application Publication No. EP 058481, each of which is incorporated by reference), copolymers of L-glutamic acid and gamma ethyl-L-glutamate (Sidman et al., 1983, Biopolymers 2:547-556), poly (2-hydroxyethyl-methacrylate) (Langer et al., 1981, J. Biomed. Mater. Res. 15:167-277 and Langer, 1982, Chem. Tech. 12:98-105), ethylene vinyl acetate (Langer et al., 1981, supra) or poly-D(-)-3-hydroxybutyric acid (European Patent Application Publication No. EP 133,988). Sustained release compositions may also include liposomes that can be prepared by any of several methods known in the art. See, e.g., Eppstein et al., 1985, Proc. Natl. Acad. Sci. U.S.A. 82:3688-3692; European Patent Application Publication Nos. EP 036,676; EP 088,046 and EP 143,949, incorporated by reference.

Pharmaceutical compositions used for *in vivo* administration are typically provided as sterile preparations. Sterilization can be accomplished by filtration through sterile filtration membranes. When the composition is lyophilized, sterilization using this method may be conducted either prior to or following lyophilization and reconstitution. Compositions for parenteral administration can be stored in lyophilized form or in a solution. Parenteral compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Aspects of the invention includes self-buffering IL-2 mutein formulations, which can be used as pharmaceutical compositions, as described in international patent application WO 06138181A2 (PCT/US2006/022599), which is incorporated by reference in its entirety herein.

As discussed above, certain embodiments provide IL-2 mutein compositions, particularly pharmaceutical Il-2 mutein Fc-fusion proteins, that comprise, in addition to the IL-2 mutein composition, one or more excipients such as those illustratively described in this section and elsewhere herein. Excipients can be used in the invention in this regard for a wide variety of purposes, such as adjusting physical, chemical, or biological properties of formulations, such as adjustment of viscosity, and or processes of the invention to improve effectiveness and or to stabilize such formulations and processes against degradation and spoilage due to, for instance, stresses that occur during manufacturing, shipping, storage, pre-use preparation, administration, and thereafter.

A variety of expositions are available on protein stabilization and formulation materials and methods useful in this regard, such as Arakawa et al., "Solvent interactions in pharmaceutical formulations," Pharm Res. 8(3): 285-91 (1991); Kendrick et al., "Physical stabilization of proteins in aqueous solution," in: RATIONAL DESIGN OF STABLE PROTEIN FORMULATIONS: THEORY AND PRACTICE,

Carpenter and Manning, eds. Pharmaceutical Biotechnology. 13: 61-84 (2002), and Randolph et al., "Surfactant-protein interactions," Pharm Biotechnol. 13: 159-75 (2002), each of which is herein incorporated by reference in its entirety, particularly in parts pertinent to excipients and processes of the same for self-buffering protein formulations in accordance with the current invention, especially as to protein pharmaceutical products and processes for veterinary and/or human medical uses.

Salts may be used in accordance with certain embodiments of the invention to, for example, adjust the ionic strength and/or the isotonicity of a formulation and/or to improve the solubility and/or physical stability of a protein or other ingredient of a composition in accordance with the invention.

As is well known, ions can stabilize the native state of proteins by binding to charged residues on the protein's surface and by shielding charged and polar groups in the protein and reducing the strength of their electrostatic interactions, attractive, and repulsive interactions. Ions also can stabilize the denatured state of a protein by binding to, in particular, the denatured peptide linkages (--CONH) of the protein. Furthermore, ionic interaction with charged and polar groups in a protein also can reduce intermolecular electrostatic interactions and, thereby, prevent or reduce protein aggregation and insolubility.

Ionic species differ significantly in their effects on proteins. A number of categorical rankings of ions and their effects on proteins have been developed that can be used in formulating pharmaceutical compositions in accordance with the invention. One example is the Hofmeister series, which ranks ionic and polar non-ionic solutes by their effect on the conformational stability of proteins in solution. Stabilizing solutes are referred to as "kosmotropic." Destabilizing solutes are referred to as "chaotropic." Kosmotropes commonly are used at high concentrations (e.g., >1 molar ammonium sulfate) to precipitate proteins from solution ("salting-out"). Chaotropes commonly are used to denture and/or to solubilize proteins ("salting-in"). The relative effectiveness of ions to "salt-in" and "salt-out" defines their position in the Hofmeister series.

Free amino acids can be used in IL-2 mutein formulations in accordance with various embodiments of the invention as bulking agents, stabilizers, and antioxidants, as well as other standard uses. Lysine, proline, serine, and alanine can be used for stabilizing proteins in a formulation. Glycine is useful in lyophilization to ensure correct cake structure and properties. Arginine may be useful to inhibit protein aggregation, in both liquid and lyophilized formulations. Methionine is useful as an antioxidant.

Polyols include sugars, e.g., mannitol, sucrose, and sorbitol and polyhydric alcohols such as, for instance, glycerol and propylene glycol, and, for purposes of discussion herein, polyethylene glycol (PEG) and related substances. Polyols are kosmotropic. They are useful stabilizing agents in both liquid and lyophilized formulations to protect proteins from physical and chemical degradation processes. Polyols also are useful for adjusting the tonicity of formulations.

Among polyols useful in select embodiments of the invention is mannitol, commonly used to ensure structural stability of the cake in lyophilized formulations. It ensures structural stability to the cake. It is generally used with a lyoprotectant, e.g., sucrose. Sorbitol and sucrose are among preferred agents for adjusting tonicity and as stabilizers to protect against freeze-thaw stresses during transport or

the preparation of bulks during the manufacturing process. Reducing sugars (which contain free aldehyde or ketone groups), such as glucose and lactose, can glycate surface lysine and arginine residues. Therefore, they generally are not among preferred polyols for use in accordance with the invention. In addition, sugars that form such reactive species, such as sucrose, which is hydrolyzed to fructose and glucose under acidic conditions, and consequently engenders glycation, also is not among preferred polyols of the invention in this regard. PEG is useful to stabilize proteins and as a cryoprotectant and can be used in the invention in this regard.

Embodiments of IL-2 mutein formulations further comprise surfactants. Protein molecules may be susceptible to adsorption on surfaces and to denaturation and consequent aggregation at air-liquid, solid-liquid, and liquid-liquid interfaces. These effects generally scale inversely with protein concentration. These deleterious interactions generally scale inversely with protein concentration and typically are exacerbated by physical agitation, such as that generated during the shipping and handling of a product.

Surfactants routinely are used to prevent, minimize, or reduce surface adsorption. Useful surfactants in the invention in this regard include polysorbate 20, polysorbate 80, other fatty acid esters of sorbitan polyethoxylates, and poloxamer 188.

Surfactants also are commonly used to control protein conformational stability. The use of surfactants in this regard is protein-specific since, any given surfactant typically will stabilize some proteins and destabilize others.

Polysorbates are susceptible to oxidative degradation and often, as supplied, contain sufficient quantities of peroxides to cause oxidation of protein residue side-chains, especially methionine. Consequently, polysorbates should be used carefully, and when used, should be employed at their lowest effective concentration. In this regard, polysorbates exemplify the general rule that excipients should be used in their lowest effective concentrations.

Embodiments of IL-2 mutein formulations further comprise one or more antioxidants. To some extent deleterious oxidation of proteins can be prevented in pharmaceutical formulations by maintaining proper levels of ambient oxygen and temperature and by avoiding exposure to light. Antioxidant excipients can be used as well to prevent oxidative degradation of proteins. Among useful antioxidants in this regard are reducing agents, oxygen/free-radical scavengers, and chelating agents. Antioxidants for use in therapeutic protein formulations in accordance with the invention preferably are water-soluble and maintain their activity throughout the shelf life of a product. EDTA is a preferred antioxidant in accordance with the invention in this regard.

Antioxidants can damage proteins. For instance, reducing agents, such as glutathione in particular, can disrupt intramolecular disulfide linkages. Thus, antioxidants for use in the invention are selected to, among other things, eliminate or sufficiently reduce the possibility of themselves damaging proteins in the formulation.

Formulations in accordance with the invention may include metal ions that are protein co-factors and that are necessary to form protein coordination complexes, such as zinc necessary to form certain insulin suspensions. Metal ions also can inhibit some processes that degrade proteins. However, metal ions also catalyze physical and chemical processes that degrade proteins.

Magnesium ions (10-120 mM) can be used to inhibit isomerization of aspartic acid to isoaspartic acid. Ca^{+2} ions (up to 100 mM) can increase the stability of human deoxyribonuclease. Mg^{+2}, Mn^{+2}, and Zn^{+2}, however, can destabilize rhDNase. Similarly, Ca^{+2} and Sr^{+2} can stabilize Factor VIII, it can be destabilized by Mg^{+2}, Mn^{+2} and Zn^{+2}, Cu^{+2} and Fe^{+2}, and its aggregation can be increased by Al^{+3} ions.

Embodiments of IL-2 mutein formulations further comprise one or more preservatives. Preservatives are necessary when developing multi-dose parenteral formulations that involve more than one extraction from the same container. Their primary function is to inhibit microbial growth and ensure product sterility throughout the shelf-life or term of use of the drug product. Commonly used preservatives include benzyl alcohol, phenol and m-cresol. Although preservatives have a long history of use with small-molecule parenterals, the development of protein formulations that includes preservatives can be challenging. Preservatives almost always have a destabilizing effect (aggregation) on proteins, and this has become a major factor in limiting their use in multi-dose protein formulations. To date, most protein drugs have been formulated for single-use only. However, when multi-dose formulations are possible, they have the added advantage of enabling patient convenience, and increased marketability. A good example is that of human growth hormone (hGH) where the development of preserved formulations has led to commercialization of more convenient, multi-use injection pen presentations. At least four such pen devices containing preserved formulations of hGH are currently available on the market. Norditropin (liquid, Novo Nordisk), Nutropin AQ (liquid, Genentech) & Genotropin (lyophilized--dual chamber cartridge, Pharmacia & Upjohn) contain phenol while Somatrope (Eli Lilly) is formulated with m-cresol.

Several aspects need to be considered during the formulation and development of preserved dosage forms. The effective preservative concentration in the drug product must be optimized. This requires testing a given preservative in the dosage form with concentration ranges that confer anti-microbial effectiveness without compromising protein stability.

As might be expected, development of liquid formulations containing preservatives are more challenging than lyophilized formulations. Freeze-dried products can be lyophilized without the preservative and reconstituted with a preservative containing diluent at the time of use. This shortens the time for which a preservative is in contact with the protein, significantly minimizing the associated stability risks. With liquid formulations, preservative effectiveness and stability should be maintained over the entire product shelf-life (about 18 to 24 months). An important point to note is that preservative effectiveness should be demonstrated in the final formulation containing the active drug and all excipient components.

IL-2 mutein formulations generally will be designed for specific routes and methods of administration, for specific administration dosages and frequencies of administration, for specific

treatments of specific diseases, with ranges of bio-availability and persistence, among other things. Formulations thus may be designed in accordance with the invention for delivery by any suitable route, including but not limited to orally, aurally, opthalmically, rectally, and vaginally, and by parenteral routes, including intravenous and intraarterial injection, intramuscular injection, and subcutaneous injection.

Once the pharmaceutical composition has been formulated, it may be stored in sterile vials as a solution, suspension, gel, emulsion, solid, crystal, or as a dehydrated or lyophilized powder. Such formulations may be stored either in a ready-to-use form or in a form (e.g., lyophilized) that is reconstituted prior to administration. The invention also provides kits for producing a single-dose administration unit. The kits of the invention may each contain both a first container having a dried protein and a second container having an aqueous formulation. In certain embodiments of this invention, kits containing single and multi-chambered pre-filled syringes (e.g., liquid syringes and lyosyringes) are provided.

The therapeutically effective amount of an IL-2 mutein-containing pharmaceutical composition to be employed will depend, for example, upon the therapeutic context and objectives. One skilled in the art will appreciate that the appropriate dosage levels for treatment will vary depending, in part, upon the molecule delivered, the indication for which the IL-2 mutein is being used, the route of administration, and the size (body weight, body surface or organ size) and/or condition (the age and general health) of the patient. In certain embodiments, the clinician may titer the dosage and modify the route of administration to obtain the optimal therapeutic effect. A typical dosage may range from about 0.1 µg /kg to up to about 1 mg/kg or more, depending on the factors mentioned above. In specific embodiments, the dosage may range from 0.5 µg /kg up to about 100 µg /kg, optionally from 2.5 µg /kg up to about 50 µg /kg.

A therapeutic effective amount of an IL-2 mutein preferably results in a decrease in severity of disease symptoms, in an increase in frequency or duration of disease symptom-free periods, or in a prevention of impairment or disability due to the disease affliction.

Pharmaceutical compositions may be administered using a medical device. Examples of medical devices for administering pharmaceutical compositions are described in U.S. Patent Nos. 4,475,196; 4,439,196; 4,447,224; 4,447, 233; 4,486,194; 4,487,603; 4,596,556; 4,790,824; 4,941,880; 5,064,413; 5,312,335; 5,312,335; 5,383,851; and 5,399,163, all incorporated by reference herein.

Methods of Treating Autoimmune or Inflammatory Disorders

In certain embodiments, an IL-2 mutein of the invention is used to treat an autoimmune or inflammatory disorder. In preferred embodiments, an IL-2 mutein Fc-fusion protein is used.

Disorders that are particularly amenable to treatment with IL-2 mutein disclosed herein include, but are not limited to, inflammation, autoimmune disease, atopic diseases, paraneoplastic autoimmune diseases, cartilage inflammation, arthritis, rheumatoid arthritis, juvenile arthritis, juvenile rheumatoid arthritis, pauciarticular juvenile rheumatoid arthritis, polyarticular juvenile rheumatoid arthritis,

systemic onset juvenile rheumatoid arthritis, juvenile ankylosing spondylitis, juvenile enteropathic arthritis, juvenile reactive arthritis, juvenile Reiter's Syndrome, SEA Syndrome (Seronegativity, Enthesopathy, Arthropathy Syndrome), juvenile dermatomyositis, juvenile psoriatic arthritis, juvenile scleroderma, juvenile systemic lupus erythematosus, juvenile vasculitis, pauciarticular rheumatoid arthritis, polyarticular rheumatoid arthritis, systemic onset rheumatoid arthritis, ankylosing spondylitis, enteropathic arthritis, reactive arthritis, Reiter's Syndrome, SEA Syndrome (Seronegativity, Enthesopathy, Arthropathy Syndrome), dermatomyositis, psoriatic arthritis, scleroderma, vasculitis, myolitis, polymyolitis, dermatomyolitis, polyarteritis nodossa, Wegener's granulomatosis, arteritis, ploymyalgia rheumatica, sarcoidosis, sclerosis, primary biliary sclerosis, sclerosing cholangitis, Sjogren's syndrome, psoriasis, plaque psoriasis, guttate psoriasis, inverse psoriasis, pustular psoriasis, erythrodermic psoriasis, dermatitis, atopic dermatitis, atherosclerosis, lupus, Still's disease, Systemic Lupus Erythematosus (SLE), myasthenia gravis, inflammatory bowel disease (IBD), Crohn's disease, ulcerative colitis, celiac disease, multiple sclerosis (MS), asthma, COPD, , rhinosinusitis, rhinosinusitis with polyps, eosinophilic esophogitis, eosinophilic bronchitis, Guillain-Barre disease, Type I diabetes mellitus, thyroiditis(e.g., Graves' disease), Addison's disease, Raynaud's phenomenon, autoimmune hepatitis, GVHD, transplantation rejection, kidney damage, hepatitis C-induced vasculitis, spontaneous loss of pregnancy, and the like.

In preferred embodiments, the autoimmune or inflammatory disorder is lupus, graft-versus-host disease, hepatitis C-induced vasculitis, Type I diabetes, multiple sclerosis, spontaneous loss of pregnancy, atopic diseases, and inflammatory bowel diseases.

Methods of Expanding Treg Cells

The IL-2 mutein or IL-2 mutein Fc-fusion proteins may be used to expand Treg cells within a subject or sample. Provided herein are methods of increasing the ratio of Tregs to non-regulatory T cells. The method comprises contacting a population of T cells with an effective amount of a human IL-2 mutein or IL-2 mutein Fc-fusion. The ratio may be measured by determining the ratio of CD3+FOXP3+ cells to CD3+FOXP3- cells within the population of T cells. The typical Treg frequency in human blood is 5-10% of total CD4+CD3+ T cells, however, in the diseases listed above this percentage may be lower or higher. In preferred embodiments, the percentage of Treg increases at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, at least 200%, at least 300%, at least 400%, at least 500%, at least 600%, at least 700%, at least 800%, at least 900%,or at least 1000%. Maximal fold increases in Treg may vary for particular diseases; however, a maximal Treg frequency that might be obtained through IL-2 mutein treatment is 50% or 60% of total CD4+CD3+ T cells. In certain embodiments, the IL-2 mutein or IL-2 mutein Fc-fusion protein is administered to a subject and the ratio of regulatory T cells (Tregs) to non-regulatory T cells within peripheral blood of a subject increases.

Because the IL-2 mutein and IL-2 mutein Fc-fusion proteins preferentially expand Tregs over other cell types, they also are useful for increasing the ratio of regulatory T cells (Tregs) to natural killer (NK) cells within the peripheral blood of a subject. The ratio may be measured by determining the ratio of CD3+FOXP3+ cells to CD16+ and/or CD56+ lymphocytes that are CD19- and CD3-.

It is contemplated that the IL-2 muteins or IL-2 mutein Fc-fusion proteins may have a therapeutic effect on a disease or disorder within a patient without significantly expanding the ratio of Tregs to non-regulatory T cells or NK cells within the peripheral blood of the patient. The therapeutic effect may be due to localized activity of the IL-2 mutein or IL-2 Fc-fusion protein at the site of inflammation or autoimmunity.

EXAMPLES

The following examples, both actual and prophetic, are provided for the purpose of illustrating specific embodiments or features of the present invention and are not intended to limit its scope.

Example 1 -- Reducing number of mutations that confer high affinity for CD25

IL-2 muteins with elevated affinity for CD25 and reduced signaling strength through IL-2Rβγ preferentially promote Treg growth and function. To reduce the potential immunogenicity, the minimum number of mutations required to achieve high affinity for CD25 was sought. The crystal structure of IL-2 in complex with its three receptors (PDB code – 2B5I) shows V69A and Q74P are located in the helical structure that interacts with CD25. This may explain why V69A and Q74P were frequently isolated in two independent IL-2 mutagenesis screens for high CD25 binding affinity (Rao et al. 2005; Thanos et al. 2006). This Example explores which of the other mutations in IL-2 mutein "2-4" identified in the screen of Rao et al. are most important to increase the affinity above that observed with V69A and Q74P alone. The following proteins were screened by flow cytometry for binding to CD25 on the surface of activated T cells. All constructs also included a C-terminal FLAG and poly-His tag for purification and detection. The specific mutations are provided in parenthesis.

HaMut1D (V69A,Q74P,N88D,C125A) (SEQ ID NO:8)
APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEALNLAPSKN
FHLRPRDLISDINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

HaMut2D (N30S,V69A,Q74P,N88D,C125A) (SEQ ID NO:9)
APTSSSTKKTQLQLEHLLLDLQMILNGINSYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEALNLAPSKN
FHLRPRDLISDINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

HaMut3D (K35R,V69A,Q74P,N88D,C125A) (SEQ ID NO:10)
APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPRLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEALNLAPSKN
FHLRPRDLISDINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

HaMut4D (T37A,V69A,Q74P,N88D,C125A) (SEQ ID NO:11)
APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLARMLTFKFYMPKKATELKHLQCLEEELKPLEEALNLAPSKN
FHLRPRDLISDINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

HaMut5D (K48E,V69A,Q74P,N88D,C125A) (SEQ ID NO:12)
APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPEKATELKHLQCLEEELKPLEEALNLAPSKN
FHLRPRDLISDINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

HaMut6D (E68D,V69A,Q74P,N88D,C125A) (SEQ ID NO:13)
APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEDALNLAPSKN
FHLRPRDLISDINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

HaMut7D (N71R,V69A,Q74P,N88D,C125A) (SEQ ID NO:14)
APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEALRLAPSKN
FHLRPRDLISDINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

HaMut8D (K35R,K48E,E68D,N88D,C125A) (SEQ ID NO:15)
APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPRLTRMLTFKFYMPEKATELKHLQCLEEELKPLEDVLNLAQSKN
FHLRPRDLISDINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

HaMut7D bound CD25 with nearly the same affinity as the original isolate "2-4" (~200 pM), indicating that mutation N71R was capable of greatly increasing the affinity above that observed with V69A, Q74P alone (HaMut1D, ~2 nM). The other constructs possessed affinities similar to or slightly higher than HaMut1D, with the exception of HaMut8D whose affinity was only slightly higher than that of WT IL-2.

Example 2 -- IL-2 muteins fused to IgG1-Fc domains for improved half-life

To reduce the dosing frequency required to achieve Treg enrichment with an IL-2 mutein, we evaluated various fusions between IL-2 and IgG1-Fc domains. The Fc domains contained point mutations to abolish effector functions mediated by IgG1, such as target cell lysis. The Fc effector function mutations utilized in our studies were either A327Q, Ala Ala (L234A+L235A) or N297G. Because the Treg-selective IL-2 muteins have partial reduction in IL-2 potency, it was important to fuse IL-2 to Fc in such a way that did not significantly impact IL-2R signaling. Thus, IL-2 muteins were tested for IL-2R activation with and without Fc fusion.

To determine if IL-2 dimerization by Fc fusion would increase IL-2R signaling strength due to increased avidity for IL-2R, a weaker IL-2 mutein (haD5) (US20110274650) was fused to the amino terminus of Fc, separated by a GGGGS (SEQ ID NO:5) linker sequence. This mutein possessed 3 mutations impacting IL-2R signaling (E15Q, H16N, N88D), 8 mutations to confer high affinity for CD25 (N29S, Y31H, K35R, T37A, K48E, V69A, N71R, Q74P) (Rao et al. 2005), and C125S to prevent cysteine mispairing and aggregation. Fusion to Fc in this manner completely abrogated the biological activity of haD5, while its high-affinity binding to cell surface CD25 was enhanced, likely due to increased avidity from dimerization.

IL-2 muteins were also fused to either the N- or C-terminus of an Fc heterodimer, such that only one chain of the Fc dimer bore the IL-2 domain. Heterodimeric pairing between two asymmetric Fc chains was promoted by electrostatic interactions between introduced lysines on one Fc chain and introduced aspartic acids on the other Fc chain. IL-2 mutein haD6 was fused to the N-terminus of one Fc chain or the other, in the event that one configuration was preferred, resulting in two protein constructs termed haD6.FcDD and haD6.FcKK. We also fused mutein haMut7D to the C-terminus of the Fc heterodimer with one or two GGGGS (SEQ ID NO:5) linkers (FcKK(G4S)haMut7D, FcKK(G4S)2haMut7D). Fusion of the IL-2 mutein haD6 to the N-terminus of the Fc heterodimer resulted in a partial loss of activity relative to free haD6 in both pSTAT5 and T cell proliferation experiments. In contrast, fusion of haMut7D to the C-terminus of the Fc heterodimer with either one or two GGGGS (SEQ ID NO:5) linkers did not alter the potency of haMut7D.

Fusion of an IL-2 mutein to the C-terminus of an Fc homodimer was also investigated. Total PBMC were activated in T75 tissue culture flasks at 300 million cells per 100 ml with 100 ng/ml anti-CD3 (OKT3). On day 3 of culture, cells were washed 3 times and rested in fresh media for 3 days. Cells were then stimulated with IL-2 variants at 10x dose titration ranging from 1pM to 10nM at a final volume of 50 µl. The level of STAT5 phosphorylation was measured using BD phosflow buffer kit. Briefly, 1 ml of BD lyse/fix phosflow buffer was added to stop stimulation. Cells were fixed for 20 min at 37°C and permeabilized with 1x BD phosflow perm buffer on ice before stained for CD4, CD25, FOXP3 and pSTAT5.

As can be seen in FIG. 1, the bioactivity of muteins haMut1D and haMut7D was not altered by fusion to the C-terminus of an Fc homodimer. Thus, fusion between the N-terminus of IL-2 and C-terminus of Fc did not compromise the agonist activity of the IL-2 muteins, even in the context of an Fc.IL-2 homodimer. In these constructs, the C125A mutation was used in place of C125S for improved manufacturing.

Example 3 -- Tuning IL-2 mutein potency to achieve preferential Treg growth

The initial panel of IL-2 muteins contained N88D alone or with 1 or 2 additional mutations impacting IL-2R signaling. A second panel of muteins was designed, all with single point mutations, with the goal of identifying muteins with either similar or slightly more potent agonism than those of the N88D series. A panel of 24 signaling mutations was identified based on predicted IL-2Rβ-interacting amino acids (crystal structure, PDB code – 2B5I). Particular substitutions were selected based on predicted decrease in the binding free energy between the mutein and IL-2Rβ. The binding free energy was calculated using EGAD computational algorithm (Handel's Laboratory, University of California at San Diego, USA). The binding free energy of a mutant is defined as $\Delta\Delta G_{mut} = \mu (\Delta G_{mut} - \Delta G_{wt})$. Where, μ (=0.1, in general) is the scaling factor used to normalize the predicted changes in binding affinity to have a slope of 1 when comparing with the experimental energies (Pokala and Handel 2005). The free energy of dissociation (ΔG) was defined as the energy difference between the complex (ΔG_{bound}) and free states (ΔG_{free}). The dissociation energy ΔGmut was calculated for each substitution.

A panel of IL-2 muteins with the following substitutions (H16E, H16Q, L19K, D20R, D20K, D20H, D20Y, M23H, D84K, D84H, S87Y, N88D, N88K, N88I, N88H, N88Y, V91N, V91K, V91H, V91R, I92H, E95K, E95R, or E95I) was expressed as C-terminal fusions to the Fc heterodimer. These constructs also contained the haMut7 mutations for high CD25 binding affinity (V69A, N71R, Q74P) and C125A for efficient folding.

The panel was screened for potency in the T cell STAT5 phosphorylation assay of Example 2, and H16E, D84K, V91N, V91K, and V91R were found to possess activity less than wild type IL-2 and more than N88D (FIG. 2).

H16E, D84K, V91N, V91K, and V91R possessed activity less than wild type IL-2 and more than N88D.

Selected muteins were also tested in T cell and NK growth assays.

For the T-cell assay, total PBMCs were activated at 3 million/ml with 100 ng OKT3. On day 2, cells were washed 3 times and rested in fresh media for 5 days. Cells were then labeled with CFSE and further cultured in a 24 well plate at 0.5 million/well in IL-2 containing media for 7 days before FACS analysis. The proliferation of T cell subsets is presented in FIG. 3 as CFSE dilution (median CFSE fluorescence).

For the NK-cell assay, MACS sorted CD16+ NK cells were cultured in IL-2 containing media for 3 days at 0.1 million/well in 96 well plates. 0.5 μCi ^{3}H-thymidine was added to each well during the final 18 hours of incubation. The results are shown in FIG. 4.

Mutants H16E, D84K, V91N, V91K, and V91R mutants were capable of stimulating Treg growth similar to WT IL-2 but were approximately 10x less potent on other T cells (FIG. 3), and approximately 100x less potent on NK cells (FIG. 4).

A separate panel of Fc.IL-2 fusion proteins was designed in which the distance between the Fc heterodimer and the mutein haMut7 (V69A, N71R, Q74P, C125A) was reduced by a series of individual amino acid truncations.

Fc.haMut7 Fc...TQKSLSLSPGKGGGGSAPTSSSTKKTQLQLEHLLLDLQMILN...haMut7 (SEQ ID NO:22)

Trunc1 Fc...TQKSLSLSSSTKKTQLQLEHLLLDLQMILN...haMut7 (SEQ ID NO:23)

Trunc2 Fc...TQKSLSLS-STKKTQLQLEHLLLDLQMILN...haMut7 (SEQ ID NO:24)

Trunc3 Fc...TQKSLSLS--TKKTQLQLEHLLLDLQMILN...haMut7 (SEQ ID NO:25)

Trunc4 Fc...TQKSLSLS---KKTQLQLEHLLLDLQMILN...haMut7 (SEQ ID NO:26)

Trunc5 Fc...TQKSLSLS----KTQLQLEHLLLDLQMILN...haMut7 (SEQ ID NO:27)

Trunc6 Fc...TQKSLSLS-----TQLQLEHLLLDLQMILN...haMut7 (SEQ ID NO:28)

Trunc7 Fc...TQKSLSLS------QLQLEHLLLDLQMILN...haMut7 (SEQ ID NO:29)

Trunc8 Fc...TQKSLSL-------QLQLEHLLLDLQMILN...haMut7 (SEQ ID NO:30)

Trunc1-Trunc4 possessed potency equal to the full length parent construct Fc.haMut7 as measured by STAT5 phosphorylation and by T cell and NK cell proliferation as described for FIGS. 2, 3, and 4. Trunc5 and Trunc6 stimulated weaker responses yet stronger than those stimulated by the N88D mutation (haD and haMut7D) and very similar to those stimulated by V91K. Trunc7 was weaker than N88D muteins, and Trunc8 had very little activity. When tested on NK cells, however, Trunc5 and Trunc6 were stronger agonists than V91K, indicating that Treg selectivity was more readily achieved with signaling mutations rather than steric hindrance by a proximal Fc domain.

Example 4 -- High CD25 affinity mutations in the context of an Fc homodimer

The mutations that conferred high CD25 binding affinity were considered advantageous because they increased tropism for CD25-high T cells, and because they promoted long term CD25::IL-2mutein association and prolonged signaling. However, reducing mutation number may reduce immunogenicity potential. The N88D or the V91K muteins, with and without the haMut1 high affinity mutations V69A and Q74P, were expressed as fusions to the C-terminus of an Fc homodimer and compared for bioactivty. In pSTAT5 stimulation assays, the homodimerization had no effect on signal strength relative to monomeric mutein. The reversion of the high affinity mutations V69A and Q74P also did not affect pSTAT5 signaling. In T cell growth assays, the high affinity mutations reduced activity on conventional CD4 T cells and CD8 T cells but not on regulatory T cells (FIG. 5). The high affinity mutations also did not alter proliferative responses in NK cells (FIG. 6).

To determine if the high affinity mutations impacted T cell responses *in vivo*, we dosed humanized mice (NOD.SCID.Il2rg-null mice reconstituted with human CD34+ hematopoietic stem cells) with the Fc.IL-2 mutein fusion proteins and monitored Treg expansion. Seven week old *NOD.SCID.Il2rg-null* (NSG) mice (Jackson Labs, Bar Harbor, ME) were irradiated (180 rad) and reconstituted with 94,000 human fetal liver $CD34^+$ hematopoietic stem cells. At 21 weeks, mice were distributed into 6 groups based on equal distribution of percent chimerism (determined by flow cytometry of PBL) and were given 1 µg sub-cutaneous injections of the indicated Fc.mutein fusion proteins or PBS on day 0 and day 7. On day 11, T cell subset frequencies in blood were determined by flow cytometry. At the low dose of 1 µg per animal, the high affinity mutations did not improve Treg expansion beyond that observed with the N88D or V91K mutations alone (FIG. 7).

Treg expansion was selective in that $FOXP3^-CD4^+$ T cells did not increase in abundance relative to total peripheral blood leukocytes (PBL) which includes a mixture of human B and T cells, and mouse myeloid cells. Furthermore, at higher doses, the high affinity mutations promoted an increase in $CD25^+FOXP3^-$ T cells, thus reducing Treg selectivity. Thus, in the context of the Fc homodimer, the high affinity mutations were not considered necessary for promoting preferential Treg growth.

Fc.WT IgG1Fc(N297G_delK)::G4S::hulL-2(C125A) (SEQ ID NO:16)

DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

GGGGS

APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLI
SNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

Fc.haMut1V91K IgG1Fc(N297G_delK)::G4S::huIL-2(V69A, Q74P, V91K, C125A) (SEQ ID NO:17)

DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

GGGGS

APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEALNLAPSKNFHLRPRDLI
SNINKIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

Fc.V91K IgG1Fc(N297G_delK)::G4S::huIL-2(V91K, C125A) (SEQ ID NO:18)

DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

GGGGS

APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLI
SNINKIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

Fc.haMut1N88D IgG1Fc(N297G_delK)::G4S::huIL-2(V69A, Q74P, N88D, C125A) (SEQ ID NO:19)

DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

GGGGS

APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEALNLAPSKNFHLRPRDLI
SDINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

Fc.N88D IgG1Fc(N297G_delK)::G4S::huIL-2(N88D, C125A) (SEQ ID NO:20)

DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

GGGGS

APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLI
SDINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

Example 5 -- Prolonged cell surface CD25 association of Fc.IL-2 muteins

An unexpected result from the humanized mouse studies was that, despite their reduced signaling capacity, the muteins induced more robust Treg enrichment relative to Fc.WT IL-2. Greater Treg enrichment and FOXP3 upregulation relative to that seen with Fc.WT was observed at a dose of 1 µg/mouse (Figure 7) and at a lower dose of 0.5 µg/mouse (FIG. 8). This increased potency *in vivo* may have resulted from reduced consumption by T cells, making more Fc.IL-2 mutein available for prolonged signaling.

In vitro and *in vivo* PK studies failed, however, to demonstrate significantly increased persistence of Fc.V91K or Fc.N88D relative to Fc.WT in supernatants from activated T cell cultures or serum from dosed mice. Because the Fc fusions bore two IL-2 mutein domains, we reasoned that increased endosomal recycling may result in prolonged cell surface association due to increased avidity for CD25. Indeed, we found that Fc.V91K and Fc.N88D persisted more efficiently than Fc.WT on the surface of previously activated T cells following a brief exposure the fusion proteins (FIG. 9).

Primary PBMCs were prestimulated for 2 days with 100 ng/ml OKT3. Cells were harvested, washed 4 times and rested for overnight in media. Cells were then pulsed with 400 pM Fc.IL-2 for 30 min at 37°C. After pulse, cells were either harvested for T0 after one wash, or washed an additional 3 times in 12 ml of warm media and cultured for 4 hours. To detect cell-associated Fc.IL-2, cells were stained with anti-human IgG-FITC (Jackson Immunoresearch) and anti-CD25-APC.

Example 6 -- Fusion sequence optimization

In preclinical studies in mice, our Fc.IL-2 muteins showed differential exposure when serum concentrations of the intact molecule were compared that of the human Fc portion only, indicative of circulating human Fc catabolite. To optimize the *in vivo* stability and pharmacokinetics of our Fc.IL-2 muteins, we characterized fusion sequence modifications for their impact on protoeolytic degradation of Fc.IL-2 muteins in systemic circulation and during recycling through the reticuloendothelial system. The following constructs were evaluated for proteolytic degradation *in vitro* and *in vivo.*

(Ala_Ala)_G4S	...TQKSLSLSPGKGGGGSAPTSSSTKKTQLQ... ha7N88D	(SEQ ID NO:31)
(N297G_delK)_G4S	...TQKSLSLSPG_GGGGSAPTSSSTKKTQLQ... ha1V91K	(SEQ ID NO:32)
(N297G_KtoA)_AAPT	...TQKSLSLSPGA_____APTSSSTKKTQLQ... ha1V91K	(SEQ ID NO:33)
(N297G_KtoA)_AAPA	...TQKSLSLSPGA_____APASSSTKKTQLQ... ha1V91K	(SEQ ID NO:34)

Stability was measured by quantitative immunoassays comparing concentrations over time of total human Fc to that of intact Fc.IL-2 mutein. Proteolysis of Fc.IL-2 muteins was verified by western blot analysis utilizing anti-IL-2 and anti-human Fc antibodies, followed by immunocapture of catabolites and characterization by mass spectrometry. Characterization by mass spectrometry of catabolites of (Ala_Ala)_G4S from *in vitro* and *in vivo* samples identified the C-terminal Lys of the Fc domain as a proteolytic cleavage site. Deletion or mutation of the C-terminal lysine of the Fc domain ((N297G_delK)_G4S and (N297G_KtoA)_AAPT) resulted in prolonged *in vitro* stability in mouse serum at 37°C compared to Fc constructs with the C-terminal lysine ((Ala_Ala)_G4S). This prolonged *in vitro* serum stability translated to greater exposure in mice as measured by the area under the Fc.IL-2 mutein serum concentration versus time curve (AUC). This prolonged stability of Fc.IL-2 muteins lacking the C-terminal Fc lysine was also observed *in vitro* in serum from cynomolgus monkeys and humans. Mutation of Thr-3 of IL-2 to Ala ((N297G_KtoA)_AAPA) resulted in decreased *in vitro* stability at 37°C (compared to (N297G_KtoA)_AAPT) in mouse serum and in separate incubations with recombinant human cathepsin D and L. This decreased *in vitro* serum stability translated to lower exposure (AUC) in mice *in vivo* for (N297G_KtoA)_AAPA compared to (N297G_KtoA)_AAPT. Characterization of catabolites of (N297G_KtoA)_AAPA from *in vitro* and *in vivo* samples by mass spectrometry identified Lys 8 and Lys 9 of the IL-2 mutein domain as residues susceptible to proteolysis which was not observed for equivalent

samples of (N297G_KtoA)_AAPT. Decreased stability at 37°C of (N297G_KtoA)_AAPA to that of (N297G_KtoA)_AAPT was also observed *in vitro* in serum from cynomolgus monkeys and humans.

Because of the importance of glycosylation in this region, and to potentially improve upon the manufacturability of the fusion protein, the fusion sequences were altered to promote N-linked rather than O-linked glycosylation, as follows.

Original

IgG1Fc(N297G_delK)::G4S::huIL-2(V91K,C125A) TQKSLSLSPGGGGGSAPTSSSTKKTQLQ (SEQ ID NO:32)

Altered

IgG1Fc(N297G_delK)::G4S::huIL-2(T3N,V91K,C125A) TQKSLSLSPGGGGGSAPNSSSTKKTQLQ (SEQ ID NO:35)

IgG1Fc(N297G_delK)::G4S::huIL-2(T3N,S5T,V91K,C125A) TQKSLSLSPGGGGGSAPNSTSTKKTQLQ (SEQ ID NO:36)

IgG1Fc(N297G_delK)::GGNGT::huIL-2(T3A,V91K,C125A) TQKSLSLSPGGGNGTAPASSSTKKTQLQ (SEQ ID NO:37)

IgG1Fc(N297G_delK)::YGNGT::huIL-2(T3A,V91K,C125A) TQKSLSLSPGYGNGTAPASSSTKKTQLQ (SEQ ID NO:38)

Example 7 – Cynomolgus Monkey PK/PD Determination

Standard IL-2 immune stimulating therapies require drug free holidays (no exposure) between dosing cycles to avoid undesirable side effects. In contrast, Treg expansion or stimulation therapies may require prolonged exposure with sustained trough drug levels (serum C_{min}) sufficient for Treg stimulation but with maximal exposures (serum C_{max}) below drug levels that lead to immune activation. This example demonstrates dosing strategies of half-life extended muteins in cynomolgus monkeys for extended target coverage (serum C_{min}) while maintaining maximal exposures (serum C_{max}) below drug levels contemplated to be necessary for proinflammatory immune activation.

Cynomolgus monkeys are dosed with Fc.V91K (IgG1Fc(N297G_delK)::G4S::huIL-2(V91K, C125A) in four groups (A-D), with three groups (A-C) dosed subcutaneously and one group (D) dosed intravenously. For each group, four biologically naïve male cynomolgus monkeys are dosed per the dosing strategy outlined below. Subcutaneous dosing of half-life extended muteins may allow for greater lymphatic absorption resulting in lower maximal exposure (serum C_{max}) and/or a more robust pharmacological response (Treg expansion). Dosing strategy for group A consists of three consecutive 10 microgram per kilogram doses on Day 0, 2, and 4 for cycle 1 and 10 microgram per kilogram on Day 14, allowing prolonged target coverage similar to a higher initial dose of 50 microgram per kilogram while maintaining a lower maximal exposure (C_{max}). The dosing strategy for group B is 50 microgram per kilogram dosed on Day 0 and 14 for comparison to Group A. The dosing strategy for group C is 50 microgram per kilogram dosed on Day 0 and 28. Allowing the determination of whether trough coverage

is required for sustaining Treg enrichment or whether a drug free holiday is beneficial between dosing cycles. The dosing strategy for the intravenous dosing arm group D is 50 microgram per kilogram dosed on Day 0, allowing a comparison of maximal exposures (C_{max}) and Treg enrichment differences to that of subcutaneous dosing.

Pharmacokinetics (quantitative immunoassay for intact molecule and total human Fc), anti-drug antibodies, shed soluble CD25, and serum cytokines (IL-1β, TNF-α, IFN-γ, IL-10, IL-5, IL-4, and IL-13) are measured at the following time points for each dose group specified:

Group A: pre-dose (first cycle; dose 1), 48 (pre-dose first cycle; dose 2), 96 (pre-dose first cycle; dose 3), 100, 104, 120, 168, 216, 264, 336 (pre-dose second cycle), 340, 344, 360, 408, 456, 504, 576, 672, 744, 840, and 1008 hours.

Group B: pre-dose (first cycle), 4, 8, 24, 72, 120, 168, 240, 336 (pre-dose second cycle), 340, 344, 360, 408, 456, 504, 576, 672, 744, 840, and 1008 hours.

Group C: pre-dose (first cycle), 4, 8, 24, 72, 120, 168, 240, 336, 408, 504, 672 (pre-dose second cycle), 676, 680, 696, 744, 792, 840, 912, 1008, 1080, and 1176 hours.

Group D: pre-dose (first cycle), 0.25, 1, 4, 8, 24, 72, 120, 168, 240, 336, 408, 504, and 672 hours.

Pharmacodynamics (immunopheotyping and enumeration of peripheral blood Tregs, non-regulatory CD4 and CD8 T cells, and NK cells) is measured at the following time points for each dose group specified:

Group A: pre-dose (first cycle; dose 1), 96 (pre-dose first cycle; dose 3), 168, 336 (pre-dose second cycle), 456, and 576 hours.

Group B: pre-dose (first cycle), 120, 240, 336 (pre-dose second cycle), 456, and 576 hours.

Group C: pre-dose (first cycle), 120, 240, 672 (pre-dose second cycle), 792, and 912 hours.

Group D: pre-dose (first cycle), 120 and 240 hours.

Hematology and clinical chemistry are assessed for all animals and dose groups pre-dose and at 24 hours post initial dose per dose group. The following parameters are evaluated.

Hematology:

- leukocyte count (total and absolute differential)
- erythrocyte count
- hemoglobin
- hematocrit
- mean corpuscular hemoglobin, mean corpuscular volume, mean corpuscular hemoglobin concentration (calculated)
- absolute reticulocytes

- platelet count
- blood cell morphology
- red cell distribution width
- mean platelet volume

Clinical Chemistry:

- alkaline phosphatase
- total bilirubin (with direct bilirubin if total bilirubin exceeds 1 mg/dL)
- aspartate aminotransferase
- alanine aminotransferase
- gamma glutamyl transferase
- urea nitrogen
- creatinine
- total protein
- albumin
- globulin and A/G (albumin/globulin) ratio (calculated)
- glucose
- total cholesterol
- triglycerides
- electrolytes (sodium, potassium, chloride)
- calcium
- phosphorus

Example 8 – Aglycosylated IgG1 Fc

Naturally occurring IgG antibodies posses a glycosylation site in the constant domain 2 of the heavy chain (CH2). For example, human IgG1 antibodies have a glycosylation site located at the position Asn297 (EU numbering). To date, the strategies for making aglycosylated antibodies involve replacing the Asn residue with an amino acid that resembles Asn in terms of physico-chemical properties (e.g., Gln) or with Ala residue which mimics the Asn side chain without the polar groups. This Example demonstrates the benefits of replacing Asn with Glycine (N297G). N297G Fc are aglcosylated molecules with better biophysical properties and manufacturability attributes (e.g., recovery during purification).

Examination of multiple known crystal structures of Fc fragments and IgG antibodies revealed considerable conformational flexibility around the glycosylated loop segment, particularly at the position Asn297 that is glycosylated. In many of the known crystal structures, Asn297 adapted positive backbone dihedral angles. Gly has high propensity to adapt positive backbone dihedral angle due to the lack of side chain atoms. Therefore, based on this conformation and structure reason, Gly may be a better replacement for Asn than N297Q or N297A.

Mutating Asn297 with Gly leads to aglcosylated molecules with much improved recovery (or efficiency) in the purification process and biophysical properties. For example, the percentage of recovery (final yield) from the protein A pool was 82.6% for the N297G mutation, compared to 45.6% for N297Q and 39.6% for N297A. SPHP column analysis revealed the lower percentage of recovery for the N297Q and N297A mutants was due to a tailing peak, which indicates high molecular weight aggregation and/or misfolded species. This result was re-confirmed at a larger, 2L scale run.

In the biopharmaceutical industry, molecules with potential need for large-scale production, e.g, potential to be sold as a drug, are assessed for a number of attributes to mitigate the risk that the molecule is not amenable to large-scale production and purification. In the manufacturability assessments, N297G revealed robustness to pH changes. N297G had no aggregation issue; whereas N297Q and N297A had 20% and 10% increase in aggregation, respectively. Although N297G had better manufacturability attributes, it was similar to N297Q and N297A in all the functional assays in which it was tested. For example, in ADCC assays, N297G lacked cytotoxicity similarly to N297Q and N297A.

Example 9 – Stabilized aglyosylated IgG1 Fc

This Example describes a method of improving stability of IgG antibody scaffolds by introducing engineered disulfide bond(s). Naturally occurring IgG antibodies are stable molecules. However, for some therapeutic applications, it may be necessary to make mutations or create aglycosylated molecules. For example, aglycosylated IgG molecules may be used in therapeutic indications where there is a need to avoid ADCC and binding to Fcgamma receptors. However, the aglycosylated IgG1 has much lower melting temperature (CH2 domain melting temperature decreases by about 10°C; 70°C to 60°C) than the glycosylated IgG1. The observed lower melting temperature negatively impacts various biophysical properties of the aglycosylated IgG1. For example, aglycosylated IgG1 has increased level of aggregation at low pH compared to glycosylated IgG1.

In order to engineer disulfide bonds, a structure based method involving distance calculation between the C-alpha atoms was initially used to identify 54 residue pairs in the Fc region for mutation to Cys. These 54 sites were further narrowed down to 4 residue pairs (V259C-L306C, R292C-V302C, A287C-L306C, and V323C-I332C). The criteria used included (i) positions within the CH2 domain, (ii) away from loops, turns and carbohydrates, (iii) away from Fcgamma receptor and FcRn interaction sites, (iv) solvent accessibility (preferred buried positions), etc.

The paired cysteine substitutions were created in the context of the aglycosylated N297G Fc. Non-reduced peptide mapping analysis revealed that 3 of the 4 engineered sites formed disulfide bond as expected and designed in that context. The V259C-L306C mutation did not form disulfide bond correctly and led to mis-pairing with the native disulfide already present in the CH2 domain. The other three designs R292C-V302C, A287C-L306C, and V323C-I332C formed disulfide bond correctly as predicted and designed. Adding the disulfide bond to the N297G mutation led to about 15C improvement in thermal stability over the N297G mutation alone. Of the R292C-V302C, A287C-L306C, and V323C-I332C disulfide variants, R292C-V302C and A287C-L306C had good pharmacokinetics when administered to rats ($t_{1/2}$ of 11 days and 9 days, respectively). This is in contrast to the pharmacokinetics

profile we observed in rats for the previously published CH2 domain disulfide bond L247C-K339C (Gong et al., *J. Biol. Chem. 2009 284: 14203-14210*), which had a $t_{1/2}$ of 5 days.

Engineering a disulfide bond in the CH2 domain improves the stability of the aglycosylated molecule on par with glycosylated IgG1 molecules (10 to 15°C improvement in the melting temperature as determined by Differential Scanning Calorimetry). The engineered sites described herein do not lead to disulfide scrambling and the disulfides are formed as predicted in approximately 100% of the population. More importantly, unlike the published disulfide bond site in the CH2 domain, the disulfide bonds described herein do not impact the rat PK.

The pharmacokinetics (PK) profile of stabilized aglycosylated antibodies was determined in cynomolgus monkeys. An IgG1 antibody having N297G, A287C, and L306C substitutions (Ab2-1) and an IgG1 antibody having N297G, R292C, and V302C substitutions (Ab2-2) were subcutaneously injected at 5 mg/kg into cynomolgus monkeys (N=2). Serum samples were collected at pre-dose, 0.5, 2, 8, 24, 48, 96, 168, 336, 504, 672, 840, 1008, 1176, 1344, 1512, and 1680 hours postdose. The samples were assayed for the Ab2-1 and Ab2-2 antibody levels by using an anti-hu IgG sandwich ELISA. To measure the serum hu IgG level in the PK study samples, the following method was used: ½ area black plate (Corning 3694) was coated with 2 µg/ml of anti-hu Fc, antibody 1.35.1 in PBS and then incubated overnight at 4°C. The plate was then washed and blocked with I-Block™ (Applied Biosystems) overnight at 4°C. If samples needed to be diluted, then they were diluted in cynomolgus monkey serum. The standards and samples were then diluted 1: 20 in 1X PBS +1M NaCl+0.5% Tween 20 and 1% BSA buffer (5% serum). The plate was washed and 50-µl samples of diluted standards and samples were transferred into an antibody 1.35.1 coated plate and incubated for 1.5 h at room temperature. The plate was washed, then 50 µl of 100 ng/ml of anti-hu Fc antibody 21.1-HRP conjugate in I-Block™ +5% BSA was added and incubated for 1.5 h. The plate was washed, then 50 µl of Pico substrate were added, after which the plate was immediately analyzed with a luminometer. Time concentration data were analyzed using non-compartmental methods with WinNonLin® (Enterprise version 5.1.1, 2006, Pharsight® Corp. Mountain View, CA).

PK exposures of Ab2-1 and Ab2-2 antibodies in cynomolgus monkeys were compared to the IgG1 antibody comprising only the N297G substitution and the IgG1 antibody comprising N297G, L247C, and K339C. The PK exposures of Ab2-1 and Ab2-2 antibodies in cynomolgus monkeys were both higher than the IgG1 antibody comprising only the N297G substitution and the IgG1 antibody comprising N297G, L247C, and K339C. Also, Ab2-2 had exposure and clearance comparable to parent IgG1 antibody.

Claims

What is claimed is:

1. A polypeptide comprising a Fc region of a human IgG1 antibody wherein said Fc region comprises a N77G mutation wherein the numbering is as provided in SEQ ID NO: 3 or 4, and said Fc region of a human IgG1 comprises at least 90% identity to the amino acid sequence set forth in SEQ ID NO:3, and wherein said Fc region comprises an A67C and L86C, or an V39C and L86C, or an R72C and V82C, or an V103C and I112C substitution within the amino acid sequence set forth in SEQ ID NO:3 or SEQ ID NO:4.

2. The polypeptide of claim 1, wherein said Fc region of a human IgG1 comprises at least 95% identity to the amino acid sequence set forth in SEQ ID NO:3.

3. An antibody comprising a Fc region of claim 1 or 2.

4. A Fc-fusion protein comprising the Fc region of claim 1 or 2.

5. A nucleic acid encoding a polypeptide of claim 1 or 2.

6. An expression vector comprising the nucleic acid of claim 5.

7. A host cell comprising the nucleic acid of claim 5.

8. A host cell comprising the expression vector of claim 6.

9. The host cell of claim 7 or claim 8, wherein the host cell is a mammalian host cell.

10. A method of making an aglycosylated IgG1 Fc-containing molecule, said method comprising:
    a) expressing a nucleic acid encoding a polypeptide of claim 1 or 2 in a mammalian cell culture; and
    b) harvesting the aglycosylated IgG1 Fc-containing molecule from said culture.