# INTERLEUKIN-2 FUSION PROTEINS AND USES THEREOF

## Field of the Invention

The present invention generally relates to fusion proteins of immunoglobulins and interleukin-2 (IL-2). In addition, the present invention relates to polynucleotides encoding such fusion proteins, and vectors and host cells comprising such polynucleotides. The invention further relates to methods for producing the fusion proteins of the invention, and to methods of using them in the treatment of disease.

## Background

Regulatory T cells (Tregs) represent specific subsets of T lymphocytes that are crucial for the maintenance of self-tolerance. These $CD4^+CD25^{hi}$ cells with suppressor function can be distinguished from effector T cells by the intracellular expression of the transcription factor FOXP3, as well as other cell markers such as $CD127^{lo}$, CTLA-$4^+$, LAP, $CD39^+$, PD-$1^+$, GARP, etc. FOXP3 is critical for Treg differentiation and function, and FOXP3 gene deficiency and mutations, both in scurfy mice and patients with immune dysregulation polyendocrinopathy, enteropathy, X-chromosome linked syndrome (IPEX), result in the breakdown of self-tolerance and the development of autoimmune diseases due to Treg deficiency or lack of function.

The autoimmune responses in type 1 diabetes, Systemic Lupus Erythematosus (SLE), multiple sclerosis, and many others are correlated with a deficiency in Tregs. Data from animal models support the hypothesis that autoimmune responses are facilitated by a failure of Tregs to control the destructive immune response to self. Type 1 diabetes is an autoimmune disease that occurs after the destruction of a majority of the insulin producing β cells in the pancreas. The frequency of type 1 diabetes is ~0.3% of the population in the US and its incidence continues to increase in the US, Europe, and in particular Scandinavia (nearly 1%) and is expected to double within the next twenty years.

The cytokine IL-2 plays a major role in the activation and function of both Tregs as well as effector T cells (Teff). A deficiency in IL-2 production or lack of responsiveness preferentially results in a loss of Treg function and an increase in the probability of autoimmunity. Because

Tregs constitutively express the high affinity IL-2 receptor at higher levels than Teff, low doses of IL-2 preferentially support the maintenance of Tregs as compared to Teff cells.

With the preferential effect of IL-2 for activating Tregs *in vitro* and *in vivo*, the potential for low dose, long-lived IL-2 therapy would seem to have a high prospect for success in autoimmune diseases. A 200 patient, double blind, placebo controlled type 1 diabetes clinical trial with IL-2 (Proleukin®) is set to begin in late 2013. Recent clinical trials with daily low dose Proleukin® ameliorated some of the signs and symptoms of chronic graft-versus-host disease (GVHD) and hepatitis C virus-induced vasculitis (Koreth et al., New Engl J Med 365, 2055-2066 (2011), Saadoun et al., New Engl J Med 365, 2067-2077 (2011)). In both studies low dose Proleukin® induced Tregs and increased the Treg:Teff ratio. However, Proleukin®'s poor PK properties make it suboptimal for maintaining low, consistent levels of IL-2 in man. Other methods being tested in clinical trials are personalized expansion of Tregs *ex vivo* followed by reinfusion, but this approach is less than ideal and represents a challenging set of quality control issues.

Thus, a new therapeutic approach that re-establishes the natural regulatory T cell (Treg) mediated dominant immune tolerance would greatly enhance the ability to treat patients with autoimmune diseases such as type 1 diabetes, multiple sclerosis, systemic lupus erythematosus, Crohn's disease as well as other autoimmune diseases and immune-based pro-inflammatory diseases such as chronic graft versus host disease, asthma, pulmonary fibrosis, chronic obstructive pulmonary disease, cardiovascular diseases such as atherosclerosis, and transplant rejection, both solid organ and bone marrow.

The IL-2 fusion proteins of the present invention preferentially activate Tregs, tipping the balance toward a higher Treg:Teff ratio and reduce the autoimmune response. They are long-lived, allowing convenient dosing schedules, and devoid of effector functions, reducing potential side effects and impairment of efficacy.

## Summary

The disclosure provides a fusion protein comprising (i) an immunoglobulin molecule comprising a modification reducing binding affinity of the immunoglobulin molecule to an Fc receptor as compared to a corresponding immunoglobulin molecule without said modification, and (ii) two interleukin-2 (IL-2) molecules.

In one aspect, the disclosure provides a fusion protein comprising (i) a human $IgG_1$-subclass immunoglobulin molecule comprising a modification reducing binding affinity of the immunoglobulin molecule to an Fc receptor as compared to a corresponding immunoglobulin molecule without said modification, and (ii) two interleukin-2 (IL-2) molecules, wherein said immunoglobulin molecule comprises the heavy chain variable region sequence of SEQ ID NO: 9 and the light chain variable region sequence of SEQ ID NO: 11, and wherein said immunoglobulin molecule comprises the amino acid substitutions L234A, L235A and P329G (EU numbering) in the immunoglobulin heavy chains.

In one embodiment, said immunoglobulin molecule is an IgG-class immunoglobulin molecule, particularly an $IgG_1$-subclass immunoglobulin molecule. In one embodiment, said immunoglobulin molecule is a human immunoglobulin molecule. In one embodiment, said immunoglobulin molecule is capable of specific binding to an antigen. In one embodiment, said immunoglobulin molecule is a monoclonal antibody. In one embodiment, said immunoglobulin molecule is not capable of specific binding to an antigen. In one embodiment, said immunoglobulin molecule comprises a heavy chain variable region sequence based on the human Vh3-23 germline sequence. In a specific embodiment, said immunoglobulin molecule comprises the heavy chain variable region sequence of SEQ ID NO: 9. In one embodiment, said immunoglobulin molecule comprises a light chain variable region sequence based on the human Vk3-20 germline sequence. In a specific embodiment, said immunoglobulin molecule comprises the light chain variable region sequence of SEQ ID NO: 11. In an even more specific embodiment, said immunoglobulin molecule comprises the heavy chain variable region sequence of SEQ ID NO: 9 and the light chain variable region sequence of SEQ ID NO: 11. In one embodiment, said immunoglobulin molecule is not capable of specific binding to an antigen, and comprises a heavy chain variable region sequence based on the human Vh3-23 germline sequence and a light chain variable region sequence based on the human Vk3-20 germline sequence.

In one embodiment, said Fc receptor is an Fcγ receptor, particularly a human Fcγ receptor. In one embodiment, said Fc receptor is an activating Fc receptor. In one embodiment, said Fc receptor is selected from the group of FcγRIIIa (CD16a), FcγRI (CD64), FcγRIIa (CD32) and FcαRI (CD89). In a specific embodiment, said Fc receptor is FcγRIIIa, particularly human FcγRIIIa. In one embodiment, said modification reduces effector function of the immunoglobulin molecule. In a specific embodiment, said effector function is antibody-dependent cell-mediated cytotoxicity (ADCC). In one embodiment, said modification is in the Fc region, particularly in the CH2 region, of said immunoglobulin molecule. In one embodiment, said immunoglobulin molecule comprises an amino acid substitution at position 329 (EU numbering) of the immunoglobulin heavy chains. In a specific embodiment, said amino acid substitution is P329G. In one embodiment, said immunoglobulin molecule comprises amino acid substitutions at positions 234 and 235 (EU numbering) of the immunoglobulin heavy chains. In a specific embodiment, said amino acid substitutions are L234A and L235A (LALA). In one embodiment, said immunoglobulin molecule comprises amino acid substitutions at positions 234, 235 and 329 (EU numbering) of the immunoglobulin heavy chains. In a particular embodiment,

said immunoglobulin molecule comprises the amino acid substitutions L234A, L235A and P329G (EU numbering) in the immunoglobulin heavy chains.

In one embodiment, said IL-2 molecules are wild-type IL-2 molecules. In one embodiment, said IL-2 molecules comprise an amino acid mutation that does not alter the binding affinity of said IL-2 molecules to an IL-2 receptor as compared to naturally occurring, native IL-2. In one embodiment, said IL-2 molecules comprise an amino acid mutation at a position corresponding to residue 125 of human IL-2. In a more specific embodiment, said amino acid mutation is the amino acid substitution C125A. In one embodiment, said IL-2 molecules are human IL-2 molecules. In a specific embodiment, said IL-2 molecules comprise the sequence of SEQ ID NO: 1 or SEQ ID NO: 3, particularly the sequence of SEQ ID NO: 3. In one embodiment, said IL-2 molecules have the sequence of SEQ ID NO: 1 or SEQ ID NO: 3, particularly the sequence of SEQ ID NO: 3. In one embodiment, said IL-2 molecules are each fused at their N-terminal amino acid to the C-terminal amino acid of one of the immunoglobulin heavy chains of said immunoglobulin molecule, optionally through a peptide linker.

In a specific embodiment, said fusion protein comprises the polypeptide sequences of SEQ ID NO: 17 and SEQ ID NO: 19. In a specific embodiment, said fusion protein comprises an immunoglobulin light chain of SEQ ID NO: 19 and an immunoglobulin heavy chain-IL-2 fusion polypeptide of SEQ ID NO: 17. In one embodiment, said fusion protein essentially consists of an immunoglobulin molecule comprising a modification reducing binding affinity of the immunoglobulin molecule to an Fc receptor as compared to a corresponding immunoglobulin molecule without said modification, two interleukin-2 (IL-2) molecules, and optionally one or more peptide linker. In one embodiment, said fusion protein essentially consists of two immunoglobulin light chains of SEQ ID NO: 19 and two immunoglobulin heavy chain-IL-2 fusion polypeptides of SEQ ID NO: 17.

The disclosure further provides, in another aspect, a polynucleotide encoding the fusion protein of the disclosure. Further provided, in another aspect, is a vector, particularly an expression vector, comprising the polynucleotide of the disclosure. In another aspect, the disclosure provides a host cell comprising the polynucleotide or the vector of the disclosure. The disclosure also provides a method for producing a fusion protein of the disclosure, comprising the steps of (i) culturing the host cell of the disclosure under conditions suitable for expression of the fusion

protein, and (i) recovering the fusion protein. Hence, in another aspect, there is provided a method for producing a fusion protein comprising (i) an immunoglobulin molecule comprising a modification reducing binding affinity of the immunoglobulin molecule to an Fc receptor as compared to a corresponding immunoglobulin molecule without said modification, and (ii) two interleukin-2 (IL-2) molecules, said method comprising the steps of (i) culturing the host cell of the disclosure under conditions suitable for expression of the fusion protein, and (ii) recovering the fusion protein. Also provided, in another aspect, is a fusion protein comprising (i) an immunoglobulin molecule comprising a modification reducing binding affinity of the immunoglobulin molecule to an Fc receptor as

compared to a corresponding immunoglobulin molecule without said modification, and (ii) two interleukin-2 (IL-2) molecules, produced by said method.

In another aspect, the disclosure provides a pharmaceutical composition comprising the fusion protein of the disclosure and a pharmaceutically acceptable carrier. In another aspect, the fusion protein or the pharmaceutical composition of the disclosure is also provided for use as a medicament. In another aspect, the fusion protein or the pharmaceutical composition of the disclosure is provided for use in the treatment or prophylaxis of an autoimmune disease. The autoimmune disease may specifically be type 1 diabetes, multiple sclerosis (MS), systemic lupus erythematosus (SLE) or Crohn's disease, most specifically type 1 diabetes, or graft-versus-host disease or transplant rejection. In another aspect, there is provided the fusion protein or the pharmaceutical composition of the disclosure for use in the treatment or prophylaxis of transplant rejection or graft-versus-host disease. Further provided is the use of the fusion protein of the disclosure for the manufacture of a medicament for the treatment of a disease in an individual in need thereof. In another aspect, the disclosure provides the use of the fusion protein of the disclosure for the manufacture of a medicament for the treatment of a disease in an individual in need thereof, wherein said disease is an autoimmune disease, transplant rejection or graft-versus-host disease. There is also provided a method of treating a disease in an individual, comprising administering to said individual a therapeutically effective amount of a composition comprising the fusion protein of the disclosure in a pharmaceutically acceptable form. In one embodiment, said disease is an autoimmune disease. In a more specific embodiment, said autoimmune disease is type 1 diabetes, multiple sclerosis (MS), systemic lupus erythematosus (SLE) or Crohn's disease. In an even more specific embodiment, said autoimmune disease is type 1 diabetes. In another embodiment said disease is transplant rejection or graft-versus-host disease. In one embodiment, said individual is a mammal, particularly a human.

Further provided, in another aspect, is the fusion protein of the disclosure for use in selective activation of regulatory T cells *in vitro* or *in vivo*. In one embodiment, said activation comprises induction of proliferation of regulatory T cells and/or induction of IL-2 receptor signaling, particularly phosphorylation of STAT5, in regulatory T cells. In one embodiment, said use is *in vitro* and said fusion protein is used at a concentration of about 1 ng/mL or less, particularly about 0.1 ng/mL or less. In another embodiment, said use is *in vivo* and said

fusion protein is used at a dose of about 20 μg/kg body weight or less, particularly about 12 μg/kg body weight or less, more particularly about 6 μg/kg body weight or less.

The disclosure also provides a method for selective activation of regulatory T cells *in vitro* or *in vivo*, comprising contacting said regulatory T cells with the fusion protein of the disclosure. In one embodiment, said activation comprises induction of proliferation of regulatory T cells and/or induction of IL-2 receptor signaling, particularly phosphorylation of STAT5, in regulatory T cells. In one embodiment, said method is *in vitro* and said fusion protein is used at a concentration of about 1 ng/mL or less, particularly about 0.1 ng/mL or less. In another

embodiment, said method is *in vivo* and said fusion protein is used at a dose of about 20 µg/kg body weight or less, particularly about 12 µg/kg body weight or less, more particularly about 6 µg/kg body weight or less.

## Brief description of the drawings

Figure 1. Purification of DP47GS IgG-IL-2 fusion protein (see SEQ ID NOs 13, 15, 19). (A) Elution profile of the Protein A affinity chromatography step. (B) Elution profile of the size exclusion chromatography step. Yield 4 mg/L. (C) Analytical capillary electrophoresis SDS (Caliper) of the final product. The following band were observed: non-reduced – 7.5% area at 111 kDa, 92.5% area at 174 kDa; reduced – 23.6% area at 29 kDa, 23.5% area at 67 kDa, 52.9% area at 82 kDa. The product contains about 7.5% "half IgG". (D) Analytical size exclusion chromatography of the final product on a TSKgel G3000 SW XL column (91% monomer content).

Figure 2. Purification of DP47GS IgG-$(IL\text{-}2)_2$ fusion protein (see SEQ ID NOs 17, 19). (A) Elution profile of the Protein A affinity chromatography step. (B) Elution profile of the size exclusion chromatography step. Yield 13 mg/L. (C) Analytical capillary electrophoresis SDS (Caliper) of the final product. The following band were observed: non-reduced – 2.3% area at 172.5 kDa, 97.7% area at 185 kDa; reduced – 18.3% area at 27.3 kDa, 0.6% area at 29.2 kDa, 81.1% area at 78.3 kDa. (D) Analytical size exclusion chromatography of the final product on a Superdex 200 column (100% monomer content).

Figure 3. CD25 (IL-2RA) and CD122 (IL-2RB) expression on $CD4^+$ Treg subsets, NK cell subsets and NKT cells. Cell surface markers were used to define $CD4^+$ Treg subsets, NKT cells and NK cells. In order to optimize staining for CD25 and CD122, intracellular FOXP3 staining was not performed. (A, B) Three regulatory $CD4^+$ T cell (Treg) populations: naïve ($CD45RA^+$, $CD25^+$; dotted line), memory ($CD45RA^-$, $CD25^+$; solid line) and activated ($CD45RA^-$, $CD25^{hi}$; dashed line). (C, D) NKT (dotted line), $CD56^{bright}$ NK cells (dashed line), $CD56^{intermediate}$ NK cells (solid line). Grey: isotype control.

Figure 4. CD25 (IL-2RA) and CD122 (IL-2RB) expression on $CD4^+$ and $CD8^+$ conventional T cell subsets. Cell surface markers were used to define naïve ($CD45RA^+$; dotted line) and memory ($CD45RA^-$; solid line) conventional $CD4^+$ T cells (A, B), memory conventional $CD8^+$ T cells ($CD45RA^-$; solid line) and $CD45RA^+$ CD8 T cells (a combination of the naïve and TEMRA

subsets; TEMRA refers to effector memory cells that have reverted to expressing CD45RA; dotted line) (C, D). Grey: isotype control.

Figure 5. Induction of pSTAT5a in human peripheral blood cell subsets in response to DP47GS IgG-IL-2. Three different human donors (C4 to C6) were assessed at separate times for the effects of various doses of DP47GS IgG-IL-2 on the induction of STAT5a phosphorylation. The results are shown for $CD4^+$ Treg subsets: activated, memory and naïve Tregs; conventional $CD4^+$ memory T effector cells; $CD56^{bright}$ NK cells; $CD8^+$ memory T effector cells; $CD4^+$ naïve T effector cells; NK cells; NKT cells; and $CD8^+$ naïve T effector + $CD45RA^+$ memory cells.

Figure 6. Induction of pSTAT5a in human peripheral blood cell subsets in response to DP47GS IgG-$(IL\text{-}2)_2$. Five different human donors (N1, N2, C4-C6) were assessed at separate times for the effects of various doses of DP47GS IgG-$(IL\text{-}2)_2$ immunoconjugate on the induction of STAT5a phosphorylation. The results are shown for $CD4^+$ Treg subsets: activated, memory and naïve Tregs; conventional $CD4^+$ memory T effector cells; $CD56^{bright}$ NK cells; $CD8^+$ memory T effector cells; $CD4^+$ naïve T effector cells; NK cells; NKT cells; and $CD8^+$ naïve T effector + $CD45RA^+$ memory cells.

Figure 7. Induction of pSTAT5a in human peripheral blood cell subsets: comparison of DP47GS IgG-IL-2 and DP47GS IgG-$(IL\text{-}2)_2$. The results for each cell subset were normalized to the maximum observed effect from each subset and the approximate EC50 for Tregs are presented in Table 2. (A) normalized results for DP47GS IgG-IL-2, (B) normalized results for DP47GS IgG-$(IL\text{-}2)_2$.

Figure 8. Detailed examination of $_{Treg}$ subset sensitivity in three donors comparing DP47GS IgG-IL-2 and DP47GS IgG-$(IL\text{-}2)_2$. Graphs represent the mean ± SD of the pSTAT5a MFI for the three donors. (A) total $CD3^+$, $CD4^+$, $FoxP3^+$ Tregs. (B) activated Tregs. (C) memory Tregs. (D) naïve Tregs.

Figure 9. DP47GS IgG-IL2 has a dose dependent effect in cynomolgus monkeys increasing regulatory T cells. The changes in whole blood $CD4^+$ $CD25^+$ $FOXP3^+$ regulatory T cells (Tregs) on day 7 post treatment are shown as (A) the absolute cell number of Tregs per $mm^3$ of whole blood and (B) the fold change in Tregs. All data are represented as the mean ± SD. Open bars: DP47GS IgG-IL-2 (n=6); shaded bars: vehicle (n=3).

Figure 10. Time and low dose effects of DP47GS IgG-IL-2 on Tregs in cynomolgus monkeys. (A) time dependent changes in Treg fold increases following dosing with 2 or 6 µg/kg DP47GS IgG-IL-2 (n=4 and 6, respectively). (B) time dependent changes in Treg absolute counts in blood after dosing with 2 or 6 µg/kg DP47GS IgG-IL-2 (n=4 and 6, respectively). All data are shown as the mean ± SD.

Figure 11. Single dose Proleukin® stimulates a transient dose dependent Treg response in cynomolgus monkeys. (A) changes in peripheral blood Treg numbers after single dose treatment with $3x10^4$ to $3x10^5$ IU/kg Proleukin®. (B) changes in Treg pSTAT5a after single dose treatment with $3x10^4$ to $3x10^5$ IU/kg Proleukin®. Data are shown as the mean ± SD.

Figure 12. Low dose DP47GS IgG-IL-2 is more effective than high dose Proleukin® in Treg induction in cynomolgus monkeys. Normal healthy cynomolgus monkeys (groups of n=5) were treated with low dose DP47GS IgG-IL-2 or high dose Proleukin® and the change in regulatory T cells tested at day 10. On days 0 and 7, DP47GS IgG-IL-2 was given SC at a dose of 16,800 IU/kg (12 µg/kg). Proleukin® treatment (200,000 IU/kg) was given SC 3 times per week (MWF) for a total of 5 doses. The results are shown as mean ± SD for (A) the change in total Tregs per $mm^3$ blood, (B) the fold increase in Tregs, and (C) the change in the ratio of Tregs to conventional $CD4^+$ $FOXP3^-$ cells. Open bars depict IL-2 treatment and shaded bars the vehicle control.

Figure 13. *Ex vivo* whole blood phosphorylated STAT5 as a sensitive biomarker for DP47GS IgG-IL-2 Treg activation *in vivo*. One and 3 days after *in vivo* administration of a single low dose of DP47GS IgG-IL-2 (12 µg/kg) to healthy cynomolgus monkeys (n=5), whole blood was collected and tested immediately without stimulation for phosphorylated STAT5 (pSTAT5a). Each monkey was bled on day 0 before treatment and the amount of pSTAT5a was measured (shaded bars) and used individually to assess the fold-changes post treatment (open bars). (A) the fold change in Treg pSTAT5a on days 1 and 3, (B) the fold change in pSTAT5a in conventional $CD4^+$ $CD45^-$ memory T cells , and (C) the fold change in in naïve T cells pSTAT5a is shown. Data are shown as the mean ± SD.

Figure 14. *Ex vivo* whole blood pSTAT5a as a sensitive biomarker for low dose DP47GS IgG-IL-2 Treg activation *in vivo*. From one to seven days after *in vivo* administration of a single low dose of DP47GS IgG-IL-2 to healthy cynomolgus monkeys, whole blood was collected and tested immediately without stimulation for pSTAT5a. Each monkey was bled on day 0 before

treatment for unstimulated levels of pSTAT5a and compared to changes in pSTAT5a post-treatment. (A) Treg pSTAT5a before and after treatment with 2 μg/kg of DP47GS IgG-IL-2 (n=4). (B) Treg pSTAT5a before and after treatment with 6 μg/kg of DP47GS IgG-IL-2 (n=6). Data are shown as the mean ± SD.

Figure 15. *Ex vivo* cynomolgus whole blood Ki-67 serves as a marker for DP47GS IgG-IL-2 induced T cell proliferation *in vivo*. The cynomolgus monkeys treated with 2 and 6 μg/kg of DP47GS IgG-IL-2 as described in Figure 14 were also monitored *ex vivo* for changes in the intracellular marker Ki-67 to assess the extent of proliferation *in vivo*. The normal steady state percentage of cells in cell cycle (Ki-67$^+$) were quantified on day 0 prior to treatment and then monitored daily for the next 7 to 11 days. (A) % Ki-67$^+$ for Tregs, (B) % Ki-67$^+$ for conventional CD4$^+$CD45$^-$ memory/effector T cells, and (C) % Ki-67$^+$ for naïve CD4$^+$CD45RA$^+$ T cells are shown. Data are shown as the mean ± SD.

Figure 16. Time and low dose effects of DP47GS IgG-(IL-2)$_2$ on Tregs in naïve healthy cynomolgus monkeys. (A) time dependent changes in Treg absolute numbers after 6 μg/kg DP47 IgG-(IL-2)$_2$. (B) time dependent changes in Treg pSTAT5a after treatment, (C) time dependent changes in the fold increase in Tregs, and (D) comparison of the fold changes in Tregs from DP47Gs IgG-IL-2 treated monkeys (open bars, 2 to 36 μg/kg) versus the DP47GS IgG-(IL-2)$_2$ treated (shaded bar, 6 μg/kg). All data are shown as the mean ± SD (n=4 to 6).

Figure 17. Time and dose dependent effects of very low dose DP47GS IgG-(IL-2)$_2$ on Tregs in naïve healthy cynomolgus monkeys. (A) time dependent changes in Treg fold increases following administration of 0.7 and 2 μg/kg DP47GS IgG-(IL-2)$_2$. (B) time dependent changes in Treg pSTAT5a measured on day 0 before treatment and on days 1-4 after treatment, (C) time dependent changes in Teff/mem cell pSTAT5a. All data are shown as the mean ± SD (n=3 at 0.7 μg/kg and n=8 at 2 μg/kg).

Figure 18. Dose dependent comparison of DP47GS IgG-IL-2 versus DP47GS IgG-(IL-2)$_2$ and their ability to increase whole blood cynomolgus Tregs. All data are presented as the mean ± SD (n=3 to 6).

Figure 19. High dose IL-2 induces eosinophilia in cynomolgus monkeys. Changes in blood eosinophil counts were monitored in all tests with Proleukin® or the immunoconjugates of IL-2. Eosinophilia was detected 7 to 14 days after treatment with high dose Proleukin® (2x10$^5$ IU/kg 3

times per week for 2 weeks) or the higher doses of DP47GS IgG-IL-2. Baseline eosinophil counts are the shaded bar on the left and those following DP47GS IgG-$(IL\text{-}2)_2$ at 6 μg/kg are the shaded bar on the right. (A) eosinophil counts from every animal in each dose group and (B) eosinophil counts only from those whose eosinophils increased after treatment. Data are shown as the mean ± SD.

Figure 20. DP47GS IgG-IL-2 has enhanced PK properties compared to Proleukin®. NOD mice were injected intraperitoneally (IP) (left panel) or subcutaneously (SC) (right panel) with the indicated doses of DP47GS IgG-IL-2 or Proleukin®. Human IL-2 was assessed in serum samples at the indicated times by a mAb-based capture assay and the limit of detection for each assay is shown as a horizontal line across each graph.

Figure 21. Both CD25 and FOXP3 increase in murine Tregs after treatment with Proleukin®, DP47GS IgG-IL-2, and DP47GS IgG-$(IL\text{-}2)_2$. BALB/c mice were treated with Proleukin® (20,000 and 100,000 IU/mouse, n=3), DP47GS IgG-IL-2, or DP47GS IgG-$(IL\text{-}2)_2$ (60, 300, or 1,500 IU/mouse, n=3), vehicle treated mice were included as unstimulated controls (n=4). Twenty-four hours after treatment, splenic Tregs were assessed for CD25 and FOXP3 levels. (A) dose dependent changes in cell surface CD25 and (B) dose dependent changes in intracellular FOXP3 were observed for all three IL2 molecules. The mean MFI for the vehicle mice was 4,900 for CD25 and 1,566 for FOXP3. The data are represented as the mean ± SD (n=3).

Figure 22. *In vivo* treatment with DP47GS IgG-IL-2 suppresses murine sheep red blood cell delayed type hypersensitivity (DTH). All data are shown for individual mice treated with vehicle (100% response), IgG-IL-2 (4,000 IU/mouse), or mouse CTLA-4-Ig as a positive control (200 μg/mouse). (A) results from NOD mice and (B) C57BL/6 mice. The magnitude of the day four DTH responses are shown as the change in paw weight compared to non-immunized mice (Δ paw weight). Data are shown as the mean ± SD.

Figure 23. *In vivo* treatment with DP47GS IgG-IL-2 (4,000 IU/mouse) suppresses the murine IgG antibody responses to KLH in (A) C57BL/6 mice 21 days after immunization and (B) NOD mice seven days after immunization. Data are shown as the mean ± SD.

## Detailed Description of the Invention

### Definitions

Terms are used herein as generally used in the art, unless otherwise defined in the following.

As used herein, the term "fusion protein" refers to a fusion polypeptide molecule comprising an immunoglobulin molecule and an IL-2 molecule, wherein the components of the fusion protein are linked to each other by peptide-bonds, either directly or through peptide linkers. For clarity, the individual peptide chains of the immunoglobulin component of the fusion protein may be linked non-covalently, e.g. by disulfide bonds.

"Fused" refers to components that are linked by peptide bonds, either directly or via one or more peptide linkers.

By "specific binding" is meant that the binding is selective for the antigen and can be discriminated from unwanted or non-specific interactions. The ability of an immunoglobulin to bind to a specific antigen can be measured either through an enzyme-linked immunosorbent assay (ELISA) or other techniques familiar to one of skill in the art, e.g. Surface Plasmon Resonance (SPR) technique (analyzed on a BIAcore instrument) (Liljeblad et al., Glyco J 17, 323-329 (2000)), and traditional binding assays (Heeley, Endocr Res 28, 217-229 (2002)). In one embodiment, the extent of binding of an immunoglobulin to an unrelated protein is less than about 10% of the binding of the immunoglobulin to the antigen as measured, e.g. by SPR. In certain embodiments, an immunoglobulin that binds to the antigen has a dissociation constant ($K_D$) of $\leq$ 1 μM, $\leq$ 100 nM, $\leq$ 10 nM, $\leq$ 1 nM, $\leq$ 0.1 nM, $\leq$ 0.01 nM, or $\leq$ 0.001 nM (e.g. $10^{-8}$ M or less, e.g. from $10^{-8}$ M to $10^{-13}$ M, e.g. from $10^{-9}$ M to $10^{-13}$ M).

"Affinity" or "binding affinity" refers to the strength of the sum total of non-covalent interactions between a single binding site of a molecule (e.g. an antibody) and its binding partner (e.g. an antigen). Unless indicated otherwise, as used herein, "binding affinity" refers to intrinsic binding affinity which reflects a 1:1 interaction between members of a binding pair (e.g. antibody and antigen). The affinity of a molecule X for its partner Y can generally be represented by the dissociation constant ($K_D$), which is the ratio of dissociation and association rate constants ($k_{off}$ and $k_{on}$, respectively). Thus, equivalent affinities may comprise different rate constants, as long as the ratio of the rate constants remains the same. Affinity can be measured by common methods known in the art, including those described herein. A particular method for measuring affinity is Surface Plasmon Resonance (SPR).

"Reduced binding", for example reduced binding to an Fc receptor, refers to a decrease in affinity for the respective interaction, as measured for example by SPR. For clarity the term includes also reduction of the affinity to zero (or below the detection limit of the analytic method), i.e. complete abolishment of the interaction. Conversely, "increased binding" refers to an increase in binding affinity for the respective interaction.

As used herein, the term "antigenic determinant" is synonymous with "antigen" and refers to a site (e.g. a contiguous stretch of amino acids or a conformational configuration made up of different regions of non-contiguous amino acids) on a polypeptide macromolecule to which an antibody binds, forming an antibody-antigen complex. Useful antigenic determinants can be found, for example, on the surfaces of cells, free in blood serum, and/or in the extracellular matrix (ECM).

As used herein, the term "single-chain" refers to a molecule comprising amino acid monomers linearly linked by peptide bonds.

The term "antibody" herein is used in the broadest sense and encompasses various antibody structures, including but not limited to monoclonal antibodies, polyclonal antibodies, multispecific antibodies (e.g., bispecific antibodies), and antibody fragments so long as they exhibit the desired antigen-binding activity.

An "antibody fragment" refers to a molecule other than an intact antibody that comprises a portion of an intact antibody that binds the antigen to which the intact antibody binds. Examples of antibody fragments include but are not limited to Fv, Fab, Fab', Fab'-SH, $F(ab')_2$, diabodies, linear antibodies, single-chain antibody molecules (e.g. scFv), and single-domain antibodies.

The term "immunoglobulin molecule" refers to a protein having the structure of a naturally occurring antibody. For example, immunoglobulins of the IgG class are heterotetrameric glycoproteins of about 150,000 daltons, composed of two light chains and two heavy chains that are disulfide-bonded. From N- to C-terminus, each immunoglobulin heavy chain has a variable region (VH), also called a variable heavy domain or a heavy chain variable domain, followed by three constant domains (CH1, CH2, and CH3), also called a heavy chain constant region. Similarly, from N- to C-terminus, each immunoglobulin light chain has a variable region (VL), also called a variable light domain or a light chain variable domain, followed by a constant light (CL) domain, also called a light chain constant region. The heavy chain of an immunoglobulin may be assigned to one of five classes, called α (IgA), δ (IgD), ε (IgE), γ (IgG), or μ (IgM), some of which may be further divided into subclasses, e.g. $\gamma_1$ ($IgG_1$), $\gamma_2$ ($IgG_2$), $\gamma_3$ ($IgG_3$), $\gamma_4$ ($IgG_4$), $\alpha_1$ ($IgA_1$) and $\alpha_2$ ($IgA_2$). The light chain of an immunoglobulin may be assigned to one of two types, called kappa (κ) and lambda (λ), based on the amino acid sequence of its constant domain. An immunoglobulin essentially consists of two Fab molecules and an Fc domain, linked via the immunoglobulin hinge region.

As used herein, "Fab fragment" refers to an immunoglobulin fragment comprising a VL domain and a constant domain of a light chain (CL), and a VH domain and a first constant domain (CH1) of a heavy chain.

The "class" of an antibody or immunoglobulin refers to the type of constant domain or constant region possessed by its heavy chain. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., $IgG_1$, $IgG_2$, $IgG_3$, $IgG_4$, $IgA_1$, and $IgA_2$. The heavy chain constant domains that correspond to the different classes of immunoglobulins are called $\alpha$, $\delta$, $\varepsilon$, $\gamma$, and $\mu$, respectively.

The term "variable region" or "variable domain" refers to the domain of an immunoglobulin or antibody heavy or light chain that is generally involved in binding the immunoglobulin or antibody to antigen. However, the immunoglobulin comprised in the fusion protein of the present invention may comprise variable regions which do not confer antigen-binding specificity. The variable domains of the heavy chain and light chain (VH and VL, respectively) of an immunoglobulin or antibody generally have similar structures, with each domain comprising four conserved framework regions (FRs) and three hypervariable regions (HVRs). See, e.g. Kindt et al., Kuby Immunology, 6th ed., W.H. Freeman and Co., page 91 (2007). A single VH or VL domain may be sufficient to confer antigen-binding specificity.

The term "hypervariable region" or "HVR", as used herein, refers to each of the regions of an immunoglobulin or antibody variable domain which are hypervariable in sequence and/or form structurally defined loops ("hypervariable loops"). Generally, native four-chain antibodies comprise six HVRs; three in the VH (H1, H2, H3), and three in the VL (L1, L2, L3). HVRs generally comprise amino acid residues from the hypervariable loops and/or from the complementarity determining regions (CDRs), the latter being of highest sequence variability and/or involved in antigen recognition. Exemplary hypervariable loops occur at amino acid residues 26-32 (L1), 50-52 (L2), 91-96 (L3), 26-32 (H1), 53-55 (H2), and 96-101 (H3) (Chothia and Lesk, J. Mol. Biol. 196, 901-917 (1987)). Exemplary CDRs (CDR-L1, CDR-L2, CDR-L3, CDR-H1, CDR-H2, and CDR-H3) occur at amino acid residues 24-34 of L1, 50-56 of L2, 89-97 of L3, 31-35B of H1, 50-65 of H2, and 95-102 of H3 (Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD (1991)). With the exception of CDR1 in VH, CDRs generally comprise the amino acid residues that form the hypervariable loops. CDRs also comprise "specificity determining residues," or "SDRs," which are residues that contact antigen. SDRs are contained within regions of the CDRs called abbreviated-CDRs, or a-CDRs. Exemplary a-CDRs (a-CDR-L1, a-

CDR-L2, a-CDR-L3, a-CDR-H1, a-CDR-H2, and a-CDR-H3) occur at amino acid residues 31-34 of L1, 50-55 of L2, 89-96 of L3, 31-35B of H1, 50-58 of H2, and 95-102 of H3 (see Almagro and Fransson, Front. Biosci. 13, 1619-1633 (2008)). Unless otherwise indicated, HVR residues and other residues in the variable domain (e.g. FR residues) are numbered herein according to Kabat et al., supra (refered to as "Kabat numbering").

"Framework" or "FR" refers to variable domain residues other than hypervariable region (HVR) residues. The FR of a variable domain generally consists of four FR domains: FR1, FR2, FR3, and FR4. Accordingly, the HVR and FR sequences generally appear in the following sequence in VH (or VL): FR1-H1(L1)-FR2-H2(L2)-FR3-H3(L3)-FR4.

A "human immunoglobulin" is one which possesses an amino acid sequence which corresponds to that of an immunoglobulin produced by a human or a human cell or derived from a non-human source that utilizes human immunoglobulin repertoires or other human immunoglobulin-encoding sequences. This definition of a human immunoglobulin specifically excludes a humanized immunoglobulin comprising non-human antigen-binding residues.

The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical and/or bind the same epitope, except for possible variant antibodies, e.g. containing naturally occurring mutations or arising during production of a monoclonal antibody preparation, such variants generally being present in minor amounts. In contrast to polyclonal antibody preparations, which typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody of a monoclonal antibody preparation is directed against a single determinant on an antigen. Thus, the modifier "monoclonal" indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies to be used in accordance with the present invention may be made by a variety of techniques, including but not limited to the hybridoma method, recombinant DNA methods, phage-display methods, and methods utilizing transgenic animals containing all or part of the human immunoglobulin loci, such methods and other exemplary methods for making monoclonal antibodies being described herein.

The term "Fc domain" or "Fc region" herein is used to define a C-terminal region of an immunoglobulin heavy chain that contains at least a portion of the constant region. The term includes native sequence Fc regions and variant Fc regions. An IgG Fc region comprises an IgG CH2 and an IgG CH3 domain. The "CH2 domain" of a human IgG Fc region usually extends

from an amino acid residue at about position 231 to an amino acid residue at about position 340. In one embodiment, a carbohydrate chain is attached to the CH2 domain. The CH2 domain herein may be a native sequence CH2 domain or variant CH2 domain. The "CH3 domain" comprises the stretch of residues C-terminal to a CH2 domain in an Fc region (i.e. from an amino acid residue at about position 341 to an amino acid residue at about position 447 of an IgG). The CH3 region herein may be a native sequence CH3 domain or a variant CH3 domain (e.g. a CH3 domain with an introduced "protuberance" ("knob") in one chain thereof and a corresponding introduced "cavity" ("hole") in the other chain thereof; see US Patent No. 5,821,333, expressly incorporated herein by reference). Such variant CH3 domains may be used to promote heterodimerization of two non-identical immunoglobulin heavy chains as herein described. In one embodiment, a human IgG heavy chain Fc region extends from Cys226, or from Pro230, to the carboxyl-terminus of the heavy chain. However, the C-terminal lysine (Lys447) of the Fc region may or may not be present. Unless otherwise specified herein, numbering of amino acid residues in the Fc region or constant region is according to the EU numbering system, also called the EU index, as described in Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD, 1991.

The term "effector functions" refers to those biological activities attributable to the Fc region of an immunoglobulin, which vary with the immunoglobulin isotype. Examples of immunoglobulin effector functions include: C1q binding and complement dependent cytotoxicity (CDC), Fc receptor binding, antibody-dependent cell-mediated cytotoxicity (ADCC), antibody-dependent cellular phagocytosis (ADCP), cytokine secretion, immune complex-mediated antigen uptake by antigen presenting cells, down regulation of cell surface receptors (e.g. B cell receptor), and B cell activation.

An "activating Fc receptor" is an Fc receptor that following engagement by an Fc region of an immunoglobulin elicits signaling events that stimulate the receptor-bearing cell to perform effector functions. Activating Fc receptors include FcγRIIIa (CD16a), FcγRI (CD64), FcγRIIa (CD32), and FcαRI (CD89). A particular activating Fc receptor is human FcγRIIIa (see UniProt accession no. P08637 (version 141)).

The term "interleukin-2" or "IL-2" as used herein, refers to any native IL-2 from any vertebrate source, including mammals such as primates (e.g. humans) and rodents (e.g. mice and rats), unless otherwise indicated. The term encompasses unprocessed IL-2 as well as any form of IL-2 that results from processing in the cell. The term also encompasses naturally occurring variants of IL-2, e.g. splice variants or allelic variants. The amino acid sequence of an exemplary human

IL-2 is shown in SEQ ID NO: 1. Unprocessed human IL-2 additionally comprises an N-terminal 20 amino acid signal peptide, which is absent in the mature IL-2 molecule.

By a "native IL-2", also termed "wild-type IL-2", is meant a naturally occurring IL-2. The sequence of a native human IL-2 molecule is shown in SEQ ID NO: 1. For the purpose of the present invention, the term wild-type also encompasses forms of IL-2 comprising one or more amino acid mutation that does not alter IL-2 receptor binding compared to the naturally occurring, native IL-2, such as e.g. a substitution of cysteine at a position corresponding to residue 125 of human IL-2 to alanine. In some embodiments wild-type IL-2 for the purpose of the present invention comprises the amino acid substitution C125A (see SEQ ID NO: 3).

The term "CD25" or "IL-2 receptor α" as used herein, refers to any native CD25 from any vertebrate source, including mammals such as primates (e.g. humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length", unprocessed CD25 as well as any form of CD25 that results from processing in the cell. The term also encompasses naturally occurring variants of CD25, e.g. splice variants or allelic variants. In certain embodiments CD25 is human CD25. The amino acid sequence of an exemplary human CD25 (with signal sequence, Avi-tag and His-tag) is shown in SEQ ID NO: 25.

The term "high-affinity IL-2 receptor" as used herein refers to the heterotrimeric form of the IL-2 receptor, consisting of the receptor γ-subunit (also known as common cytokine receptor γ-subunit, $\gamma_c$, or CD132), the receptor β-subunit (also known as CD122 or p70) and the receptor α-subunit (also known as CD25 or p55). The term "intermediate-affinity IL-2 receptor" or "IL-2 receptor βγ" by contrast refers to the IL-2 receptor including only the γ-subunit and the β-subunit, without the α-subunit (for a review see e.g. Olejniczak and Kasprzak, Med Sci Monit 14, RA179-189 (2008)). The amino acid sequences of exemplary human CD122 and CD132 (fused to an Fc region with a His-tag) are shown in SEQ ID NOs 21 and 23, respectively.

By "regulatory T cell" or "Treg cell" is meant a specialized type of $CD4^+$ T cell that can suppress the responses of other T cells. Treg cells are characterized by expression of CD4, the α-subunit of the IL-2 receptor (CD25), and the transcription factor forkhead box P3 (FOXP3) (Sakaguchi, Annu Rev Immunol 22, 531-62 (2004)) and play a critical role in the induction and maintenance of peripheral self-tolerance to antigens, including those expressed by tumors.

By "selective activation of Treg cells" is meant activation of Treg cells essentially without concomitant activation of other T cell subsets (such as $CD4^+$ T helper cells, $CD8^+$ cytotoxic T cells, NK T cells) or natural killer (NK) cells. Methods for identifying and distinguishing these cell types are described in the Examples. Activation may include induction of IL-2 receptor

signaling (as measured e.g. by detection of phosphorylated STAT5a), induction of proliferation (as measured e.g. by detection of Ki-67) and/or up-regulation of expression of activation markers (such as e.g. CD25).

The term "peptide linker" refers to a peptide comprising one or more amino acids, typically about 2-20 amino acids. Peptide linkers are known in the art or are described herein. Suitable, non-immunogenic linker peptides include, for example, $(G_4S)_n$, $(SG_4)_n$ or $G_4(SG_4)_n$ peptide linkers. "n" is generally a number between 1 and 10, typically between 2 and 4.

The term "modification" refers to any manipulation of the peptide backbone (e.g. amino acid sequence) or the post-translational modifications (e.g. glycosylation) of a polypeptide.

A "knob-into-hole modification" refers to a modification within the interface between two immunoglobulin heavy chains in the CH3 domain, wherein i) in the CH3 domain of one heavy chain, an amino acid residue is replaced with an amino acid residue having a larger side chain volume, thereby generating a protuberance ("knob") within the interface in the CH3 domain of one heavy chain which is positionable in a cavity ("hole") within the interface in the CH3 domain of the other heavy chain, and ii) in the CH3 domain of the other heavy chain, an amino acid residue is replaced with an amino acid residue having a smaller side chain volume, thereby generating a cavity ("hole") within the interface in the second CH3 domain within which a protuberance ("knob") within the interface in the first CH3 domain is positionable. In one embodiment, the "knob-into-hole modification" comprises the amino acid substitution T366W and optionally the amino acid substitution S354C in one of the antibody heavy chains, and the amino acid substitutions T366S, L368A, Y407V and optionally Y349C in the other one of the antibody heavy chains. The knob-into-hole technology is described e.g. in US 5,731,168; US 7,695,936; Ridgway et al., Prot Eng 9, 617-621 (1996) and Carter, J Immunol Meth 248, 7-15 (2001). Generally, the method involves introducing a protuberance ("knob") at the interface of a first polypeptide and a corresponding cavity ("hole") in the interface of a second polypeptide, such that the protuberance can be positioned in the cavity so as to promote heterodimer formation and hinder homodimer formation. Protuberances are constructed by replacing small amino acid side chains from the interface of the first polypeptide with larger side chains (e.g. tyrosine or tryptophan). Compensatory cavities of identical or similar size to the protuberances are created in the interface of the second polypeptide by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). Introduction of two cysteine residues at position S354 and Y349, respectively, results in formation of a disulfide bridge between the two antibody

heavy chains in the Fc region, further stabilizing the dimer (Carter, J Immunol Methods 248, 7-15 (2001)).

An amino acid "substitution" refers to the replacement in a polypeptide of one amino acid with another amino acid. In one embodiment, an amino acid is replaced with another amino acid having similar structural and/or chemical properties, e.g. conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. Non-conservative substitutions will entail exchanging a member of one of these classes for another class. For example, amino acid substitutions can also result in replacing one amino acid with another amino acid having different structural and/or chemical properties, for example, replacing an amino acid from one group (e.g., polar) with another amino acid from a different group (e.g. basic). Amino acid substitutions can be generated using genetic or chemical methods well known in the art. Genetic methods may include site-directed mutagenesis, PCR, gene synthesis and the like. It is contemplated that methods of altering the side chain group of an amino acid by methods other than genetic engineering, such as chemical modification, may also be useful. Various designations may be used herein to indicate the same amino acid substitution. For example, a substitution from proline at position 329 of the immunoglobulin heavy chain to glycine can be indicated as 329G, G329, $G_{329}$, P329G, or Pro329Gly.

"Percent (%) amino acid sequence identity" with respect to a reference polypeptide sequence is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the reference polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for aligning sequences, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes

herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc., and the source code has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available from Genentech, Inc., South San Francisco, California, or may be compiled from the source code. The ALIGN-2 program should be compiled for use on a UNIX operating system, including digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary. In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

100 times the fraction X/Y

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program.

"Polynucleotide" or "nucleic acid" as used interchangeably herein, refers to polymers of nucleotides of any length, and include DNA and RNA. The nucleotides can be deoxyribonucleotides, ribonucleotides, modified nucleotides or bases, and/or their analogs, or any substrate that can be incorporated into a polymer by DNA or RNA polymerase or by a synthetic reaction. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and their analogs. A sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may comprise modification(s) made after synthesis, such as conjugation to a label.

By a nucleic acid or polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the

polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence. As a practical matter, whether any particular polynucleotide sequence is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs, such as the ones discussed above for polypeptides (e.g. ALIGN-2).

The term "vector" as used herein, refers to a nucleic acid molecule capable of propagating another nucleic acid to which it is linked. The term includes the vector as a self-replicating nucleic acid structure as well as the vector incorporated into the genome of a host cell into which it has been introduced. Certain vectors are capable of directing the expression of nucleic acids to which they are operatively linked. Such vectors are referred to herein as "expression vectors".

The terms "host cell", "host cell line", and "host cell culture" are used interchangeably and refer to cells into which exogenous nucleic acid has been introduced, including the progeny of such cells. Host cells include "transformants" and "transformed cells," which include the primary transformed cell and progeny derived therefrom without regard to the number of passages. Progeny may not be completely identical in nucleic acid content to a parent cell, but may contain mutations. Mutant progeny that have the same function or biological activity as screened or selected for in the originally transformed cell are included herein. A host cell is any type of cellular system that can be used to generate the fusion proteins of the present invention. Host cells include cultured cells, e.g. mammalian cultured cells, such as CHO cells, BHK cells, NS0 cells, SP2/0 cells, YO myeloma cells, P3X63 mouse myeloma cells, PER cells, PER.C6 cells or hybridoma cells, yeast cells, insect cells, and plant cells, to name only a few, but also cells comprised within a transgenic animal, transgenic plant or cultured plant or animal tissue.

An "effective amount" of an agent refers to the amount that is necessary to result in a physiological change in the cell or tissue to which it is administered.

A "therapeutically effective amount" of an agent, e.g. a pharmaceutical composition, refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired therapeutic or prophylactic result. A therapeutically effective amount of an agent for example eliminates, decreases, delays, minimizes or prevents adverse effects of a disease.

An "individual" or "subject" is a mammal. Mammals include, but are not limited to, domesticated animals (e.g. cows, sheep, cats, dogs, and horses), primates (e.g. humans and non-human primates such as monkeys), rabbits, and rodents (e.g. mice and rats). Particularly, the individual or subject is a human.

The term "pharmaceutical composition" refers to a preparation which is in such form as to permit the biological activity of an active ingredient contained therein to be effective, and which contains no additional components which are unacceptably toxic to a subject to which the formulation would be administered.

A "pharmaceutically acceptable carrier" refers to an ingredient in a pharmaceutical composition, other than an active ingredient, which is nontoxic to a subject. A pharmaceutically acceptable carrier includes, but is not limited to, a buffer, excipient, stabilizer, or preservative.

As used herein, "treatment" (and grammatical variations thereof such as "treat" or "treating") refers to clinical intervention in an attempt to alter the natural course of a disease in the individual being treated, and can be performed either for prophylaxis or during the course of clinical pathology. Desirable effects of treatment include, but are not limited to, preventing occurrence or recurrence of disease, alleviation of symptoms, diminishment of any direct or indirect pathological consequences of the disease, preventing metastasis, decreasing the rate of disease progression, amelioration or palliation of the disease state, and remission or improved prognosis. In some embodiments, antibodies of the invention are used to delay development of a disease or to slow the progression of a disease.

"Autoimmune disease" refers to a non-malignant disease or disorder arising from and directed against an individual's own tissues. Examples of autoimmune diseases or disorders include, but are not limited to, inflammatory responses such as inflammatory skin diseases including psoriasis and dermatitis (e.g. atopic dermatitis); responses associated with inflammatory bowel disease (such as Crohn's disease and ulcerative colitis); dermatitis; allergic conditions such as eczema and asthma; rheumatoid arthritis; systemic lupus erythematosus (SLE) (including but not limited to lupus nephritis, cutaneous lupus); diabetes mellitus (e.g. type 1 diabetes mellitus or insulin dependent diabetes mellitus); multiple sclerosis and juvenile onset diabetes.

**Fusion proteins of the invention**

The invention provides novel immunoglobulin-IL-2 fusion proteins with particularly advantageous properties for the use in therapeutic methods as described herein.

In a first aspect, the invention provides a fusion protein comprising (i) an immunoglobulin molecule comprising a modification reducing binding affinity of the immunoglobulin molecule to an Fc receptor as compared to a corresponding immunoglobulin molecule without said modification, and (ii) two interleukin-2 (IL-2) molecules.

In one embodiment, said fusion protein essentially consists of an immunoglobulin molecule comprising a modification reducing binding affinity of the immunoglobulin molecule to an Fc receptor as compared to a corresponding immunoglobulin molecule without said modification, two interleukin-2 (IL-2) molecules, and optionally one or more peptide linker.

As shown in the Examples, a fusion protein comprising two IL-2 molecules surprisingly provides for greatly improved efficacy and selectivity in the activation of regulatory T cells, as compared to a corresponding fusion protein comprising a single IL-2 molecule.

In one embodiment, said immunoglobulin molecule is an IgG-class immunoglobulin molecule, particularly an $IgG_1$-subclass immunoglobulin molecule. In one embodiment, said immunoglobulin molecule is a human immunoglobulin molecule, i.e. it comprises fully human variable and constant regions. The sequence of an exemplary human $IgG_1$ constant region is shown in SEQ ID NO: 8. An IgG-class immunoglobulin molecule comprises (i) two immunoglobulin light chains, each comprising from N- to C-terminus a light chain variable domain (VL) and a light chain constant domain (CL), and (ii) two immunoglobulin heavy chains, each comprising from N-terminus to C-terminus a heavy chain variable domain (VH), a heavy chain constant domain (CH) 1, an immunoglobulin hinge region, a CH2 domain and a CH3 domain. The latter two domains form part of the Fc region of the immunoglobulin molecule. The two heavy chains dimerize in the Fc region.

In one embodiment of the fusion protein according to the invention, said two IL-2 molecules are each fused at their N-terminal amino acid to the C-terminal amino acid of one of the immunoglobulin heavy chains of said immunoglobulin molecule, optionally through a peptide linker. Fusion of two (identical) IL-2 molecules to the immunoglobulin heavy chains allows for simple production of the fusion protein, avoiding the formation of undesired side products and obviating the need for modifications promoting heterodimerization of non-identical heavy chains, such as a knob-into-hole modification.

Fusion of the IL-2 molecules to an immunoglobulin molecule provides for favorable pharmacokinetic properties, including a long serum half-life (due to recycling through binding to FcRn, and molecular size being well above the threshold for renal filtration), as compared to free (unfused) IL-2. Furthermore, the presence of an immunoglobulin molecule also enables simple purification of fusion proteins by e.g. protein A affinity chromatography. At the same time, however, the presence of an immunoglobulin molecule, specifically the Fc region of an immunoglobulin molecule, may lead to undesirable targeting of the fusion protein to cells expressing Fc receptors rather than to the preferred IL-2 receptor bearing cells. Moreover, the engagement of Fc receptors may lead to release of (pro-inflammatory) cytokines and undesired activation of various immune cells other than regulatory T cells. Therefore, said immunoglobulin molecule comprised in the fusion protein of the invention comprises a modification reducing binding affinity of the immunoglobulin molecule to an Fc receptor, as compared to a corresponding immunoglobulin molecule without said modification. In a specific embodiment, said Fc receptor is an Fcγ receptor, particularly a human Fcγ receptor. Binding affinity to Fc receptors can be easily determined e.g. by ELISA, or by Surface Plasmon Resonance (SPR) using standard instrumentation such as a BIAcore instrument (GE Healthcare) and Fc receptors such as may be obtained by recombinant expression. A specific illustrative and exemplary embodiment for measuring binding affinity is described in the following. According to one embodiment, Binding affinity to an Fc receptor is measured by surface plasmon resonance using a BIACORE® T100 machine (GE Healthcare) at 25°C with ligand (Fc receptor) immobilized on CM5 chips. Briefly, carboxymethylated dextran biosensor chips (CM5, GE Healthcare) are activated with N-ethyl-N'-(3-dimethylaminopropyl)-carbodiimide hydrochloride (EDC) and N-hydroxysuccinimide (NHS) according to the supplier's instructions. Recombinant ligand is diluted with 10 mM sodium acetate, pH 5.5, to 0.5-30 μg/ml before injection at a flow rate of 10 μl/min to achieve approximately 100-5000 response units (RU) of coupled protein. Following the injection of the ligand, 1 M ethanolamine is injected to block unreacted groups. For kinetics measurements, three- to five-fold serial dilutions of antibody (range between ~0.01 nM to 300 nM) are injected in HBS-EP+ (GE Healthcare, 10 mM HEPES, 150 mM NaCl, 3 mM EDTA, 0.05% Surfactant P20, pH 7.4) at 25°C at a flow rate of approximately 30-50 μl/min. Association rates ($k_{on}$) and dissociation rates ($k_{off}$) are calculated using a simple one-to-one Langmuir binding model (BIACORE ® T100 Evaluation Software version 1.1.1) by simultaneously fitting the association and dissociation sensorgrams. The equilibrium dissociation constant ($K_D$) is calculated as the ratio $k_{off}/k_{on}$. See, e.g., Chen et al., J Mol Biol 293, 865-881 (1999).

Alternatively, binding affinity antibodies to Fc receptors may be evaluated using cell lines known to express particular Fc receptors, such as NK cells expressing FcγIIIa receptor.

In one embodiment, the modification comprises one or more amino acid mutation that reduces the binding affinity of the immunoglobulin to an Fc receptor. In one embodiment the amino acid mutation is an amino acid substitution. Typically, the same one or more amino acid mutation is present in each of the two immunoglobulin heavy chains. In one embodiment said amino acid mutation reduces the binding affinity of the immunoglobulin to the Fc receptor by at least 2-fold, at least 5-fold, or at least 10-fold. In embodiments where there is more than one amino acid mutation that reduces the binding affinity of the immunoglobulin to the Fc receptor, the combination of these amino acid mutations may reduce the binding affinity of the immunoglobulin to the Fc receptor by at least 10-fold, at least 20-fold, or even at least 50-fold. In one embodiment said immunoglobulin molecule exhibits less than 20%, particularly less than 10%, more particularly less than 5% of the binding affinity to an Fc receptor as compared to a corresponding immunoglobulin molecule without said modification.

In one embodiment, said Fc receptor is an activating Fc receptor. In a specific embodiment, said Fc receptor is selected from the group of FcγRIIIa (CD16a), FcγRI (CD64), FcγRIIa (CD32) and FcαRI (CD89). In a specific embodiment the Fc receptor is an Fcγ receptor, more specifically an FcγRIIIa, FcγRI or FcγRIIa receptor. Preferably, binding affinity to each of these receptors is reduced. In an even more specific embodiment, said Fc receptor is FcγIIIa, particularly human FcγIIIa. In some embodiments binding affinity to a complement component, specifically binding affinity to C1q, is also reduced. In one embodiment binding affinity to neonatal Fc receptor (FcRn) is not reduced. Substantially similar binding to FcRn, i.e. preservation of the binding affinity of the immunoglobulin molecule to said receptor, is achieved when the immunoglobulin molecule exhibits greater than about 70% of the binding affinity of an unmodified form of the immunoglobulin molecule to FcRn. Immunoglobulin molecules comprised in the fusion proteins of the invention may exhibit greater than about 80% and even greater than about 90% of such affinity.

In one embodiment, said modification reducing binding affinity of the immunoglobulin molecule to an Fc receptor is in the Fc region, particularly the CH2 region, of the immunoglobulin molecule. In one embodiment, said immunoglobulin molecule comprises an amino acid substitution at position 329 (EU numbering) of the immunoglobulin heavy chains. In a more specific embodiment said amino acid substitution is P329A or P329G, particularly P329G. In

one embodiment, said immunoglobulin molecule comprises amino acid substitutions at positions 234 and 235 (EU numbering) of the immunoglobulin heavy chains. In a specific embodiment, said amino acid substitutions are L234A and L235A (LALA). In one embodiment said immunoglobulin molecule comprises an amino acid substitution at position 329 (EU numbering) of the antibody heavy chains and a further amino acid substitution at a position selected from position 228, 233, 234, 235, 297 and 331 of the immunoglobulin heavy chains. In a more specific embodiment the further amino acid substitution is S228P, E233P, L234A, L235A, L235E, N297A, N297D or P331S. In a particular embodiment, said immunoglobulin molecule comprises amino acid substitutions at positions P329, L234 and L235 (EU numbering) of the immunoglobulin heavy chains. In a more particular embodiment, said immunoglobulin molecule comprises the amino acid substitutions L234A, L235A and P329G (LALA P329G) in the immunoglobulin heavy chains. This combination of amino acid substitutions particularly efficiently abolishes Fcγ receptor binding of a human IgG-class immunoglobulin, as described in PCT publication no. WO 2012/130831, incorporated herein by reference in its entirety. PCT publication no. WO 2012/130831 also describes methods of preparing such modified immunoglobulin and methods for determining its properties such as Fc receptor binding or effector functions.

Immunoglobulins comprising modifications in the immunoglobulin heavy chains can be prepared by amino acid deletion, substitution, insertion or modification using genetic or chemical methods well known in the art. Genetic methods may include site-specific mutagenesis of the encoding DNA sequence, PCR, gene synthesis, and the like. The correct nucleotide changes can be verified for example by sequencing.

Immunoglobulins or antibodies which comprise modifications reducing Fc receptor binding generally have reduced effector functions, particularly reduced ADCC, as compared to corresponding unmodified immunoglobulins or antibodies. Hence, in one embodiment, said modification reducing binding affinity of the immunoglobulin molecule to an Fc receptor reduces effector function of the immunoglobulin molecule. In a specific embodiment, said effector function is antibody-dependent cell-mediated cytotoxicity (ADCC). In one embodiment, ADCC is reduced to less than 20% of the ADCC induced by a corresponding immunoglobulin molecule without said modification. Effector function of an immunoglobulin or antibody can be measured by methods known in the art. Examples of *in vitro* assays to assess ADCC activity of a molecule of interest are described in U.S. Patent No. 5,500,362; Hellstrom et al. Proc Natl Acad

Sci USA 83, 7059-7063 (1986) and Hellstrom et al., Proc Natl Acad Sci USA 82, 1499-1502 (1985); U.S. Patent No. 5,821,337; Bruggemann et al., J Exp Med 166, 1351-1361 (1987). Alternatively, non-radioactive assays methods may be employed (see, for example, ACTI™ non-radioactive cytotoxicity assay for flow cytometry (CellTechnology, Inc. Mountain View, CA); and CytoTox 96® non-radioactive cytotoxicity assay (Promega, Madison, WI)). Useful effector cells for such assays include peripheral blood mononuclear cells (PBMC) and Natural Killer (NK) cells. Alternatively, or additionally, ADCC activity of the molecule of interest may be assessed *in vivo*, e.g. in an animal model such as that disclosed in Clynes et al., Proc Natl Acad Sci USA 95, 652-656 (1998). In some embodiments binding of the immunoglobulin molecule to a complement component, specifically to C1q, is also reduced. Accordingly, complement-dependent cytotoxicity (CDC) may also be reduced. C1q binding assays may be carried out to determine whether the immunoglobulin is able to bind C1q and hence has CDC activity. See e.g. C1q and C3c binding ELISA in WO 2006/029879 and WO 2005/100402. To assess complement activation, a CDC assay may be performed (see, for example, Gazzano-Santoro et al., J Immunol Methods 202, 163 (1996); Cragg et al., Blood 101, 1045-1052 (2003); and Cragg and Glennie, Blood 103, 2738-2743 (2004)).

In addition to the immunoglobulin molecules described hereinabove and in PCT publication no. WO 2012/130831, immunoglobulins with reduced Fc receptor binding and/or effector function also include those with substitution of one or more of Fc region residues 238, 265, 269, 270, 297, 327 and 329 (U.S. Patent No. 6,737,056). Such Fc mutants include Fc mutants with substitutions at two or more of amino acid positions 265, 269, 270, 297 and 327, including the so-called "DANA" Fc mutant with substitution of residues 265 and 297 to alanine (US Patent No. 7,332,581).

$IgG_4$-subclass immunoglobulins exhibit reduced binding affinity to Fc receptors and reduced effector functions as compared to $IgG_1$ immunoglobulins. Hence, in some embodiments, said immunoglobulin molecule comprised in the fusion protein of the invention is an $IgG_4$-subclass immunoglobulin, particularly a human $IgG_4$-subclass immunoglobulin. In one embodiment said $IgG_4$-subclass immunoglobulin comprises amino acid substitutions in the Fc region at position S228, specifically the amino acid substitution S228P. To further reduce its binding affinity to an Fc receptor and/or its effector function, in one embodiment, said $IgG_4$-subclass immunoglobulin comprises an amino acid substitution at position L235, specifically the amino acid substitution L235E. In another embodiment, said $IgG_4$-subclass immunoglobulin comprises an amino acid

substitution at position P329, specifically the amino acid substitution P329G. In a particular embodiment, said $IgG_4$-subclass immunoglobulin comprises amino acid substitutions at positions S228, L235 and P329, specifically amino acid substitutions S228P, L235E and P329G. Such modified $IgG_4$-subclass immunoglobulins and their Fcγ receptor binding properties are described in PCT publication no. WO 2012/130831, incorporated herein by reference in its entirety.

In one embodiment, said immunoglobulin molecule is capable of specific binding to an antigen. In one embodiment, said immunoglobulin molecule is a monoclonal antibody. In one embodiment, said immunoglobulin molecule is not capable of specific binding to an antigen, particularly not capable of specific binding to a human antigen. The absence of specific binding of such an immunoglobulin molecule to an antigen (i.e. the absence of any binding that can be discriminated from non-specific interaction) can be determined e.g. by ELISA or surface plasmon resonance as described herein. Such an immunoglobulin molecule is particularly useful e.g. for enhancing the serum half-life of the fusion protein, where targeting to a particular tissue is not desired.

In one embodiment, said immunoglobulin molecule comprises a heavy chain variable region sequence based on the human Vh3-23 germline sequence. In a specific embodiment, said immunoglobulin molecule comprises a heavy chain variable region sequence that is at least 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 9. In one embodiment, said immunoglobulin molecule comprises a light chain variable region sequence based on the human Vk3-20 germline sequence. In a specific embodiment, said immunoglobulin molecule comprises a light chain variable region sequence that is at least 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 11. In an even more specific embodiment, said immunoglobulin molecule comprises the heavy chain variable region sequence of SEQ ID NO: 9 and the light chain variable region sequence of SEQ ID NO: 11. Immunoglobulin molecules comprising these variable region sequences are not capable of specific binding to an antigen, particularly a human antigen. They lack binding to normal tissues as well as PBMCs, have no polyreactivity and show no non-specific accumulation *in vivo* by imaging (data not shown). The variable region sequences are entirely based on human germline sequences, with the exception of the heavy chain CDR 3 wherein a GSG sequence has been introduced to generate a non-binding immunoglobulin.

In one embodiment, said IL-2 molecules are wild-type IL-2 molecules. In one embodiment, said IL-2 molecules are human IL-2 molecules. In a specific embodiment, said IL-2 molecules comprise the sequence of SEQ ID NO: 1 (native human IL-2).

In one embodiment, said IL-2 molecule comprises an amino acid substitution at a position corresponding to residue 125 of human IL-2. In one embodiment said amino acid substitution is C125A. In a specific embodiment, said IL-2 molecule comprises the sequence of SEQ ID NO: 3 (human IL-2 with the amino acid substitution C125A). Alternatively, the cysteine at position 125 may be replaced with another neutral amino acid such as serine, threonine or valine, yielding C125S IL-2, C125T IL-2 or C125V IL-2 respectively, as described in U.S. Patent no. 4,518,584. As described therein, one may also delete the N-terminal alanine residue of IL-2 yielding such mutants as des-A1 C125S or des-A1 C125A. Alternatively or conjunctively, the IL-2 molecule may include a mutation whereby methionine normally occurring at position 104 of wild-type human IL-2 is replaced by a neutral amino acid such as alanine (see U.S. Patent no. 5,206,344). Such modifications in human IL-2 may provide additional advantages such as increased expression or stability.

The IL-2 molecules comprised in the fusion protein of the invention may also be unglycosylated IL-2 molecules. For example, elimination of the O-glycosylation site of the IL-2 molecule results in a more homogenous product when the fusion protein is expressed in mammalian cells such as CHO or HEK cells. Thus, in certain embodiments the IL-2 molecule comprises a modification which eliminates the O-glycosylation site of IL-2 at a position corresponding to residue 3 of human IL-2. In one embodiment said modification which eliminates the O-glycosylation site of IL-2 at a position corresponding to residue 3 of human IL-2 is an amino acid substitution. Exemplary amino acid substitutions include T3A, T3G, T3Q, T3E, T3N, T3D, T3R, T3K, and T3P. In a specific embodiment, said modification is the amino acid substitution T3A.

In one embodiment, the fusion protein is capable of binding to IL-2 βγ receptor with an affinity constant ($K_D$) of smaller than 10 nM, particularly smaller than 3 nM, when measured by SPR at 25°C. In a specific embodiment, said IL-2 βγ receptor is human IL-2 βγ receptor. In one embodiment, the fusion protein is capable of binding to IL-2 α receptor with an affinity constant ($K_D$) of smaller than 100 nM, particularly smaller than 20 nM, when measured by SPR at 25°C. In a specific embodiment, said IL-2 α receptor is human IL-2 α receptor. A method for measuring binding affinity to IL-2 βγ or IL-2 α receptor by SPR is described herein. According to one embodiment, binding affinity ($K_D$) is measured by surface plasmon resonance using a

BIACORE® T100 machine (GE Healthcare) at 25°C with IL-2 receptors immobilized on CM5 chips. Briefly, carboxymethylated dextran biosensor chips (CM5, GE Healthcare) are activated with N-ethyl-N'-(3-dimethylaminopropyl)-carbodiimide hydrochloride (EDC) and N-hydroxysuccinimide (NHS) according to the supplier's instructions. Recombinant IL-2 receptor is diluted with 10 mM sodium acetate, pH 5.5, to 0.5-30 µg/ml before injection at a flow rate of 10 µl/minute to achieve approximately 200-1000 (for IL-2R α) or 500-3000 (for IL-2R βγ heterodimer) response units (RU) of coupled protein. Following the injection of IL-2 receptor, 1 M ethanolamine is injected to block unreacted groups. For kinetics measurements, three-fold serial dilutions of fusion protein (range between ~3 nM to 300 nM) are injected in HBS-EP+ (GE Healthcare, 10 mM HEPES, 150 mM NaCl, 3 mM EDTA, 0.05% Surfactant P20, pH 7.4) at 25°C at a flow rate of approximately 30 µl/min. Association rates ($k_{on}$) and dissociation rates ($k_{off}$) are calculated using a simple one-to-one Langmuir binding model (BIACORE ® T100 Evaluation Software version 1.1.1) by simultaneously fitting the association and dissociation sensorgrams. The equilibrium dissociation constant ($K_D$) is calculated as the ratio $k_{off}/k_{on}$. See, e.g., Chen et al., J Mol Biol 293, 865-881 (1999).

In a particular aspect, the invention provides a fusion protein comprising (i) an $IgG_1$-subclass immunoglobulin molecule comprising the amino acid substitutions L234A, L235A and P329G (EU numbering) in the immunoglobulin heavy chains, and (ii) two interleukin-2 (IL-2) molecules, each fused at its N-terminal amino acid to the C-terminal amino acid of one of the immunoglobulin heavy chains through a peptide linker. In one embodiment said immunoglobulin molecule and said IL-2 molecules are human. In a specific embodiment, said immunoglobulin molecule comprises the heavy chain variable region sequence of SEQ ID NO: 9 and the light chain variable region sequence of SEQ ID NO: 11. In a further specific embodiment, said IL-2 molecules each comprise the amino acid sequence of SEQ ID NO: 3. In an even more specific embodiment, said fusion protein comprises a polypeptide sequence that is at least about 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 17, and a polypeptide sequence that is at least about 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 19.

As shown in the Examples, the fusion protein of the invention can be used to selectively activate regulatory T cells (i.e. essentially without concomitant activation of other T cell subsets and/or NK cells). Thus, the invention particularly provides the fusion protein for use in selective activation of regulatory T cells *in vitro* or *in vivo*. In one embodiment, said use comprises

contacting regulatory T cells with said fusion protein *in vitro* or *in vivo*. In one embodiment, said use further comprises contacting other (non-regulatory) T cells with said fusion protein. In one embodiment, said use is *in vitro* and said fusion protein is used at a concentration of about 1 ng/mL or less, particularly about 0.1 ng/mL or less. In another embodiment, said use is *in vivo* and said fusion protein is used at a dose of about 20 μg/kg body weight or less, particularly about 12 μg/kg body weight or less, more particularly about 6 μg/kg body weight or less (wherein "body weight" refers to the body weight of the individual to whom the fusion protein is administered).

The invention also provides a method for selective activation of regulatory T cells *in vitro* or *in vivo*, comprising contacting said regulatory T cells with the fusion protein of the invention. In one embodiment, said method further comprises contacting other (non-regulatory) T cells with said fusion protein. In one embodiment, said activation comprises induction of proliferation and/or induction of IL-2 receptor signaling. In one embodiment, said method is *in vitro* and said fusion protein is used at a concentration of about 1 ng/mL or less, particularly about 0.1 ng/mL or less. In another embodiment, said method is *in vivo* and said fusion protein is used at a dose of about 20 μg/kg body weight or less, particularly about 12 μg/kg body weight or less, more particularly about 6 μg/kg body weight or less (wherein "body weight" refers to the body weight of the individual to whom the fusion protein is administered).

According to certain embodiments of the use or method described in the preceding paragraphs, said activation comprises induction of proliferation of regulatory T cells and/or induction of IL-2 receptor signaling in regulatory T cells. Induction of proliferation can be measured e.g. by detection of the intracellular proliferation marker Ki-67, as described in the Examples. In one embodiment, proliferation of regulatory T cells activated by the fusion protein of the invention is increased at least about 1.5-fold, at least about 2-fold, or at least about 3-fold, as compared to proliferation of non-activated regulatory T cells. In one embodiment, proliferation of other (non-regulatory) T cells and/or NK cells contacted with the fusion protein of the invention is increased less than about 1.5 fold, less than about 1.2 fold, or less than about 1.1 fold, as compared to proliferation of corresponding cells not contacted with said fusion protein. Induction of IL-2 receptor signaling can be measured e.g. by detection of phosphorylated STAT5, as described in the Examples. In one embodiment, IL-2 receptor signaling in regulatory T cells activated by the fusion protein of the invention is increased at least about 1.5-fold, at least about 2-fold, at least about 3-fold, or at least about 5-fold, as compared to IL-2 receptor signaling in non-activated

regulatory T cells. In one embodiment, IL-2 receptor signaling in other (non-regulatory) T cells and/or NK cells contacted with the fusion protein or the invention is increased less than about 1.5 fold, or less than about 1.2 fold, or less than about 1.1 fold, as compared to IL-2 receptor signaling in corresponding cells not contacted with said fusion protein.

**Polynucleotides**

The invention further provides polynucleotides encoding a fusion as described herein or a fragment thereof.

Polynucleotides of the invention include those that are at least about 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the sequences set forth in SEQ ID NOs 2, 4, 5, 6, 7, 10, 12, 18 and 20 including functional fragments or variants thereof.

The polynucleotides encoding fusion proteins of the invention may be expressed as a single polynucleotide that encodes the entire fusion protein or as multiple (e.g., two or more) polynucleotides that are co-expressed. Polypeptides encoded by polynucleotides that are co-expressed may associate through, e.g., disulfide bonds or other means to form a functional fusion protein. For example, the light chain portion of an immunoglobulin may be encoded by a separate polynucleotide from the heavy chain portion of the immunoglobulin. When co-expressed, the heavy chain polypeptides will associate with the light chain polypeptides to form the immunoglobulin.

In one embodiment, the present invention is directed to a polynucleotide encoding a fusion protein of an immunoglobulin molecule and two IL-2 molecules, or a fragment thereof, wherein the polynucleotide comprises a sequence that encodes a variable region sequence as shown in SEQ ID NO 9 or 11. In another embodiment, the present invention is directed to a polynucleotide encoding a fusion protein of an immunoglobulin molecule and two IL-2 molecules, or a fragment thereof, wherein the polynucleotide comprises a sequence that encodes a polypeptide sequence as shown in SEQ ID NO 17 or 19. In another embodiment, the invention is further directed to a polynucleotide encoding a fusion protein of an immunoglobulin molecule and two IL-2 molecules, or a fragment thereof, wherein the polynucleotide comprises a sequence that is at least about 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to a nucleic acid sequence shown SEQ ID NO 2, 4, 5, 6, 7, 10, 12, 18 or 20. In another embodiment, the invention is directed to a polynucleotide encoding a fusion protein of an immunoglobulin molecule and two IL-2 molecules, or a fragment thereof, wherein the polynucleotide comprises a nucleic acid sequence shown in SEQ ID NO 2, 4, 5, 6, 7, 10, 12, 18 or 20. In another embodiment, the invention is directed to a polynucleotide encoding a fusion protein of an immunoglobulin

molecule and two IL-2 molecules, or a fragment thereof, wherein the polynucleotide comprises a sequence that encodes a variable region sequence that is at least about 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of SEQ ID NO 9 or 11. In another embodiment, the invention is directed to a polynucleotide encoding a fusion protein of an immunoglobulin molecule and two IL-2 molecules, or a fragment thereof, wherein the polynucleotide comprises a sequence that encodes a polypeptide sequence that is at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of SEQ ID NO 17 or 19. The invention encompasses a polynucleotide encoding an a fusion protein of an immunoglobulin molecule and two IL-2 molecules, or a fragment thereof, wherein the polynucleotide comprises a sequence that encodes the variable region sequences of SEQ ID NO 9 or 11 with conservative amino acid substitutions. The invention also encompasses a polynucleotide encoding a fusion protein of an immunoglobulin molecule and two IL-2 molecules, or a fragment thereof, wherein the polynucleotide comprises a sequence that encodes the polypeptide sequences of SEQ ID NO 17 or 19 with conservative amino acid substitutions. In certain embodiments the polynucleotide or nucleic acid is DNA. In other embodiments, a polynucleotide of the present invention is RNA, for example, in the form of messenger RNA (mRNA). RNA of the present invention may be single stranded or double stranded.

**Recombinant methods**

Fusion proteins of the invention may be obtained, for example, by solid-state peptide synthesis (e.g. Merrifield solid phase synthesis) or recombinant production. For recombinant production one or more polynucleotide encoding the fusion protein (fragment), e.g., as described above, is isolated and inserted into one or more vectors for further cloning and/or expression in a host cell. Such polynucleotide may be readily isolated and sequenced using conventional procedures. In one embodiment a vector, preferably an expression vector, comprising one or more of the polynucleotides of the invention is provided. Methods which are well known to those skilled in the art can be used to construct expression vectors containing the coding sequence of a fusion protein (fragment) along with appropriate transcriptional/translational control signals. These methods include *in vitro* recombinant DNA techniques, synthetic techniques and *in vivo* recombination/genetic recombination. See, for example, the techniques described in Maniatis et al., MOLECULAR CLONING: A LABORATORY MANUAL, Cold Spring Harbor Laboratory, N.Y. (1989); and Ausubel et al., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, Greene Publishing Associates and Wiley Interscience, N.Y (1989). The expression vector can be part of a plasmid, virus, or may be a nucleic acid fragment. The expression vector includes an expression cassette

into which the polynucleotide encoding the fusion protein (fragment) (i.e. the coding region) is cloned in operable association with a promoter and/or other transcription or translation control elements. As used herein, a "coding region" is a portion of nucleic acid which consists of codons translated into amino acids. Although a "stop codon" (TAG, TGA, or TAA) is not translated into an amino acid, it may be considered to be part of a coding region, if present, but any flanking sequences, for example promoters, ribosome binding sites, transcriptional terminators, introns, 5' and 3' untranslated regions, and the like, are not part of a coding region. Two or more coding regions can be present in a single polynucleotide construct, e.g. on a single vector, or in separate polynucleotide constructs, e.g. on separate (different) vectors. Furthermore, any vector may contain a single coding region, or may comprise two or more coding regions, e.g. a vector of the present invention may encode one or more polypeptides, which are post- or co-translationally separated into the final proteins via proteolytic cleavage. In addition, a vector, polynucleotide, or nucleic acid of the invention may encode heterologous coding regions, either fused or unfused to a polynucleotide encoding the fusion protein (fragment) of the invention, or variant or derivative thereof. Heterologous coding regions include without limitation specialized elements or motifs, such as a secretory signal peptide or a heterologous functional domain. An operable association is when a coding region for a gene product, e.g. a polypeptide, is associated with one or more regulatory sequences in such a way as to place expression of the gene product under the influence or control of the regulatory sequence(s). Two DNA fragments (such as a polypeptide coding region and a promoter associated therewith) are "operably associated" if induction of promoter function results in the transcription of mRNA encoding the desired gene product and if the nature of the linkage between the two DNA fragments does not interfere with the ability of the expression regulatory sequences to direct the expression of the gene product or interfere with the ability of the DNA template to be transcribed. Thus, a promoter region would be operably associated with a nucleic acid encoding a polypeptide if the promoter was capable of effecting transcription of that nucleic acid. The promoter may be a cell-specific promoter that directs substantial transcription of the DNA only in predetermined cells. Other transcription control elements, besides a promoter, for example enhancers, operators, repressors, and transcription termination signals, can be operably associated with the polynucleotide to direct cell-specific transcription. Suitable promoters and other transcription control regions are disclosed herein. A variety of transcription control regions are known to those skilled in the art. These include, without limitation, transcription control regions, which function in vertebrate cells, such as, but not limited to, promoter and enhancer segments from cytomegaloviruses (e.g. the immediate

early promoter, in conjunction with intron-A), simian virus 40 (e.g. the early promoter), and retroviruses (such as, e.g. Rous sarcoma virus). Other transcription control regions include those derived from vertebrate genes such as actin, heat shock protein, bovine growth hormone and rabbit â-globin, as well as other sequences capable of controlling gene expression in eukaryotic cells. Additional suitable transcription control regions include tissue-specific promoters and enhancers as well as inducible promoters (e.g. promoters inducible tetracyclins). Similarly, a variety of translation control elements are known to those of ordinary skill in the art. These include, but are not limited to ribosome binding sites, translation initiation and termination codons, and elements derived from viral systems (particularly an internal ribosome entry site, or IRES, also referred to as a CITE sequence). The expression cassette may also include other features such as an origin of replication, and/or chromosome integration elements such as retroviral long terminal repeats (LTRs), or adeno-associated viral (AAV) inverted terminal repeats (ITRs).

Polynucleotide and nucleic acid coding regions of the present invention may be associated with additional coding regions which encode secretory or signal peptides, which direct the secretion of a polypeptide encoded by a polynucleotide of the present invention. For example, if secretion of the fusion is desired, DNA encoding a signal sequence may be placed upstream of the nucleic acid encoding a fusion protein of the invention or a fragment thereof. According to the signal hypothesis, proteins secreted by mammalian cells have a signal peptide or secretory leader sequence which is cleaved from the mature protein once export of the growing protein chain across the rough endoplasmic reticulum has been initiated. Those of ordinary skill in the art are aware that polypeptides secreted by vertebrate cells generally have a signal peptide fused to the N-terminus of the polypeptide, which is cleaved from the translated polypeptide to produce a secreted or "mature" form of the polypeptide. In certain embodiments, the native signal peptide, *e.g.* an immunoglobulin heavy chain or light chain signal peptide is used, or a functional derivative of that sequence that retains the ability to direct the secretion of the polypeptide that is operably associated with it. Alternatively, a heterologous mammalian signal peptide, or a functional derivative thereof, may be used. For example, the wild-type leader sequence may be substituted with the leader sequence of human tissue plasminogen activator (TPA) or mouse β-glucuronidase. The amino acid and nucleotide sequences of exemplary secretory signal peptides are shown in SEQ ID NOs 39-47.

DNA encoding a short protein sequence that could be used to facilitate later purification (e.g. a histidine tag) or assist in labeling the fusion protein may be included within or at the ends of the fusion protein (fragment) encoding polynucleotide.

In a further embodiment, a host cell comprising one or more polynucleotides of the invention is provided. In certain embodiments a host cell comprising one or more vectors of the invention is provided. The polynucleotides and vectors may incorporate any of the features, singly or in combination, described herein in relation to polynucleotides and vectors, respectively. In one such embodiment a host cell comprises (e.g. has been transformed or transfected with) a vector comprising a polynucleotide that encodes (part of) a fusion protein of the invention. As used herein, the term "host cell" refers to any kind of cellular system which can be engineered to generate the fusion proteins of the invention or fragments thereof. Host cells suitable for replicating and for supporting expression of fusion proteins are well known in the art. Such cells may be transfected or transduced as appropriate with the particular expression vector and large quantities of vector containing cells can be grown for seeding large scale fermenters to obtain sufficient quantities of the fusion protein for clinical applications. Suitable host cells include prokaryotic microorganisms, such as E. coli, or various eukaryotic cells, such as Chinese hamster ovary cells (CHO), insect cells, or the like. For example, polypeptides may be produced in bacteria in particular when glycosylation is not needed. After expression, the polypeptide may be isolated from the bacterial cell paste in a soluble fraction and can be further purified. In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for polypeptide-encoding vectors, including fungi and yeast strains whose glycosylation pathways have been "humanized", resulting in the production of a polypeptide with a partially or fully human glycosylation pattern. See Gerngross, Nat Biotech 22, 1409-1414 (2004), and Li et al., Nat Biotech 24, 210-215 (2006). Suitable host cells for the expression of (glycosylated) polypeptides are also derived from multicellular organisms (invertebrates and vertebrates). Examples of invertebrate cells include plant and insect cells. Numerous baculoviral strains have been identified which may be used in conjunction with insect cells, particularly for transfection of *Spodoptera frugiperda* cells. Plant cell cultures can also be utilized as hosts. See e.g. US Patent Nos. 5,959,177, 6,040,498, 6,420,548, 7,125,978, and 6,417,429 (describing PLANTIBODIES™ technology for producing antibodies in transgenic plants). Vertebrate cells may also be used as hosts. For example, mammalian cell lines that are adapted to grow in suspension may be useful. Other examples of useful mammalian host cell lines are monkey kidney CV1 line transformed by SV40 (COS-7); human embryonic kidney line (293 or 293T

cells as described, e.g., in Graham et al., J Gen Virol 36, 59 (1977)), baby hamster kidney cells (BHK), mouse sertoli cells (TM4 cells as described, e.g., in Mather, Biol Reprod 23, 243-251 (1980)), monkey kidney cells (CV1), African green monkey kidney cells (VERO-76), human cervical carcinoma cells (HELA), canine kidney cells (MDCK), buffalo rat liver cells (BRL 3A), human lung cells (W138), human liver cells (Hep G2), mouse mammary tumor cells (MMT 060562), TRI cells (as described, e.g., in Mather et al., Annals N.Y. Acad Sci 383, 44-68 (1982)), MRC 5 cells, and FS4 cells. Other useful mammalian host cell lines include Chinese hamster ovary (CHO) cells, including dhfr$^-$ CHO cells (Urlaub et al., Proc Natl Acad Sci USA 77, 4216 (1980)); and myeloma cell lines such as YO, NS0, P3X63 and Sp2/0. For a review of certain mammalian host cell lines suitable for protein production, see, e.g., Yazaki and Wu, Methods in Molecular Biology, Vol. 248 (B.K.C. Lo, ed., Humana Press, Totowa, NJ), pp. 255-268 (2003). Host cells include cultured cells, e.g., mammalian cultured cells, yeast cells, insect cells, bacterial cells and plant cells, to name only a few, but also cells comprised within a transgenic animal, transgenic plant or cultured plant or animal tissue. In one embodiment, the host cell is a eukaryotic cell, preferably a mammalian cell, such as a Chinese Hamster Ovary (CHO) cell, a human embryonic kidney (HEK) cell or a lymphoid cell (e.g., Y0, NS0, Sp20 cell). Standard technologies are known in the art to express foreign genes in these systems. Cells expressing a polypeptide comprising either the heavy or the light chain of an immunoglobulin, may be engineered so as to also express the other of the immunoglobulin chains such that the expressed product is an immunoglobulin that has both a heavy and a light chain.

In one embodiment, a method of producing a fusion protein according to the invention is provided, wherein the method comprises culturing a host cell comprising a polynucleotide encoding the fusion protein, as provided herein, under conditions suitable for expression of the fusion protein, and recovering the fusion protein from the host cell (or host cell culture medium).

In the fusion proteins of the invention, the components (immunoglobulin molecule and IL-2 molecule) are genetically fused to each other. Fusion proteins can be designed such that its components are fused directly to each other or indirectly through a linker sequence. The composition and length of the linker may be determined in accordance with methods well known in the art and may be tested for efficacy. Additional sequences may also be included to incorporate a cleavage site to separate the individual components of the fusion protein if desired, for example an endopeptidase recognition sequence.

In certain embodiments the fusion proteins of the invention comprise at least an immunoglobulin variable region capable of binding to an antigen. Variable regions can form part of and be

derived from naturally or non-naturally occurring antibodies and fragments thereof. Methods to produce polyclonal antibodies and monoclonal antibodies are well known in the art (see e.g. Harlow and Lane, "Antibodies, a laboratory manual", Cold Spring Harbor Laboratory, 1988). Non-naturally occurring antibodies can be constructed using solid phase-peptide synthesis, can be produced recombinantly (e.g. as described in U.S. patent No. 4,186,567) or can be obtained, for example, by screening combinatorial libraries comprising variable heavy chains and variable light chains (see e.g. U.S. Patent. No. 5,969,108 to McCafferty).

Any animal species of immunoglobulin can be used in the invention. Non-limiting immunoglobulins useful in the present invention can be of murine, primate, or human origin. If the fusion protein is intended for human use, a chimeric form of immunoglobulin may be used wherein the constant regions of the immunoglobulin are from a human. A humanized or fully human form of the immunoglobulin can also be prepared in accordance with methods well known in the art (see e. g. U.S. Patent No. 5,565,332 to Winter). Humanization may be achieved by various methods including, but not limited to (a) grafting the non-human (e.g., donor antibody) CDRs onto human (e.g. recipient antibody) framework and constant regions with or without retention of critical framework residues (e.g. those that are important for retaining good antigen binding affinity or antibody functions), (b) grafting only the non-human specificity-determining regions (SDRs or a-CDRs; the residues critical for the antibody-antigen interaction) onto human framework and constant regions, or (c) transplanting the entire non-human variable domains, but "cloaking" them with a human-like section by replacement of surface residues. Humanized antibodies and methods of making them are reviewed, e.g., in Almagro and Fransson, Front Biosci 13, 1619-1633 (2008), and are further described, e.g., in Riechmann et al., Nature 332, 323-329 (1988); Queen et al., Proc Natl Acad Sci USA 86, 10029-10033 (1989); US Patent Nos. 5,821,337, 7,527,791, 6,982,321, and 7,087,409; Jones et al., Nature 321, 522-525 (1986); Morrison et al., Proc Natl Acad Sci 81, 6851-6855 (1984); Morrison and Oi, Adv Immunol 44, 65-92 (1988); Verhoeyen et al., Science 239, 1534-1536 (1988); Padlan, Molec Immun 31(3), 169-217 (1994); Kashmiri et al., Methods 36, 25-34 (2005) (describing SDR (a-CDR) grafting); Padlan, Mol Immunol 28, 489-498 (1991) (describing "resurfacing"); Dall'Acqua et al., Methods 36, 43-60 (2005) (describing "FR shuffling"); and Osbourn et al., Methods 36, 61-68 (2005) and Klimka et al., Br J Cancer 83, 252-260 (2000) (describing the "guided selection" approach to FR shuffling). Particular immunoglobulins according to the invention are human immunoglobulins. Human antibodies and human variable regions can be produced using various techniques known in the art. Human antibodies are described generally

in van Dijk and van de Winkel, Curr Opin Pharmacol 5, 368-74 (2001) and Lonberg, Curr Opin Immunol 20, 450-459 (2008). Human variable regions can form part of and be derived from human monoclonal antibodies made by the hybridoma method (see e.g. Monoclonal Antibody Production Techniques and Applications, pp. 51-63 (Marcel Dekker, Inc., New York, 1987)). Human antibodies and human variable regions may also be prepared by administering an immunogen to a transgenic animal that has been modified to produce intact human antibodies or intact antibodies with human variable regions in response to antigenic challenge (see e.g. Lonberg, Nat Biotech 23, 1117-1125 (2005). Human antibodies and human variable regions may also be generated by isolating Fv clone variable region sequences selected from human-derived phage display libraries (see e.g., Hoogenboom et al. in Methods in Molecular Biology 178, 1-37 (O'Brien et al., ed., Human Press, Totowa, NJ, 2001); and McCafferty et al., Nature 348, 552-554; Clackson et al., Nature 352, 624-628 (1991)). Phage typically display antibody fragments, either as single-chain Fv (scFv) fragments or as Fab fragments.

In certain embodiments, the immunoglobulins comprised in the fusion proteins of the present invention are engineered to have enhanced binding affinity according to, for example, the methods disclosed in PCT publication WO 2012/020006 (see Examples relating to affinity maturation) or U.S. Pat. Appl. Publ. No. 2004/0132066, the entire contents of which are hereby incorporated by reference. The ability of the fusion proteins of the invention to bind to a specific antigenic determinant can be measured either through an enzyme-linked immunosorbent assay (ELISA) or other techniques familiar to one of skill in the art, e.g. surface plasmon resonance technique (Liljeblad, et al., Glyco J 17, 323-329 (2000)), and traditional binding assays (Heeley, Endocr Res 28, 217-229 (2002)). Competition assays may be used to identify an antibody that competes with a reference antibody for binding to a particular antigen. In certain embodiments, such a competing antibody binds to the same epitope (e.g. a linear or a conformational epitope) that is bound by the reference antibody. Detailed exemplary methods for mapping an epitope to which an antibody binds are provided in Morris (1996) "Epitope Mapping Protocols", in Methods in Molecular Biology vol. 66 (Humana Press, Totowa, NJ). In an exemplary competition assay, immobilized antigen is incubated in a solution comprising a first labeled antibody that binds to the antigen and a second unlabeled antibody that is being tested for its ability to compete with the first antibody for binding to the antigen. The second antibody may be present in a hybridoma supernatant. As a control, immobilized antigen is incubated in a solution comprising the first labeled antibody but not the second unlabeled antibody. After incubation under conditions permissive for binding of the first antibody to the antigen, excess unbound

antibody is removed, and the amount of label associated with immobilized antigen is measured. If the amount of label associated with immobilized antigen is substantially reduced in the test sample relative to the control sample, then that indicates that the second antibody is competing with the first antibody for binding to the antigen. See Harlow and Lane (1988) Antibodies: A Laboratory Manual ch.14 (Cold Spring Harbor Laboratory, Cold Spring Harbor, NY).

Fusion proteins prepared as described herein may be purified by art-known techniques such as high performance liquid chromatography, ion exchange chromatography, gel electrophoresis, affinity chromatography, size exclusion chromatography, and the like. The actual conditions used to purify a particular protein will depend, in part, on factors such as net charge, hydrophobicity, hydrophilicity etc., and will be apparent to those having skill in the art. For affinity chromatography purification an antibody, ligand, receptor or antigen can be used to which the fusion protein binds. For example, for affinity chromatography purification of fusion proteins of the invention, a matrix with protein A or protein G may be used. Sequential Protein A or G affinity chromatography and size exclusion chromatography can be used to isolate a fusion protein essentially as described in the Examples. The purity of the fusion protein can be determined by any of a variety of well-known analytical methods including gel electrophoresis, high pressure liquid chromatography, and the like. For example, the fusion proteins expressed as described in the Examples were shown to be intact and properly assembled as demonstrated by reducing and non-reducing SDS-PAGE (see e.g. Figure 2).

**Compositions, formulations, and routes of administration**

In a further aspect, the invention provides pharmaceutical compositions comprising any of the fusion proteins provided herein, e.g., for use in any of the below therapeutic methods. In one embodiment, a pharmaceutical composition comprises any of the fusion proteins provided herein and a pharmaceutically acceptable carrier. In another embodiment, a pharmaceutical composition comprises any of the fusion proteins provided herein and at least one additional therapeutic agent, e.g. as described below.

Further provided is a method of producing a fusion protein of the invention in a form suitable for administration *in vivo*, the method comprising (a) obtaining a fusion protein according to the invention, and (b) formulating the fusion protein with at least one pharmaceutically acceptable carrier, whereby a preparation of fusion protein is formulated for administration *in vivo*.

Pharmaceutical compositions of the present invention comprise a therapeutically effective amount of one or more fusion protein dissolved or dispersed in a pharmaceutically acceptable carrier. The phrases "pharmaceutical or pharmacologically acceptable" refers to molecular

entities and compositions that are generally non-toxic to recipients at the dosages and concentrations employed, i.e. do not produce an adverse, allergic or other untoward reaction when administered to an animal, such as, for example, a human, as appropriate. The preparation of a pharmaceutical composition that contains at least one fusion protein and optionally an additional active ingredient will be known to those of skill in the art in light of the present disclosure, as exemplified by Remington's Pharmaceutical Sciences, 18th Ed. Mack Printing Company, 1990, incorporated herein by reference. Moreover, for animal (e.g., human) administration, it will be understood that preparations should meet sterility, pyrogenicity, general safety and purity standards as required by FDA Office of Biological Standards or corresponding authorities in other countries. Preferred compositions are lyophilized formulations or aqueous solutions. As used herein, "pharmaceutically acceptable carrier" includes any and all solvents, buffers, dispersion media, coatings, surfactants, antioxidants, preservatives (*e.g.* antibacterial agents, antifungal agents), isotonic agents, absorption delaying agents, salts, preservatives, antioxidants, proteins, drugs, drug stabilizers, polymers, gels, binders, excipients, disintegration agents, lubricants, sweetening agents, flavoring agents, dyes, such like materials and combinations thereof, as would be known to one of ordinary skill in the art (see, for example, Remington's Pharmaceutical Sciences, 18th Ed. Mack Printing Company, 1990, pp. 1289-1329, incorporated herein by reference). Except insofar as any conventional carrier is incompatible with the active ingredient, its use in the therapeutic or pharmaceutical compositions is contemplated.

The composition may comprise different types of carriers depending on whether it is to be administered in solid, liquid or aerosol form, and whether it need to be sterile for such routes of administration as injection. Fusion proteins of the present invention (and any additional therapeutic agent) can be administered intravenously, intradermally, intraarterially, intraperitoneally, intralesionally, intracranially, intraarticularly, intraprostatically, intrasplenically, intrarenally, intrapleurally, intratracheally, intranasally, intravitreally, intravaginally, intrarectally, intratumorally, intramuscularly, intraperitoneally, subcutaneously, subconjunctivally, intravesicularly, mucosally, intrapericardially, intraumbilically, intraocularly, orally, topically, locally, by inhalation (e.g. aerosol inhalation), injection, infusion, continuous infusion, localized perfusion bathing target cells directly, via a catheter, via a lavage, in cremes, in lipid compositions (e.g. liposomes), or by other method or any combination of the forgoing as would be known to one of ordinary skill in the art (see, for example, Remington's Pharmaceutical Sciences, 18th Ed. Mack Printing Company, 1990, incorporated herein by reference). Parenteral

administration, in particular intravenous injection, is most commonly used for administering polypeptide molecules such as the fusion proteins of the invention.

Parenteral compositions include those designed for administration by injection, e.g. subcutaneous, intradermal, intralesional, intravenous, intraarterial intramuscular, intrathecal or intraperitoneal injection. For injection, the fusion proteins of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiological saline buffer. The solution may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the fusion proteins may be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use. Sterile injectable solutions are prepared by incorporating the fusion proteins of the invention in the required amount in the appropriate solvent with various of the other ingredients enumerated below, as required. Sterility may be readily accomplished, e.g., by filtration through sterile filtration membranes. Generally, dispersions are prepared by incorporating the various sterilized active ingredients into a sterile vehicle which contains the basic dispersion medium and/or the other ingredients. In the case of sterile powders for the preparation of sterile injectable solutions, suspensions or emulsion, the preferred methods of preparation are vacuum-drying or freeze-drying techniques which yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered liquid medium thereof. The liquid medium should be suitably buffered if necessary and the liquid diluent first rendered isotonic prior to injection with sufficient saline or glucose. The composition must be stable under the conditions of manufacture and storage, and preserved against the contaminating action of microorganisms, such as bacteria and fungi. It will be appreciated that endotoxin contamination should be kept minimally at a safe level, for example, less that 0.5 ng/mg protein. Suitable pharmaceutically acceptable carriers include, but are not limited to: buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride; benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium;

metal complexes (e.g. Zn-protein complexes); and/or non-ionic surfactants such as polyethylene glycol (PEG). Aqueous injection suspensions may contain compounds which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, dextran, or the like. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl cleats or triglycerides, or liposomes.

Active ingredients may be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences (18th Ed. Mack Printing Company, 1990). Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the polypeptide, which matrices are in the form of shaped articles, e.g. films, or microcapsules. In particular embodiments, prolonged absorption of an injectable composition can be brought about by the use in the compositions of agents delaying absorption, such as, for example, aluminum monostearate, gelatin or combinations thereof.

In addition to the compositions described previously, the fusion proteins may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the fusion proteins may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

Pharmaceutical compositions comprising the fusion proteins of the invention may be manufactured by means of conventional mixing, dissolving, emulsifying, encapsulating, entrapping or lyophilizing processes. Pharmaceutical compositions may be formulated in conventional manner using one or more physiologically acceptable carriers, diluents, excipients or auxiliaries which facilitate processing of the proteins into preparations that can be used pharmaceutically. Proper formulation is dependent upon the route of administration chosen.

The fusion proteins may be formulated into a composition in a free acid or base, neutral or salt form. Pharmaceutically acceptable salts are salts that substantially retain the biological activity of the free acid or base. These include the acid addition salts, e.g. those formed with the free amino groups of a proteinaceous composition, or which are formed with inorganic acids such as for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric or mandelic acid. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as for example, sodium, potassium, ammonium, calcium or ferric hydroxides; or such organic bases as isopropylamine, trimethylamine, histidine or procaine. Pharmaceutical salts tend to be more soluble in aqueous and other protic solvents than are the corresponding free base forms.

**Therapeutic methods and compositions**

Any of the fusion proteins provided herein may be used in therapeutic methods.

For use in therapeutic methods, fusion proteins of the invention would be formulated, dosed, and administered in a fashion consistent with good medical practice. Factors for consideration in this context include the particular disorder being treated, the particular mammal being treated, the clinical condition of the individual patient, the cause of the disorder, the site of delivery of the agent, the method of administration, the scheduling of administration, and other factors known to medical practitioners.

In one aspect, fusion proteins of the invention for use as a medicament are provided. In further aspects, fusion proteins of the invention for use in treating a disease are provided. In certain embodiments, fusion proteins of the invention for use in a method of treatment are provided. In one embodiment, the invention provides a fusion protein as described herein for use in the treatment of a disease in an individual in need thereof. In certain embodiments, the invention provides a fusion protein for use in a method of treating an individual having a disease comprising administering to the individual a therapeutically effective amount of the fusion protein. In certain embodiments the disease to be treated is an autoimmune disease. Exemplary autoimmune diseases include type 1 diabetes, psoriasis, asthma, rheumatoid arthritis, Crohn's disease, systemic lupus erythematosus (SLE) and multiple sclerosis. In one embodiment, the disease is transplant rejection or graft-versus-host disease. In a particular embodiment the disease is selected from the group of type 1 diabetes, Crohn's disease, SLE, and multiple sclerosis. In a more particular embodiment, the disease is type 1 diabetes. In another particular embodiment, the disease is multiple sclerosis. In further embodiments, the disease is asthma, pulmonary fibrosis or obstructive pulmonary disease. In still further embodiments, the disease is a

cardiovascular disease, particularly atherosclerosis. In certain embodiments the method further comprises administering to the individual a therapeutically effective amount of at least one additional therapeutic agent, e.g. an immunosuppressive agent if the disease to be treated is an autoimmune disease. An "individual" according to any of the above embodiments is a mammal, preferably a human.

In a further aspect, the invention provides for the use of a fusion protein of the invention in the manufacture or preparation of a medicament for the treatment of a disease in an individual in need thereof. In one embodiment, the medicament is for use in a method of treating a disease comprising administering to an individual having the disease a therapeutically effective amount of the medicament. In certain embodiments the disease to be treated is an autoimmune disease. In one embodiment, the disease is transplant rejection or graft-versus-host disease. In a particular embodiment the disease is selected from the group of type 1 diabetes, Crohn's disease, SLE, and multiple sclerosis. In a more particular embodiment, the disease is type 1 diabetes. In another particular embodiment, the disease is multiple sclerosis. In further embodiments, the disease is asthma, pulmonary fibrosis or obstructive pulmonary disease. In still further embodiments, the disease is a cardiovascular disease, particularly atherosclerosis. In one embodiment, the method further comprises administering to the individual a therapeutically effective amount of at least one additional therapeutic agent, e.g., an immunosuppressive agent if the disease to be treated is an autoimmune disease. An "individual" according to any of the above embodiments may be a mammal, preferably a human.

In a further aspect, the invention provides a method for treating a disease in an individual, comprising administering to said individual a therapeutically effective amount of a fusion protein of the invention. In one embodiment a composition is administered to said individual, comprising a fusion protein of the invention in a pharmaceutically acceptable form. In certain embodiments the disease to be treated is an autoimmune disease. In one embodiment, the disease is transplant rejection or graft-versus-host disease. In a particular embodiment the disease is selected from the group of type 1 diabetes, Crohn's disease, SLE, and multiple sclerosis. In a more particular embodiment, the disease is type 1 diabetes. In another particular embodiment, the disease is multiple sclerosis. In further embodiments, the disease is asthma, pulmonary fibrosis or obstructive pulmonary disease. In still further embodiments, the disease is a cardiovascular disease, particularly atherosclerosis. In certain embodiments the method further comprises administering to the individual a therapeutically effective amount of at least one additional therapeutic agent, e.g. an immunosuppressive agent if the disease to be treated is an

autoimmune disease. An "individual" according to any of the above embodiments may be a mammal, preferably a human.

In some embodiments, an effective amount of a fusion protein of the invention is administered to a cell. In other embodiments, a therapeutically effective amount of a fusion protein of the invention is administered to an individual for the treatment of disease.

For the prevention or treatment of disease, the appropriate dosage of a fusion protein of the invention (when used alone or in combination with one or more other additional therapeutic agents) will depend on the type of disease to be treated, the route of administration, the body weight of the patient, the type of fusion protein, the severity and course of the disease, whether the fusion protein is administered for preventive or therapeutic purposes, previous or concurrent therapeutic interventions, the patient's clinical history and response to the fusion protein, and the discretion of the attending physician. The practitioner responsible for administration will, in any event, determine the concentration of active ingredient(s) in a composition and appropriate dose(s) for the individual subject. Various dosing schedules including but not limited to single or multiple administrations over various time-points, bolus administration, and pulse infusion are contemplated herein.

The fusion protein is suitably administered to the patient at one time or over a series of treatments. Depending on the type and severity of the disease, about 1 μg/kg to 15 mg/kg (e.g. 0.1 mg/kg - 10 mg/kg) of fusion protein can be an initial candidate dosage for administration to the patient, whether, for example, by one or more separate administrations, or by continuous infusion. One typical daily dosage might range from about 1 μg/kg to 100 mg/kg or more, depending on the factors mentioned above. For repeated administrations over several days or longer, depending on the condition, the treatment would generally be sustained until a desired suppression of disease symptoms occurs. One exemplary dosage of the fusion protein would be in the range from about 0.005 mg/kg to about 10 mg/kg. In other non-limiting examples, a dose may also comprise from about 1 μg/kg body weight, about 5 μg/kg body weight, about 10 μg/kg body weight, about 50 μg/kg body weight, about 100 μg/kg body weight, about 200 μg/kg body weight, about 350 μg/kg body weight, about 500 μg/kg body weight, about 1 mg/kg body weight, about 5 mg/kg body weight, about 10 mg/kg body weight, about 50 mg/kg body weight, about 100 mg/kg body weight, about 200 mg/kg body weight, about 350 mg/kg body weight, about 500 mg/kg body weight, to about 1000 mg/kg body weight or more per administration, and any range derivable therein. In non-limiting examples of a derivable range from the numbers listed herein, a range of about 5 mg/kg body weight to about 100 mg/kg body weight, about 5

μg/kg body weight to about 500 mg/kg body weight etc., can be administered, based on the numbers described above. Thus, one or more doses of about 0.5 mg/kg, 2.0 mg/kg, 5.0 mg/kg or 10 mg/kg (or any combination thereof) may be administered to the patient. Such doses may be administered intermittently, e.g. every week or every three weeks (e.g. such that the patient receives from about two to about twenty, or e.g. about six doses of the fusion protein). An initial higher loading dose, followed by one or more lower doses may be administered. However, other dosage regimens may be useful. The progress of this therapy is easily monitored by conventional techniques and assays.

The fusion proteins of the invention will generally be used in an amount effective to achieve the intended purpose. For use to treat or prevent a disease condition, the fusion proteins of the invention, or pharmaceutical compositions thereof, are administered or applied in a therapeutically effective amount. Determination of a therapeutically effective amount is well within the capabilities of those skilled in the art, especially in light of the detailed disclosure provided herein.

For systemic administration, a therapeutically effective dose can be estimated initially from *in vitro* assays, such as cell culture assays. A dose can then be formulated in animal models to achieve a circulating concentration range that includes the $IC_{50}$ as determined in cell culture. Such information can be used to more accurately determine useful doses in humans.

Initial dosages can also be estimated from *in vivo* data, *e.g.,* animal models, using techniques that are well known in the art. One having ordinary skill in the art could readily optimize administration to humans based on animal data.

Dosage amount and interval may be adjusted individually to provide plasma levels of the fusion proteins which are sufficient to maintain therapeutic effect. Usual patient dosages for administration by injection range from about 0.1 to 50 mg/kg/day, typically from about 0.5 to 1 mg/kg/day. Therapeutically effective plasma levels may be achieved by administering multiple doses each day. Levels in plasma may be measured, for example, by HPLC.

In cases of local administration or selective uptake, the effective local concentration of the fusion protein may not be related to plasma concentration. One having skill in the art will be able to optimize therapeutically effective local dosages without undue experimentation.

A therapeutically effective dose of the fusion proteins described herein will generally provide therapeutic benefit without causing substantial toxicity. Toxicity and therapeutic efficacy of a fusion protein can be determined by standard pharmaceutical procedures in cell culture or experimental animals. Cell culture assays and animal studies can be used to determine the $LD_{50}$

(the dose lethal to 50% of a population) and the $ED_{50}$ (the dose therapeutically effective in 50% of a population). The dose ratio between toxic and therapeutic effects is the therapeutic index, which can be expressed as the ratio $LD_{50}/ED_{50}$. Fusion proteins that exhibit large therapeutic indices are preferred. In one embodiment, the fusion protein according to the present invention exhibits a high therapeutic index. The data obtained from cell culture assays and animal studies can be used in formulating a range of dosages suitable for use in humans. The dosage lies preferably within a range of circulating concentrations that include the $ED_{50}$ with little or no toxicity. The dosage may vary within this range depending upon a variety of factors, e.g., the dosage form employed, the route of administration utilized, the condition of the subject, and the like. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition (see, e.g., Fingl et al., 1975, in: The Pharmacological Basis of Therapeutics, Ch. 1, p. 1, incorporated herein by reference in its entirety).

The attending physician for patients treated with fusion proteins of the invention would know how and when to terminate, interrupt, or adjust administration due to toxicity, organ dysfunction, and the like. Conversely, the attending physician would also know to adjust treatment to higher levels if the clinical response were not adequate (precluding toxicity). The magnitude of an administered dose in the management of the disorder of interest will vary with the severity of the condition to be treated, with the route of administration, and the like. The severity of the condition may, for example, be evaluated, in part, by standard prognostic evaluation methods. Further, the dose and perhaps dose frequency will also vary according to the age, body weight, and response of the individual patient.

**Other agents and treatments**

The fusion proteins of the invention may be administered in combination with one or more other agents in therapy. For instance, a fusion protein of the invention may be co-administered with at least one additional therapeutic agent. The term "therapeutic agent" encompasses any agent administered to treat a symptom or disease in an individual in need of such treatment. Such additional therapeutic agent may comprise any active ingredients suitable for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. In certain embodiments, an additional therapeutic agent is an immunosuppressive agent.

Such other agents are suitably present in combination in amounts that are effective for the purpose intended. The effective amount of such other agents depends on the amount of fusion protein used, the type of disorder or treatment, and other factors discussed above. The fusion

proteins are generally used in the same dosages and with administration routes as described herein, or about from 1 to 99% of the dosages described herein, or in any dosage and by any route that is empirically/clinically determined to be appropriate.

Such combination therapies noted above encompass combined administration (where two or more therapeutic agents are included in the same or separate compositions), and separate administration, in which case, administration of the fusion protein of the invention can occur prior to, simultaneously, and/or following, administration of the additional therapeutic agent and/or adjuvant.

**Articles of manufacture**

In another aspect of the invention, an article of manufacture containing materials useful for the treatment, prevention and/or diagnosis of the disorders described above is provided. The article of manufacture comprises a container and a label or package insert on or associated with the container. Suitable containers include, for example, bottles, vials, syringes, IV solution bags, etc. The containers may be formed from a variety of materials such as glass or plastic. The container holds a composition which is by itself or combined with another composition effective for treating, preventing and/or diagnosing the condition and may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). At least one active agent in the composition is a fusion protein of the invention. The label or package insert indicates that the composition is used for treating the condition of choice. Moreover, the article of manufacture may comprise (a) a first container with a composition contained therein, wherein the composition comprises a fusion protein of the invention; and (b) a second container with a composition contained therein, wherein the composition comprises a further therapeutic agent. The article of manufacture in this embodiment of the invention may further comprise a package insert indicating that the compositions can be used to treat a particular condition. Alternatively, or additionally, the article of manufacture may further comprise a second (or third) container comprising a pharmaceutically-acceptable buffer, such as bacteriostatic water for injection (BWFI), phosphate-buffered saline, Ringer's solution and dextrose solution. It may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, and syringes.

## Examples

The following are examples of methods and compositions of the invention. It is understood that various other embodiments may be practiced, given the general description provided above.

### Recombinant DNA techniques

Standard methods were used to manipulate DNA as described in Sambrook et al., Molecular cloning: A laboratory manual; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989. The molecular biological reagents were used according to the manufacturer's instructions. General information regarding the nucleotide sequences of human immunoglobulin light and heavy chains is given in: Kabat, E.A. et al., (1991) Sequences of Proteins of Immunological Interest, Fifth Ed., NIH Publication No 91-3242.

### DNA sequencing

DNA sequences were determined by double strand sequencing.

### Gene synthesis

Desired gene segments where required were either generated by PCR using appropriate templates or were synthesized by Geneart AG (Regensburg, Germany) from synthetic oligonucleotides and PCR products by automated gene synthesis. In cases where no exact gene sequence was available, oligonucleotide primers were designed based on sequences from closest homologues and the genes were isolated by RT-PCR from RNA originating from the appropriate tissue. The gene segments flanked by singular restriction endonuclease cleavage sites were cloned into standard cloning / sequencing vectors. The plasmid DNA was purified from transformed bacteria and concentration determined by UV spectroscopy. The DNA sequence of the subcloned gene fragments was confirmed by DNA sequencing. Gene segments were designed with suitable restriction sites to allow sub-cloning into the respective expression vectors. All constructs were designed with a 5'-end DNA sequence coding for a leader peptide which targets proteins for secretion in eukaryotic cells. SEQ ID NOs 39-47 give exemplary leader peptides and polynucleotide sequences encoding them.

### Preparation of IL-2R βγ subunit-Fc fusions and IL-2R α subunit Fc fusion

To study IL-2 receptor binding affinity, a tool was generated that allowed for the expression of a heterodimeric IL-2 receptor. The β-subunit of the IL-2 receptor was fused to an Fc molecule that was engineered to heterodimerize (Fc(hole)) (see SEQ ID NOs 21 and 22 (human), SEQ ID NOs

27 and 28 (mouse) and SEQ ID NOs 33 and 34 (cynomolgus)) using the "knobs-into-holes" technology (Merchant et al., Nat Biotech. 16, 677-681 (1998)). The γ-subunit of the IL-2 receptor was then fused to the Fc(knob) variant (see SEQ ID NOs 23 and 24 (human), SEQ ID NOs 29 and 30 (mouse) and SEQ ID NOs 35 and 36 (cynomolgus)), which heterodimerized with Fc(hole). This heterodimeric Fc-fusion protein was then used as a substrate for analyzing the IL-2/IL-2 receptor interaction. The IL-2R α-subunit was expressed as monomeric chain with an AcTev cleavage site and an Avi His tag (SEQ ID NOs 25 and 26 (human), SEQ ID NOs 31 and 32 (mouse) and SEQ ID NOs 37 and 38 (cynomolgus)). The respective IL-2R subunits were transiently expressed in HEK EBNA 293 cells with serum for the IL-2R βγ subunit construct and without serum for the α-subunit construct. The IL-2R βγ subunit construct was purified on protein A (GE Healthcare), followed by size exclusion chromatography (GE Healthcare, Superdex 200). The IL-2R α-subunit was purified via His tag on a NiNTA column (Qiagen) followed by size exclusion chromatography (GE Healthcare, Superdex 75). Amino acid and corresponding nucleotide sequences of various receptor constructs are given in SEQ ID NOs 21-38.

**Preparation of fusion proteins**

The DNA sequences were generated by gene synthesis and/or classical molecular biology techniques and subcloned into mammalian expression vectors under the control of an MPSV promoter and upstream of a synthetic polyA site, each vector carrying an EBV OriP sequence. Fusion proteins as applied in the examples below were produced by co-transfecting exponentially growing HEK293-EBNA cells with the mammalian expression vectors using calcium phosphate-transfection. Alternatively, HEK293 cells growing in suspension were transfected by polyethylenimine (PEI) with the respective expression vectors. Alternatively, stably transfected CHO cell pools or CHO cell clones were used for production in serum-free media. Subsequently, the fusion proteins were purified from the supernatant. Briefly, fusion proteins were purified by one affinity step with protein A (HiTrap ProtA, GE Healthcare) equilibrated in 20 mM sodium phosphate, 20 mM sodium citrate pH 7.5. After loading of the supernatant, the column was first washed with 20 mM sodium phosphate, 20 mM sodium citrate, pH 7.5 and subsequently washed with 13.3 mM sodium phosphate, 20 mM sodium citrate, 500 mM sodium chloride, pH 5.45. The fusion protein was eluted with 20 mM sodium citrate, 100 mM sodium chloride, 100 mM glycine, pH 3. Fractions were neutralized and pooled and purified by size exclusion chromatography (HiLoad 16/60 Superdex 200, GE Healthcare) in final formulation buffer: 20 mM histidine, 140 mM NaCl pH 6.0. The protein concentration of

purified protein samples was determined by measuring the optical density (OD) at 280 nm, using the molar extinction coefficient calculated on the basis of the amino acid sequence. Purity and molecular weight of fusion proteins were analyzed by SDS-PAGE in the presence and absence of a reducing agent (5 mM 1,4-dithiotreitol) and stained with Coomassie blue (SimpleBlue™ SafeStain, Invitrogen). The NuPAGE® Pre-Cast gel system (Invitrogen) was used according to the manufacturer's instructions (4-20% Tris-glycine gels or 3-12% Bis-Tris). Alternatively, purity and molecular weight of molecules were analyzed by CE-SDS analyses in the presence and absence of a reducing agent, using the Caliper LabChip GXII system (Caliper Lifescience) according to the manufacturer's instructions. The aggregate content of fusion protein samples was analyzed using a Superdex 200 10/300GL analytical size-exclusion column (GE Healthcare) in 2 mM MOPS, 150 mM NaCl, 0.02% $NaN_3$, pH 7.3 running buffer at 25°C. Alternatively, the aggregate content of antibody samples was analyzed using a TSKgel G3000 SW XL analytical size-exclusion column (Tosoh) in 25 mM $K_2HPO_4$, 125 mM NaCl, 200 mM L-arginine monohydrocloride, 0.02% (w/v) $NaN_3$, pH 6.7 running buffer at 25°C.

Results of the purification and characterization of the DP47GS IgG-IL-2 and DP47GS IgG-(IL-2)$_2$ constructs are shown in Figures 1 and 2.

**Affinity to IL-2 receptors**

The affinity of the fusion proteins was determined by surface plasmon resonance (SPR) for the human, murine and cynomolgus IL-2R βγ heterodimer using recombinant IL-2R βγ heterodimer under the following conditions: ligand: human, murine and cynomolgus IL-2R β knob γ hole heterodimer immobilized on CM5 chip, analyte: DP47GS IgG-IL-2 (see SEQ ID NOs 13, 15 and 19) or DP47GS IgG-(IL-2)$_2$ (see SEQ ID NOs 17 and 19), temperature: 25°C, buffer: HBS-EP, analyte concentration: 300 nM down to 3.7 nM (1:3 dilutions), flow: 30 µl/min, association: 180 s, dissociation: 300 s, regeneration: 60 s 3M $MgCl_2$, fitting: 1:1 binding, RI≠0, Rmax=global. The affinity of the fusion proteins was also determined by surface plasmon resonance (SPR) for the human, murine and cynomolgus IL-2R α-subunit using recombinant monomeric IL-2R α-subunit under the following conditions: ligand: human, murine and cynomolgus IL-2R α-subunit immobilized on a CM5 chip, analyte: DP47GS IgG-IL-2 or DP47GS IgG-(IL-2)$_2$, temperature: 25°C, buffer: HBS-EP, analyte concentration 100 nM down to 3.1 nM (1:3 dilutions), flow: 30 µl/min, association: 60 s, dissociation: 180 s, regeneration: none, fitting: 1:1 binding, RI=0, Rmax=global.

Results of the kinetic analysis with the IL-2R βγ heterodimer or the IL-2R α-subunit are given in Table 1.

Table 1. Binding of fusion proteins to IL-2R βγ and IL-2R α.

| $K_D$ in nM | Hu IL-2R βγ | Cy IL-2R βγ | Mu IL-2R βγ | Hu IL-2R α | Cy IL-2R α | Mu IL-2R α |
|---|---|---|---|---|---|---|
| DP47GS IgG-IL-2 | 3.1 | 4.6 | 15 | 28 | 29 | 71 |
| DP47GS IgG-$(IL-2)_2$ | 2 | 3 | 8.4 | n.d. | n.d. | n.d. |

The affinity of human IL-2 to the human IL 2R βγ heterodimer is described to be around 1 nM, while the fusion proteins both have a slightly lower affinity between 2 and 3 nM. The affinity to the murine IL-2R is several times weaker than for the human and cynomolgous IL-2R.

**Expression of IL-2 receptors on immune cells**

The high-affinity trimeric IL-2 receptor is composed of the α (IL-2RA, CD25), β (IL-2RB, CD122) and γ (IL-2RG, CD132) chains and has a $K_D$ of ~10 pM. CD25 alone has only a low affinity ($K_D$ ~10 nM) for IL-2. The IL-2RB/IL-2RG dimer, which is expressed on some cell types in the absence of IL-2RA, also binds IL-2 but with an intermediate affinity ($K_D$ ~1 nM). Signalling via the IL-2 receptor is mediated by the IL-2RB and IL-2RG chains. From crystal structure analyses, IL-2RA does not seem to contact either IL-2RB or IL-2RG. It has been proposed that the basis of the cooperativity of the trimeric receptor is an entropy reduction when CD25 captures IL-2 at the cell surface for presentation to IL-2RB and IL-2RG, or alternatively a CD25-induced alteration in IL-2 conformation occurs, thus stabilizing the complex. In $FOXP3^+$ regulatory $CD4^+$ T cells, there is a large stoichiometric excess of IL-2RA as compared to the β and γ chains of the receptor supporting the hypothesis that dimers, or even larger complexes, of the α chain aid in the binding of IL-2. There is also evidence that CD25 on one cell can present IL-2 to IL-2RB/IL-2RG dimers on another cell, in a high-affinity, intercellular interaction emphasizing the unique relationship amongst the three chains composing the high affinity IL-2 receptor.

CD25 (IL-2RA) and CD122 (IL-2RB) expression on $CD4^+$ Treg subsets, NK cell subsets and NKT cells, as well as on $CD4^+$ and $CD8^+$ conventional T cell subsets was determined by FACS (Figure 3 and 4). Cell surface markers were used to define $CD4^+$ Treg subsets, NKT cells and

NK cells (Figure 3). In order to optimize staining for CD25 and CD122, intracellular FoxP3 staining was not performed. Briefly, using 150 µl blood donated by a healthy volunteer, fluorescent antibodies were incubated for 45 min at room temperature in the dark (vortexed at the beginning and after 20 min). Red blood cells were lysed with BD lysis buffer (BD FACS Lysing Solution, 349202) for 9 minutes and the remaining cells were washed (2 ml of PBS + 0.1% BSA) and fixed (1% PFA). Cells were analysed on an LSRFortessa cell analyser (Becton Dickinson) and data analysed using FloJo software (TreeStar). Treg subsets were identified using antibodies specific for TCRαβ-FITC (IP26, BioLegend), CD4-Alexa Fluor 700 (RPA-T4, BioLegend), CD127-PE/CY7 (ebioRDR5, Ebioscience), CD45RA-Pacific Blue (HI100, BioLegend), CD25-APC (2A3, M-A251, BD Biosciences) and CD122-PE (TU27, BioLegend). NK and NKT cells were stained in a separate tube with antibodies specific for TCRαβ-FITC, CD4-Alexa Fluor 700, CD8-PE/CY7 (HTT8a, BioLegend), CD56-Pacific Blue (HCD56, BioLegend), CD25-APC and CD122-PE. Following the gating of lymphocytes based on FSC/SSC and excluding doublets, naïve Tregs were identified as $TCR\alpha\beta^+$, $CD4^+$, $CD127^-$, $CD25^+$, $CD45RA^+$, memory Tregs were identified as $TCR\alpha\beta^+$, $CD4^+$, $CD127^-$, $CD25^+$, $CD45RA^-$ and activated Tregs were identified as $TCR\alpha\beta^+$, $CD4^+$, $CD127^-$, $CD25^{high}$, $CD45RA^-$. NK cells were identified as $TCR\alpha\beta^-$, $CD56^+$ and activated NK cells identified as $TCR\alpha\beta^-$, $CD56^{bright}$. NKT cells were identified as $TCR\alpha\beta^+$, $CD56^+$. Isotype controls conjugated to APC and PE were used in order to estimate background fluorescence for CD25 and CD122, respectively.

Similarly, cell surface markers were used to define naïve and memory conventional $CD4^+$ T cells (Figures 4A and 4B), memory conventional $CD8^+$ T cells and $CD45RA^+$ CD8 T cells (a combination of the naïve and TEMRA subsets; TEMRA refers to effector memory cells that have reverted to expressing CD45RA) (Figures 4C and 4D). Staining and analysis was performed as described above. Using the same tube described above to characterize $CD4^+$ Tregs, $CD4^+$ conventional naïve T cells were identified as $TCR\alpha\beta^+$, $CD4^+$, $CD127^+$, $CD25^{-/+}$, $CD45RA^+$ and $CD4^+$ conventional memory T cells were identified as $TCR\alpha\beta^+$, $CD4^+$, $CD127^+$, $CD25^{-/+}$, $CD45RA^-$. CD8 T cells were defined using TCRαβ-FITC, CD8-Alexa Fluor 700 (HTT8a, BioLegend), CD28-PE/CY7 (CD28.2, BioLegend), CD45RA-Pacific Blue, CD25-APC and CD122-PE. $CD8^+$ memory T cells were identified as $TCR\alpha\beta^+$, $CD8^+$, $CD45RA^-$. $CD8^+$ naïve and TEMRA (TEMRA refers to effector memory cells that have reverted to expressing CD45RA T cells) were identified as $TCR\alpha\beta^+$, $CD8^+$, $CD45RA^+$. CD28 was not used to distinguish $CD8^+$ naïve T cells from $CD8^+$ TEMRA T cells since the CD28 marker was not included in the pSTAT5a analysis described below (see Figure 5).

In Figures 3 and 4, the cell-specific expression of IL-2RA and IL-2RB is shown for subsets of T cells, NK cells and NK T cells in human peripheral blood (IL-2RG has essentially ubiquitous expression on hematopoietic cells since it partners with a large number of cytokine receptors). The highest level of IL-2RA is present on the three regulatory $CD4^+$ T cell (Treg) populations: naïve ($CD45RA^+$, $CD25^+$), memory ($CD45RA^-$, $CD25^+$) and activated ($CD45RA^-$, $CD25^{hi}$) (Figure 3A). On average, conventional memory $CD4^+$ T cells express approximately 10-fold less CD25 than Tregs (Figure 4A). The expression of CD25 on naïve $CD4^+$ T cells varies significantly amongst donors but is always lower than that observed on memory $CD4^+$ T cells (Figure 4A). Expression of CD25 on NK, NKT and CD8 T cells is very low or not detectable except for $CD56^{bright}$ NK cells (Figures 3C and 4C). The $CD56^{bright}$ NK and $CD56^+$ NK cells express the highest level of IL-2RB (Figure 3D), approximately 10-fold more than any of the T cell subsets, including NKT cells (Figures 3B, 3D, 4B, 4D).

**Induction of pSTAT5a in human peripheral blood cell subsets**

Following IL-2-induced oligomerization of the trimeric IL-2R, the JAK1 and JAK3 cytoplasmic protein tyrosine kinases, that are associated with the intracellular domains of IL-2RB and IL-2RG respectively, become activated. These kinases phosphorylate certain IL-2RB tyrosine residues that act as docking sites for STAT5a and STAT5b that are in turn phosphorylated. The IL-2-induced activation of several signalling pathways eventually results in the transcription of target genes that contribute to the various functions associated with the IL-2/IL-2R pathway. Since various cell types express different levels of the IL-2 receptor IL-2RA and IL-2RB molecules (Figures 3 and 4), in order to understand the integrated signalling response to IL-2 mediated by various combinations of the high and intermediate affinity receptors we measured pSTAT5a levels within individual cells by polychromatic flow cytometry.

The effects of various doses of DP47GS IgG-IL-2 or DP47GS IgG-$(IL\text{-}2)_2$ on the induction of STAT5a phosphorylation were assessed in human $CD4^+$ Treg subsets, naïve and memory conventional $CD4^+$ T cells, memory conventional $CD8^+$ T cells, $CD45RA^+$ CD8 T cells, NKT cells and NK cells (Figure 5 and 6). All subsets were characterized in a single tube for each dose. Briefly, blood from a healthy volunteer was drawn into heparinized tubes. Various concentrations of DP47GS IgG-IL-2 or DP47GS IgG-$(IL\text{-}2)_2$ were added to 500 µl of blood and incubated at 37°C. After 30 minutes the blood was lysed and fixed using pre-warmed lyse/fix buffer (Becton Dickinson #558049) for 10 minutes at 37°C, washed 2 x with PBS containing 0.2% BSA followed by permeabilization with -20°C pre-cooled methanol (Sigma, Biotech grade

#494437) for 20 minutes on ice. The cells were then extensively washed 4 x with PBS containing 0.2% BSA before FACS staining was performed using a panel of fluorescent antibodies to distinguish different lymphocyte and NK cell subpopulations and pSTAT5a status. The antibodies utilized were anti-CD4-Alexa Fluor 700 (clone RPA-T4), CD3-PerCP/Cy5.5 (UCHT1), CD45RA-PE/Cy7 (HI100), CD8-Brilliant Violet 605 (RPA-T8), CD56-Brilliant Violet 421 (HCD56), FOXP3-PE (259D) (all from BioLegend), CD25-APC (clones M-A251 & 2A3) and pSTAT5a-Alexa Fluor 488 (pY694) (Becton Dickinson). Samples were acquired using an LSRFortessa cell analyser (Becton Dickinson) and data analysed using FloJo software (TreeStar). After gating on lymphocytes and excluding doublets, Tregs were defined as $CD3^+$, $CD4^+$, $FOXP3^+$ and subdivided as $CD45^-$ $FOXP3^{hi}$ (activated Treg), $CD3^+$, $CD4^+$, $CD45RA^-$, $FOXP3^+$ (memory Treg) and $CD3^+$, $CD4^+$, $CD45^+$, $FOXP3^+$ (naïve Treg). Conventional $CD4^+$ T cells were defined as $CD3^+$, $CD4^+$, $CD45RA^+$ (naïve) and $CD3^+$, $CD4^+$, $CD45RA^-$ (memory). CD8 T cells were defined as $CD3^+$, $CD8^+$, $CD45RA^-$ (memory) and $CD3^+$, $CD8^+$, $CD45RA^+$. NKT cells were defined as $CD3^+$, $CD56^+$ and NK cells were defined as $CD3^-$, $CD56^{bright}$ (activated NK cells) or $CD3^-$, $CD56^+$ (NK cells). Intracellular pSTAT5a levels were quantified in all cell subsets at all doses.

Figure 5 shows the dose response of the DP47GS IgG-IL-2 immunoconjugate on T cells, NK cells and NK T cells in human peripheral blood from three individual donors each tested on different days. The hierarchy of responsiveness to DP47GS IgG-IL-2 was the same in all three donors and the same as that observed when recombinant human IL-2 (Proleukin®) was used (data not shown). All three Treg populations, activated ($CD45RA^-$, $CD25^{hi}$), memory ($CD45RA^-$, $CD25^+$), and naïve ($CD45RA^+$, $CD25^+$) increased pSTAT5a levels at the 0.1 ng/ml concentration of DP47GS IgG-IL-2 whereas other cell populations required either greater than 1 ng/ml ($CD56^{bright}$ NK and memory $CD4^+$ T cells) or 10-100 ng/ml (memory $CD8^+$ T cells, $CD56^+$ NK cells, naïve $CD4^+$ T cells, NKT cells and $CD45RA^+$ CD8 T cells) of DP47 IgG-IL-2 to produce detectable increases in pSTAT5a. Also see Figure 8 for more detailed dose responses by the Treg populations that display their high sensitivity for DP47GS IgG-IL-2. It is notable that the high expression of IL-2RB on NK cells with intermediate levels of CD56 (Figure 3D) as compared to IL-2RB expression on T cell subsets is not sufficient to allow Treg-like IL-2 sensitivity. Overall, activated, memory and naive Treg subsets showed the greatest sensitivity to DP47GS IgG-IL-2, while $CD56^{bright}$ NK cells and $CD4^+$ conventional memory T effector cells were 20-50 fold less sensitive. Amongst the other cell subsets analyzed for pSTAT5a increases, $CD8^+$ memory T effector cells, $CD4^+$ naïve T effector cells, NKT cells, "resting" NK cells (positive, not bright

staining for CD56), and $CD8^+$ naïve T effector + $CD45RA^+$ memory cells were relatively insensitive to the IgG-IL-2 immunoconjugate.

Figure 6 shows the dose response of DP47GS IgG-(IL-2)2 on T cells, NK cells and NK T cells in human peripheral blood from five individual donors each tested on different days. As observed for DP47GS IgG-IL-2 (Figure 5), the three Treg subsets were the cells most sensitive to DP47GS IgG-$(IL\text{-}2)_2$ induced pSTAT5a (Figures 6 and 8) and similar hierarchical dose responses were found for the other cell subsets in all five donors.

To more readily compare DP47GS IgG-IL-2 and DP47GS IgG-$(IL\text{-}2)_2$, the pSTAT5a values were normalized (Figure 7). To normalize MFI values, unstimulated pSTAT5a MFI values specific for each gated subset were subtracted from all stimulated MFI values for that cell subset. The resulting values were divided by the highest pSTAT5a MFI value obtained by that subset in the dose response. The $EC_{50}$s were estimated based on the amount of IL-2 fusion protein required to reach 50% of the maximal pSTAT5a MFI observed for that subset. As shown in Figure 7, the DP47GS IgG-$(IL2)_2$ immunoconjugate produced a more potent induction of pSTAT5a in cells constitutively expressing CD25, potentially as a consequence of increased avidity of the immunoconjugate for the high affinity IL-2 receptor. The $EC_{50}$ for pSTAT5a activation was observed to be 5-9 fold lower in Treg when directly comparing DP47GS IgG-$(IL\text{-}2)_2$ to DP47GS IgG-IL-2. Table 2 summarizes representative $EC_{50}$ values and fold-differences for pSTAT5a activation by DP47GS IgG-IL-2 vs. DP47GS IgG-$(IL\text{-}2)_2$ in the different cell subsets.

Table 2. $EC_{50}$ values and fold differences for pSTAT5a activation by DP47GS IgG-IL-2 vs. DP47GS IgG-$(IL\text{-}2)_2$ in different cell subsets.

| **T cell** | **IgG-IL-2** | **IgG-$(IL\text{-}2)_2$** | **Fold change** |
|---|---|---|---|
| activated Treg | 0.10 ng/mL | 0.020 ng/mL | 5 |
| memory Treg | 0.22 ng/mL | 0.033 ng/mL | 7 |
| naïve Treg | 0.20 ng/mL | 0.023 ng/mL | 9 |
| $CD56^{bright}$ NK | 2.0 ng/mL | 0.63 ng/mL | 3 |
| CD4 Tconv mem | 5 ng/mL | 0.7 ng/mL | 7 |
| NK cells | 35 ng/mL | 10 ng/mL | 4 |

Even at extremely limiting concentrations, DP47GS IgG-$(IL\text{-}2)_2$ produced higher levels of pSTAT5a as compared to DP47GS IgG-IL-2 (Figure 8). For this experiment, blood from three healthy volunteers was tested individually on the same day for responses to a 2-fold titration of DP47 IgG-IL-2 and DP47 IgG-$(IL\text{-}2)_2$ at limiting concentrations of IL-2. Graphs in Figure 8 represent the mean ± SD of the pSTAT5a MFI for the three donors. In addition to the three Treg subsets examined individually (Figure 8B-D), a gate was applied to assess pSTAT5a in total $CD3^+$, $CD4^+$, $FoxP3^+$ Tregs (Figure 8A). The results clearly indicate a 5-10-fold increase in potency for DP47GS IgG-$(IL\text{-}2)_2$ activation of Tregs despite only a 2-fold increase in IL-2 per molecule of IgG. Polychromatic flow cytometry was performed as described above (see Figure 5).

$CD4^+$ conventional memory T cells also responded to lower (7-fold) concentrations of DP47GS IgG-$(IL\text{-}2)_2$ as compared to DP47GS IgG-IL-2. While the $EC_{50}$ values were lower for $CD56^{bright}$ NK cells and $CD56^+$ NK cells when comparing DP47GS IgG-$(IL\text{-}2)_2$ to DP47 IgG-IL-2, the lowering was only 3-fold and 4-fold, respectively. This is likely due to the reliance of these cells on the intermediate affinity IL-2 receptor for IL-2-mediated signaling. This differential shift in the $ED_{50}$ for Tregs versus NK cells increases the preference for Treg activation several fold.

**Induction of pSTAT5a in cynomolgus peripheral blood cell subsets**

As observed in human peripheral blood, there is a preferential and similar dose-dependent induction of pSTAT5a in Treg subsets in cynomolgus peripheral blood stimulated with IL-2 (Proleukin®) (data not shown). In a direct comparison of the ability of DP47GS IgG-$(IL\text{-}2)_2$ and DP47GS IgG-IL-2 to induce pSTAT5a in the three Treg subsets, 2-8 fold less DP47GS IgG-$(IL\text{-}2)_2$ was required to reach 50% of the maximal level of pSTAT5a. Table 3 summarizes the $EC_{50}$ values for pSTAT5a activation by DP47GS IgG-IL-2 versus DP47GS IgG-$(IL\text{-}2)_2$ in the different cynomolgus Treg subsets, results that are strikingly similar to those seen with human peripheral blood (Table 2).

Similar to human whole blood, cell surface and intracellular markers were used to identify regulatory T cell subsets and conventional T cells in whole blood from normal healthy cynomolgus monkeys. Blood samples were collected on the same day from three healthy cynomolgus monkeys in sodium heparin tubes and various concentrations of DP47GS IgG-IL-2 or DP47GS IgG-$(IL\text{-}2)_2$ were added to 500 µl of blood and incubated at 37°C. After 10 min at 37°C, samples were lysed and fixed with pre-warmed BD Lyse/Fix buffer (BD Biosciences). After washing, cells were permeabilized with 1 mL methanol for 30 min on ice. Samples were

washed 3 times and stained with a panel of FOXP3-Alexa Fluor® 647 (clone: 259D, BioLegend), CD4-V500 (clone: L200, BD Biosciences), CD45RA-V450 (clone: 5H9, BD Biosciences), CD25-PE (clone: 4E3, eBioscience), pSTAT5a- Alexa Fluor® 488 (clone: 47, BD Biosciences), and Ki-67-PerCP-Cy5.5 (clone: B56, BD Biosciences) for 1 hour at 4°C. All the samples were acquired by an LSRFortessa cell analyser (Becton Dickinson) and then analysed with FlowJo software (Tree star, Inc., Ashland, USA).

Table 3. Induction of pSTAT5a in cynomolgus peripheral blood Treg subsets in response to DP47GS IgG-IL-2 and DP47GS IgG-$(IL\text{-}2)_2$.

| T cell | IgG-IL-2 | IgG-$(IL\text{-}2)_2$ | Fold change |
|---|---|---|---|
| activated Treg | 0.07 ng/mL | 0.02 ng/mL | 4 |
| memory Treg | 0.21 ng/mL | 0.025 ng/mL | 8 |
| naïve Treg | 0.040 ng/mL | 0.02 ng/mL | 2 |

**Induction of Treg number in cynomolgus monkeys**

Cynomolgus animals treated *in vivo* with DP47GS IgG-IL-2 had dose-dependent increases in the absolute number of Tregs as well as the fold increase above baseline 7 days post dosing (Figure 9A and 9B, respectively). Normal healthy cynomolgus monkeys of both sexes at ages ranging from 3 to 6 years were used in all tests and no animal was used more than once. While under anaesthesia, various doses of DP47GS IgG-IL-2 (n=4-6) or vehicle (n=3) were injected SC on the lateral dorsum. Individual doses of DP47GS IgG-IL-2 were based on body weight and formulated for injection in a vehicle of sterile PBS pH 7.2 containing 0.5% sterile normal cynomolgus serum. Blood samples were collected at various times post treatment and tested for haematological changes (CBC and Differential) with an Advia Automated Hematology Analyser as well as cell surface and intracellular markers detailed above (experimental procedures for Table 3). The changes in whole blood $CD4^+$, $CD25^+$, $FOXP3^+$, regulatory T cells on day 7 post treatment are shown in Figure 9 as the absolute cell number per $mm^3$ of whole blood (Figure 9A) and the fold change in Tregs (Figure 9B); all data are represented as the mean ± SD. At the higher doses of 25 µg/kg and 36 µg/kg DP47GS IgG-IL-2, average Treg increases of nearly 3-fold (range of 111-255%, n=6) and 4-fold (range of 110-470%, n=6), respectively, were observed. Further reduction of the SC dose of DP47GS IgG-IL-2 (12, 6, and 2 µg/kg) continued to produce correspondingly reduced changes in Treg number and fold change. Without wishing

to be bound by theory, the ~2-fold increase in Tregs (ranging from 67-133%, n=6) with the 12 µg/kg DP47GS IgG-IL2 dose represents about the desirable increase in Tregs. There is a large range in the numbers of Tregs in humans (20-90 Tregs per $mm^3$ of blood; 4 to 10% of $CD4^+$ T cells) and it is reasonable to assume that an increase of Tregs induced by IL-2 within an individual will result in an overall increase in functional suppression. It might be desirable, however, not to increase Treg numbers above the normal range for this cell population for a sustained period of time, but primarily enhance the function of these cells.

When the lower doses of DP47GS IgG-IL-2 were evaluated (2-6 µg/kg), more frequent blood samples were collected to identify optimal times for detecting changes in Tregs subsequent to DP47GS IgG-IL-2 administration (Figure 10). While changes in Tregs were present at 7 days, maximal stimulation occurred on day 4, sooner than was measured with the higher doses of DP47GS IgG-IL-2 (day 7, Figure 9).

Proleukin® and DP47GS IgG-IL-2 are comparable *in vitro* in human and cynomolgus whole blood assays when compared directly by the units of IL-2 activity used to stimulate pSTAT5a in Tregs and other IL-2 responsive cells (data not shown). With the known short half-life of Proleukin® in humans, a single dose study was done in cynomolgus monkeys to assess *in vivo* Treg induction and activation. Proleukin® produced a dose and time dependent change in Tregs measured by fold change in absolute numbers as well as pSTAT5a activation. While the increase in Treg numbers was nominal (Figure 11A: 10-40%), the Proleukin-induced increase in Treg pSTAT5a was substantial and dose dependent one day after treatment (Figure 11B).

A comparison of the ability of DP47GS IgG-IL-2 to induce an increase in Tregs *in vivo* in cynomolgus monkeys with that of Proleukin® is shown in Figure 12. Normal healthy cynomolgus monkeys (groups of n=5) were treated with low doses of DP47GS IgG-IL-2 or high doses of Proleukin® and the change in regulatory T cells tested at day 10. On days 0 and 7, DP47 IgG-IL-2 was given SC at a dose of 16,800 IU/kg (the 12 µg/kg dose shown in Figure 9). Based on published work where Proleukin® was given to type 1 diabetes patients ($4.5x10^6$ IU/person, 3 times/week) and shown to increase Tregs and the single dose data in Figure 11, Proleukin® was given SC 3 times per week (M,W,F) for a total of 5 doses each at 200,000 IU/kg (the cynomolgus equivalent of $4.5x10^6$ IU/person). The results are shown in Figure 12 as mean ± SD for the change in total Tregs per $mm^3$ blood (Figure 12A), the fold increase in number of Tregs (Figure 12B), and the change in the ratio of Tregs to conventional $CD4^+$ $FOXP3^-$ cells (Figure 12C).

Although nearly 30-fold less DP47GS IgG-IL-2 activity was administered over the 10 day period, DP47GS IgG-IL-2 induced a larger increase in the number of Tregs than Proleukin® (Figure 12A, p=0.06). The fold increase of Treg numbers above baseline (Figure 12B) and the increase of Tregs relative to conventional CD4 T cells (Figure 12C) were also larger (p=0.0011 and p=0.016, respectively) in monkeys dosed with DP47GS IgG-IL-2 as compared to Proleukin®. In humans the ratio of regulatory CD4 T cells (usually defined as $FoxP3^+$ or by a combination of surface markers) to non-regulatory CD4 T cells (referred to as conventional or effector cells) is often used to define the functional levels of Tregs in patients through time.

***In vivo* response of cynomolgus peripheral blood cell subsets to low dose DP47GS IgG-IL-2 treatment**

The *in vivo* cellular specificity of low dose IL-2 treatment is a critical parameter. We have determined that *in vivo* cell activation induced by DP47GS IgG-IL-2 or Proleukin® can be sensitively monitored by measuring pSTAT5a levels *ex vivo* in blood taken at various times after dosing cynomolgus monkeys or mice. The *in vivo* response of all cell populations that can be monitored *in vitro* (Figures 5-7) can also be examined *ex vivo*.

One and 3 days after *in vivo* administration of a single low dose of DP47GS IgG-IL-2 (12 μg/kg) to healthy cynomolgus monkeys (n=5), whole blood was collected and tested for STAT5a phosphorylation as described above (experimental procedures to Table 3). Each monkey was bled on day 0 before treatment and the amount of STAT5a phosphorylation was measured and used individually to assess fold-changes post treatment. The fold change in pSTAT5a in Tregs on days 1 and 3 is shown in Figure 13A, the fold change in pSTAT5a in conventional $CD4^+$ $CD45RA^-$ memory T cells in Figure 13B, and the fold change in pSTAT5a in conventional $CD4^+$ $CD45RA^+$ naïve T cells is in Figure 13C. The results clearly show that cynomolgus blood obtained one and three days after a single low dose (12 μg/kg) of DP47GS IgG-IL-2 showed preferential pSTAT5a increases in Treg cells as compared to memory and naïve $CD4^+$ T cells (Figure 13A-C). Single low dose DP47GS IgG-IL-2 was clearly superior to single high dose Proleukin® (Figure 11B) in producing a sustained *in vivo* Treg state of activation.

The initial studies using phosphorylation of STAT5a as an *in vivo* biomarker of Treg activation saw maximal pSTAT5a only at 1 day with single dose Proleukin® (Figure 11B) and 1 and 3 days with low dose (12 μg/kg) DP47GS IgG-IL-2 (Figure 13A). Further titration of DP47GS IgG-IL-2 combined with additional sampling times showed that *in vivo* pSTAT5a signals could be maintained for 4 days before dropping back to normal at 7 days (Figures 14A, 14B). The MFI

(mean fluorescence intensity) of the pSTAT5a signals for both the 2 μg/kg (14A, n=4) and 6 μg/kg (14B, n=6) dose suggested that less than maximal pSTAT5a signaling occurred (see Figure 16B). Even these very low doses of DP47GS IgG-IL-2 provided sustained *in vivo* signaling of Tregs and were superior to Proleukin® (Figure 11B). These results support our hypothesis that very low levels of long-lived IL-2, *i.e.* DP47GS IgG-IL-2 but not Proleukin®, can stimulate Tregs for extended periods of time *in vivo* thereby reducing the frequency of treatment needed to re-establish dominant self-tolerance and improve disease outcomes..The increase in Treg cells in the peripheral blood after low dose IL-2 treatment could reflect a change in the distribution of the cells in the body rather than an actual increase of the cells. To substantiate that Treg increases *in vivo* are at least in part due to the induction of cell division by IL-2 treatment, the intracellular marker of proliferation Ki-67 was assessed. Ki-67 is a protein that can be detected in the nucleus during $G_1$, S, $G_2$, and mitosis but is absent from resting cells that are in the $G_0$ phase of the cell cycle. The cynomolgus monkeys treated with 2 and 6 μg/kg DP47GS IgG-IL-2 described above (Figure 14) were also monitored for *ex vivo* changes in the intracellular marker Ki-67 as described (experimental procedures to Table 3) to assess the extent of proliferation *in vivo*. The percentage of cells that were in cell cycle ($Ki\text{-}67^+$) on day 0 was compared to the percentage of cells $Ki\text{-}67^+$ at 1 to 11 days post treatment. $Ki\text{-}67^+$ Tregs are shown in Figure 15A, conventional $CD4^+$ $CDRA45^-$ memory T cells are in Figure 15B, and conventional naïve $CD4^+CD45RA^+$ T cells are in Figure 15C. Cynomolgus blood cells obtained one to seven days after a single low dose of DP47GS IgG-IL-2 (6 μg/kg) showed preferential Ki-67 increases in Tregs compared to naïve conventional $CD4^+$ T cells (Figure 15A versus 15C). Unlike naïve T cells, DP47GS IgG-IL-2 (6 μg/kg) was able to stimulate proliferation of conventional memory $CD4^+$ T cells (Figure 15B). At the lowest dose of DP47GS IgG-IL-2 (2 μg/kg), there was minimal activation into cell cycle and proliferation compared to the 6 μg/kg dose..

In human and cynomolgus whole blood assays the *in vitro* activity of DP47GS IgG-$(IL\text{-}2)_2$ was in aggregate, approximately 6 fold more potent on Tregs than DP47GS IgG-IL-2 (Tables 1 and 3). Hence, the first dose into cynomolgus monkeys was 6 fold less than the highest dose of DP47GS IgG-IL-2 tested (36μg/kg). DP47GS IgG-$(IL\text{-}2)_2$ administered at 6 μg/kg (n=4) produced large increases in circulating Tregs (Figure 16A), significant and prolonged pSTAT5a in Tregs that returned to normal at 1 week (Figure 16B), and nearly a 3 fold increase in the number of Tregs (Figure 16C). The fold changes induced by DP47GS IgG-IL-2 (from Figure 9, open bars) were compared to the 6 μg/kg dose of DP47GS IgG-$(IL\text{-}2)_2$ (shaded bar) (Figure

16D). Similar to the human and cynomolgus whole blood assays, DP47GS IgG-(IL-2)$_2$ exhibited enhanced *in vivo* potency beyond its 2 fold increase in IL-2 per molecule of IgG.

Additional doses of DP47GS IgG-(IL-2)$_2$ were given to cynomolgus monkeys to assess its *in vivo* effects at very low doses (2 and 0.7 µg/kg) (Figure 17). While 2 µg/kg produced moderate fold changes (mean of 46%, ranging from 20 to 70%, n=8), the 0.7 µg/kg dose had little effect on T cell numbers (mean increase of 16%, n=3) (Figure 17A). Both low doses stimulated pSTAT5a increases in Treg (Figure 17B, n=3 each) while having little effect on Teff/mem cell pSTAT5a (Figure 17C, n=3 each).

The overarching effects of IL-2 therapy and its ability to increase Tregs in cynomolgus monkeys are presented in Figure 18. Both forms of long-lived IgG-IL-2 are potent inducers of Tregs which can be followed *in vivo* with pSTAT5a as a biomarker of activation and in this figure as the fold increase in the numbers of circulating Tregs. DP47GS IgG-(IL-2)$_2$ with its enhanced potency achieved by doubling the IL-2 molecules at the C-terminus of IgG has a dose dependent superiority over DP47GS IgG-IL-2.

Proleukin® in humans stimulates an eosinophilia when given daily at doses of $1x10^6$ to $4.5x10^6$ IU/person. In cynomolgus monkeys similar increases in eosinophils were seen after repeated treatment with Proleukin® or single doses of DP47GS IgG-IL-2 (Figure 19). The results in Figure 19A represent every animal tested (n=5-6) regardless if eosinophil numbers were normal or elevated. The data in Figure 19B represent only the monkeys that developed treatment related elevated blood eosinophils. The data are shown as the mean ± SD. Open bars are DP47GS IgG-IL-2 treated and the shaded bar on the right is from the 6 µg/kg DP47GS IgG-(IL-2)$_2$ treated monkeys from Figure 16. A summary of the results is shown in Table 4 below. Despite the equivalence of 25 µg/kg DP47GS IgG-IL-2 and 6 µg/kg DP47GS IgG-(IL-2)$_2$ on Tregs, their effect on eosinophils was markedly different, 50% responders versus 0% responders, respectively.

Table 4. Pharmacologic induction of eosinophils in cynomolgus monkeys with IL-2.

| Treatment | Dose | Group size | Eosinophilia |
|---|---|---|---|
| Proleukin® | $2x10^5$ IU/kg (x7) | 5 | 100% |
| DP47GS IgG-IL-2 | 36 µg/kg | 6 | 100% |
| DP47GS IgG-IL-2 | 25 µg/kg | 6 | 50% |

| | | | |
|---|---|---|---|
| DP47GS IgG-IL-2 | 12 µg/kg | 6 | 17% |
| DP47GS IgG-IL-2 | 6 µg/kg | 6 | 0% |
| DP47GS IgG-$(IL-2)_2$ | 6 µg/kg | 6 | 0% |

**Pharmacokinetic properties of DP47GS IgG-IL-2 in mice**

Prior to beginning functional studies in mice, the pharmacokinetic (PK) properties of DP47GS IgG-IL-2 were compared to those of Proleukin® (Figure 20).

NOD mice were injected IP (Figure 20A) or SC (Figure 20B) with the indicated doses of DP47GS IgG-IL-2 or Proleukin® in PBS containing 0.5% mouse serum and bled at various times after the injections. Doses of DP47GS IgG-IL-2 are summarized in Table 4. Human IL-2 was assessed in serum samples using mouse anti-human IL-2 mAb, BD Pharmingen, Cat #555051, clone 5344.111 to coat 96-well plates to capture the IL-2. IL-2 was detected using biotinylated mouse anti-human IL-2 mAb, BD Pharmingen, Cat # 555040, clone B33-2. Binding was visualized using Europium-conjugated streptavidin.

As described previously, Proleukin® was cleared rapidly. In contrast, DP47GS IgG-IL-2 was cleared much more slowly. Results from comparing the PK of DP47GS IgG-IL-2 in normal mice and NOD-scid CD25KO mice support the hypothesis that a major component driving the *in vivo* clearance of DP47GS IgG-IL-2 is the high affinity IL-2 receptor (data not shown).

Table 4. Doses of DP47GS IgG-IL-2 for PK study shown in Figure 20.

| **IgG-IL2 (IU/25g)** | **IgG-IL2 (mg/kg)** |
|---|---|
| 105,000 | 3.0 |
| 10,500 | 0.3 |
| 4,000 | 0.114 |
| 1,000 | 0.0286 |
| 300 | 0.0086 |

**FOXP3 and CD25 MFI increase in Tregs after treatment with IgG-IL-2**

To compare the abilities of the immunoconjugates DP47GS IgG-IL-2 and DP47GS IgG-(IL-2)$_2$, and recombinant human IL-2 (Proleukin®) to stimulate FoxP3$^+$ Treg cells *in vivo*, mice were injected subcutaneously with either Proleukin®, DP47GS IgG-IL-2, or DP47GS IgG-(IL-2)$_2$ and Tregs were monitored for changes in the expression of CD25 and FOXP3 at a previously determined optimal time of 24 hours (Figure 21).

Young healthy BALB/c mice (n=3/treatment group, n=4/vehicle control cohorts) were injected subcutaneously with either Proleukin® (20,000 or 100,000 IU), DP47GS IgG-IL-2 (60, 300, or 1,500 IU), or DP47GS IgG-(IL-2)$_2$ (60, 300, or 1,500 IU). Doses were delivered in 100 µl sterile PBS pH 7.2 containing 0.5% sterile-filtered mouse serum. After 24 hours, mice were euthanized and spleens excised. A single cell suspension of splenocytes was generated in 1 ml L-15 media and stored on ice, until further processing. A filtered aliquot of the single cell suspension, 40 µl, was transferred to FACS tubes and washed with 2 ml FACS buffer (600 x g, 5 min). Samples were then incubated with fluorochrome-conjugated antibodies directed against cell surface antigens: CD4 (clone RM4-5, fluorochrome A700), CD25 (eBio7D4, Af488), CD44 (IM7, e605), CD62L (MEL-14, PE), ICOS (C398.4A, PE/Cy7), CD103 (2E7, APC). Staining was performed for 30 min, at 4°C in 100 µl FACS buffer (PBS pH 7.2 + 0.2% BSA). Following cell surface staining, samples were washed with 4 ml FACS buffer (600 x g, 5 min) before intracellular staining (according to the eBioscience intracellular staining protocol). Briefly, samples were resuspended in 200 µl fixation/permeabilisation buffer (eBioscience #00-5521) and incubated for 1 h, 4°C. 1 ml of 1 x permeabilisation buffer (eBioscience #00-8333) was added to samples before 3 ml FACS buffer and washing (600 x g, 5 min). Intracellular antigens, Ki-67 (B56, PerCP Cy5.5) and FOXP3 (FJK-16S, e450), were stained in 100 µl 1 x permeabilisation buffer for 1 h, 4°C. Samples were washed with 4 ml FACS buffer (600 x g, 5 min - twice) and data acquired on a BD Fortessa Analyser and analysed using FlowJo software (Tree Star Inc.). Tregs were defined as CD4$^+$, FOXP3$^+$ from singlets within the lymphocyte gate; from this population, CD25 and FOXP3 mean fluorescence intensity (MFI) were calculated for all samples.

As shown in Figure 21, compared to 100,000 IU of Proleukin®, 300 IU of DP47GS IgG-IL-2 or DP47GS IgG-(IL-2)$_2$ induced similar up-regulation of CD25 while 1,500 IU was even more potent (Figure 21A). The ability to stimulate intracellular FOXP3 showed similar enhanced capabilities for the two IL-2 immunoconjugates compared to Proleukin®. In all treatment groups the data is shown as the mean ± SD. Previous studies had shown that FOXP3 and CD25 levels returned to baseline 72 hours after IL-2 treatment.

***In vivo* treatment with DP47GS IgG-IL-2 suppresses immune responses in mice**

In preliminary studies before those shown in Figure 21 we observed that a 4,000 IU DP47GS IgG-IL-2 dose activated mouse $FOXP3^+$ regulatory T cells *in vivo*; this dose was then used to assess its ability to suppress classic T dependent immune responses in mice, *i.e.* delayed type hypersensitivity (Figure 22) and an IgG anti-KLH response (Figure 23).

NOD mice and C57BL/6 mice (n=7) were immunized IV with sheep red blood cells (srbc) and challenged 3 days later with a bolus of srbc in a single hind foot to induce a delayed type hypersensitivity (DTH) response. One day after challenge, mice were euthanized with $CO_2$ and the paws excised and weighed. The magnitude of the DTH response is shown as the change in paw weight compared to non-immunized mice (Δ paw weight). DP47GS IgG-IL-2 was given SC at 4,000 IU per mouse 3 days before and on the day of srbc immunization and the vehicle was sterile PBS pH 7.2. Statistical significance was derived from the Mann Whitney test in GraphPad Prism.

Dosing DP47GS IgG-IL-2 three days before and on the day of sheep red blood cell immunization suppressed the subsequent delayed type hypersensitivity response to a sheep blood cell challenge by 51% in NOD mice (Figure 22A; p=0.0023) and 38% in C57BL/6 mice (Figure 22B; p=0.002). Mouse CTLA-4-Ig as a positive control immunosuppressant inhibited the DTH response to a similar level as DP47GS IgG-IL-2.

DP47GS IgG-IL-2 was also able to suppress KLH-specific IgG responses in C57BL/6 (78% inhibition, p=0.0007, Figure 23A) and NOD (67% inhibition, p=0.004, Figure 23B) mice. For this experiment, healthy young C57BL/6 mice (n=7-10) and NOD mice (n=13-14) were immunized IP with 100 μg of human vaccine grade KLH without adjuvant as recommended by the manufacturer (Stellar). DP47GS IgG-IL-2 treatment consisted of 1 (NOD) or 2 (C57BL/6) weekly treatments with 4,000 IU per mouse SC initiated on the day of immunization. Seven days (NOD) and 21 days (C57BL/6) after immunization, blood was collected and serum KLH-specific IgG responses were measured by ELISA.

The ability of DP47GS IgG-IL-2 to suppress immune responses *in vivo* supports the hypothesis that the regulatory T cell activation induced by low dose IL-2 produces functional regulatory T cells that mediate a reduction in the immune response.

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Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, the descriptions and examples should not be construed as limiting the scope of the invention. The disclosures of all patent and scientific literature cited herein are expressly incorporated in their entirety by reference.

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## Claims

1. A fusion protein comprising (i) a human $IgG_1$-subclass immunoglobulin molecule comprising a modification reducing binding affinity of the immunoglobulin molecule to an Fc receptor as compared to a corresponding immunoglobulin molecule without said modification, and (ii) two interleukin-2 (IL-2) molecules,

   wherein said immunoglobulin molecule comprises the heavy chain variable region sequence of SEQ ID NO: 9 and the light chain variable region sequence of SEQ ID NO: 11, and

   wherein said immunoglobulin molecule comprises the amino acid substitutions L234A, L235A and P329G (EU numbering) in the immunoglobulin heavy chains.

2. The fusion protein of claim 1, wherein said Fc receptor is an Fcγ receptor, particularly a human Fcγ receptor.

3. The fusion protein of claim 1 or 2, wherein said Fc receptor is an activating Fc receptor.

4. The fusion protein of any one of the preceding claims, wherein said Fc receptor is selected from the group of FcγRIIIa (CD16a), FcγRI (CD64), FcγRIIa (CD32) and FcαRI (CD89).

5. The fusion protein of any one of the preceding claims, wherein said Fc receptor is FcγRIIIa, particularly human FcγRIIIa.

6. The fusion protein of any one of the preceding claims, wherein said IL-2 molecules are wild-type IL-2 molecules.

7. The fusion protein of any one of the preceding claims, wherein said IL-2 molecules are human IL-2 molecules.

8. The fusion protein of any one of the preceding claims, wherein said IL-2 molecules comprise the sequence of SEQ ID NO: 1 or SEQ ID NO: 3, particularly the sequence of SEQ ID NO: 3.

9. The fusion protein of any one of the preceding claims, wherein said IL-2 molecules are each fused at their N-terminal amino acid to the C-terminal amino acid of one of the immunoglobulin heavy chains of said immunoglobulin molecule, optionally through a peptide linker.

10. The fusion protein of any one of the preceding claims, wherein the fusion protein omprises the polypeptide sequences of SEQ ID NO: 17 and SEQ ID NO: 19.

11. A polynucleotide encoding the fusion protein of any one of the preceding claims.

12. A vector, particularly an expression vector, comprising the polynucleotide of claim 11.

13. A host cell comprising the polynucleotide of claim 11 or the vector of claim 12.

14. A method for producing a fusion protein comprising (i) an immunoglobulin molecule comprising a modification reducing binding affinity of the immunoglobulin molecule to an Fc receptor as compared to a corresponding immunoglobulin molecule without said modification, and (ii) two interleukin-2 (IL-2) molecules, said method comprising the steps of (i) culturing the host cell of claim 13 under conditions suitable for expression of the fusion protein, and (ii) recovering the fusion protein.

15. A fusion protein comprising (i) an immunoglobulin molecule comprising a modification reducing binding affinity of the immunoglobulin molecule to an Fc receptor as compared to a corresponding immunoglobulin molecule without said modification, and (ii) two interleukin-2 (IL-2) molecules, produced by the method of claim 14.

16. A pharmaceutical composition comprising the fusion protein of any one of claims 1-10 or 15 and a pharmaceutically acceptable carrier.

17. The fusion protein of any one of claims 1-10 or 15, or the pharmaceutical composition of claim 16, for use as a medicament.

18. The fusion protein of any one of claims 1-10 or 15, or the pharmaceutical composition of claim 16, for use in the treatment or prophylaxis of an autoimmune disease.

19. The fusion protein or the pharmaceutical composition of claim 18, wherein said autoimmune disease is selected from the group of type 1 diabetes, systemic lupus erythematosus, Crohn's disease, ulcerative colitis, rheumatoid arthritis, eczema, dermatitis, asthma, and multiple sclerosis.

20. The fusion protein of any one of claims 1-10 or 15, or the pharmaceutical composition of claim 16, for use in the treatment or prophylaxis of transplant rejection or graft-versus-host disease.

21. Use of the fusion protein of any one of claims 1-10 or 15 for the manufacture of a medicament for the treatment of a disease in an individual in need thereof, wherein said disease is an autoimmune disease, transplant rejection or graft-versus-host disease.

22. The use of claim 21, wherein said autoimmune disease is selected from the group of type 1 diabetes, systemic lupus erythematosus, Crohn's disease, ulcerative colitis, rheumatoid arthritis, eczema, dermatitis, asthma, and multiple sclerosis.

23. The use of claims 21 or 22, wherein said individual is a mammal, particularly a human.

24. The fusion protein of any one of claims 1-10 or 15 for use in selective activation of regulatory T cells *in vitro* or *in vivo*.

25. The fusion protein of claim 24, wherein said activation comprises induction of proliferation of regulatory T cells and/or induction of IL-2 receptor signaling in regulatory T cells.

26. The fusion protein of claim 24 or 25, wherein said use is *in vitro* and said fusion protein is used at a concentration of about 1 ng/mL or less, particularly about 0.1 ng/mL or less.

27. The fusion protein of claim 24 or 25, wherein said use is *in vivo* and said fusion protein is used at a dose of about 20 µg/kg body weight or less, particularly about 12 µg/kg body weight or less, more particularly about 6 µg/kg body weight or less.