(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
3 October 2013 (03.10.2013)

WIPO | PCT

(10) International Publication Number
WO 2013/149094 A1

(51) International Patent Classification:
C07K 14/495 (2006.01)

(21) International Application Number:
PCT/US2013/034504

(22) International Filing Date:
28 March 2013 (28.03.2013)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
61/616,740 28 March 2012 (28.03.2012) US

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(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

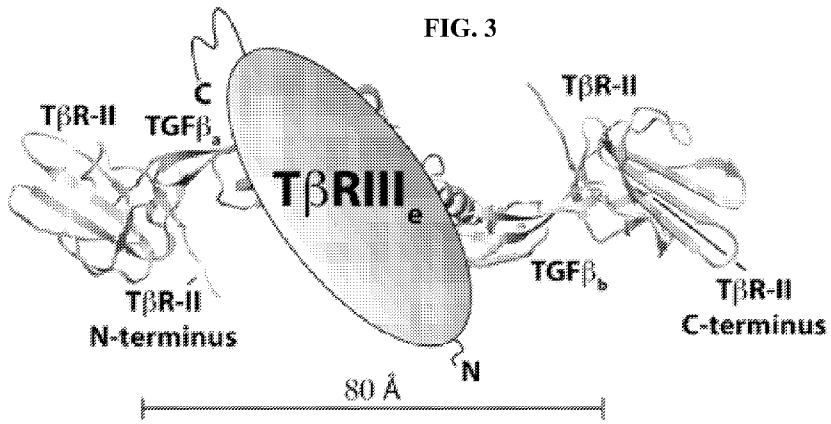
— *with international search report (Art. 21(3))*

— *with sequence listing part of description (Rule 5.2(a))*

WO 2013/149094 A1

(54) Title: TGFβ TYPE II-TYPE III RECEPTOR FUSIONS

FIG. 3



(57) Abstract: Certain embodiments are directed to novel heterotrimeric fusions in which the ectodomain of the TGF-β type II receptor (TβP?II) is coupled to the N- and C-terminal ends of the endoglin-domain of the TGF-β type III receptor (TpRIIIE). Certain embodiments are directed to novel heterotrimeric polypeptides in which the ectodomain of the TGF-β type II receptor (TI3RII) is coupled to the N- and C-terminal ends of the endoglin-domain (E domain) of the TGF-β type III receptor (TI3RIII). This trimeric receptor, known as RER, can bind all three TGF-β isoforms with sub-nanomolar affinity and is effective at neutralizing signaling induced by all three TGF-β isoforms, but not other ligands of the TGF-β superfamily, such as activins, growth and differentiation factors (GDFs), and bone morphonogenetic proteins (BMPs).

TGFβ TYPE II-TYPE III RECEPTOR FUSIONS

DESCRIPTION

STATEMENT REGARDING FEDERALLY FUNDED RESEARCH

[001] This invention was made with government support under CA079683 and GM58670 awarded by the National Cancer Institute and National Institute of General Medical Sciences, respectively. The government has certain rights in the invention.

REFERENCE TO SEQUENCE LISTING

[002] A sequence listing is being submitted electronically with this application. The sequence listing is incorporated herein by reference.

BACKGROUND

[003] Transforming growth factor beta (TGFβ) isoforms (β1, β2, and β3) are homodimeric polypeptides of 25 kDa. They are secreted in a latent form and only a small percentage of total secreted TGFβs are activated under physiological conditions. TGFβ binds to three different cell surface receptors called type I (RI), type II (RII), and type III (RIII) receptors. RI and RII are serine/threonine kinase receptors. RIII (also called betaglycan) has two TGFβ binding sites in its extracellular domain, which are called the E and U domains (BG_E and BG_U, respectively). TGFβ1 and TGFβ3 bind RII with an affinity that is 200-300 fold higher than TGF-β2 (Baardsnes et al., *Biochemistry*, 48, 2146-55, 2009); accordingly, cells deficient in RIII are 200- to 300-fold less responsive to equivalent concentrations of TGF-β2 compared to TGF-β1 and TGFβ-3 (Chiefetz, et al (1990) J. Bio. Chem, 265, 20533-20538). However, in the presence of RIII, cells respond roughly equally to all three TGF-β isoforms, consistent with reports that show that RIII can sequester and present the ligand to RII to augment TGFβ activity when it is membrane-bound (Chen et al., *J. Biol. Chem.* 272, 12862-12867, 1997; Lopez-Casillas et al., *Cell* 73, 1435-1444, 1993; Wang et al., *Cell* 67, 797-805, 1991; Fukushima et al., *J. Biol. Chem.* 268, 22710-22715, 1993; Lopez-Casillas et al., *J. Cell Biol.* 124, 557-568, 1994). Binding of TGFβ to RII recruits and activates RI through phosphorylation (Wrana et al., *Nature* 370, 341-347, 1994). The activated RI

phosphorylates intracellular Smad2 and Smad3, which then interact with Smad4 to regulate gene expression in the nucleus (Piek et al., *FASEB J.* 13, 2105-2124, 1999; Massague and Chen, *Genes & Development* 14, 627-644, 2000). Through its regulation of gene expression, TGFβ has been shown to influence many cellular functions such as cell proliferation, cell differentiation, cell-cell and cell-matrix adhesion, cell motility, and activation of lymphocytes (Massague, *Ann. Rev. Cell Biol.* 6, 597-641, 1990; Roberts and Sporn, The transforming growth factor-betas. In Peptide growth factors and their receptors I, Sporn and Roberts, eds. (Heidelberg: Springer-Verlag), pp. 419-472, 1991). TGFβ has also been shown or implicated in inducing or mediating the progression of many diseases such as osteoporosis, hypertension, atherosclerosis, hepatic cirrhosis and fibrotic diseases of the kidney, liver, and lung (Blobe et al., *N. Engl. J. Med.* 342, 1350-1358, 2000). Perhaps, the most extensively studied function of TGFβ is its role in tumor progression.

[004] TGFβs have been shown to be potent growth inhibitors in various cell types including epithelial cells (Lyons and Moses, *Eur. J. Biochem.* 187, 467-473, 1990). The mechanism of the growth inhibition by TGFβ is mainly due to the regulation of cell cycle-related proteins (Derynck, *Trends. Biochem. Sci.* 19, 548-553, 1994; Miyazono et al., *Semin. Cell Biol.* 5, 389-398, 1994). Thus, aberrant regulation of cell cycle machinery such as loss of retinoblastoma gene product during tumorigenesis can lead to loss of growth inhibition by TGFβ. Furthermore, mutational inactivation of TGFβ receptors, Smad2, and Smad4 has been reported in various carcinomas (Massague et al., *Cell* 103, 295-309, 2000). For example, loss of RI and/or RII expression is often observed in some human gastrointestinal cancers (Markowitz and Roberts, *Cytokine, Growth Factor, Rev.* 7, 93-102, 1996).

[005] While many carcinoma cells lose response to TGFβ's growth inhibition, they often overproduce active TGFβ isoforms when compared to their normal counterpart (Reiss, *Microbes and Infection* 1, 1327-1347, 1999). This is likely to result in the selection of cancer cells that are resistant to TGFβ's growth inhibitory activity. Indeed, an increased level of TGFβ1 is strongly associated with the progression of many types of malignancies and poor clinical outcome (Reiss, *Microbes and Infection* 1, 1327-1347, 1999). For example, serum TGFβ1 levels have been shown to correlate to tumor burden, metastasis, and serum prostate specific antigen (PSA) in prostate cancer patients (Adler et al., *J. Urol.* 161, 182-187, 1999; Shariat et al., *J. Clin. Oncol.* 19, 2856-2864, 2001). Consistent with these observations,

marked increase of TGFβ1 and TGFβ2 expression was observed in an aggressive androgen-independent human prostate cancer cell line when compared to its less aggressive androgen-dependent parent cell line, LNCap (Patel et al., *J. Urol.* 164, 1420-1425, 2000).

[006] Several mechanisms are believed to mediate TGFβ's tumor-promoting activity (Arteaga et al., *Breast Cancer Res. Treat.* 38, 49-56, 1996; Reiss, *Microbes and Infection* 1, 1327-1347, 1999). TGFβ is a potent immune suppressor (Sosroseno and Herminajeng, *Br. J. Biomed. Sci.* 52, 142-148, 1995). Overexpression of TGFβ1 in the rat prostate cancer cells was associated with a reduced immune response during tumor formation suggesting that TGFβ may suppress host immune response to the growing tumor (Lee et al., *Prostate* 39, 285-290, 1999). TGFβ has also been shown to be angiogenic in vivo (Fajardo et al., *Lab. Invest.* 74, 600-608, 1996; Yang and Moses, *J. Cell Biol.* 111, 731-741, 1990; Wang et al., *Proc. Natl. Acad. Sci. U.S.A.* 96, 8483-8488, 1999). Overexpression of TGFβ during cancer progression is often associated with increased angiogenesis and metastasis suggesting that TGFβ may promote metastasis by stimulating tumor blood vessel formation (Roberts and Wakefield, *Proc. Natl. Acad. Sci. U.S.A.* 100, 8621-8623, 2003). TGFβ also plays an important role in promoting bone metastasis of human prostate and breast cancers (Koeneman et al., *Prostate* 39, 246-261, 1999; Yin et al., *J. Clin. Invest* 103, 197-206, 1999). Both TGFβ1 and TGFβ2 are produced by bone tissue, which is the largest source of TGFβ in the body (Bonewald and Mundy, *Clin. Orthop.* 261-276, 1990). The latent TGFβ can be activated by proteases such as PSA and urokinase plasminogen activator, which are abundantly secreted by cancer cells (Koeneman et al., *Prostate* 39, 246-261, 1999). Taken together, TGFβ can act in tumor microenvironment to promote carcinoma growth, angiogenesis, and metastasis.

[007] Because of its involvement in the progression of various diseases, TGFβ has been targeted for the development of novel therapeutic strategies. One way of antagonizing TGFβ activity is to utilize the ectodomain of TGFβ type II receptor or type III receptor (betaglycan (BG)). It has previously been shown that ectopic expression of a soluble RIII (sBG) in human carcinoma cell lines can significantly inhibit tumor growth, angiogenesis, and metastasis when they are inoculated in athymic nude mice (Bandyopadhyay et al., *Cancer Res.* 59, 5041-5046, 1999; Bandyopadhyay et al., *Oncogene* 21, 3541-3551, 2002b). More recently, it has been shown that systemic administration of recombinant sRIII can inhibit the

growth, angiogenesis, and metastasis of the xenografts of human breast carcinoma MDA-MB-231 cells in nude mice (Bandyopadhyay et al., *Cancer Res.* 62, 4690-4695, 2002a). However, the inhibition was only partial. This could be due, in part, to the fact that the cells produced active TGFβ1 and active TGFβ2 and the anti-TGFβ potency of sRIII is 10-fold lower for TGFβ1 than for TGFβ2 (Vilchis-Landeros et al., *Biochem. J.* 355, 215-222, 2001). Interestingly, while the extracellular domain of RII (sRII) has very low affinity for TGFβ2, its affinity for TGFβ1 and TGFβ3 is more than ten times higher than that of sRIII (Lin et al., *J. Biol. Chem.* 270, 2747-2754, 1995; Vilchis-Landeros et al., *Biochem. J.* 355, 215-222, 2001).

[008] While numerous TGFβ antagonists have been prepared and tested, all have less than complete TGFβ isoform inhibiting properties. Thus, there is a need for additional TGFβ antagonists or inhibitors.

SUMMARY

[009] Certain embodiments are directed to novel heterotrimeric polypeptides in which the ectodomain of the TGF-β type II receptor (TβRII) is coupled to the N- and C-terminal ends of the endoglin-domain (E domain) of the TGF-β type III receptor (TβRIII). This trimeric receptor, known as RER, can bind all three TGF-β isoforms with sub-nanomolar affinity and is effective at neutralizing signaling induced by all three TGF-β isoforms, but not other ligands of the TGF-β superfamily, such as activins, growth and differentiation factors (GDFs), and bone morphonogenetic proteins (BMPs). The sub-nanomolar affinity of the fusion, which arises from its ability to contact the TGF-β dimer at three distinct sites, allows it to effectively compete against the endogenous receptors for TGF-β binding. The fusion proteins described herein offer significant potential as a therapeutic agent for treating diseases driven by overexpression of the TGF-β isoforms, such as cancer and fibrosis.

[010] Certain aspects are directed to a heterotrimeric fusion protein comprising (a) an amino terminal segment comprising a first TGFβ binding domain of TGFβ receptor type II, (b) a central segment comprising a endoglin-domain of TGFβ receptor type III, and (c) a carboxy terminal segment comprising a second TGFβ binding domain of TGFβ receptor type II.

[011] An example of a TGFβ type II receptor is provided as SEQ ID NO:6. Amino acids 1 to 567 of SEQ ID NO:6 is a TGFβ receptor type-2 precursor (EC_number=2.7.11.30). The signal peptide is composed of amino acid 1 to 22 of SEQ ID NO:6. The mature peptide includes amino acids 23 to 567 of SEQ ID NO:6. The ectodomain is defined by amino acids 24 to 160 of SEQ ID NO:6 (RII domain). The ectodomain is followed by a transmembrane region that spans amino acids 161 to 187 of SEQ ID NO:6. The amino terminal segment or the carboxy terminal segment of a novel heterotrimeric fusion protein described herein can comprise, independently, an amino acid segment that is 85, 90, 95, 98, or 100% identical, including all values and ranges there between, to amino acids 35, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 55, 60, 65, 70, or 75 to 145, 150, 155, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, or 170 of SEQ ID NO:6, including all values and ranges there between. The polypeptide segment's ability to bind TGFβ can be determined by using standard ligand binding assays known to those of skill in the art. In certain aspects the RII domain comprises point mutations that alter the binding affinity of the RII domain or the binding affinity of a polypeptide comprising an RII domain. In certain aspects amino acid residues 27, 30, 32, 50, 51, 52, 53, 55, 118, and 119 can be altered singly or in various combinations.

[012] An example of a TGFβ type III receptor is provided as SEQ ID NO:7 or SEQ ID NO:8. Amino acids 1 to 23 of SEQ ID NO:7 or 1 to 21 of SEQ ID NO:8 define the signal peptide. Amino acids 24-409 of SEQ ID NO:7 or 21-406 of SEQ ID NO:8 define the endoglin-like domain (E domain or region), amino acids 410 to 783 of SEQ ID NO:7 or 407-780 of SEQ ID NO:8 define the zona pellucida-like domain or uromodulin-like domain (U domain or region), and amino acids 789 to 811 of SEQ ID NO:7 or 786 to 808 of SEQ ID NO:8 define the transmembrane region. The central segment of the trimeric fusion protein can comprise an amino acid segment that is 85, 90, 95, 98, or 100% identical, including all values and ranges there between, to amino acids 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 45, 50, or 60 to 350, 355, 360, 361, 362, 364, 365, 370, 375, 380, 385, 390, 395, 400, 405 or 409 of SEQ ID NO:7 or SEQ ID NO:8, including all values and ranges there between. In certain aspects the E domain comprises point mutations that alter the binding affinity of the E domain or the binding affinity of a polypeptide comprising an E domain. In another embodiment, the central segment of the trimeric fusion protein can comprise an amino acid segment that is 85, 90, 95, 98, or 100% identical, including all values

and ranges there between, to amino acids 405, 410, 415, 420, 425, 430, 440, 445, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, or 550 to 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 690, 700, 710, 720, 730, 740, 750, 760, 770, or 780 of SEQ ID NO:7 or SEQ ID NO:8, including all values and ranges there between. The polypeptide segment's ability to bind TGFβ can be determined by using standard ligand binding assays known to those of skill in the art. In certain aspects amino acid 69, 71, 72, 90, 93, 99, 108, 115, 120, 144, 163, 192, 206, 237, 252, 274, 283, and 336 of SEQ ID NO:7 can be altered singly or in various combinations, or the corresponding amino acids of SEQ ID NO:8.

[013] In certain aspects, the fusion protein can further comprise a linker between the amino terminal segment and the central segment, and/or a linker between the central segment and the carboxy terminal segment. In a further aspect, the linkers can comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more amino acids. In certain aspects, the amino acids of the linker are additional TGFβ receptor type II or type III amino acid sequences. In other aspects, the linkers are not TGFβ receptor type II or type III amino acid sequences, i.e., heterologous linkers.

[014] In certain aspects, the amino terminal segment comprises an amino acid sequence that is 85, 90, 95, 98, or 100% identical to SEQ ID NO:3, including all values and ranges there between.

[015] In a further aspect, the central segment comprises an amino acid sequence that is 85, 90, 95, 98, or 100% identical to SEQ ID NO:4, including all values and ranges there between.

[016] In yet a further aspect, the carboxy terminal segment comprises an amino acid sequence that is 85, 90, 95, 98, or 100% identical to SEQ ID NO:5, including all values and ranges there between.

[017] In certain aspects, the fusion protein has an amino acid sequence that is 85, 90, 95, 98, or 100% identical to SEQ ID NO:2, including all values and ranges there between.

[018] In a further aspect, the fusion protein can further comprise an amino terminal signal sequence. In certain aspects, the fusion protein can further comprise an amino terminal or carboxy terminal tag. In certain aspects the tag is hexa-histidine.

[019] A peptide tag as used herein refers to a peptide sequence that is attached (for instance through genetic engineering) to another peptide or a protein, to provide a function to the resultant fusion. Peptide tags are usually relatively short in comparison to a protein to which they are fused; by way of example, peptide tags are four or more amino acids in length, such as, 5, 6, 7, 8, 9, 10, 15, 20, or 25 or more amino acids. Usually a peptide tag will be no more than about 100 amino acids in length, and may be no more than about 75, no more than about 50, no more than about 40, or no more than about 30.

[020] Peptide tags confer one or more different functions to a fusion protein (thereby "functionalizing" that protein), and such functions can include (but are not limited to) antibody binding (an epitope tag), purification, translocation, targeting, and differentiation (e.g., from a native protein). In addition, a recognition site for a protease, for which a binding antibody is known, can be used as a specifically cleavable epitope tag. The use of such a cleavable tag can provide selective cleavage and activation of a protein. Alternatively the system developed by in the Dowdy laboratory (Vocero-Akbani et al, Nat Med. 5:29-33, 1999) could be use to provide specificity of such cleavage and activation.

[021] Detection of the tagged molecule can be achieved using a number of different techniques. These include: immunohistochemistry, immunoprecipitation, flow cytometry, immunofluorescence microscopy, ELISA, immunoblotting ("western"), and affinity chromatography.

[022] Epitope tags add a known epitope (antibody binding site) on the subject protein, to provide binding of a known and often high-affinity antibody, and thereby allowing one to specifically identify and track the tagged protein that has been added to a living organism or to cultured cells. Examples of epitope tags include the myc, T7, GST, GFP, HA (hemagglutinin) and FLAG tags. The first four examples are epitopes derived from existing molecules. In contrast, FLAG is a synthetic epitope tag designed for high antigenicity (see, e.g., U.S. Pat. Nos. 4,703,004 and 4,851,341).

[023] Purification tags are used to permit easy purification of the tagged protein, such as by affinity chromatography. A well-known purification tag is the hexa-histidine (6x His) tag, literally a sequence of six histidine residues. The 6x His protein purification system is available commercially from QIAGEN (Valencia, Calif.), under the name of QIAexpress®.

[024] Certain embodiments are directed to the therapeutic use of the fusions proteins described herein. Certain aspects are directed to a method of treating a TGFβ related condition comprising administering an effective amount of a fusion protein described herein. The fusion protein can be administered to a subject, such as a mammal. The mammal being treated may have or may be at risk for one or more conditions associated with an excess of TGF-β for which a reduction in TGF-β levels may be desirable. Such conditions include, but are not limited to, fibrotic diseases (such as glomerulonephritis, neural scarring, dermal scarring, pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis), lung fibrosis, radiation-induced fibrosis, hepatic fibrosis, myelofibrosis), peritoneal adhesions, hyperproliferative diseases (e.g., cancer), burns, immune-mediated diseases, inflammatory diseases (including rheumatoid arthritis), transplant rejection, Dupuytren's contracture, and gastric ulcers. In certain aspects the fusion protein is administer intravascularly.

[025] Other terms related to the description provided herein include:

[026] The term "receptor" denotes a cell-associated protein that binds to a bioactive molecule (i.e., a ligand) and mediates the effect of the ligand on the cell. Membrane-bound receptors are characterized by a multi-domain structure comprising an extracellular ligand-binding domain and an intracellular effector domain that is typically involved in signal transduction.

[027] By "multimeric" or "heteromultimeric" is meant comprising two or more different subunits. A "heterodimeric" receptor contains two different subunits, wherein a "heterotrimeric" molecule comprises three subunits.

[028] By "soluble" multimeric receptor is meant herein a multimeric receptor, each of whose subunits comprises part or all of an extracellular domain of a receptor, but lacks part or all of any transmembrane domain, and lacks all of any intracellular domain. In general, a soluble receptor of the invention is soluble in an aqueous solution.

[029] A "fusion" protein is a protein comprising two polypeptide segments linked by a peptide bond, produced, e.g., by recombinant processes.

[030] As used herein, a "variant" polypeptide of a parent or wild-type polypeptide contains one or more amino acid substitutions, deletions and/or additions as compared to the parent or wild-type. Typically, such variants have a sequence identity to the parent or wild-type sequence of at least about 90%, at least about 95%, at least about 96%, at least about 97%, 98%, or at least about 99%, and have preserved or improved properties as compared to the parent or wild-type polypeptide. Some changes may not significantly affect the folding or activity of the protein or polypeptide; conservative amino acid substitutions, as are well known in the art, changing one amino acid to one having a side-chain with similar physicochemical properties (basic amino acid: arginine, lysine, and histidine; acidic amino acids: glutamic acid, and aspartic acid; polar amino acids: glutamine and asparagine; hydrophobic amino acids: leucine, isoleucine, valine; aromatic amino acids: phenylalanine, tryptophan, tyrosine; small amino acids: glycine, alanine, serine, threonine, methionine), small deletions, typically of one to about 30 amino acids; and small amino- or carboxyl-terminal extensions, such as an amino-terminal methionine residue, a small linker peptide of up to about 20-25 residues, or a small extension that facilitates purification (an affinity tag), such as a poly-histidine tract, protein A (Nilsson et al., EMBO 1985;14:1075 et seq.; Nilsson et al., Methods Enzymol. 1991; 198:3 et seq.), glutathione S-transferase (Smith and Johnson, Gene 1988;67:31 et seq.), or other antigenic:epitope or binding domain. See, in general Ford et al., Protein Expression and Purification 1991;2:95-107. DNAs encoding affinity tags are available from commercial suppliers.

[031] Sequence differences or "identity," in the context of amino acid sequences, can be determined by any suitable technique, such as (and as one suitable selection in the context of this invention) by employing a Needleman-Wunsch alignment analysis (see Needleman and Wunsch, *J. Mol. Biol.* (1970) 48:443453), such as is provided via analysis with ALIGN 2.0 using the BLOSUM50 scoring matrix with an initial gap penalty of −12 and an extension penalty of −2 (see Myers and Miller, CABIOS (1989) 4:11-17 for discussion of the global alignment techniques incorporated in the ALIGN program). A copy of the ALIGN 2.0 program is available, e.g., through the San Diego Supercomputer (SDSC) Biology Workbench. Because Needleman-Wunsch alignment provides an overall or global identity

measurement between two sequences, it should be recognized that target sequences which may be portions or subsequences of larger peptide sequences may be used in a manner analogous to complete sequences or, alternatively, local alignment values can be used to assess relationships between subsequences, as determined by, e.g., a Smith-Waterman alignment (*J. Mol. Biol.* (1981) 147:195-197), which can be obtained through available programs (other local alignment methods that may be suitable for analyzing identity include programs that apply heuristic local alignment algorithms such as FastA and BLAST programs).

[032] The term "isolated" can refer to a nucleic acid or polypeptide that is substantially free of cellular material, bacterial material, viral material, or culture medium (when produced by recombinant DNA techniques) of their source of origin, or chemical precursors or other chemicals (when chemically synthesized). Moreover, an isolated compound refers to one that can be administered to a subject as an isolated compound; in other words, the compound may not simply be considered "isolated" if it is adhered to a column or embedded in an agarose gel. Moreover, an "isolated nucleic acid fragment" or "isolated peptide" is a nucleic acid or protein fragment that is not naturally occurring as a fragment and/or is not typically in the functional state.

[033] Moieties of the invention, such as polypeptides or peptides may be conjugated or linked covalently or noncovalently to other moieties such as polypeptides, proteins, peptides, supports, fluorescence moieties, or labels. The term "conjugate" is broadly used to define the operative association of one moiety with another agent and is not intended to refer solely to any type of operative association, and is particularly not limited to chemical "conjugation." Recombinant fusion proteins are particularly contemplated.

[034] The term "providing" is used according to its ordinary meaning to indicate "to supply or furnish for use." In some embodiments, the protein is provided directly by administering the protein, while in other embodiments, the protein is effectively provided by administering a nucleic acid that encodes the protein. In certain aspects the invention contemplates compositions comprising various combinations of nucleic acid, antigens, peptides, and/or epitopes.

[035] An effective amount means an amount of active ingredients necessary to treat, ameliorate, or mitigate a disease or a condition related to a disease. In more specific aspects, an effective amount prevents, alleviates, or ameliorates symptoms of disease, or prolongs the survival of the subject being treated, or improves the quality of life of an individual. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any preparation used in the methods of the invention, an effective amount or dose can be estimated initially from in vitro studies, cell culture, and/or animal model assays. For example, a dose can be formulated in animal models to achieve a desired response or circulating fusion protein concentration. Such information can be used to more accurately determine useful doses in humans.

[036] Other embodiments of the invention are discussed throughout this application. Any embodiment discussed with respect to one aspect of the invention applies to other aspects of the invention as well and vice versa. Each embodiment described herein is understood to be embodiments of the invention that are applicable to all aspects of the invention. It is contemplated that any embodiment discussed herein can be implemented with respect to any method or composition of the invention, and vice versa. Furthermore, compositions and kits of the invention can be used to achieve methods of the invention.

[037] The use of the word "a" or "an" when used in conjunction with the term "comprising" in the claims and/or the specification may mean "one," but it is also consistent with the meaning of "one or more," "at least one," and "one or more than one."

[038] Throughout this application, the term "about" is used to indicate that a value includes the standard deviation of error for the device or method being employed to determine the value.

[039] The use of the term "or" in the claims is used to mean "and/or" unless explicitly indicated to refer to alternatives only or the alternatives are mutually exclusive, although the disclosure supports a definition that refers to only alternatives and "and/or."

[040] As used in this specification and claim(s), the words "comprising" (and any form of comprising, such as "comprise" and "comprises"), "having" (and any form of having, such as "have" and "has"), "including" (and any form of including, such as "includes" and

"include") or "containing" (and any form of containing, such as "contains" and "contain") are inclusive or open-ended and do not exclude additional, unrecited elements or method steps.

[041] Other objects, features and advantages of the present invention will become apparent from the following detailed description. It should be understood, however, that the detailed description and the specific examples, while indicating specific embodiments of the invention, are given by way of illustration only, since various changes and modifications within the spirit and scope of the invention will become apparent to those skilled in the art from this detailed description.

DESCRIPTION OF THE DRAWINGS

[042] The following drawings form part of the present specification and are included to further demonstrate certain aspects of the present invention. The invention may be better understood by reference to one or more of these drawings in combination with the detailed description of the specification embodiments presented herein.

[043] **FIG. 1.** SPR sensorgrams in which increasing concentrations of the TβRII and $T\beta RIII_E$ were injected over a SPR sensor surface with immobilized TGF-β2 K25R I92V K94R. The mass normalized sensorgrams are shown in panels a and b; plots of the mass normalized equilibrium response (R_{eq}) as a function of receptor concentration ([Receptor]), along with fits to $R_{eq} = (R_{max} \times [Receptor])/(K_d + [Receptor])$, are shown in panel c.

[044] **FIG. 2.** SPR sensorgrams in which increasing concentrations of the TGF-β type II receptor ectodomain were injected over immobilized TGF-β2 K25R I92V K94R in the absence (panel a) or presence (panel b) of a saturating concentration (800 nM) of the TGF-β type III receptor endoglin domain. Plots of the mass normalized equilibrium response (R_{eq}) as a function of receptor concentration ([Receptor]), along with fits to $R_{eq} = (R_{max} \times [Receptor])/(K_d + [Receptor])$, are shown in panel c.

[045] **FIG. 3.** Schematic diagram of the TGFβ:TβRII complex with the TGFβ type III receptor endoglin domain positioned in a manner that it does not sterically overlap with either of the two bound TβRII molecules. The locations on the TβRII N- and C-termini are shown.

[046] **FIG. 4.** SPR sensorgrams in which increasing concentrations of ER and RER were injected over SPR surfaces with immobilized TGF-β1, -β2, and –β3. The concentrations of injected receptor range from 10 nM downward (in two-fold increments).

[047] **FIG. 5.** SPR competition binding data in which increasing concentrations of TβRII (R), $T\beta RIII_E$-TβRII (ER), and TβRII-$T\beta RIII_E$-TβRII (RER) were pre-incubated with 0.8 nM TGF-β3 for 16 h and then injected over a high-density (20000 RU) SPR surface with the TGF-β monoclonal antibody 1D11. Data is presented in terms of the initial slope (which is directly proportional to the concentration of free TGF-β) as a function of the competitor (R, ER, or RER) concentration. Two independent measurements were performed for each of the receptor constructs studied (designated by the –a and –b suffices in the legend).

[048] **FIG. 6.** Average IC_{50} using Mv1Lu PAI1 luciferase reporter cells in 96-well plates. Assays were performed using a four-fold receptor fusion and 1D11 (neutralizing antibody) dilution series and 20 pM TGF-beta 1, 2, or 3 at 37° overnight.

[049] **FIGs. 7A-7C.** Neutralization curves comparing various traps (RR (RII-RII), RER (RII-BG_E-RII), ER (BG_E-RII), REU (RII-BG_E-BG_U, or alternatively RII-RIII), or EU (BG_E-BG_U, or alternatively RIII) and 1D11 for (A) TGF-β1, (B) TGF-β2, or TGF-β3.

[050] **FIGs. 8A-8C.** Neutralization curves for various RER preparations relative to (A) TGF-β1, (B) TGF-β2, or (c) TGF-β3

DESCRIPTION

[051] As discussed above, transforming growth factor beta (TGFβ) isoforms (β1, β2, and β3) are homodimeric polypeptides of 25 kDa. TGF-β has nine cysteine residues that are conserved among its family; eight cysteines form four disulfide bonds within the molecule, three of which form a cystine knot structure characteristic of the TGF-β superfamily, while the ninth cysteine forms a disulfide bond with the ninth cysteine of another TGF-β molecule to produce the dimer.

[052] Though a number of TGF-β inhibitors have been reported, none have been approved for clinical use. The novel TGF-β inhibitor described herein - RER – can be

produced by artificially fusing together the binding domains of the TGFβ type II receptor and and the endoglin domain of the type III receptor. The design of RER – a heterotrimeric fusion in which the ectodomain of the TGF-β type II receptor (R) has been artificially fused onto the N- and C-termini of the endoglin-like domain of the TGF-β type III receptor (E) – was conceived based on the structures of the TGF-βs bound to the their signaling receptors, TβRI and TβRII, and the results of surface plasmon resonance (SPR) binding studies which showed that:

[053] 1. The TGF-β type III receptor endoglin domain binds TGF-β dimers with a stoichiometry of 1:1. This was shown by comparing the maximal mass-normalized SPR response as increasing concentrations of the purified TGF-β type II receptor ectodomain (TβRII or R) and purified TGF-β type III receptor endoglin-like domain ($T\beta RIII_E$ or E) were injected over immobilized TGF-β2 K25R I92V K94R, a variant of TGF-β2 that binds TβRII with high affinity (FIG. 1A and 1B) (De Crescenzo et al. *J Mol Biol.* 355, 47-62, 2006; Baardsnes et al. *Biochemistry* 48, 2146-55, 2009). The maximal mass-normalized response for $T\beta RIII_E$ was found to be approximately one-half of that for TβRII, allowing the inventors to infer that $T\beta RIII_E$ must bind the TGF-β dimer with 1:1 stoichiometry since it is well established through structural studies that TβRII binds TGF-β dimers with 2:1 stoichiometry (FIG. 1C) (Hart et al., *Nat Struct Biol.* 9, 203-8, 2002; Groppe et al., *Mol Cell* 29, 157-68, 2008; Radaev et al., *Journal of Biological Chemistry* 285, 14806-14, 2010).

[054] 2. $T\beta RIII_E$ binds TGF-β dimers without displacing either of the two bound TβRIIs. This was shown by performing an SPR experiment in which increasing concentrations of TβRII were injected over immobilized TGF-β2 K25R I92V K94R in the absence or presence of a saturating concentration of $T\beta RIII_E$ (800 nM) (FIG. 2A and 2B). The data showed that the maximal mass normalized binding response for TβRII was slightly increased in the presence of 800 nM $T\beta RIII_E$ (FIG. 2C), showing that the two receptors do not compete with one another for binding TGF-β (it is impossible for more than two TβRIIs to bind the TGF-β dimer, and thus the increase in the maximal amplitude is likely caused by an experimental artifact, such as a mismatch in the concentrations of $T\beta RIII_E$ in the TβRII samples that were injected and the buffer).

[055] Together, these observations suggest that TGF-β dimers are capable of forming a heterotrimeric complex in which each TGF-β dimer binds two molecules of TβRII and one molecule of $T\beta RIII_E$. The structure of the TGF-β bound to TβRII has been reported (Hart et al., *Nat Struct Biol.* 9, 203-8, 2002; Groppe et al., *Mol Cell* 29, 157-68, 2008; Radaev et al., *Journal of Biological Chemistry* 285, 14806-14, 2010), but the structure of $T\beta RIII_E$, either alone or bound to TGF-β, has not. This has led to the hybrid structure where the precise structure of $T\beta RIII_E$ is not known, but its overall positioning between the two bound TβRIIs on the distal ends of the TGF-β dimer is known (FIG. 3).

[056] This hybrid model for binding of TβRII and $T\beta RIII_E$ led to the construction of the heterotrimeric RER (TβRII-$T\beta RIII_E$-TβRII) fusion as a novel inhibitor for binding and sequestering TGF-β. The inclusion of an additional binding domain enhanced the affinity of the fusion for the TGF-βs, especially TGF-β1 and TGF-β3, which bind TβRII with high (K_d ~ 120 nM) affinity (Baardsnes et al. *Biochemistry* 48, 2146-55, 2009; Radaev et al., *Journal of Biological Chemistry* 285, 14806-14, 2010).

[057] In comparison to the currently described RER, Genzyme's monoclonal antibody GC1008 (the humanized version of the mouse monoclonal antibody 1D11) has been shown to bind the three TGF-β isoforms with a K_d of approximately 5 – 10 nM (Grütter, et. al., *PNAS U.S.A.* 105(51): 20251-56, 2008), but it has not proven to be very effective in clinical trials for malignant melanoma and renal cell carcinoma. The reason for the lack of effectiveness might be that GC1008 does not bind the TGF-βs tightly enough to compete against the cell surface TGF-β receptors, which bind the TGF-βs at picomolar to sub-picomolar concentrations.

[058] The polypeptides described herein include high affinity heterotrimeric TGF-β inhibitors, such as RER. As described above RER has been shown to bind all three TGF-β isoforms with low nanomolar affinity to sub-nanomolar affinity. RER is more potent than the monoclonal antibody 1D11. Thus, owing to its enhanced affinity for binding TGF-β, RER more effectively competes against the cell surface receptors for binding TGF-β, and in turn blocking its disease-promoting properties in cancer and fibrosis for example.

[059] An example of an RER amino acid sequence (for example see SEQ ID NO:2) has one or more of the following features:

[060] 1. In certain aspects the TβRII sequence is human (SEQ ID NO:6), while the $T\beta RIII_E$ sequence can be rat (SEQ ID NO:7). In certain aspects the $T\beta RIII_E$ sequence can be human (SEQ ID NO:8).

[061] 2. In certain embodiments the N-terminal TβRII sequence of RER extends from residue 42 – 160 of SEQ ID NO:6, while the C-terminal TβRII sequence of RER extends from residue 48 – 160 of SEQ ID NO:6.

[062] 3. In certain embodiments the $T\beta RIII_E$ sequence extends from residue 24 – 383 of SEQ ID NO:7. In certain aspects, the $T\beta RIII_E$ sequence includes 1, 2, 3, and/or 4 single amino acid substitutions relative to the wild type rat sequence (SEQ ID NO:7), R58H, H116R, C278S, and N337A.

[063] 4. In certain embodiments there is no linker between $T\beta RIII_E$ and the C-terminal TβRII domain. In other aspects a Lys-Leu dipeptide encoded by the HindIII restriction site used to join the corresponding DNA fragments together forms a linker. It is contemplated that any dipeptide can be used.

[064] 5. In certain embodiments there is an 18 amino acid linker with the sequence Gly–Leu-Gly-Pro-Val-Glu-Ser-Ser-Pro-Gly-His-Gly-Leu-Asp-Thr-Ala-Ala-Ala (SEQ ID NO:9) that links the C-terminus of the N-terminal TβRII to the N-terminus of $T\beta RIII_E$.

[065] 6. In certain embodiments there is a C-terminal hexa-histidine tag (for purification purposes).

[066] In one example, an RER expression cassette was inserted downstream of the albumin signal peptide and an engineered NotI cloning site with the sequence Met-Lys-Trp-Val-Thr-Phe-Leu-Leu-Leu-Leu-Phe-Ile-Ser-Gly-Ser-Ala-Phe-Ser-Ala-Ala-Ala (SEQ ID NO:10). The entire albumin signal peptide was placed downstream of the CMV promoter in a modified form of pcDNA3.1 (Invitrogen) as previously described (Zou and Sun, *Cell* 134, 215-30, 2004).

[067] A plasmid expressing RER construct was transfected into CHO Lec 3.2.8.1 cells (Rosenwald et al., *Mol Cell Biol.* 9(3):914-24, 1989) and stable transfectants were selected using MSX (Zou and Sun, *Cell* 134, 215-30, 2004). The stable transfectants were in turn screened for high level expression of the RER fusion by examining the conditioned medium using a polyclonal antibody raised against the rat betaglycan ectodomain. The clone expressing RER at the highest level was expanded and ultimately transferred into serum free medium for production of conditioned medium. The RER was then purified from the conditioned medium by passing it over a NiNTA column, washing it with 25 mM Tris, 100 mM NaCl, and 10 mM imidazole, pH 8 and ultimately by eluting it with the same buffer, but with 300 mM imidazole.

[068] The isolated RER fusion protein was in turn characterized by performing an SPR experiment in which it, together with similarly prepared ER (i.e. the previously described $T\beta RIII_E$–TβRII fusion (Verona et al., *Protein Eng Des Sel.* 21, 463-73, 2008), except produced in CHO cells, not bacteria), was injected over a SPR sensor chip with immobilized TGF-β1, -β2, and -β3. This data showed comparable on-rates, but significantly slower off-rates, especially for TGF-β1 and TGF-β3 (FIG. 4). This qualitatively shows that RER binds the TGF-βs with higher affinity than ER; however, the magnitude of this increase proved to be difficult to quantify since the slow association precluded accurate measurement of the equilibrium SPR response, especially at lower concentrations of injected receptor.

[069] To further evaluate affinity, an SPR competition experiment was performed in which the commercially available TGF-β monoclonal antibody 1D11 (R&D Systems) was coupled to an SPR sensor chip at high density (20000 RU) and in turn increasing concentration of R (TβRII), ER (BG_E-RII), or RER (RII-BG_E-RII) were injected in the presence of a fixed low (0.8 nM) concentration of TGF-β3. The initial slope of these sensorgrams (which is a linear function of the free TGF-β3 concentration) was then plotted as a function of the concentration of the receptor fusion (FIG. 5). This showed that RER is indeed a more potent competitor than ER, consistent with the slower dissociation rate for RER compared to ER.

[070] RER polypeptides demonstrate more potent activity relative to similar fusion proteins. For example the average IC_{50} [nM] using Mv1Lu PAI1 luciferase reporter cells in

96-well plates is markedly lower for RER polypeptides (FIG. 6). Neutralization curves comparing various receptor fusions (RR (RII–RII, also known as T22d35), RER (RII-BG_E-RII), ER (BG_E-RII), REU (RII-BG_E-BG_U or alternatively RII-RIII), or EU (BG_E-BG_U or alternatively RIII) and 1D11 for (A) TGF-β1, (B) TGF-β2, or TGF-β3 also show an improved activity for RER polypeptides (FIG. 7 and FIG. 8).

I. Linkers

[071] In some embodiments, the invention provides a fusion protein comprising three TGF-β binding domains joined to each other directly or by a linker, such as, e.g., a short peptide linker. In some embodiments, the C terminus of the amino terminal TGF-β binding segment is joined by a peptide linker to the N terminus of the central TGF-β binding segment, and the C terminus of the center TGFβ binding segment may be joined to the N terminus of the carboxy TGFβ binding segment by a second linker. A linker is considered short if it contains 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, to 50 or fewer amino acids.

[072] Most typically, the linker is a peptide linker that contains 50 or fewer amino acids, e.g., 45, 40, 35, 30, 25, 20, 15, 10, 9, 8, 7, 6, 5, 3, 4, 2, or 1 amino acid(s). In certain aspects, the sequence of the peptide linker is a non-TGF-β type II or type III receptor amino acid sequence. In other aspects, the sequence of the peptide linker is additional TGF-β type II or type III receptor amino acid sequence, e.g., the 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, to 50 or fewer amino acids flanking the carboxy an/or amino terminal ends of the binding domains. The term additional in this context refers to amino acids in addition to those that define the segments of the heterotrimeric polypeptide as defined above. In various embodiments, the linker does not contain more than 50, 40, 20, 10, or 5 contiguous amino acids from the native receptor sequences. Typically, the linker will be flexible and allow the proper folding of the joined domains. Amino acids that do not have bulky side groups and charged groups are generally preferred (e.g., glycine, serine, alanine, and threonine). Optionally, the linker may additionally contain one or more adaptor amino acids, such as, for example, those produced as a result of the insertion of restriction sites. Generally, there will be no more than 10, 9, 8, 7, 6, 5, 4, 3, 2 adaptor amino acids in a linker.

[073] In some embodiments, the linker comprises one or more glycines, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 15, 18, or more glycines. For example, the linker may consist of (GGG)n, where n = 1, 2, 3, 4, 5, 6, 7, etc. and optional adaptor amino acids. In certain aspects, the linker is a glycine-serine linker which comprises (GGGS)n, where n = 1, 2, 3, 4, 5, etc. In view of the results disclosed herein, the skilled artisan will recognize that any other suitable peptide linker can be used in the fusion proteins of the invention, for example, as described in Alfthan et al., *Protein Eng.* 8:725-31, 1995; Argos, *J. MoI. Biol.* 211:943-58, 1990; Crasto et al., *Protein Eng.*, 13:309-12, 2000; Robinson et al., *PNAS USA*, 95:5929-34, 1998.

II. Nucleic Acids, Vectors, Host Cells

[074] The invention further provides nucleic acids encoding any of the fusion proteins of the invention, vectors comprising such nucleic acids, and host cells comprising such nucleic acids. For example, in an illustrative embodiment, the nucleic acid of the invention comprises the sequence as set forth in SEQ ID NO:1.

[075] Nucleic acids of the invention can be incorporated into a vector, e.g., an expression vector, using standard techniques. The expression vector may then be introduced into host cells using a variety of standard techniques such as liposome-mediated transfection, calcium phosphate precipitation, or electroporation. The host cells according to the present invention can be mammalian cells, for example, Chinese hamster ovary cells, human embryonic kidney cells (e.g., HEK 293), HeLa S3 cells, murine embryonic cells, or NSO cells. However, non-mammalian cells can also be used, including, e.g., bacteria, yeast, insect, and plant cells. Suitable host cells may also reside in vivo or be implanted in vivo, in which case the nucleic acids could be used in the context of in vivo or ex vivo gene therapy.

III. Methods of Making

[076] The invention also provides methods of producing (a) fusion proteins, (b) nucleic acid encoding the same, and (c) host cells and pharmaceutical compositions comprising either the fusion proteins or nucleic acids. For example, a method of producing the fusion protein according to the invention comprises culturing a host cell, containing a nucleic acid that encodes the fusion protein of the invention under conditions resulting in the expression of the fusion protein and subsequent recovery of the fusion protein. In one aspect, the fusion

protein is expressed in CHO or HEK 293 cells and purified from the medium using methods known in the art. In some embodiments, the fusion protein is eluted from a column at a neutral pH or above, e.g., pH 7.5 or above, pH 8.0 or above, pH 8.5 or above, or pH 9.0 or above.

[077] The fusion proteins, including variants, as well as nucleic acids encoding the same, can be made using any suitable method, including standard molecular biology techniques and synthetic methods, for example, as described in the following references: Maniatis (1990) Molecular Cloning, A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, and Bodansky et al. (1995) The Practice of Peptide Synthesis, 2nd ed., Spring Verlag, Berlin, Germany). Pharmaceutical compositions can also be made using any suitable method, including for example, as described in Remington: The Science and Practice of Pharmacy, eds. Gennado et al., 21th ed., Lippincott, Williams & Wilkins, 2005).

IV. Pharmaceutical Compositions And Methods of Administration

[078] The invention provides pharmaceutical compositions comprising the fusion proteins of the invention or nucleic acids encoding the fusion proteins.

[079] The fusion protein may be delivered to a cell or organism by means of gene therapy, wherein a nucleic acid sequence encoding the fusion protein is inserted into an expression vector that is administered in vivo or to cells ex vivo, which are then administered in vivo, and the fusion protein is expressed therefrom. Methods for gene therapy to deliver TGF-β antagonists are known (see, e.g., Fakhrai et al., *PNAS USA*, 93:2909-14, 1996 and U.S. patent 5,824,655).

[080] The fusion protein may be administered to a cell or organism in a pharmaceutical composition that comprises the fusion protein as an active ingredient. Pharmaceutical compositions can be formulated depending upon the treatment being effected and the route of administration. For example, pharmaceutical compositions of the invention can be administered orally, topically, transdermally, parenterally, subcutaneously, intravenously, intramuscularly, intraperitoneally, by intranasal instillation, by intracavitary or intravesical instillation, intraocularly, intraarterially, intralesionally, or by application to mucous

membranes, such as, that of the nose, throat, and bronchial tubes. The pharmaceutical composition will typically comprise biologically inactive components, such as diluents, excipients, salts, buffers, preservants, etc. Standard pharmaceutical formulation techniques and excipients are well known to persons skilled in the art (see, e.g., Physicians' Desk Reference (PDR) 2005, 59th ed., Medical Economics Company, 2004; and Remington: The Science and Practice of Pharmacy, eds. Gennado et al. 21th ed., Lippincott, Williams & Wilkins, 2005).

[081] Generally, the fusion protein of the invention may be administered as a dose of approximately from 1 μg/kg to 25 mg/kg, depending on the severity of the symptoms and the progression of the disease. The appropriate therapeutically effective dose of an antagonist is selected by a treating clinician and would range approximately from 1 μg/kg to 20 mg/kg, from 1 μg/kg to 10 mg/kg, from 1 μg/kg to 1 mg/kg, from 10 μg/kg to 1 mg/kg, from 10 μg/kg to 100 μg/kg, from 100 μg to 1 mg/kg, and from 500 μg/kg to 5 mg/kg. Effective dosages achieved in one animal may be converted for use in another animal, including human, using conversion factors known in the art (see, e.g., Freireich et al., *Cancer Chemother. Reports*, 50(4):219-244 (1996)).

V. Therapeutic And Non-Therapeutic Uses

[082] The fusion proteins of the invention may be used to capture or neutralize TGF-β, thus reducing or preventing TGF-β binding to naturally occurring TGF-β receptors.

[083] The invention includes a method of treating a subject (e.g., mammal) by administering to the mammal a fusion protein described herein or a nucleic acid encoding the fusion protein or cells containing a nucleic acid encoding the fusion protein. The mammal can be for example, primate (e.g., human), rodent (e.g., mouse, guinea pig, rat), or others (such as, e.g., dog, pig, rabbit).

[084] The mammal being treated may have or may be at risk for one or more conditions associated with an excess of TGF-β for which a reduction in TGF-β levels may be desirable. Such conditions include, but are not limited to, fibrotic diseases (such as glomerulonephritis, neural scarring, dermal scarring, pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis), lung fibrosis, radiation-induced fibrosis, hepatic fibrosis, myelofibrosis), peritoneal

adhesions, hyperproliferative diseases (e.g., cancer), burns, immune-mediated diseases, inflammatory diseases (including rheumatoid arthritis), transplant rejection, Dupuytren's contracture, and gastric ulcers.

[085] In certain embodiments, the fusion proteins, nucleic acids, and cells of the invention are used to treat diseases and conditions associated with the deposition of extracellular matrix (ECM). Such diseases and conditions include, but are not limited to, systemic sclerosis, postoperative adhesions, keloid and hypertrophic scarring, proliferative vitreoretinopathy, glaucoma drainage surgery, corneal injury, cataract, Peyronie's disease, adult respiratory distress syndrome, cirrhosis of the liver, post myocardial infarction scarring, restenosis (e.g., post- angioplasty restenosis), scarring after subarachnoid hemorrahage, multiple sclerosis, fibrosis after laminectomy, fibrosis after tendon and other repairs, scarring due to tatoo removal, biliary cirrhosis (including sclerosing cholangitis), pericarditis, pleurisy, tracheostomy, penetrating CNS injury, eosinophilic myalgic syndrome, vascular restenosis, veno-occlusive disease, pancreatitis and psoriatic arthropathy. In particular, the fusion proteins, and related aspects of the invention are particularly useful for the treatment of peritoneal fibrosis/adhesions. It is well known that antibodies are readily transferred from the peritoneal cavity into circulation. Therefore, intraperitoneal delivery of the fusion protein may provide a highly localized form of treatment for peritoneal disorders like peritoneal fibrosis and adhesions due to the advantageous concentration of the fusion protein within the affected peritoneum.

[086] The fusion proteins, nucleic acids, and cells of the invention are also useful to treat conditions where promotion of re-epithelialization is beneficial. Such conditions include, but are not limited to: diseases of the skin, such as venous ulcers, ischaemic ulcers (pressure sores), diabetic ulcers, graft sites, graft donor sites, abrasions and burns; diseases of the bronchial epithelium, such as asthma and ARDS; diseases of the intestinal epithelium, such as mucositis associated with cytotoxic treatment, esophagial ulcers (reflex disease), stomach ulcers, and small intestinal and large intestinal lesions (inflammatory bowel disease).

[087] Still further uses of the fusion proteins, nucleic acids, and cells of the invention are in conditions in which endothelial cell proliferation is desirable, for example, in stabilizing atherosclerotic plaques, promoting healing of vascular anastomoses, or in

conditions in which inhibition of smooth muscle cell proliferation is desirable, such as in arterial disease, restenosis and asthma.

[088] The fusion proteins, nucleic acids, and cells of the invention are also useful in the treatment of hyperproliferative diseases, such as cancers including, but not limited to, breast, prostate, ovarian, stomach, renal (e.g., renal cell carcinoma), pancreatic, colorectal, skin, lung, thyroid, cervical and bladder cancers, glioma, glioblastoma, mesothelioma, melanoma, as well as various leukemias and sarcomas, such as Kaposi's Sarcoma, and in particular are useful to treat or prevent recurrences or metastases of such tumors. In particular embodiments, the fusion proteins, nucleic acids, and cells of the invention are useful in methods of inhibiting cyclosporin-mediated metastases. It will of course be appreciated that in the context of cancer therapy, "treatment" includes any medical intervention resulting in the slowing of tumor growth or reduction in tumor metastases, as well as partial remission of the cancer in order to prolong life expectancy of a patient. In one embodiment, the invention is a method of treating cancer comprising administering a fusion protein, nucleic acid or cells of the invention. In particular embodiments, the condition is renal cancer, prostate cancer or melanoma.

[089] The fusion proteins, nucleic acids, and cells of the invention are also useful for treating, preventing and reducing the risk of occurrence of renal insufficiencies including, but not limited to, diabetic (type I and type II) nephropathy, radiational nephropathy, obstructive nephropathy, diffuse systemic sclerosis, pulmonary fibrosis, allograft rejection, hereditary renal disease (e.g., polycystic kidney disease, medullary sponge kidney, horseshoe kidney), nephritis, glomerulonephritis, nephrosclerosis, nephrocalcinosis, systemic lupus erythematosus, Sjogren's syndrome, Berger's disease, systemic or glomerular hypertension, tubulointerstitial nephropathy, renal tubular acidosis, renal tuberculosis, and renal infarction. In particular embodiments, the fusion proteins, nucleic acids and cells of the invention are combined with antagonists of the renin-angiotensin-aldosterone system including, but not limited to, renin inhibitors, angiotensin-converting enzyme (ACE) inhibitors, Ang Ii receptor antagonists (also known as "Ang Il receptor blockers"), and aldosterone antagonists (see, for example, WO 2004/098637).

[090] The fusion proteins, nucleic acids, and cells of the invention are also useful to enhance the immune response to macrophage-mediated infections, such as those caused by Leishmania spp., *Trypanosoma cruzi*, *Mycobacterium tuberculosis* and *Mycobacterium leprae*, as well as the protozoan *Toxoplasma gondii*, the fungi *Histoplasma capsulatum*, *Candida albicans*, *Candida parapsilosis*, and *Cryptococcus neoformans*, and Rickettsia, for example, *R. prowazekii*, *R. coronii*, and *R. tsutsugamushi*. They are also useful to reduce immunosuppression caused, for example, by tumors, AIDS or granulomatous diseases.

[091] In addition, without being bound to any particular theory, it is also believed that the fusion proteins of the invention, because they lack an immunoglobulin domain (unlike TGF-β antibodies and TGF-β receptor-Fc fusion proteins) may not be as susceptible to clearance from sites of action by the immune system (e.g., in conditions or diseases of the lung).

CLAIMS

1. A heterotrimeric fusion protein comprising:
   (a) an amino terminal segment comprising a first TGFβ binding domain of TGFβ receptor type II,
   (b) a central segment comprising a endoglin-domain of TGFβ receptor type III, and
   (c) a carboxy terminal segment comprising a second TGFβ binding domain of TGFβ receptor type II.

2. The fusion protein of claim 1, further comprising one or more linker amino acids between the amino terminal segment and the central segment, and/or one or more linker amino acids between the central segment and the carboxy terminal segment.

3. The fusion protein of claim 1, wherein the amino terminal segment comprises an amino acid sequence that is 90% identical to SEQ ID NO:3.

4. The fusion protein of claim 1, wherein the central segment comprises an amino acid sequence that is 90% identical to SEQ ID NO:4 or amino acids 21-406 of SEQ ID NO:8.

5. The fusion protein of claim 1, wherein the carboxy terminal segment comprises an amino acid sequence that is 90% identical to SEQ ID NO:5.

6. The fusion protein of claim 1, wherein the fusion protein has an amino acid sequence that is 90% identical to SEQ ID NO:2.

7. The fusion protein of claim 1, wherein the fusion protein has an amino acid sequence of SEQ ID NO:2.

8. The fusion protein of claim 1, further comprising an amino terminal signal sequence.

9. The fusion protein of claim 1, further comprising an amino terminal or carboxy terminal tag.

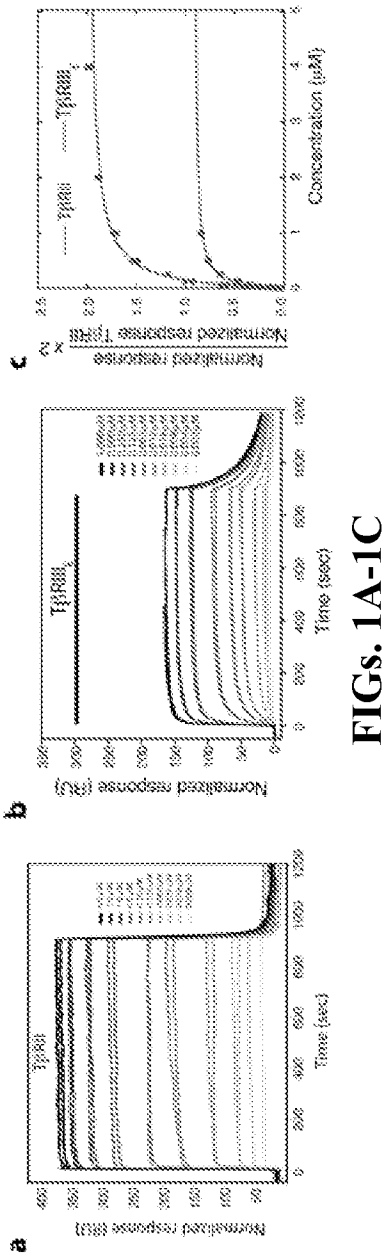
10. The fusion protein of claim 9, wherein the tag is a carboxy terminal hexa-histidine

11. A method of treating a condition related to increased expression TGFβ comprising administering an effective amount of the fusion protein of claim 1 to subject in thereof.

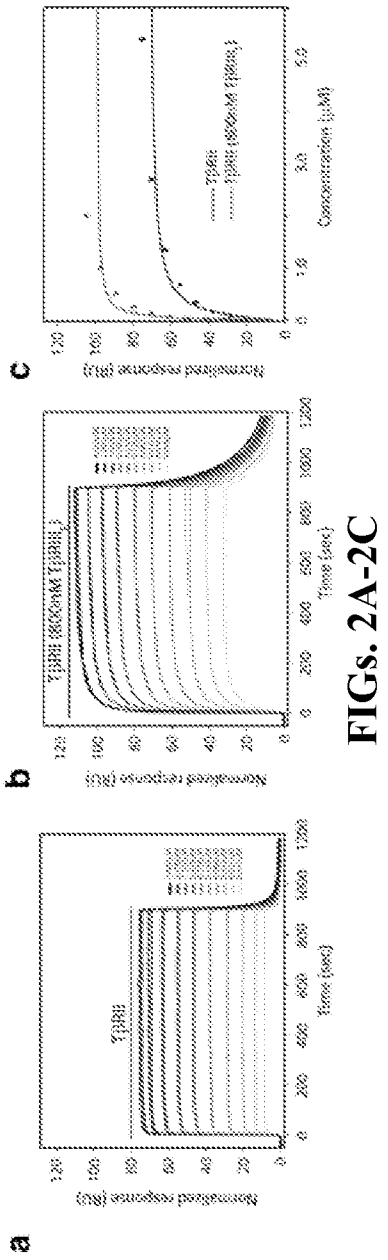
12. The method of claim 11, wherein the condition is a hyperproliferative disorder.

13. The method of claim 12, wherein the hyperproliferative disorder is cancer.

14. The method of claim 11, wherein the condition is fibrosis.



FIGs. 1A-1C



FIGs. 2A-2C

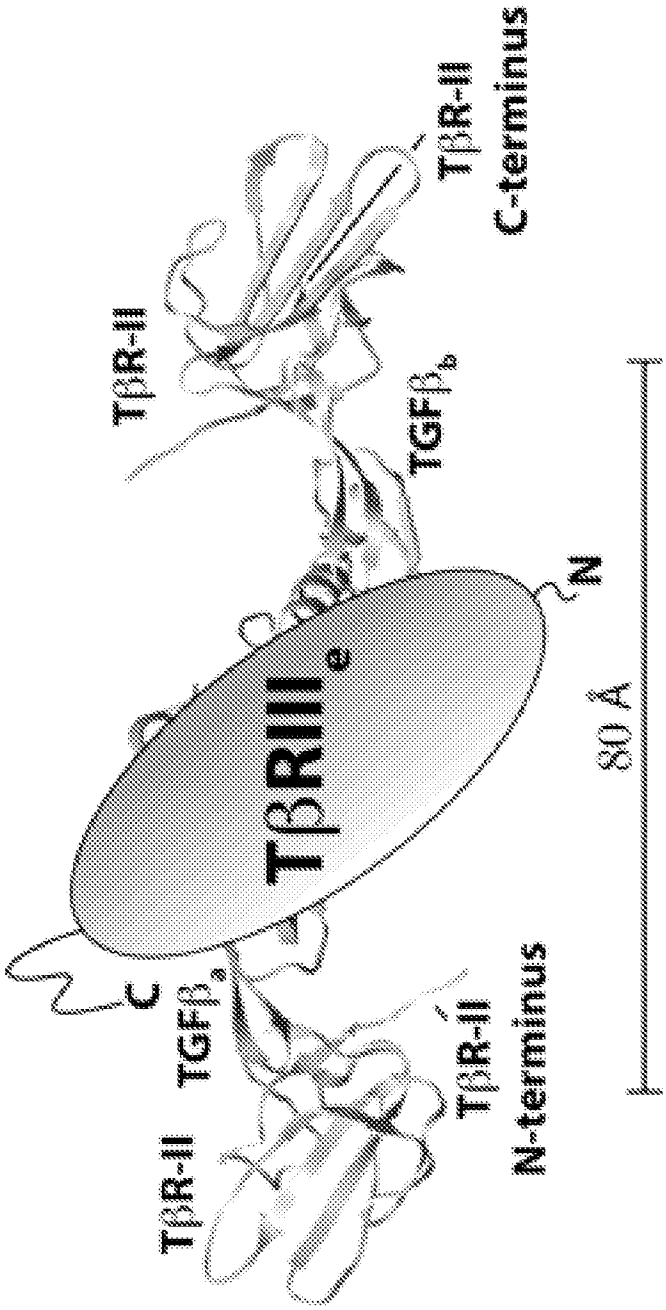

TβR-II
C-terminus
TβR-II
TGFβb
TβRIIe
N
80 Å
C
TGFβa
TβR-II
TβR-II
N-terminus

FIG. 3

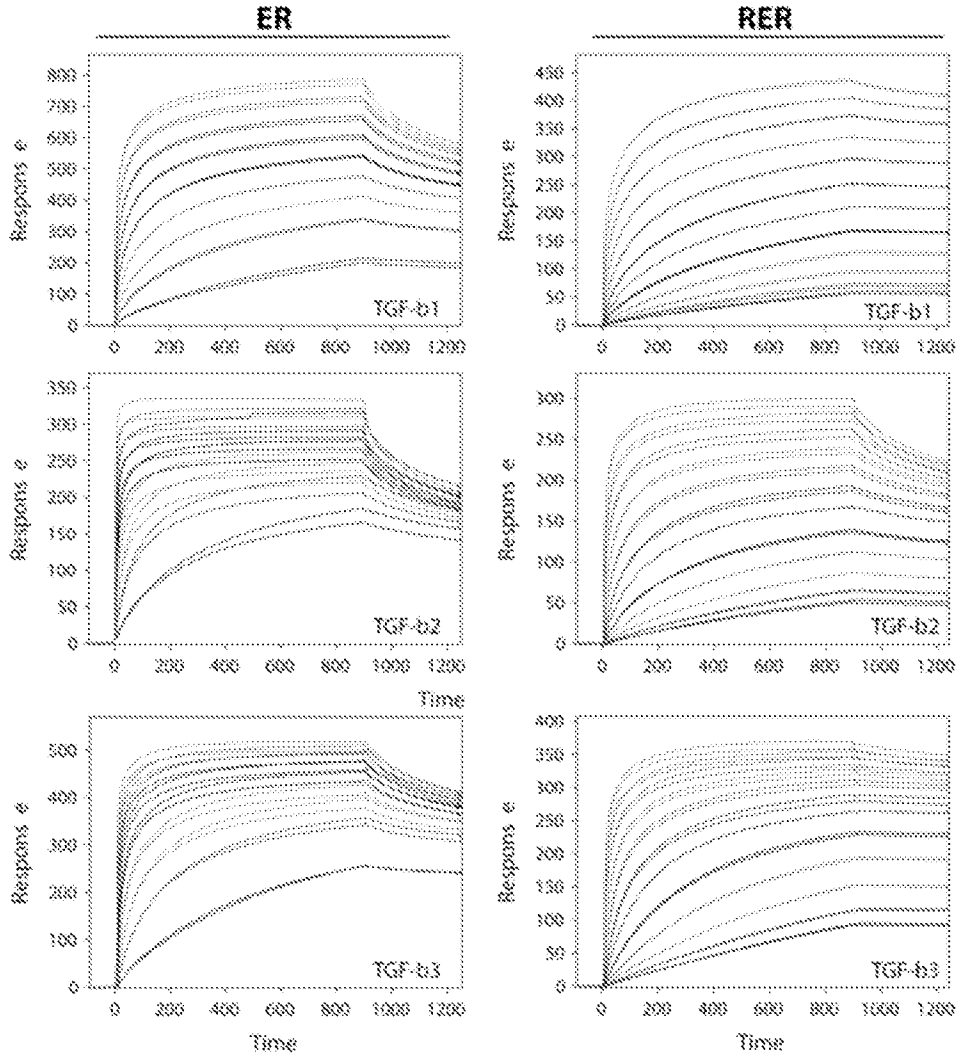


FIG. 4

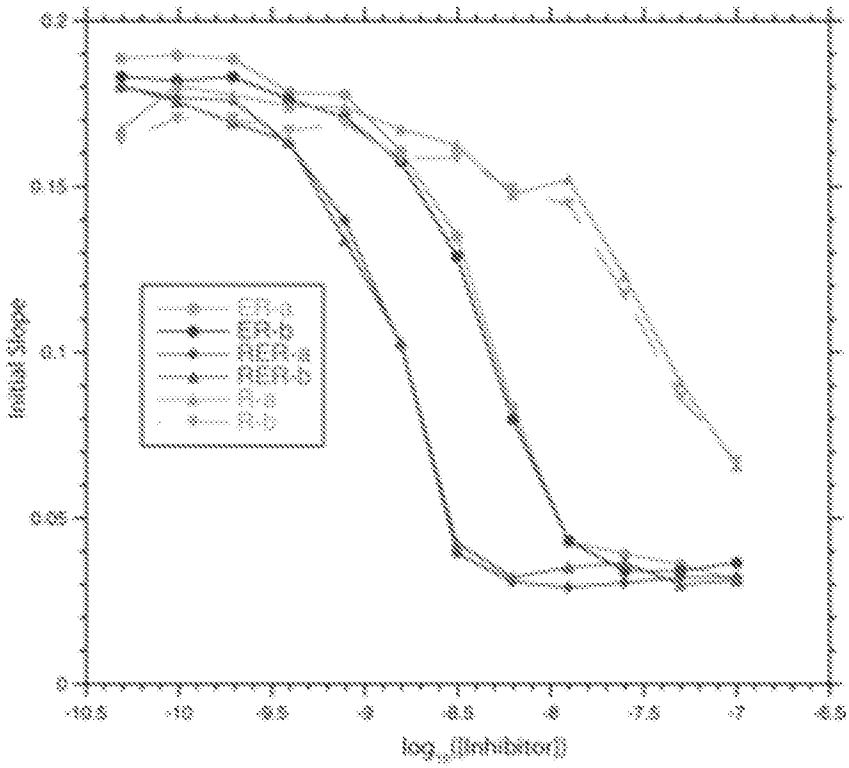


FIG. 5

Neutralization potency of various TGF-β inhibitors in a mink lung epithelial cell (Mv1Lu) luciferase reporter gene assay			
	IC_{50} (nM)	IC_{50} Std. Dev. (nM)	Number of measurements
RR (RII-RII)			
TGF-β1	1.5	0.8	4
TGF-β2	n.d.	n.d.	4
TGF-β3	0.27	0.22	4
RER (RII-BG_E-RII)			
TGF-β1	0.00051	0.00022	3
TGF-β2	0.070	0.018	3
TGF-β3	0.0033	0.0058	3
ER (BG_E-RII)			
TGF-β1	0.014	0.009	2
TGF-β2	1.2	0.3	2
TGF-β3	0.020	0.011	2
REU (RII-BG_E-BG_U, or RII-RIII)			
TGF-β1	0.18	0.04	2
TGF-β2	0.81	0.10	2
TGF-β3	0.067	0.021	2
EU (BG_E-BG_U, or RIII)			
TGF-β1	n.d.	n.d.	2
TGF-β2	n.d.	n.d.	2
TGF-β3	n.d.	n.d.	2
1D11 (Genzyme's pan isoform specific TGF-β neutralizing antibody)			
TGF-β1	0.99	0.98	2
TGF-β2	5.5	1.0	2
TGF-β3	0.093	0.016	2

FIG. 6

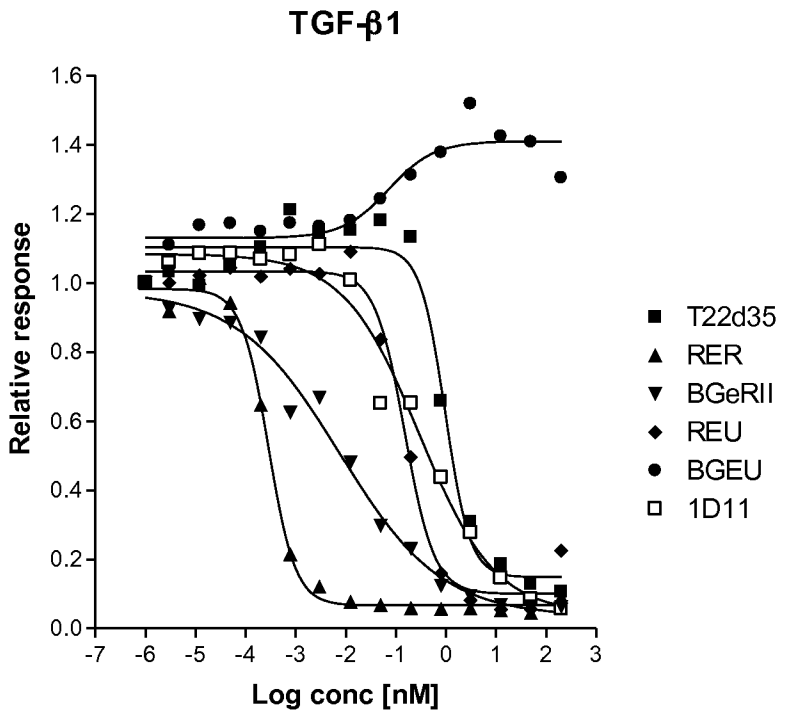

TGF-β1
Relative response
Log conc [nM]
T22d35
RER
BGeRII
REU
BGEU
1D11

FIG. 7A

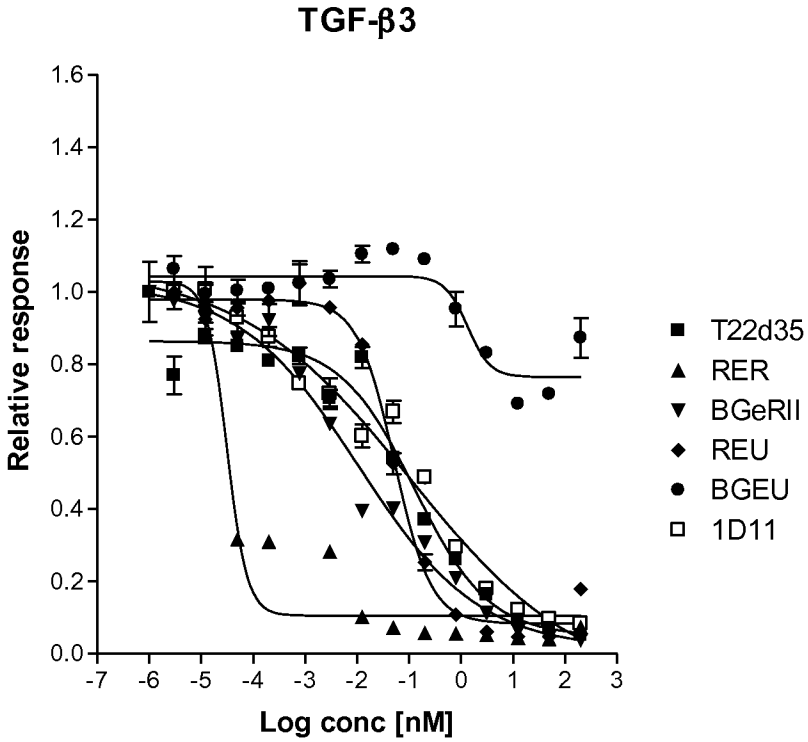

TGF-β3
Relative response
Log conc [nM]
T22d35
RER
BGeRII
REU
BGEU
1D11

FIG. 7B

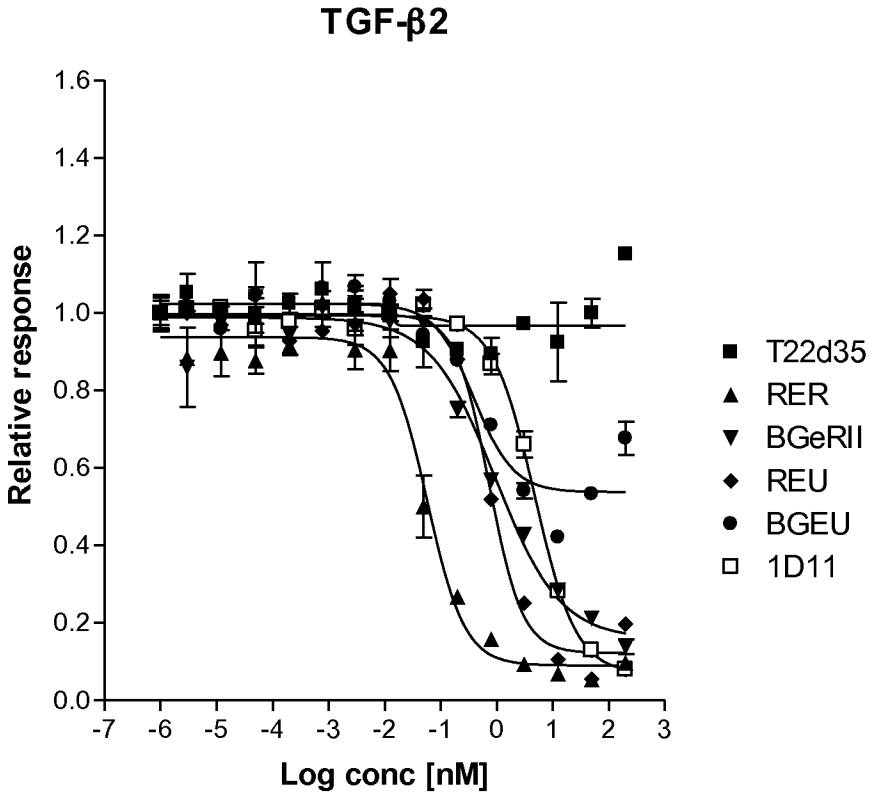

TGF-β2
Relative response
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
-7
-6
-5
-4
-3
-2
-1
0
1
2
3
Log conc [nM]
T22d35
RER
BGeRII
REU
BGEU
1D11

FIG. 7C

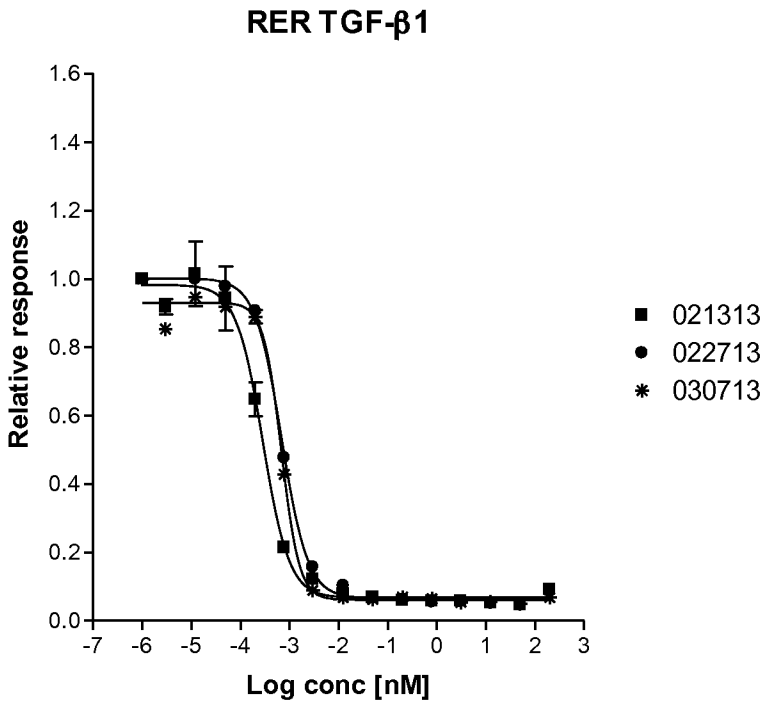

RER TGF-β1
Relative response
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
-7 -6 -5 -4 -3 -2 -1 0 1 2 3
Log conc [nM]
021313
022713
030713

FIG. 8A

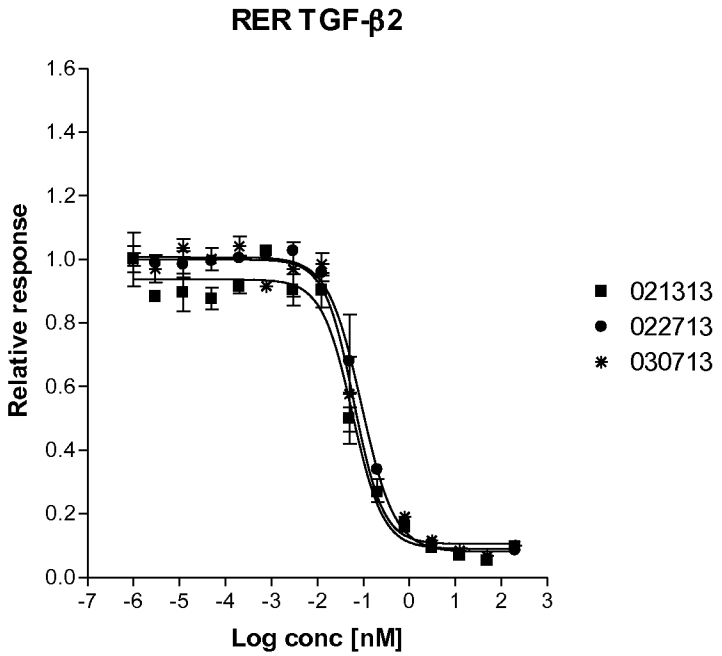

RER TGF-β2
Relative response
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
-7 -6 -5 -4 -3 -2 -1 0 1 2 3
Log conc [nM]
021313
022713
030713

FIG. 8B

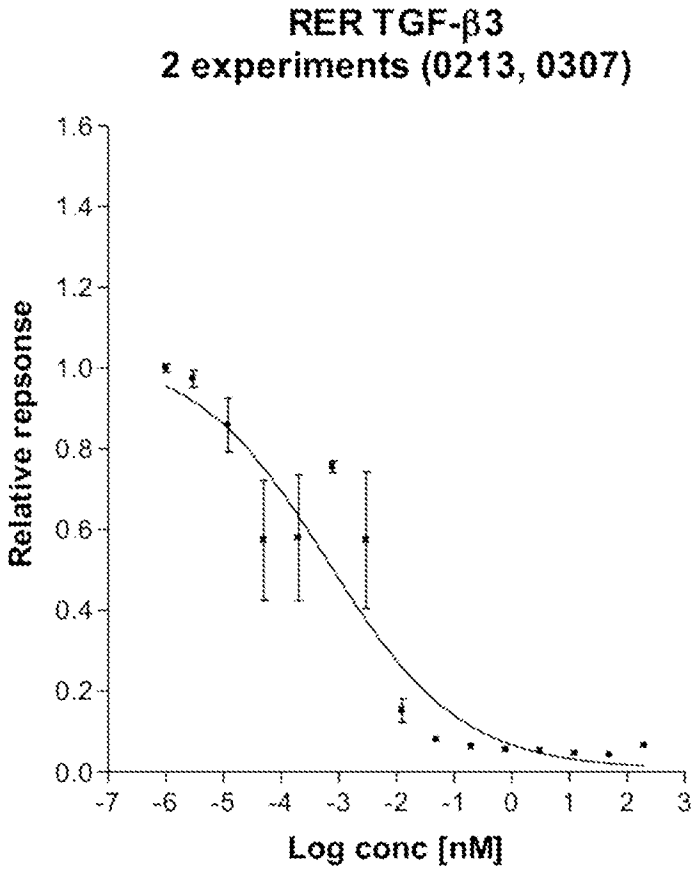

RER TGF-β3
2 experiments (0213, 0307)
Relative repsonse
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
-7
-6
-5
-4
-3
-2
-1
0
1
2
3
Log conc [nM]

FIG. 8C

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2013/034504

A. CLASSIFICATION OF SUBJECT MATTER
IPC(8) - C07K 14/495 (2013.01)
USPC - 514/8.9
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC(8) - A61K 38/00, 38/16, 38/18; C07K 14/00, 14/49, 14/495 (2013.01)
USPC - 424/198.1; 514/1.8, 7.6, 8.9, 19.3; 530/350, 399

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
CPC - A61K 38/00; C07K 14/71, 2319/32 (2013.01)

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Patbase, Google Patent, PubMed

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2007/0244042 A1 (SUN et al) 18 October 2007 (18.10.2007) entire document	1-5, 9-13
Y		8, 14
Y	US 2007/0184052 A1 (LIN et al) 09 August 2007 (09.08.2007) entire document	8, 14
A	US 2002/0004037 A1 (KOTELIANSKY et al) 10 January 2002 (10.01.2002) entire document	1-14
A	US 2010/0204104 A1 (QIU et al) 12 August 2010 (12.08.2010) entire document	1-14

☐ Further documents are listed in the continuation of Box C. ☐

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
24 May 2013	19 JUN 2013

Name and mailing address of the ISA/US	Authorized officer:
Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, Virginia 22313-1450 Facsimile No. 571-273-3201	Blaine R. Copenheaver PCT Helpdesk: 571-272-4300 PCT OSP: 571-272-7774

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2013/034504

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing filed or furnished:

   a. (means)
   - ☐ on paper
   - ☒ in electronic form

   b. (time)
   - ☒ in the international application as filed
   - ☐ together with the international application in electronic form
   - ☐ subsequently to this Authority for the purposes of search

2. ☐ In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

Specifically, SEQ ID NOs: 1-5 and amino acid residues 21-406 of SEQ ID NO:8 were searched.