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CN-A- 102 898 521
US-A- 5 869 603
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AJITH SOMINANDA ET AL: "Inhibition of Endogenous Interferon Beta by Neutralizing Antibodies Against Recombinant Interferon Beta", ARCHIVES OF NEUROLOGY., vol. 67, no. 9, 1 September 2010 (2010-09-01), XP055399988, US ISSN: 0003-9942, DOI: 10.1001/archneurol.2010.218
KATHLEEN C. F. SHEEHAN ET AL: "Selective Blockade of Interferon-[alpha] and -[beta] Reveals Their Non-

Fortsættes ...

Redundant Functions in a Mouse Model of West Nile Virus Infection", PLOS ONE, vol. 10, no. 5, 26 May 2015 (2015-05-26), page e0128636, XP055400161, DOI: 10.1371/journal.pone.0128636

RUNKEL L ET AL: "MAPPING OF IFN-BETA EPITOPES IMPORTANT FOR RECEPTOR BINDING AND BIOLOGIC ACTIVATION: COMPARISON OF RESULTS ACHIEVED USING ANTIBODY-BASED METHODS AND ALANINE SUBSTITUTION MUTAGENESIS", JOURNAL OF INTERFERON AND CYTOKINE RESEA, MARY ANN LIEBERT, NEW YORK, NY, US, vol. 21, no. 11, 1 November 2001 (2001-11-01), pages 931-941, XP009011507, ISSN: 1079-9907, DOI: 10.1089/107999001753289541

KARPUSAS MICHAEL ET AL: "The crystal structure of human interferon beta at 2.2-A resolution", PROCEEDINGS NATIONAL ACADEMY OF SCIENCES PNAS, NATIONAL ACADEMY OF SCIENCES, US, vol. 94, no. 22, 28 October 1997 (1997-10-28), pages 11813-11818, XP002160243, ISSN: 0027-8424, DOI: 10.1073/PNAS.94.22.11813

DESCRIPTION

BACKGROUND OF THE INVENTION

[0001] The interferon (IFN) family of cytokines was initially discovered by their ability to protect cells from viral infections, but it is now appreciated that this family of evolutionarily conserved cytokines can elicit a broad range of responses. The family is made up of the type I, type II, and type III IFN subfamilies, and the type I IFNs are the most diverse of all cytokine families. The human type I IFNs are encoded by 13 genes for IFN α subtypes, plus single genes for each of IFN β , IFN ω , IFN κ , and IFN ϵ . IFN β and the several IFN α isoforms are the best studied of the type I IFNs. Most IFN α proteins share 78-98% identity, and IFN β shares ~35% identity with a consensus IFN α sequence. IFN β is naturally glycosylated, whereas IFN α isoforms are typically only weakly glycosylated. All type I IFNs bind to the cell surface class II cytokine receptor IFNAR (composed of the two chains IFNAR1 and IFNAR2). IFN α has a half-life in serum of 2-3 hours, but IFN β is hydrophobic and rarely detected in serum, and these characteristics are consistent with the notion that IFN α is effective systemically, whereas IFN β acts at local sites in an autocrine/paracrine manner.

[0002] IFN production can be stimulated by exposure to microbe-derived pathogen-associated molecular patterns, including microbial nucleic acids, lipids, proteins, and lipoproteins. However, there is increasing evidence that IFN production can also be stimulated by endogenous self-components that are released during disease processes, and this is particularly relevant in the context of systemic lupus erythematosus (SLE) and other rheumatic diseases such as dermatomyositis (DM). A pathological overproduction of type I IFN expression often characterizes SLE, and IFN α is detectable in sera from a limited number of SLE patients.

[0003] Increasing evidence also points to the importance of interferon-regulated gene (IRG) expression in the manifestation of SLE disease activity/severity, as evidenced by clinical results with the anti-IFNAR antibody anifrolimab. In a placebo-controlled phase 2 study, anifrolimab reduced disease severity across multiple clinical endpoints, while simultaneously inhibiting an IRG signature by approximately 90% at both doses tested in that study.

[0004] CN 102 898 521 A discloses a murine antibody raised against human interferon beta. AJITH SOMINANDA ET AL: "Inhibition of Endogenous Interferon Beta by Neutralizing Antibodies Against Recombinant Interferon Beta", ARCHIVES OF NEUROLOGY, vol. 67, no. 9, 2010 discloses the use of polyserum preparations of patients challenged with IFN β . KATHLEEN C. F. SHEEHAN ET AL: "Selective Blockade of Interferon- [alpha] and -[beta] Reveals Their Non-Redundant Functions in a Mouse Model of West Nile Virus Infection", PLOS ONE, vol. 10, no. 5, 26 May 2015, discloses a murine antibody raised against murine interferon beta... vol. 21, no. 11, 1 November 2001 (2001-11-01), pages 931-941 discloses monoclonal anti-IFN β antibodies.

[0005] In addition to anti-IFN receptor antibody anifrolimab (anti-IFNAR), several anti-IFN α antibodies are under clinical development, such as sifalimumab, rontalizumab, and AGS-009. IFN α has been the focus of these efforts because a large body of evidence (including genetic, immunological, serological, and clinical studies) has associated IFN α with autoimmune disorders. However, based upon the scientific evidence to date it is expected that IFN β will play a role similar to IFN α in autoimmune disorders. To date therapeutic antibodies that specifically target IFN β (and not IFN α), have not been reported. Accordingly, there is an unmet need for an antibody that specially binds IFN β for use in various therapeutic or diagnostic purposes.

SUMMARY OF THE INVENTION

[0006] The invention is as defined in the claims.

[0007] In a first aspect there is provided an isolated antibody, or antigen-binding fragment thereof, that specifically binds human IFN β , comprising a VH that comprises the amino acid sequence of SEQ ID NO: 28 and VL that comprises the amino acid sequence of SEQ ID NO: 1.

[0008] In a second aspect there is provided an isolated nucleic acid molecule comprising a nucleotide sequence encoding an antibody, or antigen-binding fragment thereof, that specifically binds human IFN β and comprises a VH that comprises the amino acid sequence of SEQ ID NO: 28 and VL that comprises the amino acid sequence of SEQ ID NO: 1.

[0009] In one embodiment, the isolated nucleic acid molecule comprises the nucleotide sequence of SEQ ID NO:166 and SEQ ID NO:167.

[0010] In one embodiment the isolated nucleic acid molecule comprises the nucleotide sequence of the insert of the plasmid deposited at the ATCC and having Accession Number PTA-122726 and the nucleotide sequence of the insert of the plasmid deposited at the ATCC and having Accession Number PTA-122727.

[0011] In a third aspect there is provided a vector comprising a nucleic acid molecule of the second aspect.

[0012] In a fourth aspect there is provided a host cell comprising the nucleic acid molecule of the second aspect or a vector of the third aspect.

[0013] In a fifth aspect there is provided a method of producing an antibody, or antigen-binding fragment thereof of the first aspect, comprising culturing the host cell of the invention, under conditions wherein the antibody, or antigen-binding fragment thereof, is produced by the host cell.

[0014] In a sixth aspect there is provided a pharmaceutical composition comprising an antibody, or antigen-binding fragment thereof, of the first aspect, and a pharmaceutically acceptable excipient.

[0015] In a seventh aspect there is provided an antibody, or antigen-binding fragment thereof, of the first aspect, or the pharmaceutical composition of the sixth aspect, for use in therapy.

[0016] In one embodiment, the use is for a method of treating dermatomyositis (DM) or a method of treating systemic lupus erythematosus (SLE).

[0017] The disclosure provides antibodies, and antigen-binding fragments thereof, that bind Interferon beta (IFN β), as well as uses therefor, and associated methods.

BRIEF DESCRIPTION OF THE DRAWINGS

[0018]

FIG. 1 shows the viscosity of IFN β antibody in MOD1 buffer.

FIG. 2 is a differential scanning calorimetry (DSC) graph of antibody CTI-AF1.

FIG. 3 is the Size-Exclusion HPLC (SE-HPLC) analysis of CTI-AF1 aggregation, as a result of low-pH hold.

FIGS. 4A-4D show the SE-HPLC analysis of time points from stability studies.

FIGS. 5A-5D show graphs demonstrating that CTI-AF1 is stable over time when stored at 40°C and does not lose the ability to neutralize IFN β . CTI-AF1 was stored at various temperatures and time periods then the ability of the antibody to neutralize IFN β in an IFN dependent luciferase reporter assay was evaluated. Material stored for 1 week at 40°C (FIG. 5A, T0 equals no time at 40°C) had no loss of neutralizing activity; Storage at 40°C for two or three weeks had no impact on activity (FIG. 5C). Material that was produced after transfection of CHO cells instead of HEK293 cells or containing a mutation of amino acid 44 from a phenylalanine to a proline had no impact on neutralization (FIG. 5B). Finally, material stored for four weeks at 40°C or five weeks at room temperature (FIG. 5D) had no impact on the ability of CTI-AF1 to neutralize IFN β induced activity.

FIG. 6 depicts data showing identification of mouse anti-human IFN β hybridomas that could block the binding of IFN β to IFNAR2 by bio-layer interferometry (BLI) using the ForteBio Octet to measure molecular interaction. First, mouse anti-human IFN β Abs were captured on a protein G sensor from conditioned culture media; next, human IFN β was bound (indicated by the + hIFN- β arrow), then the Ab:IFN β complexes were exposed to the high affinity chain of the human receptor, IFNAR2 (indicated by the + IFNAR2 arrow). Non-blocking antibodies show an upward bump in the curve indicative of additional binding (as indicated by the non-neutralizer arrow, bottom), whereas neutralizing antibodies demonstrated a relatively flat curve (as indicated by neutralizer arrows, top). Several mouse hybridomas demonstrated the ability to neutralize binding of IFNAR2 to IFN β and were selected for further characterization and eventual humanization.

FIG. 7 depicts data showing determination of CTI-AF1's K_D for human IFN β by surface plasmon resonance (SPR). CTI-AF1 was captured on a CM5 sensor chip, then, starting at 2.5 nM IFN β , a 6 point, 2-fold titration series of recombinant human IFN β was flowed over CTI-AF1. The samples were run in duplicate and the concentration of IFN β is indicated to the right of the graph. For each concentration of IFN β , the thin grey lines depict the binding of IFN β in each replicate sample; the heavier grey line represents the average fitted curve calculated by the analysis program. The K_D of CTI-AF1 for human IFN β was determined to be about 36 pM.

FIGS. 8A-8B demonstrate that CTI-AF1 is a potent neutralizer of IFN β induced signaling in multiple assays. FIG. 8A shows that HEK293 cells stably transduced with an IFN stimulated response element (ISRE) luciferase reporter construct were stimulated in the presence of IFN β and titrated amounts of CTI-AF1. A dose-dependent inhibition of luminescence is seen indicating that IFN β has been neutralized. Binding of IFN β to the interferon receptor (IFNAR) is known to induce the phosphorylation of the STAT1 protein in U937 cells. FIG. 8B shows STAT1 phosphorylation analysis. U937 cells were exposed to IFN β , pre-incubated with titrated amounts of CTI-AF1 for 15 minutes, then the level of STAT1 phosphorylation was evaluated. The data show that there is a dose-dependent inhibition of STAT1 phosphorylation, indicating that IFN β dependent signals have been neutralized by CTI-AF1.

FIG. 9 demonstrates that CTI-AF1 neutralized expression of IFN stimulated gene Mx1 (MxA) in primary human dermal fibroblasts (HDF). There are a number of genes that are known to be expressed in response to stimulation with IFNs, IFN stimulated genes (ISG). Mx1 (MxA) is well characterized as a type I IFN ISG. Mx1 (MxA) gene expression after stimulation with recombinant IFN β was evaluated in primary HDF in the presence or absence of indicated amounts of CTI-AF1. Cells were stimulated for 5 hours then RNA was isolated. RNA was converted into cDNA and quantitative PCR (qPCR) was performed to determine the level of Mx1 (MxA) expression and B2M was used as a control. Data are presented as fold induction; a dose-dependent inhibition of Mx1 (MxA) gene expression was seen indicating neutralization of IFN β signaling.

FIGS. 10A-10B demonstrate that CTI-AF1 specifically neutralized IFN β . U937 cells were stimulated with either IFN β (FIG. 10A) or IFN α (FIG. 10B) for 15 minutes in the presence of neutralizing antibodies to IFN β (CTI-AF1) or IFN α (sifalimumab, SIF). CTI-AF1 inhibited IFN β dependent STAT1 phosphorylation (panel A), but had no impact on IFN α -induced STAT1 phosphorylation (panel B). As a control, a neutralizing anti-IFN α (SIF) was used in conjunction with IFN α stimulation to demonstrate IFN α dependent STAT1 phosphorylation could be inhibited.

FIG. 11 demonstrates that CTI-AF1 was a potent inhibitor of endogenous IFN β secreted by primary human dermal fibroblasts (HDF). HDF were stimulated with polyinosinic:polycytidylic acid (poly I:C) for 24 hours to induce the expression of IFN β in the presence of titrated amounts of CTI-AF1 and then Mx1 (MxA) gene expression was evaluated as described in FIG. 9. A dose-dependent inhibition of Mx1 (MxA) gene expression was seen with increasing amounts of CTI-AF1 demonstrating the antibody neutralized endogenously produced IFN β .

FIGS. 12A-12D depict CTI-AF1 serum PK and IFN β skin coverage profiles in human at 2 mg/kg IV Q4W. Profiles are shown for IFN β skin:plasma ratio of 10 (FIGS 12A and 12C) and 100 (FIGS. 12B and 12D). Note that CTI-AF1 serum PK is not impacted by IFN β skin:plasma ratio and IFN β turnover half-life. The dashed lines in panels C and D represent 95% IFN β coverage in skin.

FIGS. 13A-13D show the profiles for IFN β skin:plasma ratio of 10 (FIGS. 13A and 13C) and 100 (FIGS. 13B and 13D). Note that serum PK is not impacted by IFN β skin:plasma ratio and IFN β turnover half-life. The dashed lines in panels C and D represent 95% IFN β coverage in skin.

FIG. 14 shows the mean serum concentrations of CTI-AF1 in cynomolgus monkeys from toxicity study.

FIGS. 15A shows the sequence and secondary structure of human IFN β (SEQ ID NO:41). FIG. 15B shows the sequence alignment of human (SEQ ID NO:41), cynomolgus (SEQ ID NO:44), mouse (SEQ ID NO:42), rat (SEQ ID NO:43), and rabbit (SEQ ID NO: 45) IFN β sequences.

FIG. 16A shows the relationship between cutaneous dermatomyositis disease area and severity index (CDASI) activity and a blood 10-gene signature score. CDASI activity score ≥ 12 correlates with an elevated 10-gene blood IRG "signature" (Spearman rank correlation $r=0.61$; $p < 0.0001$). FIG. 16B shows a strong threshold effect observed with a CDASI cutoff of 12 that is associated with IRG signature cutoff of 3-fold ($p = 0.0004$, Mann-Whitney test).

FIG. 17 shows serum samples from 25 normal (unaffected) donors, 19 DM donors with a CDASI of <12, and 38 DM donors with a CDASI of ≥ 12 analyzed for the presence of IFN β protein using a high-sensitivity ELISA kit (PBL Assay Science) (Wilcoxon test 'unaffected vs CDASI <12' $p=0.39$; Wilcoxon test 'unaffected vs CDASI ≥ 12 ' $p<0.0001$).

FIGS. 18A-18B show levels of IFN α or IFN β mRNA (FIG. 18A) or an IRG signature in unaffected versus affected skin samples (FIG. 18B) in paired skin biopsies (i.e., unaffected and affected tissue) collected from 5 DM patients and evaluated by a custom Type I IFN TaqMan Low Density Array (TLDA) (96 assay array). Each data point represents the average of 2 independent qPCR reactions per sample; mean $\pm$ SEM. Panel A: Signed Rank test p-value "unaffected IFN β vs affected IFN β "=0.06; Signed Rank test p-value "unaffected IFN α vs affected IFN α "=1.0. Panel B: Signed Rank test p-value "unaffected vs affected"=0.002.

FIG. 19 is a graph showing dose-dependent CTI-AF1 inhibition of hybrid IFN α/β proteins. Absence (CID1281) or decreased (CID1280) inhibition of IFN-induced STAT1 phosphorylation indicates that insertion of the IFN α sequence has disrupted the epitope within IFN β that is recognized by CTI-AF1.

FIGS. 20A-20B shows the co-crystal structure of cyno-IFN β and Fab of CTI-AF1. Binding epitope residues are depicted in grey in FIG. 20A, and binding paratope residues are depicted in grey in FIG. 20B.

DETAILED DESCRIPTION OF THE INVENTION

1. ANTI-IFN β ANTIBODIES

A. Interferon beta (IFN β)

[0019] Interferon beta (IFN β), also known as fibroblast IFN, is a glycosylated, secreted, and approximately 22 kDa member of the type I interferon family of molecules. The sequence of human IFN β precursor is shown as SEQ ID NO: 40. A signal peptide (residues 1-21 of SEQ ID NO: 40) of the precursor is cleaved to produce mature IFN β (SEQ ID NO: 41), which shares 47% and 46% amino acid sequence identity with the mouse and rat proteins, respectively. Alignments of IFN β from various species are shown in Figure 15B. The signal peptide is underlined in the sequence below.

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MTNKLQLQIA LLLCFSTTAL SMSYNLLGEL QRSSNFQCCX LLWQINGRL YCLKDRMNF IPBRIKQLQQ
FKKDAALTI YEMLNIFAI FRQSSSTGW NETIVENLLA NVISQINHLK TVLEEKLEKE DTRGKLMS
LHLKRYYGRI LHYLKAKEYS HCAWTVRVE ILRNIFYINR LUGYLRN (Human IFN $\beta$  precursor, SEQ
ID NO:40)
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[0020] The structure of IFN β contains 5 α -helices, designated A (YNLLGFLQRSSNFQCCXKLL; SEQ ID NO:153 or residues 3-21 of SEQ ID NO:41), B (KEDAALTIYEMLNIFAI; SEQ ID NO:154 or residues 52-70 of SEQ ID NO:41), C (ETIVENLLANVYHQINHLKTVLEEK; SEQ ID NO:155 or residues 81-106 of SEQ ID NO:41), D (SLHLKRYYGRIHLHYLKA; SEQ ID NO:156 or residues 119-135 of SEQ ID NO:41), and E (HCAWTVRVEILRNIFYINRLT; SEQ ID NO:157 or residues 140-161 of SEQ ID NO:41). The five α -helices are interconnected by loops of 2 to 28 residues designated AB, BC, CD, and DE loops (Figure 15A). It has been reported that the A helix, the AB loop, and the E helix are involved in binding of IFN β to its receptor, IFNAR.

B. Anti-IFN β Antibodies

[0021] One potential drawback of an anti-IFNAR antibody (e.g., anifrolimab) is that both IFN α and IFN β cytokines bind to IFNAR. Although these two types of IFN cytokines elicit similar biological activities to a similar degree, there are significant differences in potency and cell type specific activities between these two types of IFNs. For example, IFN β elicits a markedly higher antiproliferative response in some cell types, such as embryonal carcinoma, melanoma and melanocytes, than does IFN α . Higher potency of IFN β in treatment of multiple sclerosis and certain cancers has also been observed. Blocking the activity of IFNAR, however, does not selectively modulate the activities of IFN β . Significantly, IFN α is an important cytokine in response to viral infections, such that blocking its activity may have unwanted effects. Accordingly, an antibody that specially binds IFN β , but not IFN α , would fulfill a significant unmet need for treatment of diseases that are primarily driven by IFN β .

[0022] The invention provides an isolated antibody, or antigen-binding fragment thereof, that specifically binds human IFN β . As shown in the Examples, the antibody of the invention inhibits the binding of IFN β to its receptor, and is hence referred to as a "neutralizing" antibody. Without wishing to be bound by any particular theory, the data indicate that the antibody, or antigen-binding fragment thereof, blocks, or partially blocks, the receptor binding sites of IFN β , either by competing for the same or overlapping residues from IFNAR, or by creating steric hindrance.

[0023] In certain embodiments, the antibody, or antigen-binding fragment thereof, bind to human IFN β with a binding affinity (K_D) value that is at least 100 fold less, than its K_D value for a human IFN α under substantially the same assay conditions. For example, the ratio of K_D for IFN β versus K_D for IFN α can be 1:100 or less, 1:250 or less, 1:500 or less, 1:1000 or less, 1: 2500 or less, 1:5000 or less, or 1:10,000 or less.

[0024] Mutagenesis studies and crystal structure studies also identified epitope residues in human IFN β that are recognized by anti-IFN β antibodies disclosed herein. In particular, among all IFN β residues that are within 3.8 Å from a heavy atom of the antibody ("potential" epitope residues), three different types have been identified: (i) "primary" epitope residues that are characterized as highly buried residues at the of antibody-antigen interface and zero-to-low sequence tolerance to any other amino acid substitutions at this position; (ii) "secondary" epitope residues that are characterized as residues with medium buried surface area at the interface and medium sequence tolerance to amino acid substitutions at these positions; and (iii) "Optional" epitope residues are characterized as residues with low buried surface area at the interface and high sequence tolerance to amino acid substitutions at these positions.

[0025] Provided herein are antibody CTI-AF1 and variants thereof. The antibody or antigen-binding fragment thereof comprises the following heavy chain

CDR sequences: (i) CDR-H1 comprising SEQ ID NO: 37, CDR-H2 comprising SEQ ID NO: 38, and CDR-H3 comprising SEQ ID NO: 39; and (ii) the following light chain CDR sequences: CDR-L1 comprising SEQ ID NO: 34, CDR-L2 comprising SEQ ID NO: 35, and CDR-L3 comprising SEQ ID NO: 36.

[0026] As demonstrated from the crystal structure studies, not all residues in CDRs contribute to antibody-antigen binding. As shown in Example 7 and Table 14, only limited number of CDR residues are within 3.8 Å from a heavy atom of the antigen, and are considered as potential paratope residues. Among these potential paratope residues, (i) "primary" paratope residues are those characterized as highly buried residues at the antibody-antigen interface and low sequence tolerance to any other amino acid substitutions at this position; and (ii) "secondary" paratope residues are characterized as residues with lower buried surface area at the interface and higher sequence tolerance to amino acid substitutions at these positions.

[0027] In certain embodiments, the antibody or antigen-binding fragment thereof described herein comprises (i) a CH comprising an amino acid sequence that is at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 29; and/or (ii) a CL comprising an amino acid sequence that is at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 30. Any combination of these CH and CL sequences is also encompassed by the invention.

[0028] In certain embodiments, the antibody or antigen-binding fragment thereof described herein comprises an Fc domain. The Fc domain can be derived from IgA (e.g., IgA₁ or IgA₂), IgG, IgE, or IgG (e.g., IgG₁, IgG₂, IgG₃, or IgG₄).

[0029] In certain embodiments, the antibody or antigen-binding fragment thereof described herein comprises (i) a heavy chain comprising an amino acid sequence that is at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 33; and/or (ii) a light chain comprising an amino acid sequence that is at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 32. Any combination of these heavy chain and light chain sequences is also encompassed by the invention.

[0030] The antibodies, and antigen-binding fragments thereof, provided herein include monoclonal antibodies, polyclonal antibodies, antibody fragments (e.g., Fab, Fab', F(ab')₂, Fv, Fc, etc.), chimeric antibodies, bispecific antibodies, heteroconjugate antibodies, single chain (ScFv), mutants thereof, fusion proteins comprising an antibody portion, domain antibodies (dAbs), humanized antibodies, and any other configuration of the immunoglobulin molecule that comprises an antigen recognition site of the required specificity, including glycosylation variants of antibodies, amino acid sequence variants of antibodies, and covalently modified antibodies. The antibodies and antigen-binding fragments may be murine, rat, human, or any other origin (including chimeric or humanized antibodies). In some cases the antibody is a monoclonal antibody.

[0031] The binding affinity of an antibody can be expressed as a K_D value, which refers to the dissociation rate of a particular antigen-antibody interaction. K_D is the ratio of the rate of dissociation, also called the "off-rate (k_{off})", to the association rate, or "on-rate (k_{on})". Thus, K_D equals k_{off}/k_{on} (dissociation/association) and is expressed as a molar concentration (M), and the smaller the K_D, the stronger the affinity of binding. K_D values for antibodies can be determined using methods well established in the art. Unless otherwise specified, "binding affinity" refers to monovalent interactions (intrinsic activity; e.g., binding of an antibody to an antigen through a monovalent interaction).

[0032] The antibody, or antigen-binding fragment thereof, has an affinity (K_D) value of not more than about 1×10⁻⁷ M, such as not more than about 1×10⁻⁷ M, not more than about 9×10⁻⁸ M, not more than about 8×10⁻⁸ M, not more than about 7×10⁻⁸ M, not more than about 6×10⁻⁸ M, not more than about 5×10⁻⁸ M, not more than about 4×10⁻⁸ M, not more than about 3×10⁻⁸ M, not more than about 2×10⁻⁸ M, not more than about 1×10⁻⁸ M, not more than about 9×10⁻⁹ M, not more than about 8×10⁻⁹ M, not more than about 7×10⁻⁹ M, not more than about 6×10⁻⁹ M, not more than about 5×10⁻⁹ M, not more than about 4×10⁻⁹ M, not more than about 3×10⁻⁹ M, not more than about 2×10⁻⁹ M, not more than about 1×10⁻⁹ M, not more than about 9×10⁻¹⁰ M, not more than about 8×10⁻¹⁰ M, not more than about 7×10⁻¹⁰ M, not more than about 6×10⁻¹⁰ M, not more than about 5×10⁻¹⁰ M, not more than about 4×10⁻¹⁰ M, not more than about 3×10⁻¹⁰ M, not more than about 2×10⁻¹⁰ M, not more than about 1×10⁻¹⁰ M, not more than about 9×10⁻¹¹ M, not more than about 8×10⁻¹¹ M, not more than about 7×10⁻¹¹ M, not more than about 6×10⁻¹¹ M, not more than about 5×10⁻¹¹ M, not more than about 4×10⁻¹¹ M, not more than about 3×10⁻¹¹ M, not more than about 2×10⁻¹¹ M, not more than about 1×10⁻¹¹ M, not more than about 9×10⁻¹² M, not more than about 8×10⁻¹² M, not more than about 7×10⁻¹² M, not more than about 6×10⁻¹² M, not more than about 5×10⁻¹² M, not more than about 4×10⁻¹² M, not more than about 3×10⁻¹² M, not more than about 2×10⁻¹² M, not more than about 1×10⁻¹² M, not more than about 9×10⁻¹³ M, not more than about 8×10⁻¹³ M, not more than about 7×10⁻¹³ M, not more than about 6×10⁻¹³ M, not more than about 5×10⁻¹³ M, not more than about 4×10⁻¹³ M, not more than about 3×10⁻¹³ M, not more than about 2×10⁻¹³ M, not more than about 1×10⁻¹³ M, from about 1 × 10⁻⁷ M to about 1 × 10⁻¹⁴ M, from about 9 × 10⁻⁸ M to about 1 × 10⁻¹⁴ M, from about 8 × 10⁻⁸ M to about 1 × 10⁻¹⁴ M, from about 7 × 10⁻⁸ M to about 1 × 10⁻¹⁴ M, from about 6 × 10⁻⁸ M to about 1 × 10⁻¹⁴ M, from about 5 × 10⁻⁸ M to about 1 × 10⁻¹⁴ M, from about 4 × 10⁻⁸ M to about 1 × 10⁻¹⁴ M, from about 3 × 10⁻⁸ M to about 1 × 10⁻¹⁴ M, from about 2 × 10⁻⁸ M to about 1 × 10⁻¹⁴ M, from about 1 × 10⁻⁸ M to about 1 × 10⁻¹⁴ M, from about 9 × 10⁻⁹ M to about 1 × 10⁻¹⁴ M, from about 8 × 10⁻⁹ M to about 1 × 10⁻¹⁴ M, from about 7 × 10⁻⁹ M to about 1 × 10⁻¹⁴ M, from about 6 × 10⁻⁹ M to about 1 × 10⁻¹⁴ M, from about 5 × 10⁻⁹ M to about 1 × 10⁻¹⁴ M, from about 4 × 10⁻⁹ M to about 1 × 10⁻¹⁴ M, from about 3 × 10⁻⁹ M to about 1 × 10⁻¹⁴ M, from about 2 × 10⁻⁹ M to about 1 × 10⁻¹⁴ M, from about 1 × 10⁻⁹ M to about 1 × 10⁻¹⁴ M, from about 1 × 10⁻⁷ M to about 1 × 10⁻¹³ M, from about 9 × 10⁻⁸ M to about 1 × 10⁻¹³ M, from about 8 × 10⁻⁸ M to about 1 × 10⁻¹³ M, from about 7 × 10⁻⁸ M to about 1 × 10⁻¹³ M, from about 6 × 10⁻⁸ M to about 1 × 10⁻¹³ M, from about 5 × 10⁻⁸ M to about 1 × 10⁻¹³ M, from about 4 × 10⁻⁸ M to about 1 × 10⁻¹³ M, from about 3 × 10⁻⁸ M to about 1 × 10⁻¹³ M, from about 2 × 10⁻⁸ M to about 1 × 10⁻¹³ M, from about 1 × 10⁻⁸ M to about 1 × 10⁻¹³ M, from about 9 × 10⁻⁹ M to about 1 × 10⁻¹³ M, from about 8 × 10⁻⁹ M to about 1 × 10⁻¹³ M, from about 7 × 10⁻⁹ M to about 1 × 10⁻¹³ M, from about 6 × 10⁻⁹ M to about 1 × 10⁻¹³ M, from about 5 × 10⁻⁹ M to about 1 × 10⁻¹³ M, from about 4 × 10⁻⁹ M to about 1 × 10⁻¹³ M, from about 3 × 10⁻⁹ M to about 1 × 10⁻¹³ M, from about 2 × 10⁻⁹ M to about 1 × 10⁻¹³ M, or from about 1 × 10⁻⁹ M to about 1 × 10⁻¹³ M.

[0033] The value of K_D can be determined directly by well-known methods, and can be computed even for complex mixtures by methods such as those,

for example, set forth in Caceci et al. (1984, Byte 9: 340-362). For example, the K_D may be established using a double-filter nitrocellulose filter binding assay such as that disclosed by Wong & Lohman (1993, Proc. Natl. Acad. Sci. USA 90: 5428-5432). Other standard assays to evaluate the binding ability of ligands such as antibodies towards target antigens are known in the art, including for example, ELISAs, Western blots, RIAs, and flow cytometry analysis, and other assays exemplified elsewhere herein.

[0034] One exemplary method for measuring binding affinity (K_D) value is surface plasmon resonance (SPR), typically using a biosensor system such as a BIACORE[®] system. SPR refers to an optical phenomenon that allows for the analysis of real-time biospecific interactions by detection of alterations in protein concentrations within a biosensor matrix, for example using the BIACORE[®] system. BIAcore kinetic analysis comprises analyzing the binding and dissociation of an antigen from a chip with an immobilized molecule (e.g., a molecule comprising an antigen-binding domain), on their surface; or the dissociation of an antibody, or antigen-binding fragment thereof, from a chip with an immobilized antigen. The SPR measurement can be conducted using a BIACORE[®] T100 or T200 instrument. For example, a standard assay condition for surface plasmon resonance can be based on antibody immobilization of approximately 100-500 Response Units (RU) of IgG on the SPR chip. Purified target proteins are diluted in buffer to a range of final concentrations and injected at a requisite flow rate (e.g. 10-100 μ l/min) to allow the calculation of K_a . Dissociation is allowed to proceed to establish off-rate, followed by 3 M $MgCl_2$ (or 20 mM NaOH) for regeneration of the chip surface. Sensorgrams are then analyzed using a kinetics evaluation software package. In an exemplary embodiment, the SPR assay is according to the conditions as set forth in Example 1.

[0035] For example, the binding affinity (K_D) value is measured using solution-based kinetic exclusion assay (KinExA[™]). In a particular embodiment, the KinExA measurement is conducted using a KinExA[™] 3200 instrument (Sapidyne). The Kinetic Exclusion Assay (KinExA[™]) is a general purpose immunoassay platform (basically a flow spectrofluorimeter) that is capable of measuring equilibrium dissociation constants, and association and dissociation rate constants for antigen/antibody interactions. Since KinExA[™] is performed after equilibrium has been obtained it is an advantageous technique to use for measuring the K_D of high affinity interactions where the off-rate of the interaction may be very slow. The KinExA[™] methodology can be conducted generally as described in Drake et al (2004) Analytical Biochemistry 328, 35-43.

[0036] Another method for determining the K_D of an antibody is by using Bio-Layer Interferometry, typically using OCTET[®] technology (Octet QKe system, ForteBio).

[0037] In general, an anti-IFN β antibody should bind to IFN β with high affinity, in order to effectively block the activities of IFN β . IFN β binds IFNAR1 at a K_D of about 50 nM, and to IFNAR2 at a K_D of about 100 pM. Accordingly, it is desirable that the IFN β antibody have binding affinities (K_D) in nanomolar and picomolar range, such as about 1×10^{-9} M or lower.

Activity Assays

[0038] The antibody, or antigen-binding fragment thereof, of the invention is a neutralizing antibody that reduces at least one activity of IFN β . Such activity of IFN β includes, but is not limited to, binding to IFNAR, increasing expression of an IFN β -dependent gene, and/or inducing phosphorylation of, e.g., STAT1, and/or STAT2, among other IFN β activities known in the art. Whether an antibody, or antigen-binding fragment thereof, reduces an activity of IFN β can be assessed by a number of assays. For example, assays can be used to determine whether the antibody, or antigen-binding fragment thereof: (a) inhibits the binding of IFN β to IFNAR; (b) reduces the expression level of an IFN β -dependent gene; and/or (c) inhibit IFN β -induced phosphorylation, such as phosphorylation of STAT1, and/or STAT2.

[0039] The antibody, or antigen-binding fragment thereof, inhibits the binding of IFN β to IFNAR (e.g., can be assessed by competitive binding to IFN β). For example, an assay may compare (i) the binding of IFN β to IFNAR in the presence of the antibody, or antigen-binding fragment thereof, with (ii) the binding of IFN β to IFNAR in the absence of the antibody, or antigen-binding fragment thereof. The reduction in binding of IFN β to IFNAR can be at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, in the presence of the anti-IFN β antibody, or antigen-binding fragment thereof. The expected binding of IFN β to IFNAR in the absence of the antibody, or antigen-binding fragment thereof, can be set as 100%.

[0040] The antibody, or antigen-binding fragment thereof, inhibits the binding of IFN β to IFNAR, with a half maximal inhibitory concentration (IC_{50}) of not more than about 1×10^{-7} M, not more than about 1×10^{-8} M, not more than about 1×10^{-9} M, not more than about 1×10^{-10} M, not more than about 1×10^{-11} M, not more than about 1×10^{-12} M, not more than about 1×10^{-13} M, not more than about 1×10^{-14} M, not more than about 1×10^{-15} M, from about 1×10^{-7} M to about 5×10^{-14} M, from about 1×10^{-7} M to about 1×10^{-14} M, from about 1×10^{-7} M to about 5×10^{-13} M, from about 1×10^{-7} M to about 1×10^{-13} M, from about 1×10^{-7} M to about 5×10^{-12} M, or from about 1×10^{-7} M to about 1×10^{-12} M.

[0041] The activities of an antibody, or antigen-binding fragment thereof, of the invention can also be assessed by measuring the expression level of an IFN β -dependent gene. For example, the gene can be a downstream component in the IFN β -mediated signal pathway (such as CMPK2, IFIT1, IFI27, IFIH1, IFI44, IFI44L, IFI6, ISG15, LY6E, HERC5, MX1, OAS1, OAS2, OAS3, RSAD2, XAF1, CXCL10, or any combination thereof). Alternatively, the gene can be a reporter gene (e.g., the luciferase reporter gene as used in the examples) where the expression level of the reporter gene correlates with IFN β activity (e.g., the reporter gene is operably linked to an IFN β -dependent response element). The expression level of the downstream gene or reporter gene can be assessed by a variety of methods, such as measuring the RNA level, protein level, or activity level of a protein. The assay can compare (i) the expression level of the IFN β dependent gene in the presence of the antibody, or antigen-binding fragment thereof, with (ii) the expression level of the IFN β dependent gene in the absence of the antibody, or antigen-binding fragment thereof. The reduction in expression level of a downstream gene or reporter gene can be at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, in the presence of the anti-IFN β antibody, or antigen-binding fragment thereof. The baseline expression level in the absence of the antibody, or antigen-binding fragment thereof, can be set as 100%.

[0042] The the antibody, or antigen-binding fragment thereof, inhibits the expression of an IFN β -dependent gene, with a half maximal inhibitory concentration (IC₅₀) of not more than about 1×10^{-7} M, not more than about 1×10^{-8} M, not more than about 1×10^{-9} M, not more than about 1×10^{-10} M, not more than about 1×10^{-11} M, not more than about 1×10^{-12} M, not more than about 1×10^{-13} M, not more than about 1×10^{-14} M, not more than about 1×10^{-15} M, from about 1×10^{-7} M to about 5×10^{-14} M, from about 1×10^{-7} M to about 1×10^{-14} M, from about 1×10^{-7} M to about 5×10^{-13} M, from about 1×10^{-7} M to about 1×10^{-13} M, from about 1×10^{-7} M to about 5×10^{-12} M, or from about 1×10^{-7} M to about 1×10^{-12} M. In certain embodiments, IC₅₀ of from about 1×10^{-10} M to about 1×10^{-13} M is preferred. In certain embodiments, IC₅₀ of from about 5×10^{-11} M to about 5×10^{-12} M is preferred.

[0043] The inhibitory activity of an antibody, or antigen-binding fragment thereof, can also be assessed by measuring the level of IFN β -induced phosphorylation, such as STAT1 phosphorylation, and/or STAT2 phosphorylation level. The assay can compare (i) the phosphorylation level of STAT1 and/or STAT2 in the presence of the antibody, or antigen-binding fragment thereof, with (ii) the phosphorylation level of STAT1 and/or STAT2 in the absence of the antibody, or antigen-binding fragment thereof. The reduction in phosphorylation level can be at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, in the presence of the anti-IFN β antibody, or antigen-binding fragment thereof. The baseline STAT1 phosphorylation and/or STAT2 phosphorylation level in the absence of the antibody, or antigen-binding fragment thereof, can be set as 100%.

[0044] The antibody, or antigen-binding fragment thereof, inhibits IFN β -induced phosphorylation (such as STAT1 phosphorylation, and/or STAT2 phosphorylation), with a half maximal inhibitory concentration (IC₅₀) of not more than about 1×10^{-7} M, not more than about 1×10^{-8} M, not more than about 1×10^{-9} M, not more than about 1×10^{-10} M, not more than about 1×10^{-11} M, not more than about 1×10^{-12} M, not more than about 1×10^{-13} M, not more than about 1×10^{-14} M, not more than about 1×10^{-15} M, from about 1×10^{-7} M to about 5×10^{-14} M, from about 1×10^{-7} M to about 1×10^{-14} M, from about 1×10^{-7} M to about 5×10^{-13} M, from about 1×10^{-7} M to about 1×10^{-13} M, from about 1×10^{-7} M to about 5×10^{-12} M, or from about 1×10^{-7} M to about 1×10^{-12} M. In certain embodiments, IC₅₀ of from about 1×10^{-10} M to about 1×10^{-13} M is preferred. In certain embodiments, IC₅₀ of from about 5×10^{-11} M to about 5×10^{-12} M is preferred.

[0045] The the characteristics of the antibody, or antigen-binding fragment thereof, of the invention is further assessed using other biological activity assays, e.g., in order to evaluate its potency, pharmacological activity, and potential efficacy as a therapeutic agent. Such assays are known in the art and depend on the intended use for the antibody. Examples include e.g., toxicity assays, immunogenicity assays, stability assays, and/or PK/PD profiling.

C. Nucleic Acids and Methods of Producing Anti-IFN β Antibodies

[0046] The invention also provides polynucleotides encoding the antibody, including antibody portions and modified antibodies as claimed. The invention also provides a method of making any of the polynucleotides as claimed. Polynucleotides can be made and expressed by procedures known in the art.

[0047] The sequence of a desired antibody, or antigen-binding fragment thereof, and nucleic acid encoding such antibody, or antigen-binding fragment thereof, can be determined using standard sequencing techniques. A nucleic acid sequence encoding a desired antibody, or antigen-binding fragment thereof, may be inserted into various vectors (such as cloning and expression vectors) for recombinant production and characterization. A nucleic acid encoding the heavy chain, or an antigen-binding fragment of the heavy chain, and a nucleic acid encoding the light chain, or an antigen-binding fragment of the light chain, can be cloned into the same vector, or different vectors.

[0048] In one aspect, the invention provides polynucleotides encoding the amino acid sequence of the following anti-IFN β antibody and antigen-binding portions thereof: CTI-AF1.

[0049] The invention also provides polynucleotides comprising the nucleic acid sequence set forth as SEQ ID NOs: 166 or 167.

[0050] The invention also provides polynucleotides comprising the nucleic acid sequence of the DNA insert of the plasmid deposited with the ATCC and having Accession No. PTA-122727 or the DNA insert of the plasmid deposited with the ATCC and having Accession No. PTA-122726.

[0051] In one embodiment, the VH and VL domains, or antigen-binding portion thereof, or full length HC or LC, are encoded by separate polynucleotides. Alternatively, both VH and VL, or antigen-binding portion thereof, or HC and LC, are encoded by a single polynucleotide.

[0052] Polynucleotides complementary to any such sequences are also encompassed by the present disclosure. Polynucleotides may be single-stranded (coding or antisense) or doublestranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or noncoding sequences may, but need not, be present within a polynucleotide of the present disclosure, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

[0053] Polynucleotides may comprise a native sequence (i.e., an endogenous sequence that encodes an antibody or a portion thereof) or may comprise a variant of such a sequence. Polynucleotide variants contain one or more substitutions, additions, deletions and/or insertions such that the immunoreactivity of the encoded polypeptide is not diminished, relative to a native immunoreactive molecule. The effect on the immunoreactivity of the encoded polypeptide may generally be assessed as described herein. In some embodiments, variants exhibit at least about 70% identity, in some embodiments, at least about 80% identity, in some embodiments, at least about 90% identity, and in some embodiments, at least about 95% identity to a polynucleotide sequence that encodes a native antibody or a portion thereof. These amounts are not meant to be limiting, and increments between the recited percentages are specifically envisioned as part of the disclosure.

[0054] Two polynucleotide or polypeptide sequences are said to be "identical" if the sequence of nucleotides or amino acids in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a

segment of at least about 20 contiguous positions, usually 30 to about 75, or 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

[0055] Optimal alignment of sequences for comparison may be conducted using the MegAlign® program in the Lasergene® suite of bioinformatics software (DNASTAR®, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O., 1978, A model of evolutionary change in proteins - Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J., 1990, Unified Approach to Alignment and Phylogenies pp. 626-645 Methods in Enzymology vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M., 1989, CABIOS 5:151-153; Myers, E.W. and Muller W., 1988, CABIOS 4:11-17; Robinson, E.D., 1971, Comb. Theor. 11:105; Santou, N., Nes, M., 1987, Mol. Biol. Evol. 4:406-425; Sneath, P.H.A. and Sokal, R.R., 1973, Numerical Taxonomy the Principles and Practice of Numerical Taxonomy, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J., 1983, Proc. Natl. Acad. Sci. USA 80:726-730.

[0056] In some embodiments, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (i.e., gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (i.e., the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

[0057] Variants may also, or alternatively, be substantially homologous to a native gene, or a portion or complement thereof. Such polynucleotide variants are capable of hybridizing under moderately stringent conditions to a naturally occurring DNA sequence encoding a native antibody (or a complementary sequence).

[0058] Suitable "moderately stringent conditions" include prewashing in a solution of 5X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50 °C-65 °C, 5X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

[0059] As used herein, "highly stringent conditions" or "high stringency conditions" are those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50 °C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42 °C; or (3) employ 50% formamide, 5X SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5X Denhardt's solution, sonicated salmon sperm DNA (50 µg/mL), 0.1% SDS, and 10% dextran sulfate at 42 °C, with washes at 42 °C in 0.2X SSC (sodium chloride/sodium citrate) and 50% formamide at 55 °C, followed by a high-stringency wash consisting of 0.1X SSC containing EDTA at 55 °C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

[0060] It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present disclosure. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present disclosure. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

[0061] The polynucleotides of this disclosure can be obtained using chemical synthesis, recombinant methods, or PCR. Methods of chemical polynucleotide synthesis are well known in the art and need not be described in detail herein. One of skill in the art can use the sequences provided herein and a commercial DNA synthesizer to produce a desired DNA sequence.

[0062] For preparing polynucleotides using recombinant methods, a polynucleotide comprising a desired sequence can be inserted into a suitable vector, and the vector in turn can be introduced into a suitable host cell for replication and amplification, as further discussed herein. Polynucleotides may be inserted into host cells by any means known in the art. Cells are transformed by introducing an exogenous polynucleotide by direct uptake, endocytosis, transfection, F-mating or electroporation. Once introduced, the exogenous polynucleotide can be maintained within the cell as a non-integrated vector (such as a plasmid) or integrated into the host cell genome. The polynucleotide so amplified can be isolated from the host cell by methods well known within the art. See, e.g., Sambrook *et al.*, 1989.

[0063] Alternatively, PCR allows reproduction of DNA sequences. PCR technology is well known in the art and is described in U.S. Patent Nos. 4,683,195, 4,800,159, 4,754,065 and 4,683,202, as well as PCR: The Polymerase Chain Reaction, Mullis *et al.* eds., Birkauwer Press, Boston, 1994.

[0064] RNA can be obtained by using the isolated DNA in an appropriate vector and inserting it into a suitable host cell. When the cell replicates and the DNA is transcribed into RNA, the RNA can then be isolated using methods well known to those of skill in the art, as set forth in Sambrook *et al.*, 1989, for example.

[0065] Suitable cloning and expression vectors can include a variety of components, such as promoter, enhancer, and other transcriptional regulatory sequences. The vector may also be constructed to allow for subsequent cloning of an antibody variable domain into different vectors.

[0066] Suitable cloning vectors may be constructed according to standard techniques, or may be selected from a large number of cloning vectors available in the art. While the cloning vector selected may vary according to the host cell intended to be used, useful cloning vectors will generally have the ability to self-replicate, may possess a single target for a particular restriction endonuclease, and/or may carry genes for a marker that can be used in selecting clones containing the vector. Suitable examples include plasmids and bacterial viruses, e.g., pUC18, pUC19, Bluescript (e.g., pBS SK+) and its derivatives, mp18, mp19, pBR322, pMB9, ColE1, pCR1, RP4, phage DNAs, and shuttle vectors such as pSA3 and pAT28. These and many other cloning vectors are available from commercial vendors such as BioRad, Strategene, and Invitrogen.

[0067] Expression vectors are further provided. Expression vectors generally are replicable polynucleotide constructs that contain a polynucleotide according to the disclosure. It is implied that an expression vector must be replicable in the host cells either as episomes or as an integral part of the chromosomal DNA. Suitable expression vectors include but are not limited to plasmids, viral vectors, including adenoviruses, adeno-associated viruses, retroviruses, cosmids, and expression vector(s) disclosed in PCT Publication No. WO 87/04462. Vector components may generally include, but are not limited to, one or more of the following: a signal sequence; an origin of replication; one or more marker genes; suitable transcriptional controlling elements (such as promoters, enhancers and terminator). For expression (i.e., translation), one or more translational controlling elements are also usually required, such as ribosome binding sites, translation initiation sites, and stop codons.

[0068] The vectors containing the polynucleotides of interest and/or the polynucleotides themselves, can be introduced into the host cell by any of a number of appropriate means, including electroporation, transfection employing calcium chloride, rubidium chloride, calcium phosphate, DEAE-dextran, or other substances; microprojectile bombardment; lipofection; and infection (e.g., where the vector is an infectious agent such as vaccinia virus). The choice of introducing vectors or polynucleotides will often depend on features of the host cell.

[0069] The antibody, or antigen-binding fragment thereof, may be made recombinantly using a suitable host cell. A nucleic acid encoding the antibody or antigen-binding fragment thereof can be cloned into an expression vector, which can then be introduced into a host cell, such as E. coli cell, a yeast cell, an insect cell, a simian COS cell, a Chinese hamster ovary (CHO) cell, or a myeloma cell where the cell does not otherwise produce an immunoglobulin protein, to obtain the synthesis of an antibody in the recombinant host cell. Preferred host cells include a CHO cell, a Human embryonic kidney (HEK) 293 cell, or an Sp2.0 cell, among many cells well-known in the art.

[0070] An antibody fragment can be produced by proteolytic or other degradation of a full-length antibody, by recombinant methods, or by chemical synthesis. A polypeptide fragment of an antibody, especially shorter polypeptides up to about 50 amino acids, can be conveniently made by chemical synthesis. Methods of chemical synthesis for proteins and peptides are known in the art and are commercially available.

[0071] The antibody, or antigen-binding fragment thereof, of the invention may be affinity matured. For example, an affinity matured antibody can be produced by procedures known in the art (Marks et al., 1992, Bio/Technology, 10:779-783; Barbas et al., 1994, Proc Nat. Acad. Sci, USA 91:3809-3813; Schier et al., 1995, Gene, 169:147-155; Yelton et al., 1995, J. Immunol., 155:1994-2004; Jackson et al., 1995, J. Immunol., 154(7):3310-9; Hawkins et al., 1992, J. Mol. Biol., 226:889-896; and WO2004/058184).

2. FORMULATIONS AND USES

[0072] The antibody, or antigen-binding fragment thereof, of the invention can be formulated as a pharmaceutical composition. The pharmaceutical composition may further comprise a pharmaceutically acceptable carrier, excipient, and/or stabilizer (Remington: The Science and practice of Pharmacy 20th Ed., 2000, Lippincott Williams and Wilkins, Ed. K. E. Hoover), in the form of lyophilized formulation or aqueous solution. Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations, and may comprise buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (e.g., Zn-protein complexes); and/or non-ionic surfactants such as TWEEN™, PLURONICS™ or polyethylene glycol (PEG). Pharmaceutically acceptable excipients are further described herein.

[0073] The antibody, or antigen-binding fragment thereof, of the invention can be used for various therapeutic or diagnostic purposes. For example, the antibody, or antigen-binding fragment thereof, of the invention may be used as an affinity purification agent (e.g., for in vitro purification of IFN β), as a diagnostic agent (e.g., for detecting expression of IFN β in specific cells, tissues, or serum).

[0074] Exemplary therapeutic uses of the antibody, or antigen-binding fragment include treating a rheumatic disease (such as SLE or DM) or an interferonopathy. The antibody, or antigen-binding fragment thereof, may also be used in prophylactic treatment (e.g., administering to a subject who has not exhibited a disease symptom but is susceptible to a rheumatic disease or an interferonopathy).

[0075] For therapeutic applications, the antibody, or antigen-binding fragment thereof, of the invention can be administered to a mammal, especially a human by conventional techniques, such as intravenously (as a bolus or by continuous infusion over a period of time), intramuscularly, intraperitoneally, intra-cerebrospinally, subcutaneously, intra-articularly, intrasynovially, intrathecally, orally, topically, or by inhalation. The antibody, or antigen-binding fragment thereof, of the invention also is suitably administered by intra-tumoral, peri-tumoral, intra-lesional, or peri-lesional routes.

[0076] Accordingly, although methods for treatment of the animal or human body by surgery or therapy are not encompassed by the claims, the disclosure provides a method of reducing the activity of IFN β , comprising administering to a subject (e.g., a human) in need thereof a therapeutically effective amount of the antibody, or antigen-binding fragment thereof, of the invention. However, this should be interpreted as substances and compositions for use in such treatment.

[0077] In certain cases the subject suffers from or is susceptible to a rheumatic disease. In certain embodiments, the rheumatic disease is SLE. In certain embodiments, the rheumatic disease is DM.

[0078] In certain embodiments, the subject suffers from or is susceptible to an interferonopathy.

[0079] In certain embodiments, the antibody, or antigen-binding fragment thereof, of the invention is administered subcutaneously. In certain embodiments, the antibody, or antigen-binding fragment thereof, of the invention is administered intravenously.

[0080] The pharmaceutical compositions may be administered to a subject in need thereof at a frequency that may vary with the severity of the rheumatic disease or interferonopathy. In the case of prophylactic therapy, the frequency may vary depending on the subject's susceptibility or predisposition to a

rheumatic disease or an interferonopathy.

[0081] The compositions may be administered to patients in need as a bolus or by continuous infusion. For example, a bolus administration of an antibody present as a Fab fragment may be in an amount of from 0.0025 to 100 mg/kg body weight, 0.025 to 0.25 mg/kg, 0.010 to 0.10 mg/kg or 0.10-0.50 mg/kg. For continuous infusion, an antibody present as an Fab fragment may be administered at 0.001 to 100 mg/kg body weight/minute, 0.0125 to 1.25 mg/kg/min, 0.010 to 0.75 mg/kg/min, 0.010 to 1.0 mg/kg/min. or 0.10-0.50 mg/kg/min for a period of 1-24 hours, 1-12 hours, 2-12 hours, 6-12 hours, 2-8 hours, or 1-2 hours.

[0082] For administration of an antibody present as a full-length antibody (with full constant regions), dosage amounts may be from about 1 mg/kg to about 10 mg/kg, from about 2 mg/kg to about 10 mg/kg, from about 3 mg/kg to about 10 mg/kg, from about 4 mg/kg to about 10 mg/kg, from about 5 mg/kg to about 10 mg/kg, from about 1 mg/kg to about 20 mg/kg, from about 2 mg/kg to about 20 mg/kg, from about 3 mg/kg to about 20 mg/kg, from about 4 mg/kg to about 20 mg/kg, from about 5 mg/kg to about 20 mg/kg, about 1 mg/kg or more, about 2 mg/kg or more, about 3 mg/kg or more, about 4 mg/kg or more, about 5 mg/kg or more, about 6 mg/kg or more, about 7 mg/kg or more, about 8 mg/kg or more, about 9 mg/kg or more, about 10 mg/kg or more, about 11 mg/kg or more, about 12 mg/kg or more, about 13 mg/kg or more, about 14 mg/kg or more, about 15 mg/kg or more, about 16 mg/kg or more, about 17 mg/kg or more, about 19 mg/kg or more, or about 20 mg/kg or more. The frequency of the administration would depend upon the severity of the condition. Frequency could range from three times per week to once every two or three weeks.

[0083] Additionally, the compositions may be administered to patients via subcutaneous injection. For example, a dose of 1 to 100 mg anti-IFN β antibody can be administered to patients via subcutaneous or intravenous injection administered twice a week, once a week, once every two weeks, once every three weeks, once every four weeks, once every five weeks, once every six weeks, once every seven weeks, once every eight weeks, once every nine weeks, once every ten weeks, twice a month, once a month, once every two months, or once every three months. For example, antibody CTI-AF1 has an estimated half-life of about 19 days. This half-life supports subcutaneous or intravenous injection at every 2-6 weeks, such as once every 2 weeks or once every 4 weeks.

[0084] In certain cases the half-life of the anti-IFN β antibody in human is about 5 days, about 6 days, about 7 days, about 8 days, about 9 days, about 10 days, about 11 days, about 12 days, about 13 days, about 14 days, about 15 days, about 16 days, about 17 days, about 18 days, about 19 days, about 20 days, about 21 days, about 22 days, about 23 days, about 24 days, about 25 days, about 26 days, about 27 days, about 28 days, about 29 days, about 30 days, from about 5 days to about 40 days, from about 5 days to about 35 days, from about 5 days to about 30 days, from about 5 days to about 25 days, from about 10 days to about 40 days, from about 10 days to about 35 days, from about 10 days to about 30 days, from about 10 days to about 25 days, from about 15 days to about 40 days, from about 15 days to about 35 days, from about 15 days to about 30 days, or from about 15 days to about 25 days,

[0085] The pharmaceutical composition can be administered subcutaneously or intravenously at every 2-6 weeks, with a dose from about 0.1 mg/kg to about 10 mg/kg, from about 0.5 mg/kg to about 10 mg/kg, from about 1 mg/kg to about 10 mg/kg, from about 1.5 mg/kg to about 10 mg/kg, from about 2 mg/kg to about 10 mg/kg, from about 0.1 mg/kg to about 8 mg/kg, from about 0.5 mg/kg to about 8 mg/kg, from about 1 mg/kg to about 8 mg/kg, from about 1.5 mg/kg to about 8 mg/kg, from about 2 mg/kg to about 8 mg/kg, from about 0.1 mg/kg to about 5 mg/kg, from about 0.5 mg/kg to about 5 mg/kg, from about 1 mg/kg to about 5 mg/kg, from about 1.5 mg/kg to about 5 mg/kg, from about 2 mg/kg to about 5 mg/kg, about 0.5 mg/kg, about 1.0 mg/kg, about 1.5 mg/kg, about 2.0 mg/kg, about 2.5 mg/kg, about 3.0 mg/kg, about 3.5 mg/kg, about 4.0 mg/kg, about 4.5 mg/kg, about 5.0 mg/kg, about 5.5 mg/kg, about 6.0 mg/kg, about 6.5 mg/kg, about 7.0 mg/kg, about 7.5 mg/kg, about 8.0 mg/kg, about 8.5 mg/kg, about 9.0 mg/kg, about 9.5 mg/kg, or about 10.0 mg/kg.

[0086] The pharmaceutical composition can be administered subcutaneously or intravenously at every 2-6 weeks, with a dose of about 2.0 mg/kg. The pharmaceutical composition can be administered subcutaneous or intravenously every 2-6 weeks, with a dose of from about 2.0 mg/kg to about 10.0 mg/kg.

[0087] The pharmaceutical composition can be administered subcutaneously every 2 weeks.

[0088] The antibody, or antigen-binding fragment thereof, of the invention can be used as monotherapy or in combination with other therapies to treat a rheumatic disease.

3. DEFINITIONS

[0089] Unless otherwise defined herein, scientific and technical terms used in connection with the present invention shall have the meanings that are commonly understood by those of ordinary skill in the art. Further, unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular. Generally, nomenclatures used in connection with, and techniques of, cell and tissue culture, molecular biology, immunology, microbiology, genetics and protein and nucleic acid chemistry and hybridization described herein are those well-known and commonly used in the art.

[0090] An "antigen-binding fragment" of an antibody refers to a fragment of a full-length antibody that retains the ability to specifically bind to an antigen (preferably with substantially the same binding affinity). Examples of an antigen-binding fragment includes (i) a Fab fragment, a monovalent fragment consisting of the VL, VH, CL and CH1 domains; (ii) a F(ab')₂ fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the VH and CH1 domains; (iv) a Fv fragment consisting of the VL and VH domains of a single arm of an antibody, (v) a dAb fragment (Ward et al., (1989) Nature 341:544-546), which consists of a VH domain; and (vi) an isolated complementarity determining region (CDR), disulfide-linked Fvs (dsFv), and anti-idiotypic (anti-Id) antibody and intrabody. Furthermore, although the two domains of the Fv fragment, VL and VH, are coded for by separate genes, they can be joined, using recombinant methods, by a synthetic linker that enables them to be made as a single protein chain in which the VL and VH regions pair to form monovalent molecules (known as single chain Fv (scFv)); see e.g., Bird et al. Science 242:423-426 (1988) and Huston et al., Proc. Natl. Acad. Sci. USA 85:5879-5883 (1988)). Other forms of single chain antibodies, such as diabodies, are also encompassed. Diabodies are bivalent, bispecific antibodies in which VH and VL domains are expressed on a single polypeptide chain, but using a linker that is too short to allow for pairing between the two domains on the same chain, thereby forcing the domains to pair with complementary domains of another chain and creating two antigen-binding sites (see e.g., Holliger et al. Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993); Poljak et al., 1994,

Structure 2:1121-1123).

[0091] An antibody "variable domain" refers to the variable region of the antibody light chain (VL) or the variable region of the antibody heavy chain (VH), either alone or in combination. As known in the art, the variable regions of the heavy and light chains each consist of three complementarity determining regions (CDRs), and connected by four framework regions (FR), and contribute to the formation of the antigen-binding site of antibodies.

[0092] Residues in a variable domain are numbered according Kabat, which is a numbering system used for heavy chain variable domains or light chain variable domains of the compilation of antibodies. See, Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)). Using this numbering system, the actual linear amino acid sequence may contain fewer or additional amino acids corresponding to a shortening of, or insertion into, a FR or CDR of the variable domain. For example, a heavy chain variable domain may include a single amino acid insert (residue 52a according to Kabat) after residue 52 of CDR-H2 and inserted residues (e.g. residues 82a, 82b, and 82c, according to Kabat) after heavy chain FR residue 82. The Kabat numbering of residues may be determined for a given antibody by alignment at regions of homology of the sequence of the antibody with a "standard" Kabat numbered sequence. Various algorithms for assigning Kabat numbering are available. The algorithm implemented in the 2012 release of Abysis (www.abysis.org) is used herein to assign Kabat numbering to variable regions unless otherwise noted.

[0093] Specific amino acid residue positions in an antibody (such as paratope residues) are also numbered according to Kabat.

[0094] "Complementarity Determining Regions" (CDRs) can be identified according to the definitions of the Kabat, Chothia, the accumulation of both Kabat and Chothia, AbM, contact, and/or conformational definitions or any method of CDR determination well known in the art. See, e.g., Kabat et al., 1991, Sequences of Proteins of Immunological Interest, 5th ed. (hypervariable regions); Chothia et al., 1989, Nature 342:877-883 (structural loop structures). AbM definition of CDRs is a compromise between Kabat and Chothia and uses Oxford Molecular's AbM antibody modeling software (Accelrys®). The "contact" definition of CDRs is based on observed antigen contacts, set forth in MacCallum et al., 1996, J. Mol. Biol., 262:732-745. The "conformational" definition of CDRs is based on residues that make enthalpic contributions to antigen binding (see, e.g., Makabe et al., 2008, Journal of Biological Chemistry, 283:1156-1166). Still other CDR boundary definitions may not strictly follow one of the above approaches, but will nonetheless overlap with at least a portion of the Kabat CDRs, although they may be shortened or lengthened in light of prediction or experimental findings that particular residues or groups of residues or even entire CDRs do not significantly impact antigen binding. As used herein, a CDR may refer to CDRs defined by any approach known in the art, including combinations of approaches.

[0095] In the Examples (see Table 11), the CDRs are defined as follows (numbering according to Kabat; H: heavy chain; L: light chain):

CDR-H1: H26-H35B; CDR-H2: H50-H65; CDR-H3: H95-H102

CDR-L1: L24-L34; CDR-L2: L50-L56; CDR-L3: L89-L97

[0096] "Framework" (FR) residues are antibody variable domain residues other than the CDR residues. A VH or VL domain framework comprises four framework sub-regions, FR1, FR2, FR3 and FR4, interspersed with CDRs in the following structure: FR1 - CDR1 - FR2 - CDR2 - FR3 - CDR3 - FR4. In the Examples (see Table 11), FR residues include the following (numbering according to Kabat; H: heavy chain; L: light chain):

Table 5

	FR1	FR2	FR3	FR4
Heavy Chain	H1-H25	H36-H49	H66-H94	H103-H113
Light Chain	L1-L23	L35-L49	L57-L88	L98-L107

[0097] An "epitope" refers to the area or region of an antigen (Ag) to which an antibody specifically binds, e.g., an area or region comprising amino acid residues that interact with the antibody (Ab). Epitopes can be linear or non-linear (e.g., conformational).

[0098] An antibody, or antigen-binding fragment thereof, binds substantially the same epitope as another antibody, or antigen-binding fragment thereof, when binding of the corresponding antibodies, or antigen-binding fragments thereof, are mutually exclusive. That is, binding of one antibody, or antigen-binding fragment thereof, excludes simultaneous or consecutive binding of the other antibody, or antigen-binding fragment thereof. Epitopes are said to be unique, or not substantially the same, if the antigen is able to accommodate binding of both corresponding antibodies, or antigen-binding fragments thereof, simultaneously.

[0099] The term "paratope" is derived from the above definition of "epitope" by reversing the perspective, and refers to the area or region of an antibody molecule which is involved in binding of an antigen, e.g., an area or region comprising residues that interacts with the antigen. A paratope may be linear or conformational (such as discontinuous residues in CDRs).

[0100] The epitope/paratope for a given antibody/antigen binding pair can be defined and characterized at different levels of detail using a variety of experimental and computational epitope mapping methods. The experimental methods include mutagenesis, X-ray crystallography, Nuclear Magnetic Resonance (NMR) spectroscopy, Hydrogen/deuterium exchange Mass Spectrometry (HX-MS) and various competition binding methods. As each method relies on a unique principle, the description of an epitope is intimately linked to the method by which it has been determined. Thus, the epitope/paratope for a given antibody/antigen pair will be defined differently depending on the mapping method employed.

[0101] At its most detailed level, the epitope/paratope for the interaction between an antibody (Ab) and antigen (Ag) can be defined by the spatial coordinates defining the atomic contacts present in the Ag-Ab interaction, as well as information about their relative contributions to the binding thermodynamics. At one level, an epitope/paratope residue can be characterized by the spatial coordinates defining the atomic contacts between the Ag and Ab. In one aspect, the epitope/paratope residue can be defined by a specific criterion, e.g., distance between atoms in the Ab and the Ag (e.g., a distance of equal to or less than about 4 Å (such as 3.8 Å used in the Examples here) from a heavy atom of the cognate antibody and a heavy atom of the antigen. In another aspect, an epitope/paratope residue can be characterized as participating in a hydrogen bond interaction with the cognate antibody/antigen, or with a water molecule that is also hydrogen bonded to the cognate antibody/antigen (water-mediated hydrogen bonding). In another

aspect, an epitope/paratope residue can be characterized as forming a salt bridge with a residue of the cognate antibody/antigen. In yet another aspect, an epitope/paratope residue can be characterized as a residue having a non-zero change in buried surface area (BSA) due to interaction with the cognate antibody/antigen. At a less detailed level, epitope/paratope can be characterized through function, e.g., by competition binding with other Abs. The epitope/paratope can also be defined more generically as comprising amino acid residues for which substitution by another amino acid will alter the characteristics of the interaction between the Ab and Ag (e.g. alanine scanning).

[0102] In the context of an X-ray derived crystal structure defined by spatial coordinates of a complex between an antibody, e.g., a Fab fragment or two Fab fragments, and its antigen, unless otherwise specified, an epitope residue refers to an IFN β residue (i) having a heavy atom (i.e., a non-hydrogen atom) that is within a distance of about 4 Å (e.g., 3.8 Å) from a heavy atom of the cognate antibody; (ii) participating in a hydrogen bond with a residue of the cognate antibody, or with a water molecule that is also hydrogen bonded to the cognate antibody (water-mediated hydrogen bonding), (iii) participating in a salt bridge to a residue of the cognate antibody, and/or (iv) having a non-zero change in buried surface area (BSA) due to interaction with the cognate antibody. In general, a cutoff is imposed for BSA to avoid inclusion of residues that have minimal interactions. Therefore, unless otherwise specified, epitope residues under category (iv) are selected if it has a BSA of 20 Å² or greater, or is involved in electrostatic interactions when the antibody binds to IFN β . Similarly, in the context of an X-ray derived crystal structure, unless otherwise specified or contradicted by context, a paratope residue, refers to an antibody residue (i) having a heavy atom (i.e., a non-hydrogen atom) that is within a distance of about 4 Å from a heavy atom of IFN β , (ii) participating in a hydrogen bond with an IFN β residue, or with a water molecule that is also hydrogen bonded to IFN β (water-mediated hydrogen bonding), (iii) participating in a salt bridge to a residue of IFN β , and/or (iv) having a non-zero change in buried surface area due to interaction with IFN β . Again, unless otherwise specified, paratope residues under category (iv) are selected if it has a BSA of 20 Å² or greater, or is involved in electrostatic interactions when antibody binds to IFN β . Residues identified by (i) distance or (iv) BSA are often referred to as "contact" residues.

[0103] From the fact that descriptions and definitions of epitopes, dependent on the epitope mapping method used, and obtained at different levels of detail, it follows that comparison of epitopes for different Abs on the same Ag can similarly be conducted at different levels of detail. For example, epitopes described on the amino acid level, e.g., determined from an X-ray structure, are said to be identical if they contain the same set of amino acid residues. Epitopes characterized by competition binding are said to be overlapping if the binding of the corresponding antibodies are mutually exclusive, i.e., binding of one antibody excludes simultaneous or consecutive binding of the other antibody; and epitopes are said to be separate (unique) if the antigen is able to accommodate binding of both corresponding antibodies simultaneously.

[0104] The epitope and paratope for a given antibody/antigen pair may be identified by routine methods. For example, the general location of an epitope may be determined by assessing the ability of an antibody to bind to different fragments or variant IFN β polypeptides as more fully described previously elsewhere herein. Specific residues within IFN β that make contact with specific residues within an antibody may also be determined using routine methods, such as those described in the examples. For example, antibody/antigen complex may be crystallized. The crystal structure may be determined and used to identify specific sites of interaction between the antibody and antigen.

[0105] The terms "specifically binds" and "specific binding" are terms well-understood in the art, and methods to determine such specific binding are also well known in the art. A molecule is said to exhibit "specific binding" if it reacts or associates more frequently, more rapidly, with greater duration and/or with greater affinity with a particular cell or substance, than it does with alternative cells or substances. An antibody, or antigen-binding fragment thereof, "specifically binds" to a target (e.g., IFN β) if it binds with greater affinity, avidity, more readily, and/or with greater duration than it binds other substances.

[0106] For example, an antibody, or antigen-binding fragment thereof, that specifically binds IFN β is an antibody that binds its cognate antigen (IFN β) with greater affinity, avidity, more readily, and/or with greater duration than it binds other antigens, such as other members of the IFN superfamily (e.g., INF α , IFN γ , IFN ω), or other unrelated molecules. For example, an anti-IFN β antibody can specifically binds human IFN β in a sample, but does not substantially recognize or bind other molecules in the sample under a standard binding assay condition. It is also understood that an antibody, or antigen-binding fragment thereof, which specifically binds a first target may or may not specifically bind to a second target. As such, "specific binding" does not necessarily require (although it can include) exclusive binding. Generally, but not necessarily, reference to "binding" means specific binding.

[0107] A variety of assay formats may be used to select an antibody, or antigen-binding fragment thereof, that specifically binds a molecule of interest. For example, solid-phase ELISA immunoassay, immunoprecipitation, Biacore™ (GE Healthcare), KinExA, fluorescence-activated cell sorting (FACS), Octet™ (FortéBio, Inc.) and Western blot analysis are among many assays that may be used to identify an antibody, or antigen-binding fragment thereof, that specifically binds an antigen. Typically, a specific binding will be at least twice of the background signal or noise, more typically at least 10 times of background, at least 50 times of background, at least 100 times of background, at least 500 times of background, at least 1000 of times background, or at least 10,000 times of background.

[0108] The specificity of an antibody binding may be assessed by determining and comparing the K_D values of a specific binding between an antibody and IFN β , with the K_D value of a control antibody that is known not to bind to IFN β . In general, an antibody is said to "specifically bind" an antigen when the K_D is about $\times 10^{-5}$ M or less.

[0109] An antibody, or antigen-binding fragment thereof, "does not substantially bind" to an antigen when it does not bind to said antigen with greater affinity, avidity, more readily, and/or with greater duration than it binds other antigens. Typically, the binding will be no greater than twice of the background signal or noise. In general, it binds the antigen with a K_D of 1×10^{-4} M or more, 1×10^{-3} M or more, 1×10^{-2} M or more, or 1×10^{-1} M or more.

[0110] The term "compete", as used herein with regard to an antibody, means that binding of a first antibody, or an antigen-binding portion thereof, to an antigen reduces the subsequent binding of the same antigen by a second antibody or an antigen-binding portion thereof. In general, binding of a first antibody creates steric hindrance, conformational change, or binding to a common epitope (or portion thereof), such that the binding of the second antibody to the same antigen is reduced. Standard competitive binding assays may be used to determine whether two antibodies compete with each other.

[0111] One suitable assay for antibody competition involves the use of the Biacore technology, which can measure the extent of interactions using surface plasmon resonance (SPR) technology, typically using a biosensor system (such as a BIACORE® system). For example, SPR can be used in an *in vitro* competitive binding inhibition assay to determine the ability of one antibody to inhibit the binding of a second antibody. Another assay for measuring antibody competition uses an ELISA-based approach. Furthermore, a high throughput process for "binning" antibodies based upon their competition is

described in WO2003/48731. Competition is present if one antibody, or antigen-binding fragment thereof, reduces the binding of another antibody, or antigen-binding fragment thereof, to IFN β . For example, a sequential binding competition assay may be used, with different antibodies being added sequentially. The first antibody may be added to reach binding that is close to saturation. Then, the second antibody is added. If the binding of second antibody to IFN β is not detected, or is significantly reduced (e.g., at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% reduction) as compared to a parallel assay in the absence of the first antibody (which value can be set as 100%), the two antibodies are considered as competing with each other. An exemplary antibody competition assay (and overlapping epitope analysis) by SPR is provided in Example 1.

[0112] A competitive binding assay can also be conducted in which the binding of the antibody to the antigen is compared to the binding of the target by another binding partner of that target, such as another antibody or a soluble receptor that otherwise binds the target. The concentration at which 50% inhibition occurs is known as the K_i . Under ideal conditions, the K_i is equivalent to K_D . Thus, in general, measurement of K_i can conveniently be substituted to provide an upper limit for K_D . Binding affinities associated with different molecular interactions, e.g., comparison of the binding affinity of different antibodies for a given antigen, may be compared by comparison of the K_D values for the individual antibody/antigen complexes. K_D values for antibodies or other binding partners can be determined using methods well established in the art.

[0113] An "Fc fusion" protein is a protein wherein one or more polypeptides are operably linked to an Fc polypeptide. An Fc fusion combines the Fc region of an immunoglobulin with a fusion partner. The "Fc region" may be a native sequence Fc region or a variant Fc region. Although the boundaries of the Fc region of an immunoglobulin heavy chain might vary, the human IgG heavy chain Fc region is usually defined to stretch from an amino acid residue at position Cys226, or from Pro230, to the carboxyl-terminus thereof. The numbering of the residues in the Fc region is that of the EU index as described in Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md., 1991. The Fc region of an immunoglobulin generally comprises two constant domains, CH₂ and CH₃. As is known in the art, an Fc region can be present in dimer or monomeric form.

[0114] The term "therapeutically effective amount" means an amount of an anti-IFN β antibody, or an antigen-binding fragment thereof, or a combination comprising such antibody, or antigen-binding fragment thereof, that is of sufficient quantity to achieve the intended purpose, such as decreased binding of IFN β to IFNAR, the decreased phosphorylation of STAT1 and/or STAT2, the decreased expression of IFN β -dependent gene, or otherwise causing a measurable benefit *in vivo* to a subject in need. The precise amount will depend upon numerous factors, including, but not limited to the components and physical characteristics of the therapeutic composition, intended patient population, individual patient considerations, and the like, and can be determined by one skilled in the art.

[0115] The term "treatment" includes prophylactic and/or therapeutic treatments. If it is administered prior to clinical manifestation of a disease, disorder, or condition, the treatment is considered prophylactic. Therapeutic treatment includes, e.g., ameliorating or reducing the severity of a disease, disorder, or condition, or shortening the length of the disease, disorder, or condition. Preferably, the disease, disorder, or condition is mediated by or related to IFN β binding to IFNAR.

[0116] The term "about", as used herein, refers to $\pm$ 10% of a value.

BIOLOGICAL DEPOSIT

[0117] Representative materials of the present invention were deposited in the American Type Culture Collection, 10801 University Boulevard, Manassas, Va. 20110-2209, USA, on December 18, 2015. Vector CTI-AF1-VH, having ATCC Accession No. PTA-122727, comprises a DNA insert encoding the heavy chain variable region of antibody CTI-AF1, and vector CTI-AF1-VL, having ATCC Accession No. PTA-122726, comprises a DNA insert encoding the light chain variable region of antibody CTI-AF1. The deposits were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and Regulations thereunder (Budapest Treaty).

EXAMPLES

[0118] The invention is further described in detail by reference to the following experimental examples. These examples are provided for purposes of illustration only, and are not intended to be limiting unless otherwise specified.

EXAMPLE 1. GENERATION OF ANTI-IFN β ANTIBODIES

[0119] Antibody CTI-AF1 is a humanized IgG1 antibody against the soluble cytokine interferon beta (IFN β). A mouse monoclonal antibody (mouse mAb) against human IFN β was generated by standard immunizations of female BALB/c mice with human IFN β , and subsequent hybridoma screening.

[0120] Two hybridoma clones were selected for humanization based on kinetic binding profile. The clones showed a K_D value of about 20nM and an IC₅₀ of about 20nM. Hybridoma clones were humanized by using human germline framework sequences from IGKV1-39 (DPK9 light chain variable domain; Gene Bank Accession No. X59315) and IGHV1-69 (DP10 heavy chain variable domain; Gene Bank Accession No. L22582).

[0121] Multiple rounds of affinity maturation were used to increase the affinity of the antibody. The sequences of VL region of these antibodies are shown in Table 11. All antibodies in Table 11 have the same VH sequence. In particular, CTI-AF1 showed a decrease in K_D value from 25 nM to 29 pM by introducing the following mutations in the light chain variable domain: S to G mutation in position 30, H to I and T to I mutations at position 92 and 93 respectively, and L to I mutation in position 96. No mutations were introduced in the heavy chain variable domain.

[0122] The affinities of CTI-AF antibodies to human interferon beta (IFN β) were determined by SPR as follows, using a Biacore T200 instrument. Antibodies were directly immobilized on the surface of a CM5 sensor chip at room temperature, using standard amine-coupling technique. Immobilization levels covered a range from 49 to 375 resonance units (RU). The analyte, recombinant human IFN β , was then injected in a series of dilutions ranging

from 10 nM down to 0.078 nM (2-fold dilution), at a flow rate of 30 to 50 μ L per minute for an association time ranging from 65 to 300 seconds, followed by a dissociation phase of 10 minutes. Each concentration was evaluated in duplicate. The analyte was removed by regeneration of the CM5 sensor chip surface between each cycle using 3 M MgCl_2 at pH 3.0 or 10 mM glycine-HCl at pH 1.5, followed by a buffer rinse. This regeneration step removed the bound analyte and returned the response signal to baseline. Data from the reference flow cell (without analyte) were subtracted from the antigen binding responses to remove systematic artifacts. The apparent binding affinity was determined with a 1:1 interaction model using Biacore T200 evaluation software version 2.0. The equilibrium constant K_D was determined as the ratio of the kinetic rate constants, k_d/k_a . Binding was validated by repeating the binding experiments over multiple days, using two separate instruments and different flow cells on the CM5 sensor chip. The results are shown in Table 6.

Table 6 summaries of biological activities of the antibodies in Table 11

Ab Name	K_D (M) - biacore	Response rank (Octet)	IC50 (pM) ISRE Neutralization	IC50 (pM) pSTAT1 Inhibition
CTI-AF1	3.6E-11	1	2	4
CTI-AF2	-	-	-	-
CTI-AF3	-	-	-	-
CTI-AF4	-	4	-	-
CTI-AF5	-	-	-	10
CTI-AF6	-	-	-	-
CTI-AF7	-	-	-	-
CTI-AF8	-	6	460	-
CTI-AF9	-	12	75	-
CTI-AF10	-	5	-	-
CTI-AF11	-	-	-	-
CTI-AF12	-	-	-	-
CTI-AF13	-	-	-	-
CTI-AF14	-	7	-	30
CTI-AF15	-	3	-	80
CTI-AF16	-	2	14	-
CTI-AF17	-	-	-	-
CTI-AF18	-	-	-	-
CTI-AF19	-	-	-	-
CTI-AF20	3.35E-10	8	-	20
CTI-AF21	-	11	-	-
CTI-AF22	-	-	-	-
CTI-AF23	-	9	-	-
CTI-AF24	-	-	-	-
CTI-AF25	-	-	-	-
CTI-AF26	-	-	-	-
CTI-AF27	-	10	-	70

EXAMPLE 2. BIOPHYSICAL PROPERTIES OF ANTI-IFN β ANTIBODIES

[0123] CTI-AF1 was dialyzed and concentrated to 150 mg/mL in MOD1 buffer with 10K MWCO regenerated cellulose membrane. The cynomolgus monkey ETS material was ultrafiltrated/diafiltrated into the same buffer to a final concentration of 72 mg/mL with minimal losses of product. When formulated in PBS, pH 7.2 at ~50 mg/mL, CTI-AF1 phase-separated at 2-8°C and formed a stable milky emulsion. Upon warming up to room temperature, the solution becomes clear again. In MOD1 buffer, no phase-separation occurred.

[0124] Viscosity was measured at 22°C using the mVROC viscometer. Injections were performed at 100 μ L/min using a 100 μ L Hamilton syringe. The dependence of viscosity on concentration is shown in Figure 1. Even at the maximum concentration the viscosity is still below 10 cP.

[0125] Thermal stability was evaluated using MicroCal VP-DSC (Malvern). CTI-AF1 was scanned at 1 mg/mL protein in MOD1 buffer at 1 deg/min. As shown in Figure 2, the first melting transition of this molecule occurs at 69.4°C, which is well above the known required stability threshold for commercial scale manufacturability.

[0126] Low-pH stability was evaluated by titrating protein A pool with citric acid down to pH 2.8, 3.0 and 3.4 and incubating for 5 hours at room temperature before neutralizing to pH 7.0. As shown in Figure 3, the formation of HMMS occurs only at pH 2.8, while at higher pH levels the product is stable. This stability will enable inactivation of enveloped viruses at low pH, as required for commercial manufacture.

[0127] Freeze/thaw stability was performed at 72 mg/mL in MOD1 buffer by placing an Eppendorf tube containing 1 mL of product at -80°C for 10 min, followed by thawing at room temperature. No significant aggregation was observed after 3 cycles of freeze-thaw.

[0128] Stability studies were performed at 100 mg/mL in MOD1 buffer for 6 weeks at 2-8°C (Figure 4A) and ambient temperature (22°C, Figure 4C); in MOD1 buffer at 5 mg/mL for 4 weeks at 40°C (Figure 4B); in 20 mM buffer (glutamic acid pH 4.0, histidine pH 5.8, tris pH 8.0) at 4 mg/mL for 5 or 11 days at 37°C (Figure 4D). Testing of the time points was performed by SE-HPLC. No significant increase in HMW was detected in any of the studies. Similarly analysis by CGE did not show any significant differences between the time points. Charge heterogeneity was assayed by iCE (Table 7), which showed an

increase in acidic species at 37°C (particularly at pH 8.0) and 40°C, indicating some degree of deamidation and/or oxidation. However, no major changes were detected to trigger a liquid chromatography (LS)/mass spectrometry (MS) investigation. Other stability series (2-8°C and ambient temperature) did not show significant changes in % acidic and % basic species by ICE.

[0129] The stability time points from the 40°C series were tested in the cell-based assay measuring the neutralization of IFN β activity (Figures 5 A-D). On day 1, 20,000 HEK293 ISRE-Luc (IFN β responsive luciferase reporter) cells were plated in 100 μ L of DMEM containing 10% fetal bovine serum (FBS) per well in tissue culture treated 96 well plates. Antibody solutions were prepared as 2x stocks starting at a top concentration of 1 μ M in DMEM/10% FBS, and then an 11 point, 10-fold dilution series was made with media. A 20x stock of IFN β (0.625 ng/mL) was prepared in media and added to the antibody titration stocks to a final 2x concentration. The antibody:IFN β solutions were incubated for 2 hours at 37°C, then 100 μ L of the solution was added per well and plates were cultured overnight at 37°C. On day 3, a 150 μ g/mL solution of Beetle Luciferine, potassium salt was prepared and 20 μ L/well was added and plates were incubated for 15 minutes at 37°C. Luminescence was read on an EnVision multilabel plate reader. No changes in neutralizing activity were detected.

[0130] CTI-AF1 is compatible with a formulation buffer (20 mM His, 8.5% Sucrose, 0.05 mg/mL EDTA, pH 5.8) and maintains solubility up to 150 mg/mL with acceptable viscosity.

Table 7: Charge heterogeneity in the stability samples

Sample Name	pI	Acidic	Main	Basic
HC_T0	8.74	17.3	79.5	3.2
HC_1wk4C	8.74	17.4	79.7	3
HC_2wk4C	8.75	17.5	79.1	3.3
HC_3wk4C	8.74	17.7	78.9	3.4
HC_4wk4C	8.75	18.1	78.9	3
HC_5wk4C	8.74	19.1	77.1	3.8
HC_6wk4C	8.74	17.8	79.2	3
HC_1wk25C	8.74	17.4	79.3	3.4
HC_2wk25C	8.74	17.9	78.9	3.2
HC_3wk_25C	8.73	18.2	78.5	3.4
HC_4wk25C	8.73	19.2	76.9	3.9
HC_5wk25C	8.73	19.8	76.7	3.5
HC_6wk25C	8.72	20.3	76.4	3.4
40C_1wk	8.71	23.9	70.8	5.2
40C_2wk	8.7	32.8	60.8	6.4
40C_3wk	8.7	37.4	56.7	5.9
40C_4wk	8.7	42.1	52.1	5.7
pH4_T0	8.7	18.7	78.5	2.8
pH4_5d	8.7	22	74.9	3.1
pH4_11d	8.69	25.9	67.4	6.7
PH5_8_T0	8.74	19.3	77.7	3
pH5_8_5d	8.73	21.3	75.6	3.2
pH5_8_11d	8.74	24.4	70.8	4.8
pH8_T0	8.73	21	76.3	2.7
pH8_5d	8.74	27.5	70.1	2.4
pH8_11d	8.74	34.1	63.6	2.3

EXAMPLE 3. PHARMACOLOGY

Brief Summary

[0131] CTI-AF1 is a potent and highly selective humanized IgG1 antibody against the soluble cytokine interferon beta (IFN β). *In vitro*, CTI-AF1 showed high affinity for human IFN β (K_D of 36.7+12.4 pM). The antibody showed similar EC_{50} binding for human and cynomolgus monkey IFN β (15.28 $\pm$ 2.11 pM and 25.04+5.11 pM, respectively). In human cell-based functional assays, CTI-AF1 showed potent neutralization of IFN β induced STAT1 phosphorylation (IC_{50} 7.7 $\pm$ 5.0 to 29.8+6.9 pM) and expression of a type I interferon stimulated luciferase reporter in cultured human cells (ISRE assay; IC_{50} 28.8+7.6 pM). CTI-AF1 also inhibited the IFN β -driven expression of MxA (Mx1) in gene expression assays (IC_{50} 29.4 $\pm$ 23.5 pM) and was able to inhibit IFN β endogenously expressed by human dermal fibroblasts, a disease relevant cell type, after polyinosinic:polycytidylic acid (poly I:C) stimulation.

Primary Pharmacology, In Vitro

[0132] During the initial hybridoma screening, antibodies were selected based upon their ability to block the binding of IFN β to IFNAR2, the high affinity component of the type I IFN receptor (Figure 6). In subsequent screenings post humanization and affinity maturation, antibody selection was based upon functional neutralization of IFN β in cell based assays.

[0133] SPR was used to determine the K_D of CTI-AF1 to human IFN β ; binding experiments were performed using a Biacore T200 optical biosensor equipped with research-grade CM5 sensor chip and human IFN β (Peprotech). Regeneration of the chip was performed using stripping buffer (3M MgCl $_2$ at pH 3.0 or 10mM glycine at pH 1.5) followed by a buffer rinse. CTI-AF1 was immobilized on the surface of a CM5 sensor chip at room temperature. The capture level covered a range of 50 to 375 resonance units (RU). The analyte, human IFN β , was then injected at a flow rate of 30-50 μ L per minute for an association time ranging from 65-300 seconds, followed by a dissociation phase of 10 minutes. The kinetic characterization of the interactions was performed using the traditional multi-cycle method, using a series of human IFN β concentrations from 10 nM down to 0.078125 nM in a series of 2-fold dilutions. Each concentration was evaluated in duplicate. The analyte was removed by regeneration of the array surface between each cycle using 3M MgCl $_2$ at pH 3.0 or 10 mM glycine at pH 1.5, followed by a buffer rinse. This regeneration step removed the bound analyte and returned the response signal to baseline. Data from the reference flow cell (without analyte) were subtracted from the antigen binding responses to remove systematic artifacts. The apparent binding affinity was determined using a simple 1:1 interaction model and the equilibrium constant K_D was determined as the ratio of the kinetic rate constants. The apparent binding affinity of CTI-AF1 for human IFN β was determined to be 36.7 ± 12.4 pM (Figure 7).

[0134] Binding of CTI-AF1 to human IFN β along with cynomolgus monkey, rabbit, rat and mouse orthologs and three of the nearest type I human homologs and IPN γ (type II) were evaluated in plate-based ELISAs. ELISA plates were coated overnight at 4°C with 5 μ g/mL of one of the following cytokines: human IFN β , cynomolgus monkey IFN β , rat IFN β , human IFN α 2, IFN γ , human IFN ω ; mouse IFN β or human IFN α 14(H2) were coated at 1 μ g/mL, and rabbit IFN β was coated at 10 ng/mL. All proteins were diluted in calcium and magnesium-free phosphate buffered saline. Coated plates were washed with phosphate buffered saline containing 0.05% Tween-20 (PBST) and blocked for 1 hour at room temperature with blocking buffer (PBST+0.5% BSA). Plates were washed again with PBST and primary antibodies were added to the plate at 30 nM starting concentration, followed by 1:3 dilutions in blocking buffer. For the anti-rabbit IFN β , 1:10 dilutions were performed. Plates were incubated for 1 hour at room temperature and then washed with PBST. Binding was detected with species-specific peroxidase-linked secondary antibodies and tetramethylbenzidine (TMB1) substrate. The reaction was stopped with 0.18 M sulfuric acid (H $_2$ SO $_4$) and absorbance was read at 450 nm in an EnVision multilabel reader (PerkinElmer). Table 8 shows similar reactivity for human and cynomolgus monkey IFN β , while reactivity to rabbit IFN β is 200 times lower. There was no detectable binding to rat or mouse IFN β , or to the three nearest human homologs or IFN γ (type II).

Table 8: Reactivity of CTI-AF1 to IFN β orthologs and nearest type I homologs and IPN γ as measured by ELISA

Target	Homology (%)	CTI-AF1 EC $_{50}$ (pM)
Cross-species binding		
Human IFN β	100	15.14
Cynomolgus monkey IFN β	95.7	24.67
Rabbit IFN β	56.1	2948
Rat IFN β	48.6	No binding
Mouse IFN β	47.5	No binding
Cross-reactivity		
Human IFN α 2	30.2	No binding
Human IFN α 17	38.2	No binding
Human IFN ω	29.0	No binding
Human IPN γ	13.2	No binding
<i>"No binding": when the absorbance at 450 nm was < 2x the absorbance of the blank control wells.</i>		

[0135] Two *in vitro* assays were used to demonstrate CTI-AF1 dependent inhibition of IFN β induced signals. Firstly, HEK293 cells stably transduced with a human ISRE luciferase reporter were used as a measure of IFN β dependent gene expression; on day 1, 20,000 HEK293 ISRE-Luc (IFN β responsive luciferase reporter) cells were plated in 100 μ L of DMEM containing 10% fetal bovine serum (FBS) per well in tissue culture treated 96 well plates. Antibody solutions were prepared as 2x stocks starting at a top concentration of 1 μ M in DMEM/10% FBS. An 11 point, 10-fold dilution series was made with media. A 20x stock of IFN β (28 nM, final assay concentration was 1.4 nM, the EC $_{50}$) was prepared in media and added to the antibody titration stocks to a final 2x concentration. The antibody:IFN β solutions were incubated for 2 hours at 37°C, then 100 μ L was added per well and plates were cultured overnight at 37°C. On day 3, a 150 μ g/mL solution of Beetle Luciferine, potassium salt was prepared and 20 μ L/well was added and plates were incubated for 15 minutes at 37°C. Luminescence was read on an EnVision multilabel plate reader. Figure 8A shows CTI-AF1 dose-dependent inhibition of IFN β induced luciferase activity with an IC $_{50}$ of 28.8 ± 7.6 pM.

[0136] Secondly, CTI-AF1 mediated inhibition of IFN β induced STAT1 phosphorylation was evaluated by phosflow. U937 cells, a human monocytic cell line, were grown in RPMI 1640 containing 10% FBS and 2 mM Glutamax (cRPMI). Antibody stocks were made at 4x, with a top concentration of 4 μ M (final top concentration was 1 μ M) and a 12 point, 10-fold dilution series was made in cRPMI; 25 μ L was added/well in a u-bottom 96 well tissue culture plate. An equal volume of 4x IFN β (200 pM, final concentration was 50 pM, EC $_{90}$) was added to the antibody stocks and incubated for 2 hours at 37°C. Control wells included media alone (no stimulation background pSTAT1 expression) and 50 pM IFN β only (maximum pSTAT1 signal). U937 cells were harvested, centrifuged for 5 min at 1500 rpm, room temperature and then resuspended at a concentration of 2×10^6 /mL in cRPMI warmed to 37°C; 50 μ L of cell suspension was added per well and plates placed at 37°C for 15 minutes. Next, 100 μ L of pre-warmed cytofix buffer was added and plates were placed back at 37°C for 15 minutes. Plates were removed and centrifuged as described above. Media was removed from the plates, cells resuspended and washed in 200 μ L of PBS and centrifuged again. Media was removed again, then cells were resuspended in 100 μ L of permeabilization buffer IV and incubated at room temperature for 15 minutes. At the end of the incubation, cells were centrifuged and washed as described above. After the PBS wash, cells were resuspended in 100 μ L of PBS/5% FBS; 5 μ L of TruStain FcX/well was added and plates were incubated for 10 min at 4°C. Ten microliters of Alexa Fluor 674 (AF647) conjugated anti-phospho STAT1 antibody was added per well and incubated for 20 min at 4°C. After incubation, 120 μ L of FACS buffer was added per well and plates were centrifuged as described above. The wash was repeated with 220 μ L of FACS buffer and cells were resuspended in 120 μ L of FACS buffer. A Fortessa cytometer was used to acquire the data and analysis was performed using FlowJo software. The geometric mean fluorescence intensity (Geo MFI) in the AF647 channel was calculated and prism software was used to calculate the IC $_{50}$. CTI-AF1 is a potent neutralizer of human IFN β with an IC $_{50}$ of 29.8 ± 6.9 pM (Figure 8B).

[0137] To evaluate the ability of CTI-AF1 to neutralize recombinant IFN β induced MxA (Mx1) gene expression normal human dermal fibroblasts (HDF) were plated in a T-150 flask in fibroblast culture medium. To set up the assay, cells were dislodged from the flask using trypsin/EDTA solution and plated in a 48 well plate with three wells assigned per experimental condition. On day 3, the cells were stimulated for 5 hours with culture medium spiked with 0.15 pM IFN β that was pre-incubated for 2 hours with or without dilutions of CTI-AF1 ranging from 10 nM to 0.016 nM. A combination of 0.15 pM IFN β and 50 nM of isotype control antibody was used as a negative control for the experiment. After 5 hours, cells were harvested, RNA was isolated using RNeasy micro kit and cDNA synthesized using high capacity cDNA reverse transcription kit. Taqman real time PCR analyses were performed in a Vii A7 system (Thermo Fisher) using human gene specific primer probes for *Mx1* and *B2M*. The relative quantification (fold change) was calculated from the resultant Ct values using the $\Delta\Delta C_t$ method as follows: for each condition, Ct values of the endogenous control gene (*B2M*) were subtracted from respective C_t values for target gene (*Mx1*). This was followed by normalization against the untreated sample to calculate the $\Delta\Delta C_t$ values, which were subsequently used to calculate the fold change ($2^{-\Delta\Delta C_t}$). The isotype negative control antibody had no impact on MxA (*Mx1*) expression; however, in the presence of CTI-AF1, a dose-dependent inhibition of gene transcription was seen with an IC_{50} of 29.4 ± 23.5 pM (Figure 9).

[0138] The specificity of CTI-AF1 neutralization was evaluated by using the same pSTAT assay as described earlier for Figure 8B, however, U937 cells were stimulated with either a final concentration of 20 pM IFN β or 50 pM IFN α . The different concentrations of type I IFNs were selected to provide a similar level of STAT1 phosphorylation as IFN α is a less potent activator of IFNAR signaling. A similar 12 point, 10-fold dilution series was made with sifalimumab (SIF) as a positive control for IFN α neutralization. As can be seen, CTI-AF1 specifically inhibited IFN β induced STAT1 phosphorylation, but did not inhibit phosphorylation induced by IFN α (Figures 10 A and B, respectively). A single experiment was conducted using either IFN ω (at 100 pM) or IFN α 14 (at 4 pM) and CTI-AF1 had no effect on IFN ω or IFN α 14 induced STAT1 phosphorylation.

[0139] To ensure that CTI-AF1 neutralized endogenously expressed IFN β , normal human dermal fibroblasts were seeded in a 48 well plate with three wells assigned per experimental condition. On day 3, cells were stimulated with or without a combination of 1 μ g/mL poly I:C and dilutions of CTI-AF1 (dose range: 50 pM - 100 nM) or 100 nM sifalimumab. After 2.5 and 24 hours, cells were harvested, RNA isolated using RNeasy micro kit and cDNA synthesized using high capacity cDNA reverse transcription kit. Taqman real time PCR and fold change calculations were performed as described above (Figure 9). While the amount of IFN β induced by poly I:C stimulation was unknown, a dose-dependent inhibition of MxA (*Mx1*) expression was seen in the presence of CTI-AF1 (Figure 11).

EXAMPLE 4. TRANSLATIONAL PHARMACOLOGY

[0140] The PK/PD relationship for IFN β in dermatomyositis (DM) has not been defined. There are no relevant translatable preclinical models available for DM and the preclinical efficacious concentration (C_{eff}) is not understood. A type 1 Interferon gene signature will be used clinically as a mechanistic biomarker of pharmacology modulation. Type 1 Interferon genes are typically elevated in DM and SLE patients and the mean fold-change of the type 1 Interferon gene signature has been used previously in clinical studies for anti-IFN α (sifalimumab and rontalizumab) and anti-IFNAR (anifrolumab) mAbs. However, a quantitative understanding of the gene signature modulation has not been established and the relationship between in vivo exposure, target engagement, downstream pharmacology and efficacy over time is not understood. Human efficacious dose feasibility projections are based on the ability of CTI-AF1 to neutralize >95% of IFN β in skin.

[0141] An LCMSMS assay is used to measure total IFN β in clinical serum and tissue biopsies, and in combination with CTI-AF1 clinical PK and K_D , is used to assess and confirm target engagement. Type 1 IFN gene signature in blood and skin, as well as IP-10 (CXCL10), are assessed as mechanistic biomarkers. In a subsequent Proof of Mechanism (PoM)/Early Signal of Efficacy (ESoE) study in DM patients, cutaneous dermatomyositis disease area and severity index (CDASI) is used as the primary endpoint (outcome biomarker) in addition to any relevant mechanistic biomarkers.

Pharmacokinetics-Pharmacodynamics Relationship and Human Dose

[0142] The pharmacokinetic and pharmacodynamic (PK/PD) relationships between antibody drug exposure and IFN β for CTI-AF1 have been simulated using reported PK parameters for typical IgG $_1$ therapeutics, IFN β -CTI-AF1 equilibrium binding constant, IFN β concentrations in skin and serum, and IFN β turnover half-life.

[0143] A "Site-of-Action" PK/PD model was used to predict the coverage of IFN β in DM patients. An IFN β coverage of >95% at trough was considered necessary to achieve efficacy. Skin interstitial concentrations of CTI-AF1 were assumed to be 30% of serum concentrations. The binding affinity of CTI-AF1 to IFN β determined by SPR (Biacore K_D = 36.7 pM) was used for PK/PD modeling. Consistent with this, in cell-based functional assays, CTI-AF1 showed potent neutralization of IFN β -induced STAT1 phosphorylation (IC_{50} 29.8 pM).

[0144] The median IFN β concentration in DM patient serum was 3 pg/mL (N=26); however, the IFN β concentration in DM patient skin is not known. Therefore, in the model, the impact of IFN β skin:plasma ratio was investigated at ratios of 10 and 100. Since this is a sensitive parameter for the model, these ratios were used as proposed boundary conditions to demonstrate the impact of the skin:plasma ratio on target coverage.

[0145] The *in vivo* half-life of IFN β turnover was estimated by fitting a 3-compartmental model to the human PK data for IFN β 1a, which included 3 IV doses. This fitting resulted in two different half-lives for IFN β turnover which are considered most relevant, depending on the phase and compartments considered ranging from 3 minutes (based on the initial phase) to 126 minutes (based on the effective half-life). To increase confidence in this model parameter, an IFN β assay for cynomolgus monkey serum was developed for use in cynomolgus monkey.

[0146] The IFN β skin:plasma ratio and the IFN β turnover rate are sensitive parameters for the PK/PD model. Thus, the human efficacious dose feasibility assessment was performed using the ranges described above for both IFN β skin:plasma ratio and IFN β turnover rate. Example assessments for two likely clinical ESoE dose regimens are shown in Figures 12 A-D (IV Q4W) and Figures 13A-D (SC Q1W). CTI-AF1 solubility of 150 mg/mL would enable a clinical dose of 2 mg/kg, as it can be delivered via a 1 mL injection pen. Hence a dose of 2 mg/kg was used for the dose feasibility assessments below.

[0147] Figures 12A-D show that at a dose of 2 mg/kg IV Q4W, irrespective of IFN β skin:plasma ratio, only the 126 min half-life for IFN β predicts >95% IFN β coverage in skin. If the half-life of IFN β was 3 min, >95% IFN β coverage in skin is predicted to require doses higher than 2 mg/kg.

[0148] Figures 13A-D show that at a dose of 2 mg/kg SC Q1W, irrespective of IFN β skin:plasma ratio, the 126 min half-life for IFN β predicts >95% IFN β coverage in skin. If the half-life of IFN β was 3 min, then only the IFN β skin:plasma ratio of 100 will result in >95% IFN β coverage in skin at 2 mg/kg. By contrast, if IFN β skin:plasma ratio is 10, achieving >95% coverage will require doses higher than 2 mg/kg.

Human PK/Exposure

[0149] Based on the pharmacokinetic profiles of CTI-AF1 in cynomolgus monkey, the pharmacokinetics of CTI-AF1 in human are expected to be similar to the reported values for a typical IgG₁ therapeutic. The 2-compartment pharmacokinetic parameter values are summarized in Table 9. Simulated concentration-time profiles of CTI-AF1 at projected efficacious dose levels are depicted in the top panels of Figures 12A-D and 13A-D.

Table 9: Projected Pharmacokinetic Parameters of CTI-AF1 in Human

Parameter	Definition	Projection
CL	central clearance	0.00258 mL/min/kg
V1	central volume	43.7 mL/kg
CLD	distribution clearance	0.00565 mL/min/kg
V2	peripheral volume	44.3 mL/kg
Ka	absorption rate constant for SC dosing	0.000181/min
F_sc	SC bioavailability	60%
Vdss	steady-state volume of distribution	88 mL/kg
T _{1/2}	terminal half life	19 days

Nonclinical Pharmacokinetics

[0150] IV and SC pharmacokinetics of CTI-AF1 have been assessed in cynomolgus monkeys using data from a single-dose exploratory toxicity study. Mean serum pharmacokinetic parameter values for cynomolgus monkeys are summarized in Table 10 and mean serum concentrations of CTI-AF1 are shown in Figure 14.

Table 10: Summary Table of CTI-AF1 Pharmacokinetics in Cynomolgus Monkeys

Dose (mg/kg)	Route	Cmax (μg/mL)	AUCinf (μg*hr/mL)	CL (mL/h/kg)	V _{ss} (L/kg)	T _{1/2} (h)	F (%)
10	SC	97.7	50000	n/a	n/a	379	87.3
10	IV	248	54900	0.183	0.0823	337	n/a
200	IV	4980	1000000	0.209	0.0747	273	n/a
Mean N=2 monkeys/group, 1 male and 1 female							

EXAMPLE 5. IFN β AS A TARGET FOR SLE AND DM

[0151] There is increasing evidence that IFN production is linked to SLE and other rheumatic diseases, such as DM. Moreover, the perpetuation of the SLE disease process likely involves further production of type I IFNs and a vicious pathogenic cycle.

[0152] DM is a rare autoimmune disease (about 20,000 patients in the U.S.) characterized by inflammation of skeletal muscle and skin, and, concomitantly, skeletal muscle weakness and skin rash. DM is typically associated with autoantibodies, and the pathogenesis of the disease may involve sequential binding of these autoantibodies to an endothelial autoantigen, triggering complement activation and vascular inflammation, ultimately leading to perifascicular atrophy.

[0153] As shown in Figures 16 A-B, data indicated an association of type I interferon-regulated gene (IRG) transcript "signature" in DM blood with skin rash activity, as measured by the cutaneous dermatomyositis disease area and severity index (CDASI). The highly IFN β -inducible gene MxA (Mx1) is expressed in DM perifascicular myofibers and capillaries, and blood serum IFN β - but not IFN α or IFN ω - is associated with DM, but not with other inflammatory myopathies or normal sera. These data support the notion that injury to capillaries, myofibers and skin in DM results from a pathogenic overproduction of IFN β message and protein. Data have also demonstrated an association between CDASI scores and serum levels of IFN β protein (Figure 17). Analyses of paired skin biopsies indicate the presence of both IFN β mRNA and upregulation of an IRG signature only in affected tissue (Figures 18 A-B). Taken together, these data strongly suggest that DM is an IFN β -driven disease.

[0154] Given that in many tissue contexts IFN β production may precede IFN α production and initiate a pathogenic elevation of IRG signature expression, together with the notion that DM may be a largely IFN β -driven disease, it is believed that DM and SLE share many pathogenic features and attributes. Indeed, skin lesions of DM are difficult if not impossible to distinguish histologically from those of SLE, and a diagnosis of DM skin lesions typically requires clinical determination of increased CD4⁺ and CXCR3⁺ cell types and endothelial expression of Mx1. Moreover, both DM and SLE are characterized by B cell activation and autoantibody mediated inflammation and tissue destruction.

Table 11 Sequences of anti-IFN β antibodies

Seq ID	Ab Name		Sequences (<u>CDR-L1</u> , <u>CDR-L2</u> , <u>CDR-L3</u> , <u>CDR-H1</u> , <u>CDR-H2</u> , and <u>CDR-H3</u> underlined when applicable))
1	CTI-AF1	VL	DIQMTQSPSSLSASVGDRVITTCRTSQDIGNYLNWYQQKPKGKAFKLLIYSTSLRH SGVPSRFSGSGSDFTFLTISSLQPEDFATYYCQGILLPITFGGGTKVEIK (<u>CDR-L1</u> , <u>CDR-L2</u> , <u>CDR-L3</u> : SEQ ID NOs 34, 35, and 36, respectively)
2	CTI-AF2	VL	DIQMTQSPSSLSASVGDRVITTCRTSQDIGNYLNWYQQKPKGKAFKLLIYSTSLRH SGVPSRFSGSGSDFTFLTISSLQPEDFATYYCQGIVLPITFGGGTKVEIK
3	CTI-AF3	VL	DIQMTQSPSSLSASVGDRVITTCRTSQDISNYLNWYQQKPKGKAFKLLIFSTSLRH SGVPSRFSGSGSDFTFLTISSLQPEDFATYYCQGIVLPITFGGGTKVEIK
4	CTI-AF4	VL	DIQMTQSPSSLSASVGDRVITTCRTSQDISNYLNWYQQKPKGKAFKLLIYSTSLRH SGVPSRFSGSGSDFTFLTISSLQPEDFATYYCQGIVLPITFGGGTKVEIK
5	CTI-AF5	VL	DIQMTQSPSSLSASVGDRVITTCRTSQDISNYLNWYQQKPKGKAFKLLIYTSRLR SGVPSRFSGSGSDFTFLTISSLQPEDFATYYCQGIVLPITFGGGTKVEIK
6	CTI-AF6	VL	DIQMTQSPSSLSASVGDRVITTCRTSQDIDNFWYQQKPKGKAFKLLIYSTSLRH SGVPSRFSGSGSDFTFLTISSLQPEDFATYYCQGIVLPITFGGGTKVEIK
7	CTI-AF7	VL	DIQMTQSPSSLSASVGDRVITTCRTSQDISNYLNWYQQKPKGKAFKLLIYSTSLH SGVPSRFSGSGSDFTFLTISSLQPEDFATYYCQGIVLPITFGGGTKVEIK
8	CTI-AF8	VL	DIQMTQSPSSLSASVGDRVITTCRTSQDIGNYLNWYQQKPKGKAFKLLIYSTSLRH SGVPSRFSGSGSDFTFLTISSLQPEDFATYYCQGIVLPITFGGGTKVEIK
9	CTI-AF9	VL	DIQMTQSPSSLSASVGDRVITTCRTSQDISNYLNWYQQKPKGKAFKLLIFSTSLRH SGVPSRFSGSGSDFTFLTISSLQPEDFATYYCQGSTILPITFGGGTKVEIK
10	CTI-AF10	VL	DIQMTQSPSSLSASVGDRVITTCRTSQDISNYLNWYQQKPKGKAFKLLIYSTSLRH SGVPSRFSGSGSDFTFLTISSLQPEDFATYYCQGSTILPITFGGGTKVEIK
11	CTI-AF11	VL	DIQMTQSPSSLSASVGDRVITTCRTSQDISNYLNWYQQKPKGKAFKLLIYTSRLR SGVPSRFSGSGSDFTFLTISSLQPEDFATYYCQGSTILPITFGGGTKVEIK
12	CTI-AF12	VL	DIQMTQSPSSLSASVGDRVITTCRTSQDIDNFWYQQKPKGKAFKLLIYSTSLRH SGVPSRFSGSGSDFTFLTISSLQPEDFATYYCQGSTILPITFGGGTKVEIK
13	CTI-AF13	VL	DIQMTQSPSSLSASVGDRVITTCRTSQDISNYLNWYQQKPKGKAFKLLIYSTSLH SGVPSRFSGSGSDFTFLTISSLQPEDFATYYCQGSTILPITFGGGTKVEIK
14	CTI-AF14	VL	DIQMTQSPSSLSASVGDRVITTCRTSQDISNYLNWYQQKPKGKAFKLLIFSTSLRH SGVPSRFSGSGSDFTFLTISSLQPEDFATYYCQGILLPITFGGGTKVEIK
15	CTI-AF15	VL	DIQMTQSPSSLSASVGDRVITTCRTSQDISNYLNWYQQKPKGKAFKLLIYSTSLRH SGVPSRFSGSGSDFTFLTISSLQPEDFATYYCQGILLPITFGGGTKVEIK
16	CTI-AF16	VL	DIQMTQSPSSLSASVGDRVITTCRTSQDISNYLNWYQQKPKGKAFKLLIYTSRLR SGVPSRFSGSGSDFTFLTISSLQPEDFATYYCQGILLPITFGGGTKVEIK
17	CTI-AF17	VL	DIQMTQSPSSLSASVGDRVITTCRTSQDIDNFWYQQKPKGKAFKLLIYSTSLRH SGVPSRFSGSGSDFTFLTISSLQPEDFATYYCQGILLPITFGGGTKVEIK
18	CTI-AF18	VL	DIQMTQSPSSLSASVGDRVITTCRTSQDISNYLNWYQQKPKGKAFKLLIYSTSLH SGVPSRFSGSGSDFTFLTISSLQPEDFATYYCQGILLPITFGGGTKVEIK
19	CTI-AF19	VL	DIQMTQSPSSLSASVGDRVITTCRTSQDIGNYLNWYQQKPKGKAFKLLIFSTSLRH SGVPSRFSGSGSDFTFLTISSLQPEDFATYYCQGIVLPITFGGGTKVEIK
20	CTI-AF20	VL	DIQMTQSPSSLSASVGDRVITTCRTSQDISNYLNWYQQKPKGKAFKLLIYTSRLR SGVPSRFSGSGSDFTFLTISSLQPEDFATYYCQGIVLPITFGGGTKVEIK
21	CTI-AF21	VL	DIQMTQSPSSLSASVGDRVITTCRTSQDIDNFWYQQKPKGKAFKLLIFSTSLH

Seq ID	Ab Name		Sequences (CDR-L1, CDR-L2, CDR-L3, CDR-H1, CDR-H2, and CDR-H3 underlined when applicable))
			SGVPSRPSGSGSGTDFTLTISSLPQEDFATYYCQGSTILPLTPGGGKVEIK
22	CTI-AF22	VL	DIQMTQSPSSLSASVGDRTITCRISQDIGNYLNWYQQKPKAFKLLIFSTSR ¹ HLH SGVPSRPSGSGSGTDFTLTISSLPQEDFATYYCQGSTILPLTPGGGKVEIK
23	CTI-AF23	VL	DIQMTQSPSSLSASVGDRTITCRISQDISSYLNWYQQKPKAFKLLIY ¹ TSRLR SGVPSRPSGSGSGTDFTLTISSLPQEDFATYYCQGSTILPLTPGGGKVEIK
24	CTI-AF24	VL	DIQMTQSPSSLSASVGDRTITCRISQDIDN ¹ FLQWYQQKPKAFKLLIFSTSKLH SGVPSRPSGSGSGTDFTLTISSLPQEDFATYYCQGSTILPLTPGGGKVEIK
25	CTI-AF25	VL	DIQMTQSPSSLSASVGDRTITCRISQDIGNYLNWYQQKPKAFKLLIFSTSR ¹ HLH SGVPSRPSGSGSGTDFTLTISSLPQEDFATYYCQGSTILPLTPGGGKVEIK
26	CTI-AF26	VL	DIQMTQSPSSLSASVGDRTITCRISQDISSYLNWYQQKPKAFKLLIY ¹ TSRLR SGVPSRPSGSGSGTDFTLTISSLPQEDFATYYCQGSTILPLTPGGGKVEIK
27	CTI-AF27	VL	DIQMTQSPSSLSASVGDRTITCRISQDIDN ¹ FLQWYQQKPKAFKLLIFSTSKLH SGVPSRPSGSGSGTDFTLTISSLPQEDFATYYCQGSTILPLTPGGGKVEIK
28	CTI-AF1 to ACT-AF27	VH	QVQLVQSGAEVKKPGSSVKVSCKASGYTFSRYMMHWVRQAPGQGLEWMGHIDPSD SYTYYNQKFKGRVTITADESTSTAYMELSSLRSEDTAVYCARWDYGNLLFEYWG QGTLVTVSS (CDR-H1, CDR-H2, CDR-H3: SEQ ID Nos 37, 38, and 39, respectively)
29	All CTI-AFs	CH	ASTKGPSVFPLA ¹ APSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTP PCPAPFAAGAPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVS EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI KAKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSGFFLYSKLTVDKSRWQQGNVFC ¹ SVNHEALHNHYTQKSLSLSPG (K)
30	All CTI-AFs	CL	RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQW ¹ KVDNALQSGNSQES VTEQDSKDSITYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
32	CTI-AF1	Light chain	DIQMTQSPSSLSASVGDRTITCRISQDIGNYLNWYQQKPKAFKLLIY ¹ TSRLHSC VPSRPSGSGSGTDFTLTISSLPQEDFATYYCQGSTILPLTPGGGKVEIKRTVAAP VETFPSPDEQLKSGTASVCLLNNFYPREAKVQW ¹ KVDNALQSGNSQESVTEQDSKD ITYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
33	CTI-AF1	Heavy chain	QVQLVQSGAEVKKPGSSVKVSCKASGYTFSRYMMHWVRQAPGQGLEWMGHIDPSD SYTYYNQKFKGRVTITADESTSTAYMELSSLRSEDTAVYCARWDYGNLLFEYWG QGTLVTVSSASTKGPSVFPLA ¹ APSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHCTPCPAPFAAGAPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTIKAKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRWQQGNVFC ¹ SVNHEALHNHYTQ KSLSLSPG (K)
34	CTI-AF1	CDR-L1	<u>RTSQDIGNYLN</u>
35	CTI-AF1	CDR-L2	<u>STSR¹LHS</u>
36	CTI-AF1	CDR-L3	<u>QQGIILPIT</u>
37	CTI-AF1	CDR-H1	<u>GYTFSRYMMH</u>
38	CTI-AF1	CDR-H2	<u>HIDPSDSYTYYNQKFKG</u>
39	CTI-AF1	CDR-H3	<u>WDYGNLLFEY</u>
166	CTI-AF1	VH nuclei c acid	CAGGTGCAGCTGTCGAGAGCGGCGCCGAGCTGAAGAAGCCCGCAGCAGCGTGA AGGTGAGCTGCAAGGCGACGGCTACACCTTCAGCCGGTACTGGATGCATCGGGT GCGCGAGCGCCCGCGCCAGCGCTGAGCTGGATGGGCAATCGACCCAGCGAGC AGCTACACCTACTACAACGAGAAGTCAAGGCGCGGGTGACCATCACCGCGACG AGAGCACCAGCACCCTACATGGAGCTGAGCAGCCTCGGAGCAGGACACCGC
			CGTGTACTACTGCGCCCGGTGGGACTACGGCAACCTGCTGCTTCGAGTACTGGGGC CAGGGCACCCTGGTGACCGTCTCGAGC
167	CTI-AF1	VL nuclei c acid	GACATCCAGATGACCCAGAGCCCGCAGAGCCTGAGCGCGACGCTGGGCGAOCGGG TGACCATCACCTGCGGAGCAGGCAAGGACATCGGCAACTAGCTGAACCTGGTACCA GCAGAAGCCCGGCAAGGCTTCAGGCTGCTGATCTACAGCACCAGCGCGCTGCGAC AGCGGCTGCGCCAGCGCGGTTCAGCGGACAGCGGACCGGACCGCACTTCACCTGCA GCATCAGCAGCGCTGCAGCCGAGGACTTCGCACTACTACTGCGCAGCAGGGGAT TATTTTGGCCATTACTCTTCGCGCGCGGACCAAGCTGGAGATCAAG

EXAMPLE 6. EPIOTOPE MAPPING

[0155] To elucidate the epitope recognized by CT1-AF1, hybrid IFN β proteins were made where selected portions of IFN β sequences were replaced with IFN α sequence. CT1-AF1 specifically neutralizes IFN β but not IFN α ; therefore the inability of CT1-AF1 to neutralize a given hybrid protein would indicate loss of the epitope. Hybrid proteins were produced, purified and ability to induce STAT1 phosphorylation was confirmed (Table 12).

Table 12: sequences of hybrid IFN proteins

Seq ID	Hybrid IFN name	Sequences (mutated residues underlined>
41	Human IFN β	MSYNLLGFLQ RSSNFQCCQL LWQLNGRLEY CLKDRMNFDI PEEIKQLQQF QKEDAALTIY EMLQNIFAIF RQSSSTGWN ETIVENLLAN VYHQINHLKT VLEEKLEKED FTRGKLMSSL HLKRYYGRIL HYLKAKEYSH CAWTIVRVEI LRNFYFINRL TGYLRN
158	CID1276	MSYNLLGFLQ RSSNFQCCQL LWQLNGRLEY CLKDRMNFDI PEEIKQLQQF QKEDAALTIY EMLQNIFAIF RQSSSTGWN ETIVENLLAN VYHQINHLKT VLEEKLEKED FTRGKLMSSL HLKRYYGRIL HYLKAKEYSH CAWTIVRVEI LRNFYFINRL TGYLRN
159	CID1277	MSYNLLGFLQ RSSNFQCCQL LWQLNGRLEY CLKDRHDFGI PEEIKQLQQF QKEDAALTIY EMLQNIFAIF RQSSSTGWN ETIVENLLAN VYHQINHLKT VLEEKLEKED FTRGKLMSSL HLKRYYGRIL HYLKAKEYSH CAWTIVRVEI LRNFYFINRL TGYLRN
160	CID1280	MSYNLLGFLQ RSSNFQCCQL LWQLNGRLEY CLKDRMNFDI PEEIKQLQQF QKEDAALTIY EMLQNIFAIF RQSSSTGWN ETIVDKLLTN VYHQINHLKT VLEEKLEKED FTRGKLMSSL HLKRYYGRIL HYLKAKEYSH CAWTIVRVEI LRNFYFINRL TGYLRN
161	CID1281	MSYNLLGFLQ RSSNFQCCQL LWQLNGRLEY CLKDRMNFDI PEEIKQLQQF QKEDAALTIY EMLQNIFAIF RQSSSTGWN ETIVENLLAN VYHQINHLKT VLEEKLEKED FTRGKLMSSL HLKRYYGRIL HYLKAKEYSH CAWTIVRVEI LRNFYFINRL TGYLRN
162	CID1283	MSYNLLGFLQ RSSNFQCCQL LWQLNGRLEY CLKDRMNFDI PEEIKQLQQF QKEDAALTIY EMLQNIFAIF RQSSSTGWN ETIVENLLAN VYHQINHLKT VLEEKLEKED FTRGKLMSSL HLKRYYGRIL HYLKAKEYSH CAWTIVRVEI LRNFYFINRL TGYLRN
163	CID1285	MSYNLLGFLQ RSSNFQCCQL LWQLNGRLEY CLKDRMNFDI PEEIKQLQQF QKEDAALTIY EMLQNIFAIF RQSSSTGWN ETIVENLLAN VYHQINHLKT VLEEKLEKED FTRGKLMSSL HLKRYYGRIL HYLKAKEYSH CAWTIVRVEI LRNFYFINRL TGYLRN
164	CID1286	MSYNLLGFLQ RSSNFQCCQL LWQLNGRLEY CLKDRMNFDI PEEIKQLQQF QKEDAALTIY EMLQNIFAIF RQSSSTGWN ETIVENLLAN VYHQINHLKT VLEEKLEKED FTRGKLMSSL HLKRYYGRIL HYLKAKEYSH CAWTIVRVEI LRNFYFINRL TGYLRN
165	CID1287	MSYNLLGFLQ RSSNFQCCQL LWQLNGRLEY CLKDRMNFDI PEEIKQLQQF QKEDAALTIY EMLQNIFAIF RQSSSTGWN ETIVENLLAN VYHQINHLKT VLEEKLEKED FTRGKLMSSL HLKRYYGRIL HYLKAKEYSH CAWTIVRVEI LRNFYFINRL TGYLRN

[0156] All purified hybrid proteins were able to induce STAT1 phosphorylation, however, there were differences in the biological activity. Each hybrid protein was used at the EC₅₀ concentration in the following phospho-STAT1 assay (pSTAT1). U937 cells, a human monocytic cell line, were grown in RPMI 1640 containing 10%FBS (cRPMI). Antibody stocks were made at 4x, with a top concentration of 4-400 μ M (final top concentration was 1-100 μ M) and a 11 point, 10-fold dilution series was made in cRPMI; 25 μ l was added/well in a u-bottom 96 well tissue culture plate. An equal volume of 4x hybrid or control IFN β was added at the appropriate EC₅₀ concentration to the antibody stocks and incubated for 2 hours at 37°C. Control wells included media alone (no stimulation background pSTAT1 expression) or no addition of antibody (maximum pSTAT1 signal). U937 cells were harvested, centrifuged for 5 min at 1500 rpm at room temperature and then resuspended at a concentration of 2×10^6 /ml in cRPMI warmed to 37°C; 50 μ l of cell suspension was added per well and plates placed at 37°C for 15 minutes. Next 100 μ l of pre-warmed cytofix buffer (BD Biosciences, catalog # 554655) was added and plates were placed back at 37°C for 15 minutes. Plates were removed and centrifuged as described above. Media was removed from the plates, cells resuspended and washed in 200 μ l of PBS and centrifuged again. Media was removed again, cells were resuspended in 100 μ l of permeabilization buffer IV (BD Biosciences) and incubated at room temperature for 15 minutes. At the end of the incubation, cells were centrifuged and washed as described above. After the PBS wash, cells were resuspended in 100 μ l of PBS/5% FBS (FACS buffer); 5 μ l of TruStain FcX/well (BioLegend) was added and plates were incubated for 10 min at 4°C. Ten microliters of Alexa Fluor 674 (AF647) conjugated anti-phospho STAT1 Ab (BD Biosciences) was added per well and incubated 20 min at 4°C. After incubation, 120 μ l of FACS buffer was added per well and plates were centrifuged as described above. The wash was repeated with 220 μ l of FACS buffer and cells were resuspended in 120 μ l of FACS buffer; a Fortessa cytometer (BD Biosciences) was used to acquire the

data and analysis was performed using FlowJo software (TreeStar). The geometric mean fluorescence intensity (Geo MFI) in the AF647 channel was calculated and prism software was used to calculate the IC₅₀. Data was normalized as the ratio of antibody concentration/IFN concentration and the percentage of the maximum signal was determined after subtracting the background.

[0157] U937 cells were stimulated with IFN α /IFN β hybrid proteins for 15 minutes in the presence of CTI-AF1 after which the presence of phosphorylated STAT1 was assessed by intracellular flow cytometry. CTI-AF1 did not inhibit CID1280-dependent STAT1 phosphorylation and the potency for CID1281-induced STAT1 phosphorylation neutralization was greatly reduced. CTI-AF1 neutralized STAT1 phosphorylation of all other hybrid IFN proteins with equal potency relative to human IFN β . See FIG. 19 and Table 13. These data combined indicate that the epitope residues recognized by CTI-AF1 are contained within the constructs CID1280 and CID1281, in which the IFN α sequence substitutions span amino acids 85-89 and 90-100, respectively (see Table 12).

Table 13. IC₅₀ and fold change of CTI-AF1 mediated neutralization of type I IFN-induced STAT1 phosphorylation

IFN protein	IC ₅₀ (nM)	Fold difference from IFN β
Human IFN β	0.3	
CID1276	0.2	0.7
CID1277	0.3	0.9
CID1280	47.7	161.8
CID1281	3281.0	11137.1
CID1283	0.4	1.2
CID1285	0.4	1.4
CID1286	0.4	1.4
CID1287	0.3	1.0

EXAMPLE 7. CRYSTAL STRUCTURE OF ANTI-IFN β ANTIBODIES

[0158] The co-crystals of the complex between Cynomolgus monkey IFN β and CTI-AF1 Fab were grown using the following solution as a precipitant: 19% PEG 3350, 250 mM sodium Citrate, 100 mM Bis-Tris propane pH 8.5. The crystals belong to space group P2₁ (unit cell parameters a=49.58 Å; b=91.76 Å; c=162.52 Å; β =94.86 deg) and contain two copies of complex per crystal asymmetric unit. The structure has been determined at 3.2 Å resolution using Molecular Replacement method and the refinement was performed using autoBUSTER.

[0159] CTI-AF1 Fab binds to IFN β on the side formed by two α -helices, A and C, which define the binding epitope of CTI-AF1 (Table 13)

Table 13 Epitope analysis

cyno-IFN β					human IFN β				
Structure elements	Amino Acids	Primary epitope	Secondary epitope	Optional epitope	Structural	Amino Acids	Primary epitope	Secondary epitope	Optional epitope
Helix A	Leu 5			Leu 5	Helix A	Leu 5			Leu 5
	Leu 6			Leu 6		Leu 6			Leu 6
	Phe 8		Phe 8			Phe 8		Phe 8	
	Leu 9		Leu 9			Leu 9		Leu 9	
	Ser 12		Ser 12			Ser 12		Ser 12	
	Ser 13			Ser 13		Ser 13			Ser 13
	Phe 15			Phe 15		Phe 15			Phe 15
	Gln 16		Gln 16			Gln 16		Gln 16	
Helix C	Thr 82			Thr 82	Helix C	Thr 82			Thr 82
	Asn 86		Asn 86			Asn 86		Asn 86	
	Ala 89	Ala 89				Ala 89	Ala 89		
	Asn 90		Asn 90			Asn 90		Asn 90	
	Tyr 92	Tyr 92				Tyr 92	Tyr 92		
	His 93	His 93				His 93	His 93		
	Asp 96		Asp 96			Asn 96		Asn 96	
	His 97	His 97				His 97	His 97		
Helix B	Thr 100		Thr 100		Helix B	Thr 100		Thr 100	
	Tyr 67		Tyr 67			Phe 67 is not part of the epitope on human IFN β			

[0160] All amino acids that are within 3.8 Å from of CTI-AF1 were selected as "potential" epitope residues. "Primary" epitope residues are characterized as highly buried residues at the of CTI-AF1-IFN β interface and zero-to-low sequence tolerance to any other amino acid substitutions at this position. "Secondary" epitope residues are characterized as residues with medium buried surface area at the interface and medium sequence tolerance to amino acid substitutions at these positions. "Optional" epitope residues are characterized as residues with low buried surface area at the interface and high sequence tolerance to amino acid substitutions at these positions.

[0161] The binding paratope is made up by five CDR-variable regions: CDR-H1, -H2, -H3 and CDR-L1, -L3 (Table 14). The total surface area buried under the binding interface is 1,920 Å². Analysis of CTI-AF1-IFN β binding mode reveals that the neutralizing effect of CTI-AF1 is achieved through direct

blockage on the IFNAR1 binding site.

Table 14 Paratope analysis

CDRs	Amino Acids*	Primary Paratope	Secondary paratope
CDR-H1	Trp 33H	Trp 33H	
CDR-H2	Asp 54H		Asp 54H
	Tyr 56H	Tyr 56H	
	Tyr 58H	Tyr 58H	
	Gln 61H		Gln 61H
CDR-H3	Tyr 97H	Tyr 97H	
	Gly 98H		Gly 98H
	Leu 100H		Leu 100H
CDR-L1	Gln 27L		Gln 27L
	Asp 28L		Asp 28L
	Ile 29L		Ile 29L
	Gly 30L		Gly 30L
	Tyr 32L	Tyr 32L	
CDR-L3	Ile 92L	Ile 92L	
	Ile 93L		Ile 93L
	Leu 94L	Leu 94L	

[0162] All amino acids that are within 3.8 Å from IFN β were selected as "potential" binding paratope. "Primary" paratope residues are characterized as highly buried residues at the CTI-AF1-IFN β interface and low sequence tolerance to any other amino acid substitutions at this position. "Secondary" paratope residues are characterized as residues with lower buried surface area at the interface and higher sequence tolerance to amino acid substitutions at these positions.

[0163] Table 15 summarizes the epitope-paratope interaction pairs. Table 16 summarizes epitope and paratope analysis based on BSA.

Table 15: Epitope-paratope interaction pairs

Human IFN β epitope residue	CTI-AF1 paratope residue(s)	Type of interaction
5 Leu	32L Tyr	H-bond
6 Leu	32L Tyr	H-bond
8 Phe	28L Asp, 29L Ile, 30L Gly, 32L Tyr	van der Waals
9 Leu	32L Tyr, 92L Ile	van der Waals
12 Ser	28L Asp	H-bond
	92L Ile	van der Waals
13 Ser	92L Ile	van der Waals
15 Phe	27L Gln	van der Waals
16 Gln	27L Gln	H-bond
	28L Asp, 93L Ile	van der Waals
82 Thr	61H Gln	van der Waals
86 Asn	58H Tyr, 94L Leu	van der Waals
89 Ala	58H Tyr, 94L Leu	van der Waals
90 Asn	93L Ile,	van der Waals
	94L Leu	H-bond
92 Tyr	33H Trp, 56H Tyr	van der Waals
93 His	97H Tyr, 100H Leu, 92L Ile	H-bond
		van der Waals
		H-bond
96 Asp	97H Tyr, 33H Trp	van der Waals H-bond
97 His	97H Tyr, 98H Gly, 100H Leu	van der Waals
100 Thr	97H Tyr	H-bond

Table 16: Epitope and paratope analysis based on BSA

Potential IFN β epitope residues	BSA (Å ²)
5 Leu	89.8
6 Leu	3.5
8 Phe	72.4
9 Leu	51.8
12 Ser	30.1
13 Ser	18.9
16 Gln	77.4

Potential IFN β epitope residues		BSA (A ²)
82 Thr		40.2
86 Asn		51.8
89 Ala		52.0
90 Asn		53.1
92 Tyr		75.7
93 His		119.4
Potential paratope residues	Amino Acids*	BSA (A ²)
CDR-H1	Trp 33H	34.5
CDR-H2	Asp 54H	18.7
	Tyr 56H	67.6
	Tyr 58H	69.9
	Gln 61H	52.1
CDR-H3	Tyr 97H	101.7
	Gly 98H	31.7
	Leu 100H	31.3
CDR-L1	Gln 27L	54.4
	Asp 28L	39.1
	Ile 29L	7.8
	Gly 30L	16.8
	Tyr 32L	91.9
CDR-L3	Ile 92L	80.3
	Ile 93L	55.2
	Leu 94L	79.7

EXAMPLE 8. TYPE I INTERFERON EXPRESSION PROFILES

[0164] In this example, we studied type I IFN expression profiles of 4 disease relevant cell lines in response to toll-like receptor ligand stimulation. Four types of cells were used: PBMCs, a dermal fibroblast cell line, a muscle cell line and a kidney cell line, which were stimulated with a TLR3, TLR4, TLR7/8 and TLR9 agonist in the presence and absence of anti-IFN β antibody.

[0165] Gene expression levels of Type I IFN and *Mx1* in different primary human cell types was measured using quantitative-PCR. Primary cells were cultured in the relevant media as follows: normal human dermal fibroblasts in FGM-2 bulletkit media, normal human mesangial in MsGM bulletkit media, and primary human skeletal muscle derived cells in Myotonic growth medium. Peripheral blood mononuclear cells (PBMC) were isolated by centrifugation over Ficoll-Paque Plus. Mononuclear cells were cultured in RPMI1640 supplemented with 10% FBS and penicillinstreptomycin. To measure the type I IFN gene expression, cells were seeded then stimulated with the relevant TLR ligand for 1, 2.5, 5, 8 and 24 hours. After culture, cells were harvested, RNA was isolated and cDNA was synthesized. Expression of the following genes was assessed by Taqman PCR: *IFN β* , *Mx1*, *IFNa1*, *IFNa2*, *IFNa4*, *IFNa5*, *IFNa6*, *IFNa7*, *IFNa8*, *IFNa14*, *IFNa16*, *IFNa17*, and *B2m*. Taqman real time PCR and fold change calculations were performed as described above (Figure 9).

[0166] Table 17A shows that IFN β is the predominant Type I IFN produced by various tissue resident primary human cell types upon Toll like receptor (TLR) ligand stimulation. Dermal fibroblasts, skeletal muscle cells, glomerular mesangial cells and PBMCs from normal human donors were stimulated with poly I:C (TLR3 ligand), LPS (TLR4 ligand), R848 (TLR7/8 ligand) and ODN2216 (TLR9 ligand) in a time and dose-dependent manner. Relative expression levels of *IFN β* , *Mx1*, *IFNa* (1, 2, 4, 5, 6, 7, 8, 14, 16, and 17) were measured via quantitative-PCR using B2M as the control. Relative expression of each gene is indicated as strong (+), weak (+/-) or no expression (-).

[0167] CTI-AF1 was shown to be a potent neutralizer of endogenously produced IFN β from primary human cells stimulated with TLR ligands (poly I:C, LPS, R848 or ODN2216). Cells were stimulated with the various TLR ligands in the absence or presence of titrated amounts of CTI-AF1. Expression of *Mx1* was measured 24 hours post stimulation, with the exception of PBMCs stimulated with LPS, which was measured at 6 hours. RNA isolation, cDNA synthesis and quantitative PCR were performed as described above (Figure 9). While the amount of IFN β induced by any cell type upon TLR stimulation was unknown, a dose-dependent inhibition of *Mx1* expression was seen in the presence of CTI-AF1.

[0168] Table 17B shows that CTI-AF1 is a potent inhibitor of endogenous IFN β secreted by primary human cells after poly I:C and LPS stimulation. Cells were stimulated with the indicated TLR ligand and quantitative-PCR was performed to determine the level of *Mx1* expression using *B2M* as the control. Dose-dependent inhibition of *Mx1* gene expression by CTI-AF1 is indicated by "+" while the absence of CTI-AF1 dependent *Mx1* expression inhibition is indicated by "-". Conditions where Type I IFN expression was insufficient to drive any meaningful increase in *Mx1* expression that could potentially be neutralized by CTI-AF1 is indicated as NA.

Table 17A

	Dermal Fibroblasts				Skeletal Muscle Cells				Glomerular Mesangial Cells				PBMCs			
Gene transcript	In vitro stimulation															
	Poly I:C	LPS	R848	ODN2216	Poly I:C	LPS	R848	ODN2216	Poly I:C	LPS	R848	ODN2216	Poly I:C	LPS	R848	ODN2216
<i>IFNβ</i>	+	+	-	-	+	+	-	-	+	+	-	-	+	+	+	+
<i>Mx1</i>	+	+	-	-	+	+	-	-	+	+	-	-	+	+	+	+
<i>IFNa1</i>	-	-	+/-	+/-	-	+/-	-	-	-	+/-	+/-	-	+/-	+/-	+	+
<i>IFNa2</i>	-	-	-	-	-	-	-	-	-	-	-	-	+/-	-	+	+
<i>IFNa4</i>	-	-	-	-	-	-	-	-	-	-	-	-	+/-	-	+	+
<i>IFNa5</i>	+/-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+
<i>IFNa6</i>	-	-	-	-	-	-	-	-	-	-	-	-	+/-	-	+	+
<i>IFNa7</i>	-	-	-	-	-	-	-	-	-	-	-	-	+/-	-	+	+
<i>IFNa8</i>	-	-	-	-	-	-	-	-	-	-	-	-	+/-	+/-	+	+
<i>IFNa14</i>	-	-	-	-	-	-	-	-	-	-	-	-	+/-	+/-	+	+
<i>IFNa16</i>	-	-	-	-	-	-	-	-	-	-	-	-	+/-	-	+	+
<i>IFNa17</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+

+ = strong expression; +/- = relatively weak expression; - = not detected

+ = strong expression; +/- = relatively weak expression; - = not detected

Table 17B

	Dermal Fibroblasts				Skeletal Muscle Cells				Glomerular Mesangial Cells				PBMCs			
Gene transcript	In vitro stimulation															
	PolyI:C	LPS	R848	ODN2216	PolyI:C	LPS	R848	ODN2216	PolyI:C	LPS	R848	ODN2216	PolyI:C	LPS	R848	ODN2216
<i>Mx1</i>	+	+	NA	NA	+	+	NA	NA	+	+	NA	NA	+	+	-	-
+ = dose-dependent inhibition of <i>Mx1</i> gene expression by CTI-AF1; - = no dose-dependent inhibition of <i>Mx1</i> gene expression; NA = not applicable, insufficient type I IFN expression to drive <i>Mx1</i> expression																

+ = dose-dependent inhibition of *Mx1* gene expression by CTI-AF1; - = no dose-dependent inhibition of *Mx1* gene expression; NA = not applicable, insufficient type I IFN expression to drive *Mx1* expression

Table 18: Sequences of interferon β proteins

SEQ ID	Name	Sequence
40	Human IFN β precursor	MTNRKLLQIA LLICFSTTAL SMSYNLLGFL QRSSNFQCQK LLWQLNGRLE POLKDRMNPD LPFEEKQLQQ QKEDAAITL YEMLQNIFAI FRQSSSTGW NETIVENLLA NVYHQINHLK TVLEEKLEKE DPTGRKLMSL LHLKRYGRI LHYLKAKEYS HCAWTIVRVE ILRNFFYFINR LTGYLRN
41	Mature human IFN β	MSYNLLGFLQ RSSNFQCQKL LWQLNGRLEY CLKDRMNPDI FEEKQLQQF QKEDAAITLY EMLQNIFAIF RQSSSTGWN ETIVENLLAN VYHQINHLKT VLEEKLEKED FTRGKLMSL HMKRYGRIL HYLKAKEYSH CAWTIVRVEI LRNFFYFINRL TGYLRN
42	Mature mouse IFN β	INYNQLQLQE RTNIRKQDEL LEQLNGKINL TYRADPKIPM EMTERMQKSY TAFAIQEMLQ NVFLVERNNF SSTGWNETIV VRLDELHQQ TVELKTVLEE KQERLTWEM SSTALHLKSY YWRVQRYLKL MKYNSAWMV VRAEIFRNEL IIRRLTRNFQ N
43	Mature rat IFN β	IDYNQLQFRQ STSIRTCQKL LRQLNGRLNL SYRTPDKIPM EVMHESQMEK SYTAFAIQVM LQNVFLVFRS NFSSTGWNET IVESLLDELH QQTELLEIIL KEKQERLTW VTSTTLGLK SYWVRVQRYL KDKKNSYAW MVVRAEVFRN FSIILRLNRN FQN
44	Mature Cynomolgus monkey IFN β	MSYNLLGFLQ RSSNFQCQKL LWQLNGRLEY CLKDRMNPDI FEEKQPPQF QKEDAAITLY EMLQNIYAIF RQDLSSTGWN ETIVENLLAN VYHQIDHLKT ILEEKLEKED FTRGKFVSSL HMKRYGRIL HYLKAKEYSH CAWTIVRVEI LRNFFYFINRL TGYLRN
45	Mature rabbit IFN β	MSYNSLQIQL WHGSLTCAKL LLQLNGTTED CLNERINFKV EKEIKEPQOL QKEDTTLVIF EMLNNIFDIF RKNFSSTGWN ETIVENLLGE THLQIHHLKS KINKKVTLSS IRMNLRLKSY YWRINDYLET KQYSCAWKI VQLEIFRNFS FIDMLIDYL

REFERENCES CITED IN THE DESCRIPTION

Cited references

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Patent documents cited in the description

- [CN10289821A](#) [\[0004\]](#)
- [US4683195A](#) [\[0063\]](#)
- [US4800156A](#) [\[0063\]](#)
- [US4754065A](#) [\[0063\]](#)
- [US4683202A](#) [\[0063\]](#)
- [WO8704462A](#) [\[0067\]](#)
- [WO2004058184A](#) [\[0071\]](#)
- [WO200348731A](#) [\[0111\]](#)

Non-patent literature cited in the description

- **AJITH SOMINANDA et al.**inhibition of Endogenous Interferon Beta by Neutralizing Antibodies Against Recombinant Interferon BetaARCHIVES OF NEUROLOGY., 2010, vol. 67, 9 [\[0004\]](#)
- **KATHLEEN C. F. SHEEHAN et al.**Selective Blockade of Interferon- [alpha] and -[beta] Reveals Their Non-Redundant Functions in a Mouse Model of West Nile Virus InfectionPLOS ONE, 2015, vol. 10, 5 [\[0004\]](#)
- murine antibody raised against murine interferon beta., 2001, vol. 21, 11931-941 [\[0004\]](#)
- **CACECI et al.**Byte, 1984, vol. 9, 340-362 [\[0033\]](#)
- **WONGLOHMAN**Proc. Natl. Acad. Sci. USA, 1993, vol. 90, 5428-5432 [\[0033\]](#)
- **DRAKE et al.**Analytical Biochemistry, 2004, vol. 328, 35-43 [\[0035\]](#)
- A model of evolutionary change in proteins - Matrices for detecting distant relationships**DAYHOFF, M.O.**Atlas of Protein Sequence and StructureNational Biomedical Research Foundation19780000vol. 5, 345-358 [\[0055\]](#)
- Unified Approach to Alignment and Phylogenesis**HEIN J.**Methods in EnzymologyAcademic Press, Inc.19900000vol. 183, 626-645 [\[0055\]](#)
- **HIGGINS, D.G.SHARP, P.M.**CABIOS, 1989, vol. 5, 151-153 [\[0055\]](#)
- **MYERS, E.W.MULLER W.**CABIOS, 1988, vol. 4, 11-17 [\[0055\]](#)
- **ROBINSON, E.D.**Comb. Theor., 1971, vol. 11, 105- [\[0055\]](#)
- **SANTOU, N.NES, M.**Mol. Biol. Evol., 1987, vol. 4, 406-425 [\[0055\]](#)
- **SNEATH, P.H.A.SOKAL, R.R.**Numerical Taxonomy the Principles and Practice of Numerical TaxonomyFreeman Press19730000 [\[0055\]](#)
- **WILBUR, W.J.LIPMAN, D.J.**Proc. Natl. Acad. Sci. USA, 1983, vol. 80, 726-730 [\[0055\]](#)
- PCR: The Polymerase Chain ReactionBirkaswer Press19940000 [\[0063\]](#)
- **MARKS et al.**Bio/Technology, 1992, vol. 10, 779-783 [\[0071\]](#)
- **BARBAS et al.**Proc Nat. Acad. Sci, USA, 1994, vol. 91, 3809-3813 [\[0071\]](#)
- **SCHIER et al.**Gene, 1995, vol. 169, 147-155 [\[0071\]](#)
- **YELTON et al.**J. Immunol., 1995, vol. 155, 1994-2004 [\[0071\]](#)
- **JACKSON et al.**J. Immunol., 1995, vol. 154, 73310-9 [\[0071\]](#)
- **HAWKINS et al.**J. Mol. Biol., 1992, vol. 226, 889-896 [\[0071\]](#)
- Remington: The Science and practice of PharmacyLippincott Williams and Wilkins20000000 [\[0072\]](#)
- **WARD et al.**Nature, 1989, vol. 341, 544-546 [\[0090\]](#)
- **BIRD et al.**Science, 1988, vol. 242, 423-426 [\[0090\]](#)
- **HUSTON et al.**Proc. Natl. Acad. Sci. USA, 1988, vol. 85, 5879-5883 [\[0090\]](#)
- **HOLLIGER et al.**Proc. Natl. Acad. Sci. USA, 1993, vol. 90, 6444-6448 [\[0090\]](#)
- **POLJAK et al.**Structure, 1994, vol. 2, 1121-1123 [\[0090\]](#)
- **KABAT et al.**Sequences of Proteins of Immunological InterestPublic Health Service, National Institutes of Health19910000 [\[0092\]](#) [\[0113\]](#)
- **KABAT et al.**Sequences of Proteins of Immunological Interest19910000 [\[0094\]](#)
- **CHOTHIA et al.**Nature, 1989, vol. 342, 877-883 [\[0094\]](#)
- **MACCALLUM et al.**J. Mol. Biol., 1996, vol. 262, 732-745 [\[0094\]](#)
- **MAKABE et al.**Journal of Biological Chemistry, 2008, vol. 283, 1156-1166 [\[0094\]](#)

P a t e n t k r a v

5 **1.** Isoleret antistof eller antigen-bindende fragment deraf, som specifikt binder human IFN β , omfattende en VH, der omfatter aminosyresekvensen af SEQ ID NO: 28, og VL, der omfatter aminosyresekvensen SEQ ID NO: 1.

2. Isoleret nukleinsyremolekyle, som omfatter en nukleotidsekvens, der koder for antistoffet eller antigenbindende fragment deraf ifølge krav 1.

10 **3.** Isoleret nukleinsyremolekyle ifølge krav 2, omfattende nukleotidsekvensen af SEQ ID NO:166 og SEQ ID NO:167

15 **4.** Isoleret nukleinsyremolekyle ifølge krav 2, omfattende nukleotidsekvensen af indsatsen af plasmidet deponeret ved ATCC og med accessionsnummer PTA-122726 og nukleotidsekvensen af indsatsen af plasmidet deponeret ved ATCC og har accessionsnummer PTA-122727.

20 **5.** Vektor omfattende nukleinsyremolekylet ifølge et hvilket som helst af kravene 2 til 4.

6. Værtscelle omfattende nukleinsyremolekylet ifølge et hvilket som helst af kravene 2 til 4 eller vektoren ifølge krav 5.

25 **7.** Fremgangsmåde til fremstilling af et antistof eller antigenbindende fragment deraf, omfattende dyrkning af værtscellen ifølge krav 6, under betingelser, hvor antistoffet eller det antigenbindende fragment deraf produceres af værtscellen.

30 **8.** Farmaceutisk sammensætning omfattende et antistof, eller antigen-bindende fragment deraf, ifølge krav 1, og en farmaceutisk acceptabel excipients.

9. Antistof, eller antigen-bindende fragment deraf, ifølge krav 1, eller den farmaceutiske sammensætning ifølge krav 8, til anvendelse i terapi.

5 **10.** Antistof, eller antigen-bindende fragment deraf, ifølge krav 1, eller den farmaceutiske sammensætning ifølge krav 8, til anvendelse i en fremgangsmåde til behandling af dermatomyositis (DM) eller en fremgangsmåde til behandling af systemisk lupus erythematosus (SLE).

DRAWINGS

FIG. 1

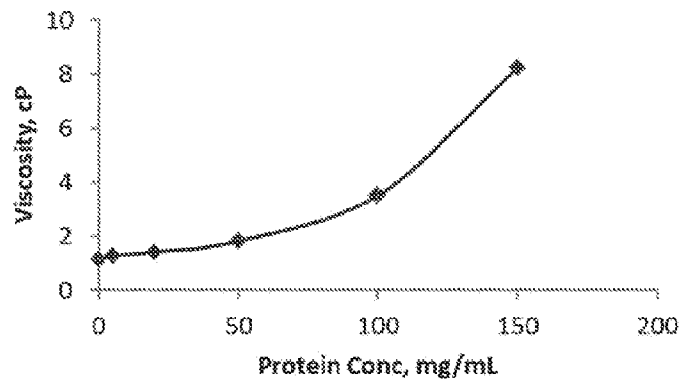
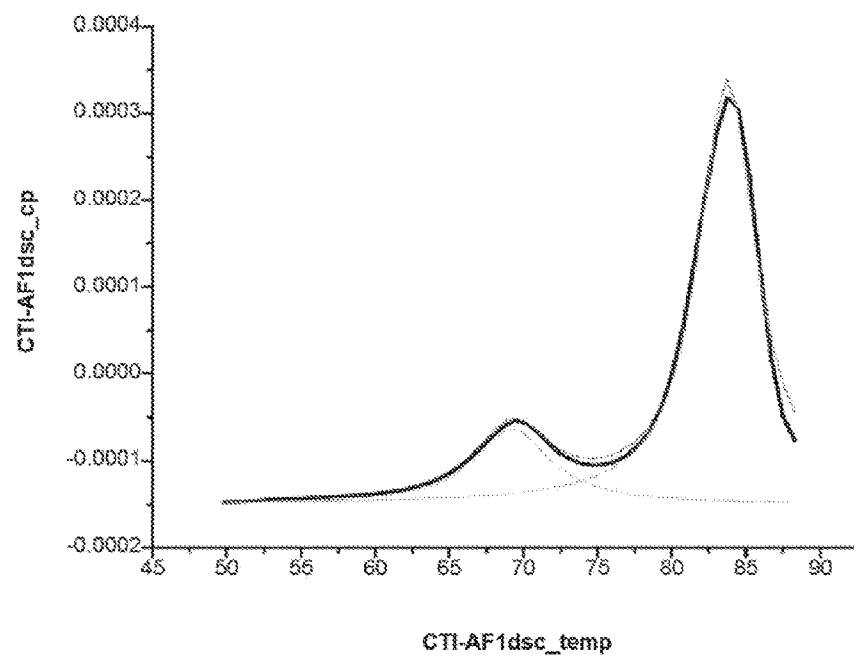


FIG. 2



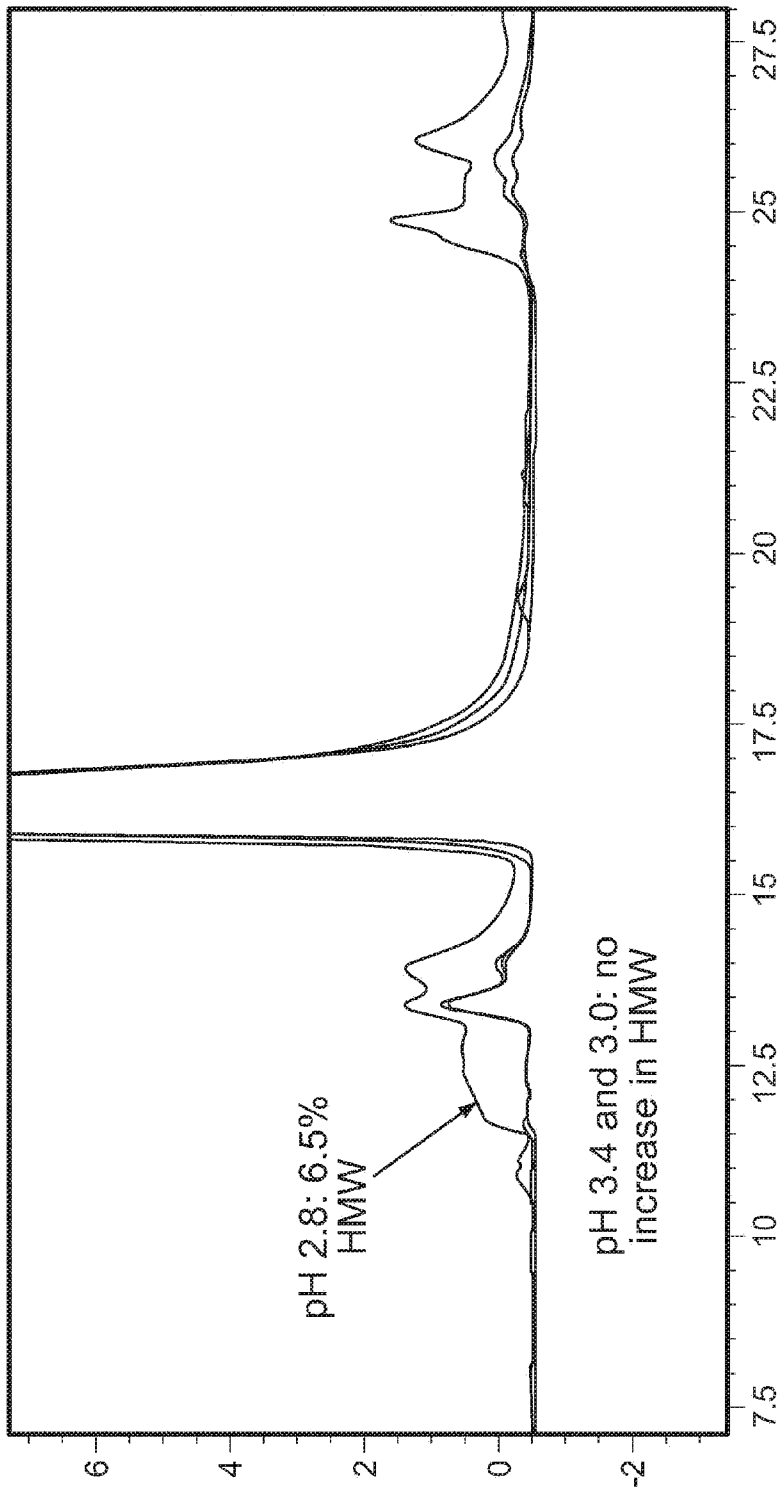
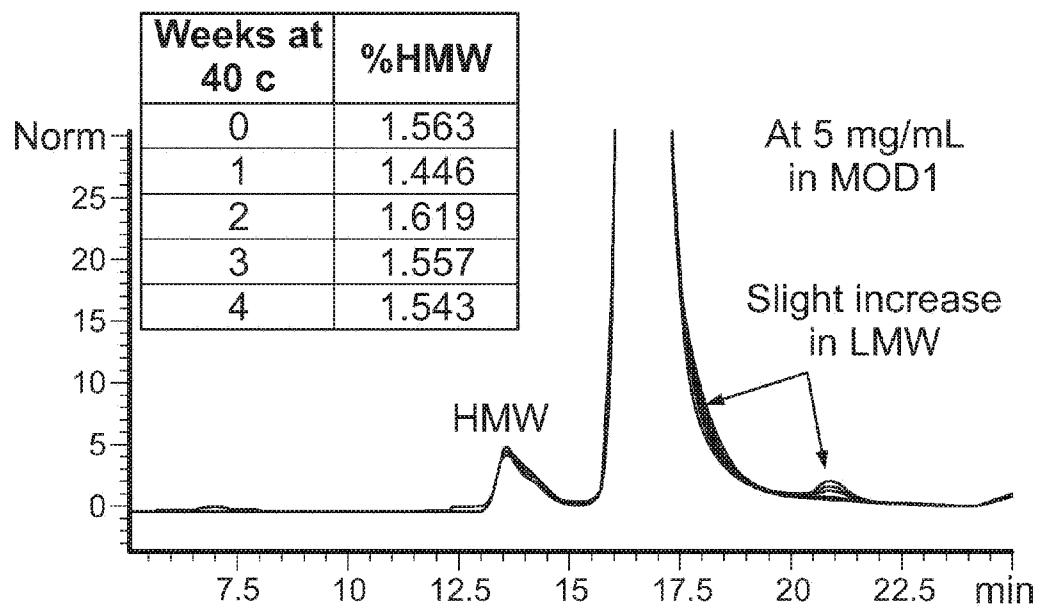
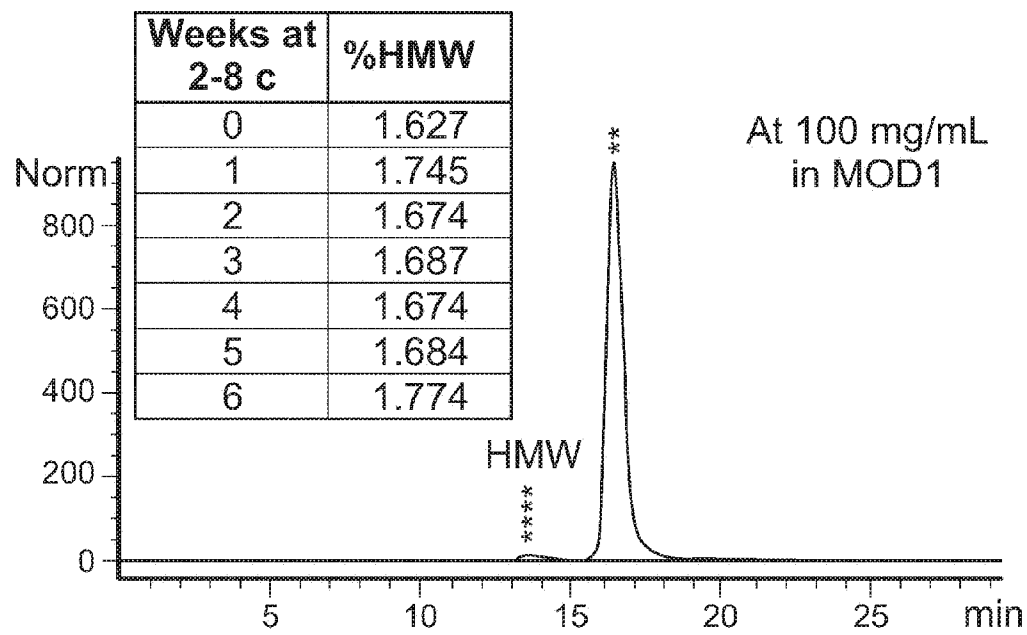


FIG. 3



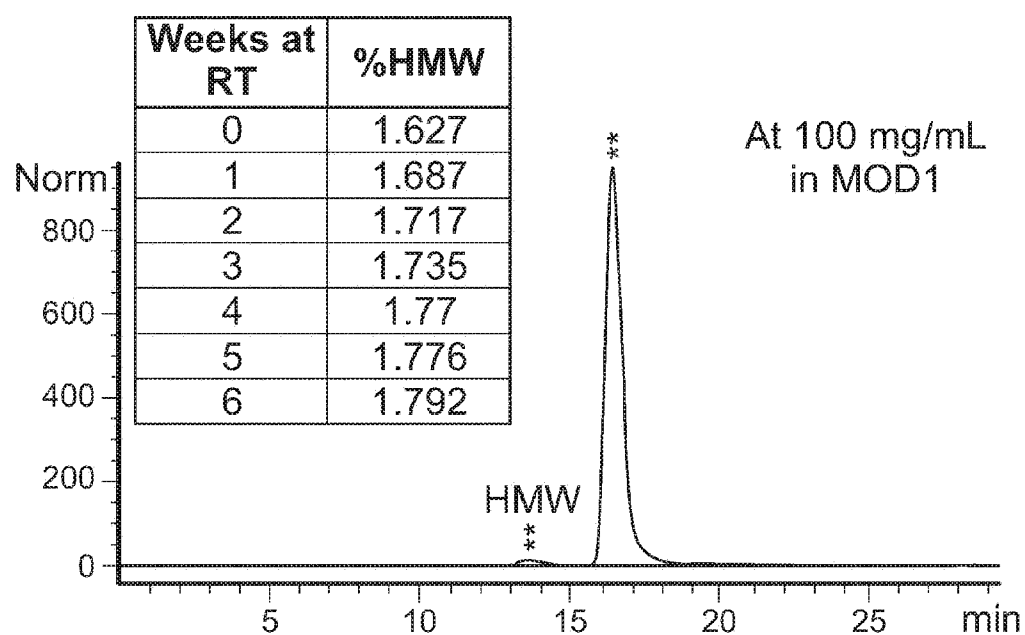


FIG. 4C

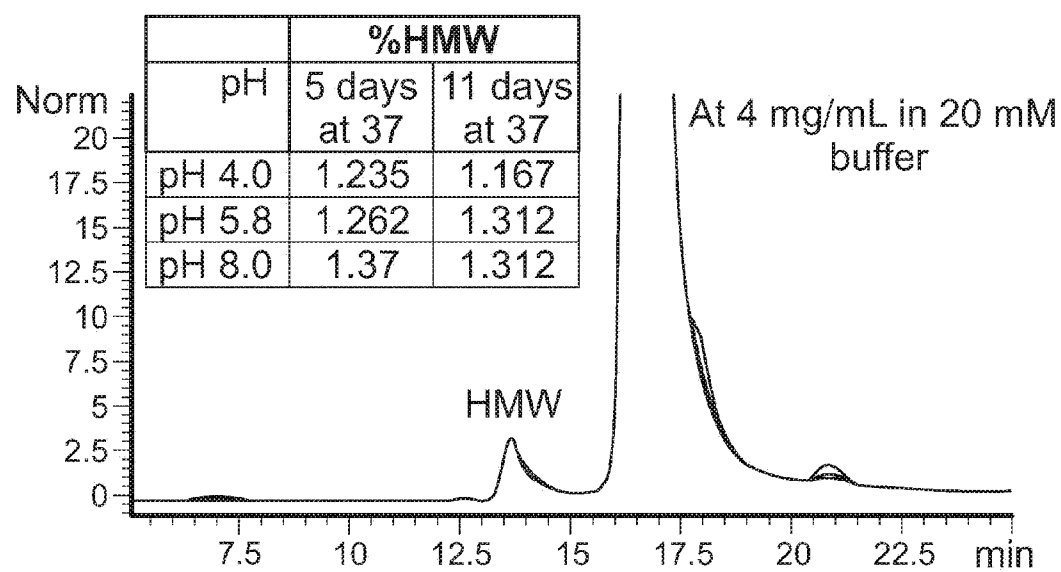


FIG. 4D

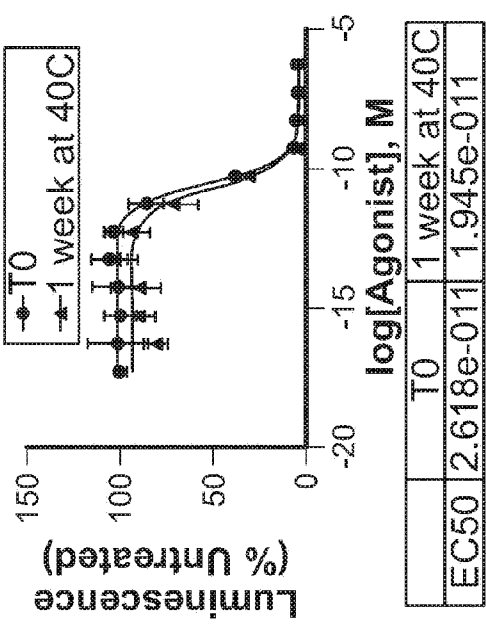


FIG. 5A

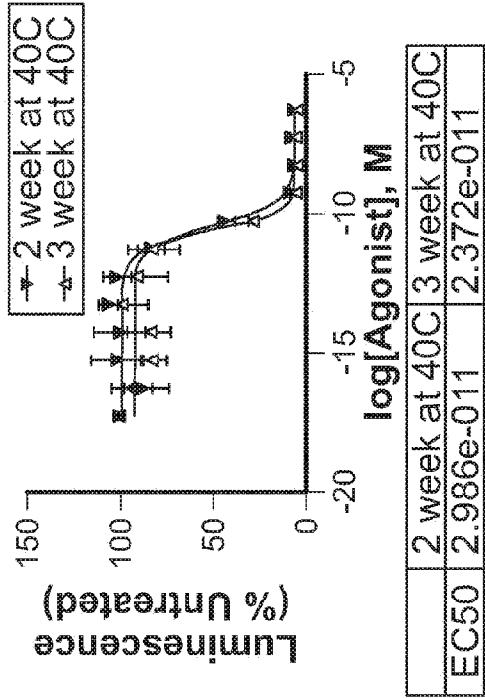


FIG. 5C

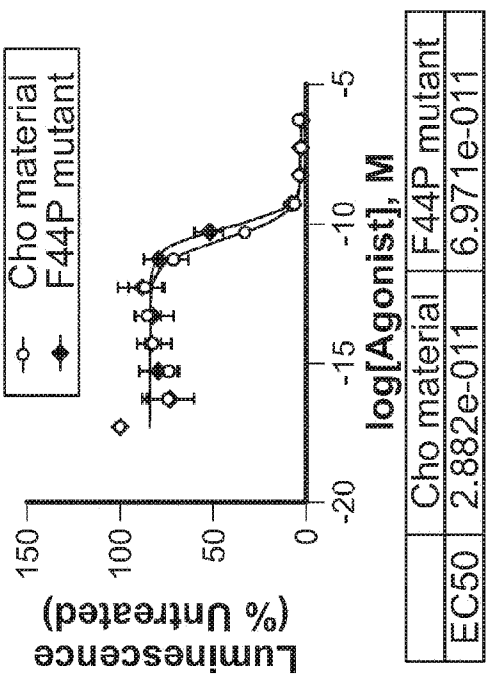


FIG. 5B

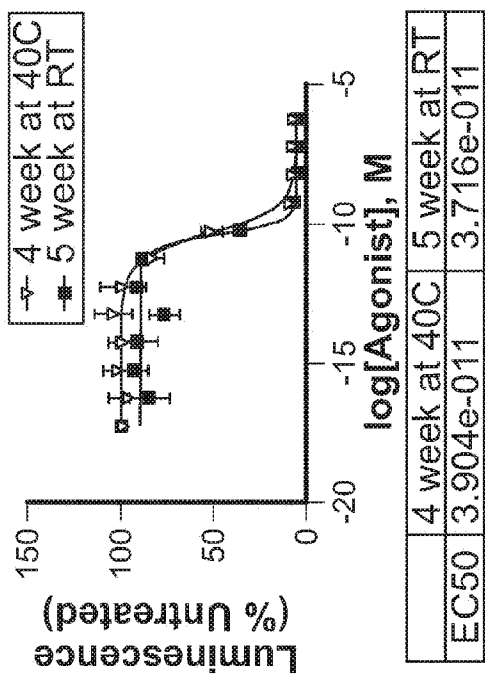


FIG. 5D

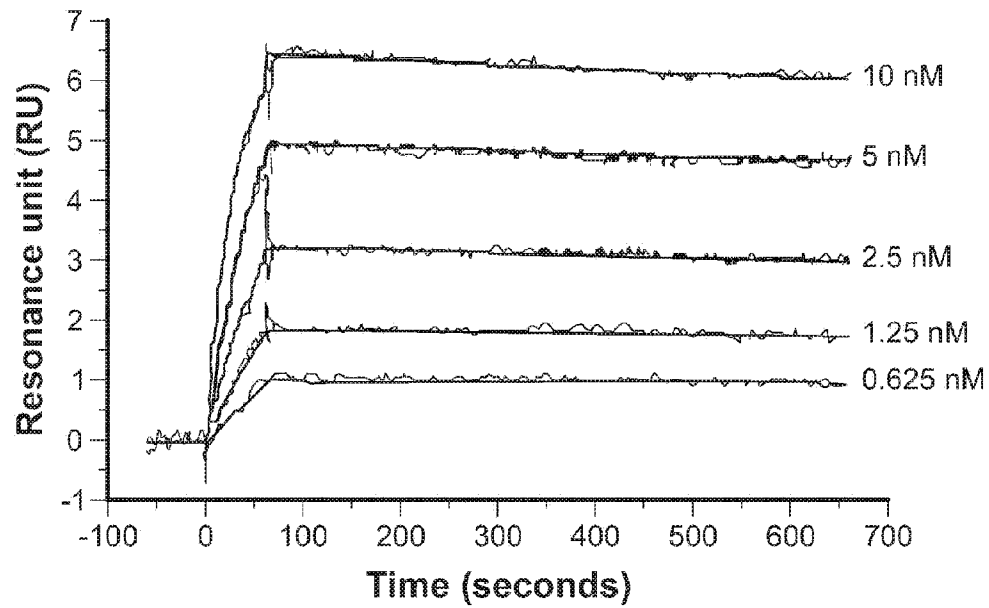
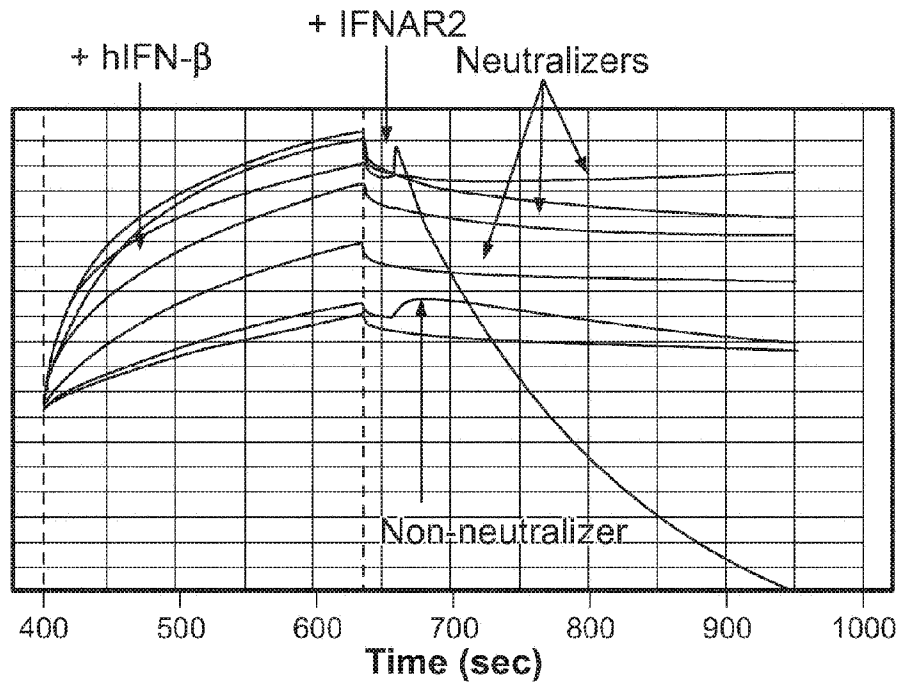


FIG. 8A

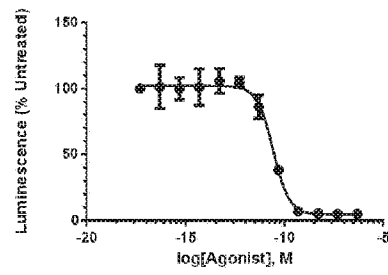


FIG. 8B

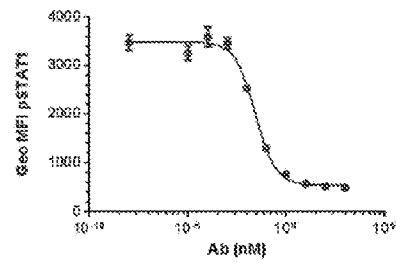
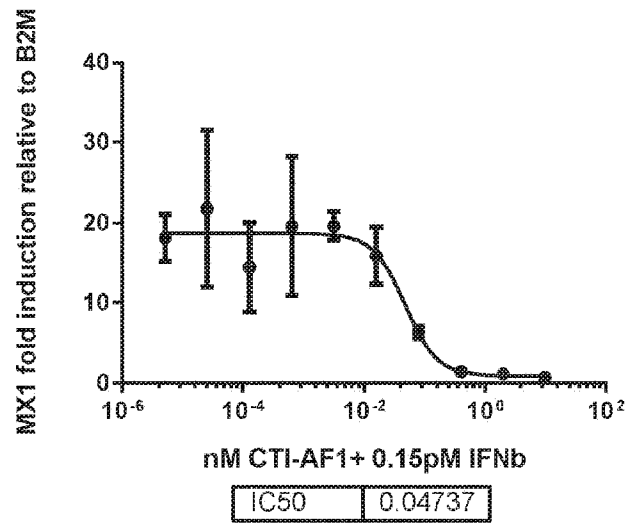


FIG. 9



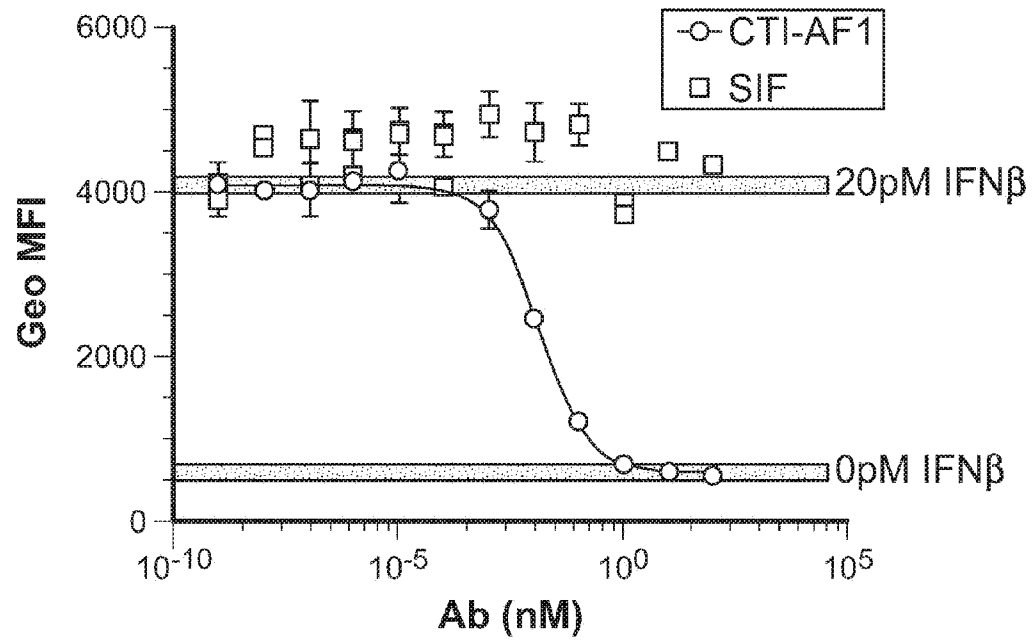


FIG. 10A

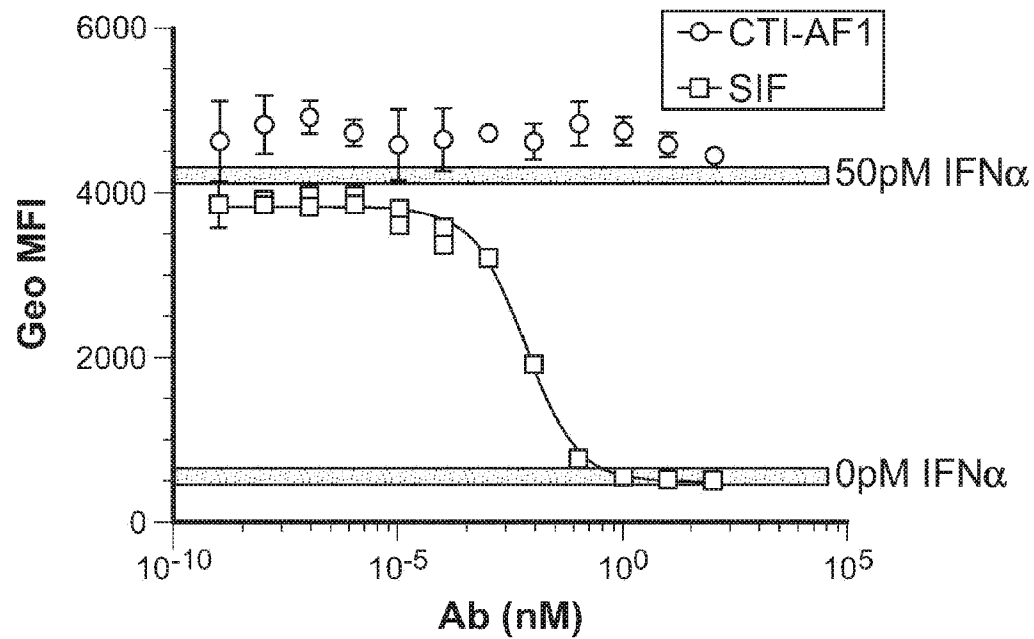
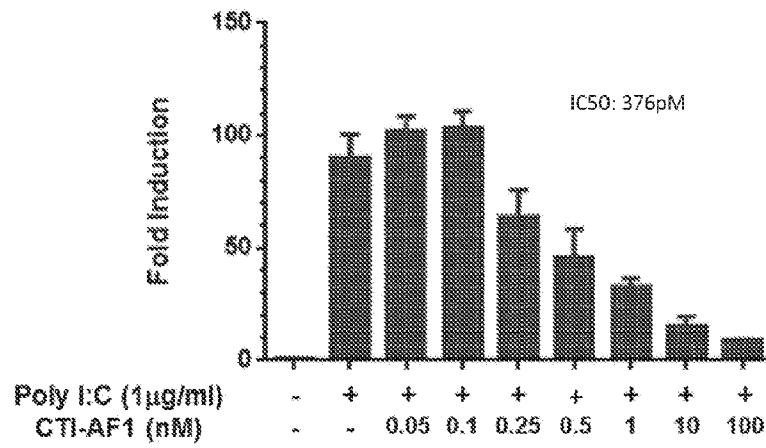


FIG. 10B

FIG. 11



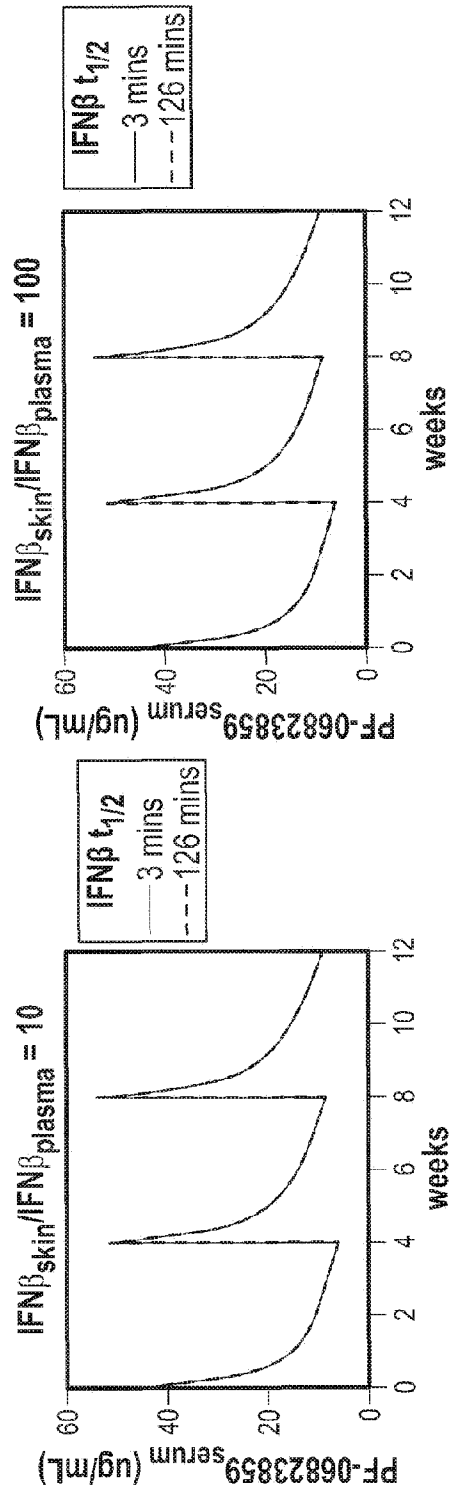


FIG. 12A

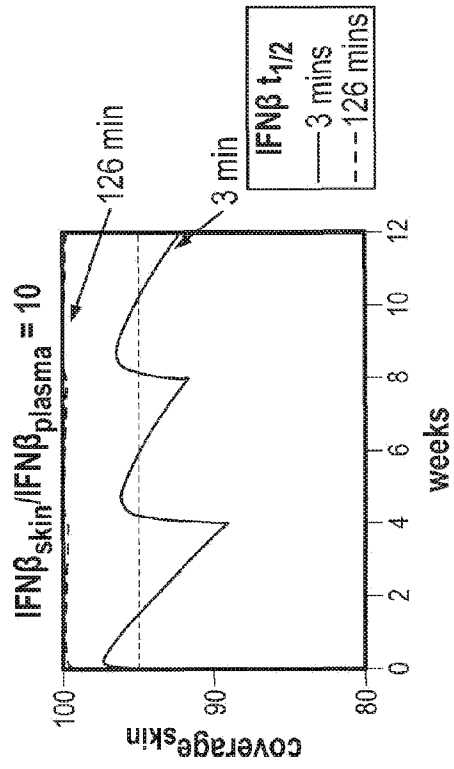


FIG. 12B

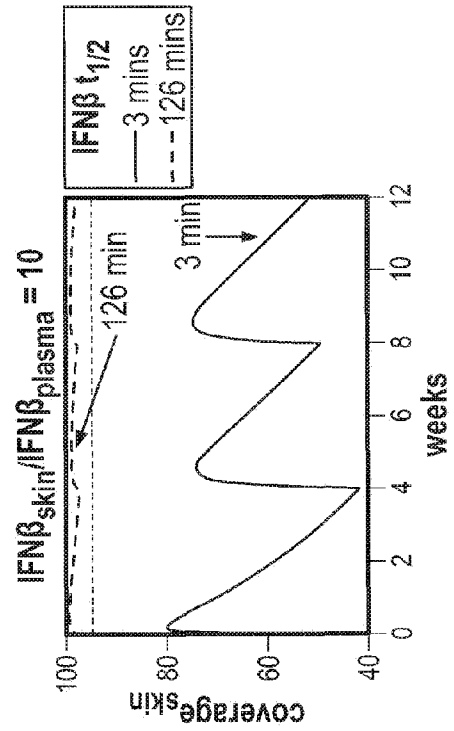


FIG. 12C

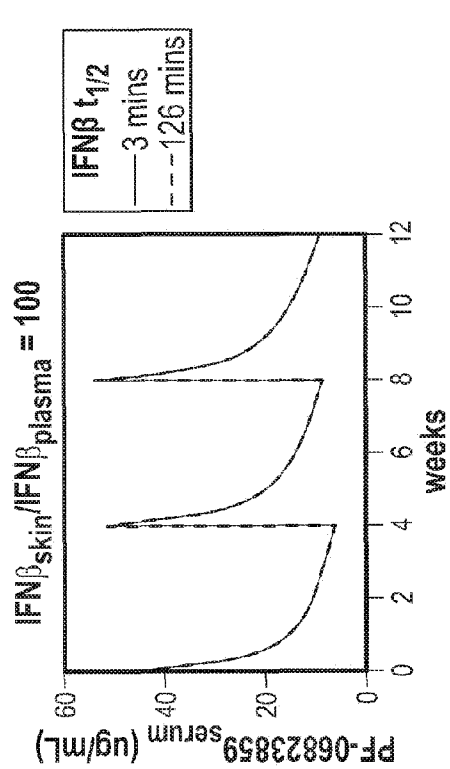


FIG. 12D

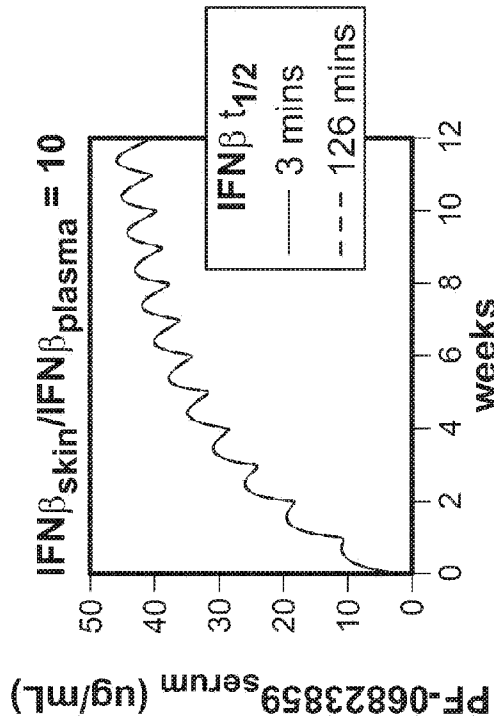


FIG. 13A

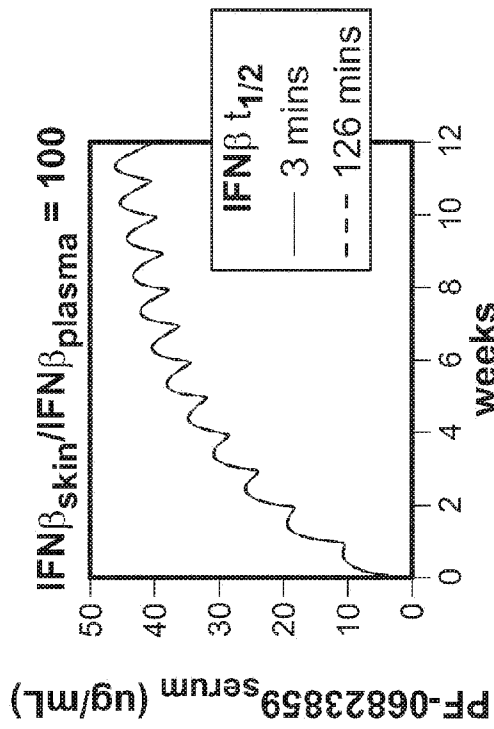


FIG. 13B

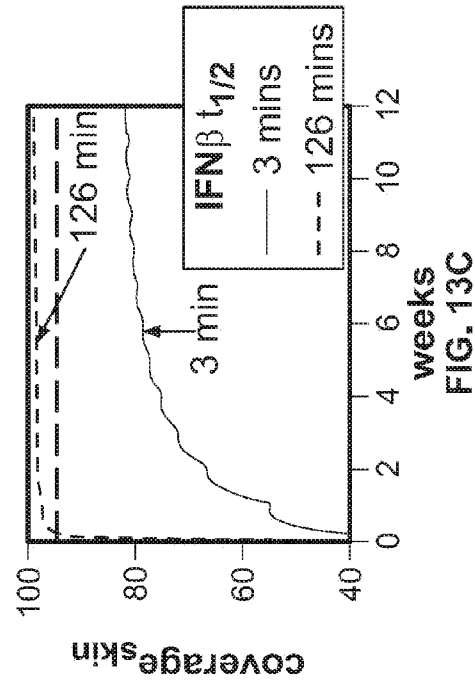


FIG. 13C

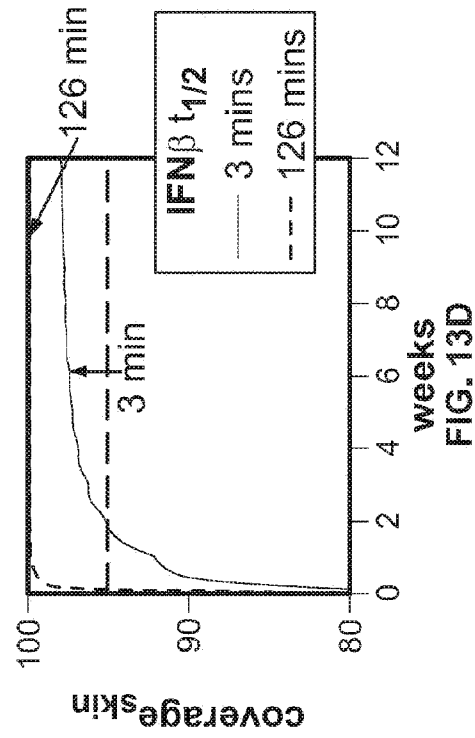
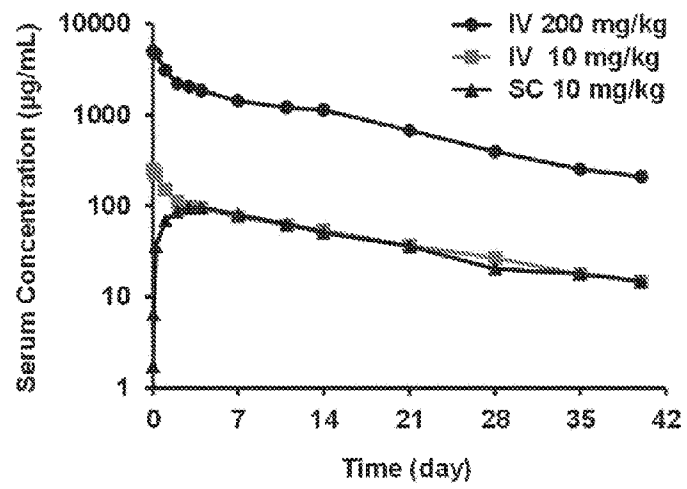


FIG. 13D

FIG. 14



```

10      20      30      40      50
MSYNLLGFLQ RSSNFQCQKL LWQLNGRLEY CLKDRMNFDI PEEIKQLQQF
|-----Helix A-----|-----AB loop-----

60      70      80      90     100
QKEDAALTIY EMLQNIFAIF RQDSSSTGWN ETIVENLLAN VYHQINHLKT
-|-----Helix B-----|---BC loop---|-----Helix C-----

110     120     130     140     150
VLEEKLEKED FTRGKLMSSL HLKRYYGRIL HYLKAKEYSH CAWTIVRVEI
-----|-----CD loop---|-----Helix D-----|---DE-|---Helix E-

160     170
LRNFYFINRL TGYLRN
-----|

```

FIG. 15A

sp P01575 mouse	INVKQLQLQERTNIRKQCQELLEQLNGKIN--LTYRADFKIPMERT--EKMQKSYTAFAIQ
sp P70499 rat	IDYKQLQFRQSTIRTCQKLLRQLNGRLN--LSYRTDFKIPMEVMHPSQMEKSYTAFAIQ
tr G1TTX4 rabbit	MSYNSLQIQLWHGSLTCAKLLQLNGTTEDCLNERINFKVPKEIKEPQQLOKEDTTLVIF
sp P01574 human	MSYNLLGFLORSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQFQKEDAALTIY
sp 077812 cyno	MSYNLLGFLORSSSFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQPQFQKEDAALTIY :.*: *: : * : ** **** : * : * : * : * : : : * : * : * : *
sp P01575 mouse	EMLQNVLVFRNFSSTGWNETIVRLLDELHQQTVFLKTVLEEKQE-ERLTWEMSSTAL
sp P70499 rat	VMLQNVLVFRSNFSSTGWNETIVESLLDELHQQTELLEIILKEKQE-ERLTWVTSTTTL
tr G1TTX4 rabbit	EMLNNIFDIFRKNFSSTGWNETLVENLLGETHLQIHHLKSKINKKVTLE----SIRMNL
sp P01574 human	EMLQNIFAIFRODSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
sp 077812 cyno	EMLQNIYAIFRQDLSSTGWNETIVENLLANVYHQIDHLKTILEEKLEKEDFTRGKFVSSL **.*.: : ** : *****. * ** : : * : * : : * : *
sp P01575 mouse	HLKSYWVRVQRYLKLKMYNSYAWMVVRAEIFRNFLLIIRRLTRNFQN
sp P70499 rat	GLKSYWVRVQRYLKDKKYNYSYAWMVVRAEVFRNFSIILRLNRNFQN
tr G1TTX4 rabbit	RLKSYWIRIMDYLETQYSNCAWKIVQLEIFRNFFSFIIMLIDYL--
sp P01574 human	HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRL
sp 077812 cyno	HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFFFINKLTGYLRN ** ** * : ** : * : ** ** : * : * : * : * : * : * : *

FIG. 15B

FIG. 16A

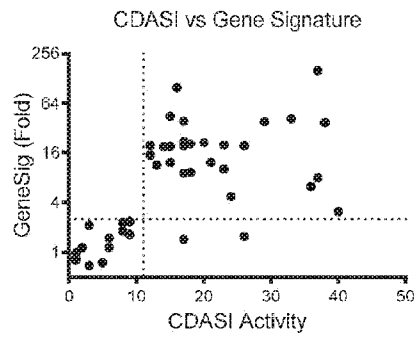


FIG. 16B

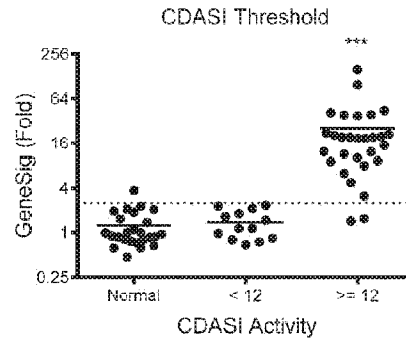


FIG. 17

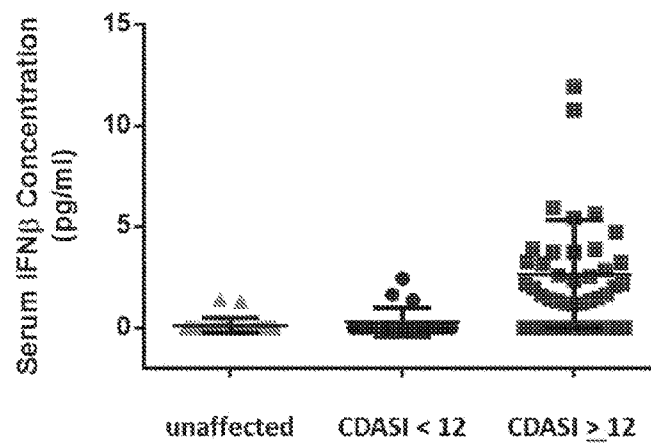


FIG. 18A

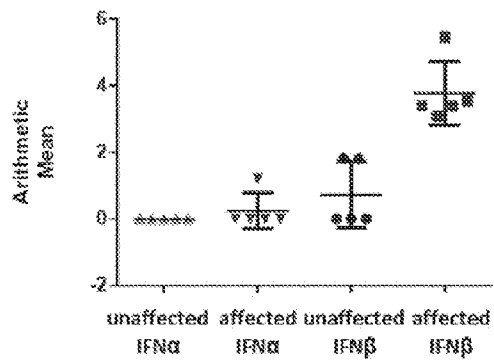


FIG. 18B

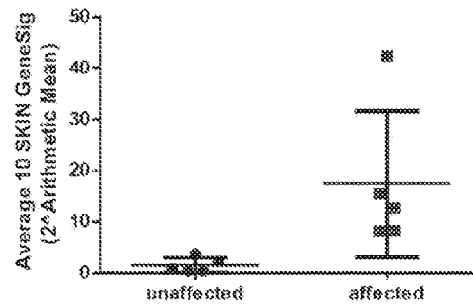
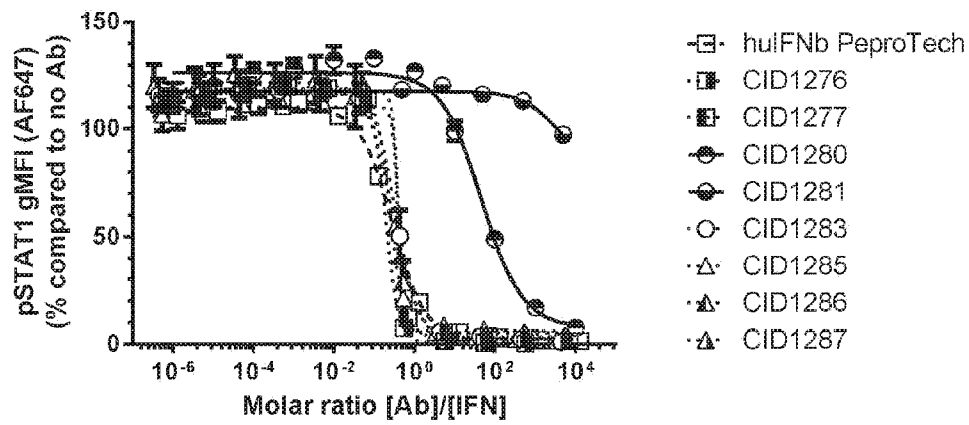


FIG. 19



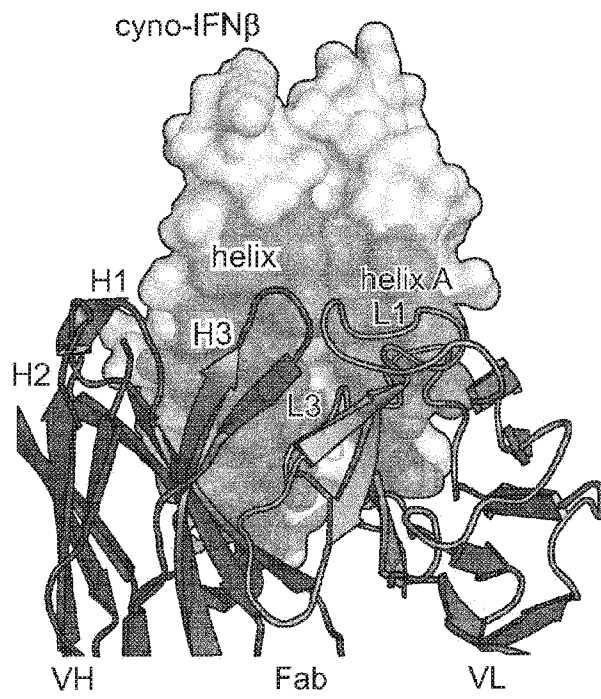


FIG. 20A

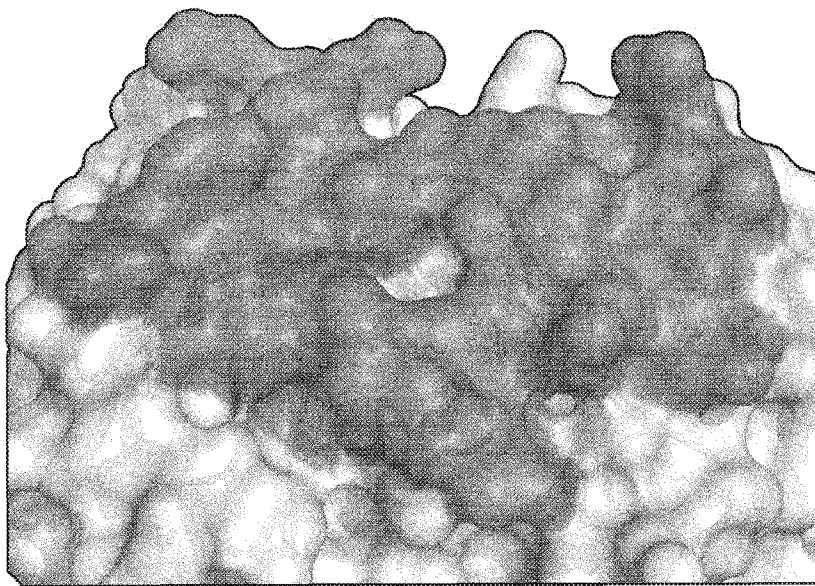


FIG. 20B

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.

