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(54) Title: CTLA4 PROTEINS AND THEIR USES

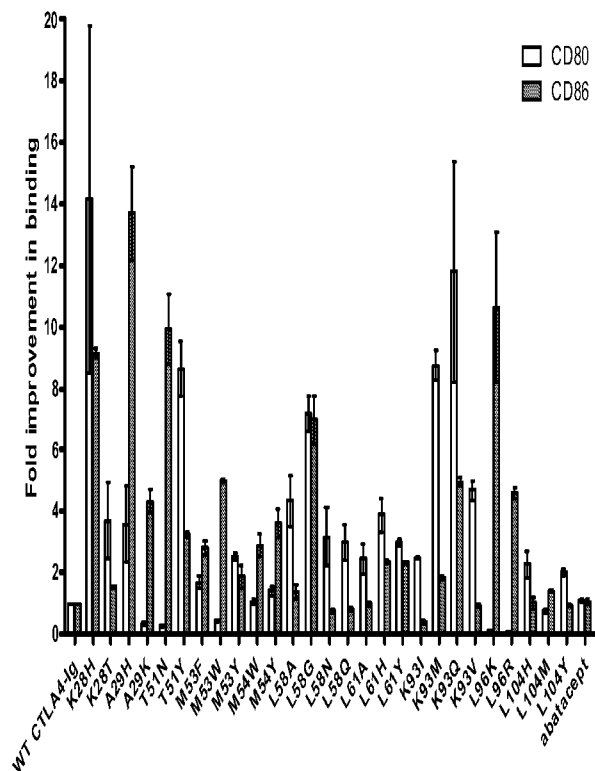


Figure 2A

(57) Abstract: The present disclosure relates to CTLA4 proteins and uses of such proteins, for example to treat diseases associated with the dysregulation of immune responses.

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CTLA4 PROTEINS AND THEIR USES

1. CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Application No. 61/313,516, filed March 12, 2010, the contents of which are incorporated by reference herein in their entirety.

1.1 SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted in ASCII format via EFS-Web and is hereby incorporated by reference in its entirety. Said ASCII copy, created on February 11, 2011, is named 237US161.txt and is 498,294 bytes in size.

2. FIELD OF THE INVENTION

[0003] The present invention relates to CTLA4 proteins, pharmaceutical compositions comprising CTLA4 proteins, and therapeutic uses of such proteins.

3. BACKGROUND

[0004] T-cell lymphocytes play a critical role in cell-mediated immunity by providing for an adaptive response to specific pathogens. T-cell activation depends on activation of at least two signaling pathways, one that is antigen specific and the other that is antigen nonspecific. A T-helper cell antigenic response requires activation of a first signaling pathway by the binding of the T-cell receptor to an antigen bound to MHC (major histocompatibility complex) on the surface of an antigen presenting cell (APC). The antigenic response also requires activation of a second signaling pathway, which produces a co-stimulatory signal, by the binding of CD28 protein on the surface of the T-cell to CD80 (B7-1) and CD86 (B7-2) on the surface of the APC. Because the antigen-

specific signal is not sufficient to generate a full antigenic response, T-cell receptor/antigen-MHC binding without co-stimulation may lead to clonal inactivation or anergy. (See, e.g., Jenkins *et al.*, 1993, *Curr. Opin. Immunol.* 5:361). The co-stimulatory pathway plays a role not only in T-cell activation and differentiation, but also in tissue migration and peripheral tolerance induction. (See Salomon *et al.*, 2001, *Ann. Rev. Immunol.* 19:225.)

[0005] Activated T-cells also express on their cell surface cytotoxic T-lymphocyte-associated antigen 4 (CTLA4), a homologue of CD28 that binds CD80 and CD86 with higher affinity. CTLA4 expression results in competitive binding to CD80 and CD86, blocking the CD80/86-CD28 interaction and terminating T-cell activation. Because these signaling pathways determine the magnitude of a T-cell response to antigen, as well as downstream responses to antigen, agents that modulate one or more costimulatory signals, e.g., by blocking one or more of the interactions between CD80/CD86 and CD28 and/or CTLA4, may be effective in treating disorders that result from dysregulated cell-mediated immune responses. (See, e.g., Mueller, *et al.*, 1989, *Annu. Rev. Immunol.* 7:445).

[0006] Suitable agents for the disruption of the CD80/86-CD28 interaction include antibodies and fusion proteins. For example, in an experimental autoimmune encephalomyelitis (EAE) model, T-cells were blocked using anti-CD80 and anti-CD86 antibodies. (See Racke, *et al.*, 1995, *J. Clin. Invest.* 96:2195). In another example, anti-CD80 and anti-CD86 antibodies were used to block type 2 *in vivo* immune responses (*i.e.*, immune responses mediated by IgG antibodies and directed against cell-surface or matrix antigens) and the production of IL-4. (Greenwald, *et al.*, 1997, *J. Immunol.* 158:4088) CD28-Ig fusion proteins have been demonstrated to interact with CD80 and/or CD86 on dendritic cells and to activate them, which results in an adjuvant activity of soluble CD28 that produces enhanced T-cell mediated immune responses *in vivo*. (Orabona *et al.*, 2004, *Nature Immunol.* 5(11):1134). Alternatively, CTLA4-Ig fusion proteins have been used to disrupt CD80/86-CD28 interactions. (See, e.g., McIntyre, *et al.*, 2005, *Drugs of the Future*, 30:873).

[0007] Recent studies of T-cell activation and the costimulatory pathway indicate that CD80 and CD86 can play different roles in immune responses, and especially in autoimmunity. Thus, blocking the binding of only one of CD80 or CD86 to CD28 has been shown to produce disparate effects *in vivo*, depending on the disease being studied and the timing of administration (*See* Salomon, 2001, *Annu. Rev. Immunol.* 19:225; Kuchroo, *et al.*, 1995, *Cell* 80:707; Racke, *et al.*, 1995, *J. Clin. Invest.* 96:2195; Lenschow *et al.*, 1995, *J. Exp. Med.* 181:1145; and Greenwald, *et al.*, *J. Immunol.*, 1997, 158:4088).

[0008] Antibodies that bind to CTLA4 and disrupt CTLA4 inhibition of CD28-mediated T-cell responses are currently in development for the treatment of various cancers. Ipilimumab, a human anti-CTLA4 IgG₁ antibody, is in Phase III trials for melanoma and in Phase II trials for breast cancer and prostate cancer. Tremelimumab, a human anti-CTLA4 IgG₂ antibody, is in Phase II trials for prostate cancer, bladder cancer, and colorectal cancer.

[0009] Fusion proteins that bind to CD80 and/or CD86 and disrupt the interaction with CTLA4 and CD28 are good candidates for the development of immunomodulatory agents. Fusion proteins allow for the engineering of proteins with, for example, improved solubility, stability, deliverability, and/or activity. One such immunomodulatory agent is the soluble fusion protein abatacept (Orencia®), developed for the treatment of rheumatoid arthritis (RA) and juvenile idiopathic arthritis, autoimmune disorders which attack the joints, causing painful swelling that can eventually result in bone erosion and joint deformity.

[0010] Abatacept is a CTLA4-Ig fusion protein consisting of the extracellular domain of human CTLA4 and a modified Fc portion of human immunoglobulin G₁ (IgG₁) that includes hinge, CH2, and CH3 domains. The CTLA4 domain provides binding activity and the Fc portion is believed to provide stability, solubility and deliverability. Abatacept inhibits the interaction of CD28 on T-cells with CD80 and/or CD86 proteins on APC cells, thereby resulting in inhibition of T-cell activation. (*See, e.g.*, Schwartz,

1992, Cell 71:1065). Accordingly, administration of abatacept results in a decrease in T-cell proliferation, activation and signaling, and attenuates the autoimmune response in rheumatoid arthritis. A second-generation soluble recombinant CTLA4-Ig fusion protein known as belatacept differs from abatacept in two amino acids and has a greater binding affinity for CD80 and CD86. Belatacept is in ongoing Phase III trials for use in kidney and other organ transplantation. (See Linsley *et al.*, 2009, Immunol. Reviews 229:307-321). A third fusion protein, MAXY-4, a protein derived from abatacept but having increased binding to CTLA4 targets, is currently in preclinical development by Perseid Therapeutics, LLC and Astellas Pharma, Inc. for treatment of autoimmune diseases and transplant rejection.

[0011] Therapy with abatacept can be cost prohibitive. Higher affinity variants of abatacept could reduce the required effective therapeutic dose and therefore reduce the cost of therapy. Moreover, because less of the agent is required to achieve a beneficial result, the risk of developing an immunogenic response to the agent itself may also be decreased. Other side-effects may also be reduced. There is a need to provide improved fusion proteins with differential binding to the CD80 and CD86 proteins, for example, by generating variants with higher relative affinity for one isoform relative to the other. Such improved variants may provide targeted immune modulation for specific conditions or pathologies. Adverse effects or exacerbation of immune responses observed in some cases of CTLA4-Ig and anti-CTLA4 antibody therapies may also be reduced.

[0012] Citation or identification of any reference in Section 2 or in any other section of this application shall not be construed as an admission that such reference is available as prior art to the present disclosure.

4. SUMMARY

[0013] The present disclosure relates to proteins comprising a CTLA4 binding domain that are capable of binding CD80 and/or CD86 and that are related in sequence to SEQ ID NO: 1 (Figure 1A). In certain aspects, the CTLA4 protein of the disclosure further

comprises a fusion partner, such as an immunoglobulin domain, which is a non-CTLA4 protein.

[0014] CTLA4 has three CDR-like loops, referred to herein (in amino- to carboxy-terminal order) as CDR-like loop 1, CDR-like loop 2 and CDR-like loop 3. The CDR-like loops of CTLA4 is shown in Figure 1B.

[0015] CTLA4 was subjected to comprehensive mutagenesis in its CDR-like loops to produce a population of variants with single point mutations. The variant population was then screened to identify point mutants that resulted in similar or increased binding affinity to CD80 or CD86 based on the variants' behavior in a population.

[0016] Variants were identified whose behavior in the population indicated a similar or higher binding affinity to CD80 or to CD86 relative to wild type CTLA4. Some of the variants were isolated from the population and their biological properties, such as binding to CD80 and CD86 (described in Example 1), inhibition of IL-2 secretion by Jurkat cells (described in Example 1) and inhibition of T-cell proliferation (described in Example 2), were further characterized. The amino acid substitutions in these variants are listed in Tables 2, 3, 5, 7, 9, 10 and 12. Other variants were not isolated from the population and their binding characteristics are based on their behavior in the population. The amino acid substitutions in these variants, which are referred to as "candidate" mutations, are listed in Tables 4, 6, 8, 11, 13, 14.

[0017] Accordingly, the present disclosure provides CTLA4 proteins comprising CDR-like loops that have at least one amino acid substitution as compared to the CDR-like loops of SEQ ID NO: 1. Exemplary substitutions in the CDR-like loops are found in Tables 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, and 14. Preferred amino acid substitutions that can be incorporated into the CTLA4 proteins of the disclosure (singly or in combination) include, but are not limited to, the amino acid substitutions K28H and A29H in CDR-like loop 1.

[0018] In certain aspects, the present disclosure provides CTLA4 proteins that have at least one amino acid substitution in the CDR-like loops as compared to SEQ ID NO: 1 and that bind with high affinity to CD80 and CD86 as compared to a wild-type CTLA4 binding domain. Exemplary substitutions in the CDR-like loops that result in high affinity binding to CD80 and CD86 are found in Table 2 and in row 1 of Table 15.

[0019] In other aspects, the present disclosure provides CTLA4 proteins that have at least one amino acid substitution in the CDR-like loops as compared to the CDR-like loops of SEQ ID NO: 1 that bind with high affinity to CD80 and with neutral affinity (*i.e.*, comparable to abatacept) to CD86 as compared to a wild-type CTLA4 binding domain. Exemplary substitutions in the CDR-like loops that result in high affinity binding to CD80 and with neutral affinity binding to CD86 are found in Tables 3, 4 and in rows 2-5 of Table 15.

[0020] In yet other embodiments, the present disclosure provides CTLA4 proteins that have at least one amino acid substitution in the CDR-like loops as compared to the CDR-like loops of SEQ ID NO: 1 that bind with high affinity to CD80 and with low affinity to CD86 as compared to a wild-type CTLA4 binding domain. Exemplary substitutions that result in high affinity binding to CD80 and low affinity binding to CD86 are found in Tables 5, 6 and in row 6 of Table 15.

[0021] In some embodiments, the present disclosure provides CTLA4 proteins that have at least one amino acid substitution in the CDR-like loops as compared to the CDR-like loops of SEQ ID NO: 1 that bind with neutral affinity to CD80 and with high affinity to CD86 as compared to a wild-type CTLA4 binding domain. Exemplary substitutions that result in neutral affinity binding to CD80 and high affinity binding to CD86 are found in Tables 7, 8 and rows 7-8 of Table 15.

[0022] In various embodiments, the present disclosure provides CTLA4 proteins that have at least one amino acid substitution in the CDR-like loops as compared to the CDR-like loops of SEQ ID NO: 1 and that bind with low affinity to CD80 and with high affinity to CD86 as compared to wild-type CTLA4 binding domain. Exemplary

substitutions that result in low affinity binding to CD80 and high affinity binding to CD86 are found in Table 9 and in row 9 of Table 15.

[0023] In certain embodiments, the present disclosure provides CTLA4 proteins that have at least one amino acid substitution in the CDR-like loops as compared to the CDR-like loops of SEQ ID NO: 1 that bind with neutral affinity to CD80 and CD86 as compared to a wild-type CTLA4 binding domain. Exemplary substitutions that result in neutral affinity binding to CD80 and CD86 are found in Tables 10, 11 and rows 10-22 of Table 15.

[0024] In various embodiments, the present disclosure provides CTLA4 proteins that have at least one amino acid substitution in the CDR-like loops as compared to the CDR-like loops of SEQ ID NO: 1 that bind with neutral affinity to CD80 and with low affinity to CD86 as compared to a wild-type CTLA4 binding domain. Exemplary substitutions that bind with neutral affinity to CD80 and with low affinity to CD86 are found in Tables 12, 13 and rows 23-26 of Table 15.

[0025] In some embodiments, the present disclosure provides CTLA4 proteins that have at least one amino acid substitution in the CDR-like loops as compared to the CDR-like loops of SEQ ID NO: 1 that bind with low affinity to CD80 and with neutral affinity to CD86 as compared to a wild-type CTLA4 binding domain. Exemplary substitutions that bind with low affinity to CD80 and with neutral affinity to CD86 are found in Table 14 and in rows 27-34 of Table 15.

[0026] In certain embodiments, the present disclosure provides a variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO: 1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO: 1 selected from K28H, K28T, A29H, T51Y, M53F, M53Y, L58G, L61H, L61Y, K93M and K93Q.

[0027] In other embodiments, the present disclosure provides a variant CTLA4 polypeptide having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO: 1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO: 1 selected from L58A, L58N, L58Q, L61A, K93V, L104H and L104Y.

[0028] In still other embodiments, the present disclosure provides a variant CTLA4 polypeptide having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO: 1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO: 1 selected from T30E, M54R, G55P, E57P, L58E, L58P, L58Y, L61F and L104I.

[0029] In various embodiments, the present disclosure provides a variant CTLA4 polypeptide having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO: 1, wherein the variant polypeptide includes the amino acid substitution K93I as compared to SEQ ID NO: 1.

[0030] In other embodiments, the present disclosure provides a variant CTLA4 polypeptide having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO: 1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO: 1 selected from L58H, L58K and D62H.

[0031] In some embodiments, the present disclosure provides a variant CTLA4 polypeptide having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO: 1, wherein the variant polypeptide includes at least one amino acid substitution selected from M54W and M54Y as compared to SEQ ID NO: 1.

[0032] In other embodiments, the present disclosure provides a variant CTLA4 polypeptide having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO: 1, wherein the variant

polypeptide has at least one amino acid substitution as compared to SEQ ID NO: 1 selected from R33D and L61W.

[0033] In still other embodiments, the present disclosure provides a variant CTLA4 polypeptide having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO: 1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO: 1 selected from A29K, T51N, M53W, L96K and L96R.

[0034] In various embodiments, the present disclosure provides a variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO: 1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO: 1 selected from G27A, Y52F, N56T and L104M.

[0035] In certain embodiments, the present disclosure provides a variant CTLA4 polypeptide having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO: 1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO: 1 selected from P26I, P26L, P26M, P26Q, P26T, P26V, K28R, A29P, A29S, T30H, T30M, T30S, V32E, R33P, T51A, Y52H, Y52M, Y52W, M53D, M54D, M54G, M54H, M54L, G55D, G55H, G55T, N56A, N56F, N56G, N56H, N56I, N56K, N56L, N56M, N56Q, N56R, N56S, N56V, N56Y, E57A, E57D, E57H, E57K, E57M, E57N, E57Q, E57R, E57S, E57T, E57V, L58I, L58R, L58T, T59I, T59M, T59N, T59Q, T59R, T59S, T59V, L61E, L61I, L61M, L61T, L61V, D62R, D63E, D63G, D63H, D63T, K93G, V94G, V94I, E95W, P99H, P99T, P99L and Y102T.

[0036] In various embodiments, the present disclosure provides a variant CTLA4 polypeptide having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO: 1, wherein the variant polypeptide includes the amino acid substitution K28Y as compared to SEQ ID NO: 1.

[0037] In certain embodiments, the present disclosure provides a variant CTLA4 polypeptide having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO: 1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO: 1 selected from P26N, G27I, G27Q, G27W, K28E, K28I, K28M, K28P, K28Q, K28V, T30I, T30L, M53E, M53L, M53N, M54A, M54Q, M54S, L58D, L58V, T59H, T59K, T59L, T59P, L61D, L61G, L61Q, L61R, D62A, D62E, D62S, D63Q, D63S and K93R.

[0038] In some embodiments, the present disclosure provides a variant CTLA4 polypeptide having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO: 1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO: 1 selected from P26R, G27D, G27P, A29N, T30K, E31D, E31G, E31P, E31R, E31T, V32G, V32H, V32T, R33E, R33G, R33I, R33M, R33N, R33Q, R33W, R33Y, T51E, T51G, T51I, T51V, Y52A, Y52D, Y52I, Y52K, Y52L, Y52Q, Y52R, Y52S, Y52T, M53H, M53P, M53S, G55A, G55I, G55L, G55N, G55Q, G55R, G55Y, E57G, E57I, E57W, E57Y, T59D, T59G, T59Y, F60D, F60G, F60H, F60L, D62G, D62I, D62W, D63A, D63Y, K93D, K93H, K93N, K93P, K93W, V94A, V94D, V94H, V94N, V94P, V94R, V94T, V94W, E95G, E95I, E95K, E95P, E95Q, E95R, E95S, E95T, E95V, E95Y, L96A, L96G, L96H, L96M, L96P, L96Q, M97D, M97G, M97I, M97N, M97S, M97V, P99I, P99M, P99W, P99Y, P100H, P100L, P100T, P100V, P100W, P101L, Y102H, Y103H, Y103L, Y103P, Y103T, and L104P.

[0039] The variant CTLA4 proteins of the disclosure can comprise one or more additional mutations or combinations of mutations selected from one or more of Tables 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, and 16-1 to 16-6.

[0040] In certain aspects, the mutations in the CDR-like loops of the variant CTLA4 polypeptides of the disclosure as compared to abatacept (SEQ ID NO: 6) do not comprise (a) A29K; (b) M53E; (c) L61Y; (d) L104M; (e) R33P; (f) T59I; (g) L61F. In other aspects, the mutations in the CDR-like loops of the variant CTLA4 polypeptides of the

disclosure as compared to abatacept (SEQ ID NO: 6) do not consist of (a) A29K; (b) M53E; (c) L61Y; (d) L104M; (e) R33P; (f) T59I; (g) L61F; (h) a combination of two or more of A29K, M53E, L61Y, L104M, R33P, T59I and L61F; or (i) a combination of three or more of A29K, M53E, L61Y, L104M, R33P, T59I and L61F. By way of example and not limitation, in specific embodiments, the mutations in the CDR-like loops of the variant CTLA4 polypeptides of the disclosure as compared to abatacept (SEQ ID NO: 6) do not comprise or consist of (1) A29K and, optionally, one, two, or more substitutions independently selected from M53E, L61Y, L104M, R33P, T59I and L61F; (2) M53E and, optionally, one, two, or more substitutions independently selected from A29K, L61Y, L104M, R33P, T59I and L61F; (3) L61Y and, optionally, one, two or more substitutions independently selected from A29K, M53E, L104M, R33P, T59I and L61F; (4) L104M and, optionally, one, two, or more substitutions independently selected from A29K, M53E, L61Y, R33P, T59I and L61F; (5) R33P and, optionally, one, two, or more substitutions independently selected from A29K, M53E, L61Y, L104M, T59I and L61F; (6) T59I and, optionally, one, two, or more substitutions independently selected from A29K, M53E, L61Y, L104M, R33P, and L61F; or (7) L61F and, optionally, one, two, or more substitutions independently selected from A29K, M53E, L61Y, L104M, R33P, and T59I.

[0041] In certain aspects, the variant CTLA4 polypeptide is a fusion protein. In certain embodiments, the fusion partner is a immunoglobulin constant domain, such as an IgG₁.

[0042] In various aspects, the CTLA4 proteins of the disclosure have sequences having at least 75% sequence identity, at least 80% sequence identity, at least 85% sequence identity, at least 90% sequence identity, at least 91% sequence identity, at least 92% sequence identity, at least 93% sequence identity, at least 94% sequence identity, at least 95% sequence identity, at least 96% sequence identity, at least 97% sequence identity, at least 98% sequence identity or at least 99% sequence identity to the amino acid sequence of a wild-type CTLA4 binding domain (amino acids 21 to 112 of SEQ ID NO: 1) or to the wild-type CTLA4 extracellular domain (SEQ ID NO: 1).

[0043] In various aspects, the CTLA4 proteins of the disclosure have up to 2, up to 3, up to 4, up to 5, up to 6, up to 7, up to 8, up to 9, or up to 10 amino acid substitutions in the CDR-like loops as compared to the CDR-like loops of SEQ ID NO: 1.

[0044] Nucleic acids comprise nucleotide sequences encoding the CTLA4 proteins of the disclosure are provided herein, as are vectors comprising nucleic acids. Additionally, prokaryotic and eukaryotic host cells transformed with a vector comprising a nucleotide sequence encoding a CTLA4 protein are provided herein, as well as eukaryotic (such as mammalian) host cells engineered to express the nucleotide sequences. Methods of producing CTLA4 proteins by culturing host cells are also provided.

[0045] The CTLA4 proteins of the disclosure are useful in the treatment of cancers, autoimmune diseases and the rejection of cell, organ or tissue graft transplants. In certain aspects, the CTLA4 proteins are useful in treating an autoimmune disease selected from rheumatoid arthritis and juvenile idiopathic arthritis.

[0046] It should be noted that the indefinite articles “a” and “an” and the definite article “the” are used in the present application, as is common in patent applications, to mean one or more unless the context clearly dictates otherwise. Further, the term “or” is used in the present application, as is common in patent applications, to mean the disjunctive “or” or the conjunctive “and.”

[0047] All publications mentioned in this specification are herein incorporated by reference. Any discussion of documents, acts, materials, devices, articles or the like that has been included in this specification is solely for the purpose of providing a context for the present disclosure. It is not to be taken as an admission that any or all of these matters form part of the prior art base or were common general knowledge in the field relevant to the present disclosure as it existed anywhere before the priority date of this application.

[0048] The features and advantages of the disclosure will become further apparent from the following detailed description of embodiments thereof.

5. BRIEF DESCRIPTION OF THE TABLES AND FIGURES

[0049] **Table 1** shows the numbering of the amino acids in the CDR-like loops of wild-type CTLA4-Ig.

[0050] **Table 2** shows mutations in the wild-type CTLA4 CDR-like loops that binding studies indicate increase affinity for CD80 and CD86.

[0051] **Table 3** shows mutations in the wild-type CTLA4 CDR-like loops that binding studies indicate increase affinity for CD80, and do not substantially impact CD86 binding.

[0052] **Table 4** shows candidate mutations that can be incorporated in the wild-type CTLA4 CDR-like loops for increasing affinity toward CD80 while not substantially impacting CD86 binding.

[0053] **Table 5** shows mutations in the wild-type CTLA4 CDR-like loops that binding studies indicate increase affinity for CD80 and decrease affinity for CD86.

[0054] **Table 6** shows candidate mutations that can be incorporated in the wild-type CTLA4 CDR-like loops for increasing affinity toward CD80 and decreasing affinity toward CD86.

[0055] **Table 7** shows mutations in the wild-type CTLA4 CDR-like loops that binding studies indicate increase affinity for CD86 while not substantially impacting CD80 binding.

[0056] **Table 8** shows candidate mutations that can be incorporated in the wild-type CTLA4 CDR-like loops for increasing affinity toward CD86 while not substantially impacting CD80 binding.

[0057] **Table 9** shows mutations in the wild-type CTLA4 CDR-like loops that binding studies indicate decrease affinity for CD80 and increase affinity for CD86.

[0058] Table 10 shows mutations in the wild-type CTLA4 CDR-like loops that binding studies indicate do not substantially impact binding to CD80 or CD86.

[0059] Table 11 shows candidate mutations that can be incorporated in the wild-type CTLA4 CDR-like loops and that do not substantially impact binding to CD80 or CD86.

[0060] Table 12 shows mutations in the wild-type CTLA4 CDR-like loops that binding studies indicate decrease affinity for CD86 while not substantially impacting binding to CD80.

[0061] Table 13 shows candidate mutations that can be incorporated in the wild-type CTLA4 CDR-like loops for decreasing affinity for CD86 while not substantially impacting CD80 binding.

[0062] Table 14 shows candidate mutations that can be incorporated in the wild-type CTLA4 CDR-like loops for decreasing affinity for CD80 while not substantially impacting CD86 binding.

[0063] Table 15 shows known mutations in the wild-type CTLA4 CDR-like loops that can be incorporated into the CTLA4 proteins of the disclosure. Row 1 shows known mutations that can be incorporated in the wild-type CTLA4 CDR-like loops for increasing affinity for CD80 and CD86. Rows 2-5 show known mutations that can be incorporated in the wild-type CTLA4 CDR-like loops for increasing affinity for CD80 while not substantially impacting CD86 binding. Row 6 shows known mutations that can be incorporated in the wild-type CTLA4 CDR-like loops for increasing affinity for CD80 while decreasing affinity for CD86. Rows 7-8 show known mutations that can be incorporated in the wild-type CTLA4 CDR-like loops for increasing affinity for CD86 while not substantially impacting CD80 binding. Row 9 shows known mutations that can be incorporated in the wild-type CTLA4 CDR-like loops for increasing affinity for CD86 while decreasing affinity for CD80. Rows 10-22 show known mutations that can be incorporated in the wild-type CTLA4 CDR-like loops which do not substantially impact CD80 or CD86 binding. Rows 23-26 show known mutations that can be incorporated in

the wild-type CTLA4 CDR-like loops for decreasing affinity for CD86 while not substantially impacting affinity for CD80. Rows 27-34 show known mutations that can be incorporated in the wild-type CTLA4 CDR-like loops for decreasing affinity for CD80 while not substantially impacting affinity for CD86.

[0064] Tables 16-1 to 16-6 show known mutations in the wild-type CTLA4 CDR-like loops that can be incorporated into the CTLA4 proteins of the disclosure.

[0065] Figures 1A-1C. **Figure 1A** shows the amino acid sequence of the human CTLA4 extracellular domain (SEQ ID NO: 1). Amino acids in the CDR-like loops (underlined) were identified by visual inspection of reported CTLA4 co-crystal structures. (Schwartz *et al.*, 2001, Nature 410:604; Stamper *et al.*, 2001, Nature 410:608). **Figure 1B** shows the sequences of the CDR-like loops of wild-type CTLA4 and the corresponding sequence identifiers. **Figure 1C** shows an alignment of (i) full-length human CTLA4 extracellular domain and containing a transmembrane domain (Genbank Accession No. NM_005214; SEQ ID NO: 5), (ii) abatacept as set forth in US Patent No. 5,434,131 (SEQ ID NO: 6); and (iii) human Fc γ 1 (SEQ ID NO: 7). The extracellular domain of wild-type CTLA4-Ig comprises amino acids 1-124 of hCTLA4, which corresponds to the CTLA4 extracellular domain. CTLA4 dimerizes through the cysteine residue at position 120. Abatacept has a glutamine residue at position 125, which is at the junction of the hCTLA4 extracellular domain and the human Fc γ 1. The CH₁ region of hFc γ 1 contains a valine at the equivalent position. The human Fc γ 1 region with the IgG₁m(a) allotype starts at position 126 and is italicized. Cysteine residues at positions 130, 136 and 139 that are present in the Fc γ 1 and are involved in disulfide bridges have been mutated to serine in abatacept. Position 148 in the CH₂ region of Fc γ 1 is mutated from proline to serine in abatacept. (Davis *et al.*, 2007, J. Rheumatol. 34(11):2204).

[0066] Figures 2A-2B show the binding of novel CTLA4-Ig variants to CD80 and CD86 as measured by competition AlphaLISA®. Relative binding activities of variants that showed improved binding to at least one of CD80 and CD86 are shown in **Figure 2A**. Relative binding activities of variants that showed equivalent binding to at least one of

CD80 and CD86 are shown in **Figure 2B**. Open and solid bars indicate the binding data with CD80 and CD86, respectively. Data are normalized with an IC_{50} value obtained from wild-type CTLA4-Ig, and are shown as the average fold improvement from two independent sets of experiments. Binding activity of abatacept that contains the mutation P148S mutation in the CH2 domain was confirmed to have negligible impact on ligand binding. Each data point of the dilution curve was duplicated in the assay plate. The average IC_{50} value of wild-type CTLA4-Ig was determined to be $0.89 \text{ nM} \pm 0.26$ and $4.26 \text{ nM} \pm 0.76$ for CD80 and CD86, respectively. Error bars represent the range of values obtained from duplicate experiments.

[0067] **Figure 3** shows the binding activity of known CTLA4-Ig variants to CD80 and CD86 as measured by competition AlphaLISA®.

[0068] **Figures 4A-4C** show the ability of wild-type and CTLA4-Ig variants to inhibit IL-2 production of Jurkat T-cells upon stimulation. **Figure 4A** shows IL-2 production from Jurkat T-cells upon stimulation with CHO-K1 cells expressing CD80 or CD86 in the presence of wild-type CTLA4-Ig or control antibody. **Figure 4B** shows full inhibition curves with titrating amounts of commercial abatacept or wild-type CTLA4-Ig or belatacept produced in-house. Relative potencies of selected CTLA-Ig variants of the disclosure in the inhibition of IL-2 production normalized with an IC_{50} value obtained from wild-type CTLA4-Ig are shown in **Figure 4C**. Error bars represent the range of values obtained from duplicate experiments.

[0069] **Figures 5A-5E** show the ability of wild-type and CTLA4-Ig variants to inhibit proliferation of primary allo-stimulated T-cells. Symbols represent means of triplicate determinations. Data are representative of at least three independent experiments.

[0070] **Figures 6A-6D** show the ability of wild-type and CTLA4-Ig variants to inhibit proliferation of secondary allo-stimulated T-cells. Symbols represent means of triplicate determinations. Data are representative of at least three independent experiments.

6. DETAILED DESCRIPTION

[0071] The present disclosure provides novel polypeptides comprising variant CD80- and/or CD86-binding fragments of CTLA4 (“CTLA4 binding domain”) that inhibit or suppress immune responses. The polypeptides of the disclosure comprise at least a CTLA4 binding domain that has one or more amino acid substitutions that maintain or alter the binding properties of CTLA4 to CD80 and/or CD86. Optionally, the variant CTLA4 binding domains are fused to a different (non-CTLA4) amino acid sequence, such as that of an immunoglobulin constant region. These novel polypeptides are collectively referred to herein as “CTLA4 proteins” or “CTLA4 polypeptides”.

6.1. CTLA4 Extracellular Domain

[0072] The variant polypeptides of the disclosure comprise an amino acid sequence that is related in sequence to the CTLA4 extracellular domain (SEQ ID NO: 1). The CTLA4 extracellular domain is a single chain polypeptide that adopts an immunoglobulin variable fold with three CDR-like loops. The variant polypeptides of the disclosure contain at least one amino acid substitution in at least one CDR-like loop as compared to CTLA4 that maintain or alter the protein’s binding properties to CD80 and/or CD86. In certain aspects, the variant CTLA4 polypeptides of the disclosure bind to CD80 and/or CD86 and block their interactions with their respective ligands, *e.g.*, CTLA4 or CD28, thereby inhibiting one or more immune cell mediated responses. The variant CTLA4 polypeptides of the disclosure can also have amino acid mutations (*e.g.*, deletions, insertions, additions or substitutions) in the non-CDR-like loop portions of the CTLA4 extracellular domain. Suitable mutations in the non-CDR-like regions of the CTLA4 extracellular domain include, but are not limited to, those disclosed, for example in U.S. Patent nos. 5,977,318; 6,107,056; 6,750,334; 7,034,121; 7,229,962; 7,432,344; 7,504,554; 7,385,045; 7,105,166; 6,090,914; 5,770,197; and U.S. Patent publication no. 2009/0258031, each of which is incorporated by reference herein in its entirety.

[0073] In certain embodiments, the variant CTLA4 polypeptides of the disclosure have an amino acid sequence that is at least 75% identical to the amino acid sequence of a

CTLA4 binding domain (*e.g.*, amino acids 21-112 of SEQ ID NO: 1). In other embodiments, the variant CTLA4 polypeptides of the disclosure have an amino acid sequence that is at least 75% identical to the amino acid sequence of the CTLA4 extracellular domain (*e.g.*, amino acids 1-124 of SEQ ID NO: 1). In various embodiments, the variant CTLA4 polypeptides of the disclosure have an amino acid sequence that is at least 80% identical, at least 85% identical, at least 90% identical, at least 91% identical, at least 92% identical, at least 93% identical, at least 94% identical, at least 95% identical, at least 96% identical, at least 97% identical, at least 98% identical or at least 99% identical to the amino acid sequence of a CTLA4 binding domain or to the amino acid sequence of a CTLA4 extracellular domain.

[0074] In some embodiments, the variant CTLA4 polypeptides of the disclosure comprise at least one mutation compared to a wild-type CTLA4 extracellular domain. In other embodiments, the variant CTLA4 polypeptides of the disclosure comprise at least one mutation compared to a wild-type CTLA4 binding domain. In other embodiments, the variant CTLA4 polypeptides of the disclosure comprise up to 2, up to 3, up to 4, up to 5, up to 6, up to 7, up to 8, up to 9, up to 10, up to 11, up to 12, up to 13, up to 14, up to 15, up to 16, up to 17, up to 18, up to 19, or up to 20 amino acid substitutions as compared to a wild-type CTLA4 extracellular domain or as compared to a wild-type CTLA4 binding domain.

[0075] In certain embodiments, the CTLA4 extracellular domain includes amino acid residues 1-124 of the human CTLA4 protein (SEQ ID NO: 1). In various embodiments, the CTLA4 polypeptide of the disclosure is a CD80- and/or CD86-binding fragment of the CTLA4 extracellular domain comprising CDR-like sequences that are related to the CDR-like sequences of CTLA4. In certain embodiments, the binding fragment comprises a portion of the CTLA4 extracellular domain starting anywhere between amino acids 1 to 12 of SEQ ID NO: 1 and ending anywhere between amino acids 112 to 124 of SEQ ID NO: 1. In certain embodiments, the binding fragment is from amino acid 12 to amino acid 112 of SEQ ID NO: 1, from amino acid 10 to amino acid 112 of SEQ ID NO: 1, from amino acid 8 to amino acid 112 of SEQ ID NO: 1, from amino acid 6 to

amino acid 112 of SEQ ID NO: 1, from amino acid 4 to amino acid 112 of SEQ ID NO: 1, from amino acid 1 to amino acid 112, amino acid 113, amino acid 114, amino acid 115, amino acid 116, amino acid 117, amino acid 118, amino acid 119, amino acid 120, amino acid 121, amino acid 122 or amino acid 123 of SEQ ID NO: 1. In yet other embodiments, the binding portion is from amino acid 12 to amino acid 114 of SEQ ID NO: 1, from amino acid 12 to amino acid 116 of SEQ ID NO: 1, from amino acid 12 to amino acid 118 of SEQ ID NO: 1, from amino acid 12 to amino acid 120 of SEQ ID NO: 1, from amino acid 12 to amino acid 122 of SEQ ID NO: 1, or from amino acid 12, amino acid 11, amino acid 10, amino acid 9, amino acid 8, amino acid 7, amino acid 6, amino acid 5, amino acid 4, amino acid 3 or amino acid 2 to amino acid 124 of SEQ ID NO: 1.

[0076] In certain embodiments, the CDR-like loops of CTLA4 are grafted onto a non-CTLA4 protein scaffold. The non-CTLA4 protein scaffold can be any protein scaffold known in the art that allows the CDR-like loops to maintain a three-dimensional structure that binds to CD80 and/or CD86. In certain embodiments, the non-CTLA4 protein scaffold is a variable domain of a camelid heavy chain antibody (VHH) or a variable domain of the shark new antigen receptor (VNAR) (“nanobodies”). In other embodiments, the scaffold can be from a protein other than an immunoglobulin. Such scaffolds for use in the CTLA4 variant proteins of the disclosure include, but are not limited to, fibronectin III (AdNectin), β -sandwich proteins (iMAB), lipocalins (Anticalin), EETI-II/AGRP (Microbody), BPTI/LACI-D1/ITI-D2 (Kunitz domain), thioredoxin (Peptide aptamer), protein A (Affibody), ankyrin repeat (DARPin), γ B-crystallin/ubiquitin (Affilin), CTLD₃ (Tetranectin) and (LDLR-A module)₃ (Avimer).

[0077] In some embodiments, the variant CTLA4 polypeptide of the disclosure is a monomer. In other embodiments, the CTLA4 polypeptide is a dimer. In certain embodiments, the CTLA4 dimer is a covalent dimer, *e.g.*, a disulfide-linked dimer. In other embodiments, the CTLA4 dimer is a non-covalent dimer. In still other embodiments, the CTLA4 polypeptide is a multimer, *e.g.*, a tetramer.

[0078] The variant CTLA4 polypeptides of the present disclosure have a binding affinity for a CTLA4 ligand. In certain embodiments the CTLA4 polypeptides have a binding affinity for the extracellular domain of human CD80, or a portion thereof. In various embodiments, the CTLA4 polypeptides have a binding affinity for the extracellular domain of human CD86, or a portion thereof.

[0079] In some embodiments, the variant CTLA4 polypeptides of the disclosure have a binding affinity for CD80 and/or CD86 that is increased compared to the binding affinity of the wild-type CTLA4 extracellular domain, *e.g.*, in the context of abatacept. As used herein, a variant with “increased affinity” for CD80 and/or CD86 (a “high affinity” variant) refers to a polypeptide of the disclosure having a binding affinity that is at least 1.5x, at least 1.75x, at least 2x, at least 2.5x, at least 3x, at least 3.5x, at least 4x, at least 4.5x, at least 5x, at least 5.5x, at least 6x, at least 6.5x, at least 7x, at least 7.5x, at least 8x, at least 8.5x, at least 9x, at least 9.5x, at least 10x, or at least 20x or greater than the binding affinity of the CTLA4 extracellular domain for CD80 and/or CD86. In other embodiments, the variant CTLA4 polypeptides of the disclosure have a binding affinity for CD80 and/or CD86 that is about equal to the binding affinity of the wild-type CTLA4 extracellular domain, *e.g.*, in the context of abatacept for CD80 and/or CD86 (a “neutral affinity” variant). As used herein, a “neutral affinity” variant has a binding affinity for CD80 and/or CD86 that is between about 0.5x and about 1.5x of the binding affinity of the CTLA4 extracellular domain for the ligand, such as about 0.6x, about 0.7x, about 0.8x, about 0.9x, about 1x, about 1.1x, about 1.2x, about 1.3x, about 1.4x or about 1.5x of the binding affinity of the CTLA4 extracellular domain. In certain embodiments, a variant polypeptide of the disclosure has a decreased binding affinity for CD80 and/or CD86 as compared to the CTLA4 extracellular domain (“low affinity” variant). As used herein, a “low affinity” variant of the disclosure has a binding affinity that is less than 0.5x, less than 0.4x, less than 0.3x, less than 0.2x, less than 0.1x, less than 0.05x, less than 0.01x or less of the binding affinity of the CTLA4 extracellular domain.

[0080] In particular embodiments a variant CTLA4 protein of the disclosure is a high affinity variant with respect to both CD80 and CD86 binding. In some embodiments, the

variant polypeptide is a high affinity variant with respect to CD80 and a neutral affinity variant with respect to CD86. In other embodiments, the variant CTLA4 polypeptide is a high affinity variant with respect to CD86 binding and neutral affinity variant with respect to CD80 binding. In still other embodiments, the variant CTLA4 protein of the disclosure is a high affinity variant with respect to CD80 binding and a low affinity variant with respect to CD86 binding. In yet other embodiments, the variant protein is a high affinity variant with respect to CD86 binding and a low affinity variant with respect to CD80 binding. In still other embodiments, the variant polypeptide of the disclosure is a neutral affinity variant with respect to both CD80 binding and CD86 binding. In various embodiments, the variant CTLA4 polypeptide of the disclosure is a low affinity variant with respect to CD86 binding and a neutral affinity variant with respect to CD80 binding. In yet other embodiments, the variant CTLA4 polypeptide of the disclosure is a neutral affinity variant with respect to CD86 binding and a low affinity variant with respect to CD80 binding.

[0081] In certain embodiments, the CTLA4 polypeptides of the disclosure comprise a variant CTLA4 binding domain in the context of full length CTLA4 (Genbank Accession No. AAL07473.1, which is incorporated herein by reference).

6.2. CTLA4 Fusion Partners

[0082] In certain aspects, the CTLA4 polypeptide of the disclosure can be a fusion protein in which the variant CTLA4 binding domain is operably linked to the amino acid sequence of another polypeptide, referred to herein as a “fusion partner.” As used herein, the term “fusion partner” refers to a non-CTLA4 polypeptide that is covalently attached to the CTLA4 polypeptide variant, either directly or through a linker sequence. In various embodiments, the C-terminus of the CTLA4 binding domain is linked to the N-terminus of the fusion partner. In some embodiments, the fusion partner can comprise a transmembrane domain and/or a cytoplasmic domain. In these embodiments, the CTLA4 fusion protein is expressed on the surface of a cell. In particular embodiments, the fusion partner comprises a polypeptide that facilitates secretion, expression and/or solubility of the CTLA4 polypeptide.

[0083] In some embodiments, the CTLA4 fusion proteins of the disclosure are monomeric. In other embodiments, the CTLA4 fusion proteins of the disclosure are dimeric, either due to covalent linkage (*e.g.*, by disulfide bonds) between the CTLA4 portions of two monomers and/or between the fusion partner polypeptides or due to non-covalent association of the CTLA4 and/or fusion partner portions of the monomers.

[0084] In some embodiments, the fusion partner is a protein or protein domain that dimerizes, such as lambda repressor, upstream binding factor, and leucine zipper domains (*e.g.*, fos/jun). In particular embodiments, the fusion partner is an immunoglobulin (Ig) Fc polypeptide, *i.e.*, the Fc domain of an Ig polypeptide, or a fragment thereof. In certain embodiments, the Fc polypeptide or fragment can be derived from various species, including, *e.g.*, human, mouse, primate, *etc.*, and can be derived from a different species than the CTLA4 binding domain to which it is linked. Thus, for example, in some embodiments, the CTLA4 binding domain is derived from a human protein and the fusion partner is derived from a mouse protein. In particular embodiments, the CTLA4 polypeptide and the fusion partner are both derived from human proteins.

[0085] In certain embodiments, the Ig Fc polypeptide comprises a first constant region (CH₁), a hinge region, a second constant region (CH₂) and a third constant region (CH₃) in the order (from the N-terminus to the C-terminus) CH₁-hinge-CH₂-CH₃. In some embodiments, the fusion partner optionally comprises a fourth constant region (CH₄). In some embodiments, the fusion partner is an immunoglobulin Fc fragment comprising the hinge region, CH₂ domain and CH₃ domain of the Ig polypeptide. In still other embodiments, the Ig Fc fragment comprises a single constant domain, such as the hinge region and a CH₁, CH₂ or CH₃ domain. In certain aspects, the Ig Fc does not have a hinge, *e.g.*, an IgM. In some embodiments, the Ig Fc polypeptide comprises a wild-type Ig Fc polypeptide. Exemplary Fc polypeptides include, but are not limited to, IgG₁, IgG₂, IgG₃, IgG₄, IgA, IgE, IgD and IgM. In particular embodiments, the Fc polypeptide is an IgG.

[0086] Alternatively, the immunoglobulin Fc fusion partner is a modified Ig polypeptide. In certain embodiments, the Fc polypeptide has one or more amino acid substitutions compared to wild-type. For example, in certain embodiments, the Fc polypeptide is a mutant IgG in which one or more cysteine residues have been substituted with another amino acid (*e.g.*, a serine residue) to eliminate one or more disulfide bonds formed between two Ig chains. In other embodiments, the Fc polypeptide is an IgG polypeptide in which one or more amino acid residues is substituted with another amino acid (*e.g.*, proline) to reduce effector function (reduced Fc receptor binding). *See* U.S. Patent Publication no. 2009/0258031.

[0087] In some embodiments, the Fc fusion partner or a fragment thereof can be modified to alter at least one constant region-mediated biological effector function relative to the corresponding wild type sequence. For example, in some embodiments, the Fc polypeptide can be modified to reduce at least one constant region-mediated biological effector function relative to an unmodified Fc region, *e.g.*, reduced binding to the Fc receptor (Fc γ R). Fc γ R binding can be reduced by mutating the immunoglobulin constant region segment at particular regions necessary for Fc γ R interactions (*see e.g.*, Canfield and Morrison, 1991, *J. Exp. Med.* 173:1483-1491; and Lund *et al.*, 1991, *J. Immunol.* 147:2657-2662). Reduction in Fc γ R binding ability of the Fc region can also reduce other effector functions which rely on Fc γ R interactions, such as opsonization, phagocytosis and antibody-dependent cellular cytotoxicity (“ADCC”).

[0088] In other embodiments, the Fc polypeptide can be modified to acquire or improve at least one constant region-mediated biological effector function relative to an unmodified Fc region, *e.g.*, to enhance Fc γ R interactions (*see, e.g.*, US 2006/0134709). For example, the Fc region can be modified to bind Fc γ RIIA, Fc γ RIIB and/or Fc γ RIIA with greater affinity than the corresponding wild type constant region.

[0089] Thus, Fc fusion proteins of the disclosure can have alterations in biological activity that result in increased or decreased opsonization, phagocytosis, or ADCC as compared to a fusion protein having the corresponding wild-type Fc region. Such

alterations are known in the art. For example, the Fc polypeptides can be modified as antibodies are modified to reduce ADCC activity, *e.g.*, as described in U.S. Patent Nos. 5,834,597 and 7,083,784; and US Patent Publication Nos. 2006/0198840, and 2007/0122403. An exemplary ADCC lowering variant corresponds to “mutant 3” shown in Figure 4 of U.S. Patent No. 5,834,597, in which residue 236 is deleted and residues 234, 235 and 237 (using EU numbering) are substituted with alanines.

[0090] In some embodiments, the Fc polypeptides for use in CTLA4 proteins of the disclosure have low levels of or lack fucose. Antibodies lacking fucose in the Fc region have been correlated with enhanced ADCC activity, especially at low doses of antibody. See Shields *et al.*, 2002, J. Biol. Chem. 277:26733-26740; Shinkawa *et al.*, 2003, J. Biol. Chem. 278:3466-73. Methods of preparing fucose-less proteins include growth in rat myeloma YB2/0 cells (ATCC CRL 1662). YB2/0 cells express low levels of FUT8 mRNA, which encodes α -1,6-fucosyltransferase, an enzyme necessary for fucosylation of polypeptides.

[0091] In yet another aspect, the proteins of the disclosure or fragments thereof can include Fc regions that have been modified to increase or reduce their binding affinities to the fetal Fc receptor, FcRn, for example by mutating the immunoglobulin constant region segment at particular regions involved in FcRn interactions (see *e.g.*, WO 2005/123780). In particular embodiments, the Ig Fc fusion partner of the IgG class is mutated such that at least one of amino acid residues 250, 314, and 428 of the heavy chain constant region is substituted alone, or in any combinations thereof, such as at positions 250 and 428, or at positions 250 and 314, or at positions 314 and 428, or at positions 250, 314, and 428, with positions 250 and 428 a specific combination. For position 250, the substituting amino acid residue can be any amino acid residue other than threonine, including, but not limited to, alanine, cysteine, aspartic acid, glutamic acid, phenylalanine, glycine, histidine, isoleucine, lysine, leucine, methionine, asparagine, proline, glutamine, arginine, serine, valine, tryptophan, or tyrosine. For position 314, the substituting amino acid residue can be any amino acid residue other than leucine, including, but not limited to, alanine, cysteine, aspartic acid, glutamic acid,

phenylalanine, glycine, histidine, isoleucine, lysine, methionine, asparagine, proline, glutamine, arginine, serine, threonine, valine, tryptophan, or tyrosine. For position 428, the substituting amino acid residues can be any amino acid residue other than methionine, including, but not limited to, alanine, cysteine, aspartic acid, glutamic acid, phenylalanine, glycine, histidine, isoleucine, lysine, leucine, asparagine, proline, glutamine, arginine, serine, threonine, valine, tryptophan, or tyrosine. Specific combinations of suitable amino acid substitutions are identified in Table 1 of U.S. Patent No. 7,217,797, which table is incorporated by reference herein in its entirety. Such mutations increase binding of the Fc polypeptide to FcRn, which protects the protein from degradation and increases its half-life.

[0092] In certain embodiments, the Fc polypeptides for use in CTLA4 fusion proteins of the disclosure have an amino acid sequence that is at least 75% identical to the amino acid sequence of human Fc γ 1 (SEQ ID NO: 7). In various embodiments, the Fc polypeptides have an amino acid sequence that is at least 80% identical, at least 85% identical, at least 90% identical, at least 91% identical, at least 92% identical, at least 93% identical, at least 94% identical, at least 95% identical, at least 96% identical, at least 97% identical, at least 98% identical or at least 99% identical to the amino acid sequence of human Fc γ 1 (SEQ ID NO: 7).

[0093] In some embodiments, the Fc polypeptides for use in CTLA4 fusion proteins of the disclosure comprise at least one mutation compared to human Fc γ 1 (SEQ ID NO: 7). In other embodiments, the variant CTLA4 polypeptides of the disclosure comprise up to 2, up to 3, up to 4, up to 5, up to 6, up to 7, up to 8, up to 9, up to 10, up to 11, up to 12, up to 13, up to 14, up to 15, up to 16, up to 17, up to 18, up to 19, or up to 20 or more amino acid substitutions as compared to wild-type human Fc γ 1.

[0094] In some embodiments, the variant CTLA4 proteins of the disclosure are fusion proteins comprising a CTLA4 binding region comprising about 124 amino acids covalently linked (either directly or indirectly) at the C-terminus to an IgG Fc fusion partner comprising about 231 amino acids (the hinge, CH₂ and CH₃ regions of the Fc). In

certain embodiments, the CTLA4 extracellular domain and the Ig Fc domain are linked via a linker, wherein the linker comprises from about 1 to about 10 amino acids. In particular embodiments, the linker comprises 1 amino acid.

[0095] In some embodiments, the variant fusion proteins of the disclosure comprise at least one amino acid substitution as compared to wild-type abatacept (SEQ ID NO: 5). In certain embodiments, the amino acid substitution is in the CTLA4 extracellular domain, *e.g.*, in a CDR-like loop of CTLA4. In other embodiments, the variant fusion proteins of the disclosure comprise at least one amino acid substitution in the CTLA4 extracellular domain and at least one amino acid substitution in the Fc domain as compared to wild-type abatacept (SEQ ID NO: 5).

[0096] In certain embodiments, the CTLA4 fusion proteins of the disclosure have an amino acid sequence that is at least 75% identical to the amino acid sequence of wild-type abatacept (SEQ ID NO: 6). In various embodiments, the fusion proteins have an amino acid sequence that is at least 80% identical, at least 85% identical, at least 90% identical, at least 91% identical, at least 92% identical, at least 93% identical, at least 94% identical, at least 95% identical, at least 96% identical, at least 97% identical, at least 98% identical or at least 99% identical to the amino acid sequence of wild-type abatacept (SEQ ID NO: 6).

[0097] In some embodiments, the CTLA4 fusion proteins of the disclosure comprise at least one mutation compared to wild-type abatacept (SEQ ID NO: 6). In other embodiments, the variant CTLA4 polypeptides of the disclosure comprise up to 2, up to 3, up to 4, up to 5, up to 6, up to 7, up to 8, up to 9, up to 10, up to 11, up to 12, up to 13, up to 14, up to 15, up to 16, up to 17, up to 18, up to 19, or up to 20 or more amino acid substitutions as compared to wild-type abatacept.

[0098] In addition to the modifications described above, a CTLA4 protein of the disclosure can be modified in the CTLA4 portion and/or the fusion partner portion to include a signal sequence for secretion from the host cell or a peptide purification sequence, *e.g.*, an epitope tag, a FLAG tag, a polyhistidine sequence, or a GST fusion. In

certain embodiments, the CTLA4 proteins of the disclosure comprise one or more modified amino acids, *e.g.*, a glycosylated amino acid, a PEGylated amino acid, a farnesylated amino acid, an acetylated amino acid, a biotinylated amino acid, an amino acid conjugated to a lipid moiety, and/or an amino acid conjugated to an organic derivatizing agent. In certain embodiments, the presence of modified amino acids is advantageous in, for example, (a) increasing polypeptide serum half-life and/or functional *in vivo* half-life, (b) reducing polypeptide antigenicity or immunogenicity, (c) increasing polypeptide storage stability, (d) increasing bioavailability, (e) decreasing effector function, and/or (f) decreasing or inhibiting undesired self-association (*e.g.*, aggregate formation) between two or more CTLA4 proteins of the disclosure. Amino acid(s) can be modified, for example, co-translationally or post-translationally during recombinant production (*e.g.*, N-linked glycosylation at N-X-S/T motifs during expression in mammalian cells) or modified by synthetic means.

[0099] In another aspect, a CTLA4 protein of the disclosure can be modified by the addition of protecting groups to the side chains of one or more the amino acids in the CTLA4 portion and/or in the fusion partner portion. Such protecting groups can facilitate transport of the polypeptides of the disclosure through membrane(s) or through certain tissue(s), for example, by reducing the hydrophilicity and increasing the lipophilicity of the polypeptides. Examples of suitable protecting groups include ester protecting groups, amine protecting groups, acyl protecting groups, and carboxylic acid protecting groups, which are known in the art (see, *e.g.*, U.S. Patent No. 6,121,236). Other modifications of the CTLA4 proteins of the disclosure, for example, by addition of polyethylene glycol or a detectable label, are discussed in Sections 5.6 and 5.7 below.

6.3. Increased Stability of CTLA4 Polypeptides

[0100] In certain aspects, the present disclosure provides CTLA4 polypeptides having increased protein stability as compared to wild-type CTLA4 Ig. The present disclosure provides CTLA4 polypeptides having single or multiple amino acid substitutions in their CDR-like loop regions as compared to the CDR-like loops of wild type CTLA4 extracellular domain and/or in the regions of the CTLA4 extracellular domain that are

outside the CDR-like loops and/or in the fusion partner polypeptide, if present, wherein at least one substitution results in increased stability of the CTLA4 polypeptide as compared to wild-type CTLA4 Ig. In certain embodiments, the increased stability is upon storage of the CTLA4 polypeptide. In other embodiments, the increased stability is due to resistance to degradation by proteases and the like. In various embodiments, the increased stability is due to increased conformational stability. In some embodiments, the increased stability is due to decreased aggregation.

[0101] In certain embodiments, the increased stability does not affect the binding affinity of the variant CTLA4 polypeptides of the disclosure to CD80 and/or CD86. In certain embodiments, the stability of a CTLA4 protein of the disclosure can be at least 0.1-fold, at least 0.2-fold, at least 0.3-fold, at least 0.4-fold, at least 0.5-fold, at least 0.6-fold, at least 0.7-fold, at least 0.8-fold, at least 0.9-fold, at least 1-fold, at least 2-fold, at least 3-fold, at least 4-fold, at least 5-fold, at least 6-fold, at least 7-fold, at least 8-fold, at least 9-fold, or at least 10-fold of the stability of wild-type CTLA4 Ig. In certain embodiments, the stability of a CTLA4 protein of the disclosure is increased relative to the stability of wild-type CTLA4 Ig in a range between any of the foregoing values, *e.g.*, 0.1-fold to 2-fold, 5-fold to 10-fold, 0.9-fold to 6-fold, or the like. In certain aspects, the stability of a CTLA4 polypeptide of the disclosure in a sample is greater than the stability of wild-type CTLA4 Ig in a sample where the samples are substantially identical (*e.g.*, are both in pharmaceutical compositions containing the same ingredients) and/or are processed or handled in substantially the same way (*e.g.*, are stored under the same conditions of temperature and humidity for the same period of time).

[0102] In certain aspects, the increased stability of a CTLA4 polypeptide of the disclosure is an increase in shelf-life. An increased shelf life can result from a decrease in amino acid oxidation (for example because an amino acid residue susceptible to oxidation, such as methionine, cysteine or tryptophan, in a CDR-like loop or in a region outside the CDR-like loops of the CTLA4 extracellular domain has been substituted relative to wild-type CTLA4-Ig). An increased shelf life can also result from a decrease in amino acid cyclization (for example because an amino acid residue susceptible to

cyclization, such as asparagines or glutamic acid) in a CDR-like loop or in a region outside the CDR-like loops of the CTLA4 extracellular domain has been substituted relative to wild-type CTLA4 Ig. An increased shelf life can also result from the elimination of an amino acid motif that is recognized by proteases that may be in protein purifications at residual levels. An increased shelf life can also result from the elimination of an amino acid motif that causes aggregation of the protein. An increased shelf life can also result from an increase in conformational stability. The increase in shelf life or conformational stability, or decrease in oxidation, cyclization, proteolysis or aggregation levels relative to wild-type CTLA4 Ig can be at least 0.1-fold, at least 0.2-fold, at least 0.3-fold, at least 0.4-fold, at least 0.5-fold, at least 0.6-fold, at least 0.7-fold, at least 0.8-fold, at least 0.9-fold, at least 1-fold, at least 2-fold, at least 3-fold, at least 4-fold, at least 5-fold, at least 6-fold, at least 7-fold, at least 8-fold, at least 9-fold, or at least 10-fold. In certain embodiments, increase in shelf life or conformational stability, or decrease in oxidation, cyclization, proteolysis or aggregation levels relative to wild-type CTLA4 Ig is in a range between any of the foregoing values, *e.g.*, 0.1-fold to 2-fold, 5-fold to 10-fold, 0.9-fold to 6-fold, or the like.

[0103] The present disclosure further provides methods for screening CTLA4 polypeptides for increased stability relative to wild-type CTLA4 Ig. In specific embodiments, the methods comprise the steps of: (a) determining the amount of full-length CTLA4 polypeptide in a first sample; and (b) comparing the amount of full-length CTLA4 polypeptide in the first sample with an amount of full-length wild-type CTLA4 Ig in a second sample. Methods of assaying for protein stability are known in the art.

6.4. Reduced Immunogenicity of CTLA4 Polypeptides

[0104] In certain aspects, the present disclosure provides CTLA4 polypeptides having reduced immunogenicity as compared to belatacept or MAXY-4 (Maxygen). The present disclosure provides CTLA4 polypeptides having single or multiple amino acid substitutions in their CDR-like loop regions as compared to the CDR-like loops of belatacept or MAXY-4 extracellular domain and/or in the regions of the CTLA4 extracellular domain that are outside the CDR-like loops and/or in the fusion partner

polypeptide, if present, wherein at least one substitution results in reduced immunogenicity of the CTLA4 polypeptide as compared to belatacept or MAXY-4. In certain embodiments, the reduced immunogenicity results from one or more amino acid substitutions that result in eliminating or mitigating one or more T cell epitopes.

[0105] In certain aspects, the CTLA4 proteins of the disclosure having reduced immunogenicity have comparable or altered biological activity as compared to belatacept or MAXY-4, *e.g.*, affinity towards CD80 and/or CD86.

[0106] In certain embodiments, the immunogenicity of a CTLA4 polypeptide of the disclosure is reduced relative to belatacept or MAXY-4. Such polypeptides generally have variant sequences relative to the CTLA4 extracellular domain and/or the fusion partner, if present. In certain embodiments, the CTLA4 polypeptides will generally have 1, 2 or 3 amino acid substitutions in one or both of the CTLA4 extracellular domain sequence and the fusion partner sequence, if present. In other embodiments, the CTLA4 polypeptides can have 4, 5, 6, 7, 8, 9, or 10 amino acid substitutions in one or both of the CTLA4 extracellular domain sequence and the fusion partner sequence, if present. In still other embodiments, the the CTLA4 polypeptides can have 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in one or both of the CTLA4 extracellular domain sequence and the fusion partner sequence, if present.

[0107] As used in the present disclosure, a variant with “reduced immunogenicity” refers to a CTLA4 polypeptide comprising a variant sequence as compared to belatacept or MAXY-4 that elicits a reduced proliferative response in peripheral blood mononuclear cells as compared to belatacept or MAXY-4. An exemplary proliferation assay that can be used to evaluate the proliferative response is set forth in Section 5.6 below. The reduced proliferative response can be reflected in terms of the percentage of responders, the stimulation index, or both.

[0108] In other embodiments, a peptide having a variant sequence as compared to the corresponding peptide in belatacept or MAXY-4 results in at least 25% fewer responders, in at least 30% fewer responders, in at least 35% fewer responders, in at least 40% fewer

responders, in at least 45% fewer responders, in at least 50% fewer responders, in at least 60% fewer responders, in at least 65% fewer responders, in at least 70% fewer responders, in at least 75% fewer responders, in at least 80% fewer responders, in at least 85% fewer responders, in at least 90% fewer responders, in at least 95% fewer responders, in at least 100% fewer responders, or a reduction in responders in a range between any of the foregoing values, *e.g.*, 25%-75% fewer responders, 50%-90% fewer responders, 60%-100% fewer responders, 70%-90% fewer responders, or the like. In certain aspects, the ability of variant peptides of belatacept or MAXY-4 to elicit a T-cell response as compared respectively to the corresponding wild-type peptides of belatacept or MAXY-4 is determined by the assay set forth in Section 5.6, below.

[0109] In other embodiments, a peptide having a variant sequence as compared to the corresponding peptide in belatacept or MAXY-4 results in a stimulation index that is at least 5% less, at least 10% less, at least 15% less, at least 20% less, at least 25% less, at least 30% less, at least 35% less, or at least 40% less than the stimulation index elicited by the corresponding peptide in wild-type CTLA4 Ig, or results in a stimulation reduced by a range between any of the foregoing values as compared to wild-type CTLA4 Ig, *e.g.*, 5%-20% less, 10%-30% less, 30%-40% less, or the like. In certain embodiments, the stimulation index is determined by the assay set forth in Section 5.6, below.

6.5. Nucleic Acids and Expression Systems

[0110] The present disclosure encompasses nucleic acid molecules encoding the CTLA4 polypeptides of the disclosure and host cells engineered to recombinantly express the polypeptides.

[0111] A CTLA4 protein of the disclosure can be prepared by recombinant expression of a nucleic acid encoding a CTLA4 binding portion or of a nucleic acid encoding a CTLA4 fusion protein in a host cell. To express a CTLA4 protein recombinantly, a host cell is transfected with one or more recombinant expression vectors carrying nucleic acids encoding the CTLA4 proteins such that the proteins are expressed in the host cell and, optionally, secreted into the medium in which the host cells are cultured, from which

medium the proteins can be recovered. Standard recombinant DNA methodologies are used to obtain nucleic acids encoding CTLA4 proteins, incorporate these nucleic acids into recombinant expression vectors and introduce the vectors into host cells, such as those described in *Molecular Cloning; A Laboratory Manual, Second Edition* (Sambrook, Fritsch and Maniatis (eds), Cold Spring Harbor, N. Y., 1989), *Current Protocols in Molecular Biology* (Ausubel, F.M. *et al.*, eds., Greene Publishing Associates, 1989) and in U.S. Patent No. 4,816,397.

[0112] The nucleic acids encoding the variant CTLA4 polypeptides of the disclosure can be synthesized in part or completely. Alternatively, nucleic acids encoding the CTLA4 binding portion are first obtained. These DNAs can be obtained from PCR of total cellular RNA of, for example, H38 (HTLV-II-associated leukemia) cell line. *See* U.S. Patent no. 5,434,131. In addition, if the CTLA4 protein is a fusion protein, nucleic acids encoding the fusion partner, *e.g.*, an immunoglobulin constant region, can be obtained by amplification and modification of germline DNA or cDNA encoding the desired fusion protein, for example using the polymerase chain reaction (PCR). A nucleic acid encoding wild-type abatacept can be synthesized and used as a template for mutagenesis to generate a variant as described herein using routine mutagenesis techniques; alternatively, a nucleic acid encoding the variant can be directly synthesized.

[0113] Once nucleic acids encoding the variant CTLA4 binding domains are obtained, the nucleic acid can be further manipulated by standard recombinant DNA techniques, for example to operatively link the CTLA4 binding domain-encoding DNA to another nucleic acid encoding another protein, *e.g.*, a fusion partner, such as an antibody constant region and/or a flexible linker. The term “operatively linked,” as used in this context, is intended to mean that the two nucleic acids are joined such that the amino acid sequences encoded by the two nucleic acids remain in-frame.

[0114] The isolated DNA encoding the CTLA4 binding domain can be converted to a nucleic acid encoding a fusion protein by operatively linking the CTLA4 binding domain-encoding DNA to another DNA molecule encoding one or more heavy chain

constant regions (CH₁, CH₂, CH₃ and, optionally, CH₄). The sequences of human heavy chain constant region nucleic acids are known in the art (see *e.g.*, Kabat, E.A., *et al.*, 1991, Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242) and nucleic acids encompassing these regions can be obtained by standard PCR amplification. The heavy chain constant region can be an IgG₁, IgG₂, IgG₃, IgG₄, IgA, IgE, IgM or IgD constant region, but in certain embodiments is an IgG₁ constant region.

[0115] To express the CTLA4 proteins of the disclosure, DNAs encoding partial or full-length proteins, obtained as described above, are inserted into expression vectors such that the nucleic acids are operatively linked to transcriptional and translational control sequences. In this context, the term “operatively linked” is intended to mean that a nucleic acid encoding a CTLA4 protein is ligated into a vector such that transcriptional and translational control sequences within the vector serve their intended function of regulating the transcription and translation of the CTLA4 protein-encoding nucleic acid. The expression vector and expression control sequences are chosen to be compatible with the expression host cell used.

[0116] The nucleic acids encoding CTLA4 proteins of the disclosure are inserted into the expression vector by standard methods (*e.g.*, ligation of complementary restriction sites on the CTLA4 protein gene fragment and vector, or blunt end ligation if no restriction sites are present). If the CTLA4 protein is a fusion protein, prior to insertion of the CTLA4 binding domain-encoding sequences, the expression vector can already carry fusion partner sequences, *e.g.*, antibody constant region sequences. For example, one approach to converting a protein of the disclosure comprising only a CTLA4 binding domain into a CTLA4 fusion protein is to insert the nucleic acid encoding the CTLA4 binding domain into expression vectors already encoding immunoglobulin Fc such that the CTLA4-encoding sequence is operatively linked to the Fc-encoding sequence within the vector. Additionally or alternatively, the recombinant expression vector can encode a signal peptide that facilitates secretion of the CTLA4 protein from a host cell. The nucleic acid encoding a CTLA4 protein can be cloned into the vector such that the signal

peptide is linked in-frame to the amino terminus of the CTLA4 protein-encoding nucleic acid. The signal peptide can be a CTLA4 signal peptide or a heterologous signal peptide, *e.g.*, an immunoglobulin signal peptide.

[0117] In addition to nucleic acids encoding CTLA4 proteins, the recombinant expression vectors of the disclosure carry regulatory sequences that control the expression of the CTLA4 protein-encoding nucleic acids in a host cell. The term “regulatory sequence” is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals) that control the transcription or translation of the nucleic acids encoding the CTLA4 proteins of the disclosure. Such regulatory sequences are described, for example, in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185 (Academic Press, San Diego, CA, 1990). It will be appreciated by those skilled in the art that the design of the expression vector, including the selection of regulatory sequences may depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. Suitable regulatory sequences for mammalian host cell expression include viral elements that direct high levels of protein expression in mammalian cells, such as promoters and/or enhancers derived from cytomegalovirus (CMV) (such as the CMV promoter/enhancer), Simian Virus 40 (SV40) (such as the SV40 promoter/enhancer), adenovirus, (*e.g.*, the adenovirus major late promoter (AdMLP)) and polyoma. For further description of viral regulatory elements, and sequences thereof, see *e.g.*, U.S. Patent No. 5,168,062 by Stinski, U.S. Patent No. 4,510,245 by Bell *et al.*, and U.S. Patent No. 4,968,615 by Schaffner *et al.*

[0118] In addition to the CTLA4 protein-encoding nucleic acids and regulatory sequences, the recombinant expression vectors of the disclosure can carry additional sequences, such as sequences that regulate replication of the vector in host cells (*e.g.*, origins of replication) and selectable marker genes. The selectable marker gene facilitates selection of host cells into which the vector has been introduced (see *e.g.*, U.S. Patents Nos. 4,399,216, 4,634,665 and 5,179,017, all by Axel *et al.*). For example, typically the selectable marker gene confers resistance to drugs, such as G418,

puromycin, blasticidin, hygromycin or methotrexate, on a host cell into which the vector has been introduced. Suitable selectable marker genes include the dihydrofolate reductase (DHFR) gene (for use in DHFR- host cells with methotrexate selection/amplification) and the neo gene (for G418 selection). For expression of the CTLA4 proteins, the expression vector(s) encoding the CTLA4 proteins is transfected into a host cell by standard techniques. The various forms of the term “transfection” are intended to encompass a wide variety of techniques commonly used for the introduction of exogenous DNA into a prokaryotic or eukaryotic host cell, *e.g.*, electroporation, lipofection, calcium-phosphate precipitation, DEAE- dextran transfection and the like.

[0119] It is possible to express the CTLA4 proteins of the disclosure in either prokaryotic or eukaryotic host cells. In certain embodiments, expression of CTLA4 proteins is performed in eukaryotic cells, *e.g.*, mammalian host cells or yeast host cells, for optimal secretion of a properly folded, post-translationally modified and immunologically active protein. Exemplary mammalian host cells for expressing the recombinant proteins of the disclosure include Chinese Hamster Ovary (CHO cells) (including DHFR- CHO cells, described in Urlaub and Chasin, 1980, Proc. Natl. Acad. Sci. USA 77:4216-4220, used with a DHFR selectable marker, *e.g.*, as described in Kaufman and Sharp, 1982, Mol. Biol. 159:601-621), NS0 myeloma cells, COS cells, 293 cells and SP2/0 cells. When recombinant expression vectors encoding CTLA4 proteins are introduced into mammalian host cells, the proteins are produced by culturing the host cells for a period of time sufficient to allow for expression of the protein in the host cells or secretion of the protein into the culture medium in which the host cells are grown. CTLA4 proteins can be recovered from the culture medium using standard protein purification methods.

[0120] Recombinant DNA technology can also be used to remove some or all of the DNA encoding the CTLA4 proteins that is not necessary for binding to a CTLA4 ligand. The molecules expressed from such truncated DNA molecules are also encompassed by the proteins of the disclosure.

[0121] Once a nucleic acid encoding one or more portions of wild-type abatacept or of a CTLA4 protein with CDR-like sequences related to the CDR-like sequences of abatacept is generated, further alterations or mutations can be introduced into the coding sequence, for example to generate nucleic acids encoding CTLA4 proteins with different CDR-like sequences, or proteins with reduced affinity to the Fc receptor.

[0122] The CTLA4 proteins of the disclosure can also be produced by chemical synthesis (*e.g.*, by the methods described in *Solid Phase Peptide Synthesis*, 2nd ed., 1984 The Pierce Chemical Co., Rockford, Ill.). Variant proteins can also be generated using a cell-free platform (see, *e.g.*, Chu *et al.*, *Biochemia No. 2*, 2001 (Roche Molecular Biologicals)).

[0123] Once a CTLA4 protein of the disclosure has been produced by recombinant expression, it can be purified by any method known in the art for purification of proteins, for example, using antibodies reactive with the CTLA4 binding domain of a protein of the disclosure, or chromatography (*e.g.*, ion exchange, affinity, such as affinity for CD80 and/or CD86, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique. Further, the CTLA4 proteins of the present disclosure can be fused to heterologous polypeptide sequences described herein or otherwise known in the art to facilitate purification.

[0124] Once isolated, a CTLA4 protein can, if desired, be further purified, *e.g.*, by high performance liquid chromatography (See, *e.g.*, Fisher, *Laboratory Techniques In Biochemistry And Molecular Biology* (Work and Burdon, eds., Elsevier, 1980)), or by gel filtration chromatography on a SuperdexTM 75 column (Pharmacia Biotech AB, Uppsala, Sweden).

6.6. Biological Activities of CTLA4 Proteins

[0125] In various embodiments, the CTLA4 proteins of the disclosure have certain biological activities, such as competing with abatacept for binding to CD80 and/or CD86, or blocking T-cell response.

[0126] Accordingly, in certain embodiments, CTLA4 proteins of the disclosure compete with abatacept for binding to CD80 or CD86. The ability to compete for binding to CD80 or CD86 can be tested using a competition assay. In one example of a competition assay, the AlphaLISA® (Amplified Luminescent Proximity Homogeneous) or AlphaScreen® assay can be used as a non-wash alternative to ELISA. In the AlphaLISA® assay, the ligand, CD80 or CD86 fused with a tag (*e.g.*, C λ -HA) is bound to AlphaLISA® acceptor beads conjugated with an anti-tag antibody (*e.g.*, goat anti-human C λ) and biotinylated abatacept is bound to AlphaScreen® streptavidin-coated donor beads (PerkinElmer, Waltham, MA). In the absence of competing CTLA4 variants, abatacept interacts with CD80 or CD86 and produces a signal at 615 nm. Addition of unlabeled CTLA4 variant competes with the abatacept/CD80 or CD86 interaction, reducing fluorescence quantitatively to enable determination of relative binding affinities. Abatacept can be biotinylated with Sulfo-NHS-Biotin using standard methods and dialyzed in PBS. Conjugation of AlphaLISA® acceptor beads is performed by following the “AlphaLISA® Assay Development Guide” (PerkinElmer). The binding is performed in a 384-well AlphaPlate (PerkinElmer) in assay buffer (*e.g.*, 1% BSA, 0.01% Tween20 in PBS (pH 7.1)). Each well contains 0.5 nM biotinylated abatacept, 1:4 serially diluted CTLA4 competitor starting from 40nM, 0.078 μ g/ml CD80, and 5 μ g/ml goat anti-human C λ -conjugated acceptor beads. The plate is incubated in the dark for 1 h at room temperature. Streptavidin donor beads are then added to each well at 5 μ g/ml. The plate is incubated in the dark at room temperature for an additional 30 min, after which it is read on an EnVision reader (PerkinElmer). Data are fit using nonlinear regression with the software GRAPHPAD PRISM (GraphPad, San Diego).

[0127] For CD86 binding, 8nM biotinylated abatacept, 1:4 serially diluted competitor starting from 100nM, 0.1 μ g/ml CD86 and 10 μ g/ml goat anti-human C λ -conjugated acceptor beads are first incubated and then 10 μ g/ml streptavidin donor beads are added. Variations on this competition assay can also be used to test competition between CTLA4 proteins of the disclosure and abatacept. For example, in certain aspects, the CTLA4 protein is used as a reference and abatacept is used as a test molecule. Additionally,

instead of soluble CD80 or CD86, membrane-bound ligand expressed on the surface of cells (*e.g.*, mammalian cells such as CHO) in culture can be used. Other formats for competition assay are known in the art and can be employed.

[0128] In various embodiments, a CTLA4 protein of the disclosure reduces the binding of labeled abatacept by at least 10%, by at least 20%, by at least 30%, by at least 40%, by at least 50%, by at least 60%, by at least 70%, by at least 80%, by at least 90%, by at least 95%, by at least 99%, or by a percentage ranging between any of the foregoing values (*e.g.*, a CTLA4 protein of the disclosure reduces the binding of labeled abatacept by 10% to 40%, 50% to 70%, by 40% to 60% or by 80% to 99%) when the CTLA4 protein is used at a concentration of 0.01 µg/ml, 0.025 µg/ml, 0.05 µg/ml, 0.075 µg/ml, 0.1 µg/ml, 0.25 µg/ml, 0.5 µg/ml, 0.75 µg/ml, 1 µg/ml, 2 µg/ml, 10 µg/ml, 50 µg/ml, 100 µg/ml or at a concentration ranging between any of the foregoing values (*e.g.*, at a concentration ranging from 0.1 µg/ml to 2 µg/ml).

[0129] In certain aspects, the CTLA4 variants of the disclosure are tested for their ability to elicit a T-cell response. In particular, CTLA4 peptides are synthesized using a multi-pin format by Mimotopes (Adelaide, Australia). The CTLA4 polypeptide sequences can be synthesized, for example, as 15-mer peptides overlapping by 12 amino acids. Peptides are resuspended in DMSO (Sigma-Aldrich) at approximately 1-2 mg/ml. Stock peptides are kept frozen at -20°C. For isolation of peripheral blood mononuclear cells, community donor buffy coat products can be purchased from the Stanford Blood Center, Palo Alto, CA. Buffy coat material is diluted 1:1 v:v with DPBS containing no calcium or magnesium. Diluted buffy coat material (25-35 mls) is underlayered in 50 ml conical centrifuge tubes (Sarsted or Costar) with 12.5 mls of FicollPaque-PLUS (GE Healthcare). The samples are centrifuged at 900 g for 30 minutes at room temperature. Peripheral blood mononuclear cells (PBMC) are collected from the interface. DPBS is added to bring the final volume to 50 mls and the cells are centrifuged at 350 g for 5 minutes. Pelleted cells are resuspended in DPBS and counted. For isolation of dendritic cells, T75 culture flasks (Costar) are seeded with 10⁸ freshly isolated PBMC in a total volume of 30 mls AIM V media (Invitrogen). Excess PBMC are frozen at -80°C in 90% fetal calf

serum (FCS), 10% DMSO at 5×10^7 cells/ml. T75 flasks were incubated at 37°C in 5% CO₂ for 2 hours. Nonadherent cells are removed, and the adherent monolayer is washed with DPBS. To differentiate dendritic cells from monocytes, 30 mls of AIM V media containing 800 units/ml of GM-CSF (R and D Systems) and 500 units/ml IL-4 (R and D Systems) are added. Flasks are incubated for 5 days. On day 5 IL-1 α (Endogen) and TNF α (Endogen) are added to 50 pg/ml and 0.2 ng/ml, respectively. Flasks are incubated for two more days. On day 7, dendritic cells are collected by the addition of 3 mls of 100 mM EDTA containing 0.5 to 1.0 mg Mitomycin C (Sigma-Aldrich) for a final concentration of 10 mM EDTA and 16.5 to 33 μ g/ml Mitomycin C. Flasks are incubated an additional hour at 37°C and 5% CO₂. Dendritic cells are collected, and washed in AIM V media 2-3 times. For cell culture, on day 7, previously frozen autologous PBMC are thawed quickly in a 37°C water bath. Cells are immediately diluted into DPBS or AIM V media and centrifuged at 350g for 5 minutes. CD4⁺ cells are enriched by negative selection using magnetic beads (Easy-Sep CD4⁺ kit, Stem Cell Technologies). Autologous CD4⁺ T cells and dendritic cells are cocultured at 2×10^5 CD4⁺ T-cells per 2×10^4 dendritic cells per well in 96 well round bottomed plates (Costar 9077). Peptides are added at approximately 5 μ g/ml. Control wells contain the DMSO (Sigma) vehicle alone at 0.25% v:v. Positive control wells contain DMSO at 0.25% and tetanus toxoid (List Biologicals or CalBioChem) at 1 μ g/ml. Cultures are incubated for 5 days. On day 5, 0.25 μ Ci per well of tritiated thymidine (Amersham or GE Healthcare) is added. Cultures are harvested on day 6 to filtermats using a Packard Filtermate Cell harvester. Scintillation counting is performed using a Wallac MicroBeta 1450 scintillation counter (Perkin Elmer). Average background CPM values are calculated by averaging individual results from 6 to 12 replicates. The CPM values of the four positive control wells are averaged. Replicate or triplicate wells for each peptide are averaged.

[0130] Stimulation index values for the positive control and the peptide wells are calculated by dividing the average experimental CPM values by the average control values. In order to be included in the dataset, a stimulation index of greater than 3.0 in the tetanus toxoid positive control wells is required. A response is noted for any peptide

resulting in a stimulation index of 2.95 or greater. Peptides are tested using peripheral blood samples from a group of 100 donors. Responses to all peptides are compiled. For each peptide tested, the percentage of the donor set that responds with a stimulation index of 2.95 or greater is calculated. In addition, the average stimulation index for all donors is calculated. CD4⁺ T-cell epitope peptides are identified by an analysis of the percent responses to the peptides within the set of 100 donors. The average percent response and standard deviation are calculated for all peptides tested describing the CTLA4 polypeptide. A response rate greater than or equal to the average background response plus three standard deviations is considered a potential CD4⁺ T-cell epitope.

[0131] In other aspects, a CTLA4 polypeptide of the disclosure inhibits activity of CD80 and/or CD86 in a range of *in vitro* assays, such as cell proliferation, cytokine (*e.g.*, IL-2) production and cell adhesion.

[0132] In some embodiments, the activity assayed is immunosuppressive activity of the CTLA4 polypeptides of the disclosure. In particular, human blood freshly collected from donors is diluted with an equal volume of PBS and fractionated to isolate PMBCs using a Histopaque (Sigma) Ficoll gradient as per the manufacturer's instructions. PMBCs are diluted in RPMI medium (Sigma) supplemented with 10% FBS (Hyclone) and 1x PSG (penicillin, streptomycin and glutamine) (Invitrogen) and added to 96-well culture plates (BD Biosciences) at a density of 1×10^5 cells/well. CTLA4 proteins to be tested are serially diluted in the same medium and added to wells in quadruplicate. Cell proliferation is initiated by addition of PPD antigen (purified protein derivative from *Mycobacterium tuberculosis*, Mycos) to a final concentration of 5µl/ml. After incubation at 37°C for 5 days, ³H thymidine (GE Healthcare) is added at 1 µCi/well and plates are incubated at 37 °C for an additional 18 hours. Cells are harvested with a cell harvester (FilterMate Omnifilter-96 Harvester, Perkin Elmer) using the manufacturer's recommended conditions and measured for ³H thymidine incorporation using a scintillation counter (Wallac Trilux). Cell proliferation data are analyzed with GraphPad Prism 5 software using a non-linear regression curve fit model (sigmoidal dose-response,

variable slope) and the least-squares fit method. The IC₅₀ parameters for each variant and their associated 95% confidence intervals are determined.

[0133] In certain embodiments, the activity assayed is inhibition of proliferation of primary and secondary allo-stimulated T-cells. In particular, the activity can be measured by the proliferation of human peripheral blood CD4⁺ T-cells, for example as described by Larsen *et al.*, 2005, *Am. J. Transplant.* 5:443-453. In primary allo-response assays, human CD4⁺ T-cells (3-10 x 10⁴/well) are isolated and incubated with irradiated human B lymphoblastoid cell lines expressing equivalent amounts of CD80 and CD86 (*e.g.*, PM cells, 8.0 x 10³/well), along with varying concentrations of wild-type CTLA4-Ig or CTLA4 proteins of the disclosure. Primary allogenic stimulation assays proceed for 6 days before addition of 0.5μCi/well of [³H]-thymidine for the final 7h of culture. For secondary allogenic stimulation assays, viable cells from 7-day primary allo-stimulated T-cells are isolated by differential density centrifugation and rested for 24h. T-cells are then restimulated (secondary stimulation) by adding PM cells in the same ratio as above in the presence of titrating amounts of wild-type CTLA4-Ig or CTLA4 proteins of the disclosure. T-cells are stimulated for 3 days, pulsed with [³H]-thymidine for the final 7h of culture and harvested as above. Alternatively, the proliferation of primary and secondary allo-stimulated T-cells can be assayed as described in Example 2 below.

[0134] In various embodiments, the activity of CTLA4 variants of the disclosure can be measured by inhibition of cytokine production. For example, in specific embodiments, the cytokine is IL-2 produced by Jurkat T cells (Cox *et al.*, 1999, *Protein Expr. Purif.* 17(1):26-32). Jurkat cells (1.0 x 10⁵/well) are stimulated with 10μg/mL PHA-L and cells (*e.g.*, CHO-K1, 2.5 x 10⁴/well) expressing recombinant CD80 or CD86 in the presence of titrating amounts of wild-type CTLA4-Ig or CTLA4 proteins of the disclosure. After 24 hours of culture, IL-2 concentration in the culture supernatant is measured using, for example, an AlphaLISA® Human IL-2 kit (Perkin Elmer). Alternatively, IL-2 concentration can be measured by other methods known in the art (*e.g.*, ELISA).

[0135] Alternatively, in another embodiment, the inhibition of cytokine production can be measured in the culture media of secondary allo-stimulated T-cells (Larsen *et al.*, 2005, *Am. J. Transplant.* 5:443-453). Aliquots of culture supernatants from T-cells allo-stimulated for 3 days as described in secondary allo-stimulation assay above are removed prior to addition of [³H]-thymidine. The level of cytokine production (*e.g.*, IFN γ , IL-2, IL-4) is measured using bead-based assays such as Luminex® (Invitrogen) or other methods known in the art (*e.g.*, ELISA).

[0136] In certain embodiments, the activity assayed is cell adhesion. In particular, cells (*e.g.*, CHO cells) recombinantly expressing CD80 or CD86 on the cells surface are diluted in medium, *e.g.*, 10% FBS in RPMI, and seeded in 96-well plates and grown to confluence. When confluent, cells are incubated with a CTLA4 protein of the disclosure or abatacept or are used as a negative control. Unbound protein is removed from the cells by washing with warm medium. Purified T-cells that are either unstimulated or are prestimulated with 1 μ g/ml anti-CD3 monoclonal antibody (30 min at 37°C). T-cells (1×10^5 cells/well in 100 μ l medium) are seeded onto the CD80 or CD86 expressing cells and allowed to adhere for 30 min at 37°C. Nonadherent cells are removed by washing each well three times with warm medium and counted (*e.g.*, by trypan blue exclusion) in triplicate. Cell adherence to the CHO cells is calculated as (the number of nonadherent cells/total number of input cells) X 100%. Alternatively, T-cells can be incubated with a fluorescent dye such as calcein AM (Molecular Probes, Eugene OR) according to the manufacturer's instructions before being seeded into the wells. After incubation with T-cells, removal of medium containing non-adherent T-cells and washing, plates are read by a fluorescence multi-well plate reader. Percent of T-cell adhesion is derived from the formula: (specific adhesion in the presence of test fusion protein – background adhesion)/(specific adhesion in the presence of abatacept – background adhesion).

6.7. Kinetic Properties of CTLA4-Ig Fusion Proteins

[0137] In certain embodiments, the CTLA4 proteins of the disclosure have high affinity for CD80 and CD86. As used herein, variant proteins with “high affinity” for CD80 and/or CD86 have at least a 1.5-fold improvement in binding affinity as compared to

abatacept. In other embodiments, the CTLA4 proteins of the disclosure have high affinity for CD80 and neutral affinity for CD86. In various embodiments, the CTLA4 proteins of the disclosure have high affinity for CD80 and low affinity for CD86. In still other embodiments, the CTLA4 proteins of the disclosure have high affinity for CD86 and neutral affinity for CD80. As used herein, variant proteins with “neutral affinity” for CD80 and/or CD86 have at least 0.5-fold but less than 1.5-fold improvement in binding affinity as compared to abatacept. In various embodiments, the CTLA4 proteins of the disclosure have low affinity for CD80 and high affinity for CD86. In still other embodiments, the CTLA4 proteins of the disclosure have neutral affinity for both CD80 and CD86. In some embodiments, the CTLA4 proteins of the disclosure have neutral affinity for CD80 and low affinity for CD86. In other embodiments, the CTLA4 proteins of the disclosure have low affinity for CD80 and neutral affinity for CD86. As used herein, a variant with “low affinity” for CD80 and/or CD86 has less than 0.5-fold improvement in binding affinity as compared to abatacept.

[0138] In specific embodiments, the CTLA4 proteins of the present disclosure have specific association rate constants (k_{on} or k_a values), dissociation rate constants (k_{off} or k_d values), affinity constants (K_A values), dissociation constants (K_D values) and/or IC_{50} values. In various embodiments, binding constants for the interaction of the CTLA4 proteins with either CD80 or CD86 extracellular domain can be determined using surface plasmon resonance according to the method disclosed in Karlsson *et al.*, 1991, J. Immunol. Methods 145:229-240. In certain aspects, such values are selected from the following embodiments.

[0139] In specific embodiments, the CTLA4 proteins of the disclosure bind to CD80 with a k_{on} of at least $10^2 M^{-1}s^{-1}$, at least $5 \times 10^2 M^{-1}s^{-1}$, at least $10^3 M^{-1}s^{-1}$, at least $5 \times 10^3 M^{-1}s^{-1}$, at least $10^4 M^{-1}s^{-1}$, at least $5 \times 10^4 M^{-1}s^{-1}$, at least $10^5 M^{-1}s^{-1}$, at least $5 \times 10^5 M^{-1}s^{-1}$, at least $10^6 M^{-1}s^{-1}$, at least $5 \times 10^6 M^{-1}s^{-1}$, at least $10^7 M^{-1}s^{-1}$, at least $5 \times 10^7 M^{-1}s^{-1}$, at least $10^8 M^{-1}s^{-1}$, at least $5 \times 10^8 M^{-1}s^{-1}$, at least $10^9 M^{-1}s^{-1}$, at least $5 \times 10^9 M^{-1}s^{-1}$ or with a k_{on} of any range between any pair of the foregoing values (*e.g.*, $5 \times 10^4 M^{-1}s^{-1}$ to $10^6 M^{-1}s^{-1}$ or $10^2 M^{-1}s^{-1}$ to $5 \times 10^5 M^{-1}s^{-1}$).

[0140] In certain embodiments, the CTLA4 proteins of the disclosure bind to CD86 with a k_{on} of at least $10^2 M^{-1}s^{-1}$, at least $5 \times 10^2 M^{-1}s^{-1}$, at least $10^3 M^{-1}s^{-1}$, at least $5 \times 10^3 M^{-1}s^{-1}$, at least $10^4 M^{-1}s^{-1}$, at least $5 \times 10^4 M^{-1}s^{-1}$, at least $10^5 M^{-1}s^{-1}$, at least $5 \times 10^5 M^{-1}s^{-1}$, at least $10^6 M^{-1}s^{-1}$, at least $5 \times 10^6 M^{-1}s^{-1}$, at least $10^7 M^{-1}s^{-1}$, at least $5 \times 10^7 M^{-1}s^{-1}$, at least $10^8 M^{-1}s^{-1}$, at least $5 \times 10^8 M^{-1}s^{-1}$, at least $10^9 M^{-1}s^{-1}$, at least $5 \times 10^9 M^{-1}s^{-1}$ or with a k_{on} of any range between any pair of the foregoing values (e.g., $5 \times 10^4 M^{-1}s^{-1}$ to $10^6 M^{-1}s^{-1}$ or $10^3 M^{-1}s^{-1}$ to $5 \times 10^5 M^{-1}s^{-1}$).

[0141] In certain embodiments, the CTLA4 proteins of the disclosure bind to CD80 with a k_{off} of $2 s^{-1}$ or less, $1.5 s^{-1}$ or less, $1 s^{-1}$ or less, $0.5 s^{-1}$ or less, $0.1 s^{-1}$ or less, $5 \times 10^{-2} s^{-1}$ or less, $10^{-2} s^{-1}$ or less, $5 \times 10^{-3} s^{-1}$ or less, $10^{-3} s^{-1}$ or less, $5 \times 10^{-4} s^{-1}$ or less, $10^{-4} s^{-1}$ or less, $5 \times 10^{-5} s^{-1}$ or less, $10^{-5} s^{-1}$ or less, $5 \times 10^{-6} s^{-1}$ or less, $10^{-6} s^{-1}$ or less, $5 \times 10^{-7} s^{-1}$ or less, $10^{-7} s^{-1}$ or less, $5 \times 10^{-8} s^{-1}$ or less, $10^{-8} s^{-1}$ or less, or with a k_{off} rate of any range between any pair of the foregoing values (e.g., $1 s^{-1}$ to $5 \times 10^{-3} s^{-1}$, or $5 \times 10^{-5} s^{-1}$ to $10^{-8} s^{-1}$).

[0142] In some embodiments, the CTLA4 proteins of the disclosure bind to CD86 with a k_{off} of $10 s^{-1}$ or less, $5 s^{-1}$ or less, $1 s^{-1}$ or less, $0.5 s^{-1}$ or less, $0.1 s^{-1}$ or less, $5 \times 10^{-2} s^{-1}$ or less, $10^{-2} s^{-1}$ or less, $5 \times 10^{-3} s^{-1}$ or less, $10^{-3} s^{-1}$ or less, $5 \times 10^{-4} s^{-1}$ or less, $10^{-4} s^{-1}$ or less, $5 \times 10^{-5} s^{-1}$ or less, $10^{-5} s^{-1}$ or less, $5 \times 10^{-6} s^{-1}$ or less, $10^{-6} s^{-1}$ or less, $5 \times 10^{-7} s^{-1}$ or less, $10^{-7} s^{-1}$ or less, $5 \times 10^{-8} s^{-1}$ or less, $10^{-8} s^{-1}$ or less, or with a k_{off} rate of any range between any pair of the foregoing values (e.g., $1 s^{-1}$ to $5 \times 10^{-3} s^{-1}$, or $5 \times 10^{-5} s^{-1}$ to $10^{-8} s^{-1}$).

[0143] In some embodiments, a CTLA4 protein of the disclosure binds to CD80 with a K_A (k_{on}/k_{off}) of at least at least $5 \times 10^5 M^{-1}$, at least $10^5 M^{-1}$, at least $5 \times 10^6 M^{-1}$, at least $10^6 M^{-1}$, at least $5 \times 10^7 M^{-1}$, at least $10^7 M^{-1}$, at least $10^8 M^{-1}$, at least $5 \times 10^8 M^{-1}$, at least $10^9 M^{-1}$, at least $5 \times 10^9 M^{-1}$, at least $5 \times 10^{10} M^{-1}$, at least $10^{10} M^{-1}$, at least $5 \times 10^{11} M^{-1}$, at least $10^{11} M^{-1}$, at least $5 \times 10^{12} M^{-1}$, at least $10^{12} M^{-1}$, at least $5 \times 10^{13} M^{-1}$, at least $10^{13} M^{-1}$, at least $5 \times 10^{14} M^{-1}$, at least $10^{14} M^{-1}$, at least $5 \times 10^{15} M^{-1}$, at least 10^{15}

M^{-1} , or with a K_A of any range between any pair of the foregoing values (e.g., $5 \times 10^5 M^{-1}$ to $5 \times 10^{13} M^{-1}$ or $5 \times 10^8 M^{-1}$ to $5 \times 10^{15} M^{-1}$).

[0144] In some embodiments, a CTLA4 protein of the disclosure binds to CD86 with a K_A (k_{on}/k_{off}) of at least $5 \times 10^4 M^{-1}$, at least $10^4 M^{-1}$, at least $5 \times 10^5 M^{-1}$, at least $10^5 M^{-1}$, at least $5 \times 10^6 M^{-1}$, at least $10^6 M^{-1}$, at least $10^7 M^{-1}$, at least $5 \times 10^7 M^{-1}$, at least $10^8 M^{-1}$, at least $5 \times 10^8 M^{-1}$, at least $5 \times 10^9 M^{-1}$, at least $10^9 M^{-1}$, at least $5 \times 10^{10} M^{-1}$, at least $10^{10} M^{-1}$, at least $5 \times 10^{11} M^{-1}$, at least $10^{11} M^{-1}$, at least $5 \times 10^{12} M^{-1}$, at least $10^{12} M^{-1}$, at least $5 \times 10^{13} M^{-1}$, at least $10^{13} M^{-1}$, at least $5 \times 10^{14} M^{-1}$, at least $10^{14} M^{-1}$, or with a K_A of any range between any pair of the foregoing values (e.g., $5 \times 10^4 M^{-1}$ to $10^{13} M^{-1}$ or $5 \times 10^7 M^{-1}$ to $5 \times 10^{13} M^{-1}$).

[0145] In various embodiments, a CTLA4 of the disclosure binds to CD80 with a K_D (k_{off}/k_{on}) of $5 \times 10^{-6} M$ or less, $10^{-6} M$ or less, $5 \times 10^{-7} M$ or less, $10^{-7} M$ or less, $5 \times 10^{-8} M$ or less, $10^{-8} M$ or less, $5 \times 10^{-9} M$ or less, $10^{-9} M$ or less, $5 \times 10^{-10} M$ or less, $10^{-10} M$ or less, $5 \times 10^{-11} M$ or less, $10^{-11} M$ or less, $5 \times 10^{-12} M$ or less, $10^{-12} M$ or less, $5 \times 10^{-13} M$ or less, $10^{-13} M$ or less, $5 \times 10^{-14} M$ or less, $10^{-14} M$ or less, $5 \times 10^{-15} M$ or less, $10^{-15} M$ or less, or with a K_D of any range between any pair of the foregoing values (e.g., $10^{-7} M$ to $5 \times 10^{-13} M$, or $5 \times 10^{-9} M$ to $10^{-15} M$).

[0146] In various embodiments, a CTLA4 protein of the disclosure binds to CD86 with a K_D (k_{off}/k_{on}) of $10^{-5} M$ or less, $5 \times 10^{-6} M$ or less, $10^{-6} M$ or less, $5 \times 10^{-7} M$ or less, $10^{-7} M$ or less, $5 \times 10^{-8} M$ or less, $10^{-8} M$ or less, $5 \times 10^{-9} M$ or less, $10^{-9} M$ or less, $5 \times 10^{-10} M$ or less, $10^{-10} M$ or less, $5 \times 10^{-11} M$ or less, $10^{-11} M$ or less, $5 \times 10^{-12} M$ or less, $10^{-12} M$ or less, $5 \times 10^{-13} M$ or less, $10^{-13} M$ or less, $5 \times 10^{-14} M$ or less, $10^{-14} M$ or less, $5 \times 10^{-15} M$ or less, $10^{-15} M$ or less, or with a K_D of any range between any pair of the foregoing values (e.g., $10^{-6} M$ to $5 \times 10^{-10} M$, or $5 \times 10^{-9} M$ to $10^{-15} M$).

[0147] In some embodiments, the CTLA4 protein of the disclosure binds to CD80 and inhibits the binding of CD80 to abatacept in a binding assay (e.g., an AlphaLISA® competition assay) at an IC_{50} value of less than 1000 nM, less than 750 nM, less than 500 nM, less than 100 nM, less than 50 nM, less than 10 nM, less than 5 nM, less than 1 nM,

less than 0.75 nM, less than 0.5 nM, less than 0.25 nM, less than 0.1 nM, less than 5×10^{-2} nM, less than 10^{-2} nM, less than 5×10^{-3} nM, less than 10^{-3} nM, less than 5×10^{-4} nM, or less than 10^{-4} nM, or with an IC_{50} of any range between any pair of the foregoing values (e.g., 100 nM to 5×10^{-2} nM or 0.5 nM and 5×10^{-4} nM).

[0148] In some embodiments, the CTLA4 protein of the disclosure binds to CD86 and inhibits the binding of CD86 to abatacept in a binding assay (e.g., an AlphaLISA® competition assay) at an IC_{50} value of less than 1000 nM, less than 500 nM, less than 100 nM, less than 50 nM, less than 10 nM, less than 5 nM, less than 1 nM, less than 0.75 nM, less than 0.5 nM, less than 0.25 nM, less than 0.1 nM, less than 5×10^{-2} nM, less than 10^{-2} nM, less than 5×10^{-3} nM, less than 10^{-3} nM, less than 5×10^{-4} nM, or less than 10^{-4} nM, or with an IC_{50} of any range between any pair of the foregoing values (e.g., 100 nM to 5×10^{-2} nM or 0.5 nM and 5×10^{-4} nM).

[0149] In certain embodiments, the kinetic properties of a fusion protein of the disclosure are comparable to, or improved relative to, abatacept in a comparable assay. For example, in certain embodiments, a CTLA4 protein of the disclosure binds to CD80 and/or CD86 with a k_{on} rate ranging from approximately 0.05x to 1000x of the k_{on} of abatacept, for example a k_{on} of 0.06x of the k_{on} of abatacept, a k_{on} of 0.08x of the k_{on} of abatacept, a k_{on} of 0.1x of the k_{on} of abatacept, a k_{on} of 0.5x of the k_{on} of abatacept, a k_{on} of 1x of the k_{on} of abatacept, a k_{on} of 1.1x of the k_{on} of abatacept, a k_{on} of 1.2x of the k_{on} of abatacept, a k_{on} of 1.3x of the k_{on} of abatacept, a k_{on} of 1.4x of the k_{on} of abatacept, a k_{on} of 1.5x of the k_{on} of abatacept, a k_{on} of 1.6x of the k_{on} of abatacept, a k_{on} of 1.6x of the k_{on} of abatacept, a k_{on} of 1.7x of the k_{on} of abatacept, a k_{on} of 1.8x of the k_{on} of abatacept, a k_{on} of 1.9x of the k_{on} of abatacept, a k_{on} of 2x of the k_{on} of abatacept, a k_{on} of 2.25x of the k_{on} of abatacept, a k_{on} of 2.5x of the k_{on} of abatacept, a k_{on} of 2.75x of the k_{on} of trazituzumab, a k_{on} of 3x of the k_{on} of abatacept, a k_{on} of 4x of the k_{on} of abatacept, a k_{on} of 5x of the k_{on} of abatacept, a k_{on} of 6x of the k_{on} of abatacept, a k_{on} of 7x of the k_{on} of abatacept, a k_{on} of 8x of the k_{on} of abatacept, a k_{on} of 9x of the k_{on} of abatacept, a k_{on} of 10x of the k_{on} of abatacept, a k_{on} of 15x of the k_{on} of abatacept, a k_{on} of 20x of the k_{on} of abatacept, a k_{on} of 50x of the k_{on} of abatacept, a k_{on} of 75x of the k_{on} of abatacept, a k_{on} of

100x of the k_{on} of abatacept, a k_{on} of 150x of the k_{on} of abatacept, a k_{on} of 200x of the k_{on} of abatacept, or a k_{on} ranging between any pair of the foregoing values, *e.g.*, a k_{on} of 0.1x-75x of the k_{on} of abatacept, a k_{on} of 5x-100x of the k_{on} of abatacept, a k_{on} of 0.05x-1000x of the k_{on} of abatacept, a k_{on} of 0.75x-250x of the k_{on} of abatacept, *etc.*

[0150] In various embodiments, a CTLA4 protein of the disclosure binds to CD80 and/or CD86 with a k_{off} rate ranging from about 0.001x to about 3x of the k_{off} of abatacept, for example a k_{off} of 0.002x of the k_{off} of abatacept, a k_{off} of 0.003x of the k_{off} of abatacept, a k_{off} of 0.004x of the k_{off} of abatacept, a k_{off} of 0.005x of the k_{off} of abatacept, a k_{off} of 0.006x of the k_{off} of abatacept, a k_{off} of 0.0075x of the k_{off} of abatacept, a k_{off} of 0.01x of the k_{off} of abatacept, a k_{off} of 0.025x of the k_{off} of abatacept, a k_{off} of 0.05x of the k_{off} of abatacept, a k_{off} of 0.075x of the k_{off} of abatacept, a k_{off} of 0.1x of the k_{off} of abatacept, a k_{off} of 0.25x of the k_{off} of abatacept, a k_{off} of 0.5x of the k_{off} of abatacept, a k_{off} of 0.75x of the k_{off} of abatacept, a k_{off} of 1x of the k_{off} of abatacept, a k_{off} of 1.25x of the k_{off} of abatacept, a k_{off} of 1.5x of the k_{off} of abatacept, a k_{off} of 1.75x of the k_{off} of abatacept, a k_{off} of 2x of the k_{off} of abatacept, a k_{off} of 2.25x of the k_{off} of abatacept, a k_{off} of 2.5x of the k_{off} of abatacept, a k_{off} of 3x of the k_{off} of abatacept, a k_{off} of 4x of the k_{off} of abatacept, a k_{off} of 5x of the k_{off} of abatacept, or a k_{off} ranging between any pair of the foregoing values, *e.g.*, a k_{off} of 0.01x to 1.25x of the k_{off} of abatacept, a k_{off} of 0.05x to 2.5x of the k_{off} of abatacept, or a k_{off} of 0.006x to 0.1x of the k_{off} of abatacept, *etc.*

[0151] In other embodiments, a CTLA4 protein of the disclosure binds to CD80 and/or CD86 with a K_A (k_{on}/k_{off}) ranging from about 0.1x to about 1000x of the K_A of abatacept, for example a K_A of 0.2x of the K_A of abatacept, a K_A of 0.25x of the K_A of abatacept, a K_A of 0.5x of the K_A of abatacept, a K_A of 0.75 of the K_A of abatacept, a K_A of 1x of the K_A of abatacept, a K_A of 2x of the K_A of abatacept, a K_A of 3x of the K_A of abatacept, a K_A of 4x of the K_A of abatacept, a K_A of 5x of the K_A of abatacept, a K_A of 10x of the K_A of abatacept, a K_A of 15x of the K_A of abatacept, a K_A of 20x of the K_A of abatacept, a K_A of 30x of the K_A of abatacept, a K_A of 40x of the K_A of abatacept, a K_A of 50x of the K_A of abatacept, a K_A of 75x of the K_A of abatacept, a K_A of 100x of the K_A of abatacept, a K_A of 200x of the K_A of abatacept, a K_A of 250x of the K_A of abatacept, a K_A of 300x of

the K_A of abatacept, a K_A of 350X of the K_A of abatacept, a K_A of 400x of the K_A of abatacept, a K_A of 500x of the K_A of abatacept, a K_A of 750x of the K_A of abatacept, a K_A of 1000x of the K_A of abatacept, or a K_A ranging between any pair of the foregoing values, *e.g.*, a K_A of 0.1x to 100x of the K_A of abatacept, a K_A of 10x to 50x of the K_A of abatacept, or a K_A of 5x to 50x of the K_A of abatacept, *etc.*

[0152] In still other embodiments, a CTLA4 protein of the disclosure binds to CD80 and/or CD86 with a K_D (k_{off}/k_{on}) ranging from about 0.001x to 10x of the K_D of abatacept, or example a K_D of 0.001x of the K_D of abatacept, a K_D of 0.002x of the K_D of abatacept, a K_D of 0.003x of the K_D of abatacept, a K_D of 0.004x of the K_D of abatacept, a K_D of 0.005x of the K_D of abatacept, a K_D of 0.0075x of the K_D of abatacept, a K_D of 0.01x of the K_D of abatacept, a K_D of 0.025x of the K_D of abatacept, a K_D of 0.05x of the K_D of abatacept, a K_D of 0.075x of the K_D of abatacept, a K_D of 0.1x of the K_D of abatacept, a K_D of 0.2x of the K_D of abatacept, a K_D of 0.3x of the K_D of abatacept, a K_D of 0.4x of the K_D of abatacept, a K_D of 0.5x of the K_D of abatacept, a K_D of 0.75x of the K_D of abatacept, a K_D of 1x of the K_D of abatacept, a K_D of 1.5x of the K_D of abatacept, a K_D of 2x of the K_D of abatacept, a K_D of 3x of the K_D of abatacept, a K_D of 4x of the K_D of abatacept, a K_D of 5x of the K_D of abatacept, a K_D of 6x of the K_D of abatacept, a K_D of 7x of the K_D of abatacept, a K_D of 8x of the K_D of abatacept, a K_D of 9x of the K_D of abatacept, a K_D of 10x of the K_D of abatacept, or a K_D ranging between any pair of the foregoing values, *e.g.*, a K_D of 0.001x to 0.5x of the K_D of abatacept, a K_D of 0.1x to 4x of the K_D of abatacept, a K_D of 0.05 to 1x of the K_D of abatacept, *etc.*

[0153] In certain embodiments, a CTLA4 protein of the disclosure binds to CD80 and/or CD86 and inhibits cell growth or IL2 production at a IC_{50} value ranging from about 0.001x to 10x of the IC_{50} of abatacept, for example at an IC_{50} of 0.005 of the IC_{50} of abatacept, at an IC_{50} of 0.01x of the IC_{50} of abatacept, at an IC_{50} of 0.05x of the IC_{50} of abatacept, at an IC_{50} of 0.1x of the IC_{50} of abatacept, at an IC_{50} of 0.2x of the IC_{50} of abatacept, at an IC_{50} of 0.3x of the IC_{50} of abatacept, at an IC_{50} of 0.4x of the IC_{50} of abatacept, at an IC_{50} of 0.5x of the IC_{50} of abatacept, at an IC_{50} of 0.6x of the IC_{50} of abatacept, at an IC_{50} of 0.7x of the IC_{50} of abatacept, at an IC_{50} of 0.8x of the IC_{50} of

abatacept, at an IC₅₀ of 0.9x of the IC₅₀ of abatacept, at an IC₅₀ of 1x of the IC₅₀ of abatacept, at an IC₅₀ of 1.5x of the IC₅₀ of abatacept, at an IC₅₀ of 2x of the IC₅₀ of abatacept, at an IC₅₀ of 3x of the IC₅₀ of abatacept, at an IC₅₀ of 4x of the IC₅₀ of abatacept, at an IC₅₀ of 5x of the IC₅₀ of abatacept, at an IC₅₀ of 6x of the IC₅₀ of abatacept, at an IC₅₀ of 7x of the IC₅₀ of abatacept, at an IC₅₀ of 8x of the IC₅₀ of abatacept, at an IC₅₀ of 9x of the IC₅₀ of abatacept, at an IC₅₀ of 10x of the IC₅₀ of abatacept, at an IC₅₀ of 100x of the IC₅₀ of the IC₅₀ of abatacept, at an IC₅₀ of 500x of the IC₅₀ of abatacept, at an IC₅₀ of 1000x of the IC₅₀ of abatacept, or an IC₅₀ ranging between any pair of the foregoing values, *e.g.*, an IC₅₀ of 0.005 to 0.2 of the IC₅₀ of abatacept, an IC₅₀ of 0.1x to 1.5x of the IC₅₀ of abatacept, an IC₅₀ of 0.2x to 2x of the IC₅₀ of abatacept, *etc.* In certain embodiments, a single substitution in the CDR-like loops can result in the foregoing differences in IC₅₀ as compared to abatacept, wherein a CTLA4-Ig fusion protein of the disclosure can comprise such substitution and up to 5 additional substitutions, up to 10 additional substitutions, up to 15 additional substitutions or up to 20 additional substitutions in the CDR-like loops as compared to abatacept.

6.8. CTLA4 Protein Conjugates

[0154] The CTLA4 proteins of the disclosure include conjugates that are modified, *e.g.*, by the covalent attachment of any type of molecule to the protein, such that covalent attachment does not interfere with binding to CD80 or CD86.

[0155] In certain aspects, a CTLA4 protein of the disclosure can be conjugated to an effector moiety or a label. The term “effector moiety” as used herein includes, for example, antineoplastic agents, drugs, toxins, biologically active proteins, for example enzymes, antibody or antibody fragments, synthetic or naturally occurring polymers, nucleic acids (*e.g.*, DNA and RNA), radionuclides, particularly radioiodide, radioisotopes, chelated metals, nanoparticles and reporter groups such as fluorescent compounds or compounds which can be detected by NMR or ESR spectroscopy.

[0156] In one example, CTLA4 proteins can be conjugated to an effector moiety, such as a cytotoxic agent, a radionuclide or drug moiety to modify a given biological response.

The effector moiety can be a protein or polypeptide, such as, for example and without limitation, a toxin (such as abrin, ricin A, *Pseudomonas* exotoxin, or Diphtheria toxin), a signaling molecule (such as α -interferon, β -interferon, nerve growth factor, platelet derived growth factor or tissue plasminogen activator), an immunosuppressant (such as cyclosporine A, tacrolimus, Campath-1H or a glucocorticoid) or anti-inflammatory agent (such as aspirin or naproxen) or a biological response modifier such as an antibody, anti-lymphocyte globulin, protein or cytokine (*e.g.*, an anti-TNF α antibody or an antibody that affects cell migration, such as natalizumab).

[0157] In another example the effector moieties can be cytotoxins or cytotoxic agents. Examples of cytotoxins and cytotoxic agents include taxol, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof.

[0158] Effector moieties also include, but are not limited to, antimetabolites (*e.g.*, methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (*e.g.*, mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclophosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C5 and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (*e.g.*, daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (*e.g.*, dactinomycin (formerly actinomycin), bleomycin, mithramycin, anthramycin (AMC), calicheamicins or duocarmycins), and anti-mitotic agents (*e.g.*, vincristine and vinblastine).

[0159] Other effector moieties can include radionuclides such as, but not limited to, ^{111}In and ^{90}Y , Lu^{177} , Bismuth 213 , Californium 252 , Iridium 192 and Tungsten 187 /Rhenium 188 and drugs such as, but not limited to, alkylphosphocholines, topoisomerase I inhibitors, taxoids and suramin.

[0160] Techniques for conjugating such effector moieties to proteins are well known in the art (see, *e.g.*, Hellstrom *et al.*, *Controlled Drug Delivery*, 2nd Ed., at pp. 623-53 (Robinson *et al.*, eds., 1987)); Thorpe *et al.*, 1982, *Immunol. Rev.* 62:119-58 and Dubowchik *et al.*, 1999, *Pharmacology and Therapeutics* 83:67-123).

[0161] In certain aspects, a CTLA4 protein is conjugated to a small molecule toxin. In certain exemplary embodiments, a CTLA4 protein of the disclosure is conjugated to a dolastatin or dolostatin peptidic analog or derivative, *e.g.*, an auristatin (U.S. Patent Nos. 5,635,483 and 5,780,588). The dolastatin or auristatin drug moiety may be attached to the antibody through its N (amino) terminus, C (carboxyl) terminus or internally (WO 02/088172). Exemplary auristatin embodiments include the N-terminus linked monomethylauristatin drug moieties DE and DF, as disclosed in U.S. Patent No. 7,498,298, which is hereby incorporated by reference in its entirety (disclosing, *e.g.*, linkers and methods of preparing monomethylvaline compounds such as MMAE and MMAF conjugated to linkers).

[0162] In other exemplary embodiments, small molecule toxins include but are not limited to calicheamicin, maytansine (U.S. Patent No. 5,208,020), trichothene, and CC1065. In one embodiment of the disclosure, the CTLA4 protein is conjugated to one or more maytansine molecules (*e.g.*, about 1 to about 10 maytansine molecules per protein molecule). Maytansine may, for example, be converted to May-SS-Me which may be reduced to May-SH3 and reacted with a protein (Chari *et al.*, 1992, *Cancer Research* 52: 127-131) to generate a maytansinoid-protein or maytansinoid-Fc fusion conjugate. Structural analogues of calicheamicin that can also be used include but are not limited to γ 11, γ 31, γ 31, N-acetyl- γ 11, PSAG, and θ 11, (Hinman *et al.*, 1993, *Cancer Research* 53:3336-3342; Lode *et al.*, 1998, *Cancer Research* 58:2925-2928; U.S. Patent No. 5,714,586; U.S. Patent No. 5,712,374; U.S. Patent No. 5,264,586; U.S. Patent No. 5,773,001).

[0163] In certain aspects, a CTLA4 protein of the disclosure can be attached to an immunosuppressant agent. Such agents include glucocorticoids, cytostatic agents,

antibodies, drugs that act on immunophilins, statins and other agents such as interferons (*e.g.*, INF- β and INF- γ), opioids, TNF binding agents (*e.g.*, infliximab, etanercept, adalimumab, curcumin and catechins), mycophenolate, IL-1 receptor antagonists, and other small molecule agents (*e.g.*, fingolimod, myriocin). Exemplary glucocorticoids include, but are not limited to, hydrocortisone, prednisone, prednisolone, methylprednisone, dexamethasone, betamethasone, triamcinolone, beclometasone, fludrocortisone acetate, deoxycorticosterone acetate, and aldosterone. Exemplary cytostatic agents include but are not limited to cyclophosphamide, nitrosoureas, platinum compounds, methotrexate, azathioprine, mercaptopurine, pyrimidine analogs, protein synthesis inhibitors, and antibiotics such as dactinomycin, anthracyclines, mitomycin C, bleomycin and mithramycin. Exemplary immunosuppressant antibodies include, but are not limited to, anti-CD20 antibodies, anti-IL2 receptor antibodies (daclizumab, basiliximab), Campath-1H, anti- $\alpha_4\beta_1$ integrin antibodies, anti-IL-15 antibodies, anti-IL-6 receptor antibodies, and anti-CD3 antibodies (muromonab). Exemplary agents that act on immunophilins include but are not limited to cyclosporin, tacrolimus, and sirolimus.

[0164] In certain embodiments, CTLA4 proteins of the present disclosure can be attached to an anti-inflammatory agent. Exemplary anti-inflammatory agents include, but are not limited to, non-steroidal anti-inflammatories such as ibuprofen, aspirin, naproxen, diflunisal, ketoprofen, nabumetone, piroxicam, diclofenac, indomethacin, sulindac, tolmetin, etodolac, ketorolac, oxaprozin, and celecoxib, and glucocorticoids, which also have immunosuppressive activity.

[0165] In one example CTLA4 proteins of the present disclosure can be attached to poly(ethyleneglycol) (PEG) moieties. In one particular example the PEG moieties can be attached through any available amino acid side-chain or terminal amino acid functional group located in the protein, for example any free amino, imino, thiol, hydroxyl or carboxyl group. Such amino acids can occur naturally in the protein or can be engineered into the protein using recombinant DNA methods. See for example U.S. Patent No. 5,219,996. Multiple sites can be used to attach two or more PEG molecules. PEG moieties can be covalently linked through a thiol group of at least one cysteine residue

located in the CTLA4 protein. Where a thiol group is used as the point of attachment, appropriately activated effector moieties, for example thiol selective derivatives such as maleimides and cysteine derivatives, can be used. The CTLA4 proteins can be attached to PEG or other hydrophilic synthetic polymers, such as polypropylene glycol or polyoxyalkylene, using techniques well known in the art, such as those described in U.S. Patent Nos. 4,179,337, 4,301,144, 4,496,689, 4,640,835, 4,670,417, and 4,791,192, or to a polymer such as polyvinylalcohol or polyvinylpyrrolidone (PVP).

[0166] The word “label” when used herein refers to a detectable compound or composition which can be conjugated directly or indirectly to a CTLA4 protein of the disclosure. The label can itself be detectable (*e.g.*, radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, can catalyze chemical alteration of a substrate compound or composition which is detectable. Useful fluorescent moieties include, but are not limited to, fluorescein, fluorescein isothiocyanate, rhodamine, 5-dimethylamine-1-naphthalenesulfonyl chloride, phycoerythrin and the like. Useful enzymatic labels include, but are not limited to, alkaline phosphatase, horseradish peroxidase, glucose oxidase and the like.

[0167] Additional CTLA4 protein conjugates that are useful for, *inter alia*, diagnostic purposes, are described in Section 5.7 below.

6.9. Diagnostic uses of CTLA4 Proteins

[0168] The CTLA4 proteins of the disclosure, including those proteins that have been modified, *e.g.*, by biotinylation, horseradish peroxidase, or any other detectable moiety (including those described in Section 5.6), can be advantageously used for diagnostic purposes.

[0169] In particular, the CTLA4 proteins can be used, for example, but not limited to, to bind to CD80 and/or CD86 for leukocyte typing *in vitro* to define B-cell maturational stages, for detecting B-cell associated diseases, for isolation of CD80- and/or CD86-positive cells, and for *in vitro* and *in vivo* diagnostic methods. (See, *e.g.*, Yokochi *et al.*,

1982, *J. Immunol.* 128(2):823-27.) For example, the proteins can be used in immunoassays for qualitatively and quantitatively measuring levels of CD80- and/or CD86-positive cells in biological samples. General guidance for performing such diagnostic techniques are found in, for example, Harlow *et al.*, *Antibodies: A Laboratory Manual*, Second Edition (Cold Spring Harbor Laboratory Press, 1988) and Hampton R *et al.*, *Serological Methods A Laboratory Manual*, (APS Press, 1990), each of which is incorporated by reference herein in its entirety.

[0170] In certain embodiments, the CTLA4 proteins of the disclosure can be used in assays to identify other agents, *e.g.*, anti-CTLA4 antibodies or fragments thereof, that are capable of regulating T-cell/B-cell interactions. In particular, the assays identify agents capable of inhibiting the binding of a protein of the disclosure to CD80 and/or CD86. Assays useful for screening agents that regulate T-cell/B-cell interactions are known in the art and include, but are not limited to, competition ELISA assays.

[0171] The present disclosure further encompasses CTLA4 proteins or fragments thereof conjugated to a diagnostic agent. The proteins can be used diagnostically, for example, to detect expression of a target of interest in specific cells, tissues, or serum; or to monitor the development or progression of an immunologic response as part of a clinical testing procedure to, *e.g.*, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling the protein to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, radioactive materials, positron emitting metals using various positron emission tomographies, and nonradioactive paramagnetic metal ions. The detectable substance can be coupled or conjugated either directly to the protein (or fragment thereof) or indirectly, through an intermediate (such as, for example, a linker known in the art) using techniques known in the art. Examples of enzymatic labels include luciferases (*e.g.*, firefly luciferase and bacterial luciferase; U.S. Patent No. 4,737,456), luciferin, 2,3-dihydrophthalazinediones, malate dehydrogenase, urease, peroxidase such as horseradish peroxidase (HRPO), alkaline phosphatase, β -galactosidase, acetylcholinesterase, glucoamylase, lysozyme, saccharide oxidases (*e.g.*,

glucose oxidase, galactose oxidase, and glucose-6-phosphate dehydrogenase), heterocyclic oxidases (such as uricase and xanthine oxidase), lactoperoxidase, microperoxidase, and the like. Examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin; and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{111}In or ^{99}Tc .

[0172] The disclosure provides for the detection of expression of CD80 and/or CD86 comprising contacting a biological sample (*e.g.*, cells, tissues or bodily fluids) using one or more CTLA4 proteins of the disclosure (optionally conjugated to a detectable moiety), and detecting whether or not the sample is positive for CD80- and/or CD86-expressing cells, or whether the sample has altered (*e.g.*, reduced or increased) numbers of cells expressing CD80 and/or CD86 as compared to a control sample.

[0173] Diseases that can be diagnosed using the present methods include, but are not limited to, the diseases described herein. In certain embodiments, the tissue or body fluid is peripheral blood, peripheral blood leukocytes, biopsy tissues such as breast or lymph node biopsies, and tissue.

6.10. Therapeutic Methods Using CTLA4 Proteins

6.10.1. Clinical Benefits

[0174] The CTLA4 proteins of the disclosure interact with CD80 and/or CD86 on antigen presenting cells and regulate the interaction of T-cells with CD80/CD86-positive cells. Accordingly, the proteins of the disclosure are useful for treating pathological conditions involving dysregulated T-cell interactions with CD80/CD86-positive cells, including antigen presenting cells.

[0175] As described above in Section 5.1, in certain embodiments, the variant CTLA4 polypeptides of the disclosure have different binding affinities for CD80 and CD86. In

other embodiments, the variant CTLA4 polypeptides of the disclosure have comparable binding affinities for both CD80 and CD86. CD80 and CD86 bind to T-cell surface proteins (*e.g.*, CD28 and CTLA4) and elicit different biological effects. For example, the binding of CD86 to CD28 on naive T-cells initiates T-cell responses. Thus, inhibiting or reducing CD86 binding to CD28, for example, by administering a variant CTLA4 polypeptide of the disclosure with high or neutral binding affinity for CD86, can inhibit the initiation of the T-cell response and lead to T-cell anergy. Furthermore, binding of CD80 to CTLA4 terminates the T-cell response. Therefore, inhibiting or reducing CD80 binding to CTLA4 on T-cells, for example, by administering a variant CTLA4 polypeptide of the disclosure for high or neutral binding affinity for CD80, can block the termination of responses and prolong T-cell responses.

[0176] Accordingly, in certain embodiments, variant CTLA4 polypeptides with high binding affinity for CD80 and with low binding affinity for CD86, or variant CTLA4 polypeptides with neutral binding affinity for CD80 and with low binding affinity for CD86 are useful for treating conditions requiring enhanced T-cell mediated killing of cells, such as cancer. In other embodiments, variant CTLA4 proteins with high affinity or neutral binding affinity for CD86 and low affinity for CD80, or variant CTLA4 proteins with high binding affinity for both CD80 and CD86 are useful for treating conditions resulting from enhanced T-cell mediated killing of cells, such as autoimmune diseases, or tissue, organ or cell transplant rejection.

[0177] In certain embodiments, the proteins of the disclosure are useful for treating neoplasms. The proteins of the disclosure are useful in the treatment of tumors, including cancers and benign tumors. Examples of cancer to be treated herein include, but are not limited to, melanoma, breast cancer, prostate cancer, bladder cancer and colorectal cancer. More particular examples of such cancers include squamous cell cancer, lung cancer (including small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung, and squamous carcinoma of the lung), cancer of the peritoneum, hepatocellular cancer, gastric or stomach cancer (including gastrointestinal cancer), pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma,

breast cancer, colon cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney or renal cancer, liver cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma and various types of head and neck cancer, as well as multiple myeloma, B-cell lymphoma (including low grade/follicular non-Hodgkin's lymphoma (NHL); small lymphocytic (SL) NHL; intermediate grade/follicular NHL; intermediate grade diffuse NHL; high grade immunoblastic NHL; high grade lymphoblastic NHL; high grade small non-cleaved cell NHL; bulky disease NHL; mantle cell lymphoma; AIDS-related lymphoma; and Waldenstrom's Macroglobulinemia); chronic lymphocytic leukemia (CLL); acute lymphoblastic leukemia (ALL); Hairy cell leukemia; chronic myeloblastic leukemia; and post-transplant lymphoproliferative disorder (PTLD), as well as abnormal vascular proliferation associated with phakomatoses, edema (such as that associated with brain tumors), and Meigs' syndrome.

[0178] More particularly, cancers that are amenable to treatment with the CTLA4 proteins of the disclosure include those that are CD80 and/or CD86 positive. In some embodiments, the variant proteins of the disclosure useful for cancer treatment have high affinity for CD80 and low affinity for CD86. In other embodiments, the variant proteins of the disclosure useful for cancer treatment have neutral affinity for CD80 and low affinity for CD86.

[0179] In certain aspects, the cancer treatment methods include before the step of administering to the patient a CTLA4 protein of the disclosure, a step of detecting CD80 and/or CD86 on cancer cells. Said detecting step can be accomplished by any method known in the art, including, but not limited to, an immunohistochemistry assay to measure CD80 and/or CD86 protein levels on cancer cells. In certain embodiments, immunohistochemistry assays can be performed using a labeled anti-CD80 and/or anti-CD86 antibodies.

[0180] In various embodiments, the proteins of the disclosure are useful for treating autoimmune diseases. In some embodiments, the proteins of the disclosure are useful for treating patients with an autoimmune disease who have not been previously treated for

the disease. In other embodiments, the proteins of the disclosure are useful for treating patients with an autoimmune disease who had an inadequate response to treatment with methotrexate, a disease-modifying antirheumatic drug, or an anti-TNF α antagonist. In various embodiments, the CTLA4 proteins of the disclosure are useful for treating an autoimmune disease selected from rheumatoid arthritis and juvenile idiopathic arthritis. In some embodiments, the proteins of the disclosure are useful for treating an autoimmune disease selected from ankylosing spondylitis, scleroderma, multiple sclerosis, and systemic lupus erythematosus.

[0181] More particularly, the CTLA4 proteins of the disclosure are useful for treating an autoimmune disease selected from acute disseminated encephalomyelitis (ADEM), acute necrotizing hemorrhagic leukoencephalitis, Addison's disease, agammaglobulinemia, allergic asthma, allergic rhinitis, alopecia areata, amyloidosis, ankylosing spondylitis, anti-GBM/anti-TBM nephritis, antiphospholipid syndrome (APS), autoimmune aplastic anemia, autoimmune dysautonomia, autoimmune hepatitis, autoimmune hyperlipidemia, autoimmune immunodeficiency, autoimmune inner ear disease (AIED), autoimmune myocarditis, autoimmune pancreatitis, autoimmune retinopathy, autoimmune thrombocytopenic purpura (ATP), autoimmune thyroid disease, axonal & neuronal neuropathies, Balo disease, Behcet's disease, bullous pemphigoid, cardiomyopathy, Castleman disease, celiac sprue (nontropical), Chagas disease, autoimmune conditions associated with chronic fatigue syndrome or fibromyalgia, chronic inflammatory demyelinating polyneuropathy (CIDP), chronic recurrent multifocal osteomyelitis (CRMO), Churg-Strauss syndrome, icatricial pemphigoid/benign mucosal pemphigoid, Crohn's disease, Cogans syndrome, cold agglutinin disease, congenital heart block, coxsackie myocarditis, CREST disease, essential mixed cryoglobulinemia, demyelinating neuropathies, dermatomyositis, Devic's disease (neuromyelitis optica), discoid lupus, Dressler's syndrome, endometriosis, eosinophilic fasciitis, erythema nodosum, experimental allergic encephalomyelitis, Evans syndrome, fibrosing alveolitis, giant cell arteritis (temporal arteritis), glomerulonephritis, Goodpasture's syndrome, Graves' disease, Guillain-Barre syndrome, Hashimoto's encephalitis, Hashimoto's thyroiditis,

hemolytic anemia, Henoch-Schonlein purpura, herpes gestationis, hypogammaglobulinemia, idiopathic thrombocytopenic purpura (ITP), IgA nephropathy, immunoregulatory lipoproteins, inclusion body myositis, insulin-dependent diabetes (type1), interstitial cystitis, juvenile arthritis, juvenile diabetes, Kawasaki syndrome, Lambert-Eaton syndrome, leukocytoclastic vasculitis, lichen planus, lichen sclerosus, ligneous conjunctivitis, linear IgA disease (LAD), lupus (SLE), Lyme disease, Meniere's disease, microscopic polyangiitis, mixed connective tissue disease (MCTD), Mooren's ulcer, Mucha-Habermann disease, multiple sclerosis, myasthenia gravis, myositis, narcolepsy, neuromyelitis optica (see Devic's), neutropenia, ocular cicatricial pemphigoid, optic neuritis, palindromic rheumatism, PANDAS (Pediatric Autoimmune Neuropsychiatric Disorders Associated with Streptococcus), paraneoplastic cerebellar degeneration, paroxysmal nocturnal hemoglobinuria (PNH), Parry Romberg syndrome, Parsonage-Turner syndrome, pars planitis (peripheral uveitis), pemphigus, peripheral neuropathy, perivenous encephalomyelitis, pernicious anemia, POEMS syndrome, polyarteritis nodosa, type I, II, & III autoimmune polyglandular syndromes, polymyalgia rheumatica, polymyositis, postmyocardial infarction syndrome, postpericardiotomy syndrome, progesterone dermatitis, primary biliary cirrhosis, primary sclerosing cholangitis, psoriasis, psoriatic arthritis, idiopathic pulmonary fibrosis, pyoderma gangrenosum, pure red cell aplasia, Raynauds phenomenon, reflex sympathetic dystrophy, Reiter's syndrome, relapsing polychondritis, restless legs syndrome, retroperitoneal fibrosis, rheumatic fever, rheumatoid arthritis, sarcoidosis, Schmidt syndrome, scleritis, scleroderma, Sjogren's syndrome, sperm & testicular autoimmunity, stiff person syndrome, subacute bacterial endocarditis (SBE), sympathetic ophthalmia, Takayasu's arteritis, temporal arteritis/Giant cell arteritis, thrombocytopenic purpura (TTP), Tolosa-Hunt syndrome, transverse myelitis, ulcerative colitis, undifferentiated connective tissue disease (UCTD), uveitis, vasculitis, vesiculobullous dermatosis, vitiligo, and Wegener's granulomatosis.

[0182] In certain embodiments, the variant proteins of the disclosure useful for treating an autoimmune disease have high affinity for CD86 and low affinity for CD80. In other

embodiments, the variant proteins of the disclosure useful for treating an autoimmune disease have neutral affinity for CD86 and low affinity for CD80. In other embodiments, the variant proteins of the disclosure have high affinity for both CD86 and CD80.

[0183] In various embodiments, the CTLA4 proteins of the disclosure are useful for treating rejection of cell, organ and tissue graft transplants, graft versus host disease and/or for inducing xenograft tolerance, *e.g.*, islet xenograft tolerance in patients with type 1 diabetes mellitus. In some embodiments, the variant proteins of the disclosure have high affinity for CD86 and low affinity for CD80. In other embodiments, the variant proteins of the disclosure have neutral affinity for CD86 and low affinity for CD80. In still other embodiments, the variant proteins of the disclosure have high affinity for both CD86 and CD80.

[0184] In some embodiments, the proteins of the disclosure are useful for treating infections caused by the proliferation of viruses that depend on T-cell activation. Such viruses include, but are not limited to, HTLV-1, HIV-1 and HIV2 viruses.

[0185] Accordingly, the present disclosure provides methods of treating any of the foregoing diseases in a patient in need thereof, comprising: administering to the patient a CTLA4 protein of the disclosure. Optionally, said administration is repeated, *e.g.*, after one day, two days, three days, five days, one week, two weeks, three weeks, one month, five weeks, six weeks, seven weeks, eight weeks, two months or three months. The repeated administration can be at the same dose or at a different dose. The administration can be repeated once, twice, three times, four times, five times, six times, seven times, eight times, nine times, ten times, or more. For example, according to certain dosage regimens a patient receives CTLA4 therapy for a prolonged period of time, *e.g.*, 6 months, 1 year or more. In various embodiments, periods of CTLA4 therapy are alternated with periods of no CTLA4 therapy. The amount of protein administered to the patient is in certain embodiments a therapeutically effective amount. As used herein, a “therapeutically effective” amount of a CTLA4 protein can be administered as a single dose or over the course of a therapeutic regimen, *e.g.*, over the course of a week, two

weeks, three weeks, one month, three months, six months, one year, or longer.

Exemplary therapeutic regimens are described in Section 5.8.4 below.

[0186] In certain embodiments, the CTLA4 therapy is commenced at or near the onset of disease, such as from 1 day to 6 months after onset of the disease. In some embodiments, CTLA4 therapy is commenced after the disease has progressed, such as from 6 months to 1 year, 2 years, or 3 years or more after the onset of disease. In other embodiments, CTLA4 therapy is administered during periods of disease remission. In still other embodiments, CTLA4 therapy is administered during periods of active disease. The timing of administration of CTLA4 therapy will depend upon factors known to the skilled artisan, such as the nature of the disease and the role of the CD28-CD80/CD86 costimulatory pathway in the disease being treated.

[0187] According to the present disclosure, treatment of a disease encompasses the treatment of patients already diagnosed as having any form of the disease at any clinical stage or manifestation; the delay of the onset or evolution or aggravation or deterioration of the symptoms or signs of the disease; and/or preventing and/or reducing the severity of the disease.

[0188] A “subject” or “patient” to whom the CTLA4 proteins of the disclosure is administered is preferably a mammal such as a non-primate (*e.g.*, cow, pig, horse, cat, dog, rat, *etc.*) or a primate (*e.g.*, monkey or human). In certain embodiments, the subject or patient is a human. In certain aspects, the human is an adult patient. In other aspects, the human is a pediatric patient.

6.10.2. Pharmaceutical Compositions and Routes of Administration

[0189] Compositions comprising a CTLA4 protein of the disclosure and, optionally one or more additional therapeutic agents, such as the combination therapeutic agents described in Section 5.8.3 below, are provided herein. The compositions will usually be supplied as part of a sterile, pharmaceutical composition that will normally include a

pharmaceutically acceptable carrier. This composition can be in any suitable form (depending upon the desired method of administering it to a patient).

[0190] The CTLA4 proteins of the disclosure can be administered to a patient by a variety of routes such as orally, transdermally, subcutaneously, intranasally, intravenously, intramuscularly, intraocularly, topically, intrathecally and intracerebroventricularly. The most suitable route for administration in any given case will depend on the particular protein, the subject, and the nature and severity of the disease and the physical condition of the subject.

[0191] For treatment of indications described herein, the effective dose of CTLA4 protein of the disclosure can range from about 0.1 to about 75 mg/kg per single (*e.g.*, bolus) administration, multiple administrations or continuous administration, or to achieve a serum concentration of 0.01-5000 µg/ml serum concentration per single (*e.g.*, bolus) administration, multiple administrations or continuous administration, or any effective range or value therein depending on the condition being treated, the route of administration and the age, weight and condition of the subject. In certain embodiments, *e.g.*, for the treatment of rheumatoid arthritis, each dose can range from about 0.2 mg to about 50 mg per kilogram of body weight, for example from about 0.5 mg to about 20 mg per kilogram body weight. The CTLA4 protein can be formulated as an aqueous solution and administered by infusion.

[0192] Pharmaceutical compositions can be conveniently presented in unit dose forms containing a predetermined amount of a CTLA4 protein of the disclosure per dose. Such a unit can contain for example but without limitation 0.1 mg to 5 g, for example 1 mg to 1 g, 100 mg to 500 mg, or 10 mg to 50 mg. Pharmaceutically acceptable carriers for use in the disclosure can take a wide variety of forms depending, *e.g.*, on the condition to be treated or route of administration.

[0193] Therapeutic formulations of the CTLA4 proteins of the disclosure can be prepared for storage as lyophilized formulations or aqueous solutions by mixing the protein having the desired degree of purity with optional pharmaceutically-acceptable carriers,

excipients or stabilizers typically employed in the art (all of which are referred to herein as “carriers”), i.e., buffering agents, stabilizing agents, preservatives, isotonifiers, non-ionic detergents, antioxidants, and other miscellaneous additives. See, Remington’s Pharmaceutical Sciences, 16th edition (Osol, ed. 1980). Such additives must be nontoxic to the recipients at the dosages and concentrations employed.

[0194] Buffering agents help to maintain the pH in the range which approximates physiological conditions. They can be present at concentration ranging from about 2 mM to about 50 mM. Suitable buffering agents for use with the present disclosure include both organic and inorganic acids and salts thereof such as citrate buffers (*e.g.*, monosodium citrate-disodium citrate mixture, citric acid-trisodium citrate mixture, citric acid-monosodium citrate mixture, *etc.*), succinate buffers (*e.g.*, succinic acid monosodium succinate mixture, succinic acid-sodium hydroxide mixture, succinic acid disodium succinate mixture, *etc.*), tartrate buffers (*e.g.*, tartaric acid-sodium tartrate mixture, tartaric acid-potassium tartrate mixture, tartaric acid-sodium hydroxide mixture, *etc.*), fumarate buffers (*e.g.*, fumaric acid-monosodium fumarate mixture, fumaric acid disodium fumarate mixture, monosodium fumarate-disodium fumarate mixture, *etc.*), gluconate buffers (*e.g.*, gluconic acid-sodium gluconate mixture, gluconic acid-sodium hydroxide mixture, gluconic acid-potassium gluconate mixture, *etc.*), oxalate buffer (*e.g.*, oxalic acid-sodium oxalate mixture, oxalic acid-sodium hydroxide mixture, oxalic acid-potassium oxalate mixture, *etc.*), lactate buffers (*e.g.*, lactic acid-sodium lactate mixture, lactic acid-sodium hydroxide mixture, lactic acid-potassium lactate mixture, *etc.*) and acetate buffers (*e.g.*, acetic acid-sodium acetate mixture, acetic acid-sodium hydroxide mixture, *etc.*). Additionally, phosphate buffers, histidine buffers and trimethylamine salts such as Tris can be used.

[0195] Preservatives can be added to retard microbial growth, and can be added in amounts ranging from 0.2%-1% (w/v). Suitable preservatives for use with the present disclosure include phenol, benzyl alcohol, meta-cresol, methyl paraben, propyl paraben, octadecyldimethylbenzyl ammonium chloride, benzalconium halides (*e.g.*, chloride, bromide, and iodide), hexamethonium chloride, and alkyl parabens such as methyl or

propyl paraben, catechol, resorcinol, cyclohexanol, and 3-pentanol. Isotonicifiers sometimes known as “stabilizers” can be added to ensure isotonicity of liquid compositions of the present disclosure and include polyhydric sugar alcohols, for example trihydric or higher sugar alcohols, such as glycerin, erythritol, arabitol, xylitol, sorbitol and mannitol. Stabilizers refer to a broad category of excipients which can range in function from a bulking agent to an additive which solubilizes the therapeutic agent or helps to prevent denaturation or adherence to the container wall. Typical stabilizers can be polyhydric sugar alcohols (enumerated above); amino acids such as arginine, lysine, glycine, glutamine, asparagine, histidine, alanine, ornithine, L-leucine, 2-phenylalanine, glutamic acid, threonine, *etc.*, organic sugars or sugar alcohols, such as lactose, trehalose, stachyose, mannitol, sorbitol, xylitol, ribitol, myoinositol, galactitol, glycerol and the like, including cyclitols such as inositol; polyethylene glycol; amino acid polymers; sulfur containing reducing agents, such as urea, glutathione, thioctic acid, sodium thioglycolate, thioglycerol, α -monothioglycerol and sodium thio sulfate; low molecular weight polypeptides (*e.g.*, peptides of 10 residues or fewer); proteins such as human serum albumin, bovine serum albumin, gelatin or immunoglobulins; hydrophylic polymers, such as polyvinylpyrrolidone monosaccharides, such as xylose, mannose, fructose, glucose; disaccharides such as lactose, maltose, sucrose and trisaccharides such as raffinose; and polysaccharides such as dextran. Stabilizers can be present in the range from 0.1 to 10,000 weights per part of weight active protein.

[0196] Non-ionic surfactants or detergents (also known as “wetting agents”) can be added to help solubilize the therapeutic agent as well as to protect the therapeutic protein against agitation-induced aggregation, which also permits the formulation to be exposed to shear surface stressed without causing denaturation of the protein. Suitable non-ionic surfactants include polysorbates (20, 80, *etc.*), polyoxamers (184, 188 *etc.*), Pluronic polyols, polyoxyethylene sorbitan monoethers (TWEEN®-20, TWEEN®-80, *etc.*). Nonionic surfactants can be present in a range of about 0.05 mg/ml to about 1.0 mg/ml, for example about 0.07 mg/ml to about 0.2 mg/ml.

[0197] Additional miscellaneous excipients include bulking agents (*e.g.*, starch), chelating agents (*e.g.*, EDTA), antioxidants (*e.g.*, ascorbic acid, methionine, vitamin E), and cosolvents.

[0198] The formulation herein can also contain a combination therapeutic agent in addition to the CTLA4 protein of the disclosure. Examples of suitable combination therapeutic agents are provided in Section 5.8.3 below.

[0199] The dosing schedule for administration by infusion can vary from once every six months to daily depending on a number of clinical factors, including the type of disease, severity of disease, and the patient's sensitivity to the CTLA4 protein.

[0200] The dosage of a CTLA4 protein of the disclosure to be administered will vary according to the particular antibody, the type of disease, the subject, and the severity of the disease, the physical condition of the subject, the therapeutic regimen (*e.g.*, whether a combination therapeutic agent is used), and the selected route of administration; the appropriate dosage can be readily determined by a person skilled in the art.

[0201] It will be recognized by one of skill in the art that the optimal quantity and spacing of individual dosages of a CTLA4 protein of the disclosure will be determined by the nature and extent of the condition being treated, the form, route and site of administration, and the age and condition of the particular subject being treated, and that a physician will ultimately determine appropriate dosages to be used. This dosage can be repeated as often as appropriate. If side effects develop, the amount and/or frequency of the dosage can be altered or reduced, in accordance with normal clinical practice.

6.10.3. Combination Therapy

[0202] Described below are combinatorial methods in which the CTLA4 proteins of the disclosure can be utilized. The combinatorial methods of the disclosure involve the administration of at least two agents to a patient, the first of which is a CTLA4 protein of the disclosure, and the second of which is a combination therapeutic agent. The CTLA4

protein and the combination therapeutic agent can be administered simultaneously, sequentially or separately.

[0203] The combinatorial therapy methods of the present disclosure can result in a greater than additive effect, providing therapeutic benefits where neither the CTLA4 protein nor the combination therapeutic agent is administered in an amount that is alone therapeutically effective.

[0204] In the present methods, the CTLA4 protein of the disclosure and the combination therapeutic agent can be administered concurrently, either simultaneously or successively. As used herein, the CTLA4 protein of the disclosure and the combination therapeutic agent are said to be administered successively if they are administered to the patient on the same day, for example during the same patient visit. Successive administration can occur 1, 2, 3, 4, 5, 6, 7 or 8 hours apart. In contrast, the CTLA4 antibody of the disclosure and the combination therapeutic agent are said to be administered separately if they are administered to the patient on the different days, for example, the CTLA4 protein of the disclosure and the combination therapeutic agent can be administered at a 1-day, 2-day or 3-day, one-week, 2-week or monthly intervals. In the methods of the present disclosure, administration of the CTLA4 protein of the disclosure can precede or follow administration of the combination therapeutic agent.

[0205] As a non-limiting example, the CTLA4 protein of the disclosure and combination therapeutic agent can be administered concurrently for a period of time, followed by a second period of time in which the administration of the CTLA4 protein of the disclosure and the combination therapeutic agent is alternated.

[0206] Because of the potentially synergistic effects of administering a CTLA4 protein of the disclosure and a combination therapeutic agent, such agents can be administered in amounts that, if one or both of the agents is administered alone, is/are not therapeutically effective.

[0207] In certain aspects, the combination therapeutic agent is a chemotherapeutic agent, an anti-rheumatic, an anti-inflammatory agent, a radiotherapeutic, an immunosuppressive agent, or a cytotoxic drug.

[0208] Anti-rheumatic drugs for use in the combination therapies described herein include, but are not limited to, anakinra, auranofin, azathioprine, chloroquine, D-penicillamine, gold sodium thiomalate, hydroxychloroquine, Myocrisin, sulfasalazine methotrexate, cyclophosphamide, leflunomide, and minocycline.

[0209] In certain embodiments, the anti-rheumatic drug is a TNF- α antagonist including, but not limited to, agents such as infliximab (REMICADE®; Centocor) or a derivative, analog or antigen-binding fragment thereof, adalimumab (HUMIRA®; Abbott) or a derivative, analog or antigen-binding fragment thereof, golimumab (SIMPONI™; Centocor), or a derivative, analog or antigen-binding fragment thereof, certolizumab pegol (CIMZIA®, UCB) or a derivative, analog or antigen-binding fragment thereof, etanercept (ENBREL®, Amgen) or a fragment, derivative or analog thereof, IL-10, thalidomide, xanthine derivatives such as pentoxifylline, and Bupropion (WELLBUTRIN®, GlaxoSmithKline).

[0210] For treatment of cancer, a cancer vaccine can be used in combination with a CTLA4 protein of the disclosure. Suitable cancer vaccines include those that are targeted to cancer-causing viruses, such as the hepatitis B vaccine for liver cancer and the human papilloma virus vaccine for cervical cancer (Gardasil® and Cervarix®). Other cancer vaccines that can be used in the combination with the methods of the disclosure include, but are not limited to, Provenge® (Dendreon, Seattle WA) and GVAX® for prostate cancer, OncoVex^{GM-CSF} for melanoma (BioVex, Woburn MA), Lucanix™ for non-small cell lung cancer, Stimuvax® for breast cancer, and Oncophage® for kidney cancer (Antigenics, Lexington MA). In certain embodiments, a cancer vaccine is administered prior to administration of a CTLA4 polypeptide of the disclosure.

[0211] For treatment of cancer, autoimmune diseases, or transplant rejection an anti-inflammatory agent can be used in combination with the CTLA4 proteins of the

disclosure. Suitable anti-inflammatory agents for use in the methods described herein include, but are not limited to, ibuprofen, aspirin, naproxen, diflunisal, ketoprofen, nabumetone, piroxicam, diclofenac, indomethacin, sulindac, tolmetin, etodolac, ketorolac, oxaprozin, celecoxib, acetaminophen, diphenhydramine, meperidine, dexamethasone, pentasa, mesalazine, asacol, codeine phosphate, benorylate, and fenbufen.

[0212] For treatment of autoimmune diseases or transplant rejection, an immunosuppressant can be used in combination with the CTLA4 proteins of the disclosure. Suitable immunosuppressants for use in the methods described herein include, but are not limited to, hydrocortisone, prednisone, prednisolone, methylprednisone, dexamethasone, betamethasone, triamcinolone, beclometasone, fludrocortisone acetate, deoxycorticosterone acetate, aldosterone, cyclophosphamide, nitrosoureas, platinum compounds, methotrexate, azathioprine, mercaptopurine, pyrimidine analogs, protein synthesis inhibitors, dactinomycin, anthracyclines, mitomycin C, bleomycin, mithramycin, rapamycin, cyclosporin, tacrolimus, sirolimus, mycophenolic acid, mizoribine, 15-deoxyspergualin, mycophenolate mofetil (MMF), anti-thymocyte globulin, an anti-CD20 antibody or derivative, analog or antigen binding fragment thereof, an anti-IL2 receptor antibody (daclizumab, basiliximab) or a derivative, analog or antigen binding fragment thereof, Campath-1H, an anti- $\alpha_4\beta_1$ integrin antibody or a derivative, analog or antigen binding fragment thereof, an anti-IL-15 antibody or a derivative, analog or antigen binding fragment thereof, an anti-IL-6 receptor antibody or a derivative, analog or antigen binding fragment thereof, an anti-CD3 antibody (muromonab) or a derivative, analog or antigen binding fragment thereof, an anti-MHC antibody, or a derivative, analog or antigen binding fragment thereof, an anti-CD2 antibody, or a derivative, analog or antigen binding fragment thereof, an anti-CD4 antibody, or a derivative, analog or antigen binding fragment thereof, an anti-CD11a/CD18 antibody, or a derivative, analog or antigen binding fragment thereof, an anti-CD7 antibody, or a derivative, analog or antigen binding fragment thereof, an anti-CD27 antibody, or a derivative, analog or antigen binding fragment thereof, an anti-

CD80 and/or anti-CD86 antibody (*e.g.*, ATCC HB-253, ATCC CRL-2223, ATCC CRL-2226, ATCC HB-301, ATCC HB-11341, etc), or a derivative, analog or antigen binding fragment thereof, an anti-CD40 antibody (*e.g.*, ATCC HB-9110), or a derivative, analog or antigen binding fragment thereof, or a derivative, analog or antigen binding fragment thereof, an anti-CD45 antibody, or a derivative, analog or antigen binding fragment thereof, an anti-CD58 antibody, or a derivative, analog or antigen binding fragment thereof, an anti-CD137 antibody, or a derivative, analog or antigen binding fragment thereof, an anti-ICOS antibody, or a derivative, analog or antigen binding fragment thereof, an anti-CD150 antibody, or a derivative, analog or antigen binding fragment thereof, an anti-OX40 antibody, or a derivative, analog or antigen binding fragment thereof, an anti-4-1BB antibody, or a derivative, analog or antigen binding fragment thereof, and low molecular weight adhesion antagonists such as LFA-1 antagonists, selectin antagonists and VLA-4 antagonists.

[0213] Other immunomodulatory compounds for use in the combination methods described herein include, but are not limited to, soluble gp39 (also known as CD40 ligand (CD40L), CD154, T-BAM, TRAP), soluble CD29, soluble CD40, soluble CD80 (*e.g.*, ATCC 68627), soluble CD86, soluble CD28 (*e.g.*, 68628), soluble CD56, soluble Thy-1, soluble CD3, soluble TCR, soluble VLA-4, soluble VCAM-1, soluble LECAM-1, soluble ELAM-1, soluble CD44, antibodies reactive with gp39 (*e.g.*, ATCC HB-10916, ATCC HB-12055 and ATCC HB-12056), antibodies reactive with CD28 (*e.g.*, ATCC HB-11944 or mAb 9.3 as described by Martin *et al.* (J. Clin. Immun. 4(1):18-22, 1980), antibodies reactive with LFA-1 (*e.g.*, ATCC HB-9579 and ATCC TIB-213), antibodies reactive with LFA-2, antibodies reactive with IL-12, antibodies reactive with IFN- γ , antibodies reactive with CD48, antibodies reactive with any ICAM (*e.g.*, ICAM-1 (ATCC CRL-2252), ICAM-2 and ICAM-3), antibodies reactive with CTLA4 (*e.g.*, ATCC HB-304), antibodies reactive with Thy-1, antibodies reactive with CD56, antibodies reactive with CD29, antibodies reactive with TCR, antibodies reactive with VLA-4, antibodies reactive with VCAM-1, antibodies reactive with LECAM-1, antibodies reactive with ELAM-1, antibodies reactive with CD44.

[0214] For treatment of cancers, chemotherapeutic agents can suitably be used in combination with the CTLA4 proteins of the disclosure. Chemotherapeutic agents include, but are not limited to, radioactive molecules, toxins, also referred to as cytotoxins or cytotoxic agents, which includes any agent that is detrimental to the viability of cells, agents, and liposomes or other vesicles containing chemotherapeutic compounds. Examples of suitable chemotherapeutic agents include but are not limited to 1- dehydrotestosterone, 5-fluorouracil decarbazine, 6-mercaptopurine, 6-thioguanine, actinomycin D, adriamycin, aldesleukin, an anti- $\alpha 5\beta 1$ integrin antibody, alkylating agents, allopurinol sodium, altretamine, amifostine, anastrozole, anthramycin (AMC), anti-mitotic agents, cisdichlorodiamine platinum (II) (DDP) cisplatin), diamino dichloro platinum, anthracyclines, antibiotics, antimetabolites, asparaginase, BCG live (intravesical), betamethasone sodium phosphate and betamethasone acetate, bicalutamide, bleomycin sulfate, busulfan, calcium leucouorin, calicheamicin, capecitabine, carboplatin, lomustine (CCNU), carmustine (BSNU), Chlorambucil, Cisplatin, Cladribine, Colchicin, conjugated estrogens, Cyclophosphamide, Cyclothosphamide, Cytarabine, Cytarabine, cytochalasin B, Cytosan, Dacarbazine, Dactinomycin, dactinomycin (formerly actinomycin), daunirubicin HCL, daunorubicin citrate, denileukin difitox, Dexrazoxane, Dibromomannitol, dihydroxy anthracin dione, Docetaxel, dolasetron mesylate, doxorubicin HCL, dronabinol, *E. coli* L-asparaginase, eolociximab, emetine, epoetin- α , *Erwinia* L-asparaginase, esterified estrogens, estradiol, estramustine phosphate sodium, ethidium bromide, ethinyl estradiol, etidronate, etoposide citrororum factor, etoposide phosphate, filgrastim, floxuridine, fluconazole, fludarabine phosphate, fluorouracil, flutamide, folinic acid, gemcitabine HCL, glucocorticoids, goserelin acetate, gramicidin D, granisetron HCL, hydroxyurea, idarubicin HCL, ifosfamide, interferon α -2b, irinotecan HCL, letrozole, leucovorin calcium, leuprolide acetate, levamisole HCL, lidocaine, lomustine, maytansinoid, mechlorethamine HCL, medroxyprogesterone acetate, megestrol acetate, melphalan HCL, mercaptopurine, mesna, methotrexate, methyltestosterone, mithramycin, mitomycin C, mitotane, mitoxantrone, nilutamide, octreotide acetate, ondansetron HCL, paclitaxel, pamidronate disodium, pentostatin, pilocarpine HCL, plimycin, polifeprosan 20 with carmustine implant,

porfimer sodium, procaine, procarbazine HCL, propranolol, rituximab, sargramostim, streptozotocin, tamoxifen, taxol, teniposide, teniposide, testolactone, tetracaine, thioepa chlorambucil, thioguanine, thiotepa, topotecan HCL, toremifene citrate, tretinoin, valrubicin, vinblastine sulfate, vincristine sulfate, and vinorelbine tartrate.

[0215] Sometimes, for treatment of cancers it may be beneficial to also administer one or more cytokines to the patient. In a preferred embodiment, the CTLA4 protein is co-administered with a growth inhibitory agent. Suitable dosages for the growth inhibitory agent are those presently used and may be lowered due to the combined action (synergy) of the growth inhibitory agent and CTLA4 protein.

6.10.4. Therapeutic Regimens

[0216] The present disclosure provides therapeutic regimens involving the administration of the CTLA4-Ig fusion proteins of the disclosure. The therapeutic regimen will vary depending on the patient's age, weight, and disease condition. The therapeutic regimen can continue for 2 weeks to indefinitely. In specific embodiments, the therapeutic regimen is continued for 2 weeks to 6 months, from 3 months to 5 years, from 6 months to 1 or 2 years, from 8 months to 18 months, or the like. The therapeutic regimen can be a non-variable dose regimen or a multiple-variable dose regimen.

[0217] For the dosage exemplary regimens described below, the CTLA4-Ig fusion proteins can be administered as a sterile, preservative-free solution for intravenous infusion.

[0218] For treatment of rheumatoid arthritis in adults weighing less than 60 kg, a CTLA4-Ig fusion protein of the disclosure is administered intravenously at an initial dose of 50 mg to 750 mg. In specific embodiments, the initial dose is 100-600 mg, 250-500 mg, 300-550 mg, 350-500 mg, 50-250 mg, or 400-600 mg. Following the initial dose, a CTLA4-Ig fusion protein of the disclosure is administered intravenously at 2 weeks and 4 weeks after the first infusion and every 4 weeks thereafter at a dose of 50-750 mg, such

as 100-600 mg, such as 250-500 mg, such as 300-550 mg, such as 50-250 mg or at a dose of 400-600 mg.

[0219] For treatment of rheumatoid arthritis in adults weighing between 60 kg and 100 kg, a CTLA4-Ig fusion protein of the disclosure is administered intravenously at an initial dose of 75 mg to 1000 mg. In specific embodiments, the initial dose is 100-850 mg, 250-800 mg, 300-750 mg, 400-700 mg, 75-500 mg, 500-1000 mg or 600-800 mg. Following the initial dose, a CTLA4-Ig fusion protein of the disclosure is administered intravenously at 2 weeks and 4 weeks after the first infusion and every 4 weeks thereafter at a dose of 75-900 mg, such as 100-850 mg, such as 250-800 mg, such as 300-750 mg, such as 400-700 mg, such as 75-500 mg, such as 500-1000 mg or such as 600-800 mg.

[0220] For treatment of rheumatoid arthritis in adults weight more than 100 kg, a CTLA4-Ig fusion protein of the disclosure is administered intravenously at an initial dose of 100 mg to 1500 mg. In specific embodiments, the initial dose is 250-1250 mg, 500-1100 mg, 750-1000 mg, 100-800 mg, 250-900 mg or 700-1200 mg. Following the initial dose, a CTLA4-Ig fusion protein of the disclosure is administered intravenously at 2 weeks and 4 weeks after the first infusion and every 4 weeks thereafter at a dose of 100 mg to 1500 mg, such as 250-1250 mg, such as 500-1100 mg, such as 750-1000 mg, such as 100-800 mg, such as 250-900 mg or such as 700-1200 mg.

[0221] For treatment of juvenile idiopathic arthritis in patients between the ages of 6 and 17 who weigh less than 75 kg, a CTLA4-Ig fusion protein of the disclosure is administered intravenously at an initial dose of 0.1 to 15 mg/kg. In specific embodiments, the initial dose is 0.2-12.5 mg/kg, 0.5-12 mg/kg, 1-10.5 mg/kg, 2-10 mg/kg, 3-9 mg/kg, or 4-8.5 mg/kg. Following the initial dose, a CTLA4-Ig fusion protein of the disclosure is administered intravenously at 2 weeks and 4 weeks after the first infusion and every 4 weeks thereafter at a dose of 0.1 to 15 mg/kg, such as 0.2-12.5 mg/kg, 0.5-12 mg/kg, 1-10.5 mg/kg, 2-10 mg/kg, 3-9 mg/kg, or 4-8.5 mg/kg.

[0222] For treatment of juvenile idiopathic arthritis in patients aged 6 to 17 years who weigh more than 75 kg, a CTLA4-Ig fusion protein of the disclosure is administered

intravenously at an initial dose of 75 mg to 1000 mg. In specific embodiments, the initial dose is 100-850 mg, 250-800 mg, 300-750 mg, 400-700 mg, 75-500 mg, 500-1000 or 600-800 mg. Following the initial dose, a CTLA4-Ig fusion protein of the disclosure is administered intravenously at 2 weeks and 4 weeks after the first infusion and every 4 weeks thereafter at a dose of 75-900 mg, such as 100-850 mg, such as 250-800 mg, such as 300-750 mg, such as 400-700 mg, such as 75-500 mg, such as 500-1000 mg or such as 600-800 mg. In these embodiments, the maximum does should not exceed 1000 mg.

[0223] In certain embodiments, the CTLA4-Ig fusion proteins of the disclosure are used to treat patients with rheumatoid arthritis who have had an inadequate response to methotrexate therapy or to therapy with an anti-TNF α agent (*e.g.*, etanercept (Enbrel®), infliximab (Remicade®), adalimumab (Humira®), certolizumab pegol (Cimzia®), or sTNFR-IgG (lenercept)).

6.10.5. Diagnostic and Pharmaceutical Kits

[0224] Encompassed by the present disclosure are pharmaceutical kits containing the CTLA4 proteins (including conjugates of CTLA4 proteins) of the disclosure. The pharmaceutical kit is a package comprising the CTLA4 protein of the disclosure (*e.g.*, either in lyophilized form or as an aqueous solution) and one or more of the following:

- A combination therapeutic agent, for example as described in Section 5.8.3 above;
- A device for administering the CTLA4 protein, for example a pen, needle and/or syringe; and
- Pharmaceutical grade water or buffer to resuspend the antibody if the protein is in lyophilized form.

[0225] In certain aspects, each unit dose of the CTLA4 protein is packaged separately, and a kit can contain one or more unit doses (*e.g.*, two unit doses, three unit doses, four

unit doses, five unit doses, eight unit doses, ten unit doses, or more). In a specific embodiment, the one or more unit doses are each housed in a syringe or pen.

[0226] Diagnostic kits containing the CTLA4 proteins (including protein conjugates) of the disclosure are also encompassed herein. The diagnostic kit is a package comprising the CTLA4 protein of the disclosure (*e.g.*, either in lyophilized form or as an aqueous solution) and one or more reagents useful for performing a diagnostic assay. Where the CTLA4 protein is labeled with an enzyme, the kit can include substrates and cofactors required by the enzyme (*e.g.*, a substrate precursor which provides the detectable chromophore or fluorophore). In addition, other additives can be included, such as stabilizers, buffers (*e.g.*, a block buffer or lysis buffer), and the like. In certain embodiments, the CTLA4 protein included in a diagnostic kit is immobilized on a solid surface, or a solid surface (*e.g.*, a slide) on which the protein can be immobilized is included in the kit. The relative amounts of the various reagents can be varied widely to provide for concentrations in solution of the reagents which substantially optimize the sensitivity of the assay. In a specific embodiment, the protein and one or more reagents can be provided (individually or combined) as dry powders, usually lyophilized, including excipients which on dissolution will provide a reagent solution having the appropriate concentration.

7. **EXAMPLE 1: IDENTIFICATION OF VARIANTS OF CTLA4-IG WITH AFFINITY TO CD80 AND CD86**

7.1. **Materials and Methods**

7.1.1. **Production of CD80 and CD86 proteins**

[0227] CD80 and CD86 protein were expressed as monomeric secreted fusion proteins. The extracellular domain of either CD80 or CD86 was fused with human lambda constant region containing a Cys to Ser mutation to disrupt the intermolecular disulfide bond (Akamatsu *et al.*, 2007, J. Immunol. Methods 327:40). The CD80-C λ or CD86-C λ fusion protein was expressed transiently in the culture supernatant of 293T cells. The production levels of these fusion proteins were estimated by ELISA, using goat anti-

human lambda light chain antibody (Biosource, Camarillo, CA) for capturing and horseradish peroxidase (HRP)-conjugated goat anti-human lambda chain antibody (Southern Biotech, Birmingham, AL) for detection.

7.1.2. Binding of CTLA4-Ig variants to CD80 and CD86

[0228] CD80 or CD86 fused with a C λ -HA tag was bound to AlphaLISA[®] acceptor beads conjugated with goat anti-human C λ antibody and biotinylated abatacept was bound to AlphaScreen[®] streptavidin-coated donor beads (Perkin Elmer, Waltham, MA). Abatacept was biotinylated with Sulfo-NHS-Biotin using standard methods and dialyzed in PBS. Conjugation of AlphaLISA[®] acceptor beads was performed by following the manufacturer's instructions ("AlphaLISA[®] Assay Development Guide", Perkin Elmer). The binding assay was performed in a 384-well AlphaPlate (Perkin Elmer) in assay buffer (1% BSA, 0.01% Tween20 in PBS (pH 7.1)). Each well contained 0.5 nM biotinylated abatacept, 1:4 serially diluted unlabeled CTLA4-Ig variant protein starting from 40nM, 0.078 μ g/ml CD80, and 5 μ g/ml goat anti-human C λ -conjugated acceptor beads. The plate was incubated in the dark for 1 h at room temperature. Streptavidin donor beads were subsequently added to each well at 5 μ g/ml. The plate was incubated in the dark at room temperature for an additional 30 min, after which it was read on an EnVision reader (Perkin Elmer). Data were fit using nonlinear regression with the software GRAPHPAD PRISM (GraphPad, San Diego). For the CD86 binding assays, 8nM biotinylated abatacept, 1:4 serially diluted unlabeled CTLA4-Ig variant protein starting from 100nM, 0.1 μ g/ml CD86 and 10 μ g/ml goat anti-human C λ -conjugated acceptor beads were incubated in the AlphaPlate as described above, followed by addition of 10 μ g/ml streptavidin donor beads.

7.1.3. Production Of Cell Lines Expressing Cell-Surface CD80 Or CD86

[0229] Genes encoding full-length human CD80 and CD86 were subcloned into appropriate mammalian expression vectors. Each plasmid containing cDNA of CD80 or CD86 was transfected into CHO-K1 (ATCC) cells by Lipofectamine 2000 (Invitrogen) and selected for stable transfection in F12K media (45% DMEM, 45% F12K, 10% FBS)

containing 0.5 mg/ml G418. The 1% of single clones with the highest expression of CD80 or CD86 on the cell surface were sorted by FACS and cultured to establish stable cell lines. The expression levels between two cell lines were confirmed to be roughly equivalent to each other.

7.1.4. Potency Of CTLA4-Ig Variants In The Inhibition Of IL-2 Production Of Jurkat T Cells

[0230] Jurkat cells (3.0×10^5 /well) and CHO-K1 that stably expressed CD80 or CD86 (1.0×10^4 /well) were incubated in the presence of 10 μ g/ml PHA-P with titrating amounts of abatacept or CTLA4 proteins of the disclosure. After 24 hours, supernatants were assayed using an AlphaLISA[®] Human IL-2 kit to measure the amount of secreted IL-2.

7.2. Results

[0231] A total of 27 high affinity variants and 4 neutral affinity variants for binding of either CD80 or CD86 were confirmed by AlphaLISA[®]. The CTLA4-Ig variant having the mutation K28H showed the highest affinity among 19 high affinity CTLA4-Ig variants for CD80, with a binding affinity that was 11.9-fold greater than the binding affinity of wild-type CTLA4-Ig for CD80 (Figure 2A). The CTLA4-Ig variant having the mutation A29H showed the highest affinity among 18 high affinity CTLA4-Ig variants for CD86, with a binding affinity that was 14.2-fold greater than the binding affinity of wild-type CTLA4-Ig for CD86 (Figure 2A).

[0232] The mutations A29Y and L104E are those incorporated into belatacept (LEA29, Bristol-Myers Squibb) and were re-identified as high affinity variants in the present analysis (Figure 3). Belatacept showed 22-fold and 32-fold improvement over wild-type CTLA4-Ig in binding to CD80 and CD86, respectively, in the AlphaLISA[®] assay (data not shown).

[0233] In a typical 24 hour assay without blocking agent, 2.1-3.5 ng/ml of IL-2 was produced in the culture supernatant of Jurkat T-cells stimulated by PMA and CHO-K1 cells stably expressing CD80 or CD86. In the presence of blocking agents such as CTLA4-Ig proteins or anti-CD80 or anti-CD86 antibodies, the production of IL-2 was

inhibited through blocking of the costimulatory signal. No IL-2 was produced by Jurkat cells in the absence of PHA-P or CHO-K1 negative for CD80 or CD86 expression. Similarly, no IL-2 was detected in the culture supernatant of CHO-K1 cultured in the absence of Jurkat cells (Figure 4A).

[0234] Inhibition curves of wild-type CTLA4-Ig and abatacept were found to overlap substantially when Jurkat T-cells were stimulated by PMA and CHO-K1 cells expressing either CD80 or CD86 (Figure 4B). This result indicates that wild-type CTLA4-Ig and abatacept inhibit IL-2 production by Jurkat cells to the same extent (*i.e.*, have similar potency). The average IC_{50} value of wild-type CTLA4-Ig was determined to be 1.2 nM and 17.2 nM for CD80 and CD86, respectively. Although the two amino acid mutations in belatacept as compared to wild-type CTLA4-Ig resulted in a 22-fold improvement in binding toward CD80, belatacept showed only a 2.0-fold improvement in potency for inhibition of CD80-mediated T-cell activation over wild-type CTLA4-Ig or abatacept. In contrast, the resulting 32-fold improvement in binding of CD86 in belatacept produced an 11.5-fold improvement in potency for inhibition of CD86-mediated T-cell activation.

[0235] The 7.2-fold to 11.9-fold improvement in affinity toward CD80 of the CTLA4 variants of disclosure resulted in from 1.1-fold to 2.2-fold improvement in potency for inhibition of CD80-mediated T-cell activation. In contrast, the 7.0-fold to 14.2-fold improvement in affinity toward CD86 of the CTLA4 variants of the disclosure resulted in from 2.4-fold to 6.2-fold improvement in potency for inhibition of CD86-mediated T-cell activation. The K28H and A29H CTLA4-Ig variants respectively showed the highest affinity for CD80 and CD86 as well as the highest potency for inhibition of T-cell activation. Accordingly, a mutation that confers higher affinity binding to a ligand typically results in improved potency in inhibition of T-cell activation. Likewise, a variant with neutral affinity resulted in no significant difference in biological activity (Y52F).

[0236] These results indicate that variants having higher binding affinity for CD86 as compared to wild-type protein show better potency as compared to variants having higher

binding affinity for CD80, which is similar to the results obtained for belatacept. This can be explained by the avidity effect, which has a greater impact on biological activity when the base-line binding affinity is lower. The binding affinity of wild-type CTLA4-Ig to CD80 is likely to be too high to gain further improvement through avidity. In contrast, wild-type CTLA4-Ig has a 13-fold lower affinity for CD86 than for CD80 (Collins et al, 2002, Immunity 17: 201-210), which means that the affinity of CTLA4-Ig variants for CD86 can be improved. The avidity effect can be seen in the results obtained with the CTLA4-Ig variant having the mutation L96K (Figure 4C). Although this variant showed significant reduction in CD80 binding affinity (10-fold lower as compared to wild-type CTLA4-Ig), the potency of this variant was only 2.4-fold lower than that of wild-type CTLA4-Ig due to the increased impact of avidity on biological activity of this low affinity variant.

8. EXAMPLE 2: EVALUATION OF POTENCY OF CTLA4-IG VARIANTS TO INHIBIT T-CELL PROLIFERATION

8.1. Materials and Methods: Potency of CTLA4-Ig Variants for Inhibiting T-cell Proliferative Responses *In Vitro*

[0237] The human diffuse large B cell lymphoma cell line SU-DHL-6 (ATCC CRL-2959) expresses both CD80 and CD86 on the cell surface. SU-DHL-6 cells were maintained in RPMI 1640 containing 10% FBS. Peripheral blood mononuclear cells (PBMC) were isolated from human whole blood or buffy coat by Ficoll-Paque Plus (GE Healthcare, Piscataway, NJ) density gradient centrifugation as described in the instruction manual of Leucosep Greiner Bio-One, Germany). Human peripheral CD4⁺ T cells were isolated from PBMC using EasySep Negative Selection Human CD4⁺ T cell Enrichment Kit (STEMCELL Technologies, Canada). T-cells were cultured in RPMI 1640 medium containing 10% heat-inactivated FBS, β -mercaptoethanol and 100U/ml Penicillin-Streptomycin. The resulting culture contained CD4⁺ above 90% in purity.

[0238] To set up the assays, varying concentrations of CTLA4-Ig or its variants diluted in 50 μ L of media were added to each well of round-bottom 96-well microtiter plates in triplicate. CD4⁺ T cells (1×10^5) were then mixed with freshly irradiated (10,000 rad) B

lymphoma cell line (2×10^4) in a 5:1 responder-stimulator ratio in 150 μL of culture media. The cells were added to CTLA4-Ig or variant-containing wells resulting in a final volume of 200 μL per well. The primary allogenic stimulation assays were incubated at 37°C in 5% CO_2 for 5 days. tritiated thymidine at 0.5 $\mu\text{Ci}/\text{well}$ were added for additional 18hr of culture. Cells were harvested with a cell harvester (Filtermate Omnifilter-96 Harvester, Perkin Elmer) using the manufacturer's recommended conditions and [^3H] thymidine incorporation was measured using a scintillation counter (Wallac Trilux). For secondary allogenic stimulation assays, 6-day primary allo-stimulated T cells were harvested, isolated by Ficoll-Paque Plus density gradient centrifugation and rested in complete medium for 24 hr. T cells were then restimulated for 3 days with freshly irradiated B lymphoma cells at the same ratio as above in the presence of CTLA4-Ig and its mutants. The secondary stimulation assays were incubated at 37°C for 2 days before addition of 0.5 $\mu\text{Ci}/\text{well}$ of [^3H]-thymidine for the final 18hr of culture. Cell harvesting was performed as indicated above. Cell proliferation data are analyzed with GraphPad Prism 5 software using a non-linear regression curve fit method.

[0239] To evaluate the potency of CTLA4-Ig variants for inhibiting alloantigen-stimulated T- cell proliferation, purified CD4^+ T-cells were stimulated with an allogenic B-cell line, SU-DHL-6, positive for both CD80 and CD86 (confirmed by FACS, data not shown). Inhibition curves of wild-type CTLA4-Ig and commercial abatacept closely overlap each other, indicating equivalent potency in inhibition of proliferative response in CD4^+ T-cells. All variants with improved binding to CD80 and/or CD86 showed greater inhibition of proliferative responses of CD4^+ T-cells in both primary and secondary responses. Improvement in IC_{50} was observed in a range of 1.5 to 20-fold and 1.5 to 10-fold for primary and secondary responses, respectively (Figures 5 and 6). Overall, affinity improvement to CD80 and/or CD86 inhibits primary proliferative responses of CD4^+ T-cells greater than secondary responses, reflecting the reduced dependency of memory T-cells on costimulatory molecules for secondary responses (Croft *et al.*, 1997, Crit. Rev. Immunol. 17: 89).

[0240] Among the eight variants tested, the A29H mutation resulted in the maximum potency for inhibition of both primary and secondary proliferative responses, approximately 20-fold and 10-fold, respectively. The K28H mutation was the second best in potency with approximately 12-fold and 8-fold improvement in inhibiting primary and secondary responses, respectively (Figures 5 and 6). The A29H mutation showed a 14-fold improvement in binding activity toward CD86, but only a 3.0-fold improvement in binding to CD80. On the other hand, the K28H mutant showed more balanced improvement to both ligands, being 12-fold and 9.5-fold for CD80 and CD86, respectively (Figure 2A). Since the A29H mutation resulted in the best improvement in inhibition of both primary and secondary proliferative response, increased affinity for CD86 may have more impact on potency, assuming that the binding kinetics and protein stability of the A29H and K28H mutations are equivalent.

[0241] The L96K mutation resulted in ~11-fold reduction in CD80 binding while improving CD86-binding for ~11-fold. Another example of higher CD86 binding with reduced binding toward CD80 is T51N (10-fold to CD86 and 0.25-fold to CD80). Because both variants did not show reduction in potency in inhibiting primary or secondary responses, loss of binding toward CD80 at least up to 11-fold seems to be well compensated by the improved binding to CD86. Another possible explanation is that, since CD80 is known to form dimers (Ikemuzu *et al.*, 2000, *Immunity* 12:51), loss of affinity of at least up to 11-fold may have minimal impact on the avidity provided by CD80.

[0242] In conclusion, higher affinity to either ligand results in improved potency in inhibition of proliferative response in alloantigenic stimulation, consistent with the results from 24hr assay using Jurkat and CHO cell lines expressing CD80 or CD86 (Figure 4). Both CD80 and CD86 can contribute to primary and secondary allo-responses, however, it is possible to contribute at different levels under the condition where differential levels of ligand expression and other costimulatory/adhesion molecules are involved.

9. SPECIFIC EMBODIMENTS, CITATION OF REFERENCES

[0243] All publications, patents, patent applications and other documents cited in this application are hereby incorporated by reference in their entireties for all purposes to the same extent as if each individual publication, patent, patent application or other document were individually indicated to be incorporated by reference for all purposes.

[0244] While various specific embodiments have been illustrated and described, it will be appreciated that various changes can be made without departing from the spirit and scope of the invention(s).

WHAT IS CLAIMED IS:

1. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO:1, wherein the variant polypeptide comprises one or more of the amino acid substitutions K28H, A29H, T51N, T51Y, L58G, K93Q, K93M, and L96K as compared to SEQ ID NO:1.

2. The variant CTLA4 polypeptide of claim 1, which comprises the amino acid substitution A29H.

3. The variant CTLA4 polypeptide of claim 2, which comprises the amino acid substitution K28H.

4. The variant CTLA4 polypeptide of claim 1, which comprises the amino acid substitution K28H.

5. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO:1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO:1 selected from K28H, K28T, A29H, T51Y, M53F, M53Y, L58G, L61H, L61Y, K93M and K93Q.

6. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO:1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO:1 selected from L58A, L58N, L58Q, L61A, K93V, L104H and L104Y.

7. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO:1, wherein the variant polypeptide has at least one

amino acid substitution as compared to SEQ ID NO:1 selected from T30E, M54R, G55P, E57P, L58E, L58P, L58Y, L61F and L104I.

8. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO:1, wherein the variant polypeptide includes the amino acid substitution K93I as compared to SEQ ID NO:1 .

9. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO:1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO:1 selected from L58H, L58K and D62H.

10. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO:1, wherein the variant polypeptide includes at least one amino acid substitution selected from M54W and M54Y as compared to SEQ ID NO:1 .

11. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO:1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO:1 selected from R33D and L61W.

12. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO:1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO:1 selected from A29K, T51N, M53W, L96K and L96R.

13. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to

amino acids 21 to 112 of SEQ ID NO:1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO:1 selected from G27A, Y52F, N56T and L104M.

14. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO:1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO:1 selected from P26I, P26L, P26M, P26Q, P26T, P26V, K28R, A29P, A29S, T30H, T30M, T30S, V32E, R33P, T51A, Y52H, Y52M, Y52W, M53D, M54D, M54G, M54H, M54L, G55D, G55H, G55T, N56A, N56F, N56G, N56H, N56I, N56K, N56L, N56M, N56Q, N56R, N56S, N56V, N56Y, E57A, E57D, E57H, E57K, E57M, E57N, E57Q, E57R, E57S, E57T, E57V, L58I, L58R, L58T, T59I, T59M, T59N, T59Q, T59R, T59S, T59V, L61E, L61I, L61M, L61T, L61V, D62R, D63E, D63G, D63H, D63T, K93G, V94G, V94I, E95W, P99H, P99T, P99L and Y102T.

15. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO:1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO:1 selected from P26N, G27I, G27Q, G27W, K28E, K28I, K28M, K28P, K28Q, K28V, T30I, T30L, M53E, M53L, M53N, M54A, M54Q, M54S, L58D, L58V, T59H, T59K, T59L, T59P, L61D, L61G, L61Q, L61R, D62A, D62E, D62S, D63Q, D63S and K93R.

16. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO:1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO:1 selected from P26R, G27D, G27P, A29N, T30K, E31D, E31G, E31P, E31R, E31T, V32G, V32H, V32T, R33E, R33G, R33I, R33M, R33N, R33Q, R33W, R33Y, T51E, T51G, T51I, T51V, Y52A, Y52D, Y52I, Y52K, Y52L, Y52Q, Y52R, Y52S, Y52T, M53H, M53P, M53S, G55A, G55I,

G55L, G55N, G55Q, G55R, G55Y, E57G, E57I, E57W, E57Y, T59D, T59G, T59Y, F60D, F60G, F60H, F60L, D62G, D62I, D62W, D63A, D63Y, K93D, K93H, K93N, K93P, K93W, V94A, V94D, V94H, V94N, V94P, V94R, V94T, V94W, E95G, E95I, E95K, E95P, E95Q, E95R, E95S, E95T, E95V, E95Y, L96A, L96G, L96H, L96M, L96P, L96Q, M97D, M97G, M97I, M97N, M97S, M97V, P99I, P99M, P99W, P99Y, P100H, P100L, P100T, P100V, P100W, P101L, Y102H, Y103H, Y103L, Y103P, Y103T, and L104P.

17. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO:1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO:1 selected from K28S and L61P, wherein when the lysine at position 3 in CDR-like loop 1 of said CTLA4 polypeptide is serine, the alanine at position 4 of CDR-like loop 1 is not arginine, and wherein when the leucine at position 11 in CDR-like loop 2 of said CTLA4 polypeptide is proline, the leucine at position 8 of CDR-like loop 2 is not serine.

18. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO:1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO:1 selected from G27H, G27T, K28N and M54K, wherein CDR-like loop 1 in said CTLA4 polypeptide does not consist of a CDR-like loop 1 sequence set forth in Tables 16-1 to 16-6, and wherein when the lysine at position 3 of CDR-like loop 1 is asparagine, the leucine at position 8 of CDR-like loop 2 is not serine.

19. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO:1, wherein the variant polypeptide includes the substitution G27S as compared to SEQ ID NO:1, and wherein the leucine at position 8 of CDR-like loop 2 in said CTLA4 polypeptide is not serine.

20. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO:1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO:1 selected from A29T and A29W, and wherein the leucine at position 12 of CDR-like loop 3 is not glutamic acid.

21. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO:1, wherein the variant polypeptide includes the substitution T30G as compared to SEQ ID NO:1, wherein the alanine at position 4 of CDR-like loop 1 in said CTLA4 polypeptide is not tyrosine, and wherein the leucine at position 12 of CDR-like loop 3 is not glutamic acid.

22. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO:1, wherein the variant polypeptide includes the substitution K28G as compared to SEQ ID NO:1, and wherein CDR-like loop 1 in said CTLA4 polypeptide does not consist of a CDR-like loop 1 sequence set forth in Tables 16-1 to 16-6.

23. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO:1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO:1 selected from P26H, P26K, P26S, A29V, T30A, T30D, T30N, T30Q, T30Y, M53V, M54V, G55E, N56D, L58S, T59A, D62N, and K93E, and wherein CDR-like loop 1, CDR-like loop 2 or CDR-like loop 3 in said CTLA4 polypeptide do not consist of a CDR-like loop 1, CDR-like loop 2 or CDR-like loop 3 sequence set forth in Tables 16-1 to 16-6.

24. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO:1, wherein the variant polypeptide includes the

substitution K28D as compared to SEQ ID NO:1, and wherein the alanine at position 4 in CDR-like loop 1 of said CTLA4 polypeptide is not glycine.

25. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO:1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO:1 selected from P26A, G27V, K28A, and V32I, and wherein CDR-like loop 1 or CDR-like loop 2 in said CTLA4 polypeptide do not consist of a CDR-like loop 1 or CDR-like loop 2 sequence set forth in Tables 16-1 to 16-6.

26. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 15 to 115 of SEQ ID NO:1, wherein the variant polypeptide includes the substitution A29G as compared to SEQ ID NO:1, and wherein the lysine at position 3 in CDR-like loop 1 of said CTLA4 polypeptide is not aspartic acid.

27. A variant CTLA4 polypeptide comprising an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 21 to 112 of SEQ ID NO:1, wherein the variant polypeptide has at least one amino acid substitution as compared to SEQ ID NO:1 selected from G27R, A29Q, T30R, D63K, and L104V, and wherein CDR-like loop 1 or CDR-like loop 2 in said CTLA4 polypeptide do not consist of a CDR-like loop 1 or CDR-like loop 2 sequence set forth in Tables 16-1 to 16-6.

28. The variant CTLA4 polypeptide of any one of claims 4 to 27, which further comprises the amino acid substitution A29Y as compared to SEQ ID NO:1.

29. The variant CTLA4 polypeptide of any one of claims 1 to 28, which further comprises the amino acid substitutions L104E as compared to SEQ ID NO:1.

30. The variant CTLA4 polypeptide of any one of claims 1 to 29, which comprises an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to amino acids 1 to 124 of SEQ ID NO:1.

31. The variant CTLA4 polypeptide of any one of claims 1 to 30, which comprises one or more additional mutations or combinations of mutations selected from one or more of Tables 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, and 16-1 to 16-6.

32. The variant CTLA4 polypeptide of any one of claims 1 to 30, wherein the substitutions in the CDR-like loops of said variant CTLA4 polypeptide as compared to abatacept (SEQ ID NO:6) do not comprise or consist of (a) A29K; (b) M53E; (c) L61Y; (d) L104M; (e) R33P; (f) T59I; (g) L61F; (h) a combination of two or more of A29K, M53E, L61Y, L104M, R33P, T59I and L61F; or (i) a combination of three or more of A29K, M53E, L61Y, L104M, R33P, T59I and L61F.

33. The variant CTLA4 polypeptide of any one of claims 1 to 30, wherein the substitutions in the CDR-like loops of said variant CTLA4 polypeptide as compared to abatacept (SEQ ID NO:6) do not comprise or consist of A29K.

34. The variant CTLA4 polypeptide of any one of claims 1 to 30, wherein the substitutions in the CDR-like loops of said variant CTLA4 polypeptide as compared to abatacept (SEQ ID NO:6) do not comprise or consist of M53E.

35. The variant CTLA4 polypeptide of any one of claims 1 to 30, wherein the substitutions in the CDR-like loops of said variant CTLA4 polypeptide as compared to abatacept (SEQ ID NO:6) do not comprise or consist of L61Y.

36. The variant CTLA4 polypeptide of any one of claims 1 to 30, wherein the substitutions in the CDR-like loops of said variant CTLA4 polypeptide as compared to abatacept (SEQ ID NO:6) do not comprise or consist of L104M.

37. The variant CTLA4 polypeptide of any one of claims 1 to 30, wherein the substitutions in the CDR-like loops of said variant CTLA4 polypeptide as compared to abatacept (SEQ ID NO:6) do not comprise or consist of R33P.

38. The variant CTLA4 polypeptide of any one of claims 1 to 30, wherein the substitutions in the CDR-like loops of said variant CTLA4 polypeptide as compared to abatacept (SEQ ID NO:6) do not comprise or consist of T59I.

39. The variant CTLA4 polypeptide of any one of claims 1 to 30, wherein the substitutions in the CDR-like loops of said variant CTLA4 polypeptide as compared to abatacept (SEQ ID NO:6) do not comprise or consist of L61F.

40. The variant CTLA4 polypeptide of any one of claims 1 to 30, wherein the substitutions in the CDR-like loops of said variant CTLA4 polypeptide as compared to abatacept (SEQ ID NO:6) do not comprise or consist of a combination of two or more of A29K, M53E, L61Y, L104M, R33P, T59I and L61F.

41. The variant CTLA4 polypeptide of any one of claims 1 to 30, wherein the substitutions in the CDR-like loops of said variant CTLA4 polypeptide as compared to abatacept (SEQ ID NO:6) do not comprise or consist of a combination of three or more of A29K, M53E, L61Y, L104M, R33P, T59I and L61F.

42. The variant CTLA4 polypeptide of any one of claims 1 to 41, which comprises up to 10, up to 9, up to 8, up to 7, up to 6, up to 5, up to 4 amino acid, or up to 3 or up to 2 substitutions as compared to amino acids 21 to 112 of SEQ ID NO:1.

43. The variant CTLA4 polypeptide of any one of claims 1 to 42, which comprises up to 10, up to 9, up to 8, up to 7, up to 6, up to 5, up to 4, up to 3 or up to 2 substitutions as compared to amino acids 1 to 124 of SEQ ID NO:1.

44. The variant CTLA4 polypeptide of any one of claims 1 to 27, wherein the only substitutions in the polypeptide are those recited in claims 1 to 27, respectively, as compared to amino acids 21 to 112 of SEQ ID NO:1.

45. The variant CTLA4 polypeptide of any one of claims 1 to 27, wherein the only substitutions in the polypeptide are those recited in claims 1 to 27, respectively, as compared to amino acids 1 to 124 of SEQ ID NO:1.

46. The variant CTLA4 polypeptide of any one of claims 1 to 45 which is a fusion protein.

47. The variant CTLA4 polypeptide of claim 46, wherein the fusion protein comprises a CTLA4 extracellular domain linked to an immunoglobulin constant region and optionally a signal sequence.

48. The variant CTLA4 polypeptide of claim 46 or claim 47, which comprises an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to abatacept (SEQ ID NO:6).

49. The variant CTLA4 polypeptide of claim 46, which comprises up to 10, up to 9, up to 8, up to 7, up to 6, up to 5, up to 4, up to 3 or up to 2 substitutions as compared to abatacept (SEQ ID NO:6).

50. The variant CTLA4 polypeptide of claim 49, wherein the only mutations in the polypeptide are those recited in claims 1 to 20, respectively, as compared to abatacept (SEQ ID NO:6).

51. The CTLA4 polypeptide of claim 47, wherein the CTLA4 extracellular domain and the immunoglobulin constant region are linked by way of a hinge.

52. The variant CTLA4 polypeptide of claim 51, which comprises an amino acid sequence having at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity to abatacept (SEQ ID NO:6).

53. The variant CTLA4 polypeptide of claim 52, which comprises up to 10, up to 9, up to 8, up to 7, up to 6, up to 5, up to 4, up to 3 or up to 2 substitutions as compared to abatacept (SEQ ID NO:6).

54. The variant CTLA4 polypeptide of claim 50, wherein the only mutations in the polypeptide are those recited in claims 1 to 20, respectively, as compared to abatacept (SEQ ID NO:6).

55. The CTLA4 polypeptide of any one of claims 47, 48 or 51, wherein the immunoglobulin constant region is selected from an IgG1, an IgG2, and IgG3 or an IgG4.

56. The CTLA4 protein of claim 55, wherein the immunoglobulin constant region is an IgG1.

57. The variant CTLA4 polypeptide of any one of claims 1 to 56, wherein the amino acid at the position corresponding to residue 120 in SEQ ID NO:1 is a cysteine.

58. The variant CTLA4 polypeptide of any one of claims 1 to 57, which has a binding affinity for CD80 that is less than 0.5-fold of the binding affinity for CD80 of a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:1 or SEQ ID NO:6.

59. The variant CTLA4 polypeptide of any one of claims 1 to 57, which has a binding affinity for CD80 that is from about 0.5- to about 1.5-fold greater than the binding affinity for CD80 of a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:1 or SEQ ID NO:6.

60. The variant CTLA4 polypeptide of any one of claims 1 to 57, which has a binding affinity for CD80 that is more than 1.5-fold greater than the binding affinity for CD80 of a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:1 or SEQ ID NO:6.

61. The variant CTLA4 polypeptide of any one of claims 1 to 57, which has a binding affinity for CD86 that is less than 0.5-fold of the binding affinity for CD86 of a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:1 or SEQ ID NO:6.

62. The variant CTLA4 polypeptide of any one of claims 1 to 57, which has a binding affinity for CD86 that is from about 0.5- to about 1.5-fold greater than the binding affinity for CD86 of a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:1 or SEQ ID NO:6.

63. The variant CTLA4 polypeptide of any one of claims 1 to 57, which has a binding affinity for CD86 that is more than 1.5-fold greater than the binding affinity for CD86 of a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:1 or SEQ ID NO:6.

64. The variant CTLA4 polypeptide of any one of claims 1 to 63 which is purified.

65. The variant CTLA4 polypeptide of claim 64 which is purified to at least 85%, at least 90%, at least 95% or at least 98% homogeneity.

66. A variant CTLA4 polypeptide-drug conjugate comprising a variant CTLA4 polypeptide of any one of claims 1 to 65.

67. A pharmaceutical composition comprising a CTLA4 polypeptide according to any one of claims 1 to 65 or a CTLA4 polypeptide-drug conjugate according to claim 66, and a pharmaceutically acceptable carrier.

68. A nucleic acid comprising a nucleotide sequence encoding a CTLA4 polypeptide according to any one of claims 1 to 63.

69. A vector comprising the nucleic acid of claim 68.

70. A prokaryotic host cell transformed with the vector according to claim 69.

71. A eukaryotic host cell transformed with the vector according to claim 69.

72. A eukaryotic host cell engineered to express the nucleic acid of claim 68.

73. The eukaryotic host cell of claim 72 which is a mammalian host cell.

74. A method of producing a CTLA4 polypeptide comprising (a) culturing the eukaryotic host cell of claim 72 or claim 73 and (b) recovering the CTLA4 polypeptide.

75. A method of treating cancer comprising administering to a human in need thereof a therapeutically effective amount of a CTLA4 polypeptide according to any one of claims 1-65, a CTLA4 polypeptide-drug conjugate according to claim 66, or a pharmaceutical composition according to claim 67.

76. A method of treating an autoimmune disease comprising administering to a human in need thereof a therapeutically effective amount of a CTLA4 polypeptide according to any one of claims 1-65, a CTLA4 polypeptide-drug conjugate according to claim 66, or a pharmaceutical composition according to claim 67.

77. The method according to claim 76, wherein the autoimmune disease is selected from rheumatoid arthritis and juvenile idiopathic arthritis.

78. A method of treating or preventing rejection of a cell, organ or tissue graft transplant comprising administering to a human in need thereof a therapeutically effective amount of a CTLA4 polypeptide according to any one of claims 1-65, a CTLA4 polypeptide-drug conjugate according to claim 66, or a pharmaceutical composition according to claim 67.

79. The method of any one of claims 74 to 78, further comprising prior to said administering testing for CTLA4 expression in a tissue affected by said cancer, autoimmune disease or rejection, respectively.

CDR-like Loop No.	Residue	Position in CDR-like Loop	Position in Polypeptide Chain
1 (SEQ ID NO: 2)	P	1	26
	G	2	27
	K	3	28
	A	4	29
	T	5	30
	E	6	31
	V	7	32
	R	8	33
2 (SEQ ID NO: 3)	T	1	51
	Y	2	52
	M	3	53
	M	4	54
	G	5	55
	N	6	56
	E	7	57
	L	8	58
	T	9	59
	F	10	60
	L	11	61
	D	12	62
	D	13	63
3 (SEQ ID NO: 4)	K	1	93
	V	2	94
	E	3	95
	L	4	96
	M	5	97
	Y	6	98
	P	7	99
	P	8	100
	P	9	101
	Y	10	102
	Y	11	103
	L	12	104

Table 1

WT	Position in Polypeptide Chain/Position in CDR-like Loop	High affinity substitutions for CD80 and CD86 binding	SEQ ID NO:
CDR-like Loop 1			
K	28/3	H, T	8,9
A	29/4	H	10
CDR-like Loop 2			
T	51/1	Y	11
M	53/3	F, Y	12,13
L	58/8	G	14
L	61/11	H, Y	15,16
CDR-like Loop 3			
K	93/1	M, Q	17,18

Table 2

WT	Position in Polypeptide Chain/Position in CDR-like Loop	High affinity substitutions for CD80 binding/ Neutral substitutions for CD86 binding	SEQ ID NO:
CDR-like Loop 2			
L	58/8	A, N, Q	19,21
L	61/11	A	22
CDR-like Loop 3			
K	93/1	V	23
L	104/12	H, Y	24,,25

Table 3

WT	Position in Polypeptide Chain/Position in CDR-like Loop	Candidate high affinity substitutions for CD80 binding/ Neutral substitutions for CD86 binding	SEQ ID NO:
CDR-like Loop 1			
T	30/5	E	26
CDR-like Loop 2			
M	54/4	R	27
G	55/5	P	28
E	57/7	P	29
L	58/8	E, P, Y	30, 31, 32
L	61/11	F	33
CDR-like Loop 3			
L	104/12	I	34

Table 4

WT	Position in Polypeptide Chain/Position in CDR-like Loop	High affinity substitutions for CD80 binding/ Low affinity substitutions for CD86 binding	SEQ ID NO:
CDR-like Loop 3			
K	93/1	I	35

Table 5

WT	Position in Polypeptide Chain/Position in CDR-like Loop	Candidate high affinity substitutions for CD80 binding/ Low affinity substitutions for CD86 binding	SEQ ID NO:
CDR-like Loop 2			
L	58/8	H, K	36, 37
D	62/12	H	38

Table 6

WT	Position in Polypeptide Chain/Position in CDR-like Loop	Neutral substitutions for CD80 binding/ High affinity substitutions for CD86 binding	SEQ ID NO:
CDR-like Loop 2			
M	54/4	W, Y	39, 40

Table 7

WT	Position in Polypeptide Chain/Position in CDR-like Loop	Candidate neutral substitutions for CD80 binding/ High affinity substitutions for CD86 binding	SEQ ID NO:
CDR-like Loop 1			
R	33/8	D	41
CDR-like Loop 2			
L	61/11	W	42

Table 8

WT	Position in Polypeptide Chain/Position in CDR-like Loop	Low affinity substitutions for CD80 binding/ High affinity substitutions for CD86 binding	SEQ ID NO:
CDR-like Loop 1			
A	29/4	K	43
CDR-like Loop 2			
T	51/1	N	44
M	53/3	W	45
CDR-like Loop 3			
L	96/4	K, R	46, 47

Table 9

WT	Position in Polypeptide Chain/Position in CDR-like Loop	Neutral substitutions for CD80 and CD86 binding	SEQ ID NO:
CDR-like Loop 1			
G	27/2	A	48
CDR-like Loop 2			
Y	52/2	F	49
N	56/6	T	50
CDR-like Loop 3			
L	104/12	M	51

Table 10

WT	Position in Polypeptide Chain/Position in CDR-like Loop	Candidate neutral substitutions for CD80 and CD86 binding	SEQ ID NO:
CDR-like Loop 1			
P	26/1	I, L, M, Q, T, V	52, 53, 54, 55, 56, 57
K	28/3	R	58
A	29/4	P, S	59, 60
T	30/5	H, M, S	61, 63
V	32/7	E	64
R	33/8	P	65
CDR-like Loop 2			
T	51/1	A	66
Y	52/2	H, M, W	67, 68, 69
M	53/3	D	70
M	54/4	D, G, H, L	71, 72, 73, 74
G	55/5	D, H, T	75, 76, 77
N	56/6	A, F, G, H, I, K, L, M, Q, R, S, V, Y	78 to 90, respectively
E	57/7	A, D, H, K, M, N, Q, R, S, T, V	91 to 101, respectively
L	58/8	I, R, T	102, 103, 104
T	59/9	I, M, N, Q, R, S, V	105 to 111, respectively
L	61/11	E, I, M, T, V	112, 113, 114, 115, 116
D	62/12	R	117
D	63/13	E, G, H, T	118, 119, 120, 121
CDR-like Loop 3			
K	93/1	G	122
V	94/2	G, I	123, 124
E	95/3	W	125
P	99/7	H, T, L	126, 127, 128
Y	102/10	T	129

Table 11

WT	Position in Polypeptide Chain/Position in CDR-like Loop	Neutral substitutions for CD80 binding/ low affinity substitutions for CD86 binding	SEQ ID NO:
CDR-like Loop 1			
K	28/3	Y	130

Table 12

WT	Position in Polypeptide Chain/Position in CDR-like Loop	Candidate neutral substitutions for CD80 binding/ low affinity substitutions for CD86 binding	SEQ ID NO:
CDR-like Loop 1			
P	26/1	N	131
G	27/2	I, Q, W	132, 133, 134
K	28/3	E, I, M, P, Q, V	135 to 140, respectively
T	30/5	I, L	141, 142
CDR-like Loop 2			
M	53/3	E, L, N	143, 144, 145
M	54/4	A, Q, S	146, 147, 148
L	58/8	D, V	149, 150
T	59/9	H, K, L, P	151, 152, 153, 154
L	61/11	D, G, Q, R	155, 156, 157, 158
D	62/12	A, E, S	159, 160, 161
D	63/13	Q, S	162, 163
CDR-like Loop 3			
K	93/1	R	164

Table 13

WT	Position in Polypeptide Chain/Position in CDR-like Loop	Candidate low affinity substitutions for CD80 binding/ Neutral substitutions for CD86 binding	SEQ ID NO:
CDR-like Loop 1			
P	26/1	R	165
G	27/2	D, P	166, 167
A	29/4	N	168
T	30/5	K	169
E	31/6	D, G, P, R, T	170, 171, 172, 173, 174
V	32/7	G, H, T	175, 176, 177
R	33/8	E, G, I, M, N, Q, W, Y	178 to 185, respectively
CDR-like Loop 2			
T	51/1	E, G, I, V	186, 187, 188, 189
Y	52/2	A, D, I, K, L, Q, R, S, T	190 to 198, respectively
M	53/3	H, P, S	199, 200, 201
G	55/5	A, I, L, N, Q, R, Y	202 to 208, respectively
E	57/7	G, I, W, Y	209, 210, 211, 212
T	59/9	D, G, Y	213, 214, 215
F	60/10	D, G, H, L	216, 217, 218, 219
D	62/12	G, I, W	220, 221, 222
D	63/13	A, Y	223, 224
CDR-like Loop 3			
K	93/1	D, H, N, P, W	225, 226, 227, 228, 229
V	94/2	A, D, H, N, P, R, T, W	230 to 237, respectively
E	95/3	G, I, K, P, Q, R, S, T, V, Y	238 to 247, respectively
L	96/4	A, G, H, M, P, Q	248 to 253, respectively
M	97/5	D, G, I, N, S, V	254 to 259, respectively
P	99/7	I, M, W, Y	260, 261, 262, 263
P	100/8	H, L, T, V, W	264, 265, 266, 267, 268
P	101/9	L	269
Y	102/10	H	270
Y	103/11	H, L, P, T	271, 272, 273, 274
L	104/12	P	275

Table 14

Row #	WT	Position in Polypeptide Chain/Position in CDR-like Loop	Substitutions	SEQ ID NO:
CDR-like Loop 3				
1	L	104/12	E	276
CDR-like Loop 1				
2	G	27/2	H, T	277, 278
3	K	28/3	G, N, S	279, 280, 281
CDR-like Loop 2				
4	M	54/4	K	282
5	L	61/11	P	283
CDR-like Loop 1				
6	G	27/2	S	284
CDR-like Loop 1				
7	A	29/4	T, W, Y	285, 286, 287
CDR-like Loop 2				
8	T	51/1	S	288
CDR-like Loop 1				
9	T	30/5	G	289
CDR-like Loop 1				
10	P	26/1	H, K, S	290, 291, 292
11	A	29/4	G, V	293, 294
12	T	30/5	A, D, N, Q, Y	295, 296, 297, 298, 299
CDR-like Loop 2				
13	M	53/3	V, I	300-301
14	M	54/4	V	302
15	G	55/5	E	303
16	N	56/6	D	304
17	L	58/8	S	305
18	T	59/9	A	306
19	D	62/12	N	307
CDR-like Loop 3				
20	K	93/1	E	308
21	Y	98/6	I	309
22	L	104/12	Q, W	310-311

Table 15

Row #	WT	Position in Polypeptide Chain/Position in CDR-like Loop	Substitutions	SEQ ID NO:
CDR-like Loop 1				
23	P	26/1	A	312
24	G	27/2	V	313
25	K	28/3	A, D	314-315
26	V	32/7	I	316
CDR-like Loop 1				
27	G	27/2	R	317
28	A	29/4	Q	318
29	T	30/5	R	319
CDR-like Loop 2				
30	D	63/13	K	320
CDR-like Loop 3				
31	K	93/1	S	321
32	Y	98/6	P	322
33	P	100/8	A	323
34	L	104/12	D, S, V	324, 325, 326

Table 15, continued

SEQ ID NO:	26	27	28	29	30	31	32	33	SEQ ID NO:	51	52	53	54	55	56	57	58	59	60	61	62	63	SEQ ID NO:	83	84	85	86	87	88	89	90	91	92	93	94				
	P	G	K	A	T	E	V	R	3	T	Y	M	M	G	N	E	L	T	F	L	D	D	4	K	V	E	L	M	Y	P	P	P	Y	Y	L				
327						S			3														4																
328								S	3														4																
2									331	S													4																
2									3														333	S															
2									3														334					P											
2									3														335												P				
2									3														336	A		A													
2									3														337				A												
2									3														338					A											
2									3														339							A									
2									3														340								A								
2									3														341										A						
2									3														342												A				
2									3														343				A	A	A	A	A	A	A	A					
329			A				A	A	3														4																
2									332			I											4																
330				Y					3														344															E	
2									3														345						F										

Table 16-1

SEQ ID NO:	26	27	28	29	30	31	32	33	SEQ ID NO:	51	52	53	54	55	56	57	58	59	60	61	62	63	SEQ ID NO:	93	94	95	96	97	98	99	100	101	102	103	104		
2	P	G	K	A	T	E	V	R	3	T	Y	M	M	G	N	E	L	T	F	L	D	D	4	K	V	E	L	M	Y	P	P	P	Y	Y	L		
2									3														355													E	
2									3														356														S
2									3														357														T
2									3														358														A
2									3														359														W
2									3														360														Q
2									3														361														K
2									3														362														R
2									3														363														G
2									3														364														D
346					G				3														365														E
347					N				3														365														E
348				Y					3														365														E
349				L					3														365														E
350				W					3														365														E
351				T					3														365														E
352	K	R	G	V	Q				3														4														
353	Y	T	G	Y	G				3														4														
354	Y	R	N	Q	Q				3														4														

Table 16-2

SEQ ID NO:	26	27	28	29	30	31	32	33	SEQ ID NO:	51	52	53	54	55	56	57	58	59	60	61	62	63	SEQ ID NO:	93	94	95	96	97	98	99	100	101	102	103	104			
2	P	G	K	A	T	E	V	R	3	T	Y	M	H	G	N	E	L	T	F	L	D	D	4	K	V	E	L	M	Y	P	P	P	Y	Y	L			
366	P	Y	D	G	Q				3														4															
367	H	V	S	R	R				3														4															
2									3														368				A											
2									3														369					A										
2									3														370						A									
2									3														371							A								
2									3														372								A							
2									3														373									A						
2									3														374					D										
2									3														375					E										
2									3														376					F										
2									3														377					G										
2									3														378					H										
2									3														379					I										
2									3														380					K										
2									3														381					L										
2									3														382					M										
2									3														383					N										
2									3														384					P										

Table 16-3

SEQ ID NO:	26	27	28	29	30	31	32	33	SEQ ID NO:	51	52	53	54	55	56	57	58	59	60	61	62	63	SEQ ID NO:	93	94	95	96	97	98	99	100	101	102	103	104	
2	P	G	K	A	T	E	V	R	3	T	Y	M	M	G	N	E	L	T	F	L	D	D	4	K	V	E	L	M	Y	P	P	P	Y	Y	L	
2									3														401					Q								
2									3														402					R								
2									3														403					S								
2									3														404					T								
2									3														405					V								
2									3														406					W								
385			Y						3														4													
2									392			T											4													
386	A			A					393		T	V	E	D									47				L								V	
387	S			D					394			V	E	D									408													V
388	S		N	A	K	F			395		T	V	E					A		N		409													A	
389				Y					396			T											4													
390	S		N	A					397		T	V	E	D			A						408													V
390	S		N	A					398		T	V	E				A						409													A
2									399		V					S							410	E												
2									400							S							410	E												
391	S								400							S							410	E												

Table 16-4

SEQ ID NO.	26	27	28	29	30	31	32	33	SEQ ID NO.	51	52	53	54	55	56	57	58	59	60	61	62	63	SEQ ID NO.	93	94	95	96	97	98	99	100	101	102	103	104			
2	P	G	K	A	T	E	V	R	3	T	Y	M	M	G	N	E	L	T	F	L	D	D	4	K	V	E	L	M	Y	P	P	P	Y	Y	L			
2									414							S			P			423	E															
411			N						415							S						423	E															
2									416						D							4																
412				N					417					E								4																
412				N					418				K	E								4																
412				N					419				K	E	D							4																
412				N					420				V	E	D							4																
412				N					421				K		D							4																
412				N					421				K		D							424															E	
412				N					422				K									4																
412				N					422				K									424															E	
413				N		I			422				K									4																
413				N		I			422				K									424																E
413				N		I			419				K	E	D							4																
413				N		I			418				K	E								4																
413				N		I			421				K		D							4																

Table 16-5

SEQ ID NO:	26	27	28	29	30	31	32	33	SEQ ID NO:	51	52	53	54	55	56	57	58	59	60	61	62	63	SEQ ID NO:	93	94	95	96	97	98	99	100	101	102	103	104		
2	P	G	K	A	T	E	V	R	3	T	Y	M	M	G	N	E	L	T	F	L	D	D	4	K	V	E	L	M	Y	P	P	P	Y	Y	L		
425					N		I		437				K		D								449													E	
425					N		I		438						D								4														
426							I		438						D								4														
426							I		437				K		D								4														
427	H						I		439					E	D								4														
427	H						I		437				K		D								4														
428					D		I		440				E		D								4														
429	H				D		I		439					E	D								4														
430	H				N		I		437				K		D								4														
431	H				N				439					E	D								4														
431	H				N				441				V	E	D								4														
432	H	N			A		I		442				K	E	D								4														
433	H	N			D		I		443				E	E	D								4														
433	H	N			D		I		444				V	E	D							K	4														
2									445											K			4														
2									3														450			F											
2									3														449														E
434					I				3														4														
435								F	3														4														
2									446	C													4														
2									447	K													4														
2									3														451			M											
436					Y				448											Y			449													E	

Table 16-6

	1	2	3	4
123456789	0123456789	0123456789	0123456789	0123456789
MHVAQPAVV	LASSRGIASF	VCEYAS <u>PGKA</u>	<u>TEVR</u> VTVLRQ	ADSQVTEVCA
5	6	7	8	9
0123456789	0123456789	0123456789	0123456789	0123456789
<u>ATYMMGNELT</u>	<u>FLDD</u> SICTGT	SSGNQVNLT <u>I</u>	QGLRAMDTGL	YICK <u>VELMYP</u>
1	1	1		
0	1	2		
0123456789	0123456789	01234		
<u>PPYYL</u> GIGNG	TQIYVIDPEP	CPDSD		

FIGURE 1A

CDR-like loop No.	Sequence	SEQ ID NO.
1	PGKATEVR	2
2	TYMMGNELTFLDD	3
3	KVELMYPPPYL	4

FIGURE 1B

		1	2	3	4
	123456789	0123456789	0123456789	0123456789	0123456789
hCTLA-4	MHVAQPAVV	LASSRGIASF	VCEYASPGKA	<u>TEVRVTVLRQ</u>	ADSQVTEVCA
Abatacept	MHVAQPAVV	LASSRGIASF	VCEYASPGKA	<u>TEVRVTVLRQ</u>	ADSQVTEVCA
	5	6	7	8	9
	0123456789	0123456789	0123456789	0123456789	0123456789
hCTLA-4	<u>ATYMMGNELT</u>	<u>FLDDSICTGT</u>	SSGNQVNLT	QGLRAMDTGL	YICKVELMYP
Abatacept	<u>ATYMMGNELT</u>	<u>FLDDSICTGT</u>	SSGNQVNLT	QGLRAMDTGL	YICKVELMYP
	1	1	1	1	1
	0	1	2	3	4
	0123456789	0123456789	0123456789	0123456789	0123456789
hCTLA-4	<u>PPYYLGIGNG</u>	TQIYVIDPEP	CPDSDFLW	LAAVSSGLFF	YSFLLTAVSL
Abatacept	<u>PPYYLGIGNG</u>	TQIYVIDPEP	CPDSDQEPKS	<u>SDKTHTSPPS</u>	<u>PAPELLGGSS</u>
Human Fcγ1			VEPKS	CDKTHTCPPC	PAPELLGGPS
	1	1	1	1	1
	5	6	7	8	9
	0123456789	0123456789	0123456789	0123456789	0123456789
hCTLA-4	SKMLKKRSPL	TTGVYVKMPP	TEPECEKQFQ	PYFIPIN	
Abatacept	<u>VFLFPPKPKD</u>	<u>TLMISRTPEV</u>	<u>TCVVVDVSHE</u>	<u>DPEVKFNWYV</u>	<u>DGVEVHNAKT</u>
Human Fcγ1	<u>VFLFPPKPKD</u>	<u>TLMISRTPEV</u>	<u>TCVVVDVSHE</u>	<u>DPEVKFNWYV</u>	<u>DGVEVHNAKT</u>
	2	2	2	2	2
	0	1	2	3	4
	0123456789	0123456789	0123456789	0123456789	0123456789
Abatacept	<u>KPREEQYNST</u>	<u>YRVVSVLTVL</u>	<u>HQDWLNGKEY</u>	<u>KCKVSNKALP</u>	<u>APIEKTISKA</u>
Human Fcγ1	<u>KPREEQYNST</u>	<u>YRVVSVLTVL</u>	<u>HQDWLNGKEY</u>	<u>KCKVSNKALP</u>	<u>APIEKTISKA</u>
	2	2	2	2	2
	5	6	7	8	9
	0123456789	0123456789	0123456789	0123456789	0123456789
Abatacept	<u>KGQPREPQVY</u>	<u>TLPPSRDEL</u>	<u>KNQVSLTCLV</u>	<u>KGFYPSDIAV</u>	<u>EWESNGQPEN</u>
Human Fcγ1	<u>KGQPREPQVY</u>	<u>TLPPSRDEL</u>	<u>KNQVSLTCLV</u>	<u>KGFYPSDIAV</u>	<u>EWESNGQPEN</u>
	3	3	3	3	3
	0	1	2	3	4
	0123456789	0123456789	0123456789	0123456789	0123456789
Abatacept	<u>NYKTTPPVLD</u>	<u>SDGSFFLYSK</u>	<u>LTVDKSRWQQ</u>	<u>GNVFSCSVMH</u>	<u>EALHNHYTQK</u>
Human Fcγ1	<u>NYKTTPPVLD</u>	<u>SDGSFFLYSK</u>	<u>LTVDKSRWQQ</u>	<u>GNVFSCSVMH</u>	<u>EALHNHYTQK</u>
	3				
	5				
	01234567				
Abatacept	<u>SLSLSPGK</u>				
Human Fcγ1	<u>SLSLSPGK</u>				

FIGURE 1C

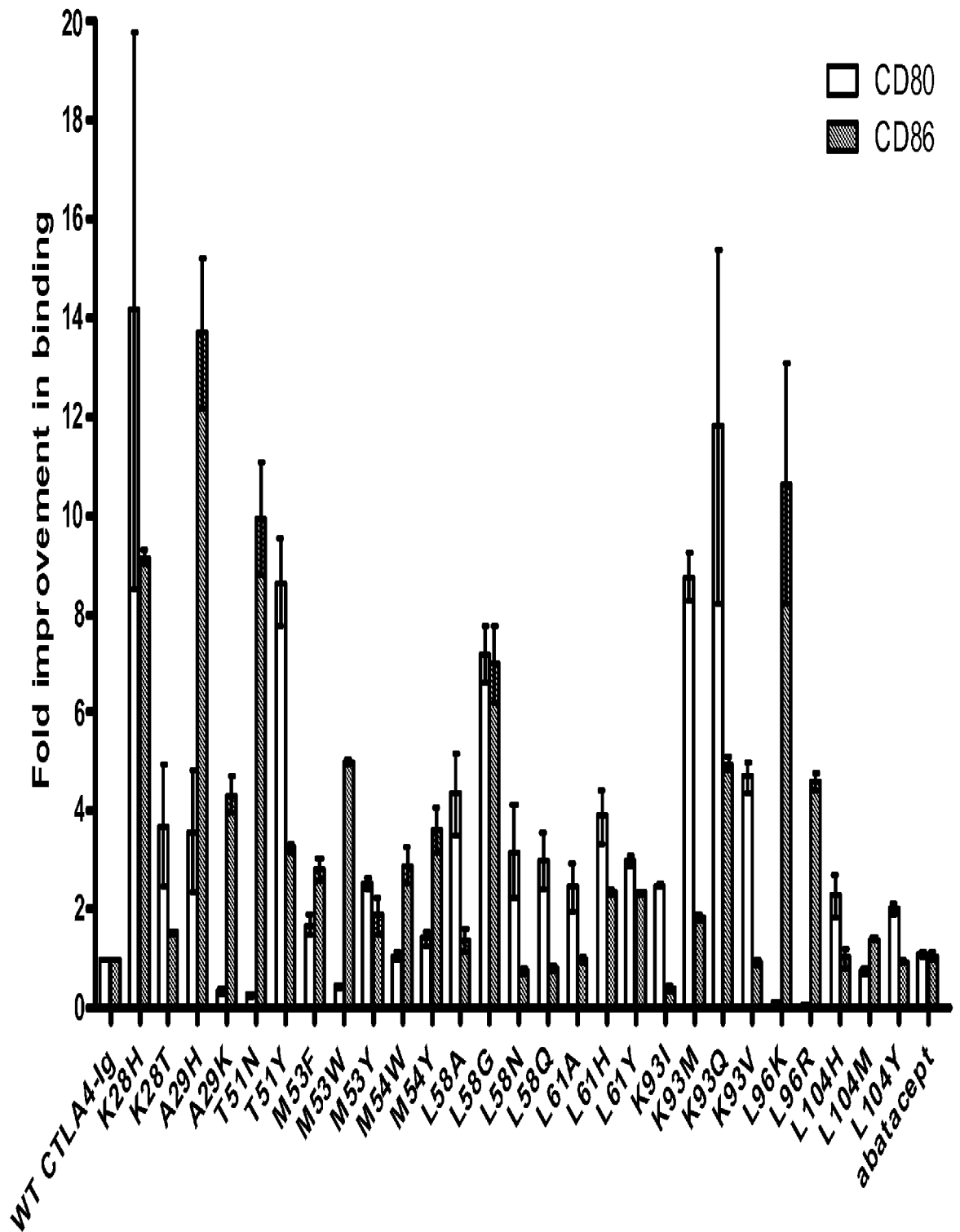


Figure 2A

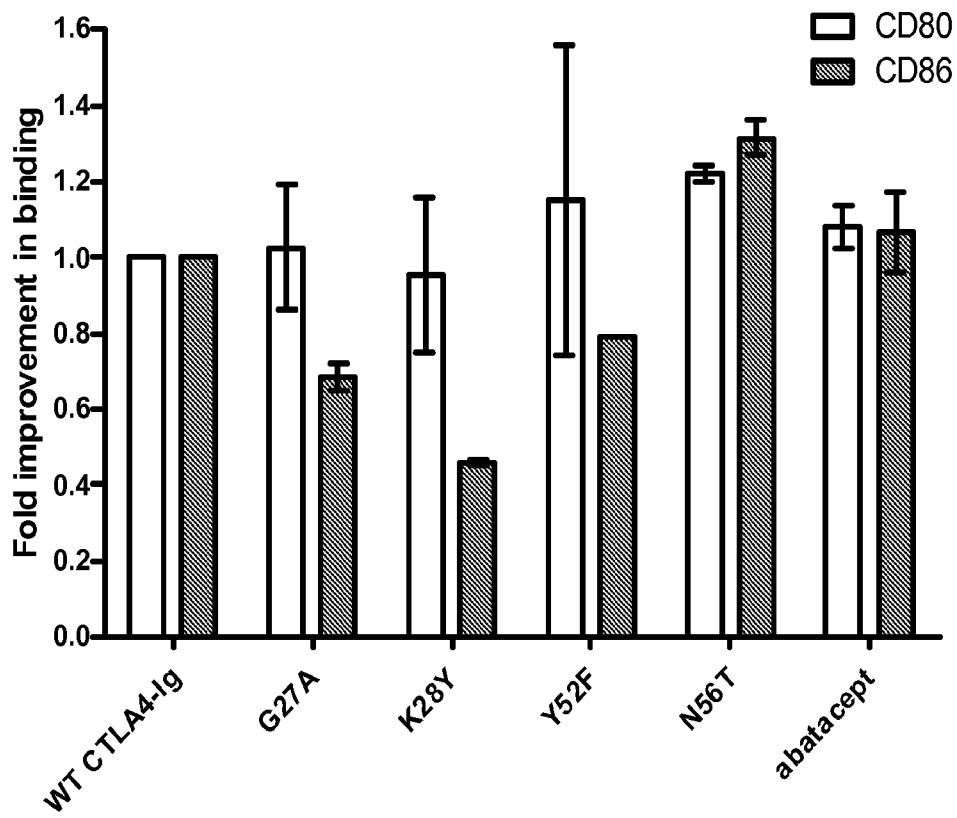


Figure 2B

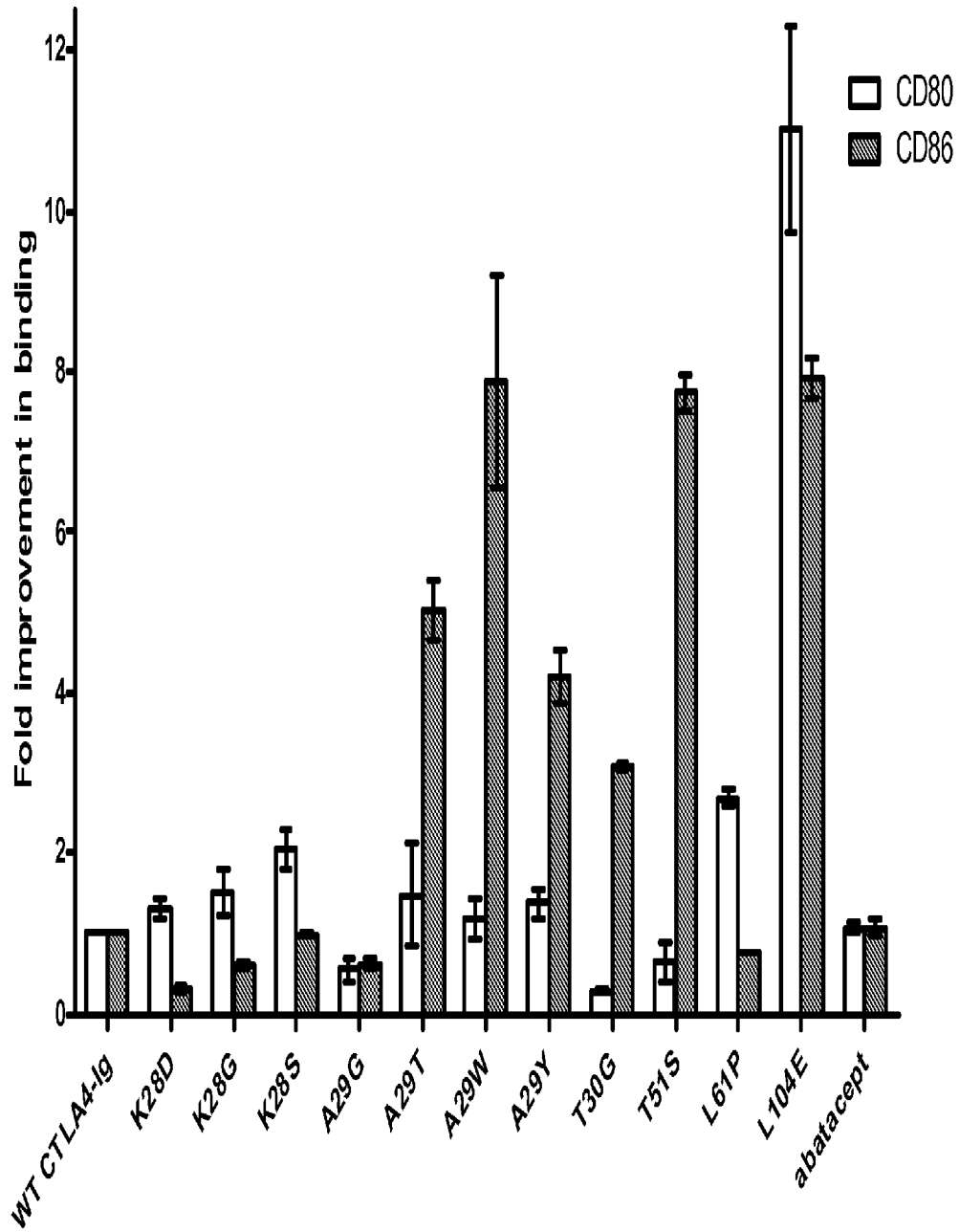


Figure 3

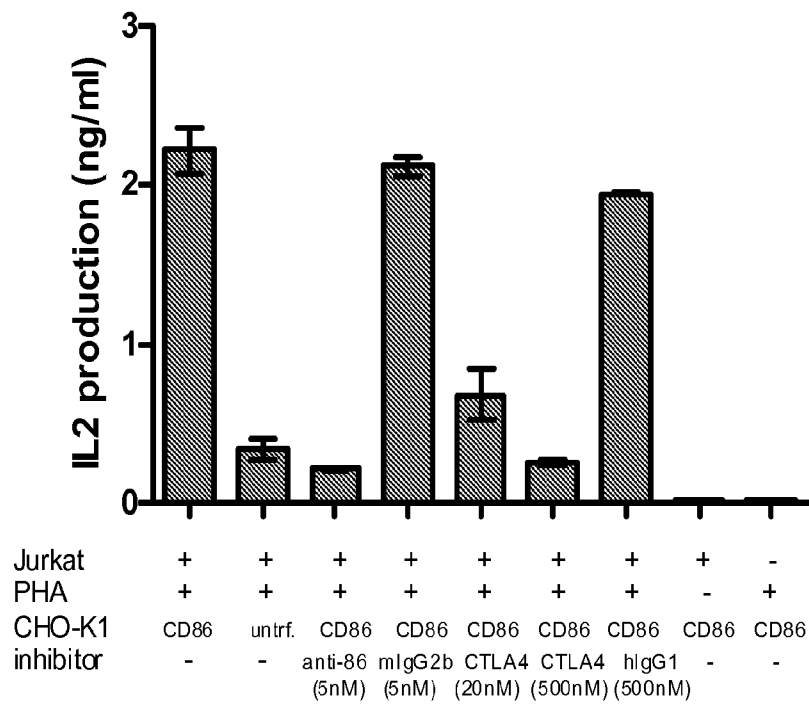
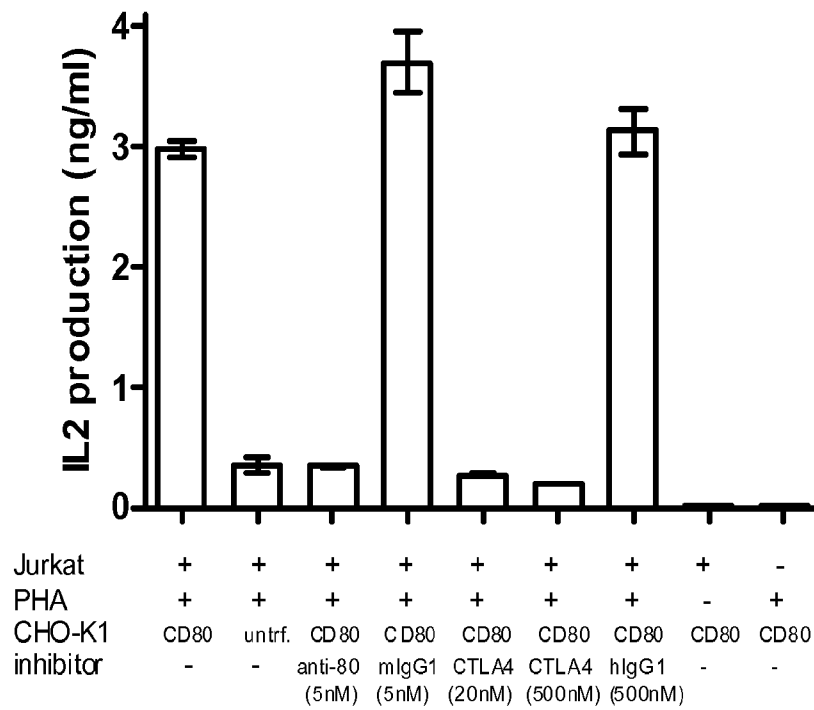


Figure 4A

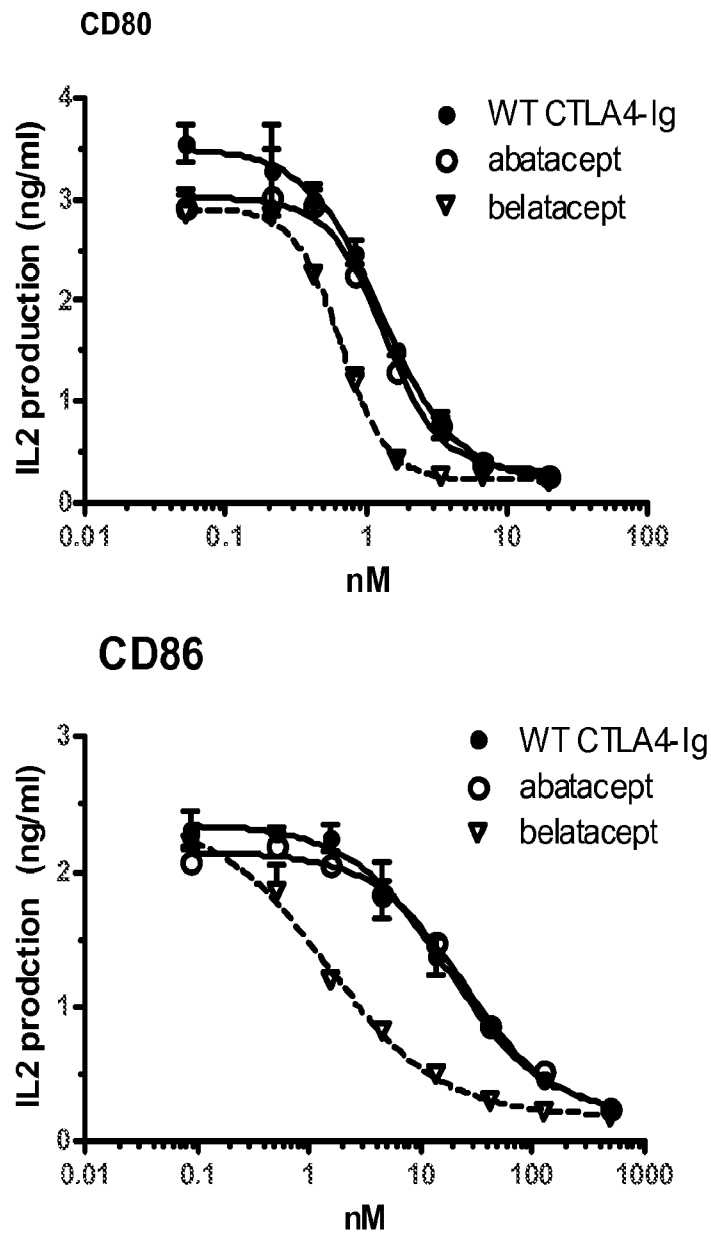


Figure 4B

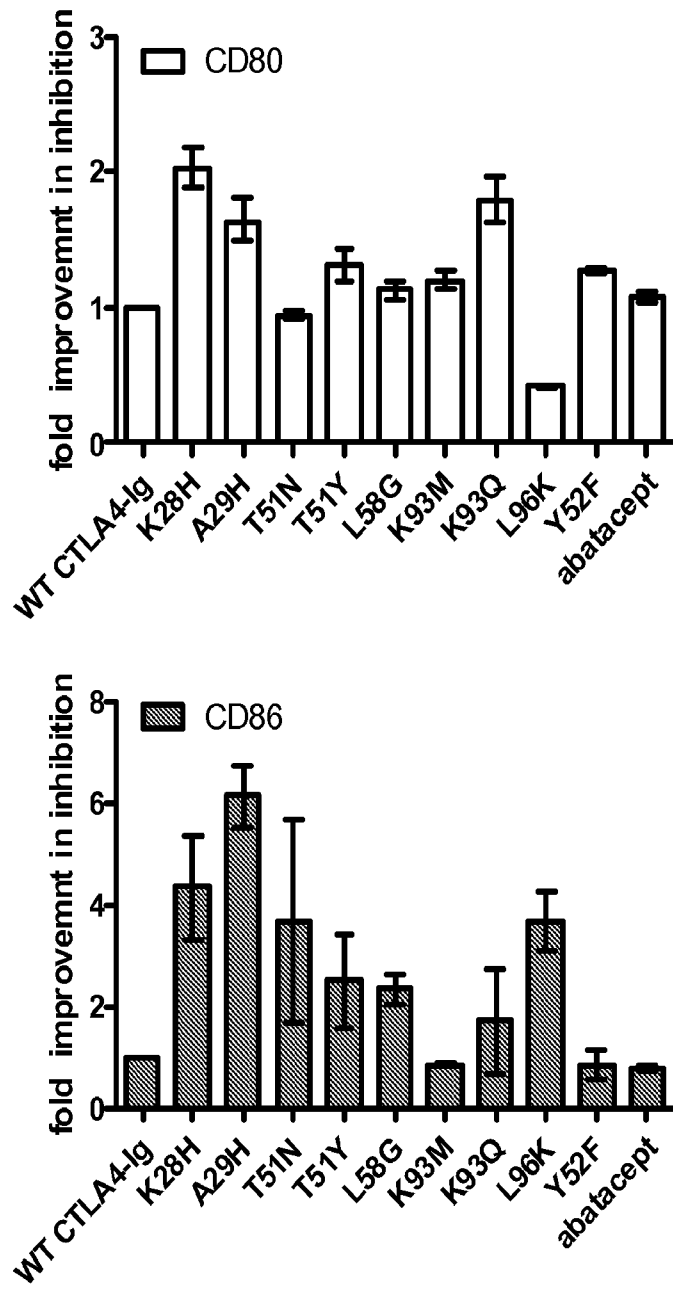


Figure 4C

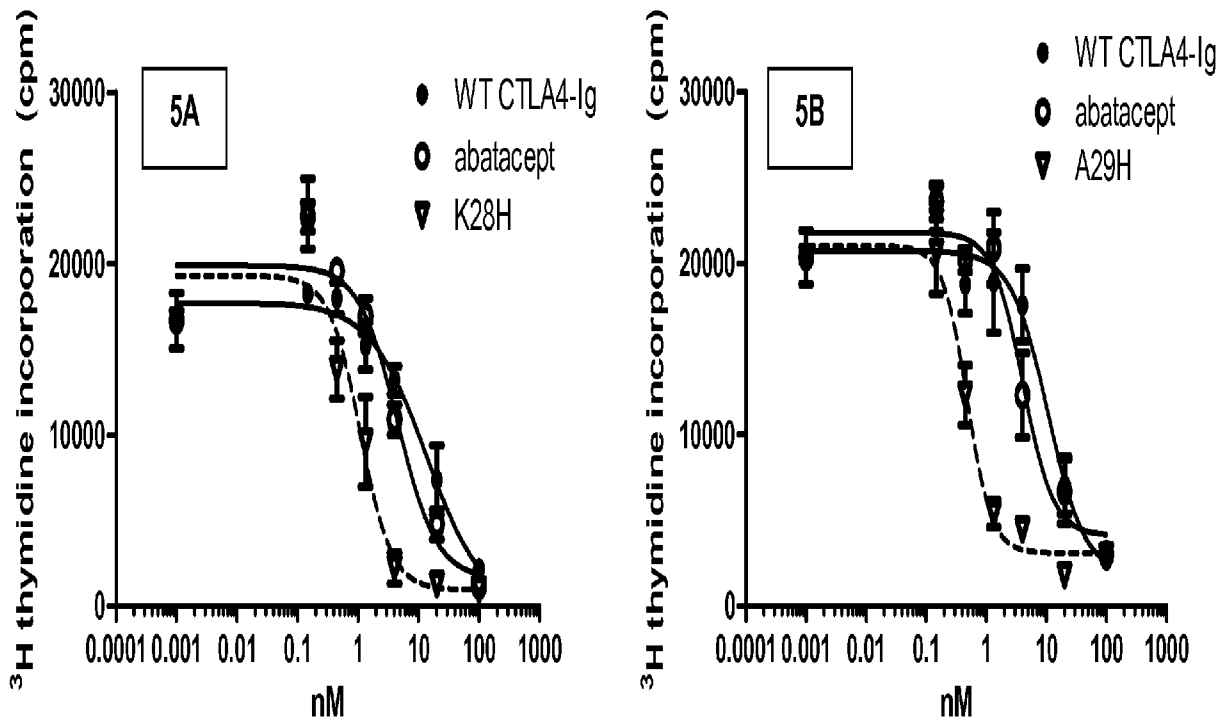


Figure 5

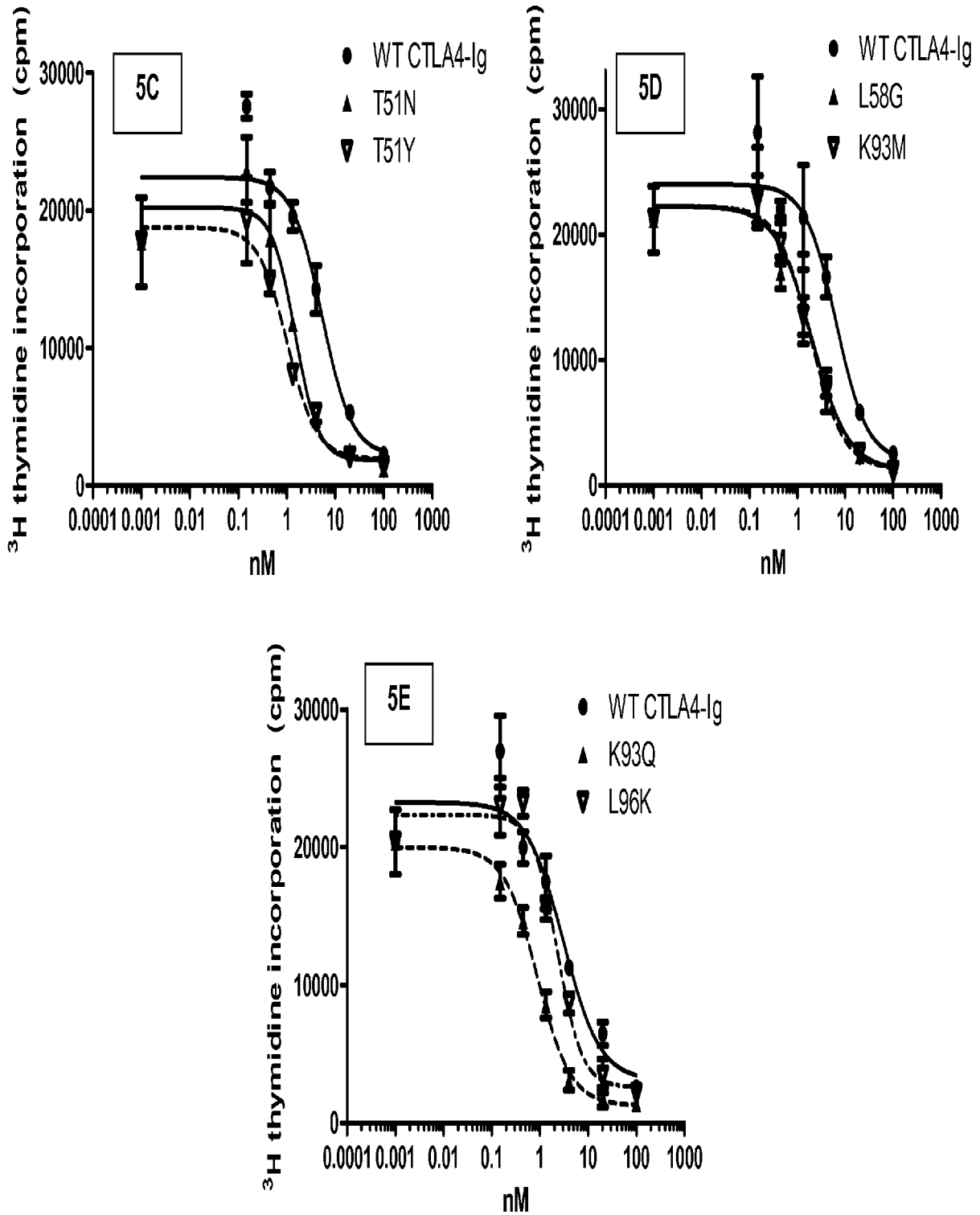


Figure 5, continued

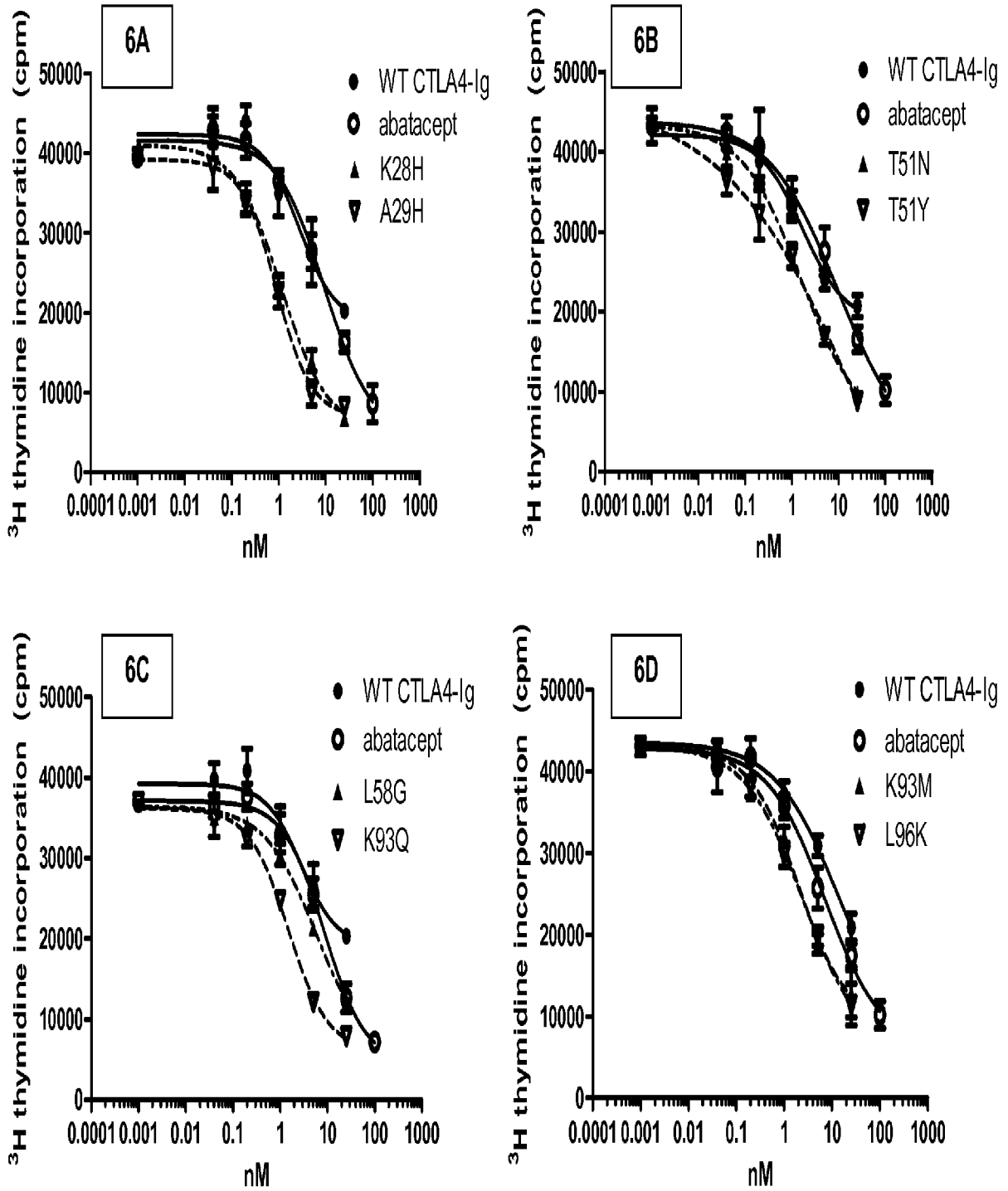


Figure 6