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DESCRIPTION

CROSS-REFERENCE TO RELATED APPLICATION

[0001] The present application claims the benefit of U.S. Provisional Application No. 61/931,363, filed January 24, 2014.

GOVERNMENT SUPPORT

[0002] This invention was made with government support under grant numbers R01 AI056152 and R01 NS051245 awarded by the National Institutes of Health. The government has certain rights in the invention.

BACKGROUND OF THE INVENTION

[0003] Systemic lupus erythematosus (SLE) is a multi-organ autoimmune disease with varied clinical manifestations, ranging from cutaneous pathologies to life threatening renal disease (reviewed in Tsokos 2011). Although auto-antibodies are critical to the pathogenesis of SLE, abnormal CD4⁺ T cell responses make a key contribution, as CD4⁺ T cell depletion in lupus-prone mouse models results in reduced anti-dsDNA IgG autoantibody production and prolonged survival (Wofsy *et al.* 1985; Santoro *et al.* 1988). Notably, although it is well accepted that dysregulated T lymphocyte effector functions are key to lupus onset and progression, how lupus-promoting T lymphocytes evade peripheral tolerance mechanisms is less well understood.

[0004] As a mechanism to maintain tolerance to ubiquitous self-antigens, naive T lymphocytes typically require both TCR stimulation and co-stimulatory signals in order to obtain an activation threshold sufficient for clonal expansion and elaboration of effector functions (reviewed in Iannone and Lapadula 2012). Activation of the CD28 pathway is a critical naive T lymphocyte co-stimulatory pathway, as it is typically responsible for the surface expression of the high affinity IL2R alpha chain (CD25) and the production of IL2, which are requisites for clonal expansion (Mondino and Jenkins 1994). Interactions between the TCR and antigen- MHC complexes, in the absence of co-stimulation, typically result in functional inactivation of naive T lymphocyte clones and inhibition of a sustained immune response (reviewed in Tivol *et al.* 1996). Significantly, CD4⁺ T lymphocytes obtained from SLE patients and murine disease models intrinsically possess a lower threshold of activation (Stekman *et al.* 1991; Desai-Mehta *et al.* 1996; Mohan *et al.* 1999; Vratsanos *et al.* 2001; Bouzazhah *et al.* 2003). Although it is known that lupus-promoting CD4⁺ T lymphocytes possess a lower activation threshold, mechanistic insight into this pathogenic process is limited. Moreover, the therapeutic efficacy of treatment strategies, which target CD4⁺ cell activation defects, remains inconclusive (Iannone and Lapadula 2012). A lower threshold of CD4⁺ T lymphocyte activation is compounded by the observation that CD4⁺ T cells in lupus have a preferential bias toward excessive type I and type II (IFN γ) interferon signaling (Takahashi *et al.* 1996; Balomenos *et al.* 1998). Notably suppressor of cytokine signaling-1 (SOCS1) critically regulates IFN γ (the sole type II interferon) (reviewed in Knosp and Johnston 2012) and type I

interferon signaling (Piganis *et al.* 2011). SOCS1 is a member of a cytokine inducible family of intracellular proteins that is essential for the regulation of cytokine signaling and T lymphocyte effector functions (reviewed in Knosp and Johnston 2012). Although SOCS1 is critical in the regulation of IFN γ and type I interferon signaling, a defined role of SOCS1 in the prevention of human lupus pathology is less clear.

[0005] The binding of interferon molecules to ligand specific receptors results in a cascade of events in which Janus kinases (JAKs) are activated through phosphorylation, followed by activation and phosphorylation of signal transducing and activators of transcription (STAT) molecules (Platanias and Fish 1999; Kutenko and Pestka 2000). The STAT molecules then translocate to the nucleus where they mediate the transcription of interferon specific genes, which notably include SOCS1. SOCS1, which is also referred to as STAT induced STAT inhibitor-1, then inhibits the ability of the JAK molecules to mediate STAT activation thereby creating a classic feedback inhibition loop (reviewed in (Knosp and Johnston 2012)). Mice lacking the SOCS1 gene (SOCS1^{-/-}) develop a severe inflammatory disease, characterized by fatty degeneration of the liver, leukocyte infiltration into vital organs, and death within three weeks of birth (Alexander *et al.* 1999). This Src-homology type 2 (SH2) domain containing protein also possesses two functional domains: (i) the kinase inhibitory region (KIR), which inhibits JAK2 tyrosine kinase phosphorylation; and (ii) the SOCS box, which targets JAK associated cytokine receptors for lysosomal or proteosomal degradation (reviewed in Knosp and Johnston 2012). The KIR region of SOCS1 possesses significant immuno-regulatory properties, as transgenic mice that possess this functional domain, but lack the SOCS box, do not develop SOCS1^{-/-} associated perinatal lethality (Zhang *et al.* 2001). Additionally, it has recently been shown that a SOCS1 mimetic peptide, corresponding to the KIR region of SOCS1 (SOCS1-KIR), has potent regulatory capacity both *in vitro* and *in vivo* (Jager *et al.* 2011; Collins *et al.* 2011). Although SOCS1 is essential for the regulation of immune events that are associated with lupus onset and progression, strategies to target the SOCS1 regulatory pathway as a lupus therapeutic are limited.

[0006] It has recently been shown that, upon disease onset, splenocytes from (NZBxNZW)F₁ mice, a classic model of SLE, display enhanced STAT1 activation and reduced SOCS1 expression (Sharabi *et al.* 2009). Moreover, treatment of this mouse model with the tolerogenic peptide, hCDR1, increased SOCS1 expression and ameliorated lupus disease (Sharabi *et al.* 2009). Notably, SOCS1^{+/-} mice, which possess one functional allele of SOCS1, develop disease symptoms similar to human lupus, including anti-dsDNA autoantibody production and glomerulonephritis at greater than 6 months of age (Fujimoto *et al.* 2004). Though murine studies clearly show an association between reduced SOCS1 expression and increased disease pathology, the exact mechanisms by which SOCS1 deficiency leads to murine lupus development have not been elucidated.

BRIEF SUMMARY OF THE INVENTION

[0007] In one aspect of the invention, there is provided a peptide mimetic of a suppressor of cytokine signaling (SOCS) protein, wherein said peptide binds to the activation loop of and inhibits the activity of a tyrosine kinase, wherein said peptide comprises two copies of the amino acid sequence of SEQ ID NO: 1, or a functional fragment of said peptide that binds to the activation loop of and inhibits said tyrosine kinase activity, wherein the functional fragment is not a monomer of the amino acid sequence of SEQ ID NO: 1.

[0008] In another aspect, there is provided a polynucleotide comprising a nucleotide sequence that encodes one or more peptides of the invention, or an expression construct comprising said polynucleotide.

[0009] In a further aspect, there is provided a composition comprising a peptide of the invention, optionally encapsulated in a liposome, or a polynucleotide or expression construct of the invention, wherein said composition optionally comprises a suitable carrier, diluent or buffer.

[0010] Further provided is a peptide of the invention, a polynucleotide or expression construct of the invention, or a composition of the invention, for use as a medicament.

[0011] Additionally provided is a peptide of the invention, a polynucleotide or expression construct of the invention, or a composition of the invention, for use in a method for treating or preventing an autoimmune disorder and/or inflammatory disorder and/or oncological disorder in a person or animal.

[0012] Finally, there is provided an *in vitro* method for inhibiting the growth of a cancer or tumor cell, or for inhibiting activation of a tyrosine kinase in a cell, comprising contacting or providing the cell with an effective amount of a peptide of the invention, a polynucleotide or expression construct of the invention, or a composition of the invention.

[0013] The subject invention concerns peptide mimetics of SOCS proteins and their use. A peptide mimetic of the disclosure can bind to a SOCS1 and a SOCS3 target protein. A peptide mimetic of the disclosure can comprise the amino acid sequence of SEQ ID NO:1 and/or SEQ ID NO:2 and/or SEQ ID NO:51, or a functional fragment or variant thereof. A peptide of the disclosure can comprise multiple copies of the mimetic sequence. A peptide of the disclosure can comprise two or more copies of SEQ ID NO:1 and/or SEQ ID NO:2 and/or SEQ ID NO:51. A peptide mimetic of the disclosure can comprise the amino acid sequence of SEQ ID NO:3 and/or SEQ ID NO:4 and/or SEQ ID NO:52, or a functional fragment or variant thereof.

[0014] The disclosure also pertains to methods of treating and/or preventing autoimmune conditions and/or disorders. One or more peptide mimetics of the disclosure can be used to treat an autoimmune condition or disorder in a person or animal. A mimetic of the disclosure can be used to treat SLE or multiple sclerosis (MS) in a person or animal. Alternatively, a peptide mimetic of the disclosure can be used to treat an autoimmune skin disorder, such as psoriasis. A peptide mimetic of the disclosure can comprise the amino acid sequence of SEQ ID NO:1 and/or SEQ ID NO:2 and/or SEQ ID NO:51, or a functional fragment or variant thereof. A peptide of the disclosure can comprise multiple copies of the mimetic sequence. A peptide of the disclosure can comprise two or more copies of SEQ ID NO:1 and/or SEQ ID NO:2 and/or SEQ ID NO:51. A peptide mimetic of the disclosure can comprise the amino acid sequence of SEQ ID NO:3 and/or SEQ ID NO:4 and/or SEQ ID NO:52, or a functional fragment or variant thereof.

[0015] We show herein that lupus free, SOCS1^{+/-} mice possess an increased proportion of peripheral CD4⁺T cells bearing an activated cell phenotype. Through *in vitro* analysis, we show that CD28 signaling and subsequent Akt phosphorylation are dispensable for SOCS1^{+/-} CD4⁺T lymphocyte activation. Therefore, these SOCS1 deficient cells possess a lower activation threshold. We also demonstrate that naive SOCS1^{+/-} cells, which are biased toward a Th1 phenotype, can readily undergo regulatory T cell differentiation, but are biased against Th17 differentiation. Additionally, we show that a

mimetic peptide of the SOCS1 kinase inhibitory region, SOCS-KIR, has the capacity to inhibit excessive CD4⁺ T cell activation, proliferation, and IFN γ signaling. Finally, we demonstrate that peripheral blood mononuclear cells (PBMCs) from SLE patients have reduced SOCS1 expression, which is correlated with SLE disease activity-associated markers, type I IFN signature and serum complement component 3 (C3) levels.

BRIEF DESCRIPTION OF THE DRAWINGS

[0016] The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Patent and Trademark Office upon request and payment of the necessary fee.

Figures 1A-1C. *SOCS1*^{+/-} mice exhibit CD4⁺ T cell accumulation and enhanced CD4⁺ T cell activation in the periphery. (Figure 1A) *SOCS1*^{+/+} or *SOCS1*^{+/-} CD4⁺CD8⁻ thymocyte frequency was assessed by flow cytometry (left). Flow diagrams are representative of 9 independent experiments, which are presented graphically in the middle. Absolute CD4⁺CD8⁻ cell counts were calculated from each experiment and are presented on the right. (Figure 1B) LNs and spleen from *SOCS1*^{+/+} or *SOCS1*^{+/-} mice were pooled and CD4⁺ frequency was assessed by flow cytometry (left). Flow diagrams are representative of 8 independent experiments, which are presented graphically in the middle. Absolute CD4⁺ cell counts were calculated from each experiment and are presented on the right. (Figure 1C) *SOCS1*^{+/+} or *SOCS1*^{+/-} CD4⁺CD25⁺ and CD4⁺CD69⁺T cell frequencies within pooled LNs and spleen were assessed by flow cytometry (left). Flow diagrams are representative of 9 independent experiments, which are presented graphically in the middle. Absolute CD4⁺CD25⁺ and CD4⁺CD69⁺ cell counts were calculated from each experiment and are presented on the right. Results are shown as mean $\pm$ s.e.m. Statistical comparisons were performed using the Mann-Whitney U test (*P < 0.05).

Figures 2A-2D. CD28 co-stimulation is dispensable for activation and expansion of *SOCS1*^{+/-} CD4⁺ T lymphocytes. CD4⁺CD25⁻ T cells from *SOCS1*^{+/+} or *SOCS1*^{+/-} mice were stimulated with α CD3 antibodies alone or with α CD3 and α CD28 antibodies for 72 h. (Figure 2A) The frequencies of CD25 and CD69 expressing cells were assessed by flow cytometry. Flow cytometry histograms are representative of 4 independent experiments. (Figure 2B) Proliferation was assessed by CFSE labeling (top), cell counts (middle), and [³H] thymidine incorporation (bottom). Flow cytometry graphs to assess CFSE labeling are representative of 4 independent experiments. (Figure 2C) pAkt and Akt proteins were assessed by western blotting (top). pAkt relative intensities are displayed graphically (bottom). Blots and graphs are representative of 4 independent experiments. (Figure 2D) IFN γ secretion was measured by ELISA (n=3). Results are shown as mean $\pm$ s.e.m. Statistical comparisons were performed using the Mann-Whitney U test (*P<0.05, ***P<0.0005). α CD3=anti-CD3, α CD28=anti-CD28, WT= *SOCS1*^{+/+}, HT=*SOCS1*^{+/-}.

Figures 3A-3E. Th17, but not Treg, induction is dysregulated in *SOCS1*^{+/-} CD4⁺ T lymphocytes. (Figure 3A) Naive *SOCS1*^{+/+} or *SOCS1*^{+/-} CD4⁺CD25⁻ T cells were placed under control (α CD3, α CD28) or Treg inducing conditions for 3 d and Foxp3 expression was measured by intracellular staining and flow cytometry. Histograms on the left are representative of 4 independent experiments, which are

displayed graphically on the right. (Figure 3B) Naive *SOCS1*^{+/+} or *SOCS1*^{+/-} CD4⁺CD25⁻ T cells were placed under control or Th17 inducing conditions for 5 d. IL-17A expression was measured by intracellular staining and flow cytometry. Histograms on the left are representative of 10 independent experiments, which are shown graphically on the right. (Figure 3C) *IL-17a* and *ROR γ t* mRNA expression were measured by qPCR (left and right, respectively) and IL-17A secretion was assessed by ELISA (middle). Graphs of IL-17A qPCR and ELISA are representative of 10 independent experiments and graph of *ROR γ t* qPCR is representative of 5 independent experiments. (Figures 3D and 3E) Naive *SOCS1*^{+/+} or *SOCS1*^{+/-} CD4⁺CD25⁻ T cells were CFSE labeled and were placed under the indicated conditions for 3d in Figure 3D and 5 d in Figure 3E. Cell proliferation and Foxp3 expression (Figure 3D) or IL-17A expression (Figure 3E) were measured by flow cytometry. Flow diagrams in (Figure 3D) and (Figure 3E) are representative of 5 experiments. Results are shown as mean $\pm$ s.e.m. Statistical comparisons were performed using the Mann-Whitney U test (**P<0.0005). iTh17 = Th17 inducing conditions. *IL-17a* and *ROR γ t* expression is relative to β -actin.

Figures 4A-4D. *SOCS1*^{+/-} CD4⁺ T cells display Th1 bias under Th17 inducing conditions. (Figures 4A and 4B) *SOCS1*^{+/+} or *SOCS1*^{+/-} CD4⁺CD25⁻ T cells were placed under Th17 inducing conditions or left unstimulated for 5 d. (Figure 4A) *IFN γ* and *Tbet* expression were assessed by qPCR (n=4). (Figure 4B) *IFN γ* ⁺ cells were assessed by intracellular staining and flow cytometry. Flow diagrams are representative of 4 independent experiments. (Figure 4C) *IFN γ* ⁺ and/or IL-17A⁺ cells were assessed as in (Figure 4B). Flow diagrams are representative of 4 independent experiments. (Figure 4D) Frequencies of IL-17A producing cells were identified by intracellular staining and flow cytometry following Th17 induction of *SOCS1*^{+/+}, *SOCS1*^{+/-}, or *SOCS1*^{+/-}*IFN γ* ^{-/-} CD4⁺CD25⁻ T cells. Results are representative of 4 independent experiments. Results are shown as mean $\pm$ s.e.m. Statistical comparisons were performed using the Mann-Whitney U test (*P<0.05). iTh17 = Th17 inducing conditions. *IFN γ* and *Tbet* expression is relative to β -actin.

Figures 5A-5D. *SOCS1*-KIR treatment inhibits perturbed *SOCS1*^{+/-} CD4⁺ T cell activation, proliferation, and *IFN γ* production. (Figures 5A and 5B) *SOCS1*^{+/+} or *SOCS1*^{+/-} CD4⁺CD25⁻ T cells were stimulated with α CD3 antibodies alone or with α CD3 + *SOCS1*-KIR peptide (20 μ M) for 72 h. (Figure 5A) CD25 expressing cells were assessed by flow cytometry. Results are representative of 4 independent experiments. (Figure 5B) Proliferation was assessed by CFSE labeling and flow cytometry, cell counts, and [³H] thymidine incorporation. n=4. (Figures 5C and 5D) *SOCS1*^{+/+} or *SOCS1*^{+/-} CD4⁺CD25⁻ T cells were placed under Th17 inducing conditions in the absence or presence of *SOCS1*-KIR peptide (20 μ M) (Figure 5C) *IFN γ* expression, relative to β -actin., was assessed by qPCR (left) and ELISA (right) (n=4). (Figure 5D) pSTAT1 and STAT1 protein expressions were assessed by western blotting. Results are representative of 4 independent experiments. Statistical comparisons were performed using Mann-Whitney U test. (*P<0.05). iTh17 = Th17 inducing conditions, WT= *SOCS1*^{+/+}, and HT=*SOCS1*^{+/-}.

Figures 6A-6C. *SOCS1* expression is relevant to human SLE. (Figure 6A) PMBCs were isolated from whole blood taken from SLE patients or healthy controls and *SOCS1* was measured via qPCR, relative to GAPDH. (Figure 6B) For each patient, *SOCS1* expression was correlated with *IFN γ* expression (left) and monocyte CD64 MFI (right). (Figure 6C) *SOCS1* expression in patients was also correlated with C3 levels (left) and C4 levels (right). Results shown as mean $\pm$ s.e.m. Statistical comparisons between healthy controls and SLE patients were performed using the Mann-Whitney U test (**P < 0.005).

Spearman's correlation was chosen for statistical analyses in (Figure 6B) and (Figure 6C). MFI=Mean Fluorescent intensity.

Figures 7A-7C. *SOCS1*^{+/-} mice are free of SLE-like pathology at <6 months of age. (Figure 7A) Concentrations of total IgG antibodies and IgG autoantibodies specific for ssDNA and dsDNA antigens in *SOCS1*^{+/+} or *SOCS1*^{+/-} mice, <6 months of age, were measured by ELISA. (Figure 7B) Proteinuria was assessed in *SOCS1*^{+/+} and *SOCS1*^{+/-} mice, <6 months of age. (Figure 7C) Schematic timeline for autoantibody production by *SOCS1*^{+/-} mice and display of age range of *SOCS1*^{+/+} and *SOCS1*^{+/-} mice chosen for experiments. Results are shown as mean ± s.e.m. Statistical comparisons were performed using the Mann-Whitney U test.

Figure 8. *SOCS1*^{+/-} mice possess a normal peripheral CD4⁺CD25⁺Foxp3⁺ cell frequency. LNs and spleen from *SOCS1*^{+/+} or *SOCS1*^{+/-} mice were pooled and the CD4⁺CD25⁺Foxp3⁺ frequency was assessed by flow cytometry. Results shown as mean ± s.e.m. Statistical comparisons *SOCS1*^{+/+} and *SOCS1*^{+/-} mice were performed using the Mann-Whitney U test.

Figures 9A and 9B. *SOCS1* expression is not affected by chloroquine treatment, but is increased by dexamethasone treatment. (Figure 9A) PBMCs, taken from healthy controls, were treated with (Figure 9A) chloroquine diphosphate salt at the indicated molar concentrations for 12 and 24 h or (Figure 9B) dexamethasone at the indicated molar concentrations for 3, 6, 12, or 24 h. Post treatment, *SOCS1* expression, relative to *GAPDH*, was assessed via qPCR. Results shown as mean ± s.e.m. The Kruskal-Wallis test followed by the Dunn's Multiple Comparison Test was chosen to assess statistical significance. (*P<0.05).

Figures 10A and 10B. *SOCS1* expression is not correlated with age or SLEDAI. PMBCs were isolated from whole blood taken from SLE patients or healthy controls (HCs) and *SOCS1* expression was measured via qPCR, relative to *GAPDH*. (Figure 10A) *SOCS1* expression was compared between age-matched HCs and SLE patients. (Figure 10B) *SOCS1* expression in SLE patients was correlated with the SLE disease activity index (SLEDAI). Spearman's correlation was chosen for statistical analyses.

Figure 11. *SOCS1* dimer is more effective than monomer at inhibitory iTh17 induction. CD4⁺CD25⁻ T cells from B6 mice were in the presence of Th17 inducing conditions in the presence of *SOCS1* monomer or dimer for 5 days. Cells were re-stimulated with PMA, ionomycin, and brefeldin, followed by staining with anti-CD4, anti-IL17, and anti-CD25 antibodies.

Figures 12A-12C. *SOCS1*^{+/-} mice develop lupus pathology. (Figure 12A) Schematic showing time frame in which lupus pathology occurs in *SOCS1*^{+/-} mice. (Figure 12B) Model showing regulation of the Th1/IFN gamma pathway by *SOCS1* (depicted from Egwuagu and Larkin, 2013). (Figure 12C) Graph showing relative expression of *SOCS1* in spleen taken from *SOCS1*^{+/+} (wild-type) and *SOCS1*^{+/-} mice.

Figures 13A-13C. *SOCS1*-KIR inhibits CD28 independent proliferation and activation of CD4⁺*SOCS1*^{+/-} T lymphocytes. *SOCS1*-KIR treatment inhibits perturbed *SOCS1*^{+/-} CD4⁺ T cell activation and proliferation. (Figures 13A and 13B) *SOCS1*^{+/+} or *SOCS1*^{+/-}, CD4⁺CD25⁻ T cells were stimulated with αCD3 antibodies alone or with αCD3 + *SOCS1*-KIR peptide for 72 h. (Figure 13A) Proliferation was assessed by CFSE labeling and flow cytometry. (Figure 13B) CD25 expressing cells were assessed by flow cytometry. (Figure 13C) *SOCS1*^{+/+} or *SOCS1*^{+/-}, CD4⁺CD25⁻ T cells were

treated under the indicated conditions in the absence or presence of SOCS 1-KIR peptide followed by analysis of pSTAT1 and STAT1 protein expressions by western blotting. Results are representative of ≥ 3 independent experiments. Statistical comparisons were performed using Mann-Whitney U test. (* $P < 0.05$). Th17 = Th17 inducing conditions, WT=SOCS1^{+/+}, and HT=SOCS1^{+/-}.

Figure 14. SOCS1 expression in SLE patient PBMC is deficient, and inversely correlated with disease activity. (Left) PMBCs were isolated from whole blood taken from SLE patients or healthy controls and SOCS1 was measured via qPCR, relative to GAPDH. (middle) For each patient, SOCS1 expression was correlated with monocyte CD64 MFI. (right) SOCS1 expression in patients was also correlated with C3 levels. Results shown as mean $\pm$ s.e.m. Statistical comparisons between healthy controls and SLE patients were performed using the Mann-Whitney U test (** $P < 0.005$). Spearman's correlation was chosen for statistical analyses. MFI=Mean Fluorescent intensity.

Figures 15A-15F. SOCS1-KIR inhibition of lethal inflammatory pathology in SOCS1^{-/-} mice is correlated to enhanced regulatory T cell homeostasis. (Figure 15A) Kaplan Meier curve showing survival of SOCS1^{-/-} (black square; n=7) or CD4⁺/SOCS1-KIR treatment (purple triangles, n=12). Numbers of mice in each group are indicated in parentheses. Mice were euthanized when moribund with survival comparisons by Mantel-Cox. Statistical significance denoted by asterisks. (Figure 15B) Photographs of H&E stains depicting heart and liver tissues of 2 week old SOCS1^{-/-}, SOCS1^{-/-} mice receiving dual treatments, or littermate control mice. Photographs shown of H&E stained liver and heart of untreated SOCS1^{-/-} (N=8) and WT (N=7) mice are representative of 100% of samples analyzed. Photographs shown of H&E stained liver and heart of SOCS1^{-/-} mice receiving combined treatments are representative of 2 out of 5 mice in regard to heart samples and 1 out of 5 mice in regards to liver tissue. (Figure 15C) Graph showing average daily weights of SOCS1^{-/-} mice untreated (n=16), CD4⁺/SOCS1-KIR treatment (n=12), or WT littermate controls (n=9) over a two week period. (Figure 15D) Photographs of 2 week old SOCS1^{-/-} mice, SOCS1^{-/-} mice receiving dual treatment, and WT littermate controls. (Figure 15E) Graphs showing IFN γ levels within the sera of 2 week old WT (n=7) or SOCS1^{-/-} mice with (n=8) and without (n=10) CD4⁺/SOCS1-KIR treatment, measured by ELISA. (Figure 15F) Graphs showing absolute numbers of CD4⁺Foxp3⁺ lymphocytes present in two week old SOCS1^{-/-} and WT littermate control mice with or without CD4⁺/SOCS1-KIR treatment and WT 6-8 week old adult mice. Each dot is representative of an individual mouse with averages denoted by lines. Statistics were performed using unpaired, two-tailed t test comparing treated SOCS1^{-/-} to untreated SOCS1^{-/-} 2wk. Statistical significance is denoted by asterisks. *, $p \leq 0.05$; **, $p \leq 0.005$; ***, $p \leq 0.0005$.

Figures 16A-16E. SOCS1 and SOCS3 levels are decreased in SLE patients when compared to healthy controls: (Figure 16A) Graphs showing average SOCS1 and SOCS3 mRNA expression (mean $\pm$ SE) via real time RT-PCR, relative to GAPDH in SLE patients (N=33) versus controls (N=11) (Figure 16B). Simple linear regression correlating SOCS1 vs SOCS3 gene expression at the 95% confidence level within SLE patients. Correlation was considered significant at 0.05 level (2 tailed). (Figure 16C) Graph showing average SOCS1 and SOCS3 protein levels (arbitrary Units mean $\pm$ SE) within SLE patients (N=32) compared to controls (N=6). (Figure 16D) Individual basal protein level comparisons between SOCS1 and SOCS3 within SLE patients. The mean values of healthy controls (n=6) are represented as solid red circles with the values of individual SLE patients being represented as respective black dotted lines. (Figure 16E) Western blot analysis of SOCS1, SOCS3, pAKT, pERK1/2 and pSTAT1 in human SLE patients (N=32) and healthy controls (N=6) relative to loading control

GAPDH. * represents significant Pearson correlation; ^ represents a t-test with significant mean difference. Correlation was considered significant at 0.05 level (2 tailed).

Figures 17A-17C. Dysregulated STAT1 activation in SLE patients is correlated SOCS1 deficiency SOCS1 and SOCS3 protein levels in comparison to phosphorylated proteins: (Figure 17A) Graphical representation (arbitrary Units mean $\pm$ SE) of pAKT and AKT; pERK1/2 and ERK1/2; pSTAT1 and STAT1 protein levels of SLE patients (N=32) as compared to controls (N=6). (Figure 17B) Individual basal level comparison of SOCS 1 to phosphorylated proteins (pAKT; pERK1/2; pSTAT1) from individual SLE patients (N=32) that are represented as solid black circles. (Figure 17C) Represents the individual basal level comparison of SOCS3 to phosphorylated proteins (pAKT; pERK1/2; pSTAT1) of individual SLE patients (N=32). The mean values of healthy controls (n=6) are represented as solid red circles and the means for SLE patients are represented as black dotted line respectively. * represents significant Pearson correlation; ^ represents a t-test with significant mean difference. Correlation was considered significant at 0.05 level (2 tailed).

Figures 18A-18B. Inverted pSTAT1/SOCS1 ratio correlates to significantly enhanced MHC class 1 levels amongst SLE patients. (Figure 18A) Graph showing pSTAT1/SOCS1 ratios (from Figure 17B) bearing a distinctly positive or negative slope, where each number denotes an individual patient. (dotted line denotes location where slope=1). (Figure 18B) Graphical representation comparing MHC class 1 message levels (HLA-HQ-DQR and HQ-DAR) in patients bearing high versus low pSTAT1/SOCS1 ratio, showing an inverted SOCS1/pSTAT1 ratio in protein levels correlated to significantly enhanced MHC class I message levels amongst SLE patients.

Figures 19A-19D. IFN gamma and IL27 mRNA levels are positively correlated to SOCS1 mRNA levels: (Figure 19A) IFN γ and IL-27 mRNA expression was measured (mean $\pm$ SE) via real time RT-PCR, relative to GAPDH in SLE patients (N=33) and controls (N=11). (Figure 19B) Simple linear regressions correlating IFN γ mRNA expression with SOCS1 and SOCS3 mRNA and protein expression in SLE patients at 95% confidence level. to (Figure 19C) Simple linear regressions correlating IL-27 mRNA expression with SOCS1 and SOCS3 mRNA and protein expression in SLE patients with 95% confidence level. to (Figure 19D) Simple linear regressions correlating CD64 (MFI) with SOCS1 and SOCS3 gene and protein expression were achieved for SLE patients to with 95% confidence level. * represents significant Pearson correlation; ^ represents a t-test with significant mean difference. Correlation was considered significant at 0.05 level (2 tailed).

Figures 20A-20F. Subgroup analysis of SOCS1 and SOCS3 expression in SLE patients with and without prednisone treatment: Active SLEDIA and inactive SLEDIA SLE patients with and without prednisone treatment were analyzed for SOCS1 and SOCS3 mRNA and protein expression relative to GAPDH, in comparison to controls (N=6). Protein expression represented by graph (Figure 20A) Active SLEDIA (Figure 20B) Inactive SLEDIA; Phosphorylated protein expression of pAKT; pERK1/2 and pSTAT1 represented by graph (Figure 20C) Active SLEDIA (Figure 20D) Inactive SLEDIA and mRNA expression represented by graph (Figure 20E) Active SLEDIA (Figure 20F) Inactive SLEDIA in comparison to healthy controls respectively (N=6). Results shown are mean $\pm$ SE; * represents significant Pearson correlation; ^ represents a t-test with significant mean difference. Correlation was considered significant at 0.05 level (2 tailed).

BRIEF DESCRIPTION OF THE SEQUENCES

[0017]

SEQ ID NO:1 (⁵³DTHFRTFRSHSDYRRI) is a SOCS1-KIR peptide.

SEQ ID NO:2 (⁵³DTHARTARSHSDYRRI) is a SOCS1-KIR2A peptide.

SEQ ID NO:3 (⁵³DTHFRTFRSHSDYRRIGGGGGGDTHFRTFRSHSDYRRI) is a SOCS 1-KIR dimer peptide.

SEQ ID NO:4 (DTHARTARSHSDYRRIGGGGGGDTHARTARSHSDYRRI) is a SOCS 1-KIR2A dimer peptide.

SEQ ID NOs:5-26 are amplification primers.

SEQ ID NO:27 (RRRRRRRRRDTHFRTFRSHSDYRRI) is a SOCS1-KIR peptide.

SEQ ID NO:28 (RRRRRRRRRDTHARTARSHSDYRRI) is a SOCS1-KIR2A peptide.

SEQ ID NO:29:

(RRRRRRRRRDTHFRTFRSHSDYRRIGGGGGGDTHFRTFRSHSDYRRI) is a SOCS 1-KIR dimer peptide.

SEQ ID NO:30:

(RRRRRRRRRDTHARTARSHSDYRRIGGGGGGDTHARTARSHSDYRRI) is a SOCS 1-KIR2A dimer peptide.

SEQ ID NOs:31-49 are examples of cell penetrating peptides that can be used with the disclosure.

SEQ ID NO:50 (WLVFFVIFYFFR) is a Tkip peptide.

SEQ ID NO:51 (LRLKTFSSKSEYQLVV) is a SOCS3-KIR peptide.

SEQ ID NO:52 (LRLKTFSSKSEYQLVGGGGGGLRLKTFSSKSEYQLVV) is a SOCS3-KIR dimer peptide.

SEQ ID NO:53 (RRRRRRRRRLRLKTFSSKSEYQLVV) is a SOCS3-KIR peptide.

SEQ ID NO:54:

(RRRRRRRRRLRLKTFSSKSEYQLVGGGGGGLRLKTFSSKSEYQLVV) is a SOCS3-KIR dimer peptide.

DETAILED DESCRIPTION OF THE INVENTION

[0018] In one aspect of the invention, there is provided a peptide mimetic of a suppressor of cytokine signaling (SOCS) protein, wherein said peptide binds to the activation loop of and inhibits the activity of a tyrosine kinase, wherein said peptide comprises two copies of the amino acid sequence of SEQ ID NO: 1, or a functional fragment of said peptide that binds to the activation loop of and inhibits said tyrosine kinase activity, wherein the functional fragment is not a monomer of the amino acid sequence of SEQ ID NO: 1.

[0019] The tyrosine kinase may be a JAK protein, for example a JAK2 protein.

[0020] The peptide may comprise one or more linker amino acids, for example, glycine amino acids, inserted between said copies of said amino acid sequences that bind to and inhibit said tyrosine kinase activity. The peptide may comprise the amino acid sequence of SEQ ID NO:3, or a functional fragment of said peptide that binds to the activation loop of and inhibits said tyrosine kinase activity, wherein the functional fragment is not a monomer of the amino acid sequence of SEQ ID NO: 1.

[0021] The peptide may comprise a protein or nucleic acid that is attached to said peptide and that targets delivery to a cell and/or that provides for translocation of said peptide across a biological membrane of said cell.

[0022] A lipophilic group, such as a palmitoyl-lysine group, may be attached to said peptide. The lipophilic group may comprise one or more arginine and/or lysine amino acids at the N-terminus, the C-terminus, or both the N-terminus and C-terminus of said peptide. The peptide may comprise the amino acid sequence of SEQ ID NO:29, or a functional fragment of said peptide that binds to the activation loop of and inhibits said tyrosine kinase activity, wherein the functional fragment is not a monomer of the amino acid sequence of SEQ ID NO: 1. The lipophilic group may comprise a fatty acid moiety, such as capric acid, lauric acid, myristic acid, palmitic acid, stearic acid, arachidic acid, behenic acid, lignoceric acid, or cerotic acid.

[0023] In another aspect, there is provided a polynucleotide comprising a nucleotide sequence that encodes one or more peptides of the invention, or an expression construct comprising said polynucleotide.

[0024] In a further aspect, there is provided a composition comprising a peptide of the invention, optionally encapsulated in a liposome, or a polynucleotide or expression construct of the invention, wherein said composition optionally comprises a suitable carrier, diluent or buffer.

[0025] Further provided is a peptide of the invention, a polynucleotide or expression construct of the invention, or a composition of the invention, for use as a medicament.

[0026] Additionally provided is a peptide of the invention, a polynucleotide or expression construct of the invention, or a composition of the invention, for use in a method for treating or preventing an autoimmune disorder and/or inflammatory disorder and/or oncological disorder in a person or animal.

[0027] Finally, there is provided an *in vitro* method for inhibiting the growth of a cancer or tumor cell, or for inhibiting activation of a tyrosine kinase in a cell, comprising contacting or providing the cell with an effective amount of a peptide of the invention, a polynucleotide or expression construct of the invention, or a composition of the invention.

[0028] The subject invention concerns peptide mimetics of SOCS proteins and their use. A peptide mimetic of the disclosure can bind to a SOCS1 and a SOCS3 tyrosine kinase target protein. A peptide mimetic of the disclosure can bind to a JAK2 and TYK2 tyrosine kinase. A peptide mimetic of the disclosure can comprise the amino acid sequence of SEQ ID NO:1 or SEQ ID NO:2 or SEQ ID NO:51, or a functional fragment or variant thereof. A peptide of the disclosure can comprise multiple copies of the mimetic sequence. A peptide of the disclosure can comprise two or more copies of SEQ ID NO:1 or

SEQ ID NO:2 or SEQ ID NO:51. A peptide mimetic of the disclosure can comprise the amino acid sequence of SEQ ID NO:3 or SEQ ID NO:4 or SEQ ID NO:52, or a functional fragment or variant thereof.

[0029] The disclosure also pertains to methods of treating and/or preventing autoimmune conditions and/or disorders. One or more peptide mimetics or polynucleotides of the invention, or a composition comprising one or more of the peptide mimetics or polynucleotides, can be used to treat an autoimmune condition or disorder in a person or animal by administering an effective amount of a mimetic peptide or composition of the invention to the person or animal. A mimetic of the invention can be used to treat MS or SLE in a person or animal. A mimetic of the invention can be used to treat an autoimmune skin disorder, such as psoriasis. A peptide mimetic used with a method of the disclosure can comprise the amino acid sequence of SEQ ID NO:1 or SEQ ID NO:2 or SEQ ID NO:51, or a functional fragment or variant thereof. A peptide used with a method of the disclosure can comprise multiple copies of the mimetic sequence. Peptides with multiple copies of a mimetic sequence can optionally comprise one or more linker amino acids between the mimetic sequences. The linker amino acid can be glycine. A peptide used with a method of the disclosure can comprise two or more copies of SEQ ID NO:1 or SEQ ID NO:2 or SEQ ID NO:51. A peptide mimetic used with a method of the disclosure can comprise the amino acid sequence of SEQ ID NO:3 or SEQ ID NO:4 or SEQ ID NO:52, or a functional fragment or variant thereof.

[0030] The disclosure also pertains to methods of treating and/or preventing disorders and/or conditions associated with activated tyrosine kinases in a person or animal by administering an effective amount of one or more mimetic peptide, polynucleotide, or composition of the invention to the person or animal. The tyrosine kinase can be a JAK kinase. The JAK kinase can be JAK2 kinase. A peptide mimetic used with a method of the disclosure can comprise the amino acid sequence of SEQ ID NO:1 or SEQ ID NO:2 or SEQ ID NO:51, or a functional fragment or variant thereof. A peptide used with a method of the disclosure can comprise multiple copies of the mimetic sequence. A peptide used with a method of the disclosure can comprise two or more copies of SEQ ID NO:1 or SEQ ID NO:2 or SEQ ID NO:51. A peptide mimetic used with a method of the disclosure can comprise the amino acid sequence of SEQ ID NO:3 or SEQ ID NO:4 or SEQ ID NO:52, or a functional fragment or variant thereof.

[0031] The disclosure also pertains to methods of treating and/or preventing neurological disorders and/or conditions that have an inflammatory component associated with them by administering an effective amount of one or more mimetic peptide, polynucleotide, or composition of the invention. A peptide mimetic of the invention can be used to treat Parkinson's disease or ALS. A peptide mimetic used with a method of the disclosure can comprise the amino acid sequence of SEQ ID NO:1 or SEQ ID NO:2 or SEQ ID NO:51, or a functional fragment or variant thereof. A peptide used with a method of the disclosure can comprise multiple copies of the mimetic sequence. A peptide used with a method of the disclosure can comprise two or more copies of SEQ ID NO:1 or SEQ ID NO:2 or SEQ ID NO:51. A peptide mimetic used with a method of the disclosure can comprise the amino acid sequence of SEQ ID NO:3 or SEQ ID NO:4 or SEQ ID NO:52, or a functional fragment or variant thereof.

[0032] A peptide of the invention can comprise a lipophilic sequence or moiety that facilitates penetration through a cell membrane for entry into a cell. A peptide of the invention can comprise one or more arginine and/or lysine amino acids at one or both termini of the peptide. A peptide of the invention can comprises one or more arginine amino acids at the N-terminus of the peptide. For example, a peptide can comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more arginine and/or lysine amino acids

at one or both termini. A peptide of the disclosure can have the amino acid sequence shown in SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:52, or SEQ ID NO:54. A peptide of the invention can comprise a fatty acid moiety, *e.g.*, a carboxylic acid with a long aliphatic tail, attached to the peptide. Examples of fatty acids contemplated within the scope of the invention include, but are not limited to, caprylic acid, capric acid, lauric acid, myristic acid, palmitic acid, stearic acid, arachidic acid, behenic acid, lignoceric acid, and cerotic acid. A peptide of the invention can comprise a palmitate or palmitic acid (hexadecanoic acid) attached to the peptide, typically at the N- and/or C-terminus of the peptide. A peptide of the invention can comprise a nuclear localization sequence (NLS).

[0033] As those skilled in the art can readily appreciate, there can be a number of variant sequences of a protein found in nature, in addition to those variants that can be artificially created by the skilled artisan in the lab. The peptides of the disclosure can encompass those specifically exemplified herein, as well as any natural variants thereof, as well as any variants which can be created artificially, so long as those variants retain the desired biological activity.

[0034] The peptides contemplated in the disclosure can include the specific peptides exemplified herein as well as equivalent peptides which may be, for example, somewhat longer or shorter than the peptides exemplified herein. For example, using the teachings provided herein, a person skilled in the art could readily make peptides having from 1 to about 5, 10, 15, 20, 25, 30, 35, 40, 50, 60, 70 or more amino acids added to, or removed from, either end of the disclosed peptides using standard techniques known in the art. Amino acids can be removed from the N-terminus of a peptide of the disclosure. For example, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 50, 60, 70 or more amino acids can, independently, be removed from either or both ends of a peptide of the disclosure. Preferably, any added amino acids would be the same as the corresponding amino acids of a mature full-length SOCS protein. The skilled artisan, having the benefit of the teachings disclosed in the subject application, could easily determine whether a variant peptide retained the biological activity of the specific peptides exemplified herein. Such a longer or shorter peptide would be within the disclosure as long as said peptide does not encompass the entire full-length SOCS protein and said longer or shorter peptide retains substantially the same relevant biological activity as the peptides exemplified herein. For example, a longer or shorter variant of the SOCS 1-KIR (SEQ ID NO: 1) or SOCS 1-KIR2A (SEQ ID NO:2) or SOCS3-KIR (SEQ ID NO:51) peptide would fall within the disclosure if the variant peptide had the ability to mimic SOCS function, *e.g.*, bind to the activation loop of a tyrosine kinase.

[0035] Also within the disclosure are peptides which have the same amino acid sequences of a peptide exemplified herein except for amino acid substitutions, additions, or deletions within the sequence of the peptide, as long as these variant peptides retain substantially the same relevant biological activity as the peptides specifically exemplified herein. For example, conservative amino acid substitutions within a peptide which do not affect the ability of the peptide to, for example, to mimic SOCS1 function would be within the disclosure. Thus, the peptides disclosed herein should be understood to include variants and fragments, as discussed above, of the specifically exemplified sequences.

[0036] The subject invention further includes polynucleotides comprising nucleotide sequences which encode the peptides of the invention. A polynucleotide of the disclosure can comprise a nucleotide sequence which encodes a peptide comprising one or more of the amino acid sequences of SEQ ID NO:1, 2, 3, 4, 27, 28, 29, 30, 51, 52, 53, or 54. These nucleotide sequences can be readily constructed by those skilled in the art having the knowledge of the protein and peptide amino acid sequences which are presented herein. As would be appreciated by one skilled in the art, the degeneracy of the genetic

code enables the artisan to construct a variety of nucleotide sequences that encode a particular peptide or protein. The choice of a particular nucleotide sequence could depend, for example, upon the codon usage of a particular expression system.

[0037] The disclosure contemplates the use of the peptides described herein in pharmaceutical compositions for administration to an animal or human for the treatment of clinically important disease conditions that are amenable to treatment with a full-length SOCS protein. For example, using the teachings described herein, the skilled artisan can use the subject invention to modulate the immune response of an animal or human. The peptides of the subject invention can be prepared in pharmaceutically acceptable carriers or diluents for administration to humans or animals in a physiologically tolerable form. Materials and methods for preparing such compositions are known in the art.

[0038] The peptides of the subject invention can be administered using a variety of techniques that are known in the art. One or more peptides of the invention can be administered as a topical preparation to the skin or an external membrane of a person or animal. The peptides can be encapsulated in liposomes that are targeted to specific cells or tissues and the liposome-encapsulated peptides delivered to the cells or tissue either *in vitro*, *in vivo*, or *ex vivo*. Procedures for preparing liposomes and encapsulating compounds within the liposome are well known in the art. See, for example, U.S. Patent No. 5,252,348, which issued to Schreier et al. Peptides can also be conjugated or attached to other molecules, such as an antibody, that targeted a specific cell or tissue. Peptides can also be administered using a drug delivery system similar to that described in U.S. Patent No. 4,625,014, which issued to Senter et al.

[0039] Also disclosed is the use of the claimed peptides to produce antibodies, both polyclonal and monoclonal. These antibodies can be produced using standard procedures well known to those skilled in the art. These antibodies may be used as diagnostic and therapeutic reagents. For example, antibodies that bind to the SOCS 1-KIR (SEQ ID NO:1) peptide can be used as an antagonist to block the function of SOCS protein. Antibodies that are reactive with the peptides of the subject invention can also be used to purify SOCS protein from a crude mixture.

[0040] An antibody that is contemplated by the disclosure on can be in any of a variety of forms, including a whole immunoglobulin, an antibody fragment such as Fv, Fab, and similar fragments, as well as a single chain antibody that includes the variable domain complementarity determining regions (CDR), and similar forms, all of which fall under the broad term "antibody," as used herein.

[0041] The term "antibody fragment" refers to a portion of a full-length antibody, generally the antigen binding or variable region. Examples of antibody fragments include Fab, Fab', F(ab')₂ and Fv fragments. Papain digestion of antibodies produces two identical antigen binding fragments, called the Fab fragment, each with a single antigen binding site, and a residual "Fc" fragment, so-called for its ability to crystallize readily. Pepsin treatment of an antibody yields an F(ab')₂ fragment that has two antigen binding fragments, which are capable of cross-linking antigen, and a residual other fragment (which is termed pFc'). Additional fragments can include diabodies, linear antibodies, single-chain antibody molecules, and multispecific antibodies formed from antibody fragments. As used herein, "antigen binding fragment" with respect to antibodies, refers to, for example, Fv, F(ab) and F(ab')₂ fragments.

[0042] Antibody fragments can retain an ability to selectively bind with the antigen or analyte are contemplated within the disclosure and include:

1. (1) Fab is the fragment of an antibody that contains a monovalent antigen-binding fragment of an antibody molecule. A Fab fragment can be produced by digestion of whole antibody with the enzyme papain to yield an intact light chain and a portion of one heavy chain.
2. (2) Fab' is the fragment of an antibody molecule can be obtained by treating whole antibody with pepsin, followed by reduction, to yield an intact light chain and a portion of the heavy chain. Two Fab' fragments are obtained per antibody molecule. Fab' fragments differ from Fab fragments by the addition of a few residues at the carboxyl terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region.
3. (3) (Fab')₂ is the fragment of an antibody that can be obtained by treating whole antibody with the enzyme pepsin without subsequent reduction. F(ab')₂ is a dimer of two Fab' fragments held together by two disulfide bonds.
4. (4) Fv is the minimum antibody fragment that contains a complete antigen recognition and binding site. This region consists of a dimer of one heavy and one light chain variable domain in a tight, non-covalent association (V_H-V_L dimer). It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the V_H-V_L dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.
5. (5) Single chain antibody ("SCA"), defined as a genetically engineered molecule containing the variable region of the light chain (V_L), the variable region of the heavy chain (V_H), linked by a suitable polypeptide linker as a genetically fused single chain molecule. Such single chain antibodies are also referred to as "single-chain Fv" or "sFv" antibody fragments. Generally, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains that enables the sFv to form the desired structure for antigen binding. For a review of sFv fragments, see Pluckthun in *The Pharmacology of Monoclonal Antibodies*, vol. 113, Rosenberg and Moore eds. Springer-Verlag, N.Y., pp. 269 315 (1994).

[0043] Antibodies within the disclosure can be of any isotype, including IgG, IgA, IgE, IgD, and IgM. IgG isotype antibodies can be further subdivided into IgG1, IgG2, IgG3, and IgG4 subtypes. IgA antibodies can be further subdivided into IgA1 and IgA2 subtypes.

[0044] Antibodies of the disclosure can be genus or species specific to a target. Antibodies can be prepared using standard techniques known in the art. Antibodies can be polyclonal or monoclonal antibodies. Monoclonal antibodies can be prepared using standard methods known in the art (Kohler *et al.*, 1975). Antibodies can be mammalian antibodies, including mouse, rat, goat, rabbit, pig, dog, cat, monkey, chimpanzee, ape, or human.

[0045] The subject invention also concerns compositions comprising one or more peptides of the invention. The composition can further comprises a suitable carrier, diluent, or buffer. Compositions contemplated within the disclosure can comprise one or more peptides or polynucleotides of the invention and, optionally, one or more other compounds for treating autoimmune conditions or other conditions associated with activated tyrosine kinases. For example, a peptide of the invention can be

provided in a composition with one or more of cyclophosphamide, methotrexate, mycophenolate, azathioprine, leflunomide, and prednisone. The composition can comprise a peptide of the invention in a pharmaceutically or physiologically acceptable carrier, buffer, or diluent.

[0046] Peptides, polynucleotides, antibodies, and other agents of the disclosure can be modified so as to enhance uptake into a cell. A lipophilic group can be attached to a peptide, polynucleotide, or other agent of the disclosure. A palmitic acid can be attached to a peptide of the invention. A palmitoyl-lysine group can be attached to the peptide, for example at the N-terminus of the peptide. Other methods for enhancing uptake of a peptide, polynucleotide, and antibody into a cell are known in the art and are contemplated within the disclosure.

[0047] Peptides, polynucleotides, antibodies, compositions, and other agents of the disclosure can also be delivered into cells by encapsulation of the peptide, polynucleotide, antibody, and other agents of the disclosure within a liposome. Methods for encapsulation of peptides, polynucleotides, antibodies, and other agents of the disclosure within liposomes are well known in the art.

[0048] Peptides having substitution of amino acids other than those specifically exemplified in the subject peptides are also contemplated by the disclosure. For example, non-natural amino acids can be substituted for the amino acids of a peptide of the invention, so long as the peptide having substituted amino acids retains substantially the same activity as the peptide in which amino acids have not been substituted. Examples of non-natural amino acids include, but are not limited to, ornithine, citrulline, hydroxyproline, homoserine, phenylglycine, taurine, iodotyrosine, 2,4-diaminobutyric acid, α -amino isobutyric acid, 4-aminobutyric acid, 2-amino butyric acid, γ -amino butyric acid, ϵ -amino hexanoic acid, 6-amino hexanoic acid, 2-amino isobutyric acid, 3-amino propionic acid, norleucine, norvaline, sarcosine, homocitrulline, cysteic acid, τ -butylglycine, τ -butylalanine, phenylglycine, cyclohexylalanine, β -alanine, fluoro-amino acids, designer amino acids such as β -methyl amino acids, C-methyl amino acids, N-methyl amino acids, and amino acid analogues in general. Non-natural amino acids also include amino acids having derivatized side groups. Furthermore, any of the amino acids in the protein can be of the D (dextrorotary) form or L (levorotary) form.

[0049] Amino acids can be generally categorized in the following classes: non-polar, uncharged polar, basic, and acidic. Conservative substitutions whereby a peptide having an amino acid of one class is replaced with another amino acid of the same class fall within the disclosure so long as the peptide having the substitution still retains substantially the same biological activity as a peptide that does not have the substitution. Table 1 below provides a listing of examples of amino acids belonging to each class.

Table 1.	
Class of Amino Acid	Examples of Amino Acids
Nonpolar	Ala, Val, Leu, Ile, Pro, Met, Phe, Trp
Uncharged Polar	Gly, Ser, Thr, Cys, Tyr, Asn, Gln
Acidic	Asp, Glu
Basic	Lys, Arg, His

[0050] Single letter amino acid abbreviations are defined in Table 2.

Table 2.	
Letter Symbol	Amino Acid
A	Alanine
B	Asparagine or aspartic acid
c	Cysteine
D	Aspartic Acid
E	Glutamic Acid
F	Phenylalanine
G	Glycine
H	Histidine
I	Isoleucine
K	Lysine
L	Leucine
M	Methionine
N	Asparagine
P	Proline
Q	Glutamine
R	Arginine
S	Serine
T	Threonine
V	Valine
w	Tryptophan
Y	Tyrosine
Z	Glutamine or glutamic acid

[0051] The peptides of the present invention can be formulated into pharmaceutically-acceptable salt forms. Pharmaceutically-acceptable salt forms include the acid addition salts and include hydrochloric, hydrobromic, nitric, phosphoric, carbonic, sulphuric, and organic acids like acetic, propionic, benzoic, succinic, fumaric, mandelic, oxalic, citric, tartaric, maleic, and the like. Pharmaceutically-acceptable base addition salts include sodium, potassium, calcium, ammonium, and magnesium salts. Pharmaceutically-acceptable salts of the peptides of the invention can be prepared using conventional techniques.

[0052] The disclosure also concerns polynucleotide expression constructs that comprise a polynucleotide of the present invention comprising a nucleotide sequence encoding a peptide of the present invention. The polynucleotide can encode a peptide comprising the amino acid sequence shown in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, or SEQ ID NO:54, or a fragment or variant thereof that exhibits substantially the same activity as the full-length non-variant peptide.

[0053] As used herein, the term "expression construct" refers to a combination of nucleic acid sequences that provides for transcription of an operably linked nucleic acid sequence. As used herein, the term "operably linked" refers to a juxtaposition of the components described wherein the components are in a relationship that permits them to function in their intended manner. In general, operably linked components are in contiguous relation.

[0054] Expression constructs of the disclosure n will also generally include regulatory elements that are functional in the intended host cell in which the expression construct is to be expressed. Thus, a person of ordinary skill in the art can select regulatory elements for use in, for example, bacterial host cells, yeast host cells, plant host cells, insect host cells, mammalian host cells, and human host cells. Regulatory elements include promoters, transcription termination sequences, translation termination sequences, enhancers, and polyadenylation elements.

[0055] An expression construct of the disclosure can comprise a promoter sequence operably linked to a polynucleotide sequence encoding a peptide of the invention. Promoters can be incorporated into a polynucleotide using standard techniques known in the art. Multiple copies of promoters or multiple promoters can be used in an expression construct of the invention. A promoter can be positioned about the same distance from the transcription start site as it is from the transcription start site in its natural genetic environment. Some variation in this distance is permitted without substantial decrease in promoter activity. A transcription start site is typically included in the expression construct.

[0056] For expression in animal cells, an expression construct of the disclosure can comprise suitable promoters that can drive transcription of the polynucleotide sequence. If the cells are mammalian cells, then promoters such as, for example, actin promoter, metallothionein promoter, NF-kappaB promoter, EGR promoter, SRE promoter, IL-2 promoter, NFAT promoter, osteocalcin promoter, SV40 early promoter and SV40 late promoter, Lck promoter, BMP5 promoter, TRP-1 promoter, murine mammary tumor virus long terminal repeat promoter, STAT promoter, or an immunoglobulin promoter can be used in the expression construct. The baculovirus polyhedrin promoter can be used with an expression construct of the disclosure for expression in insect cells. Promoters suitable for use with an expression construct of the disclosure in yeast cells include, but are not limited to, 3-phosphoglycerate kinase promoter, glyceraldehyde-3-phosphate dehydrogenase promoter, metallothionein promoter, alcohol dehydrogenase-2 promoter, and hexokinase promoter.

[0057] For expression in prokaryotic systems, an expression construct of the disclosure can comprise promoters such as, for example, alkaline phosphatase promoter, tryptophan (trp) promoter, lambda P_L promoter, β-lactamase promoter, lactose promoter, phoA promoter, T3 promoter, T7 promoter, or tac promoter (de Boer *et al.*, 1983).

[0058] If the expression construct is to be provided in a plant cell, plant viral promoters, such as, for example, the cauliflower mosaic virus (CaMV) 35S (including the enhanced CaMV 35S promoter (see, for example U.S. Patent No. 5,106,739)) or 19S promoter can be used. Plant promoters such as prolifera promoter, Ap3 promoter, heat shock promoters, T-DNA 1'- or 2'-promoter of *A. tumefaciens*, polygalacturonase promoter, chalcone synthase A (CHS-A) promoter from petunia, tobacco PR-1a promoter, ubiquitin promoter, actin promoter, alcA gene promoter, pin2 promoter (Xu *et al.*, 1993), maize Wipl promoter, maize trpA gene promoter (U.S. Patent No. 5,625,136), maize CDPK gene promoter, and RUBISCO SSU promoter (U.S. Patent No. 5,034,322) can also be used. Seed-specific promoters such as the promoter from a β-phaseolin gene (of kidney bean) or a glycinin gene (of soybean), and others, can also be used. Constitutive promoters (such as the CaMV, ubiquitin, actin, or

NOS promoter), tissue-specific promoters (such as the E8 promoter from tomato), developmentally-regulated promoters, and inducible promoters (such as those promoters that can be induced by heat, light, hormones, or chemicals) are contemplated for use with the polynucleotides of the invention.

[0059] Expression constructs of the disclosure may optionally contain a transcription termination sequence, a translation termination sequence, signal peptide sequence, and/or enhancer elements. Transcription termination regions can typically be obtained from the 3' untranslated region of a eukaryotic or viral gene sequence. Transcription termination sequences can be positioned downstream of a coding sequence to provide for efficient termination. Signal peptides are a group of short amino terminal sequences that encode information responsible for the relocation of an operably linked peptide to a wide range of post-translational cellular destinations, ranging from a specific organelle compartment to sites of protein action and the extracellular environment. Targeting a peptide to an intended cellular and/or extracellular destination through the use of operably linked signal peptide sequence is contemplated for use with the peptides of the invention. Chemical enhancers are cis-acting elements that increase gene transcription and can also be included in the expression construct. Chemical enhancer elements are known in the art, and include, but are not limited to, the CaMV 35S enhancer element, cytomegalovirus (CMV) early promoter enhancer element, and the SV40 enhancer element. DNA sequences which direct polyadenylation of the mRNA encoded by the structural gene can also be included in the expression construct.

[0060] Unique restriction enzyme sites can be included at the 5' and 3' ends of the expression construct to allow for insertion into a polynucleotide vector. As used herein, the term "vector" refers to any genetic element, including for example, plasmids, cosmids, chromosomes, phage, virus, and the like, which is capable of replication when associated with proper control elements and which can transfer polynucleotide sequences between cells. Vectors contain a nucleotide sequence that permits the vector to replicate in a selected host cell. A number of vectors are available for expression and/or cloning, and include, but are not limited to, pBR322, pUC series, M13 series, and pBLUESCRIPT vectors (Stratagene, La Jolla, CA).

[0061] Polynucleotides, vectors, and expression constructs of the disclosure can be introduced into a cell by methods known in the art. Such methods include transfection, microinjection, electroporation, lipofection, cell fusion, calcium phosphate precipitation, and by biolistic methods. A polynucleotide or expression construct of the disclosure can be introduced *in vivo* via a viral vector such as adeno-associated virus (AAV), herpes simplex virus (HSV), papillomavirus, adenovirus, and Epstein-Barr virus (EBV). Attenuated or defective forms of viral vectors that can be used with the disclosure are known in the art. Typically, defective virus is not capable of infection after the virus is introduced into a cell. Polynucleotides, vectors, and expression constructs of the disclosure can also be introduced *in vivo* via lipofection (DNA transfection via liposomes prepared from synthetic cationic lipids) (Felgner *et al.*, 1987). Synthetic cationic lipids (LIPOFECTIN, Invitrogen Corp., La Jolla, CA) can be used to prepare liposomes to encapsulate a polynucleotide, vector, or expression construct of the disclosure. A polynucleotide, vector, or expression construct of the disclosure can also be introduced *in vivo* as naked DNA using methods known in the art, such as transfection, microinjection, electroporation, calcium phosphate precipitation, and by biolistic methods.

[0062] Polynucleotides and peptides of the disclosure can also be defined in terms of more particular identity and/or similarity ranges with those exemplified herein. The sequence identity will typically be greater than 60%, preferably greater than 75%, more preferably greater than 80%, even more preferably greater than 90%, and can be greater than 95%. The identity and/or similarity of a sequence

can be 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% as compared to a sequence exemplified herein. Unless otherwise specified, as used herein percent sequence identity and/or similarity of two sequences can be determined using the algorithm of Karlin and Altschul (1990), modified as in Karlin and Altschul (1993). Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul *et al.* (1990). BLAST searches can be performed with the NBLAST program, score = 100, wordlength = 12, to obtain sequences with the desired percent sequence identity. To obtain gapped alignments for comparison purposes, Gapped BLAST can be used as described in Altschul *et al.* (1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (NBLAST and XBLAST) can be used. See NCBI/NIH website.

[0063] The disclosure also contemplates those polynucleotide molecules (encoding peptides of the invention) having sequences which are sufficiently homologous with the polynucleotide sequences encoding a peptide of the invention so as to permit hybridization with that sequence under standard stringent conditions and standard methods (Maniatis, T. *et al.*, 1982). As used herein, "stringent" conditions for hybridization refers to conditions wherein hybridization is typically carried out overnight at 20-25 C below the melting temperature (T_m) of the DNA hybrid in 6x SSPE, 5x Denhardt's solution, 0.1% SDS, 0.1 mg/ml denatured DNA. The melting temperature is described by the following formula (Beltz, G.A. *et al.*, 1983):

$$T_m = 81.5 \text{ } ^\circ\text{C} + 16.6 \text{ Log}[\text{Na}^+] + 0.41(\%G+C) - 0.61(\% \text{ formamide}) - 600/\text{length of duplex in base pairs.}$$

[0064] Washes are typically carried out as follows:

1. (1) Twice at room temperature for 15 minutes in 1x SSPE, 0.1% SDS (low stringency wash).
2. (2) Once at $T_m - 20 \text{ } ^\circ\text{C}$ for 15 minutes in 0.2x SSPE, 0.1% SDS (moderate stringency wash).

[0065] As used herein, the terms "nucleic acid" and "polynucleotide sequence" refer to a deoxyribonucleotide or ribonucleotide polymer in either single- or double-stranded form, and unless otherwise limited, would encompass known analogs of natural nucleotides that can function in a similar manner as naturally-occurring nucleotides. The polynucleotide sequences include both the DNA strand sequence that is transcribed into RNA and the RNA sequence that is translated into protein. The polynucleotide sequences include both full-length sequences as well as shorter sequences derived from the full-length sequences. It is understood that a particular polynucleotide sequence includes the degenerate codons of the native sequence or sequences which may be introduced to provide codon preference in a specific host cell. The polynucleotide sequences falling within the disclosure further include sequences which specifically hybridize with the sequences coding for a peptide of the disclosure. The polynucleotide includes both the sense and antisense strands as either individual strands or in the duplex.

[0066] The disclosure also concerns methods for inhibiting tyrosine kinases, such as JAK2 and TYK2, in a cell. A cell can be contacted with an effective amount of one or more peptide, polynucleotide, or a composition of the disclosure. The peptide can have the amino acid sequence of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30,

SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, or SEQ ID NO:54, or a fragment or variant thereof that exhibits tyrosine kinase inhibitory activity. The composition can comprises a peptide of the disclosure and an anti-inflammatory drug or an immunosuppressant. The cell can be a human or mammalian cell. The cell can be a keratinocyte, a fibroblast, a macrophage, or a lymphocyte. Peptides, polynucleotides, compositions, and/or other agents of the disclosure can be delivered to a cell either through direct contact of peptide, *etc.* with the cell or via a carrier means. Carrier means for delivering compositions to cells are known in the art and include encapsulating the composition in a liposome moiety, and attaching the peptide or polynucleotide to a protein or nucleic acid that is targeted for delivery to the target cell. Published U.S. Patent Application Nos. 20030032594 and 20020120100 disclose amino acid sequences that can be coupled to another peptide, protein, or nucleic acid and that allows the peptide, protein, or nucleic acid to be translocated across biological membranes. Published U.S. Patent Application No. 20020035243 also describes compositions for transporting biological moieties, such as peptides and proteins across cell membranes for intracellular delivery. Peptides can also be delivered using a polynucleotide that encodes a subject peptide. The polynucleotide can be delivered to the cell where it is taken up and the polynucleotide is transcribed into RNA and the RNA is translated into the encoded peptide. Methods of the disclosure can be conducted *in vitro* or *in vivo*.

[0067] The disclosure also concerns methods for preventing or treating an autoimmune and/or inflammatory disorder in a patient. The disorder may be SLE. The disorder can be multiple sclerosis (MS) or experimental allergic encephalitis (EAE). The disorder can be rheumatoid arthritis (RA). The disorder can be psoriasis. The disorder can be uveitis. The disorder can be diabetes. Any autoimmune and/or inflammatory disorder, including, but not limited to, amyotrophic lateral sclerosis, dermatitis, autoimmune peripheral neuropathy, autoimmune thrombocytopenic purpura, autoimmune lymphoproliferative syndrome (ALPS), Crohn's disease, Goodpasture's syndrome, Graves' disease Guillain-Barré syndrome (GBS), idiopathic thrombocytopenic purpura, myasthenia gravis, psoriatic arthritis, rheumatoid arthritis, Sjögren's syndrome, ulcerative colitis, and vasculitis, is included within the disclosure. An effective amount of one or more peptide, polynucleotide, and/or composition of the disclosure can be administered to a patient having an autoimmune and/or inflammatory disorder and who is in need of treatment thereof. Optionally, the patient is a person or animal at risk of developing an autoimmune and/or inflammatory disorder. In the method, the peptide can have the amino acid sequence in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, or SEQ ID NO:54, or a fragment or variant thereof that exhibits tyrosine kinase inhibitory activity. Methods of the disclosure can also further comprise administering one or more compounds or drugs useful for treating an autoimmune and/or inflammatory disorder. Examples of such compounds or drugs include non-steroidal anti-inflammatory drugs (NSAIDs) (such as aspirin, acetaminophen, ibuprofen, nabumetone, and celecoxib), corticosteroids, cyclophosphamide, methotrexate, azathioprine, belimumab, teriflunomide, interferon beta-1a, interferon beta-1b, glatiramer acetate, fingolimod, mitoxantrone, dimethyl fumarate, and/or natalizumab. Such compounds or drugs can be administered prior to, in conjunction with, and/or subsequent to administration of a peptide, polynucleotide, and/or composition of the disclosure. The patient can be a human or other mammal, such as a dog, cat, or horse, or other animals having the disorder. Methods of the disclosure can optionally comprise identifying that a person or animal has or may develop a disorder and is in need of treatment or prevention. Means for administering and formulating peptides and polynucleotides for administration to a patient are known in the art, examples of which are described herein. Peptides, polynucleotides, and/or compositions of the disclosure can be delivered to a cell either through direct contact of peptide, polynucleotide, or composition with the cell or via a carrier means. A peptide, polynucleotide, or composition of the disclosure can comprise an attached group that enhances cellular uptake of the peptide. The peptide,

polynucleotide, or composition can be attached to an antibody that binds to a targeted cell. The peptide, polynucleotide, or composition can be encapsulated in a liposome. Peptides can also be delivered using a polynucleotide that encodes a peptide. Any polynucleotide having a nucleotide sequence that encodes a peptide of the invention is contemplated. The polynucleotide can be delivered to the cell where it is taken up and the polynucleotide is transcribed into RNA and the RNA is translated into the encoded peptide.

[0068] The disclosure also concerns methods for treating an oncological disorder (e.g., cancer) or an autoimmune disorder in a patient. An effective amount of one or more peptide, polynucleotide, or composition of the disclosure can be administered to a patient having an oncological disorder or an autoimmune disorder and who is in need of treatment thereof. The disclosure also concerns methods for inhibiting the growth of a cancer cell by contacting the cell *in vitro* or *in vivo* with an effective amount of a peptide, polynucleotide, or composition of the disclosure. The peptide can have the amino acid sequence in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, or SEQ ID NO:54, or a fragment or variant thereof that exhibits tyrosine kinase inhibitory activity. Methods of the disclosure can also further comprise administering or contacting a cell with one or more compounds for treating an oncological or autoimmune disorder. Such compounds can be administered prior to, in conjunction with, and/or subsequent to administration of a peptide, polynucleotide, and/or composition of the disclosure. Methods of the disclosure can optionally include identifying a patient who is or may be in need of treatment of an oncological or autoimmune disorder. The patient can be a human or other mammal, such as a primate (monkey, chimpanzee, ape, *etc.*), dog, cat, cow, pig, or horse, or other animals having an oncological disorder. Means for administering and formulating peptides, polynucleotides, or compositions of the disclosure for administration to a patient are known in the art, examples of which are described herein. A SOCS1-KIR (SEQ ID NO:1) peptide, or a peptide dimer (SEQ ID NO:3 or SEQ ID NO:29), or a SOCS3-KIR (SEQ ID NO:51) peptide, or a peptide dimer (SEQ ID NO:52 or SEQ ID NO:54), or a polynucleotide encoding the peptide, can be used to treat a person or animal having the disorder. Oncological disorders within the disclosure include, but are not limited to, cancer and/or tumors of the anus, bile duct, bladder, bone, bone marrow, bowel (including colon and rectum), breast, eye, gall bladder, kidney, mouth, larynx, esophagus, stomach, testis, cervix, head, neck, ovary, lung, mesothelioma, neuroendocrine, penis, skin, spinal cord, thyroid, vagina, vulva, uterus, liver, muscle, pancreas, prostate, blood cells (including lymphocytes and other immune system cells), and brain. Specific cancers contemplated for treatment include carcinomas, Kaposi's sarcoma, melanoma, mesothelioma, soft tissue sarcoma, pancreatic cancer, lung cancer, leukemia (hairy cell, acute lymphoblastic, acute myeloid, chronic lymphocytic, chronic myeloid, and other), and lymphoma (Hodgkin's and non-Hodgkin's), and follicular lymphoma, and multiple myeloma.

[0069] Examples of cancers that can be treated according to the disclosure are listed in Table 3.

Table 3. Examples of Cancer Types

Acute Lymphoblastic Leukemia, Adult	Hairy Cell Leukemia
Acute Lymphoblastic Leukemia, Childhood	Head and Neck Cancer
Acute Myeloid Leukemia, Adult	Hepatocellular (Liver) Cancer, Adult (Primary)
Acute Myeloid Leukemia, Childhood	Hepatocellular (Liver) Cancer, Childhood (Primary)
Adrenocortical Carcinoma	
Adrenocortical Carcinoma, Childhood	Hodgkin's Lymphoma, Adult

AIDS-Related Cancers	Hodgkin's Lymphoma, Childhood
AIDS-Related Lymphoma	Hodgkin's Lymphoma During Pregnancy
Anal Cancer	Hypopharyngeal Cancer
Astrocytoma, Childhood Cerebellar Astrocytoma, Childhood Cerebral	Hypothalamic and Visual Pathway Glioma, Childhood
Basal Cell Carcinoma	Intraocular Melanoma
Bile Duct Cancer, Extrahepatic	Islet Cell Carcinoma (Endocrine Pancreas)
Bladder Cancer	
Bladder Cancer, Childhood	Kaposi's Sarcoma
Bone Cancer, Osteosarcoma/Malignant	Kidney (Renal Cell) Cancer
Fibrous Histiocytoma	Kidney Cancer, Childhood
Brain Stem Glioma, Childhood	
Brain Tumor, Adult	Laryngeal Cancer
Brain Tumor, Brain Stem Glioma, Childhood	Laryngeal Cancer, Childhood
	Leukemia, Acute Lymphoblastic, Adult
Brain Tumor, Cerebellar Astrocytoma, Childhood	Leukemia, Acute Lymphoblastic, Childhood
	Leukemia, Acute Myeloid, Adult
Brain Tumor, Cerebral	Leukemia, Acute Myeloid, Childhood
Astrocytoma/Malignant Glioma, Childhood	Leukemia, Chronic Lymphocytic
	Leukemia, Chronic Myelogenous
Brain Tumor, Ependymoma, Childhood	Leukemia, Hairy Cell
	Lip and Oral Cavity Cancer
Brain Tumor, Medulloblastoma, Childhood	Liver Cancer, Adult (Primary)
	Liver Cancer, Childhood (Primary)
Brain Tumor, Supratentorial Primitive	Lung Cancer, Non-Small Cell
Neuroectodermal Tumors, Childhood	Lung Cancer, Small Cell
Brain Tumor, Visual Pathway and	Lymphoma, AIDS-Related
Hypothalamic Glioma, Childhood	Lymphoma, Burkitt's
Brain Tumor, Childhood	Lymphoma, Cutaneous T-Cell, see Mycosis
Breast Cancer	Fungoides and Sézary Syndrome
Breast Cancer, Childhood	Lymphoma, Hodgkin's, Adult
Breast Cancer, Male	Lymphoma, Hodgkin's, Childhood
Bronchial Adenomas/Carcinoids, Childhood	Lymphoma, Hodgkin's During Pregnancy
	Lymphoma, Non-Hodgkin's, Adult

Burkitt's Lymphoma	Lymphoma, Non-Hodgkin's, Childhood
	Lymphoma, Non-Hodgkin's During Pregnancy
Carcinoid Tumor, Childhood	
Carcinoid Tumor, Gastrointestinal	Lymphoma, Primary Central Nervous System
Carcinoma of Unknown Primary	
Central Nervous System Lymphoma, Primary	Macroglobulinemia, Waldenström's
Cerebellar Astrocytoma, Childhood	Malignant Fibrous Histiocytoma of Bone/Osteosarcoma
Cerebral Astrocytoma/Malignant	Medulloblastoma, Childhood
Glioma, Childhood	Melanoma
Cervical Cancer	Melanoma, Intraocular (Eye)
Childhood Cancers	Merkel Cell Carcinoma
Chronic Lymphocytic Leukemia	Mesothelioma, Adult Malignant
Chronic Myelogenous Leukemia	Mesothelioma, Childhood
Chronic Myeloproliferative Disorders	Metastatic Squamous Neck Cancer with Occult Primary
Colon Cancer	
Colorectal Cancer, Childhood	Multiple Endocrine Neoplasia Syndrome, Childhood
Cutaneous T-Cell Lymphoma, see Mycosis Fungoides and Sézary Syndrome	Multiple Myeloma/Plasma Cell Neoplasm
	Mycosis Fungoides
	Myelodysplastic Syndromes
Endometrial Cancer	Myelodysplastic/Myeloproliferative Diseases
Ependymoma, Childhood	Myelogenous Leukemia, Chronic
Esophageal Cancer	Myeloid Leukemia, Adult Acute
Esophageal Cancer, Childhood	Myeloid Leukemia, Childhood Acute
Ewing's Family of Tumors	Myeloma, Multiple
Extracranial Germ Cell Tumor, Childhood	Myeloproliferative Disorders, Chronic
Extragenital Germ Cell Tumor	Nasal Cavity and Paranasal Sinus Cancer
Extrahepatic Bile Duct Cancer	Nasopharyngeal Cancer
Eye Cancer, Intraocular Melanoma	Nasopharyngeal Cancer, Childhood
Eye Cancer, Retinoblastoma	Neuroblastoma
	Non-Hodgkin's Lymphoma, Adult
Gallbladder Cancer	Non-Hodgkin's Lymphoma,

	Childhood
Gastric (Stomach) Cancer	Non-Hodgkin's Lymphoma During
Gastric (Stomach) Cancer, Childhood	Pregnancy
Gastrointestinal Carcinoid Tumor	Non-Small Cell Lung Cancer
Germ Cell Tumor, Extracranial, Childhood	
	Oral Cancer, Childhood
Germ Cell Tumor, Extragonadal	Oral Cavity Cancer, Lip and
Germ Cell Tumor, Ovarian	Oropharyngeal Cancer
Gestational Trophoblastic Tumor	Osteosarcoma/Malignant Fibrous
Glioma, Adult	Histiocytoma of Bone
Glioma, Childhood Brain Stem	Ovarian Cancer, Childhood
Glioma, Childhood Cerebral	Ovarian Epithelial Cancer
Astrocytoma	Ovarian Germ Cell Tumor
Glioma, Childhood Visual Pathway and Hypothalamic	Ovarian Low Malignant Potential Tumor
	Pancreatic Cancer
Skin Cancer (Melanoma)	Pancreatic Cancer, Childhood
Skin Carcinoma, Merkel Cell	Pancreatic Cancer, Islet Cell
Small Cell Lung Cancer	Paranasal Sinus and Nasal Cavity Cancer
Small Intestine Cancer	Parathyroid Cancer
Soft Tissue Sarcoma, Adult	Penile Cancer
Soft Tissue Sarcoma, Childhood	Pheochromocytoma
Squamous Cell Carcinoma, see Skin Cancer (non-Melanoma)	Pineoblastoma and Supratentorial Primitive
	Neuroectodermal Tumors, Childhood
Squamous Neck Cancer with Occult	Pituitary Tumor
Primary, Metastatic	Plasma Cell Neoplasm/Multiple Myeloma
Stomach (Gastric) Cancer	Pleuropulmonary Blastoma
Stomach (Gastric) Cancer, Childhood	Pregnancy and Breast Cancer
Supratentorial Primitive	Pregnancy and Hodgkin's Lymphoma
Neuroectodermal Tumors, Childhood	Pregnancy and Non-Hodgkin's Lymphoma
	Primary Central Nervous System Lymphoma
T-Cell Lymphoma, Cutaneous, see Mycosis Fungoides and Sézary	Prostate Cancer
Syndrome	Rectal Cancer

Testicular Cancer	Renal Cell (Kidney) Cancer
Thymoma, Childhood	Renal Cell (Kidney) Cancer, Childhood
Thymoma and Thymic Carcinoma	Renal Pelvis and Ureter, Transitional Cell Cancer
Thyroid Cancer	
Thyroid Cancer, Childhood	Retinoblastoma
Transitional Cell Cancer of the Renal Pelvis and Ureter	Rhabdomyosarcoma, Childhood
Trophoblastic Tumor, Gestational	Salivary Gland Cancer
	Salivary Gland Cancer, Childhood
Unknown Primary Site, Carcinoma of, Adult	Sarcoma, Ewing's Family of Tumors
	Sarcoma, Kaposi's
Unknown Primary Site, Cancer of, Childhood	Sarcoma, Soft Tissue, Adult
	Sarcoma, Soft Tissue, Childhood
Unusual Cancers of Childhood	Sarcoma, Uterine
Ureter and Renal Pelvis, Transitional	Sezary Syndrome
Cell Cancer	Skin Cancer (non-Melanoma)
Urethral Cancer	Skin Cancer, Childhood
Uterine Cancer, Endometrial	
Uterine Sarcoma	
Vaginal Cancer	
Visual Pathway and Hypothalamic	
Glioma, Childhood	
Vulvar Cancer	
Waldenström's Macroglobulinemia Wilms' Tumor	

[0070] For the treatment of oncological disorders, the peptides, polynucleotides, and compositions of this disclosure can be administered to a patient in need of treatment in combination with other antitumor or anticancer substances and/or with radiation and/or photodynamic therapy and/or with surgical treatment to remove a tumor. These other substances or treatments may be given at the same as or at different times from the peptides, polynucleotides, and compositions of this disclosure. For example, the peptides, polynucleotides, and compositions of the disclosure can be used in combination with mitotic inhibitors such as taxol or vinblastine, alkylating agents such as cyclophosphamide or ifosfamide, antimetabolites such as 5-fluorouracil or hydroxyurea, DNA intercalators such as adriamycin or bleomycin, topoisomerase inhibitors such as etoposide or camptothecin, antiangiogenic agents such as angiostatin, antiestrogens such as tamoxifen, and/or other anti-cancer drugs or antibodies, such as, for example, GLEEVEC (Novartis Pharmaceuticals Corporation) and HERCEPTIN (Genentech, Inc.), respectively. Peptides, polynucleotides, and compositions of the invention can be used in combination with proteasome inhibitors, including, but not limited to, Bortezomib, Carfilzomib, and Salinosporamide A. The disclosure also concerns methods for inhibiting

the growth of a cancer cell by contacting the cell *in vitro* or *in vivo* with an effective amount of a peptide, polynucleotide, or composition of the disclosure.

[0071] Many tumors and cancers have viral genome present in the tumor or cancer cells. For example, Epstein-Barr Virus (EBV) is associated with a number of mammalian malignancies. The peptides, polynucleotides, and compositions of the disclosure can also be used alone or in combination with anticancer or antiviral agents, such as ganciclovir, azidothymidine (AZT), lamivudine (3TC), *etc.*, to treat patients infected with a virus that can cause cellular transformation and/or to treat patients having a tumor or cancer that is associated with the presence of viral genome in the cells.

[0072] The methods of the disclosure can be used with humans and other animals. The other animals contemplated include domesticated, agricultural, or zoo- or circus-maintained animals. Domesticated animals include, for example, dogs, cats, rabbits, ferrets, guinea pigs, hamsters, pigs, monkeys or other primates, and gerbils. Agricultural animals include, for example, horses, mules, donkeys, burros, cattle, cows, pigs, sheep, and alligators. Zoo- or circus-maintained animals include, for example, lions, tigers, bears, camels, giraffes, hippopotamuses, and rhinoceroses.

[0073] One or more of the peptides of the disclosure can be provided in the form of a multiple peptide construct. Such a construct can be designed so that multiple peptides are linked to each other by intervening moieties wherein the intervening moieties are subsequently cleaved or removed following administration of the multiple peptide construct to a patient. Methods for constructing multiple peptide constructs are known in the art. For example, peptides of the present invention can be provided in the form of a multiple antigenic peptide (MAP) construct. The preparation of MAP constructs has been described in Tam (1988). MAP constructs utilize a core matrix of lysine residues onto which multiple copies of an immunogen are synthesized. Multiple MAP constructs, each containing different peptides, can be prepared and administered in accordance with methods of the disclosure. A multiple peptide construct can be prepared by preparing the subject peptides having at least one metal chelating amino acid incorporated therein, preferably at the amino and/or carboxy terminal of the peptide as described, for example, in U.S. Patent No. 5,763,585. The peptides are then contacted with a solid support having attached thereto a metal ion specific for the metal chelating amino acid of the peptide. A multiple peptide construct of the disclosure can provide multiple copies of the exact same peptide, including variants or fragments of a subject peptide, or copies of different peptides of the disclosure.

[0074] Therapeutic application of the subject peptides, polynucleotides, and compositions containing them, can be accomplished by any suitable therapeutic method and technique presently or prospectively known to those skilled in the art. The peptides and polynucleotides can be administered by any suitable route known in the art including, for example, topical, oral, nasal, rectal, parenteral, subcutaneous, or intravenous routes of administration. Administration of the peptides and polynucleotides of the disclosure can be continuous or at distinct intervals as can be readily determined by a person skilled in the art.

[0075] Compounds and compositions useful in the disclosure can be formulated according to known methods for preparing pharmaceutically useful compositions. Formulations are described in detail in a number of sources which are well known and readily available to those skilled in the art. For example, Remington's Pharmaceutical Science by E.W. Martin describes formulations which can be used in connection with the subject invention. In general, the compositions of the subject invention will be formulated such that an effective amount of the bioactive peptide or polynucleotide is combined with a suitable carrier in order to facilitate effective administration of the composition. The compositions used

in the methods can also be in a variety of forms. These include, for example, solid, semisolid, and liquid dosage forms, such as tablets, pills, powders, liquid solutions or suspension, suppositories, injectable and infusible solutions, and sprays. The preferred form depends on the intended mode of administration and therapeutic application. The compositions also preferably include conventional pharmaceutically acceptable carriers and diluents which are known to those skilled in the art. Examples of carriers or diluents for use with the subject peptides and polynucleotides include, but are not limited to, water, saline, oils including mineral oil, ethanol, dimethyl sulfoxide, gelatin, cyclodextrans, magnesium stearate, dextrose, cellulose, sugars, calcium carbonate, glycerol, alumina, starch, and equivalent carriers and diluents, or mixtures of any of these. Formulations of the peptide or polynucleotide of the invention can also comprise suspension agents, protectants, lubricants, buffers, preservatives, and stabilizers. To provide for the administration of such dosages for the desired therapeutic treatment, pharmaceutical compositions of the invention will advantageously comprise between about 0.1% and 45%, and especially, 1 and 15% by weight of the total of one or more of the peptide or polynucleotide based on the weight of the total composition including carrier or diluent.

[0076] The peptides, polynucleotides, and compositions of the subject invention can also be administered utilizing liposome technology, slow release capsules, implantable pumps, and biodegradable containers. These delivery methods can, advantageously, provide a uniform dosage over an extended period of time.

[0077] The subject peptides and polynucleotides can also be modified by the addition of chemical groups, such as PEG (polyethylene glycol). PEGylated peptides typically generate less of an immunogenic response and exhibit extended half-lives *in vivo* in comparison to peptides that are not PEGylated when administered *in vivo*. Methods for PEGylating proteins and peptides known in the art (see, for example, U.S. Patent No. 4,179,337). The subject peptides and polynucleotides can also be modified to improve cell membrane permeability. Cell membrane permeability can be improved by attaching a lipophilic moiety, such as a steroid, to the peptide or polynucleotide. Peptides and polynucleotides of the disclosure can comprise a cell-penetrating peptide (CPP). CPPs are typically short peptides that are highly cationic and typically include several arginine and/or lysine amino acids. CPPs can be classified as hydrophilic, amphiphilic, or periodic sequence. A CPP can be provided at the terminus of a peptide or polynucleotide. Examples of CPPs include, but are not limited to penetratin or antennapedia PTD (RQIKWFFQNRRMKWKK) (SEQ ID NO:31), TAT (YGRKKRRQRRR) (SEQ ID NO:32), SynB1 (RGGRLSYSRRRFSTSTGR) (SEQ ID NO:33), SynB3 (RRLSYSRRRF) (SEQ ID NO:34), PTD-4 (PIRRRKLRRLK) (SEQ ID NO:35), PTD-5 (RRQRRTSKLMKR) (SEQ ID NO:36), FHV Coat-(35-49) (RRRRNRTRNRNRVR) (SEQ ID NO:37), BMV Gag-(7-25) (KMTRAQRRAAARRNRWTAR) (SEQ ID NO:38), HTLV-II Rex-(4-16) (TRRQRTRRRARRNR) (SEQ ID NO:39), D-Tat (GRKKRRQRRRPPQ) (SEQ ID NO:40), R9-Tat (GRRRRRRRRRPPQ) (SEQ ID NO:41), Transportan (GWTLSAGYLLGKINLKALAALAKKIL) (SEQ ID NO:42) chimera, MAP (KLALKLALKLALALKLA) (SEQ ID NO:43), SBP (MGLGLHLLVLAALQGAWSQPKKKRKV) (SEQ ID NO:44), FBP (GALFLGWLGAAGSTMGAWSQPKKKRKV) (SEQ ID NO:45), MPG (ac-GALFLGFLGAAGSTMGAWSQPKKKRKV-cya) (SEQ ID NO:46), MPG(Δ NLS) (ac-GALFLGFLGAAGSTMGAWSQPKSKRKV-cya) (SEQ ID NO:47), Pep-1 (ac-KETWWETWWTEWSQPKKKRKV-cya) (SEQ ID NO:48), and Pep-2 (ac-KETWFETWFTEWSQPKKKRKV-cya) (SEQ ID NO:49). Other CPPs can have only arginine (R) or only lysine (K) amino acids, e.g., having a formula (R)_n or (K)_n, where n = an integer from 3 to 20. Other groups known in the art for providing for cell membrane permeability can be linked to peptides and polynucleotides of the present invention.

[0078] The disclosure also concerns a packaged dosage formulation comprising in one or more containers at least one peptide, polynucleotide, and/or composition of the disclosure formulated in a pharmaceutically acceptable dosage. The package can contain discrete quantities of the dosage formulation, such as tablet, capsules, lozenge, and powders. The quantity of peptide and/or polynucleotide in a dosage formulation and that can be administered to a patient can vary from about 1 mg to about 5000 mg, or about 1 mg to about 2000 mg, or more typically about 1 mg to about 500 mg, or about 5 mg to about 250 mg, or about 10 mg to about 100 mg.

[0079] The disclosure also concerns kits comprising one or more peptides, polynucleotides, compositions, compounds, or molecules of the disclosure in one or more containers. A kit can contain a peptide, polynucleotide, and/or composition of the present invention. A kit can comprise a peptide comprising the amino acid sequence shown in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, or SEQ ID NO:54, or a fragment or variant of the peptide that exhibits substantially the same activity as the full-length non-variant peptide e.g., tyrosine kinase inhibitory activity. A kit of the disclosure can also comprise, in addition to a peptide, polynucleotide, and/or composition of the invention, one or more compounds, biological molecules, or drugs for treating an autoimmune or an oncological disorder. For example, a kit can comprise one or more of non-steroidal anti-inflammatory drugs (NSAIDs) (such as aspirin, acetaminophen, ibuprofen, nabumetone, and celecoxib), corticosteroids, cyclophosphamide, methotrexate, azathioprine, belimumab, teriflunomide, interferon beta-1a, interferon beta-1b, glatiramer acetate, fingolimod, mitoxantrone, dimethyl fumarate, and/or natalizumab. A kit can comprise one or more of mitotic inhibitors such as taxol or vinblastine, alkylating agents such as cyclophosphamide or ifosfamide, antimetabolites such as 5-fluorouracil or hydroxyurea, DNA intercalators such as adriamycin or bleomycin, topoisomerase inhibitors such as etoposide or camptothecin, antiangiogenic agents such as angiostatin, antiestrogens such as tamoxifen, and/or other anti-cancer drugs or antibodies, such as, for example, GLEEVEC (imatinib) (Novartis Pharmaceuticals Corporation) and HERCEPTIN (trastuzumab) (Genentech, Inc.), respectively.

[0080] A kit of the disclosure includes instructions or packaging materials that describe how to administer a peptide, polynucleotide, compositions, compounds, or molecules of the kit. Containers of the kit can be of any suitable material, e.g., glass, plastic, metal, etc., and of any suitable size, shape, or configuration. A peptide, polynucleotide, compositions, compounds, or molecules of the disclosure can be provided in the kit as a solid, such as a tablet, pill, or powder form. A peptide, polynucleotide, compositions, compounds, or molecules of the disclosure can be provided in the kit as a liquid or solution. The kit may comprise an ampoule or syringe containing a peptide, polynucleotide, compositions, compounds, or molecules of the disclosure in liquid or solution form.

[0081] The disclosure concerns peptide mimetics of suppressor of cytokine signaling 1 (SOCS 1) and methods of use. They are active against SOCS targets, including both SOCS 1 and SOCS3 tyrosine kinase targets. SOCS1 and SOCS3 are two important intracellular protein members of the eight-member SOCS family. SOCS1 and SOCS3 are particularly important physiologically in modulation of the immune system in protection against autoimmune diseases such as multiple sclerosis, lupus erythematosus, and psoriasis. The SOCS mimetics of the disclosure possess broad anti-autoimmune properties. The mimetics are small peptides (see, for example, SEQ ID NOs:1-4, 27-30, and 51-54) that have the common property of binding to the activation loop of the JAK2 and/or TYK2 tyrosine kinases. These JAK kinases play a critical role of mediation of signal transduction events of cytokines that have been implicated or associated with a range of autoimmune disorders. Notably, chemical

tyrosine kinase inhibitors are currently utilized in various inflammation based cancers and leukocytic proliferative disorders. As such, SOCS mimetics of the disclosure are an attractive alternative to chemical tyrosine kinase inhibitors which possess significant negative side effects.

[0082] The SOCS mimetics of the disclosure can be engineered for cell membrane penetration where they can bind to the JAKs in the cytoplasm of the cell. The mimetics were developed to bind to JAK2 and/or TYK2 at the activation loop of the JAKs. The SOCS1-KIR mimetic as a dimer with a six glycine (G) linker (SEQ ID NO:3) significantly increased the avidity for the activation loop of JAK2 with increased anti-cellular activity. Thus, multimers increase binding for increased biological effect. The N-terminus of SOCS 1 and SOCS3 contain a short 12 amino acid kinase inhibitory region (KIR). Studies by others showed that KIR was important for SOCS1 and SOCS3 function, but not by binding to the activation loop of JAK2 and TYK2. Thus, our demonstration of such binding played an important role in our reasoning that analogs or sequences of KIR should function as SOCS mimetics if internalized in the cell.

[0083] The disclosure can be used in gene therapy to treat a disease or condition in a person or animal. The disorder can be SLE. The disorder can be multiple sclerosis (MS) or experimental allergic encephalitis (EAE). The disorder can be rheumatoid arthritis (RA). The disorder can be psoriasis. The disorder can be uveitis. The disorder can be diabetes or vascular problems such as vascular plaque accumulation. Any autoimmune and/or inflammatory disorder, including, but not limited to, amyotrophic lateral sclerosis, dermatitis, autoimmune peripheral neuropathy, autoimmune thrombocytopenic purpura, autoimmune lymphoproliferative syndrome (ALPS), Crohn's disease, Goodpasture's syndrome, Graves' disease Guillain-Barré syndrome (GBS), idiopathic thrombocytopenic purpura, myasthenia gravis, Parkinson's disease, psoriatic arthritis, rheumatoid arthritis, Sjögren's syndrome, ulcerative colitis, and vasculitis, is included within the disclosure. A polynucleotide of the invention can be incorporated into a cell or cells of a person or animal, and the polynucleotide expressed in the cell to produce a peptide of the invention. A cell can be removed from the body of the person or animal, the polynucleotide incorporated into the cell, and the cell then reintroduced back into the body of the person or animal and the polynucleotide expressed in the cell. The polynucleotide can be stably incorporated into the genome of the cell. The polynucleotide can be provided in an expression construct that provides for expression of the polynucleotide in the cell. The peptide expressed in the cell can be transported outside the cell and into the extracellular space of the person or animal.

[0084] Any methods of the disclosure can optionally include a step of identifying a person or animal who is or who may be in need of treatment or prevention of a disease, disorder, or condition.

[0085] Biological samples refer to a fluid or tissue composition obtained from a human or animal. Biological samples within the scope of the invention include, but are not limited to, cells, whole blood, peripheral blood, blood plasma, bone marrow, spleen, serum, urine, tears, saliva, sputum, exhaled breath, nasal secretions, pharyngeal exudates, bronchoalveolar lavage, tracheal aspirations, interstitial fluid, lymph fluid, meningeal fluid, amniotic fluid, glandular fluid, feces, perspiration, mucous, vaginal or urethral secretion, cerebrospinal fluid, and transdermal exudate. A biological sample also includes experimentally separated fractions of all of the preceding solutions or mixtures containing homogenized solid material, such as feces, cells, tissues, and biopsy samples.

[0086] The disclosure also concerns methods for diagnosing and/or monitoring progression of an autoimmune or inflammatory disorder such as systemic lupus erythematosus (SLE) or a similar or related condition in a person or animal. The disorder can be Sjögren's syndrome or dermatitis. A

method of the disclosure can comprise optionally obtaining a biological sample from the person or animal, and determining SOCS1 and/or SOCS3 RNA and/or protein levels of a cell from the person or animal, wherein reduced levels are indicative of SLE in the person or animal. The levels can be compared to the levels of a normal or healthy control person or animal. The levels can be compared to levels from the same person or animal obtained at an earlier time point. The levels can be compared to a predetermined baseline level. Any method for screening or determining RNA or protein levels can be used with the methods. SOCS1 and/or SOCS3 RNA levels can be determined using RT-PCR. RNA levels can be determined using a cDNA or oligonucleotide microarray assay, or a Northern blot assay. SOCS1 and/or SOCS3 protein levels can be determined using an antibody based assay, including, but not limited to, Western blotting or an ELISA assay. The method also further comprises treating the person or animal for SLE if the results are indicative that the person or animal has SLE or a similar or related condition. Treatment can include administration of any known and/or approved treatment for SLE, including but not limited to, prednisone and plaquenil. Treatment can include the use or administration of one or more peptide mimetics of the invention. The level of STAT1 activation can also be determined, wherein reduced SOCS1 levels in an SLE patient are correlated with enhanced STAT1 activation (phosphorylation of STAT1). The level of interferon gamma (IFN γ) and/or interleukin-27 (IL27) can also be determined, wherein reduced IFN γ in an SLE patient is positively correlated with SOCS1 and SOCS3 levels.

[0087] The disclosure also concerns methods for screening for a drug or compound to treat an autoimmune or inflammatory disorder, such as SLE or a similar or related condition in a person or animal. A method can comprise optionally obtaining a biological sample from the person or animal, and determining SOCS 1 and/or SOCS3 RNA and/or protein levels of a cell from the person or animal, wherein the person or animal has received a drug or compound for treating the disorder or the person or animal has received a drug or compound that is being evaluated for efficacy in treating the disorder prior to determining SOCS1 and/or SOCS3 levels in the person or animal. A drug or compound that increases levels of SOCS1 and/or SOCS3 in the person or animal would be indicative of a drug or compound that may be beneficial in treating a disorder in a person or animal. Levels of SOCS 1 and/or SOCS3 can be compared to baseline levels of SOCS1 and/or SOCS3 from the same person or animal taken prior to administration of the drug or compound. The levels of SOCS1 and/or SOCS3 can be compared to an established baseline level of SOCS1 and/or SOCS3 of patients having the disorder. The levels of SOCS1 and/or SOCS3 RNA and/or protein can be determined at various time intervals for the person or animal, e.g., every day, every few days, every week, every two weeks, every month, every two or three months, or any other time interval. Any method for screening or determining RNA or protein levels can be used with the methods. SOCS1 and/or SOCS3 RNA levels can be determined using RT-PCR. RNA levels can be determined using a cDNA or oligonucleotide microarray assay, or a Northern blot assay.

[0088] The disclosure also concerns methods for monitoring the progression of an autoimmune or inflammatory disorder, such as SLE or a similar or related condition in a person or animal. A method of the disclosure comprises optionally obtaining a biological sample from the person or animal, and determining SOCS1 and/or SOCS3 RNA and/or protein levels of a cell from the person or animal, wherein decreasing levels are indicative of worsening of disease and increasing levels are indicative of improvement of disease in the person or animal. The levels of SOCS1 and/or SOCS3 RNA and/or protein can be determined at various time intervals for the person or animal, e.g., every day, every few days, every week, every two weeks, every month, every two or three months, or any other time interval recommended or required by a clinician. The levels of SOCS 1 and/or SOCS3 RNA and/or protein can be compared to previously determined levels of the person or animal being evaluated or to a level of a

control person or animal or to a predetermined baseline level. Any method for screening or determining RNA or protein levels can be used with the methods. SOCS1 and/or SOCS3 RNA levels can be determined using RT-PCR. RNA levels can be determined using a cDNA or oligonucleotide microarray assay, or a Northern blot assay.

MATERIALS AND METHODS FOR EXAMPLES 1-12

[0089] Mice. SOCS1^{+/-} and SOCS1^{+/+} (WT) mice were generated as previously described (Collins *et al.* 2011). Briefly, SOCS1^{+/-} mice, on a C56BL/6 genetic background, were purchased from the St. Jude animal facility (Memphis, TN) and mated, generating WT, SOCS1^{+/-}, and SOCS1^{-/-} mice. SOCS1^{+/-} and WT littermate control mice were chosen for experiments. SOCS1^{+/-}IFN γ ^{-/-} mice were also purchased from the St. Jude animal facility. Mice were maintained under specific pathogen free conditions at the University of Florida Cancer and Genetics Animal Care Facility.

[0090] Genotyping. Mouse genotyping was performed similar to (Collins *et al.* 2011). In brief, mouse tail clips (1mm) were degraded using the DNAeasy Blood and Tissue Kit (Quiagen, Valencia, CA) to extract DNA, followed by quantitative PCR (qPCR) to assess of the presence SOCS1 using iQTM SYBR Green Supermix (BioRad, Hercules, CA) and primers specific for SOCS1 (forward: 5'-GACACTCACTTCCGCACCTT-3' (SEQ ID NO:5); reverse: 5'-GAAGCAGTTCCGTTGGCGACT-3') (SEQ ID NO:6) or β -actin (forward: 5'-CCACAGCACTGTAGGGTTTA-3' (SEQ ID NO:7); reverse: 5'ATTGTCTTTCTTCTGCCGTTCTC-3' (SEQ ID NO:8)) (200 nM) which were used to amplify and quantify relative amounts of DNA on a PTC-200 Peltier Thermal Cycler with a CHROMO 4 Continuous Fluorescence Detector (BioRad, Hercules, CA). Mouse genotype was determined by relative expression of SOCS1. Expression was calculated using the $\Delta\Delta$ CT method.

[0091] Human Subjects. 17 SLE patients (16 females and 1 male; mean age: 48) and 8 healthy controls (5 females and 3 males; mean age: 30) were enrolled in this study. All SLE patients were diagnosed by the 1982 SLE criteria (Tan *et al.* 1982). Subjects with active infections and patients treated with mofetil mycophenolate, azathioprine, methotrexate, or systemic corticosteroids were excluded. This study was approved by the University of Florida Institutional Review Board (IRB).

[0092] Isolation of Human PBMCs. PBMCs were purified from heparinized blood by Ficoll-Paque gradient centrifugation. Briefly, whole blood was diluted with PBS (1:1) and gently layered on the Ficoll (Lymphocyte Separation Medium; Cellgro, Manassas, VA). Cells were centrifuged continuously at 400xg for 20 minutes. PBMCs were collected from the interface layer and washed 3 times with PBS. After isolation, PBMCs were harvested for CD64 surface staining, as previously described (Li *et al.* 2010), or lysed with RNA lysis buffer (Promega) and stored at -80°C until RNA extraction and qPCR protocols were performed.

[0093] Peptide Synthesis. The SOCS1-KIR peptide (⁵³DTHFRFTRSHSDYRRI) (SEQ ID NO:1) was synthesized using conventional fluorenylmethylcarbonyl chemistry, as previously described (Szente *et al.* 1994) using an Applied Biosystems 431A automated peptide synthesizer (Applied Bio- systems, Carlsbad, CA). For cell penetration, using a semi-automated protocol (Thiam *et al.* 1999), we added a lipophilic group (palmitoyl-lysine) to the amino terminus as a final step. The peptide was characterized using mass spectrometry and purified by HPLC. Once synthesized, SOCS1-KIR peptide was

resuspended in DMSO (Sigma- Aldrich, St. Louis, MO) and used for *in vitro* cell culture experiments.

[0094] Surface and Intracellular Staining. To assess *ex vivo* T cell populations, single-cell suspensions were obtained from the thymus or pooled lymph nodes (axillary, brachial, cervical, inguinal, and mesenteric) and spleen. Aliquots of these organ-specific cell suspensions were stained as with the following monoclonal antibodies (mAb): anti-CD4-Pacific Blue (RM4-5; BD Biosciences, San Diego, CA) and anti-CD8a-Alexa Flour 700 (53-6.7; BD Biosciences). To determine the activation status of peripheral CD4⁺ T cells, *ex vivo*, LN and spleen suspensions were also stained with anti-CD25-allophycocyanin (PC61; BD Biosciences) and anti-CD69-APC (H1.2F3; BD Biosciences). To assess CD4⁺ T cell activation, *in vitro*, the same mAbs toward CD25 and CD69 were used as previously described for *ex vivo* experiments.

[0095] Foxp3 and IL-17A intracellular staining (ICS) were employed to assess *in vitro* Treg and Th17 induction, respectively. For Foxp3 ICS, cells were fixed and permeabilized using the reagents provided by the Foxp3 / Transcription Factor Staining Buffer Set (eBioscience). Cells were then stained with anti-Foxp3-FITC (FJK-16s; eBioscience) Ab. For IL-17A and IFN γ ICS, prior to staining, cells were incubated with PMA (50ng/ml), ionomycin (1 μ M; Sigma - Aldrich, St. Louis, MO), and brefeldin A (10 μ g/ml; MP Biomedicals, Solon, OH) for 4 hours at 37°C, as previously described (Bedoya *et al.* 2013). Cells were then fixed and permeabilized using the reagents provided by the Intracellular Cytokine Staining Starter Kit -Mouse (BD Biosciences). Following fixation and permeabilization, cells were stained with an anti-IL17A-Alexa Flour 700 or an anti-IFN γ -PE mAb. After staining (surface and ICS), a total of 50,000 live events were collected on an LSRII (BD Pharmingen) and analyzed using FlowJo software (Tree Star, San Carlos, CA).

[0096] Magnetic Cell Separation. For each mouse, CD4⁺CD25⁻ T cells were enriched using a regulatory T cell isolation kit and magnetic-activated cell sorting (MACS) technology (Miltenyi Biotec, Bergisch Gladbach, Germany). After isolation, flow cytometry was used to assess the purity of CD4⁺CD25⁻ T cell populations used in experiments, and found to be typically $\geq 90\%$.

[0097] In Vitro T Cell Differentiation. CD4⁺CD25⁻ T lymphocytes (1 $\times 10^5$ /well) were cultured in triplicate at 37°C (5% CO₂) in RPMI 1640 (Cellgro 10-040-CV) containing 10% FBS (INVITROGEN™ GIBCO®) 1% antibiotic/antimycotic (Herndon, VA), and 50 μ M β -ME (MP Biomedicals, Solon, OH). For Treg differentiation, cells were stimulated with 2 μ g/ml plate-bound anti-CD3 mAb (BD Pharmingen; clone: 145-2C11), 2 μ g/ml soluble anti-CD28 mAb (BD Pharmingen; clone: 37.51), and 2ng/ml human TGF-1 (R&D Systems). Cells were incubated for 72 hours and assessed for Treg differentiation by ICS for Foxp3. For Th17 differentiation, cells were stimulated with 10 μ g/ml plate-bound anti-CD3 mAb (BD Pharmingen; clone: 145.2C11), 15 μ g/ml soluble anti-CD28 mAb (BD Pharmingen; clone 37.51), 5ng/ml human TGF- β (R&D Systems), and 20ng/ml IL-6 (Ebioscience). CD4⁺CD25⁻ cells stimulated with plate-bound anti-CD3 mAb and soluble anti-CD28 mAb, or plate-bound anti-CD3 mAb alone, served as stimulation controls for both Treg and Th17 differentiation assays. For assays that included SOCS1-KIR mimetic peptide, 20 μ M SOCS1-KIR peptide was added in culture at time zero in conjunction with Th17 inducing reagents. Cells were collected after 5 days and assessed for activation and Th17 differentiation.

[0098] Proliferation Assays. CD4⁺ T cell proliferation was assessed by CFSE staining, ³H thymidine

incorporation, and absolute cell counts. MACS purified CD4⁺CD25⁻ T cells, isolated from LN and spleen suspension, were stimulated in triplicate (96 well roundbottom plate; 1×10⁵ cells/well) with 10µg/ml anti-CD3 (BD Pharmingen; clone: 145.2C11) alone or in addition to 1.5µg/ml anti-CD28 (BD Pharmingen; clone 37.51) at 37°C (5% CO₂) in RPMI 1640 (Cellgro; 10-040-CV) containing 10% FBS (INVITROGEN™ GIBCO®), 1% antibiotic/antimycotic (Herndon, VA), and 50µM β-ME (MP Biomedicals, Solon, OH). After 72 h of incubation, cell cultures were either pulsed with 0.5 mCi ³H thymidine (GE Healthcare; Arlington Heights, IL) or counted and harvested for assessment by flow cytometry. In cultures analyzed by flow cytometry, T lymphocytes were labeled with 10µg/ml CFSE prior to culture as previously described (Cozzo *et al.* 2003). ³H thymidine pulsed T lymphocytes were harvested 16-18 hours after initial pulse followed by the ³H thymidine incorporation assessment using a Beckman LS3801 Liquid Scintillation System. Absolute cell numbers of CD4⁺CD25⁻ lymphocytes were obtained via Trypan Blue exclusion.

[0099] RNA Extraction and qPCR. Using the Promega RNA extraction protocol, total RNA was extracted from human PBMCs *ex vivo* or from mouse CD4⁺CD25⁻ cells after being cultured under control (anti-CD3 and anti-CD28) or Th17 inducing conditions in the presence or absence of SOCS1-KIR peptide. cDNA synthesis and qPCR were performed as described in (Collins *et al.* 2011), with modifications. Briefly, cDNA synthesis was performed using the iQ cDNA synthesis kit (Bio-rad; Hercules, CA). To amplify the target and house-keeping genes present in cDNA, qPCR was subsequently performed using the iQ SYBR Green Supermix (Bio-Rad) and gene-specific primers (Table 4). The amplification reactions took place in a PTC-200 Peltier Thermal Cycler with a CHROMO 4 Continuous Fluorescence Detector (BioRad). The reaction protocol is as follows: one 2-3 min cycle at 95° C, followed by 50 cycles of denaturation (95° C, 15s), annealing (30s) (see Table 4 for primer specific temperature), and extension (72° C, 30s). To confirm amplicon specificity, melting curve analysis was performed. The fold change in expression was calculated using the ΔΔCT method.

[0100] In Vitro Cytokine Secretion Analysis. SOCS1^{+/-} and WT CD4⁺CD25⁻ T cells were plated and stimulated in triplicate with plate-bound anti-CD3 alone (BD Pharmingen; clone: 145.2C11), plate-bound anti-CD3 and anti-CD28 (BD Pharmingen; clone 37.51), or Th17 inducing conditions for 5 days as previously described (Bedoya *et al.* 2013). After the incubation period, 100µl of culture supernatant was collected from each well. Harvested supernatants were used to perform IL-17A and IFNγ ELISAs, as previously described (Lau *et al.* 2011). IL-17A capture (555068) and detection (555067) mAb, and IFN-γ cytokine standard (554587) were purchased from BD Biosciences. IL-17 cytokine standard (14-8171-80), IFN-γ capture (16-7313-85) and IFNγ detection (13-7311-85) mAbs were purchased from eBioscience.

[0101] IgG Antibody Assessment. Total IgG and anti-dsDNA IgG levels were measured by ELISA as in Morel *et al.* (Morel *et al.* 2000). For the anti-ssDNA IgG ELISA, ssDNA was generated by heating rat dsDNA at 100°C for 10 minutes, followed by a 5-minute incubation on ice. The resulting ssDNA was then used to coat the wells of flat-bottomed 96 well plate. Relative units of anti-DNA IgG were standardized using serum taken from C56BL/6 triple congenic (B6.TC) mice, which coexpress three lupus susceptibility loci (*Sle1*, *Sle2*, and *Sle3*) and develop severe lupus-like disease (Morel *et al.* 2000). 1:100 dilution of B6.TC serum was set to an equivalent of 100 units.

[0102] Western Blotting. MACS purified CD4⁺CD25⁻ T cells were stimulated with anti-CD3 Ab

(10µg/ml), anti-CD3 (10µg/ml) and anti-CD28 (1.5µg/ml) Abs, or Th17 inducing conditions in the presence or absence of SOCS1-KIR peptide as previously described. 2×10^7 cells from each condition were lysed with 100µl of RIPA lysis buffer containing complete protease inhibitor (Santa Cruz; product number: SC-24948). Equal quantities of protein were loaded and separated in 4%-12% SDS-PAGE gel (Biorad). Separated proteins were transferred to nitrocellulose membrane (Amersham; HYBOND™-N+). The membrane was then blocked, probed with primary anti-pAkt (ser473) (catalogue #: 9271) or anti-pSTAT1 (Tyr701) (catalogue #: 9171) antibody and then with appropriate secondary antibodies conjugated to HRP, and visualized with the ECL detection system according to the manufacturer's instructions (Pierce; Product # 32106). Akt (catalogue #: 9272) and STAT1 (catalogue #: 9172) immunoblots were performed to confirm equal loading.

[0103] Statistical Analysis. GraphPad Prism v.5 was used to calculate the statistically significant differences between two different groups using the nonparametric, Mann-Whitney U test. For multiple comparisons tests, the nonparametric Kruskal-Wallis test was performed, followed by the Dunn's Multiple Comparisons post-test. For correlation data, the nonparametric Spearman correlation test was performed. A 95% confidence limit, defined by p values ≤ 0.05 , was considered significant and is indicated within the figures.

[0104] Following are examples that illustrate procedures for practicing the invention. These examples should not be construed as limiting. All percentages are by weight and all solvent mixture proportions are by volume unless otherwise noted.

Example 1-SOCS1^{+/-} mice exhibit CD4 T cell accumulation and enhanced CD4⁺ T cell activation in the periphery

[0105] In this study we selected SOCS1^{+/-} mice between 2 and 5 months of age, which are free of overt lupus pathology (Figure 7 and Fujimoto *et al.* 2004), to assess how SOCS1 deficiency precipitates CD4⁺ T lymphocyte mediated autoimmunity. We first assessed whether distinctions were present within the thymic and peripheral pools of CD4⁺ T lymphocytes in SOCS1^{+/-} mice. Although the frequency and absolute numbers of CD4⁺CD8⁻ thymocytes within SOCS1^{+/-} and WT littermate controls were indistinct (Figure 1A), CD4⁺ T lymphocytes in the periphery of SOCS1^{+/-} mice were two fold higher in frequency, and four-fold higher in absolute cell number, when compared to WT littermate controls (Figure 1B). As T lymphocyte activation may also contribute to lupus progression (Stekman *et al.* 1991; Desai-Mehta *et al.* 1996; Mohan *et al.* 1999; Vratsanos *et al.* 2001; Bouzahzah *et al.* 2003), we next assessed differences in the CD4⁺ T cell activation marker, CD25, directly *ex-vivo*. Indeed, SOCS1^{+/-} mice possessed an increased frequency and nearly 3-fold more peripheral CD4⁺ T lymphocytes (6.9×10^6 vs. 2.4×10^6) that were also CD25⁺ when compared to WT (Figure 1C). This increase in CD25 expression was not due to increases in Tregs, as levels of Foxp3⁺ T lymphocytes were indistinct between SOCS1^{+/-} mice and littermate controls (Figure 8). In addition to CD25 expression, activation of CD4⁺ T lymphocytes can also be analyzed by the presence of the early activation marker CD69 (Testi *et al.* 1994; Larkin *et al.* 2007). CD4⁺CD69⁺ T lymphocytes were also higher in both frequency and absolute number within SOCS1^{+/-} mice (Figure 1C). Together, these data show that SOCS1^{+/-} mice, which develop CD4 T cell-mediated lupus, possess significantly more activated CD4⁺ T lymphocytes,

which may contribute to disease progression.

Example 2-CD28 co-stimulation of SOCS1^{+/-} CD4⁺ T lymphocytes is dispensable for activation and clonal expansion

[0106] Having observed enhanced CD4⁺ T cell activation within the periphery of SOCS1^{+/-} mice, we next conducted *in vitro* assays to characterize this observation mechanistically. Given that conventional T lymphocytes (Tcon) require signaling through both TCR and CD28 for activation (reviewed in Tivol *et al.* 1996), we next stimulated MACs purified, CD4⁺CD25⁻ T lymphocytes with antibodies specific to CD3 and CD28 (α CD3/ α CD28), *in vitro*. After 72 hours of incubation, α CD3/ α CD28 activated CD4⁺ T lymphocyte populations were greater than 70% CD25⁺, independent of SOCS 1 expression (Figure 2A). In similar fashion, α CD3/ α CD28 treatment mediated comparable CD69 up-regulation in both SOCS1^{+/-} and littermate control T lymphocytes (Figure 2A). Notably, however, whereas α CD3 treatment mediated limited CD25 high expression in SOCS1 sufficient CD4⁺ T cells, 45% of SOCS1^{+/-} counterparts had high levels of CD25 expression with α CD3 treatment alone (Figure 2A). Moreover the percentage of CD69^{hi} was also greater in α CD3 treated SOCS1^{+/-}CD4⁺ T lymphocytes compared to SOCS1^{+/+}CD4⁺ controls (Figure 2A).

[0107] Since clonal expansion (e.g., proliferation) occurs subsequent to CD4⁺ T cell activation (Mondino and Jenkins 1994), we then assessed T cell proliferation under α CD3/ α CD28 treatment or α CD3 alone. Consistent with CD25 and CD69 frequencies (Figure 2A), SOCS1^{+/-} CD4⁺ T lymphocyte proliferation (as assessed by CFSE, absolute cell counts, and ³H thymidine incorporation) was statistically indistinguishable to that of littermate controls when stimulated by α CD3/ α CD28, (Figure 2B). Strikingly, however, α CD3 treatment alone mediated significantly more proliferation of SOCS1^{+/-} CD4⁺ T lymphocytes as depicted by a higher percentage of CFSE^{lo} cells (54.6 ± 0.9 vs. 34.0 ± 3.2), 3 fold higher absolute cell numbers, and 6 fold greater ³H thymidine incorporation (Figure 2B). In summary, these results indicate that SOCS^{+/-} CD4⁺ T cells have a reduced threshold for activation and clonal expansion *in vitro*.

Example 3-SOCS1^{+/-} CD4⁺ T cells exhibit reduced P-Akt requirement for activation

[0108] As SOCS 1^{+/-}CD4⁺ T lymphocytes exhibited significant activation and proliferation in the absence of CD28 stimulation, we next examined Akt activation, which is involved in signaling downstream of CD28 (Parry *et al.* 1997). Strikingly, although we observed significantly more proliferation and activation of SOCS1^{+/-} CD4⁺ T lymphocytes under α CD3 treatment alone, Akt phosphorylation subsequent to α CD3 treatment was significantly reduced in SOCS1^{+/-} mice compared to littermate controls (Figure 2C). The differences in p-Akt were observed in spite of comparable amounts of total Akt under α CD3 treatment (Figure 2C). Consistent with the activation and proliferation results noted previously (Figure 2A, Figure 2B), p-Akt levels were indistinct between SOCS1^{+/-} and WT cells incubated with α CD3/ α CD28 (Figure 2C). Together, these results suggest a limited requirement

for CD28 co-stimulatory signals in the CD4⁺ T lymphocyte phenotype present in lupus-prone, SOCS1^{+/-} mice.

Example 4-TCR stimulated SOCS1^{+/-} T cells display heightened IFN γ production

[0109] As CD4⁺ T cell activation is associated with cytokine production, and IFN γ production has been associated with lupus onset (Balomenos *et al.* 1998; Haas *et al.* 1998; Nakashima *et al.* 1999; Akahoshi *et al.* 1999; Karonitsch *et al.* 2009), we next analyzed IFN γ production under CD3 and CD3/CD28 stimulatory conditions. Although IFN γ production by SOCS1^{+/-} was consistently higher than WT mice when subjected to α CD3/ α CD28 conditions, distinctions in IFN γ production reached profound significance under α CD3 treatment, with IFN γ levels 4 fold higher in SOCS1^{+/-} lymphocytes compared to those obtained from WT littermates (Figure 2D). Notably, the production of IFN γ by SOCS1^{+/-} T lymphocytes under α CD3 treatment alone was comparable to IFN γ production by T lymphocytes receiving additional CD28 stimulation (Figure 2D). Therefore, prior to disease onset, SOCS1 deficiency leads to the development of CD4⁺ T cells that are hyper-responsive to TCR stimulation - resulting in hyper-activation and abnormal Th1 phenotypic expression.

Example 5-SOCS^{+/-} naïve CD4⁺ T cells undergo normal Treg induction, but abnormal Th17 induction

[0110] As proper T cell differentiation is critical to the maintenance of immune homeostasis and inhibition of autoimmunity (reviewed in Hirahara *et al.* 2013), we next investigated the plasticity of SOCS1^{+/-}CD4⁺ T lymphocytes through incubation under regulatory and Th17 inducing conditions. While flow cytometric analysis of Treg induction (as denoted by the frequency of Foxp3⁺ cells) revealed no difference in Treg induction between SOCS1^{+/-} and WT CD4⁺ T cells (Figure 3A), it is noteworthy that there was a significant reduction in the percentage of SOCS1^{+/-}IL-17A⁺ cells, subsequent to incubation under Th17 inducing conditions (Figure 3B). Reduced Th17 differentiation of SOCS1^{+/-} lymphocytes was confirmed by qPCR and ELISA, which showed reduced levels of IL-17A message, secreted IL-17A protein, and decreased levels of the Th17 specific transcription factor ROR γ t (Figure 3C).

[0111] As it has been previously shown that cytokine production and terminal differentiation of lymphocytes are functions of cell division (Gett and Hodgkin 1998), we next assessed whether differences in proliferation contributed to differential IL-17A production. Purified, CFSE labeled CD4⁺CD25⁻ cells from either SOCS1^{+/-} or WT littermate controls were cultured under α CD3/ α CD28 stimulation, iTreg inducing conditions, iTh17 inducing conditions, or left unstimulated. The treated cultures were subsequently assessed for Foxp3 or IL17 production as a function of proliferation. Treatment with α CD3/ α CD28 alone failed to mediate either extensive Foxp3 expression, or IL17 production, in either SOCS1^{+/-} or WT lymphocytes (Figure 3D, 3E). As expected, the induction of Foxp3⁺ Tregs and Th17 CD4⁺ T lymphocytes upon incubation with TGF- β alone and TGF- β and IL6, respectively, was consistent with published reports (Mangan *et al.* 2006; Bedoya *et al.* 2013) (Figure

3D, Figure 3E). Moreover, consistent with results observed in Figure 3A, the frequencies of Foxp3⁺CD4⁺ T lymphocytes were similar, independent of SOCS1 expression and CFSE dilution (Figure 3D). Although the overall frequency of SOCS1^{+/-} IL-17A⁺ CD4⁺ lymphocytes was reduced compared to WT (6.5 ± 0.5 vs. 3.1 ± 0.2 ; SOCS1^{+/-} vs. WT), dilutions in CFSE, indicative of division cycles, were indistinct (Figure 3E). Notably, unlike Treg induction, which began independently of proliferation, IL-17A production was not readily apparent until the third division (Figure 3D vs. Figure 3E). Taken together, these data indicate that while SOCS1^{+/-} CD4⁺ T cells have the capacity to undergo normal Treg induction, SOCS1 deficient cells have a reduced capacity to undergo proper Th17 differentiation.

Example 6-SOCS1^{+/-} CD4⁺ T Cells display heightened IFN γ expression, even under Th17 inducing conditions

[0112] Considering the Th1 bias observed in TCR stimulated SOCS1^{+/-} CD4⁺ T cells, we hypothesized that the reduced capacity of SOCS1^{+/-} T cells to undergo Th17 differentiation could be due to dysregulated IFN γ signaling. To test this hypothesis, we placed SOCS1^{+/-} or WT cells under Th17 inducing (iTh17) conditions and first assessed mRNA expression of IFN γ and T-bet, the IFN γ promoting transcription factor (Szabo *et al.* 2002). As can be seen, IFN γ expression was more than 2-fold greater in SOCS1^{+/-} cells in comparison to WT controls (Figure 4A). In parallel with the heightened IFN γ message expression, T-bet expression was also enhanced more than 2 fold (Figure 4A). Heightened expression was also seen at the protein level as intracellular staining revealed that unstimulated SOCS1^{+/-} cells possessed an IFN γ ⁺ cell frequency that was approximately 1.5 fold greater than WT counterparts (Figure 4B). Additionally, under iTh17 conditions, we noted a 5-fold increase in the population of SOCS1^{+/-} IFN γ ⁺ cells (Figure 4B). Moreover, the reduction in IFN γ producing WT CD4⁺ T lymphocytes subsequent to Th17 induction (more than 80%) was not as readily observed in SOCS1^{+/-} under the same conditions (only 38%, Figure 4B). In addition, the changes in IFN γ and IL17 production were not due to changes in IL17⁺IFN γ ⁺ dual cytokine expressing T lymphocytes (Figure 4C). Taken together, these results suggest that preferential expression of IFN γ by SOCS1^{+/-} CD4⁺ T cells inhibits Th17 induction.

[0113] To confirm the role of IFN γ in the reduced Th17 differentiation of SOCS1^{+/-} CD4⁺ T cells, we assessed Th17 differentiation in SOCS1^{+/-} CD4⁺ T cells taken from SOCS1^{+/-} IFN γ ^{-/-} mice. While Th17 differentiation of SOCS1^{+/-} cells resulted in a 2.3% CD4⁺IL-17A⁺ population, intracellular staining revealed a 4.8% population in SOCS1^{+/-}IFN γ ^{-/-} cells, that was statistically indistinct from WT controls (Figure 4D). Taken together, these data show that preferential expression of IFN γ by SOCS1^{+/-} CD4⁺ T lymphocytes precludes Th17 differentiation.

Example 7-SOCS1-KIR treatment inhibits aberrant activation and proliferation of SOCS1^{+/-} CD4⁺ T Cells.

[0114] As SOCS1 deficiency in SOCS1^{+/-} CD4⁺ T lymphocytes results in aberrant activation and proliferation (Figure 1 - Figure 5), it is possible that partial restoration of SOCS1 signaling can moderate dysregulation. We have previously shown that a peptide able to partially mimic SOCS1 function, SOCS1-KIR, could both regulate immune homeostasis and prevent EAE when administered *in vivo* (Jager *et al.* 2011; Collins *et al.* 2011). We next assessed the ability of SOCS-KIR to reduce the excessive activation observed in SOCS1^{+/-} CD4⁺ T lymphocytes. As can be seen, SOCS 1-KIR was sufficient to inhibit excessive α CD3 mediated CD25 up-regulation by SOCS 1^{+/-} CD4⁺ T lymphocytes, while mediating limited effects on CD25 expression in WT counterparts (Figure 5A). SOCS1-KIR also reduced proliferation of both WT and SOCS1^{+/-} CFSE labeled T lymphocytes (Figure 5B). Notably, SOCS1-KIR reduced the activation and proliferation of α CD3 treated SOCS1^{+/-} CD4⁺ T lymphocytes to levels comparable to WT receiving α CD3 stimulation (Figure 5B). Absolute cell counts and ³H thymidine incorporation confirmed the SOCS1-KIR mediated inhibition of T lymphocyte proliferation (Figure 5B). Moreover, SOCS 1-KIR treatment resulted in a 2-fold reduction in IPN γ mRNA expression and protein production (Figure 5C). Together, these data show that dysregulated activation and proliferation of SOCS1^{+/-} CD4 T cells, which have significant implications in autoimmune development, are moderated by the SOCS-KIR peptide.

Example 8-SOCS1-KIR inhibits excessive STAT1 signaling present in SOCS1^{+/-} CD4⁺ T cells under Th17 inducing conditions

[0115] As STAT1 α is rapidly phosphorylated upon IPN γ binding to the IPN γ receptor (Greenlund *et al.* 1995; Schroder *et al.* 2004) we next evaluated the capacity of SOCS1-KIR to regulate STAT1 α phosphorylation under Th17 inducing conditions. Although little STAT1 was phosphorylated in WT CD4⁺ T lymphocytes cultured under Th17 conditions, phosphorylation of STAT1 was readily apparent in SOCS1^{+/-}CD4⁺ T lymphocytes (Figure 5D). Significantly, SOCS1-KIR drastically reduced the enhanced STAT1 activation in SOCS1^{+/-} cells (Figure 5D). Therefore, the capacity of SOCS 1-KIR to normalize IPN γ production is partly through regulation of STAT1 signaling.

Example 9-Reduced SOCS1 levels observed in SLE patients

[0116] Although SOCS1 deficiency has been associated to lupus-like pathology in mice (Sharabi *et al.* 2009; Fujimoto *et al.* 2004), clinical relevance to this observation in human SLE is less clear. Therefore, to determine whether differences in SOCS1 expression are relevant to human SLE, we assessed SOCS1 expression in peripheral blood mononuclear cells (PBMCs) taken from SLE patients and healthy controls. Although anti-malarials and glucocorticoids are common standard of care medications used to treat SLE (reviewed in Gurevitz *et al.* 2013), their effects on the modulation of SOCS1 expression in human leukocytes are unknown. Therefore, prior to selecting our patient population, we treated healthy control PBMCs with an antimalarial, chloroquine, and a glucocorticoid, dexamethasone, *in vitro* and assessed SOCS1 expression. Our pilot study revealed that SOCS1 expression was affected by dexamethasone but not chloroquine (Figure 9). As such, patients prescribed glucocorticoids were excluded from our study. Strikingly, as can be seen in Figure 6, SOCS1 mRNA expression was significantly decreased in SLE patients in comparison to healthy controls (Figure 6A). The differences in SOCS1 expression were likely not due to age, as deficiencies in SOCS1

expression were readily observed in SLE patients compared to age-matched controls (Figure 10A).

[0117] Given that both type I and type II IFNs have been shown to play a key role in the immunopathogenesis of human SLE, and that SOCS1 is a critical regulator of the signaling of these cytokines (Takahashi *et al.* 1996; Balomenos *et al.* 1998; Piganis *et al.* 2011; Alexander *et al.* 1999; Santiago-Raber *et al.* 2003), we next investigated whether SOCS1 expression was related to IPN γ and/or monocyte CD64 expression (which is a marker for the type I IFN signature in SLE patients (Li *et al.* 2010)). While no significant correlation was observed between SOCS1 and IPN γ , a strong negative correlation was noted when SOCS1 was correlated with monocyte CD64 (Figure 6B). Notably, the patient with the lowest SOCS1 expression displayed the highest CD64 (Figure 6B), indicating that SOCS1 expression is indeed related to the pathogenic type I IFN signature observed in SLE patients.

[0118] We next investigated whether SOCS1 expression was associated with disease activity, as defined by SLE disease activity index (SLEDAI) scores, and serum complement component 3 (C3) and serum complement component 4 (C4) levels. C3 and C4 levels were examined because decreases in free complement molecules in serum are indicative of increased levels of immune complexes and disease activity (reviewed in Pickering and Walport 2000). Though there was no correlation between SOCS1 and SLEDAI scores (Figure 10B) or between SOCS1 and C4 levels (Figure 6C), a strong positive correlation was observed between SOCS1 and C3 (Figure 6C). Notably, the patients with the two highest SOCS1 expression levels displayed the lowest CD64 mean fluorescent intensities and possessed the highest C3 levels (Figure 6B vs. Figure 6C). Given that studies involving SLE patients and murine models of the disease have shown that type I IFNs play significant role in immune complex formation (Santiago-Raber *et al.* 2003; Ronnblom *et al.* 1991; Jorgensen *et al.* 2007; Nacionales *et al.* 2007), the observation that SOCS1 expression is highest in patients with both a low type 1 IFN signature and a high C3 level suggests that SOCS1 may be a key molecule involved in preventing excessive immune complex formation in SLE patients through regulation of type 1 IFN signaling. Taken together, these results strongly implicate a role of SOCS1 in the prevention of the autoimmune pathology observed in human SLE patients.

Example 10

[0119] Cytokine dysregulation and T lymphocyte effector function imbalances significantly contribute to SLE onset and progression. Foundational studies, including the classical MRL lupus model and many human SLE studies have outlined the importance of CD4⁺ T cells in both autoantibody production and glomerulonephritis (Stekman *et al.* 1991; Desai-Mehta *et al.* 1996; Mohan *et al.* 1999; Vratsanos *et al.* 2001; Bouzazah *et al.* 2003). Significantly, several murine studies have implicated deficiencies in SOCS1, which regulates cytokine production and T lymphocyte effector functions, with lupus progression (Sharabi *et al.* 2009; Fujimoto *et al.* 2004; Hanada *et al.* 2003). However the role of SOCS 1 in the regulation of lupus-associated T lymphocyte abnormalities is less clear. In this study, we have shown that SOCS1 regulates T lymphocyte activation and effector functions in SOCS1^{+/-} mice, which develop lupus-like pathology. Moreover, we show that SOCS1 deficiency is strongly correlated to human lupus disease.

[0120] It is well accepted that although T cells possessing TCR bearing specificity to self are eliminated through central tolerance, nevertheless potentially self-reactive T lymphocytes evade negative selection and persist in the periphery (Picca *et al.* 2006). In this study we show that SOCS1-specific

aberrations in CD4⁺ T lymphocytes are evident within the periphery of SOCS1^{+/-} mice as opposed to the thymus, thus implicating a peripheral tolerance defect. Prior to anti-DNA autoantibody production, activated CD4⁺ T cells readily accumulated in the periphery of SOCS1^{+/-} lupus-prone mice. Significantly, peripheral accumulation of T lymphocytes is also readily present in the classical MRL lupus model (Jabs *et al.* 1992). Moreover, CD4⁺ T cells in murine and human lupus are known to display a hyper-activated phenotype, which contributes to pathogenic autoantibody production (Stekman *et al.* 1991; Desai-Mehta *et al.* 1996; Mohan *et al.* 1999; Vratsanos *et al.* 2001; Bouzazhah *et al.* 2003). Our results here expand upon those previous studies, by showing that decreased levels of SOCS1 expression are sufficient to mediate both lympho-accumulation and CD4⁺ T lymphocyte hyper-activation.

[0121] The peripheral accumulation of CD4⁺ T lymphocytes in SOCS1^{+/-} mice and rodent models of SLE underscores the fact that peripheral tolerance mechanisms must be in place to inhibit the onset of autoimmune diseases such as SLE. In addition to TCR stimulation, the additional requirement of co-stimulation in order to obtain full activation of naive CD4 T lymphocytes serves to limit aberrant peripheral activation and autoimmune events (reviewed in Tivol *et al.* 1996). Engagement of the CD28 receptor by APC associated B7 molecules is one of the best characterized co-stimulatory interactions (Mondino and Jenkins 1994). In this study we show that under conditions of limited SOCS1 expression, dependence on the CD28 pathway for full CD4⁺ T lymphocyte activation is significantly diminished. This was reflected not only in significant activation, in the absence of CD28 stimulation, but also in the diminished role of activated Akt in the activation process. It is well established that T cell activation is abnormal in lupus (Stekman *et al.* 1991; Desai-Mehta *et al.* 1996; Mohan *et al.* 1999; Vratsanos *et al.* 2001; Bouzazhah *et al.* 2003; Zielinski *et al.* 2005). In addition, previous studies have shown that SOCS1^{-/-}CD28^{-/-} mice possessed high levels of anti-dsDNA antibodies (Hanada *et al.* 2003). Although this result was interpreted to mean that T lymphocyte help was not required, an alternative interpretation, supported by this study, is that CD28 co-stimulation is not required for B cell help mediated by SOCS1 deficient T lymphocytes. Notably, several studies implicate the phosphatidylinositol 3 Kinase (PI3K)/Akt pathway in regulating the balance between conventional T lymphocyte (Tcon) effector functions and Foxp3 Treg development (Cheng *et al.* 2011; Pierau *et al.* 2009). As these studies show a reduced threshold for T lymphocyte activation under conditions of SOCS1 deficiency, these findings extend upon previous studies by implicating a role of SOCS1 deficiency in the hyper-activated CD4⁺ T lymphocyte population characterized in both SLE patients and classical murine lupus models.

[0122] An important hallmark of a properly functioning immune system is the generation of a cytokine milieu sufficient to mediate the elimination of distinct microorganisms or cancerous cells. Significantly, an important characteristic of an autoimmune promoting immune system is the production of a dysregulated cytokine milieu (reviewed in Yoshimura *et al.* 2012). For example, CD4⁺ T cells in lupus have been shown to display enhanced IPN γ production due to a Th1 bias (Takahashi *et al.* 1996). Our studies show that STAT1 is highly activated in SOCS1^{+/-} CD4⁺ T lymphocytes, even under Th17 inducing conditions. As it has been previously shown that IL-6 inhibition of Th1 differentiation is mediated by SOCS1 (Diehl *et al.* 2000), it appears likely that SOCS1 expression also serves to regulate IL-17 production in environments with IPN γ present.

[0123] Dysregulated regulatory T cell (Treg) function has been strongly implicated in lupus onset (Valencia *et al.* 2007; Suen *et al.* 2009; Yan *et al.* 2008). In this study we show that SOCS1 expression

did not influence the induction of Foxp3⁺ Tregs. This was in spite of the Th1 bias present in SOCS1^{+/-} CD4⁺ T lymphocytes. This finding is novel, given the conflicting studies regarding the role of Th1 related cytokines and Treg development (Caretto *et al.* 2010; Feng *et al.* 2011). Notably we have previously shown that the lethal IPN γ mediated auto-inflammatory disease that occurs in SOCS1^{-/-} mice was correlated with a decreased peripheral Treg population (Collins *et al.* 2011). Moreover, it was shown by the Yoshimura group that SOCS1^{-/-}Foxp3⁺ Tregs, lack suppressor function and can be induced to produce the inflammatory cytokines IPN γ and IL-17 (Takahashi *et al.* 2011). It is tempting to speculate SOCS1 expression regulates the stability of the Treg lineage, even with heterozygous expression. Additional studies are necessary to further characterize the role of SOCS1 in peripheral Treg homeostasis and function.

[0124] The identification of genetic defects involved in SLE onset/progression is critical, as therapeutic strategies incorporating this knowledge can then be utilized for treatment development. Genetic defects can be mediated through gene polymorphisms or nonfunctional alleles. Although haplotype expression of particular genes may not be generally associated with dysregulated immunity, it is clear that, whereas complete deficiency of the SOCS 1 gene in rodent models results in lethality, heterozygous expression mediates lupus-like pathology. Significantly, we show that SOCS1 production by PBMCs is significantly lower in SLE patients compared to healthy controls. To date, there have been two studies examining SOCS1 levels in lupus patients with conflicting results (Tsao *et al.* 2008; Chan *et al.* 2010). One study found no differences in SOCS1 with respect to lupus (Tsao *et al.* 2008), while a second study found higher levels of SOCS 1 within patients with significant disease (Chan *et al.* 2010). Although it remains unclear why the results of these two studies differ from the results acquired in our study, it is likely that differences in samples sizes and patient exclusionary criteria contribute. As our pilot study (and a recently published murine study (Bhattacharyya *et al.* 2011)) showed that glucocorticoids increase SOCS1 expression, in contrast to the previous studies, we excluded patients that were prescribed glucocorticoids.

[0125] We also show that SOCS1 expression is inversely proportional to SLE disease as measured by C3 levels and type 1 interferon signature. It is likely that a statistical correlation could not be established between C4 and SOCS1 because genetic deficiencies in CD4, independent of inflammation, are common in lupus patients (reviewed in Pickering and Walport 2000).

[0126] Elucidation of the mechanisms by which lupus pathogenesis occurs is critical for the development of treatment strategies, which target the specific immune dysregulation. We show that a peptide mimic of the kinase inhibitory region of SOCS1, SOCS1-KIR, was sufficient to inhibit aberrant T cell activation and IFN signaling. SOCS 1-KIR binds to and inhibits the function of JAK2, making it a natural JAK2 tyrosine kinase inhibitor. Studies are currently underway to determine whether chemical JAK2 kinase inhibitors used to treat patients with myeloproliferative neoplasms, may have efficacy in the treatment of SLE (Pardanani *et al.* 2011; Wang *et al.* 2010). SOCS 1 limits the signaling of several cytokines involved in lupus onset including the cytokines interferon gamma (IPN γ), interferon α (IFN α), B lymphocyte activating factor (BLyS), and interleukin 6 (reviewed in Alexander 2002). As humanized monoclonal antibodies against BLyS, IFN α , and IPN γ are in clinical trials for treating lupus (Ledford 2011), it is tempting to speculate that strategies focused on enhancing SOCS1 could work in synergy with antibody or standard of care treatments for SLE - especially since SOCS1 expression is reduced in SLE patients.

Table 4. Mouse (mus) and Human (hu) mRNA Primer Sequences and Annealing Temperatures

mRNA	Forward Primer	Reverse Primer	Annealing Temperature (°C)
mus-Actin	5'-CCTTCCTTCTTGGGT A TGGA-3' (SEQ ID NO:9)	5'-GGAGGAGCAA TGA TCTTGA T -3' (SEQ ID NO:10)	55
mus-IFN γ	5'-AACT A TTTT AACTCAAGTGGCA T -3' (SEQ ID NO:11)	5'-AGGTGTGA TTCAA TGACG-3' (SEQ ID NO:12)	55
mus-Tbet	5'-GGGAGAACTTTGAGTCCA-3' (SEQ ID NO:13)	5'-GAAGGTCGGGGTAGAAA-3' (SEQ ID NO:14)	50
mus-IL-17A	5'-ACTCTCCACCGCAATGA-3' (SEQ ID NO:15)	5'-CTCTTCAGGACCAGGAT-3' (SEQ ID NO:16)	55
mus-ROR γ t	5'-ACAGCCACTGCA TTCCCAGTTT -3' (SEQ ID NO:17)	5'-TCTCGGAAGGACTTGCAGACA T -3' (SEQ ID NO:18)	63
mus-SOCS1	5'-GACACTCACTTCCGCACCTT-3' (SEQ ID NO:19)	5'-GAAGCAGTTCCGTTGGCACT-3' (SEQ ID NO:20)	57
hu-GAPDH	5'-TGCACCACCAACTGCTTAG-3' (SEQ ID NO:21)	5'-GAGGCAGGGATGATGTTC-3' (SEQ ID NO:22)	59
hu-SOCS1	5' - GGGAGCGGATGGGTGTAGG-3' (SEQ ID NO:23)	5' - AGAGGTAGGAGGTGCGAGTTC-3' (SEQ ID NO:24)	59
hu-IFN γ	5' - TGACCAGAGCA TCCAAAAGA-3' (SEQ ID NO:25)	5' - CTCTTCGACCTCGAAACAGC-3' (SEQ ID NO:26)	59

Example 11-SOCS1 dimer is more effective than SOCS1 monomer at inhibiting Th17 induction and CD4+ T cell activation *in vitro*.

[0127] Induction of Th17 cells, iTh17, and the effect of treatment on induction is illustrated in Figure 11. CD4⁺CD25⁻ T cells from C56BL/6 mice were incubated for 5 days at 37°C under 1) control conditions (anti-CD3 (10 μ g/ml), anti-CD28 (1.5 μ g/ml)); 2) Th17 inducing conditions (anti-CD3, anti-CD28, IL-6 (20ng/ml), TGF- β (5ng/ml)); 3) Th17 inducing conditions with SOCS 1 monomer (20 μ M), or Th17 inducing conditions with SOCS 1 dimer (20 μ M). Following a 5-day incubation, cells were re-stimulated with phorbol myristic acetate (PMA) (50ng/ml), ionomycin (1 μ M), and brefeldin A (10 μ g/ml). To assess Th17 differentiation, cells were stained with anti-CD4 and anti-IL-17A antibodies. To assess activation, cells were stained with anti-CD4 and anti-CD25 antibodies.

[0128] The data indicate the inhibitory effect of our SOCS mimetics on iTh17 induction. The 16 amino acid mimetic, SOCS1-KIR, encompasses the KIR of SOCS1 (Yoshimura *et al.* 2012). The SOCS1-KIR dimer used here was synthesized as we indicate for the antagonist above with the poly-glycine linker in symmetrical orientation. The SOCS mimetic dimer had greater inhibitory effects on iTh17 than did the monomer. We expect similar enhanced effects of SOCS dimeric antagonist compared to monomer.

Example 12

[0129] Lupus does not occur at birth, implicating that the clinical manifestations observed in lupus are due to the accumulation of pathological autoimmune events, decreases in regulatory mechanisms, or a combination of these processes. Notably, defects in two well established tolerance mechanisms, regulatory T cells (Tregs) and Suppressor of cytokine signaling-1 (SOCS 1), have recently been implicated in lupus progression. Significantly, we have shown that SOCS1 is critically involved in the stability of peripheral Tregs. We also showed that a peptide which mimics SOCS1 function can enhance Tregs numbers and prolong the survival of mice with lethal auto-inflammatory disease (see Figures 12-15).

Conclusions:

[0130] SOCS1^{+/-} mice develop lupus and possibly mimic a SOCS1 deficiency present in human lupus patients.

[0131] SOCS1 expression in lupus patients is inversely correlated to disease activity marker CD64, and directly correlated to C3 complement molecules (which typically decrease with increasing disease activity).

[0132] T cells, present in SOCS1^{+/-} mice possess a lower threshold of activation, consistent with other lupus rodent models and PBMCs from lupus patients. Notably, SOCS1-KIR can inhibit aberrant proliferation, CD25 up-regulation, and STAT 1 activation.

[0133] Mice deficient in SOCS1 (SOCS 1^{-/-}) die of a perinatal auto-inflammatory disease within 3 weeks after birth. The administration of SOCS-KIR peptide combined with CD4 T cells could extend the life of SOCS^{-/-} mice, improve the quality of life (size and overall health improvement), and prevent/delay leukocytic infiltration into heart and liver.

[0134] Inhibition of perinatal lethality in SOCS1^{-/-} mice is correlated to enhanced peripheral homeostasis of Foxp3+CD4+ Tregs, with 2 week old SOCS1^{-/-} mice possessing comparable absolute numbers of Tregs as adult mice.

MATERIALS AND METHODS FOR EXAMPLES 13 - 17

[0135] Patients and Clinical samples. The UF Institutional scientific research and review board (IRB) on human subjects approved the study protocol. Written informed consent were obtained from all patients and controls in the study. In all, 34 SLE patients and 11 healthy controls were enrolled in the present study (Table 5). All SLE patients fulfilled the 1982 American College of Rheumatology (ACR) revised criteria for SLE (Tan *et al.* 1982). The patient's age ranged from 22 to 73 years while the healthy controls age ranged from 27 to 55 years. Healthy controls (N=11) were recruited from the outpatient clinics at the participating institutions. All patients underwent baseline investigations as per clinical

requirements. Disease activity was assessed by the SLE disease activity index (SLEDAI) (Bombardier *et al.* 1992).

Table 5. SLE patients included in the study (N=34)

Patient No.	Age/Gender	SLEDAI	Prednisone (mg)	Plaquenil (mg)
1	27/F	2	0	0
2	36/F	2	0	(100 or 300)
3	63/F	4	20	400
4	53/F	10	20	0
5	69/M	2	25	200
6	73/F	2	0	0
7	31/F	6	0	400
8	38/F	ND	0	400
9	28/F	0	0	400
10	45/F	4	10	400
11	55/F	10	5	400
12	62/F	ND	0	400
13	55/F	ND	0	200
14	59/F	0	0	400
15	22/F	ND	20	400
16	41/F	2	10	400
17	23/F	ND	5	400
18	58/F	0	0	0
19	32/F	0	0	100 mg Quinacrine
20	67/F	0	2.5	400
21	39/F	7	0	400
22	61/M	ND	8	0
23	61/F	ND	5	400
24	46/F	0	0	100 mg Quinacrine
25	66/F	0	0	200
26	51/F	4	10	400
27	66/F	ND	0	400
28	44/F	ND	4	400
29	28/F	4	40	400
30	56/F	2	0	200
31	44/F	0	0	200
32	64/F	0	5	400
33	29/F	ND	ND	ND
34	18/F	ND	ND	ND

[0136] Preparation of Peripheral blood mononuclear cells (PBMCs) and total RNA extraction.

PBMCs were purified from heparinized blood by Ficoll-Hypaque gradient centrifugation. Briefly, whole blood was diluted with PBS (1:1) and gently layered on Ficoll (Lymphocyte Separation Medium; Cellgro, Manassas, VA). Cells were centrifuged continuously at 400xg for 20 minutes. PBMCs were collected from the interface layer and washed 3 times with PBS. After isolation, PBMCs were lysed with RNA lysis buffer (Promega) and stored at -80° C until RNA extraction and qPCR protocols were performed.

[0137] Reverse transcription-polymerase chain reaction (RT-PCR).

RT-PCR was performed to determine the transcript levels of SOCS1, SOCS3 and STAT1 genes in PBMCs, relative to GAPDH. In brief, cDNA synthesis was performed using the iQ cDNA synthesis kit (Bio-Rad; Hercules, CA). The qPCR was subsequently performed using the iQ SYBR Green Super mix (Bio-Rad) and gene-specific primers for SOCS1, SOCS3, IFN- γ and IL-27. The real time RT-PCR reaction was performed on CFX connectTM-Real time system. The PCR for the target gene and GAPDH was duplicated twice for each sample and the results were corrected for GAPDH expression as an internal control. Further the data was analyzed using CFX ManagerTM software version 3.0 (Bio-Rad technologies, Inc.).

[0138] Western blot analysis.

Frozen PMBC cell pellets were thawed and lysed in RIPA lysis buffer (Santa Cruz Technologies, Inc.) followed by protein estimation through BSA 2.0 mg/ml standard curve preparation with Pierce protein assay reagents (Thermo Scientific Product # 23209). Equal quantities of proteins were loaded and separated in 4%-12% SDS PAGE gel (Bio-rad) and separated proteins were transferred to nitrocellulose membrane (Bio-Rad Laboratories, Hercules, CA). The membranes were then blocked and incubated with polyclonal anti-rabbit antibodies specific to the KIR regions of SOCS1 and SOCS3 (a kind gift from Dr. Howard Johnson Labs, UF), anti-pSTAT1; anti-pERK1/2; anti-pAKT and for total STAT1; ERK1/2 and AKT respectively (Cell signaling). Further probed with appropriate secondary antibodies conjugated to HRP, and visualized with the ECL detection system according to the manufacturer's instruction (Pierce; Thermo Scientific) The GAPDH was used as a loading control. The results were calculated as densitometry arbitrary units using the J image online software.

[0139] Statistical analysis.

The statistical analysis were achieved by the software Graph Pad prism v.5. Data were presented as mean $\pm$ standard deviation (SE). Student t-test was used for non-paired samples with a 95% confidence limit. Simple linear regressions and Pearson's correlation were used to measure the correlation among different parameters with a 95% confidence limit. P-value was set at $p < 0.05$ to be statically significant.

Example 13-Reduced mRNA and Protein levels of SOCS1 and SOCS3 in SLE patients

[0140] In order to assess whether deficiencies in regulatory proteins could possibly contribute to the well-established cytokine signaling defects present in SLE patients, we first measured SOCS1 and SOCS3 mRNA expression in SLE patients in relation to healthy controls. As can be seen in Figure 16A, the mean SOCS 1 message levels in PBMC isolated from SLE patients was two-fold lower than that of controls ($p \leq 0.01$). Although not statistically significant, SOCS3 message levels were also consistently lower in patients compared to controls. In addition, linear regression analysis between SOCS1 and SOCS3 message levels from SLE patients showed a positive correlation ($r^2 = 0.5696$ ($p < 0.0001$) between expression levels (Figure 16B).

[0141] As it has been previously shown, in rodent systems, that SOCS mRNA undergoes significant posttranscriptional regulation (Warren S 2004), we next assessed SOCS1 and SOCS3 protein levels from the same patients that we evaluated message expression. Consistent with mRNA levels, the mean SOCS1 protein levels were approximately 3 fold lower in SLE patients compared to controls ($P \leq 0.0001$). Notably, reductions in the mean SOCS3 protein levels present in the PBMC of SLE patients did reach statistical significance when compared to controls (Figure 16C) ($P \leq 0.001$). Analysis of SOCS1 and SOCS3 mean protein levels, present in healthy controls, again showed comparable levels of the two proteins as denoted by the red dots within Figure 16D. However, analysis of SOCS1 and SOCS3 protein levels within the peripheral blood of individual SLE patients showed comparable variation. Although 15/24 of the SLE patients has comparable levels of SOCS 1 and SOCS3, 6/24 has higher levels of SOCS3 and 3/24 had strikingly higher levels of SOCS1 levels of the two proteins within individuals (Figure 16D). Together, these results show that SOCS1 and SOCS3 levels are significantly lower in SLE patients compared to controls.

Example 14-Reduced SOCS1 protein levels, in SLE patients, are correlated with enhanced STAT1 activation

[0142] We next assessed the activation of the inflammatory markers Akt, Erk1/2, and STAT1 by phosphorylation in SLE patients versus controls. While the average levels of pAkt and pErk1/2 protein levels were statistically indistinct (Figure 17A as determined by average densitometric analysis of western data present in Figure 16E), pSTAT1 levels were statistically higher in SLE patients compared to controls. Higher pSTAT1 levels were present in the PBMC of SLE patients compared to controls despite overall higher Akt, Erk1/2, and STAT1 proteins levels in healthy controls (Figure 17A). In order to assess a relationship between the KIR containing SOCS1 and SOCS3 proteins with the inflammatory markers Akt, Erk1/2, and STAT1; comparisons were performed between the individual SLE patients and the average levels expressed by healthy controls. Figure 17B shows that healthy controls, 23/26, and 20/26 of the SLE patients, respectively, possessed pAkt and pErk1/2 levels that were negatively associated with SOCS1 and SOCS3 protein levels. Notably, although healthy controls and 22/26 of the SLE patients possessed low pSTAT1 levels and high SOCS3 levels, in 15/26 of the patients pSTAT1 levels were visibly elevated in comparison to SOCS1 levels. Indeed, 57% (8/14) of SLE patients bearing SOCS1 protein levels below the SLE patient mean possessed pSTAT1 proteins levels that were elevated in relation to SOCS1. Together these data suggest that reduced levels of SOCS1, in SLE patients is correlated to enhanced activation of STAT1.

Example 15-Inverted pSTAT1/SOCS1 ratio correlates to significantly enhanced MHC class 1 levels amongst SLE patients

[0143] Given that nearly 60% of the SLE patients possessed a striking inverted pSTAT1/SOCS1 ratio, we next sought to examine whether this inverted ratio could have any bearing on immunological dysregulation events associated with lupus pathology. As such, we first identified individual patients from Figure 17B that possessed pSTAT1/SOCS1 ratios that were greater or lower than 1 (Figure 18A). We next segregated the SLE patients based on the presence of a pSTAT/SOCS1 ratio of greater or less than 1, followed by the assessment of MHC class I mRNA levels. As can be clearly seen in Figure 18B, patients bearing a high pSTAT1/SOCS1 ratio also possessed higher levels of MHC class 1

message expression which reached statistical significance with HLA-HQ:DAR. Given the importance of MHC associated antigen presentation to the progression of SLE, this result suggests that a high pSTAT1/SOCS1 ratio may be predictive of SLE pathology, and further implicates reduced SOCS1 signaling to SLE disease progression.

Example 16-IFN γ production is positively correlated to SOCS1 protein levels

[0144] As it has been previously shown in rodent models that SOCS 1/3 induction can be mediated by several pro-inflammatory cytokines, we next assessed a relationship between SOCS1/3 induction in SLE patients and IL27, IPN γ , and type 1 interferon signaling. Notably, we observed a significantly lower level of IPN γ message levels in patients versus control samples, while IL27 levels were comparable (Figure 18A). We next compared SOCS1/3 message and protein levels, in SLE patients, with IPN γ message levels, IL27 message levels, and CD64 expression (which has been shown to be a marker of a type 1 interferon signature). Although SOCS1 and SOCS3 protein levels yielded no statistically significant relationship between IPN γ , IL27, or CD64; SOCS1 and SOCS3 message levels in SLE patients were positively correlated to both IPN γ and IL27 (Figures 18B, 18C, and 18D). Together, these data support the notion that IPN γ signaling may be important in the production of SOCS1 protein.

Example 17-Prednisone treatment is correlated with enhanced SOCS1 and SOCS3 protein levels

[0145] In order to analyze the possible effects of prednisone treatment and SLE disease activity on KIR containing protein expression, subgroup analyses among SLE patients was performed. As can be seen in Figure 19, patients receiving prednisone consistently had higher SOCS1 protein levels than those not receiving prednisone, reaching significance among patients with an inactive SLEDIA score (n=9, p=p<0.001). In contrast, prednisone treatment had no effect of SOCS3 protein levels. In terms of cellular activation, patients receiving prednisone treatment had higher levels of pErk1/2 activation, again reaching statistical significance within inactive SLEDIA patients. Notably, prednisone treatment had no effect on either SOCS 1/3 message expression or STAT1 phosphorylation (Figure 19B). Together, these data show that enhanced SOCS1 levels were present in patients receiving prednisone treatment, but with no observed differences in STAT1 phosphorylation.

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P a t e n t k r a v

- 5 **1.** Peptidmimetikum af en suppressor af cytokinsignaleringsprotein (SOCS), hvor peptidet binder til aktiveringsløkken af og inhiberer aktiviteten af en tyrosinkinase, hvor peptidet omfatter to kopier af aminosyresekvensen af SEQ ID NO: 1, eller et funktionelt fragment af peptidet, der binder til aktiveringsløkken af og inhiberer tyrosinkinaseaktiviteten, hvor det funktionelle fragment ikke er en monomer af aminosyresekvensen af SEQ ID NO: 1.
- 10 **2.** Peptid ifølge krav 1, hvor tyrosinkinasen er et JAK-protein, for eksempel et JAK2-protein.
- 15 **3.** Peptid ifølge krav 1, hvor peptidet omfatter en eller flere linkeraminosyrer, for eksempel glycinaminosyrer, der er indsat mellem kopierne af aminosyresekvenserne, som binder til og inhiberer tyrosinkinaseaktiviteten.
- 20 **4.** Peptid ifølge krav 3, hvor peptidet omfatter aminosyresekvensen af SEQ ID NO:3, eller et funktionelt fragment af peptidet, der binder til aktiveringsløkken af og inhiberer tyrosinkinaseaktiviteten, hvor det funktionelle fragment ikke er en monomer af aminosyresekvensen af SEQ ID NO: 1.
- 25 **5.** Peptid ifølge krav 1, hvor peptidet omfatter et protein eller en nukleinsyre, der er bundet til peptidet, og som målretter levering til en celle, og/eller som sørger for translokation af peptidet over en biologisk membran af cellen, og/eller hvor peptidet er modificeret ved tilsætning af en polyethylenglycol-(PEG)-gruppe.
- 30 **6.** Peptid ifølge krav 1, hvor en lipofil gruppe, såsom en palmitoyl-lysingruppe, er knyttet til peptidet, eller hvor et cellepenetrerende peptid (CPP), for eksempel en CPP, der omfatter aminosyresekvensen af en hvilken som helst af SEQ

ID NOS: 31 til 49, er tilvejebragt ved en terminal ende af peptidet.

5 **7.** Peptid ifølge krav 6, hvor den lipofile gruppe omfatter en eller flere arginin- og/eller lysinaminosyrer ved den N-terminale ende, den C-terminale ende eller både den N-terminale og C-terminale ende af peptidet.

10 **8.** Peptid ifølge krav 7, hvor peptidet omfatter aminosyresekvensen af SEQ ID NO:29, eller et funktionelt fragment af peptidet, der binder til aktiveringsløkken af og inhiberer tyrosinkinaseaktiviteten, hvor det funktionelle fragment ikke er en monomer af aminosyresekvensen af SEQ ID NO: 1.

15 **9.** Peptid ifølge krav 6, hvor den lipofile gruppe omfatter en fedtsyredel, såsom caprinsyre, laurinsyre, myristinsyre, palmitinsyre, stearinsyre, arachidinsyre, behensyre, lignocerinsyre eller cerotsyre.

20 **10.** Polynukleotid, der omfatter en nukleotidsekvens, der koder for et eller flere peptider ifølge et hvilket som helst af kravene 1-9, eller et ekspressionskonstrukt, der omfatter polynukleotidet.

25 **11.** Sammensætning omfattende et peptid ifølge et hvilket som helst af kravene 1-9, eventuelt indkapslet i et liposom, eller polynukleotid eller ekspressionskonstrukt ifølge krav 10, hvor sammensætningen eventuelt omfatter en egnet bærer, et egnet fortyndingsmiddel eller en egnet buffer.

30 **12.** Peptid ifølge et hvilket som helst af kravene 1-9, polynukleotid eller ekspressionskonstrukt ifølge krav 10 eller sammensætning ifølge krav 11 til anvendelse som et medikament.

30 **13.** Peptid ifølge et hvilket som helst af kravene 1-9, polynukleotid eller ekspressionskonstrukt ifølge krav 10 eller sammensætning ifølge 11 til anvendelse i en fremgangsmåde til behandling eller forebyggelse af en autoimmun

lidelse og/eller inflammatorisk lidelse og/eller onkologisk lidelse hos en person eller et dyr.

5 **14.** Peptid ifølge et hvilket som helst af kravene 1-9, polynukleotid eller ekspressionskonstrukt ifølge krav 10, sammensætning ifølge krav 11 eller peptid til anvendelse ifølge krav 12 eller 13, hvor peptidet er et uforgrenet peptid.

10 **15.** *In vitro*-fremgangsmåde til inhibering af væksten af en cancer- eller tumor-celle eller til inhibering af aktivering af en tyrosinkinase i en celle, omfattende at bringe cellen i kontakt med eller forsyne cellen med en effektiv mængde af et peptid ifølge et hvilket som helst af kravene 1-9 eller 14, eller en polynukleotid eller et ekspressionskonstrukt ifølge krav 10 eller 14, eller en sammensætning ifølge krav 11 eller 14.

DRAWINGS

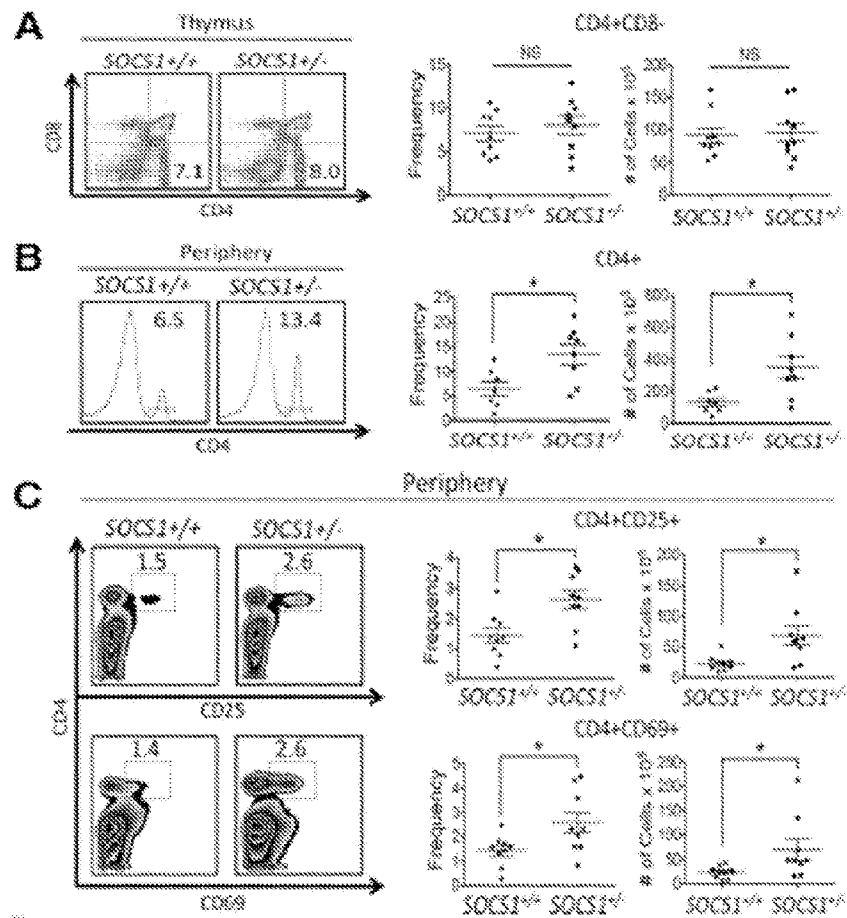


FIG. 1

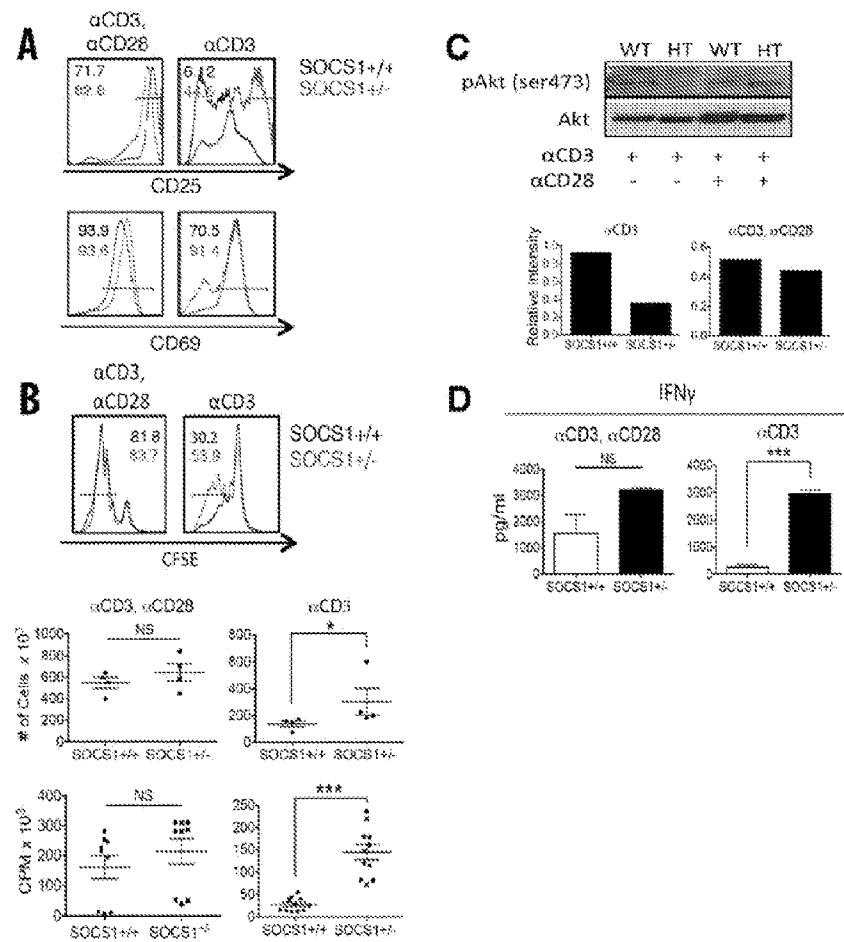


FIG. 2

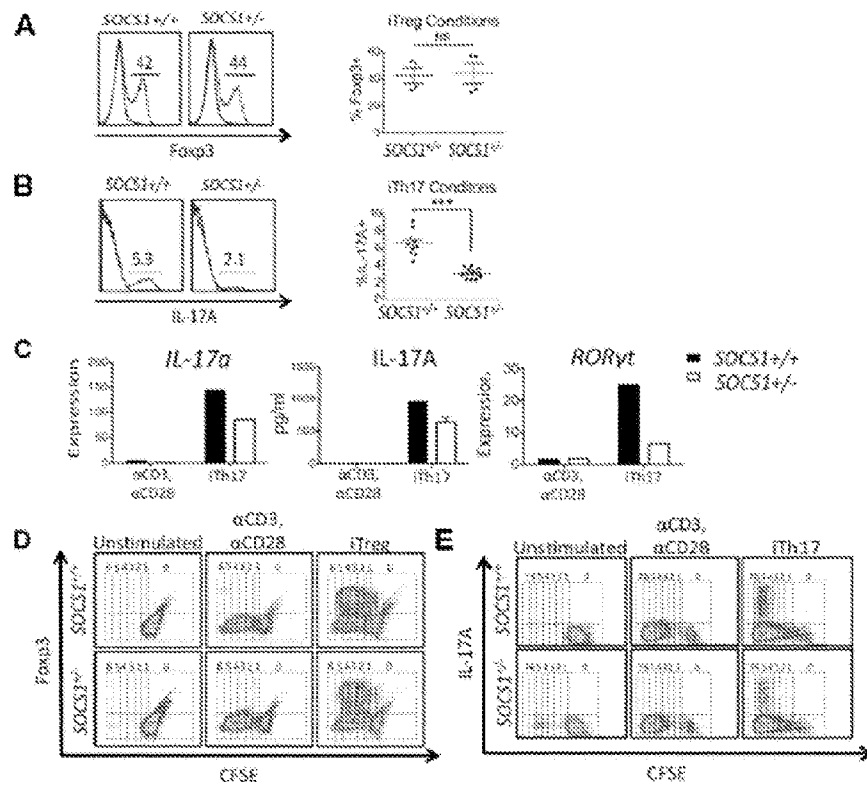


FIG. 3

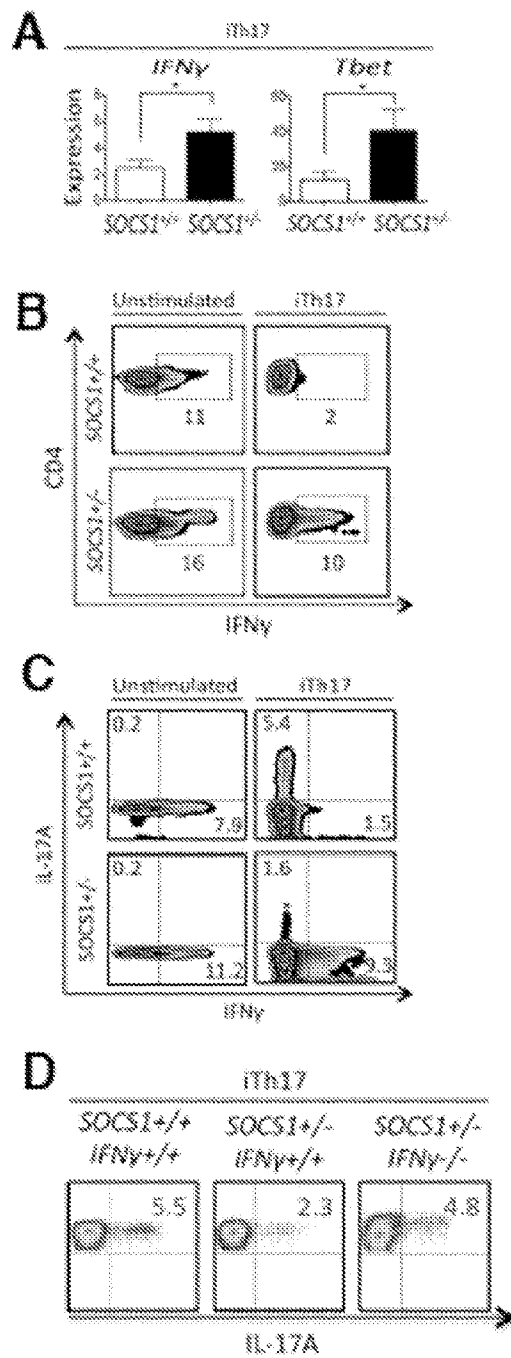


FIG. 4

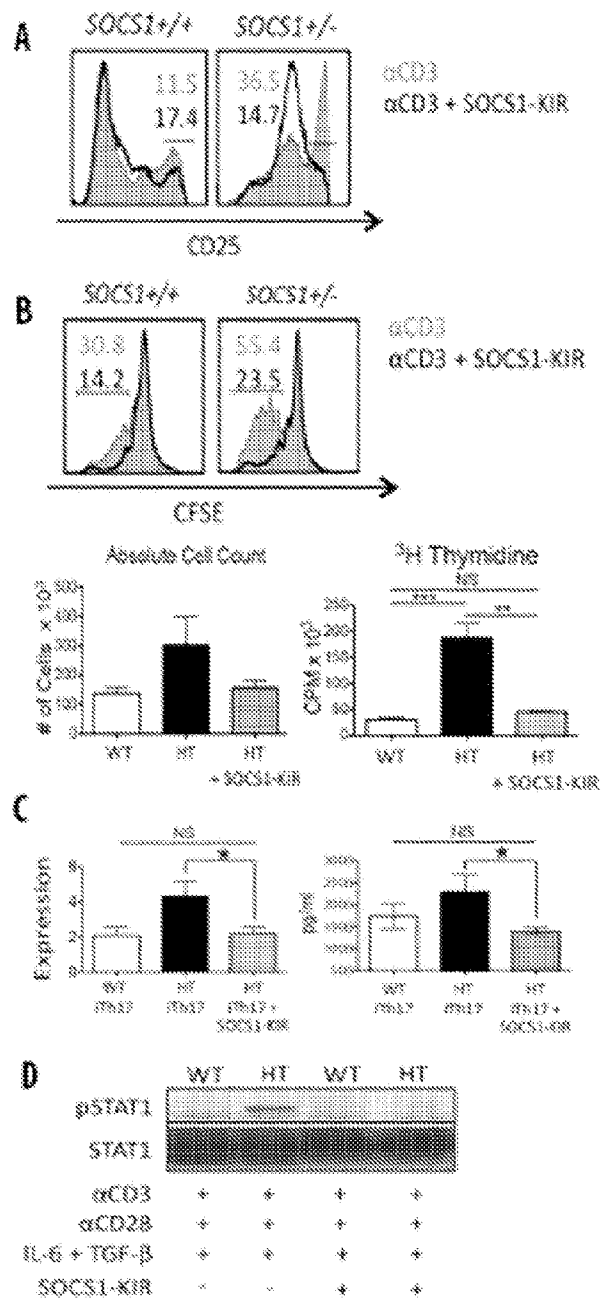


FIG. 5

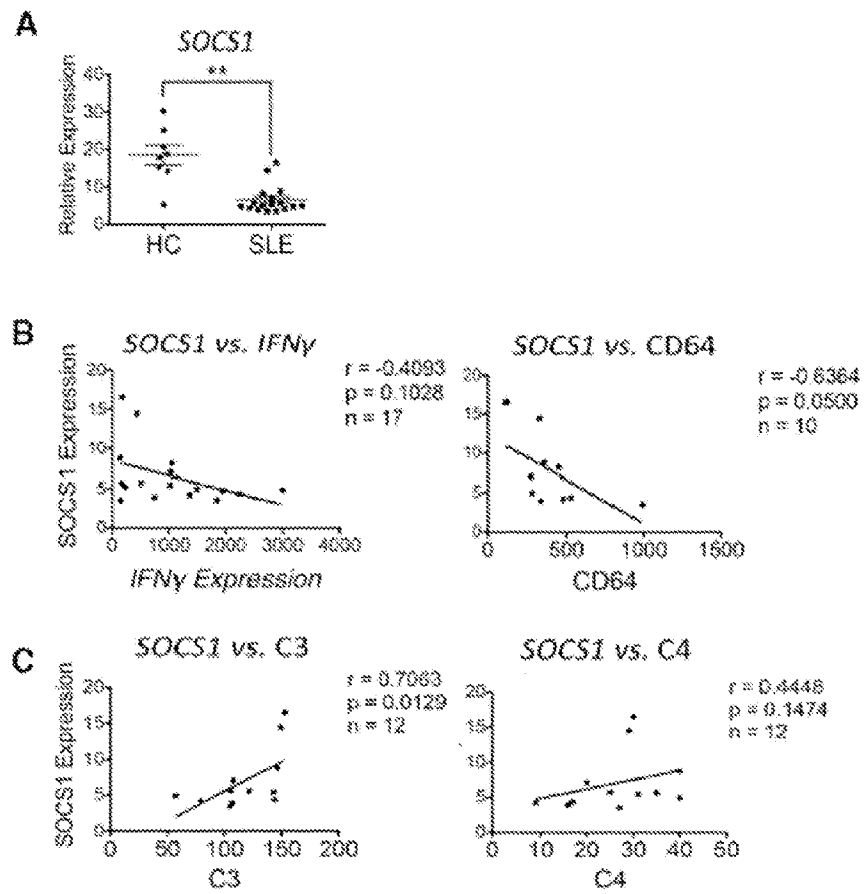


FIG. 6

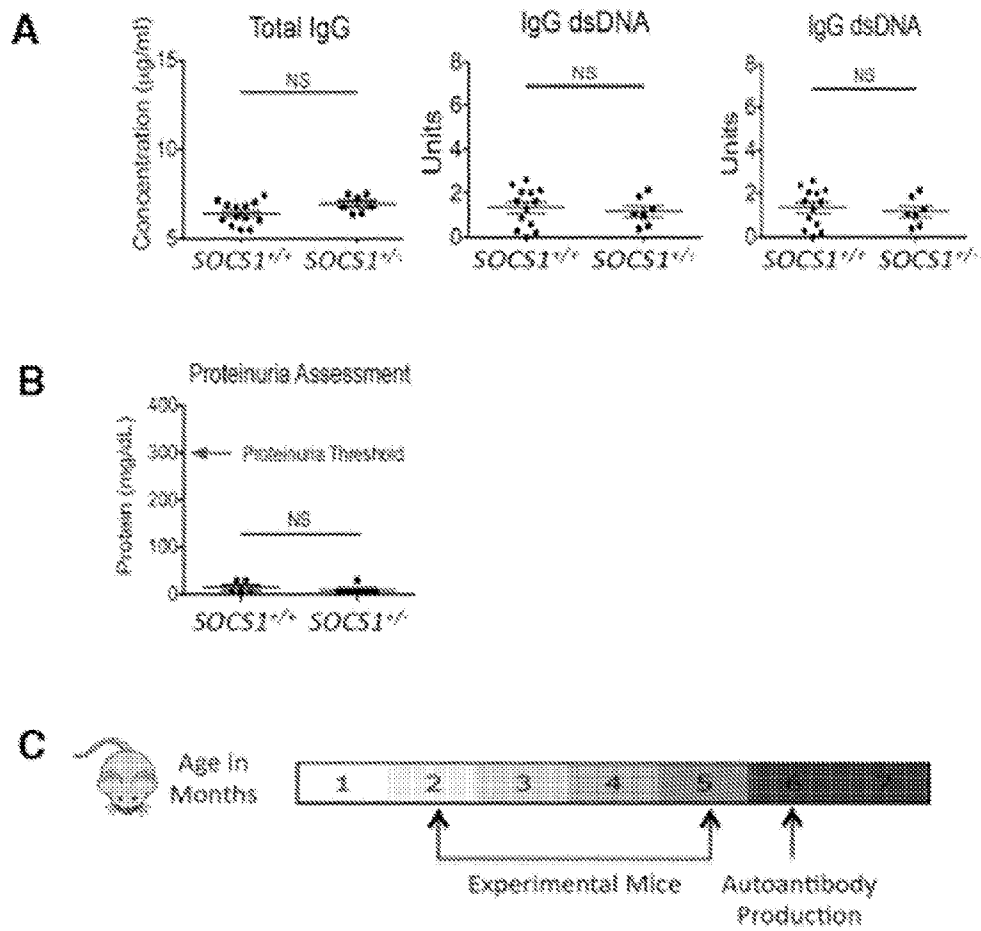


FIG. 7

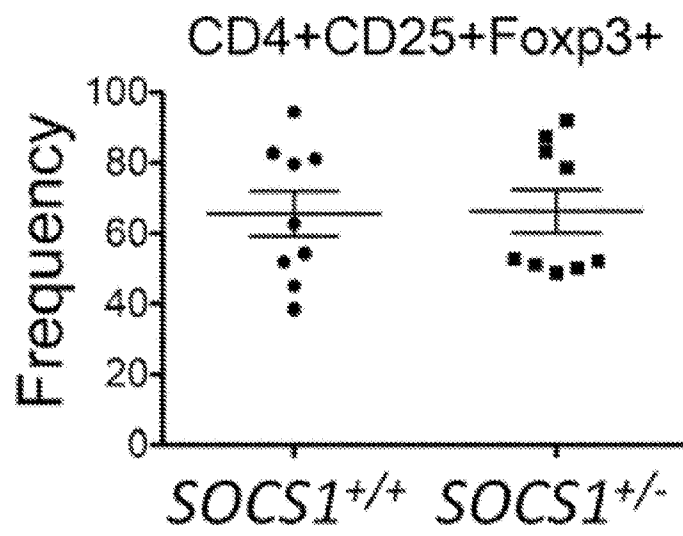


FIG. 8

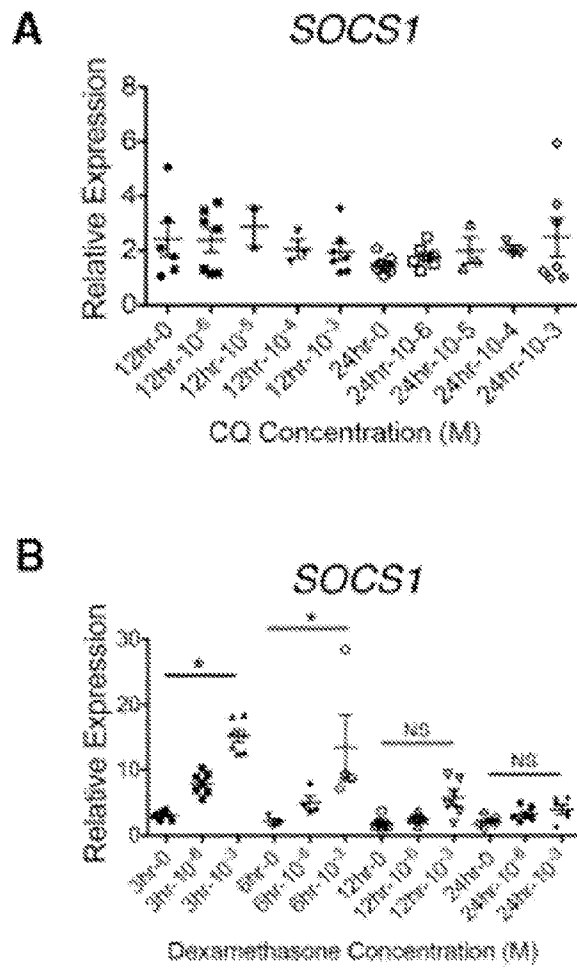


FIG. 9

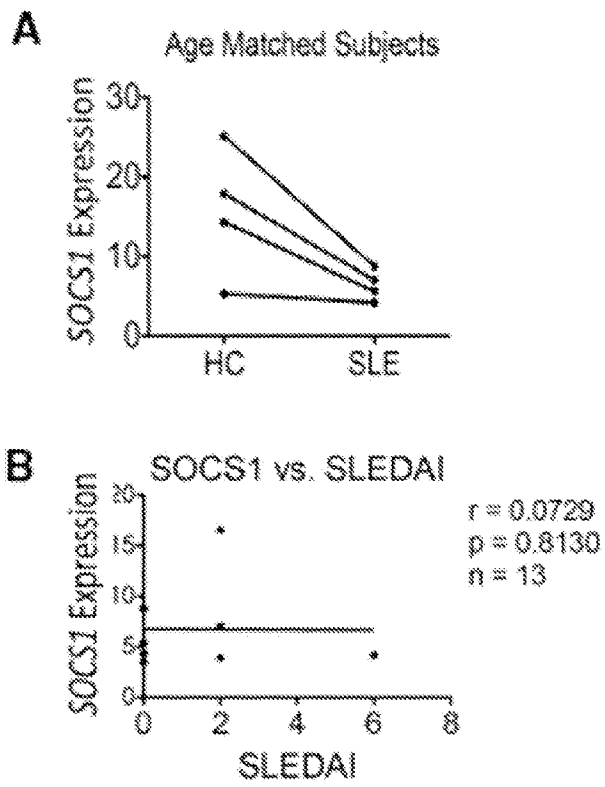


FIG. 10

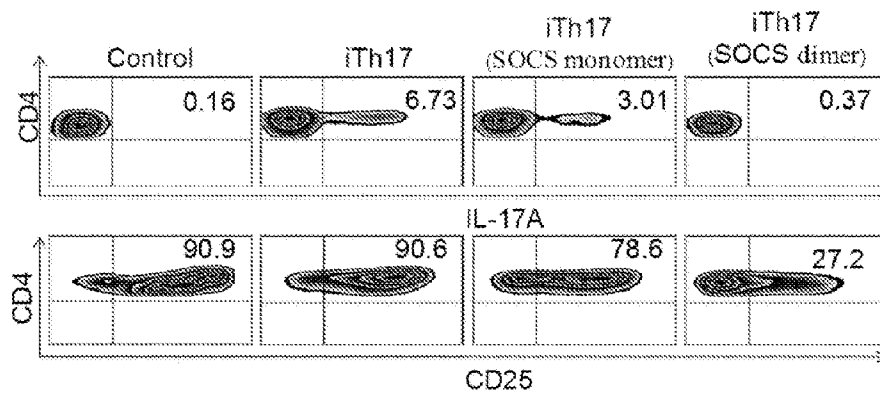


FIG. 11

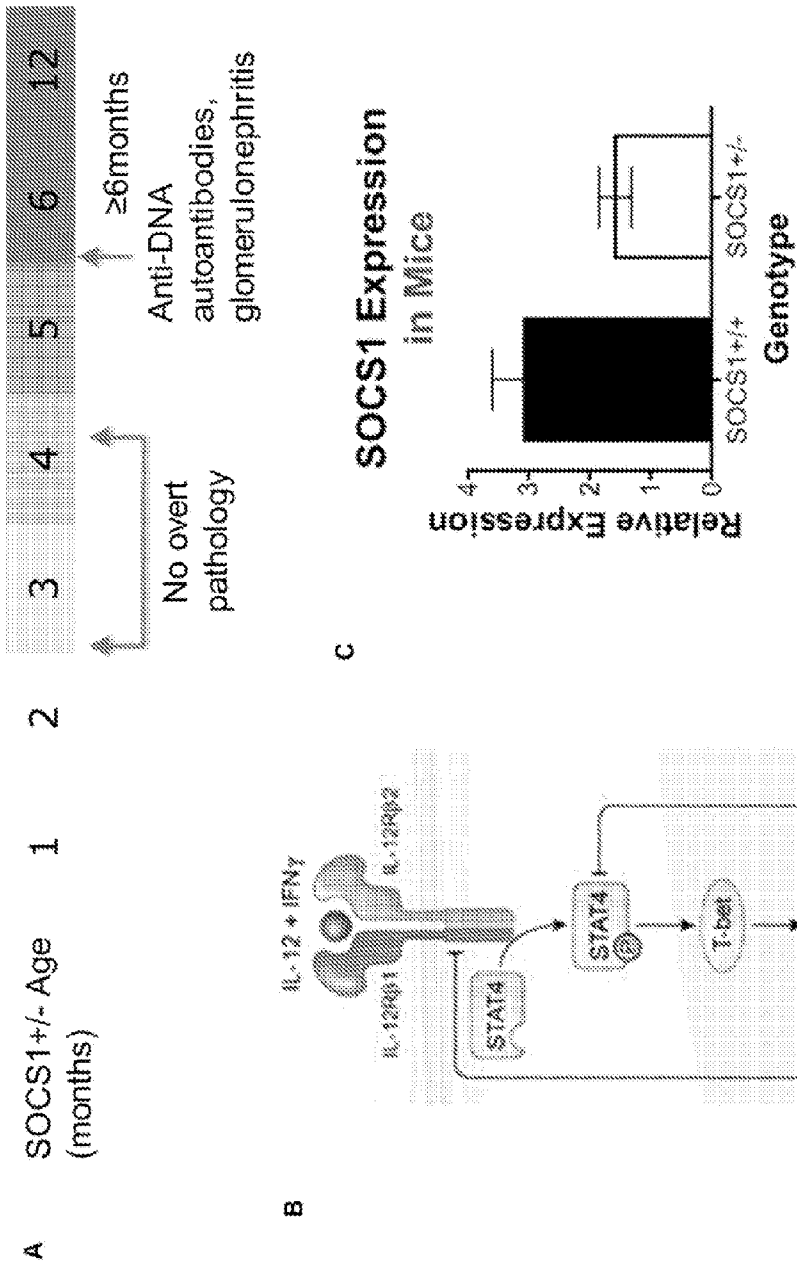


FIG. 12

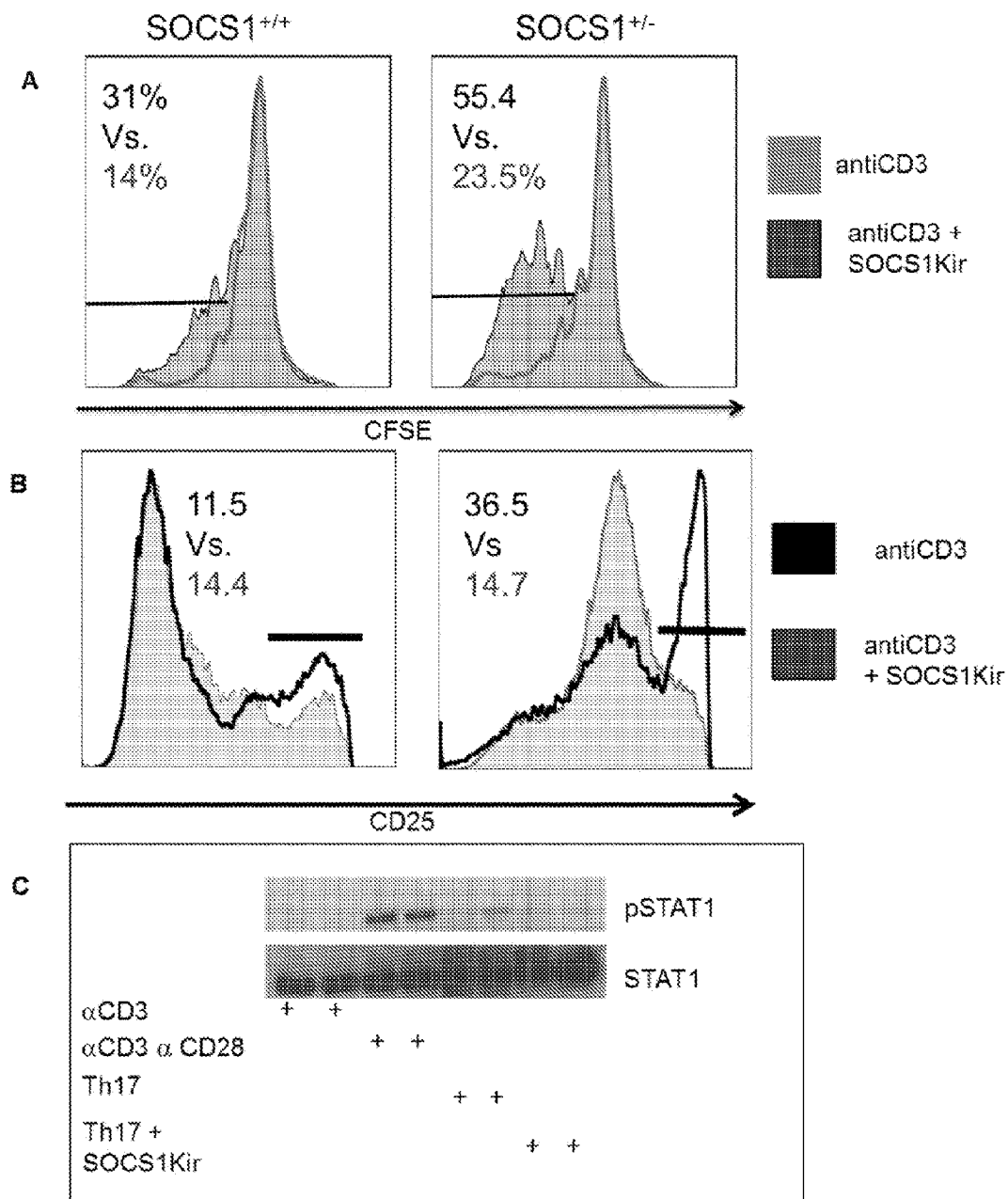


FIG. 13

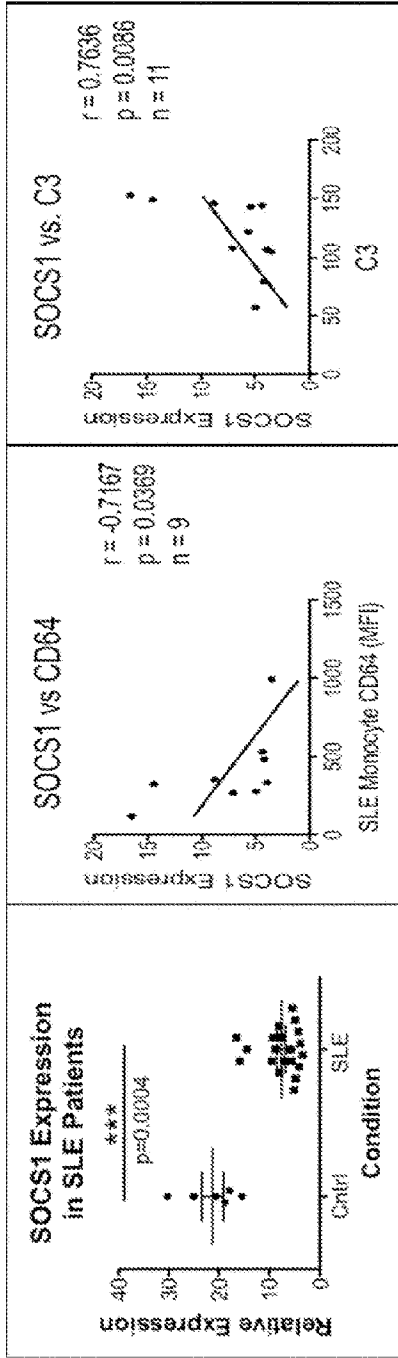


FIG. 14

FIG. 15

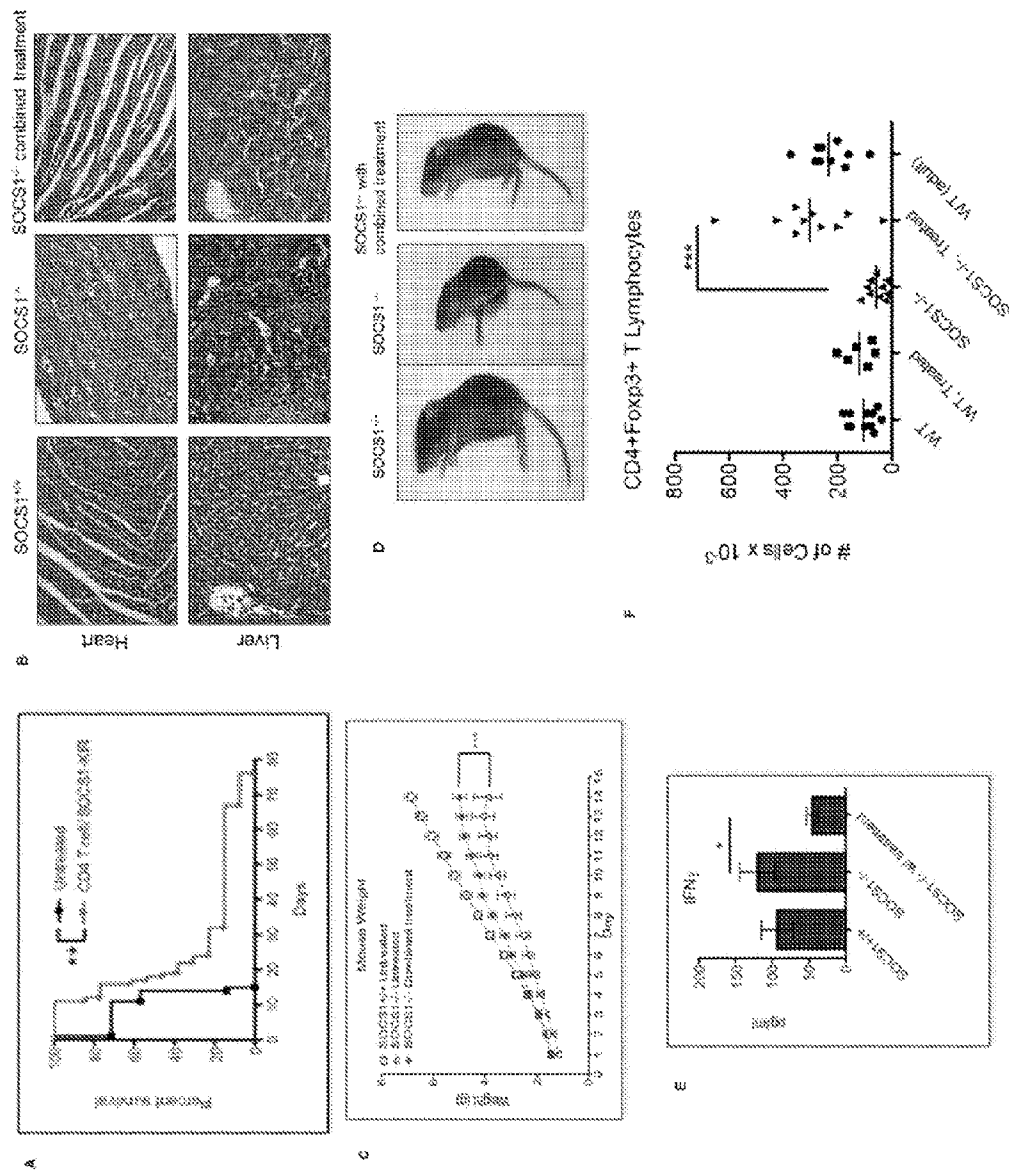


FIG. 16

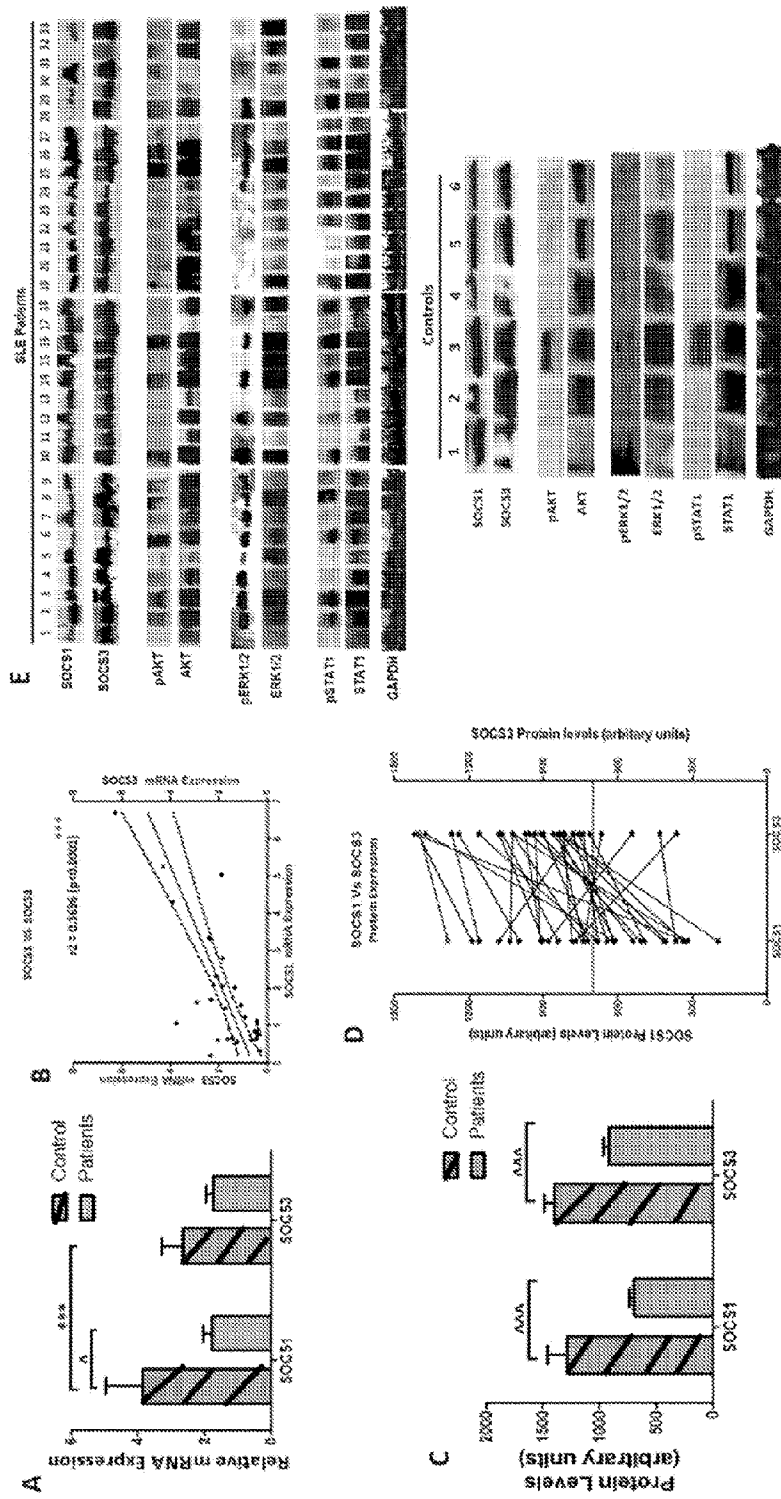


FIG. 18

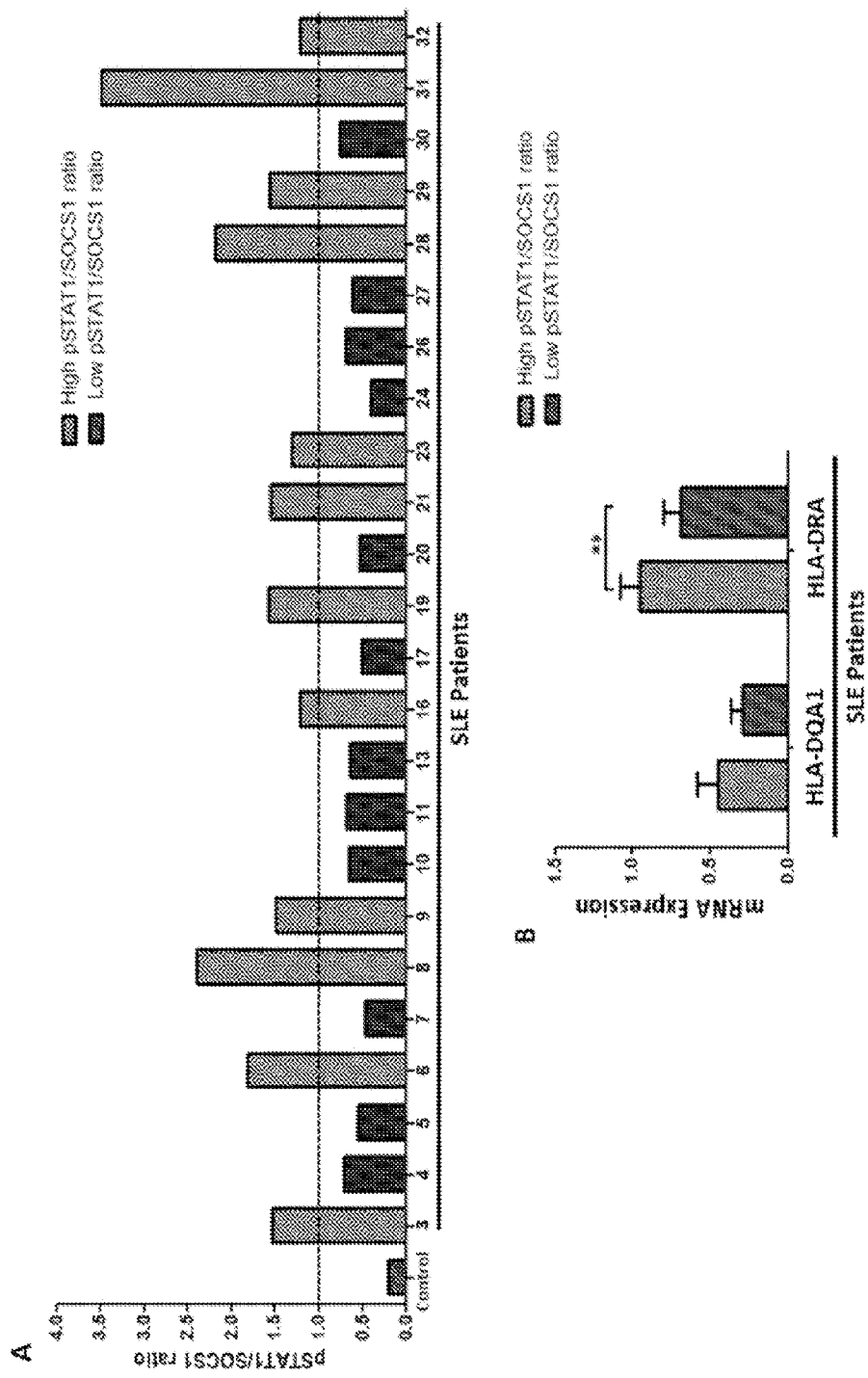


FIG. 19

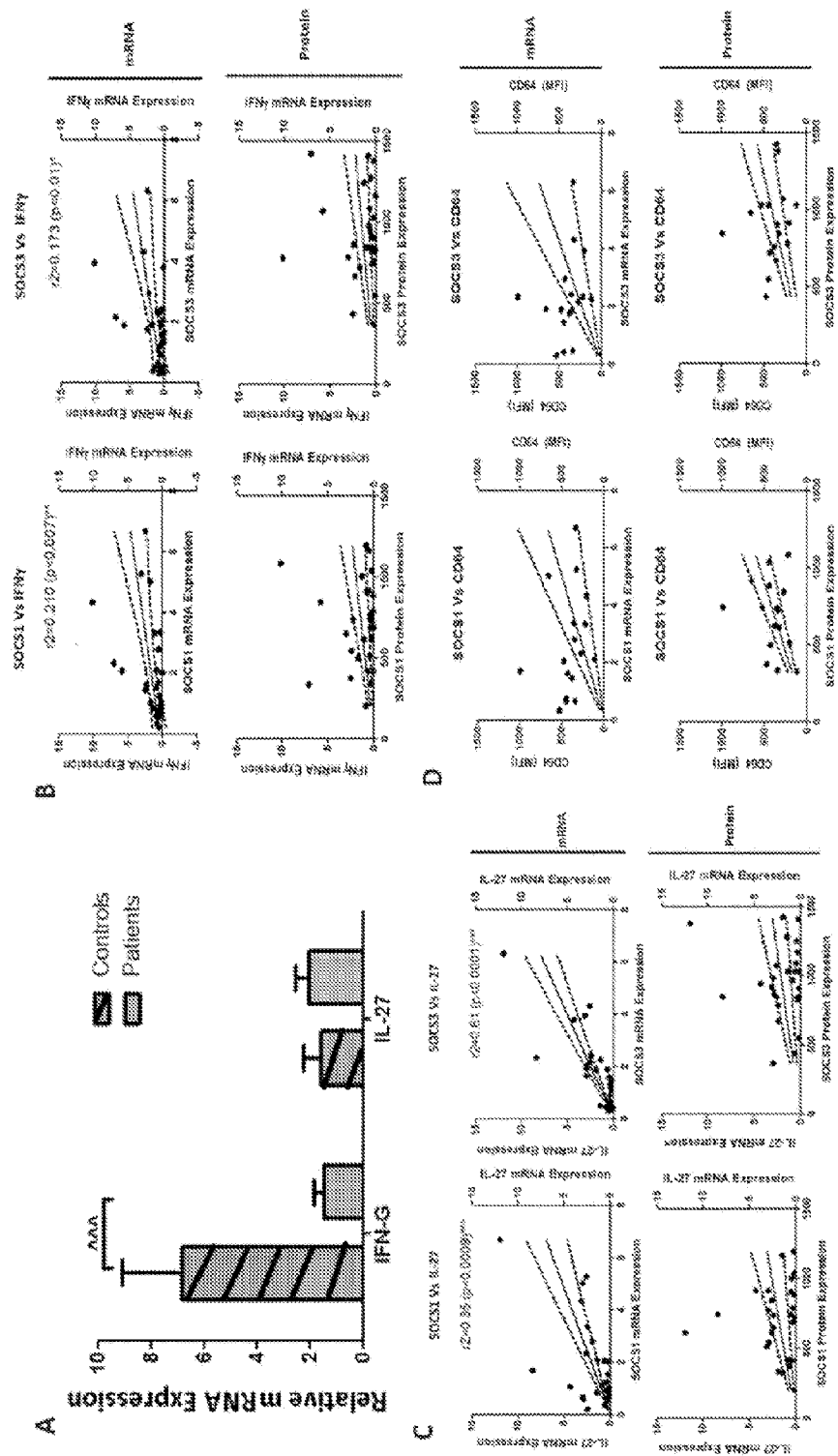
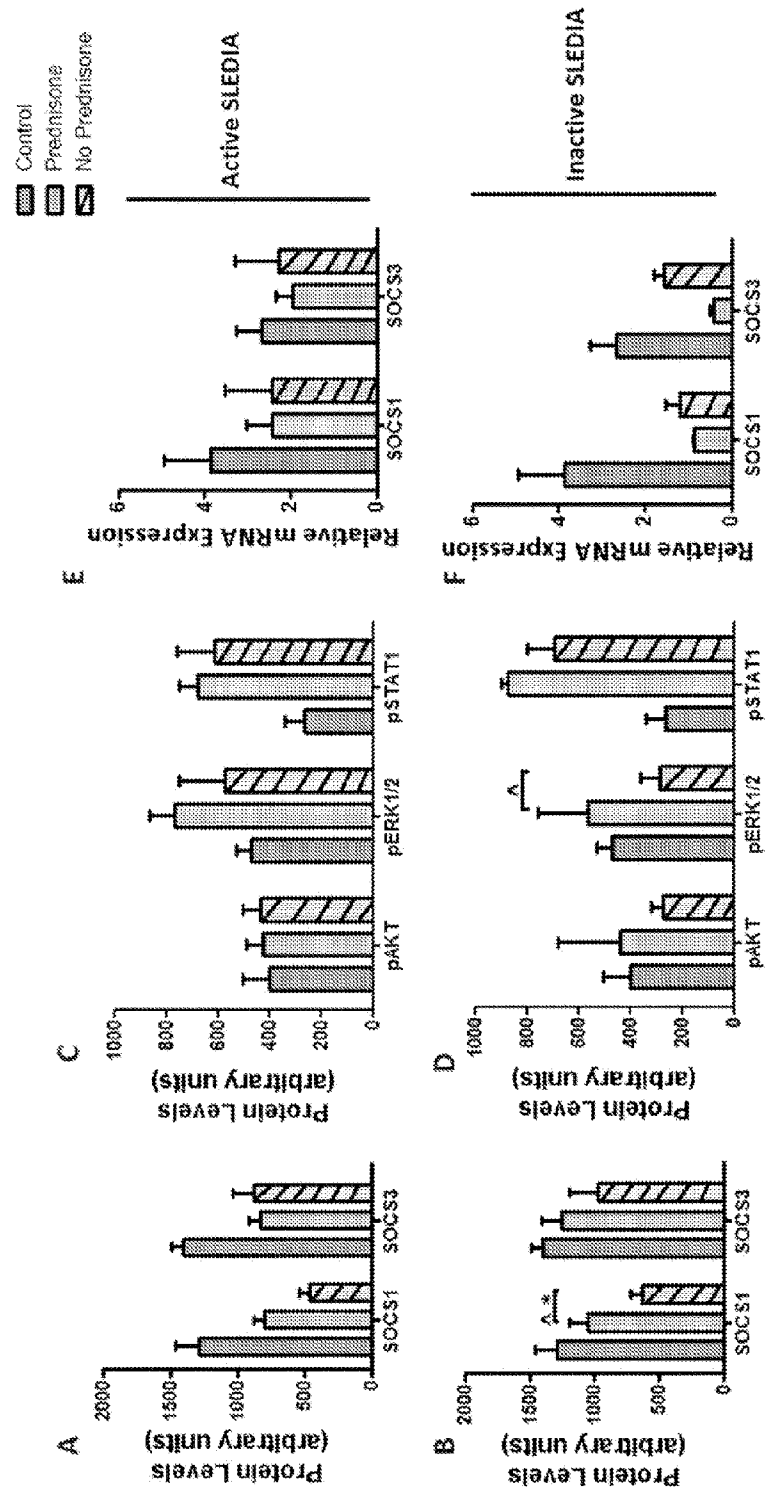


FIG. 20



SEKVENSLISTE

Sekvenslisten er udeladt af skriftet og kan hentes fra det Europæiske Patent Register.

The Sequence Listing was omitted from the document and can be downloaded from the European Patent Register.

