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(54) **OLIGORIBONUCLEOTIDES AND METHODS OF USE THEREOF FOR TREATMENT OF FIBROTIC CONDITIONS AND OTHER DISEASES**

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(57) **ABSTRACT**

The invention relates to a double-stranded compound, preferably an oligoribonucleotide (siRNA), which down-regulates the expression of a human TGaseII gene at the post-transcriptional level. The invention also relates to a pharmaceutical composition comprising the compound, or a vector capable of expressing the oligoribonucleotide compound, and a pharmaceutically acceptable carrier. The present invention also contemplates a method of treating a patient suffering from a fibrotic disease such as pulmonary, kidney and liver fibrosis or ocular, scarring comprising administering to the patient the pharmaceutical composition in a therapeutically effective dose so as to thereby treat the patient. The invention also relates to treatment of fibrotic and other diseases by use of antibodies to TGaseII polypeptide.

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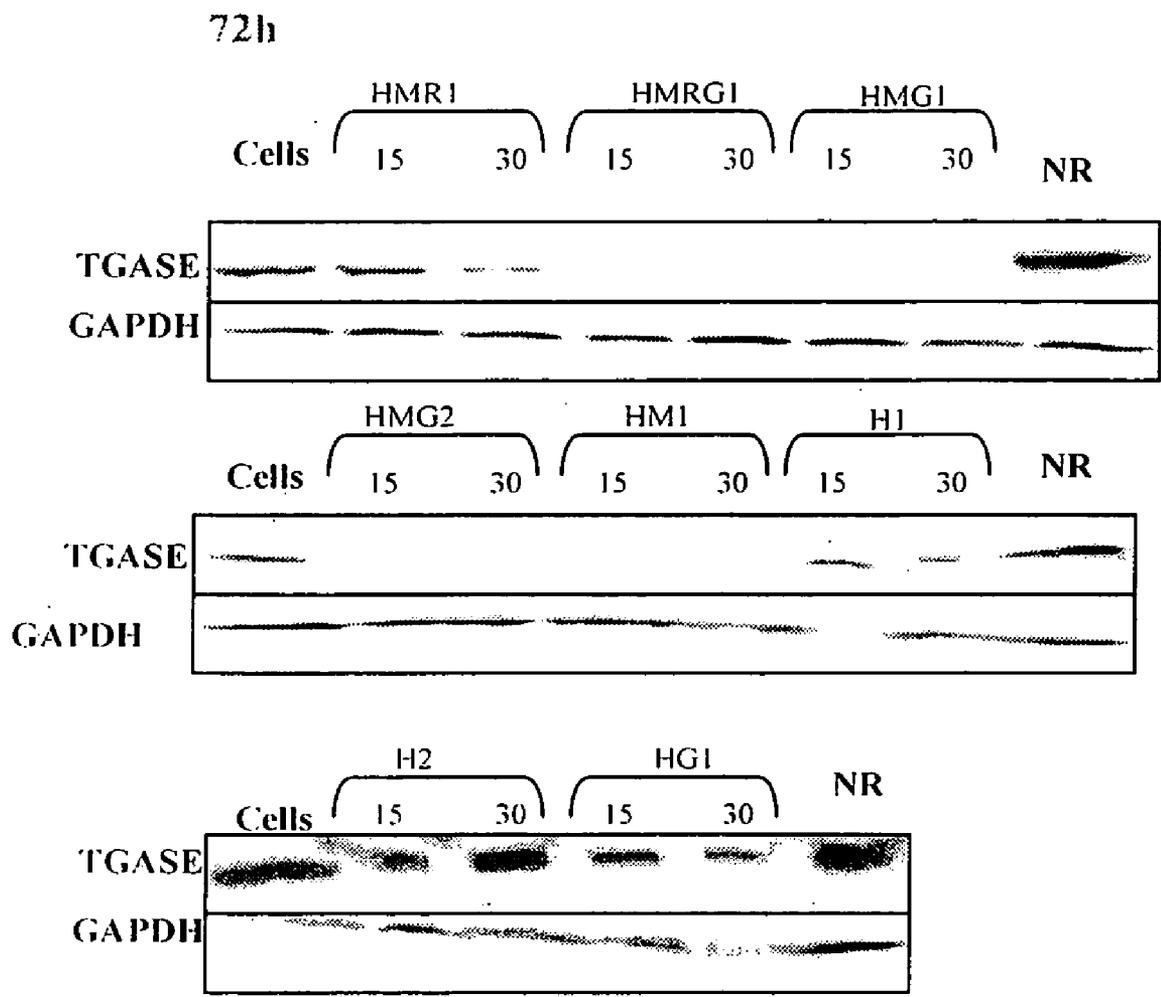
FIGURE 1.

ATGGCCGAGG AGCTGGTCTT AGAGAGGTGT GATCTGGAGC TGGAGACCAA TGGCCGAGAC CACCACACGG 70
CCGACCTGTG CCGGGAGAAG CTGGTGGTGC GACGGGGCCA GCCCTTCTGG CTGACCCTGC ACTTTGAGGG 140
CCGCAACTAC GAGGCCAGTG TAGACAGTCT CACCTTCAGT GTCGTGACCG GCCCAGCCCC TAGCCAGGAG 210
GCCGGGACCA AGGCCCGTTT TCCACTAAGA GATGCTGTGG AGGAGGGTGA CTGGACAGCC ACCGTGGTGG 280
ACCAGCAAGA CTGCACCCTC TCGCTGCAGC TCACCACCCC GGCCAACGCC CCCATCGGCC TGTATCGCCT 350
CAGCCTGGAG GCCTCCACTG GCTACCAGGG ATCCAGCTTT GTGCTGGGCC ACTTCATTTT GCTCTTCAAC 420
GCCTGGTGCC CAGCGGATGC TGTGTACCTG GACTCGGAAG AGGAGCGGCA GGAGTATGTC CTCACCCAGC 490
AGGGCTTTAT CTACCAGGGC TCGGCCAAGT TCATCAAGAA CATACTTGG AATTTTGGGC AGTTTGAAGA 560
TGGGATCCTA GACATCTGCC TGATCCTTCT AGATGTCAAC CCCAAGTTC TGAAGAACGC CGGCCGTGAC 630
TGCTCCCGCC GCAGCAGCCC CGTCTACGTG GGCCGGGTGG TGAGTGGCAT GGTCAACTGC AACGATGACC 700
AGGGTGTGCT GCTGGGACGC TGGGACAACA ACTACGGGGA CGGCGTCAGC CCCATGTCCT GGATCGGCAG 770
CGTGGACATC CTGCGGCGCT GGAAGAACCA CGGCTGCCAG CGCGTCAAGT ATGGCCAGTG CTGGGTCTTC 840
GCCGCCGTGG CCTGCACAGT GCTGAGGTGC CTGGGCATCC CTACCCGCGT CGTGACCAAC TACAACCTCG 910
CCCATGACCA GAACAGCAAC CTTCTCATCG AGTACTCCG CAATGAGTTT GGGGAGATCC AGGGTGACAA 980
GAGCGAGATG ATCTGGAAT TCCACTGCTG GGTGGAGTCG TGGATGACCA GGCCGGACCT GCAGCCGGGG 1050
TAGGAGGGCT GGCAGGCCCT GGACCCAACG CCCCAGGAGA AGAGCGAAGG GACGTAATGC TGTGGCCAG 1120
TTCAGTTTCG TGCCATCAAG GAGGGCGACC TGAGCACCAA GTACGATGCG CCCTTTGTCT TTGCGGAGGT 1190
CAATGCCGAC GTGGTAGACT GGATCCAGCA GGACGATGGG TCTGTGCACA AATCCATCAA CCGTTCCTG 1260
ATCGTTGGGC TGAAGATCAG CACTAAGAGC GTGGGCCGAG ACGAGCGGGA GGATATCACC CACACCTACA 1330
AATACCCAGA GGGGTCCTCA GAGGAGAGGG AGGCCTPCAC AAGGGCGAAC CACCTGAACA AACTGGCCGA 1400
GAAGGAGGAG ACAGGGATGG CCATGCGGAT CCGTGTGGGC CAGAGCATGA ACATGGGCAG TGACTTTGAC 1470
GTCTTTGCCC ACATACCAA CAACACCGCT GAGGAGTACG TCTGCCGCTT CCTGCTCTGT GCCCGCACCG 1540
TCAGCTACAA TGGGATCTTG GGGCCCGAGT GTGGCACCAA GTACCTGCTC AACCTCAACC TGGAGCCTTT 1610
CTCTGAGAAG AGCGTTCCTC TTTGCATCCT CTATGAGAAA TACCGTACT GCCTTACGGA GTCCAACCTC 1680
ATCAAGGTGC GGGCCCTCCT CGTGGAGCCA GTTATCAACA GCTACCTGCT GGCTGAGAGG GACCTCTACC 1750
TGGAGAATCC AGAAATCAAG ATCCGGATCC TTGGGGAGCC CAAGCAGAAA CGCAAGCTGG TGGCTGAGGT 1820
GTCCCTGCAG AACCCGCTCC CTGTGGCCCT GGAAGGCTGC ACCTTCACTG TGGAGGGGGC CGGCCTGACT 1890
GAGGAGCAGA AGACGGTGA GATCCAGAC CCCGTGGAGG CAGGGGAGGA AGTTAAGGTG AGAATGGACC 1960
TGCTGCCGCT CCACATGGGC CTCCACAAGC TGGTGGTGAA CTTGAGAGC GACAAGCTGA AGGCTGTGAA 2030
GGGCTTCCGG AATGTCATCA TTGGCCCCG CTA 2064

FIGURE 2.

MAEELVLERC DLELETNGRD HHTADLCREK LVVRRGQPFW LTLHFEGRNY EASVDSLTFE VVTGPAPSQE 70
AGTKARFPLR DAVEEGDWTG TVVDQDCTL SLQLTTPANA FIGLYRLSLE ASTGYQGSSF VLGHFILLFN 140
AWCPADAVYL DSEERQEVV LTQQGFYQG SAKFIKNIPW NFGQFEDGIL DICLILLDVN PKFLKNAGRD 210
CSRRSSPVYV GRVSGMVNC NDDQGVLLGR WDNNYGDGVS PMSWIGSVDI LRRWKNHGCQ RVKYQCWVF 280
AAVACTVLRC LGIPTRVVTN YNSAHDQNSN LLIEYFRNEF GEIQGDKSEM IWNFHCWVES WMTRPDLQPG 350
YEGWQALDPT PQEKSEGTYC CGPVPVRAIK EGDLSKYDA PFVFAEVNAD VVDWIIQDDG SVHKSINRSL 420
IVGLKISTKS VGRDEREDIT HTYKYPEGSS EEREAFTRAN HLNKLAKEEE TGMAMRIRVG QSMNMGSDFD 490
VFAHITNNTA EEYVCRLLLC ARTVSYNGIL GPECGTKYLL NLNLEPFSEK SVPLCILYEK YRDCLTESNL 560
IKVRALLVEP VINSYLLAER DLYLENPEIK IRILGEPKQK RKLVAEVSLO NPLPVALEGC TFTVEGAGLT 630
EEQKTVEIPD PVEAGEEVKV RMDLLPLHMG LHKLVVNFES DKLKAVKGR NVIIGPA 687

FIGURE 3.



OLIGORIBONUCLEOTIDES AND METHODS OF USE THEREOF FOR TREATMENT OF FIBROTIC CONDITIONS AND OTHER DISEASES

[0001] This application claims priority of U.S. Provisional patent applications No. 60/540,687, filed Jan. 30, 2004 and No. 60/641,522, filed Jan. 4, 2005, both of which are hereby incorporated by reference in their entirety.

[0002] Throughout this application various patent and scientific publications are cited. The disclosures of these publications in their entireties are hereby incorporated by reference into this application to more fully describe the state of the art to which this invention pertains.

BACKGROUND OF THE INVENTION

[0003] siRNAs and RNA interference

[0004] RNA interference (RNAi) is a phenomenon involving double-stranded (ds) RNA-dependent gene specific post-transcriptional silencing. Originally, attempts to study this phenomenon and to manipulate mammalian cells experimentally were frustrated by an active, non-specific antiviral defense mechanism which was activated in response to long dsRNA molecules; see Gil et al. 2000, *Apoptosis*, 5:107-114. Later it was discovered that synthetic duplexes of 21 nucleotide RNAs could mediate gene specific RNAi in mammalian cells, without the stimulation of the generic antiviral defence mechanisms see Elbashir et al. *Nature* 2001, 411:494-498 and Caplen et al. *Proc Natl Acad Sci* 2001, 98:9742-9747. As a result, small interfering RNAs (siRNAs), which are short double-stranded RNAs, have become powerful tools in attempting to understand gene

[0005] Thus, RNA interference (RNAi) refers to the process of sequence-specific post-transcriptional gene silencing in mammals mediated by small interfering RNAs (siRNAs) (Fire et al, 1998, *Nature* 391, 806) or microRNAs (miRNAs) (Ambros V. *Nature* 431:7006,350-355(2004); and Bartel D P. *Cell*. 2004 Jan. 23; 116(2): 281-97 *MicroRNAs: genomics, biogenesis, mechanism, and function*). The corresponding process in plants is commonly referred to as specific post-transcriptional gene silencing or RNA silencing and is also referred to as quelling in fungi. An siRNA is a double-stranded RNA molecule which down-regulates or silences (prevents) the expression of a gene/mRNA of its endogenous (cellular) counterpart. RNA interference is based on the ability of dsRNA species to enter a specific protein complex, where it is then targeted to the complementary cellular RNA and specifically degrades it. Thus, the RNA interference response features an endonuclease complex containing an siRNA, commonly referred to as an RNA-induced silencing complex (RISC), which mediates cleavage of single-stranded RNA having a sequence complementary to the antisense strand of the siRNA duplex. Cleavage of the target RNA may take place in the middle of the region complementary to the antisense strand of the siRNA duplex (Elbashir et al 2001, *Genes Dev.*, 15, 188). In more detail, longer dsRNAs are digested into short (17-29 bp) dsRNA fragments (also referred to as short inhibitory PNAs—"siRNAs") by type III RNases (DICER, DROSHA, etc., Bernstein et al., *Nature*, 2001, v.409, p.363-6; Lee et al., *Nature*, 2003, 425, p.415-9). The RISC protein complex recognizes these fragments and complementary mRNA. The whole process is culminated by endonuclease cleavage of target mRNA (McManus&Sharp, *Nature Rev Genet* , 2002,

v.3, p.737-47; Paddison &Hannon, *Curr Opin Mol Ther.* 2003 June; 5(3): 217-24). For information on these terms and proposed mechanisms, see Bernstein E., Denli A M. Hannon G J: 2001 *The rest is silence*. *RNA*. I; 7(11): 1509-21; Nishikura K.: 2001 *A short primer on RNAi. RNA-directed RNA polymerase acts as a key catalyst*. *Cell*. I 16; 107(4): 415-8 and PCT publication WO 01/36646 (Glover et al).

[0006] The selection and synthesis of siRNA corresponding to known genes has been widely reported; see for example Chalk A M, Wahlestedt C, Sonnhammer E L. 2004 *Improved and automated prediction of effective siRNA* *Biochem. Biophys. Res. Commun.* Jun. 18; 319(1): 264-74; Sioud M, Leirdal M., 2004, *Potential design rules and enzymatic synthesis of siRNAs*, *Methods Mol Biol.*; 252:457-69; Levenkova N, Gu Q, Rux J. J. 2004 *Gene specific siRNA selector* *Bioinformatics*. I 12; 20(3): 430-2. and Ui-Tei K, Naito Y, Takahashi F, Haraguchi T, Ohki-Hamazaki H, Juni A, Ueda R, Saigo K., *Guidelines for the selection of highly effective siRNA sequences for mammalian and chick RNA interference* *Nucleic Acids Res.* 2004 I 9;32(3):936-48. See also Liu Y, Braasch D A, Nulf C J, Corey D R. *Efficient and isoform-selective inhibition of cellular gene expression by peptide nucleic acids*, *Biochemistry*, 2004 I 24;43(7):1921-7. See also PCT publications WO 2004/015107 (Atugen) and WO 02/44321 (Tuschl et al), and also Chiu Y L, Rana T M. *siRNA function in RNAi. a chemical modification analysis*, *RNA* 2003 September;9(9):1034-48 and I Patent Nos.5898031 and 6107094 (Crooke) for production of modified/ more stable siRNAs.

[0007] Several groups have described the development of DNA-based vectors capable of generating siRNA within cells. The method generally involves transcription of short hairpin RNAs that are efficiently processed to form siRNAs within cells. Paddison et al. *PNAS* 2002, 99:1443-1448; Paddison et al. *Genes & Dev* 2002, 16:948-958; Sui et al. *PNAS* 2002, 8:5515-5520; and Brummelkamp et al. *Science* 2002, 296:550-553. These reports describe methods to generate siRNAs capable of specifically targeting numerous endogenously and exogenously expressed genes.

[0008] siRNA has recently been successfully used for inhibition in primates; for further details see Tolentino et al., *Retina* 24(1) February 2004 1 132-138.

[0009] Transglutaminase (TGase) Family

[0010] Transglutaminases (EC 2.3.2.13) are a family of enzymes that catalyze the crosslinking of proteins by epsilon-gamma glutamyl lysine isopeptide bonds. The family comprises 9 different enzymes among which are the factor XIIIa (plasma transglutaminase), keratinocyte transglutaminase (TGaseI), epidermal transglutaminase (TGaseIII), prostate transglutaminase (TGaseIV), and tissue-type transglutaminase (TGaseII). Although the overall primary structure of these enzymes is different, they all share a common amino acid sequence at the active site (Y-G-Q-C-W) and a strict calcium dependence for their activity (Lesort M, Tucholski J, Miller M L, Johnson G V, *Tissue transglutaminase: a possible role in neurodegenerative diseases. Prog Neurobiol.* 2000 August; 61(5):439-63).

[0011] Transglutaminase II. Transglutaminase II (TGaseII) also known as Protein-glutamine gamma-glutamyltransferase, TGase C, TGC, TG(C), and tissue-type transglutaminase, is a unique multifunctional enzyme with dual enzymatic activity:

- [0012] 1) The enzyme acts as a TGase protein (Ca²⁺ activated, GTP-inactivated) with crosslinking activities (i.e. it catalyzes reactions resulting in protein cross-links and/or covalent incorporation of biogenic amines). TGase further catalyzes the formation of a covalent glutamyl—lysyl bond, a unique isopeptide bond that is highly resistant to proteolysis and denaturants and that cannot be disrupted by any known vertebrate endopeptidase.
- [0013] 2) The enzyme also acts as a GTP-binding protein that transduces the activating signal from alpha 1 B and alpha 1 D adrenergic receptors, from TP alpha thromboxane A2 receptor and from oxytocin receptor to phospholipase C delta 1 (i.e. it activates inositol phosphate production, Ca²⁺ mobilization etc.). It has been shown that both alpha 1D adrenergic receptor and PLC act as guanine nucleotide exchanging factor for transglutaminase 11 (Baek K J, Kang S, Damron D, Im M, *Phospholipase C-delta1 is a guanine nucleotide exchanging factor for transglutaminase II (G alpha h) and promotes alpha 1B-adrenoreceptor-mediated GTP binding and intracellular calcium release. J Biol Chem.* 2001 Feb. 23;276(8):5591-7).
- [0014] The dual function of this enzyme is separate and the active sites are located at different positions (Im M. J, Russell M A, Feng J F, *Transglutaminase II. a new class of GTP-binding protein with new biological functions.* Cell Signal. 1997 November;9(7):477-82), and inhibition of crosslinking activity of TGaseII may be achieved without the interference with its G-protein function.
- [0015] TGaseII: Subcellular Localization and Fibrosis Related Intracellular Signaling Activity
- [0016] TgaseII is ubiquitously expressed and can be found in association with ECM and intracellularly, both as membrane bound and as cytosolic protein. The GTP-binding activity is higher in the membrane fraction of TGase and the cross-linking activity is higher in the cytosolic and extracellular fraction. On the cell surface, TGase binds to fibronectin via its 42 kDa gelatin-binding domain. The cross-linking of fibronectin with collagen contributes to structural stabilization of the ECM rendering the matrix resistant to proteolysis by matrix metalloproteinases. Thus TGaseII, by favoring deposition of extracellular proteins and inhibiting breakdown of said proteins, contributes to ECM accumulation, a phenomenon that is central to the formation of tissue fibrosis.
- [0017] In addition, TGase mediates the binding of latent TGF-beta to the ECM, a required step for a proper subsequent processing of this pro-fibrotic factor, which finally results in the release of active TGF-beta (Le et al., *Connect Tissue Res.* 2001;42(4):245-53. Rosenthal et al., *Arthritis Rheum.* 2000 August;43(8): 1729-33).
- [0018] In the cytoplasm, TGaseII may activate RhoA, a small G protein of the ras family known to have an important role in cytoskeletal rearrangement, regulation of cell morphology and differentiation. Activation of TGaseII results in an increased transamidation of RhoA, which then functions as a constitutively active G-protein showing increased binding to and activation of its downstream target ROCK-2 (Rho-associated kinase) (Singh et al. *EMBO J.* 2001 May 15;20(10):2413-23). The specific ROCK kinase inhibitor, Y-27632, showed anti-fibrotic effect in UO model of renal fibrosis as well as in the models of liver or lung fibrosis (Nagatoya K, Moriyama T, Kawada N, Takeji M, Oseto S, Murozono T, Ando A, Imai E, Hori M. Y-27632 was found to prevent tubulointerstitial fibrosis in mouse kidneys with unilateral urethral obstruction. *Kidney Int.* 2002 May;61(5):1684-95; Murata T, Arii S, Nakamura T, Mori A, Kaido T, Furuyama H, Furumoto K, Nakao T, Isobe N, Imamura M, *Inhibitory effect of Y-27632, a ROCK inhibitor, on progression of rat liver fibrosis in association with inactivation of hepatic stellate cells. J Hepatol.* 2001 October;35(4):474-81; Shimizu Y, Dobashi K, Iizuka K, Horie T, Suzuki K, Tukagoshi H, Nakazawa T, Nakazato Y, Mori M, *Contribution of small GTPase Rho and its target protein ROCK in a murine model of lung fibrosis.* Am J Respir Crit Care Med. 2001 January;163(1):210-7). Recently, a unique function of TGaseII contributing to activation of NFkB, a transcription factor with a well-documented pro-fibrotic activity was described (Baud et al., *J Soc Biol.* 2002;196(4):269-73, Lee et al. *J Biol Chem.* 2004 Dec. 17;279(51):53725-35).
- [0019] Fibrotic Diseases
- [0020] Fibrotic diseases are all characterized by the excess deposition of a fibrous material within the extracellular matrix, which contributes to abnormal changes in tissue architecture and interferes with normal organ function. Unfortunately, although fibrosis is widely prevalent, debilitating and often life threatening, there is no effective treatment currently available.
- [0021] All tissues damaged by trauma respond by the initiation of a wound-healing program. Fibrosis, a type of disorder characterized by excessive scarring, occurs when the normal self-limiting process of wound healing response is disturbed, and causes excessive production and deposition of collagen. As a result, normal organ tissue is replaced with scar tissue, which eventually leads to the functional failure of the organ.
- [0022] Fibrosis may be initiated by diverse causes and in various organs. Liver cirrhosis, pulmonary fibrosis, sarcoidosis, keloids and kidney fibrosis are all chronic conditions associated with progressive fibrosis, thereby causing a continuous loss of normal tissue function.
- [0023] Acute fibrosis (usually with a sudden and severe onset and of short duration) occurs as a common response to various forms of trauma including accidental injuries (particularly injuries to the spine and central nervous system), infections, surgery, ischemic illness (e.g. cardiac scarring following heart attack), burns, environmental pollutants, alcohol and other types of toxins, acute respiratory distress syndrome, radiation and chemotherapy treatments).
- [0024] For further information on different types of fibrosis see: Molina V, Blank M, Shoenfeld Y. (2002), "*Fibrotic diseases*", *Harefuah*, 141(11): 973-8, 1009; Yu L, Noble NA, Border WA (2002), "*Therapeutic strategies to halt renal fibrosis*", *Curr Opin Pharmacol.* 2(2):177-81; Keane W F, Lyle P A. (2003), "*Recent advances in management of type 2 diabetes and nephropathy: lessons from the RENAL study*", *Am J Kidney Dis.* 41(3 Suppl 2): S22-5; Bohle A, Kressel G, Muller C A, Muller G A. (1989), "*The pathogenesis of chronic renal failure*", *Pathol Res Pract.* 185(4):421-40; Kikkawa R, Togawa M, Isono M, Isshiki K,

Haneda M. (1997), "Mechanism of the progression of diabetic nephropathy to renal failure", *Kidney Int Suppl.* 62:S39-40; Bataller R, Brenner D A. (2001), "Hepatic stellate cells as a target for the treatment of liver fibrosis", *Semin Liver Dis.* 21(3):437-51; Gross T J, Hunninghake G W, (2001) "Idiopathic pulmonary fibrosis", *N Engl J Med.* 345(7):517-25; Frohlich E D. (2001) "Fibrosis and ischemia: the real risks in hypertensive heart disease", *Am J Hypertens.*14(6 Pt 2):194S-199S.

[0025] Liver Fibrosis

[0026] Liver fibrosis (LF) is a generally irreversible consequence of hepatic damage of several etiologies. In the Western world, the main etiologic categories are: alcoholic liver disease (30-50%), viral hepatitis (30%), biliary disease (5-10%), primary hemochromatosis (5%), and drug-related and cryptogenic cirrhosis of unknown etiology(10-15%). Wilson's disease, α_1 -antitrypsin deficiency and other rare diseases also have liver fibrosis as one of the symptoms Scheinberg IH, Sternlieb I, *Wilson disease and idiopathic copper toxicosis.* *Am J Clin Nutr* 1996 May;63(5):842S-5S; Parfrey H, Mahadeva R, Lomas D A., *Alpha(1)-antitrypsin deficiency, liver disease and emphysema.* *Int J Biochem Cell Biol.* 2003 July;35(7):1009-14.

[0027] Liver cirrhosis, the end stage of liver fibrosis, frequently requires liver transplantation and is among the top ten causes of death in the Western world.

[0028] Anti-inflammatory agents, which cause inhibition of activation of hepatic stellate cells, stimulation of growth of hepatocytes and inhibition of post translational modification of collagen have all been used to treat liver fibrosis. However, due to the lack of selective targeting, these treatments suffer from, inter alia, the drawbacks of severe side effects,.

[0029] For more information see Friedman S L. (2003), "Liver fibrosis—from bench to bedside", *J Hepatol.* 38 Suppl 1:S38-53; Albanis E, Safadi R, Friedman S L. (2003), "Treatment of hepatic fibrosis: almost there", *Curr Gastroenterol Rep.* 5(1):48-56. See also Grenard P, Bresson-Hadni S, El Alaoui S, Chevallier M, Vuitton D A, Ricard-Blum S., *Transglutaminase-mediated cross-linking is involved in the stabilization of extracellular matrix in human liver fibrosis.* *J Hepatol.* 2001 September;35(3):367-75 ;Mirza A, Liu S L, Frizell E, Zhu J, Maddukuri S, Martinez J, Davies P, Schwarting R, Norton P, Zern M A., *A role for tissue transglutaminase in hepatic injury and fibrogenesis, and its regulation by NF-kappaB.* *Am J Physiol.* 1997 February;272(2 Pt 1):G28 1-8).

[0030] Kidney Fibrosis and Related Conditions

[0031] Chronic Renal Failure (CRF)

[0032] Chronic renal failure is a gradual and progressive loss of the ability of the kidneys to excrete wastes, concentrate urine, and conserve electrolytes. CRF is slowly progressive. It most often results from any disease that causes gradual loss of kidney function, and fibrosis is the main pathology that produces CRF.

[0033] Diabetic Nephropathy

[0034] Diabetic nephropathy, hallmarks of which are glomerulosclerosis and tubulointerstitial fibrosis, is the single most prevalent cause of end-stage renal disease in the

modern world, and diabetic patients constitute the largest population on dialysis. Such therapy is costly and far from optimal. Transplantation offers a better outcome but suffers from a severe shortage of donors. More targeted therapies against diabetic nephropathy (as well as against other types of kidney pathologies) are not developed, since molecular mechanisms underlying these pathologies are largely unknown. Identification of an essential functional target gene that is modulated in the disease and affects the severity of the outcome of diabetes nephropathy has a high diagnostic as well as therapeutic value.

[0035] Origins of kidney Pathology

[0036] Many pathological processes in the kidney (e.g., glomerular nephritis, physical obstructions, toxic injuries, metabolic and immunological diseases) eventually culminate in similar or identical morphological changes, namely glomerulosclerosis and tubulointerstitial fibrosis. Thus, different types of insults converge on the same single genetic program resulting in two hallmarks of fibrosis: the proliferation of fibroblasts and overproduction by them of various protein components of connective tissue. In addition, thickening of the basal membrane in the glomeruli accompanies interstitial fibrosis and culminates in glomerulosclerosis. See also Johnson TS, Skill NJ, El Nahas A M, Oldroyd S D, Thomas G L, Douthwaite J A, Haylor J L, Griffin M, *Transglutaminase transcription and antigen translocation in experimental renal scarring.* *J Am Soc Nephrol.* 1999 October;10(10):2146-57; Johnson T S, Griffin M, Thomas G L, Skill J, Cox A, Yang B, Nicholas B, Birckbichler P J, Muchaneta-Kubara C, Meguid El Nahas A, *The role of transglutaminase in the rat subtotal nephrectomy model of renal fibrosis.* *J Clin Invest.* 1997 Jun. 15;99(12):2950-60).

[0037] Pulmonary Fibrosis

[0038] Interstitial pulmonary fibrosis (IPF) is scarring of the lung caused by a variety of inhaled agents including mineral particles, organic dusts, and oxidant gases, or by unknown reasons (idiopathic lung fibrosis). The disease afflicts millions of individuals worldwide, and there are no effective therapeutic approaches. A major reason for the lack of useful treatments is that few of the molecular mechanisms of disease have been defined sufficiently to design appropriate targets for therapy (Lasky . J A., Brody A R. (2000), "Interstitial fibrosis and growth factors", *Environ Health Perspect.*; 108 Suppl 4:751-62).

[0039] The cellular substrate of pathogenesis of pulmonary fibrosis includes endothelial and epithelial cell injury, production of inflammatory cells and their mediators, and fibroblast activation., Fibrosis is believed to be related to a dysregulation in cross-talk between inflammatory and structural cells, mediated by various cytokines, chemokines and growth factors, which are responsible for the maintenance of tissue homeostasis and which coordinate the response to injury (Kelly M, Kolb M, Bonniaud P, Gauldie J. (2003), "Re-evaluation of fibrogenic cytokines in lung fibrosis" *Curr Pharm Des.* 9(1):39-49).

[0040] Conventional therapy consisting of glucocorticoids or cytotoxic drugs is usually ineffective in preventing progression of the disease. It is believed that further understanding of the molecular mechanisms of endothelial and epithelial cell injury, inflammatory reaction, fibroblast proliferation, collagen deposition and lung repair, is necessary

for the development of effective treatments against pulmonary fibrosis (Kuwano K, Hagimoto N, Hara N. (2001), "Molecular mechanisms of pulmonary fibrosis and current treatment", *Curr Mol Med.* 1(5):551-73). See also Griffin M, Smith L L, Wynne J., *Changes in transglutaminase activity in an experimental model of pulmonary fibrosis induced by Paraquat.* *Br. J. Exp. Pathol.* 1979 December; 60(6):653-61).

[0041] Cardiac Fibrosis

[0042] Heart failure is unique among the major cardiovascular disorders in that it alone is increasing in prevalence while there has been a striking decrease in other conditions. Some of this can be attributed to the aging of the populations of the United States and Europe. The ability to salvage patients with myocardial damage is also a major factor, as these patients may develop progression of left ventricular dysfunction due to deleterious remodeling of the heart.

[0043] The normal myocardium is composed of a variety of cells, cardiac myocytes and noncardiomyocytes, which include endothelial and vascular smooth muscle cells and fibroblasts. (Weber KT. (2000), "Fibrosis and hypertensive heart disease", *Curr Opin Cardiol.* 15(4):264-72).

[0044] Structural remodeling of the ventricular wall is a key determinant of clinical outcome in heart disease. Such remodeling involves the production and destruction of extracellular matrix proteins, cell proliferation and migration, and apoptotic and necrotic cell death. Cardiac fibroblasts are crucially involved in these processes, producing growth factors and cytokines that act as autocrine and paracrine factors, as well as extracellular matrix proteins and proteinases. Recent studies have shown that the interactions between cardiac fibroblasts and cardiomyocytes are essential for the progression of cardiac remodeling of which the net effect is deterioration in cardiac function and the onset of heart failure (Manabe I, Shindo T, Nagai R. (2002), "Gene expression in fibroblasts and fibrosis: involvement in cardiac hypertrophy", *Circ Res.* 13;91(12):1103-13).

[0045] The use of agents to block the renin-angiotensin-aldosterone and sympathetic nervous systems has been shown to inhibit (and sometimes even reverse) cardiac remodeling and to improve the clinical course of patients with cardiac dysfunction. However, drugs aiming at direct inhibition or reduction of fibrosis are not yet available. See also Greenberg B. (2001), "Treatment of heart failure: state of the art and perspectives", *J Cardiovasc Pharmacol.* 38 Suppl 2:S59-63, Zhang Z, Vezza R, Plappert T, McNamara P, Lawson J A, Austin S, Pratico D, Sutton M S, FitzGerald G A, *COX-2-dependent cardiac failure in Gh/tTG transgenic mice.* *Circ Res.* 2003 May 30;92(10):1153-61. Epub 2003 Apr. 17; Hwang K C, Gray C D, Sweet W E, Moravec C S, Im M J., *Alpha 1-adrenergic receptor coupling with Gh in the failing human heart.* *Circulation.* 1996 Aug. 15;94(4):718-26.

[0046] Neurological Diseases

[0047] Polyglutamine diseases are a group of neurological diseases that are caused by expansion of CAG trinucleotide repeats coding for polyglutamine insert. Polyglutamine diseases include Huntington's disease (HD), spinobulbar muscular atrophy, dentatorubral-pallidoluysian atrophy and spinocerebellar ataxias (SCAs) 1, 2, 3, 6, 7 and 17. All these diseases are characterized by the presence of expansion of

polyglutamine stretches (exceeding 35-40 glutamines), thus forming intranuclear aggregates, which leads to neuronal death. Alzheimer's disease (AD) is the most common cause of cognitive impairment in older patients and is expected to increase greatly in prevalence. Neurofibrillary degeneration, associated with the formation of paired helical filaments (PHF), is one of the critical neuropathological hallmarks of Alzheimer's disease (AD). Parkinson disease is a neurodegenerative disorder of aging characterized by a selective and progressive loss of dopaminergic neurons within the substantia nigra. See also Mastroberardino P G, Iannicola C, Nardacci R, Bernassola F, De Laurenzi V, Melino G, Moreno S, Pavone F, Oliverio S, Fesus L, Piacentini M. *Tissue transglutaminase ablation reduces neuronal death and prolongs survival in a mouse model of Huntington's disease.* *Cell Death Differ.* 2002 September;9(9):873-80; Karpuz M V, Becher M W, Springer J E, Chabas D, Youssef S, Pedotti R, Mitchell D, Steinman L., *Prolonged survival and decreased abnormal movements in transgenic model of Huntington disease, with administration of the transglutaminase inhibitor cystamine.* *Nat Med.* 2002 February;8(2):143-9; Citron B A, Suo Z, SantaCruz K, Davies P J, Qin F, Festoff B W., *Protein crosslinking, tissue transglutaminase, alternative splicing and neurodegeneration.* *Neurochem Int.* 2002 January;40(1):69-78; Chen J S, Mehta K., *Tissue transglutaminase: an enzyme with a split personality.* *Int J Biochem Cell Biol.* 1999 Aug.;31(8):817-36.

[0048] Osteoarthritis

[0049] Among the main characteristics of osteoarthritis are the degradation of articular cartilage and the formation of new bone at the joint edges, so-called osteophytes. See Van den Berg W B., *Growth factors in experimental osteoarthritis: transforming growth factor beta pathogenic?* *J Rheumatol Suppl.* 1995 February;43:143-5; Scharstuhl A, Glansbeek H L, Van Beuningen H M, Vitters E L, Van der Kraan P M.; Van den Berg W B., *Inhibition of endogenous TGF-beta during experimental osteoarthritis prevents osteophyte formation and impairs cartilage repair.* *J Immunol.* 2002 Jul. 1; 169(1):507-14; Karpouzas G A, Terkeltaub R A., *New developments in the pathogenesis of articular cartilage calcification.* *Curr Rheumatol Rep.* 1999 Dec; 1(2):121-7.

[0050] Ocular Diseases

[0051] Age-related cataracts: Cataracts are characterized by aggregation and covalent cross-linking of the crystallins, the major structural proteins of the eye lens, resulting in increase light scattering, opacification and cataract. Disturbance of calcium homeostasis in the tissue is one of the factors implicated in cataractogenesis. see Shridas et al., *FEBS Lett.* 2001 Jun. 22;499(3):245-50; Shin et al, *J Biol Chem.* 2004 Apr. 9;279(15):15032-9; Wan et al., *Br J Ophthalmol.* 2002 November;86(11):1293-8. and Takeuchi N, Kamei A. *Biol Pharm Bull.* 2000 March;23(3):283-90.

[0052] Proliferative vitreoretinopathy Proliferative vitreoretinopathy (PVR) is the most common complication following retinal detachment and associated with a retinal hole or break. PVR refers to the growth of cellular membranes within the vitreous cavity and on the front and back surfaces of the retina containing retinal pigment epithelial (RPE) cells. These membranes, which are essentially scar tissues, exert traction on the retina and may result in recurrences of retinal detachment, even after an initially successful retinal detachment procedure.

[0053] Migration and adhesion of dislocated retinal pigment epithelial (RPE) cells to a fibronectin-rich extracellular matrix is an initial step in proliferative vitreoretinopathy (PVR). See also Casaroli-Marano R P et al Invest Ophthalmol Vis Sci. 1999 August;40(9):2062-72). and Priglinger S et al, Invest Ophthalmol Vis Sci. 2004 March;45(3):955-63; Priglinger et al., Invest Ophthalmol Vis Sci. 2003 January;44(1):355-64.

[0054] Fibrosis following glaucoma filtering operation. The goal of the glaucoma filtration procedure is to create a new passageway by which aqueous fluid inside the eye can escape, thereby lowering the pressure. The filter, therefore, allows the drainage of fluid from inside the anterior chamber of the eye to a "pocket" created between the conjunctiva, which is the outermost covering of the eye, and the sclera, which is the underlying white anatomical structure of the eye. The fluid is eventually absorbed by blood vessels. Unfortunately, due to postoperative scarring, the generated drainage system may be blocked requiring additional surgical intervention(s).

[0055] Current anti-scarring regimens (Mitomycin C or 5FU) are limited due to the complications involved (e.g. blindness) e.g. see Cordeiro M F, Gay J A, Khaw P T., *Human anti-transforming factor-beta2 antibody: a new glaucoma anti-scarring agent Invest Ophthalmol Vis Sci.* 1999 September;40(10):2225-34.

[0056] In conclusion, there are no effective modes of therapy for the diseases described above, and there is a need, therefore, to develop novel effective compounds and methods of treatment for these purposes.

SUMMARY OF THE INVENTION

[0057] The invention provides novel double stranded oligoribonucleotides. These oligoribonucleotides inhibit human TGaseII via the mechanism of RNA interference. The invention also provides a pharmaceutical composition comprising such an oligoribonucleotide, and a vector capable of expressing the oligoribonucleotide. The present invention also provides a method of treating a patient suffering from a fibrosis-related pathology comprising administering to the patient the oligoribonucleotide typically as a pharmaceutical composition, in a therapeutically effective dose so as to thereby treat the patient. The present invention also contemplates treating other diseases and conditions. The invention also relates to treatment of fibrotic and other diseases by use of an antibody to TGaseII polypeptide.

BRIEF DESCRIPTION OF THE FIGURES

[0058] FIG. 1. This figure sets forth the nucleotide sequence of the human TGaseII cDNA—(gi|13653650|ref|XM 009482.3|—ORF)—SEQ ID NO:1.

[0059] FIG. 2. This figure sets forth the amino acid sequence of the human TGaseII corresponding polypeptide—SEQ ID NO:2.

[0060] FIG. 3. Western Blot results demonstrating the effect of various TGaseII siRNAs on human TGaseII polypeptide expression.

[0061] The figure demonstrates the activity of various siRNAs in reducing expression of human TGase polypeptide

in HeLa cells, 72 hr following siRNA transfection. GAPDH expression serves as control for protein loading. The numbers 15 and 30 represent concentration of the oligonucleotide in nM. "Cells" (first lane in each panel) stands for—nontransfected control cells. The last lane in each panel contains protein extracts from HeLa cells transfected with non-relevant (NR) siRNA, to ensure that the decrease in TGaseII expression is specific to the anti TGase siRNAs activity.

DETAILED DESCRIPTION OF THE INVENTION

[0062] The present invention provides a method for treatment of various pathologies, as recited below, in a subject in need of such treatment which comprises: administering to the subject an amount of an inhibitor of TGaseII polypeptide sufficient to effect a substantial inhibition of the TGaseII activity so as to thereby treat the subject. The TGaseII inhibitor may be L683685, an antibody to TGaseII polypeptide or an siRNA to TGaseII RNA or any of the TGaseII inhibitors known in the art (for further information on such inhibitors see for example: U.S. Pat. No. 5,021,440; 4,968,713 and 5,098,707). In particular the present invention relates to specific siRNAs targeting TGaseII RNA and the use thereof. The use of neutralizing antibodies against TGaseII is also disclosed. The present invention relates generally to compounds which down-regulate expression of the human TGaseII gene particularly to novel small interfering RNAs (siRNAs), and to the use of these novel siRNAs in the treatment of various diseases and medical conditions in particular fibrotic diseases, diseases related to fibrotic scarring and other diseases related to aberrant expression of Transglutaminase II.

[0063] The present invention provides methods and compositions for inhibiting expression of the target TGaseII gene in vivo. In general, the method includes administering oligoribonucleotides, such as small interfering RNAs (i.e., siRNAs) that are targeted to a particular mRNA and hybridize to, or interact with, it under biological conditions (within the cell), or a nucleic acid material that can produce siRNA in a cell, in an amount sufficient to down-regulate expression of a target gene by an RNA interference mechanism. In particular, the subject method can be used to inhibit expression of the TGaseII gene for treatment of disease.

[0064] Thus, the inhibitor of TGaseII expression (transcription or translation) or polypeptide activity may be inner alia siRNA, antibodies, preferably neutralizing antibodies or fragments thereof, including single chain antibodies, antisense oligonucleotides, antisense DNA or RNA molecules, proteins, polypeptides and peptides including peptidomimetics and dominant negatives, and also expression vectors expressing all the above. Additional inhibitors may be small chemical molecules, which generally have a molecular weight of less than 2000 daltons, more preferably less than 1000 daltons, even more preferably less than 500 daltons. These inhibitors may act as follows: small molecules may affect expression and/or activity; antibodies may affect activity; all kinds of antisense may affect TGaseII expression; and dominant negative polypeptides and peptidomimetics may affect activity; expression vectors may be used inter alia for delivery of antisense or dominant-negative polypeptides or antibodies.

[0065] In accordance with the present invention, the siRNA molecules or inhibitors of Transglutaminase II, such

as antibodies, may be used as drugs to treat various pathologies including fibrosis related pathologies (as defined below) and also to treat ocular diseases including cataract, cardiovascular diseases, neurological diseases, polyglutamine diseases (including Huntington's disease (HD), spinobulbar muscular atrophy, dentatorubral-pallidoluysian atrophy and spinocerebellar ataxias (SCAs) 1, 2, 3, 6, 7 and 17), Alzheimer's and Parkinson's disease and osteoarthritis.

[0066] As used herein, the term "Transglutaminase II gene", or "TGaseII gene", or "TGase gene" is defined as any homolog of TGaseII gene having preferably 90% homology, more preferably 95% homology, and even more preferably 98% homology to the amino acid encoding region of SEQ ID NO:1, or nucleic acid sequences which bind to the TGaseII gene under conditions of highly stringent hybridization, which are well-known in the art (for example, see Ausubel et al., Current Protocols in Molecular Biology, John Wiley and Sons, Baltimore, Md. (1988), updated in 1995 and 1998).

[0067] As used herein, the term "Transglutaminase II polypeptide", or "TGaseII polypeptide", or "TGase" is defined as any homolog of TGaseII polypeptide having preferably 90% homology, more preferably 95% homology, and even more preferably 98% homology to SEQ ID NO:2, as either full-length or fragments or a domain thereof, as a mutant of the polypeptide encoded by a spliced variant nucleic acid sequence, as a chimera with other polypeptides, provided that any of the above has the same or substantially the same biological function as the TGaseII polypeptide. TGaseII polypeptide, or a TGaseII polypeptide homolog, may be present in different forms, including but not limited to soluble protein, membrane-bound (either in purified membrane preparations or on a cell surface), bead-bound, or any other form presenting TGaseII protein or fragments and polypeptides derived thereof.

[0068] As used herein, an "interactor" is a molecule with which TGaseII binds or interacts or activates in nature; for example, a molecule on the surface of a TGaseII polypeptide expressing cell, a molecule on the surface of a second cell or a cytoplasmic molecule. An interactor may be a ligand that is activated by TGaseII alone or by TGaseII as part of a complex with other components. An interactor may be a component of a signal transduction pathway that facilitates transduction of an extracellular signal from TGaseII through the cell membrane and into the cell. An interactor, for example, can be a second intercellular protein that mediates downstream signaling from TGaseII. The interactor is a molecule with which TGase binds in competition with a known TGase substrate (e.g. fibronectin).

[0069] As used herein, the term "lysyl donor" or "K donor" is defined as any polypeptide having the ability to donate a lysyl side chain to allow the formation of gamma-glutamyl-lysine bonds during transglutamination process.

[0070] As used herein, the term "glutamyl donor" or "Q donor" is defined as any polypeptide having the ability to donate glutamine side chain to allow the formation of gamma-glutamyl-lysine bonds during transglutamination process.

[0071] The present invention provides double-stranded oligoribonucleotides (siRNAs), which down-regulate the expression of TGaseII. The downregulation of the expres-

sion of transglutaminase II can be measured by e.g., measuring the amount of the lysyl-glutamyl crosslinked material produced in the presence of the siRNAs or by direct assessment of the amounts of TGaseII mRNA or polypeptide. The amount of TGaseII mRNA may be measured by e.g., by Northern blotting, RNase protection, RT-PCR or real-time PCR. The amount of TGaseII polypeptide may be measured by immunoblotting or by immunoprecipitation or by ELISA with TGaseII-specific antibodies.

[0072] An siRNA of the invention is a duplex oligoribonucleotide in which the sense strand is derived from the mRNA sequence of gene TGaseII, and the antisense strand is complementary to the sense strand. In general, some deviation from the target mRNA sequence is tolerated without compromising the siRNA activity (see e.g. Czauderna et al 2003 Nucleic Acids Research 31(11), 2705-2716). An siRNA of the invention inhibits gene expression on a post-transcriptional level with or without destroying the mRNA. Without being bound by theory, siRNA may target the mRNA for specific cleavage and degradation and/or may inhibit translation from the targeted message.

[0073] There are at least two variant TGaseII polypeptides, for which the GeneBank references are variant 2 NM_198951.1 GI:39777598 and variant 1NM_004613.2 GI:39777596. The sequence given in **FIG. 1** is the nucleotide sequence of variant 2 (GI:39777598). Both variants and any other similar minor variants are included in the definition of TGaseII polypeptide and in the definition of the TGaseII genes encoding them.

[0074] As used herein, the term "TGaseII gene" is defined as the naturally-occurring human gene including any allelic variant thereof as well as any homolog of the TGaseII gene having preferably 90% homology, more preferably 95% homology, and even more preferably 98% homology to the amino acid encoding region of SEQ ID NO: 1 or nucleic acid sequences which bind to the TGaseII gene under conditions of highly stringent hybridization, which are well-known in the art (for example, see Ausubel et al., Current Protocols in Molecular Biology, John Wiley and Sons, Baltimore, Md. (1988), updated in 1995 and 1998).

[0075] As used herein, the term "TGaseII", or "TGaseII polypeptide" is defined as the naturally-occurring polypeptide product of the gene including any allelic variant thereof as well as any homolog of the TGaseII polypeptide having preferably 90% homology, more preferably 95% homology, and even more preferably 98% homology to SEQ ID NO:2, as either full-length or a fragment or a domain thereof, as a mutant or the polypeptide encoded by a spliced variant nucleic acid sequence, as a chimera with other polypeptides, provided that any of the above has the same or substantially the same biological function as the TGaseII polypeptide. More particularly, the invention provides a compound having the structure:

5'(N)_x-Z 3' (antisense strand)

3'Z-(N')_y5' (sense strand)

[0076] wherein each N and N' is a ribonucleotide which may be modified or unmodified in its sugar residue and (N)_x and (N')_y is oligomer in which each consecutive N or N' is joined to the next N or N' by a covalent bond;

[0077] wherein each of x and y is an integer between 19 and 40;

- [0078] wherein each of Z and Z' may be present or absent, but if present is dTdT and is covalently attached at the 3' terminus of the strand in which it is present;
- [0079] and wherein the sequence of (N)_x comprises any one of the antisense sequences present in Tables A, B and C
- [0080] It will be readily understood by those skilled in the art that the compounds of the present invention consist of a plurality of nucleotides which are linked through covalent linkages. Each Such covalent linkage may be a phosphodiester linkage, a phosphothioate linkage, or a combination of both, along the length of the nucleotide sequence of the individual strand. Other possible backbone modifications are described inter alia in U.S. Pat. Nos. 5,587,361; 6,242,589; 6,277,967; 6,326,358; 5,399,676; 5,489,677; and 5,596,086.
- [0081] In particular embodiments, x and y are preferably an integer between about 19 to about 27, most preferably from about 19 to about 23. In a particular embodiment of the compound of the invention, x may be equal to y (viz., x=y) and in preferred embodiments x=y=19 or x=y=21. In a particularly preferred embodiment x=y=19.
- [0082] In one embodiment of the compound of the invention, Z and Z' are both absent; in another embodiment one of Z or Z' is present.
- [0083] In one embodiment of the compound of the invention, all of the ribonucleotides of the compound are unmodified in their sugar residues.
- [0084] In some embodiments of the compound of the invention, at least one ribonucleotide is modified in its sugar residue, preferably a modification at the 2' position. The modification at the 2' position results in the presence of a moiety which is preferably selected from the group comprising amino, fluoro, methoxy, alkoxy and alkyl groups. In a presently most preferred embodiment the moiety at the 2' position is methoxy (2'-O-methyl).
- [0085] In some embodiments of the invention, alternating ribonucleotides are modified in both the antisense and the sense strands of the compound.
- [0086] In particularly preferred embodiments of the invention, the antisense strand is phosphorylated at the 5' terminus, and may or may not be phosphorylated at the 3' terminus; and the sense strand may or may not be phosphorylated at the 5' terminus and at the 3' terminus.
- [0087] In another embodiment of the compound of the invention, the ribonucleotides at the 5' and 3' termini of the antisense strand are modified in their sugar residues, and the ribonucleotides at the 5' and 3' termini of the sense strand are unmodified in their sugar residues.
- [0088] The invention further provides a vector capable of expressing any of the aforementioned oligoribonucleotides in unmodified form in a cell after which appropriate modification may be made.
- [0089] The invention also provides a composition comprising one or more of the compounds of the invention in a carrier, preferably a pharmaceutically acceptable carrier.
- [0090] The invention also provides a composition comprising a carrier and one or more of the compounds of the

invention in an amount effective to down-regulate expression in a cell of a human TGaseII gene, which compound comprises a sequence substantially complementary to the Sequence of (N)_x.

[0091] The invention also provides a method of down-regulating the expression of a human TGaseII gene by at least 50% as compared to a control comprising contacting an mRNA transcript of the gene with one or more of the compounds of the invention.

[0092] In one embodiment the compound is down-regulating TGaseII, whereby the down-regulation of TGaseII is selected from the group comprising down-regulation of TGaseII function (which may be examined by an enzymatic assay or a binding assay with a known interactor of the native gene/polypeptide, inter alia), down-regulation of TGaseII protein (which may be examined by Western blotting, ELISA or immuno-precipitation, inter alia) and down-regulation of TGaseII mRNA expression (which may be examined by Northern blotting, quantitative RT-PCR, in-situ hybridisation or microarray hybridisation, inter alia).

[0093] The invention also provides a method of treating a patient suffering from fibrosis or a fibrosis-related pathology, comprising administering to the patient a composition of the invention in a therapeutically effective dose so as to thereby treat the patient.

[0094] The invention also provides a method of treating a patient suffering from a pathology related to aberrant cross-linking of cellular proteins via Transglutaminase II comprising administering to the patient a composition of the invention in a therapeutically effective dose so as to thereby treat the patient.

[0095] The invention also provides a use of a therapeutically effective dose of one or more compounds of the invention for the preparation of a composition for promoting recovery in a patient suffering from fibrosis or a fibrosis-related pathology or a pathology related to aberrant crosslinking of cellular proteins via Transglutaminase II.

[0096] Fibrotic diseases or diseases in which fibrosis is evident (fibrosis-related pathology) include both acute and chronic forms of fibrosis of organs, including all etiological variants of the following: pulmonary fibrosis, including interstitial lung disease and fibrotic lung disease, liver fibrosis, cardiac fibrosis including myocardial fibrosis, kidney fibrosis including chronic renal failure, skin fibrosis including scleroderma, keloids and hypertrophic scars; myelofibrosis (bone marrow fibrosis); all types of ocular scarring including proliferative vitreoretinopathy (PVR) and scarring resulting from surgery to treat cataract or glaucoma; inflammatory bowel disease of variable etiology, macular degeneration, Grave's ophthalmopathy, drug induced ergotism, psoriasis, glioblastoma in Li-Fraumeni syndrome, sporadic glioblastoma, myeloid leukemia, acute myelogenous leukemia, myelodysplastic syndrome, myeloproliferative syndrome, gynecological cancer-, Kaposi's sarcoma, Hansen's disease, and collagenous colitis .

[0097] The compounds of the invention may be used to treat many other diseases and conditions apart from fibrotic diseases. Other indications may be ocular diseases including cataract, cardiovascular diseases especially cardiac hypertrophy, atherosclerosis/restenosis, neurological diseases, including polyglutamine diseases (such as Huntington's

disease), spinobulbar muscular atrophy, dentatorubral-pallidoluysian atrophy and spinocerebellar ataxias (SCAs) 1, 2, 3, 6, 7 and 17, Alzheimer's disease and Parkinson's disease.

[0098] The compound may have homologs wherein up to two of the ribonucleotides in each terminal region a base is altered; the terminal region refers to the four terminal ribonucleotides e.g. refers to bases 1-4 and/or 16-19 in a 19-mer sequence and to bases 1-4 and/or 18-21 in a 21-mer sequence.

[0099] The preferred oligonucleotides of the invention are the oligonucleotides listed in Tables A, B and C, preferably the oligonucleotides targeting human cDNA. The most preferred oligonucleotides of the invention are the oligonucleotides having inhibitory activity as demonstrated in Table D, preferably oligonucleotides targeting human TGaseII cDNA.

[0100] The presently most preferred compound of the invention is a blunt-ended 19-mer oligonucleotide, i.e. $x=y=19$ and Z and Z' are both absent; the oligonucleotide is phosphorylated at the 5' position of the antisense strand and at the 3' position of the sense strand wherein alternating ribonucleotides are modified at the 2' position in both the antisense and the sense strands, wherein the moiety at the 2' position is methoxy (2'-O-methyl) and wherein the ribonucleotides at the 5' and 3' termini of the antisense strand are modified in their sugar residues, and the ribonucleotides at the 5' and 3' termini of the sense strand are unmodified in their sugar residues. The presently most preferred such compound is TG_HMRG1. The antisense strand of TG_HMRG1 has SEQ ID NO: 22 and the sense strand has SEQ ID NO: 4. Other preferred compounds are TG_HMG1 and TG_HM1, which have the antisense strand represented by SEQ ID NOS: 23 and 25 respectively and the sense strand represented by SEQ ID NO: 5 and 7 respectively.

[0101] In one aspect of the invention the oligonucleotide comprises a double-stranded structure, whereby such double-stranded structure comprises

[0102] a first strand and a second strand, whereby

[0103] the first strand comprises a first stretch of contiguous nucleotides and the second strand comprises a second stretch of contiguous nucleotides, whereby

[0104] the first stretch is either complementary or identical to a nucleic acid sequence coding for TGaseII and whereby the second stretch is either identical or complementary to a nucleic acid sequence coding for TGaseII.

[0105] In an embodiment the first stretch and/or the second stretch comprises from about 14 to 40 nucleotides, preferably about 18 to 30 nucleotides, more preferably from about 19 to 27 nucleotides and most preferably from about 19 to 23 nucleotides, in particular from about 19 to 21 nucleotides. In such an aspect the oligonucleotide may be from 17-40 nucleotides in length. Additionally, further nucleic acids according to the present invention comprise at least 14 contiguous nucleotides of any one of the SEQ. ID. NO.3 to SEQ ID NO: 416 and more preferably 14 contiguous nucleotide base pairs at any end of the double-stranded structure comprised of the first stretch and second stretch as described above.

[0106] The term "treatment" as used herein refers to administration of a therapeutic substance effective to ameliorate symptoms associated with a disease or condition, to lessen the severity or cure the disease or condition, or to prevent the disease or condition from occurring.

[0107] In a particular embodiment, the administration comprises intravenous administration. In another particular embodiment the administration comprises topical or local administration.

[0108] Additionally, the present invention provides a method of regulating a pathology or disease (as recited above) in a patient in need of such treatment by administering to a patient a therapeutically effective dose of at least one antisense (AS) oligonucleotide or at least one siRNA against the nucleic acid sequences or a dominant negative peptide directed against the TGaseII sequences or TGaseII proteins or an antibody directed against the TGaseII polypeptide.

[0109] Delivery: Delivery systems aimed specifically at the enhanced and improved delivery of siRNA into mammalian cells have been developed, see, for example, Shen et al (FEBS letters 539: 111-114 (2003)), Xia et al., Nature Biotechnology 20: 1006-1010 (2002), Reich et al., Molecular Vision 9: 210-216 (2003), Sorensen et al. (J.Mol.Biol. 327: 761-766 (2003), Lewis et al., Nature Genetics 32: 107-108 (2002) and Simeoni et al., Nucleic Acids Research 31, 11: 2717-2724 (2003). siRNA has recently been successfully used for inhibition in primates; for further details see Tolentino et al., Retina 24(1) February 2004 I 132-138. Respiratory formulations for siRNA are described in U.S. patent application No. 2004/0063654 of Davis et al. Cholesterol-conjugated siRNAs (and other steroid and lipid conjugated siRNAs) can be used for delivery (see Soutschek et al Nature 432: 173-177(2004) *Therapeutic silencing of an endogenous gene by systemic administration of modified siRNAs*; and Lorenz et al. Bioorg. Med. Chemistry. Lett. 14:4975-4977 (2004) *Steroid and lipid conjugates of siRNAs to enhance cellular uptake and gene silencing in liver cells*.

[0110] The siRNAs or pharmaceutical compositions of the present invention are administered and dosed in accordance with good medical practice, taking into account the clinical condition of the individual patient, the disease to be treated, the site and method of administration, scheduling of administration, patient age, sex, body weight and other factors known to medical practitioners.

[0111] The "therapeutically effective dose" for purposes herein is thus determined by such considerations as are known in the art. The dose must be effective to achieve improvement including but not limited to improved survival rate or more rapid recovery, or improvement or elimination of symptoms and other indicators as are selected as appropriate measures by those skilled in the art. The compounds of the present invention can be administered by any of the conventional routes of administration. It should be noted that the compound can be administered as the compound or as pharmaceutically acceptable salt and can be administered alone or as an active ingredient in combination with pharmaceutically acceptable carriers, solvents, diluents, excipients, adjuvants and vehicles. The compounds can be administered orally, subcutaneously or parenterally including intravenous, intraarterial, intramuscular, intraperitoneally,

and intranasal administration as well as intrathecal and infusion techniques. Implants of the compounds are also useful. Liquid forms may be prepared for injection, the term including subcutaneous, transdermal, intravenous, intramuscular, intrathecal, and other parental routes of administration. The liquid compositions include aqueous solutions, with and without organic cosolvents, aqueous or oil suspensions, emulsions with edible oils, as well as similar pharmaceutical vehicles. In addition, under certain circumstances the compositions for use in the novel treatments of the present invention may be formed as aerosols, for intranasal and like administration. The patient being treated is a warm-blooded animal and, in particular, mammals including man. The pharmaceutically acceptable carriers, solvents, diluents, excipients, adjuvants and vehicles as well as implant carriers generally refer to inert, non-toxic solid or liquid fillers, diluents or encapsulating material not reacting with the active ingredients of the invention and they include liposomes and microspheres. Examples of delivery systems useful in the present invention include U. S. Pat. Nos. 5,225,182; 5,169,383; 5,167,616; 4,959,217; 4,925,678; 4,487,603; 4,486,194; 4,447,233; 4,447,224; 4,439,196; and 4,475,196. Many other such implants, delivery systems, and modules are well known to those skilled in the art. In one specific embodiment of this invention topical and transdermal formulations are particularly preferred.

[0112] In general, the active dose of compound for humans is in the range of from 1 ng/kg to about 20-100 mg/kg body weight per day, preferably about 0.01 mg to about 2-10 mg/kg body weight per day, in a regimen of one dose per day or twice or three or more times per day for a period of 1-4 weeks or longer. Treatment for many years or even lifetime treatment is also envisaged for some of the indications disclosed herein.

[0113] The present invention also provides for a process of preparing a pharmaceutical composition, which comprises:

[0114] obtaining at least one double stranded siRNA compound of the invention; and

[0115] admixing said compound with a pharmaceutically acceptable carrier.

[0116] The present invention also provides for a process of preparing a pharmaceutical composition, which comprises admixing a compound of the present invention with a pharmaceutically acceptable carrier.

[0117] In a preferred embodiment, the compound used in the preparation of a pharmaceutical composition is admixed with a carrier in a pharmaceutically effective dose. In a particular embodiment the compound of the present invention is conjugated to a steroid or to a lipid or to another suitable molecule e.g. to cholesterol.

[0118] Modifications or analogs of nucleotides can be introduced to improve the therapeutic properties of the nucleotides. Improved properties include increased nuclease resistance and/or increased ability to permeate cell membranes.

[0119] Accordingly, the present invention also includes all analogs of, or modifications to, a oligonucleotide of the invention that does not substantially affect the function of the polynucleotide or oligonucleotide. In a preferred embodiment such modification is related to the base moiety

of the nucleotide, to the sugar moiety of the nucleotide and/or to the phosphate moiety of the nucleotide.

[0120] In embodiments of the invention, the nucleotides can be selected from naturally occurring or synthetically modified bases. Naturally occurring bases include adenine, guanine, cytosine, thymine and uracil. Modified bases of the oligonucleotides include inosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl-, 2-propyl- and other alkyladenines, 5-halo uracil, 5-halo cytosine, 6-aza cytosine and 6-aza thymine, pseudo uracil, 4-thiuracil, 8-halo adenine, 8-aminoadenine, 8-thiol adenine, 8-thiolalkyl adenines, 8-hydroxyl adenine and other 8-substituted adenines, 8-halo guanines, 8-amino guanine, 8-thiol guanine, 8-thioalkyl guanines, 8-hydroxyl guanine and other substituted guanines, other aza and deaza adenines, other aza and deaza guanines, 5-trifluoromethyl uracil and 5-trifluoro cytosine.

[0121] In addition, analogs of nucleotides can be prepared wherein the structures of the nucleotides are fundamentally altered and are better suited as therapeutic or experimental reagents. An example of a nucleotide analog is a peptide nucleic acid (PNA) wherein the deoxyribose (or ribose) phosphate backbone in DNA (or RNA) is replaced with a polyamide backbone similar to that found in peptides. PNA analogs have been shown to be resistant to degradation by enzymes and to have extended lives in vivo and in vitro. Further, PNAs have been shown to bind more strongly to a complementary DNA sequence than to a DNA molecule. This observation is attributed to the lack of charge repulsion between the PNA strand and the DNA strand. Other modifications that can be made to oligonucleotides include polymer backbones, cyclic backbones, or acyclic backbones.

[0122] In one embodiment the modification is a modification of the phosphate moiety, whereby the modified phosphate moiety is selected from the group comprising phosphothioate.

[0123] The compounds of the present invention can be synthesized by any of the methods that are well-known in the art for synthesis of ribonucleic (or deoxyribonucleic) oligonucleotides. Such synthesis is, among others, described in Beaucage S. L. and Iyer R. P., *Tetrahedron* 1992; 48: 2223-2311, Beaucage S. L. and Iyer R. P., *Tetrahedron* 1993; 49: 6123-6194 and Caruthers M. H. et. al., *Methods Enzymol.* 1987; 154: 287-313, the synthesis of thioates is, among others, described in Eckstein F., *Annu. Rev. Biochem.* 1985; 54: 367-402, the synthesis of RNA molecules is described in Sproat B., in *Humana Press* 2005 Edited by Herdewijn P.; Kap. 2: 17-31 and respective downstream processes are, among others, described in Pingoud A. et. al., in *IRL Press* 1989 Edited by Oliver R. W. A.; Kap. 7: 183-208 and Sproat B., in *Humana Press* 2005 Edited by Herdewijn P.; Kap. 2: 17-31 (supra).

[0124] Other synthetic procedures are known in the art e.g. the procedures as described in Usman et al., 1987, *J. Am. Chem. Soc.*, 109, 7845; Scaringe et al., 1990, *Nucleic Acids Res.*, 18, 5433; Wincott et al., 1995, *Nucleic Acids Res.* 23, 2677-2684; and Wincott et al., 1997, *Methods Mol. Bio.*, 74, 59, and these procedures may make use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. The modified (e.g. 2'-O-methylated) nucleotides and unmodified nucleotides are incorporated as desired.

[0125] The oligonucleotides of the present invention can be synthesized separately and joined together post-synthetically.

cally, for example, by ligation (Moore et al., 1992 *Science* 256, 9923; Draper et al., International PCT publication No. WO93/23569; Shabarova et al., 1991, *Nucleic Acids Research* 19, 4247; Bellon et al., 1997, *Nucleosides & Nucleotides*, 16, 951; Bellon et al., 1997, *Bioconjugate Chem.* 8, 204), or by hybridization following synthesis and/or deprotection.

[0126] It is noted that a commercially available machine (available, inter alia, from Applied Biosystems) can be used; the oligonucleotides are prepared according to the sequences disclosed herein. Overlapping pairs of chemically synthesized fragments can be ligated using methods well known in the art (e.g., see U.S. Pat. No. 6,121,426). The strands are synthesized separately and then are annealed to each other in the tube. Then, the double-stranded siRNAs are separated from the single-stranded oligonucleotides that were not annealed (e.g. because of the excess of one of them) by HPLC. In relation to the siRNAs or siRNA fragments of the present invention, two or more such sequences can be synthesized and linked together for use in the present invention.

[0127] The compounds of the invention can also be synthesized via a tandem synthesis methodology, as described in US patent application publication No. US2004/0019001 (McSwiggen), wherein both siRNA strands are synthesized as a single contiguous oligonucleotide fragment or strand separated by a cleavable linker which is subsequently cleaved to provide separate siRNA fragments or strands that hybridize and permit purification of the siRNA duplex. The linker can be a polynucleotide linker or a non-nucleotide linker.

[0128] The compounds of the present invention can be delivered either directly or with viral or non-viral vectors. When delivered directly the sequences are generally rendered nuclease resistant.

[0129] Alternatively the sequences can be incorporated into expression cassettes or constructs such that the sequence is expressed in the cell as discussed herein below. Generally the construct contains the proper regulatory sequence or promoter to allow the sequence to be expressed in the targeted cell. Vectors optionally used for delivery of the compounds of the present invention are commercially available, and may be modified for the purpose of delivery of the compounds of the present invention by methods known to one of skill in the art.

[0130] It is also envisaged that a long double stranded oligonucleotide (typically 25-500 nucleotides in length) comprising one or more of the sequences of the oligonucleotides of the invention may be delivered and may be processed intracellularly by endogenous cellular complexes (e.g. by DICER as described above) to produce smaller double stranded oligonucleotides which are oligonucleotides of the invention.

[0131] As used herein, the term "polypeptide" refers to, in addition to a polypeptide, an oligopeptide, peptide and a full protein.

[0132] Animal model systems: Testing the active siRNAs of the invention may be done in predictive animal models. Several models for kidney fibrosis are described in Example 3.

[0133] Two models of liver fibrosis in rats are the Bile Duct Ligation (BDL) with sham operation as controls, and CCl₄ poisoning, with olive oil fed animals as controls, as described in the following references: Lotersztajn S, Julien B, Teixeira-Clerc F, Grenard P, Mallat A, *Hepatic Fibrosis: Molecular Mechanisms and Drug Targets*. Annu Rev Pharmacol Toxicol. 2004 Oct. 07; Uchio K, Graham M, Dean N M, Rosenbaum J, Desmouliere A., *Down-regulation of connective tissue growth factor and type I collagen mRNA expression by connective tissue growth factor antisense oligonucleotide during experimental liver fibrosis*. Wound Repair Regen. 2004 January-February; 12(1):60-6. ;and. Xu X Q, Leow C K, Lu X, Zhang X, Liu J S, Wong W H, Asperger A, Deininger S, Eastwood Leung H C., *Molecular classification of liver cirrhosis in a rat model by proteomics and bioinformatics* Proteomics. 2004 October;4(10):3235-45.

[0134] Models for ocular scarring are well known in the art e.g. Sherwood M B et al., *J Glaucoma*. 2004 October;13(5):407-12. *A new model of glaucoma filtering surgery in the rat*; Miller M H et al., *Ophthalmic Surg*. 1989 May;20(5):350-7. *Wound healing in an animal model of glaucoma fistulizing surgery in the rabbit*, vanBockxmeer F M et al., *Retina*. 1985 Fall-Winter; 5(4): 239-52. *Models for assessing scar tissue inhibitors*; Wiedemann P et al., *J Pharmacol Methods*. 1984 August; 12(1): 69-78. *Proliferative vitreoretinopathy: the rabbit cell injection model for screening of antiproliferative drugs*.

[0135] Models of cataract are described in the following publications: The role of Src family kinases in cortical cataract formation. Zhou J, Menko AS. *Invest Ophthalmol Vis Sci*. 2002 July;43(7):2293-300; Bioavailability and anti-cataract effects of a topical ocular drug delivery system containing disulfiram and hydroxypropyl-beta-cyclodextrin on selenite-treated rats. Wang S, Li D, Ito Y, Nabekura T, Wang S, Zhang J, Wu C. *Curr Eye Res*. 2004 July;29(1):51-8; and Long-term organ culture system to study the effects of UV-Airradiation on lens transglutaminase. Weinreb O, Dovrat A.; *Curr Eye Res*. 2004 July;29(1):51-8.

[0136] Antibody Production

[0137] By the term "antibody" as used in the present invention is meant both poly- and mono-clonal complete antibodies as well as fragments thereof, such as Fab, F(ab')₂, and Fv, which are capable of binding the epitopic determinant. These antibody fragments retain the ability to selectively bind with its antigen or receptor and are exemplified as follows, inter alia:

[0138] (1) Fab, the fragment which contains a monovalent antigen-binding fragment of an antibody molecule can be produced by digestion of whole antibody with the enzyme papain to yield a light chain and a portion of the heavy chain;

[0139] (2) (Fab')₂, the fragment of the antibody that can be obtained by treating whole antibody with the enzyme pepsin without subsequent reduction; F(ab')₂ is a dimer of two Fab fragments held together by two disulfide bonds;

[0140] (3) Fv, defined as a genetically engineered fragment containing the variable region of the light chain and the variable region of the heavy chain expressed as two chains; and

- [0141] (4) Single chain antibody (SCA), defined as a genetically engineered molecule containing the variable region of the light chain and the variable region of the heavy chain linked by a suitable polypeptide linker as a genetically fused single chain molecule.
- [0142] Such fragments having antibody functional activity can be prepared by methods known to those skilled in the art (e.g. Bird et al. (1988) *Science* 242:423-426)
- [0143] Conveniently, antibodies may be prepared against the immunogen or portion thereof, for example, a synthetic peptide based on the sequence, or prepared recombinantly by cloning techniques or the natural gene product and/or portions thereof may be isolated and used as the immunogen. Immunogens can be used to produce antibodies by standard antibody production technology well known to those skilled in the art, as described generally in Harlow and Lane (1988), *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., and Borrebaeck (1992), *Antibody Engineering—A Practical Guide*, W. H. Freeman and Co., NY.
- [0144] For producing polyclonal antibodies a host, such as a rabbit or goat, is immunized with the immunogen or immunogen fragment, generally with an adjuvant and, if necessary, coupled to a carrier; antibodies to the immunogen are collected from the sera. Further, the polyclonal antibody can be absorbed such that it is monospecific; that is, the sera can be absorbed against related immunogens so that no cross-reactive antibodies remain in the sera, rendering it monospecific.
- [0145] For producing monoclonal antibodies the technique involves hyperimmunization of an appropriate donor with the immunogen, generally a mouse, and isolation of splenic antibody-producing cells. These cells are fused to an immortal cell, such as a myeloma cell, to provide a fused cell hybrid that is immortal and secretes the required antibody. The cells are then cultured, in bulk, and the monoclonal antibodies harvested from the culture media for use.
- [0146] For producing recombinant antibody see generally Huston et al. (1991) "Protein engineering of single-chain Fv analogs and fusion proteins" in *Methods in Enzymology* (JJ Langone, ed., Academic Press, New York, N.Y.) 203:46-88; Johnson and Bird (1991) "Construction of single-chain Fvb derivatives of monoclonal antibodies and their production in *Escherichia coli* in *Methods in Enzymology* (JJ Langone, ed., Academic Press, New York, N.Y.) 203:88-99; Mernaugh and Mernaugh (1995) "An overview of phage-displayed recombinant antibodies" in *Molecular Methods In Plant Pathology* (RP Singh and US Singh, eds., CRC Press Inc., Boca Raton, Fla.:359-365). In particular scFv antibodies are described in WO 2004/007553 (Tedesco and Marzari). Additionally, messenger RNAs from antibody-producing B-lymphocytes of animals, or hybridoma can be reverse-transcribed to obtain complementary DNAs (cDNAs). Antibody cDNA, which can be full or partial length, is amplified and cloned into a phage or a plasmid. The cDNA can be a partial length of heavy and light chain cDNA, separated or connected by a linker. The antibody, or antibody fragment, is expressed using a suitable expression system to obtain recombinant antibody. Antibody cDNA can also be obtained by screening pertinent expression libraries.
- [0147] The antibody can be bound to a solid support substrate or conjugated with a detectable moiety or be both bound and conjugated as is well known in the art. (For a general discussion of conjugation of fluorescent or enzymatic moieties see Johnstone & Thorpe (1982.), *Immunochemistry in Practice*, Blackwell Scientific Publications, Oxford). The binding of antibodies to a solid support substrate is also well known in the art (for a general discussion, see Harlow & Lane (1988) *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Publications, New York; and Borrebaeck (1992), *Antibody Engineering—A Practical Guide*, W. H. Freeman and Co.). The detectable moieties contemplated with the present invention can include, but are not limited to, fluorescent, metallic, enzymatic and radioactive markers such as biotin, gold, ferritin, alkaline phosphatase, β -galactosidase, peroxidase, urease, fluorescein, rhodamine, tritium, ^{14}C and iodination.
- [0148] Additional compounds which are also considered to be useful in the treatment of the diseases and disorders discussed herein may be antisense DNA molecules (which can be generated using the sequence in FIG. 1 by methods known in the art), catalytic RNAs such as ribozymes, polypeptides such as dominant negative peptides (which can be generated using the sequence in FIG. 2 by methods known in the art) or other polypeptide inhibitors. Antisense DNA molecules which comprise the siRNA sequences disclosed herein (with the appropriate nucleic acid modifications stemming from the differences between DNA and RNA) are particularly desirable and may be used in the same capacity as their corresponding siRNAs for all uses and methods disclosed herein.
- [0149] Screening of TGase Inactivating Compounds
- [0150] Some of the compounds and compositions of the present invention may be used in a screening assay for identifying and isolating compounds that modulate the activity of TGaseII, in particular compounds that modulate fibrotic disease or fibrosis-related pathology. The compounds to be screened comprise inter alia substances such as small chemical molecules, antibodies especially neutralizing antibodies, inhibitory polypeptides and dominant negative peptides.
- [0151] The inhibitory activity of the compounds of the present invention on TGaseII polypeptide enzymatic activity or binding of the compounds of the present invention to TGaseII may be used to determine the interaction of an additional compound with the TGaseII polypeptide, e.g., if the additional compound competes with the antibodies or dominant-negative peptides of the present invention for TGaseII inhibition, or if the additional compound rescues said inhibition. The inhibition or activation can be tested by various means, such as, inter alia, assaying for the product of the activity of the TGaseII polypeptide or displacement of binding compound from the TGaseII polypeptide in radioactive or fluorescent competition assays.
- [0152] The present invention additionally provides for a process of obtaining a compound capable of inhibiting the enzymatic activity of a TGaseII polypeptide, preferably a human TGaseII polypeptide, that comprises the steps of:
- [0153] (i) contacting the TGaseII polypeptide or cells expressing the TGaseII polypeptide with the compound, a lysyl donor and with a glutamyl donor which is a biological molecule;
- [0154] (ii) removing excess lysyl donor from the mixture of step (i);

- [0155] (iii) measuring the amount of the lysyl-glutamyl crosslinked material produced in the presence of the compound;
- [0156] (iv) comparing the amount of lysyl-glutamyl crosslinked material measured in step (iii) to that measured in the absence of the compound under controlled conditions, wherein a decrease in the amount of lysyl-glutamyl crosslinked material is indicative of inhibition of the TGaseII polypeptide activity by the compound; and
- [0157] (v) identifying the compound as an inhibitor of TGaseII polypeptide activity.
- [0158] In one embodiment of all the processes described herein, the TGaseII polypeptide used in such process comprises consecutive amino acids, the sequence of which is set forth in SEQ ID NO: 2.
- [0159] In another embodiment, the lysyl donor of step (i) is tagged and the measurement in step (iii) is of the tag related read-out, and wherein, a decrease in the read-out level is indicative of inhibition of the TGaseII polypeptide activity by the compound.
- [0160] The glutamyl donor which is a biological molecule may be e.g. fibronectin. or collagen.
- [0161] In another embodiment, the lysyl donor used in such process is cadaverin tagged with a dansyl fluorescent tag.
- [0162] In another embodiment the lysyl donor used in such process is tagged with biotin, and in a specific embodiment, the lysyl donor is biotin cadaverine. Biotin is detected by streptavidin (or a modified streptavidin such as nutrivadin) conjugated to readouts known in the art (e.g. conjugated to horseradish peroxidase, wherein the amount of horseradish peroxidase is quantified using tetramethylbenzidine as a substrate).
- [0163] in yet another embodiment of the invention, the glutamyl donor in the provided process may be an extracellular matrix protein or a cellular protein. The extracellular matrix protein is selected from the group consisting of: fibronectin, collagen, osteonectin, ECM-gel (e.g. Sigma E-1270), and the intracellular protein is selected inter alia from the group consisting of: RhoA, filamin, spectrin, vimentin, HSP90, HSP60, (see Orru S, Caputo I, D'Amato A, Ruoppolo M, Esposito C *Proteomics identification of acyl-acceptor and acyl-donor substrates for transglutaminase in a human intestinal epithelial cell line. Implications for celiac disease. J Biol Chem.* 2003 Aug. 22;278(34):31766-73).
- [0164] In a different embodiment, the compound is contacted with cells expressing the TGaseII polypeptide. The cells that may be used in such process may either be separated or present in a tissue. The cells may express the TGaseII polypeptide naturally or as a result of having been transfected with TGaseII gene, either transiently or stably or may over-express the TGaseII gene and the activity of TGaseII will be compared between over-expressors to normal TGaseII expressing cells. In a further embodiment, the glutamyl donor is either a natural product of the cells or it is added from outside.
- [0165] In a different embodiment, the TGaseII polypeptide is contacted with the compound. The TGaseII polypeptide can be either immobilized or free in a solution. In an embodiment of the provided screening process the glutamyl donor is immobilized.
- [0166] In a further embodiment, the processes provided for obtaining a compound capable of inhibiting the activity of human TGaseII may comprise a further step in which prior to step (i) TGaseII is contacted with a second compound known to bind TGaseII.
- [0167] In one embodiment of the invention, the tag read-out in the provided processes described herein is the interaction of biotin with neutravidin conjugated to horseradish peroxidase, wherein the amount of cell-bound horseradish peroxidase is quantified using TMB (tetramethylbenzidine) as a substrate.
- [0168] In yet a further embodiment, the compound obtained by the provided process inhibits the activity of the TGaseII polypeptide at least 2-fold more effectively than it inhibits the activity of at least one other member of the TGase family, and more preferably the inhibition is at least 10-fold, 50-fold and even 100-fold more effective. In such process, either the TGaseII polypeptide or the second compound may be immobilized.
- [0169] In one another embodiment, the compound obtained by any of the provided processes is an antibody.
- [0170] The invention further provides a process of obtaining a compound which modulates the activity of a TGaseII polypeptide, preferably a human TGaseII polypeptide, which comprises the steps of:
- [0171] (i) contacting the TGaseII polypeptide with an interactor with which the TGaseII polypeptide interacts specifically in vivo;
- [0172] (ii) contacting the TGaseII polypeptide or the interactor with said compound; and
- [0173] (iii) measuring the effect of the compound on the interaction between TGaseII polypeptide and the interactor by measuring a parameter related to fibrosis; and
- [0174] (iv) comparing the effect measured in step (iii) with the effect measured in the absence of the compound, a change in the effect measured indicating that the compound modulates the activity of the human TGaseII polypeptide.
- [0175] In one embodiment of the invention the compound obtained by the provided process inhibits the activity of a human TGaseII polypeptide.
- [0176] In another embodiment of the invention the TGaseII polypeptide in such process comprises consecutive amino acids, the sequence of which is set forth in SEQ ID NO: 2. In a further embodiment either the TGaseII polypeptide or the interactor are immobilized.
- [0177] In a further embodiment of the invention, the parameter measured in any of the provided processes is related to a pathology characterized by TGaseII up-regulation in general and to fibrosis related pathologies as defined above, and also to cataract, cardiovascular diseases, neurological disorders, polyglutamine diseases including Huntington's disease (HD), spinobulbar muscular atrophy, dentatorubral-pallidolusian atrophy and spinocerebellar ataxias (SCAs) 1, 2, 3, 6, 7 and 17), Alzheimer's and Parkinson's disease, coeliac disease and osteoarthritis. It is another object of the present invention to provide a process

of obtaining a compound capable of inhibiting the activity of a human TGaseII polypeptide that comprises the steps of:

- [0178] (i) contacting the TGaseII polypeptide or cells expressing the TGaseII polypeptide with a plurality of compounds, a tagged lysyl donor and with a glutamyl donor which is a biological molecule;
- [0179] (ii) washing excess tagged lysyl donor from the mixture of step (i); and
- [0180] (iii) measuring the tag related read-out in the presence of the plurality of compounds;
- [0181] (iv) comparing the tag read-out measured in step (iii) to that measured in the absence of the plurality of compounds under controlled conditions, wherein a decrease in the read-out level is indicative of inhibition of the TGaseII polypeptide activity by the plurality of compounds;
- [0182] (v) separately determining which compound or compounds present in the plurality inhibit the activity of a human TGaseII.
- [0183] It is another aspect of the present invention to provide a cell-based process of obtaining a compound capable of inhibiting the activity of a TGaseII polypeptide, preferably human TGaseII polypeptide, that comprises the steps of:
 - [0184] (i) contacting cells expressing active TGaseII polypeptide with the compound and with a lysyl donor;
 - [0185] (ii) removing excess lysyl donor from the mixture of step (i);
 - [0186] (iii) measuring the amount of lysyl-glutamyl crosslinked material produced in the presence of the compound;
 - [0187] (iv) comparing the amount of lysyl-glutamyl crosslinked material measured in step (iii) to that measured in the absence of the compound under controlled conditions, wherein a decrease in the amount of lysyl-glutamyl crosslinked material is indicative of inhibition of the TGaseII polypeptide activity by the compound; and
 - [0188] (v) identifying the compound as an inhibitor of TGaseII polypeptide
- [0189] It is another aspect of the present invention to provide a cell-based process of obtaining a compound capable of inhibiting the activity of a human TGaseII polypeptide that comprises the steps of:
 - [0190] a. contacting cells expressing the TGaseII polypeptide with a plurality of compounds and with a lysyl donor;
 - [0191] b. removing excess lysyl donor from the mixture of step (i); and
 - [0192] c. measuring the amount of the lysyl-glutamyl crosslinked material produced in the presence of the plurality of compounds;
 - [0193] d. comparing the amount of lysyl-glutamyl crosslinked material measured in step (iii) to that measured in the absence of the plurality of compounds under controlled conditions, wherein a decrease in the amount of lysyl-glutamyl crosslinked

material is indicative of inhibition of the TGaseII polypeptide activity by the plurality of compounds; and

- [0194] (e) separately determining which compound or compounds present in the plurality inhibit the activity of a human TGaseII.
- [0195] Methods
- [0196] General Methods in Molecular Biology
- [0197] Standard molecular biology techniques known in the art and not specifically described were generally followed as in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, New York (1989), and as in Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley and Sons, Baltimore, Md. (1989) and as in Perbal, *A Practical Guide to Molecular Cloning*, John Wiley & Sons, New York (1988), and as in Watson et al., *Recombinant DNA*, Scientific American Books, New York and in Birren et al (eds) *Genome Analysis: A Laboratory Manual Series*, Vols. 1-4 Cold Spring Harbor Laboratory Press, New York (1998) and methodology as set forth in U.S. Pat. Nos. 4,666,828; 4,683,202; 4,801,531; 5,192,659 and 5,272,057 and incorporated herein by reference. Polymerase chain reaction (PCR) was carried out generally as in *PCR Protocols: A Guide To Methods And Applications*, Academic Press, San Diego, Calif. (1990). In situ (in cell) PCR in combination with Flow Cytometry can be used for detection of cells containing specific DNA and mRNA sequences (e.g. Testoni et al., 1996, *Blood* 87:3822.) Methods of performing RT-PCR are also well known in the art.
- [0198] The present invention is illustrated in detail below with reference to Examples, but is not to be construed as being limited thereto.

EXAMPLES

Example 1

- [0199] Design of Active siRNA Compounds
- [0200] Using proprietary algorithms and the known sequence of cDNA of TGaseII (SEQ ID NO:1), the sequences of many potential siRNAs were generated. These are shown in the Tables below. Note that the abbreviations for species are: H: human; M: mouse; R: rat; G: guinea pig; C: cow.
- [0201] Table A shows 18 siRNAs that have so far been chemically synthesized and tested for activity (see Example 2). All these siRNAs are 19-mers. In Table A the sense strands of siRNAs 1-18 have SEQ ID NOS: 3-20 respectively, and the antisense strands of siRNAs 1-18 have SEQ ID NOS: 21-38 respectively.
- [0202] Table B below shows 153 additional 19-mer siRNAs, which have been generated by the proprietary algorithms but not yet tested for activity. In Table B, the sense strands of siRNAs 1-153 have SEQ ID NOS: 39-191, respectively, and the antisense strands of siRNAs 1-153 have SEQ ID NOS: 192-344 respectively.
- [0203] Table C below shows 36 additional 21-mer siRNAs that have been generated by the proprietary algorithms. In Table C, the sense strands of siRNAs 1-36 have SEQ ID NOS: 345-380 respectively, and the antisense strands of siRNAs 1-36 have SEQ ID NOS: 381-416, respectively.

TABLE A

No.name	Sense strand	Antisense strand	Species	NM_198951 (human)	NM_009373 (mouse)	NM_198851 (RAT)	M19646.1 (GP)
1 TG_HMR1	ACAAGAGCGAGAUGAUCUG	CAGAUCAUCUCGCUCUUGU	hum_mus_rat	[1077– 1095]	[1069– 1087]	[1033– 1051]	
2 TG_HMRG1	AGAGCGAGAUGAUCUGGAA	UCCAGAUCAUCUCGCUCU	hum_mus_rat_GP	[1080– 1098]	[1072– 1090]	[1036– 1054]	[1048– 1066]
3 TG_HMG1	ACCCCAAGUCCUGAAGAA	UUCUUCAGGAACUUGGGU	hum_mus_GP	[699–717]	[691–709]		[667–685]
4 TG_HMG2	GCGAGAUGAUCUGGAACUU	AAGUUCAGAUCAUCUCGC	hum_mus_GP	[1083– 1101]	[1075– 1093]		[1051– 1069]
5 TG_HM1	CAAAUCCAUAACCGUCC	GGAACGGUUGAUGGAUUUG	hum_mus	[1339– 1357]	[1331– 1349]		
6 TG_M1	GAACAUCCAUGAGAAACUU	AAGUUUCUCAUGGAUGUUC	mus		2599–2617		
7 TG_M2	CGACCUAUGCCAAGAGAAA	UUUCUCUUGGCAUAGGUCG	mus		164–182		
8 TG_M3	GGUGUGAUUUGGAGAUAUCA	UGAAUCCAAAUCACACC	mus		118–136		
9 TG_M4	CCAACCACCGAACAACU	AGUUUUGUUCAGGUGGUUG	mus_rat		[1468– 1486]	[1432– 1450]	
10 TG_M5	GAACAAACUGGCAGAGAAA	UUUCUCGCCAGUUUGUUC	mus_rat		[1478– 1496]	[1442– 1460]	
11 TG_M6	GCUCUGUCAAGUUCAUCA	UUGAUGAACUUGACAGAGC	mus_rat		601–619		
12 TG_M7	GAUCCCUACUCUGAGAACA	UGUUCUCAGAGUAGGGAUC	mus_rat		1692–1637		
13 TG_M8	CCAGAGUGGUGACCAACUA	UAGUUGGUCACCACUCUGG	mus_rat		[976–994]	[940–958]	
14 TG_M9	GCAACAAGAGCGAGAUGAU	AUCAUCUCGCUCUUGUUGC	mus_rat		[1066– 1084]	[1030– 1048]	
15 TG_M10	GCAACCUGCUCUACGAGUA	UACUCGAGAGCAGGUUGC	mus_rat		[1018– 1036]	[982– 1000]	
16 TG_H1	GUGACCUAACCCAUAGCA	UGCUAAGUGGUUAGGUCAC	hum	1773–1791			
17 TG_H2	GUAGUGACCUAACCCAUUA	UAAGUGGUUAGGUCACUAC	hum	1770–1788			
18 TG_HG1	GACGUGGGACAACAACUA	UAGUUGUUGCCAGCGUC	hum_GP	[816–834]			[784–802]

[0204]

TABLE B

No.Method	Sense siRNA	AntiSense siRNA	human GI 39777598	Mouse GI 31543859	Rat GI 42476286	Guinea- pig GI 387604	Cow GI 31343554	species
1 Cross Sp	UCCACUCGCGGGUGGAGU	ACUCCACCCAGCAGUGGAA	1100– 1118	1092– 1110	1056– 1074	1068– 1086	1046– 1064	hmrgc
2 Cross Sp	AAGAGCGAGAUGAUCUGGA	UCCAGAUCAUCUCGCUCUU	1079– 1097	1071– 1089	1035– 1053	1047– 1065	1025– 1043	hmrgc
3 Cross Sp	CAAGAGCGAGAUGAUCUGG	CCAGAUCAUCUCGCUCUUG	1078– 1096	1070– 1088	1034– 1052	1046– 1064	1024– 1042	hmrgc
4 Cross Sp	AACCACCGAACAACUGG	CCAGUUUGUUCAGGUGGU	1478– 1496	1470– 1488	1434– 1452	–	1424– 1442	hmr
5 Cross Sp	ACCACCGAACAACUGGC	GCCAGUUUGUUCAGGUGGU	1479– 1497	1471– 1489	1435– 1453	–	1425– 1442	hmr
6 Cross Sp	CUGGAACUCCACUCUGG	CCAGCAGUGGAAGUCCAG	1093– 1111	1085– 1103	1049– 1067	1061– 1079	1039– 1057	hm

TABLE B-continued

No.	Method	Sense siRNA	AntiSense siRNA	human GI	Mouse GI	Rat GI	Guinea-	Cow GI	species
				39777598	31543859	42476286	pig GI 387604	31343554	
7	Cross	Sp AACUUCCACUGCUGGGUGG	CCACCCAGCAGUGGAAGUU	1097-1115	1089-1107	1056-1071	1065-1083	1043-1061	hm
8	Cross	Sp AGGAGAAGAGCGAAGGGAC	GUCCCUUCGCUCUUCUCCU	1185-1203	1177-1195	1141-1156	-	1131-1149	hm
9	Cross	Sp UGAUCUGGAACUCCACUG	CAGUGGAAGUCCAGAUCA	1089-1107	1081-1099	-	1057-1075	1035-1053	hm
10	Cross	Sp GAGCGAGAUGAUCUGGAAC	GUUCCAGAUCAUCUCGCUC	1081-1099	1073-1091	1037-1054	1049-1067	1027-1045	hm
11	Cross	Sp UCUGGAACUCCACUGCUG	CAGCAGUGGAAGUCCAGA	1092-1110	1084-1102	1048-1066	1060-1078	1038-1056	hm
12	Cross	Sp GAUCUGGAACUCCACUGC	GCAGUGGAAGUCCAGAUCA	1090-1108	1082-1100	-	1058-1076	1036-1054	hm
13	Cross	Sp GAGAUGAUCUGGAACUCC	GGAAGUCCAGAUCAUCUC	1085-1103	1077-1095	1041-1059	1053-1071	1031-1049	hm
14	Cross	Sp AGCGAGAUGAUCUGGAACU	AGUUCAGAUCAUCUCGCU	1082-1100	1074-1092	1038-1054	1050-1068	1028-1046	hm
15	Cross	Sp AGAUGAUCUGGAACUCCA	UGGAAGUCCAGAUCAUCU	1086-1104	1078-1096	1042-1060	1054-1072	1032-1050	hm
16	Cross	Sp CCCCAAGUUCUGAAGAAC	GUUCUUCAGGAACUUGGGC	700-718	692-710	656-671	668-685	646-659	hm
17	Cross	Sp AUCUGGAACUCCACUGCUG	AGCAGUGGAAGUCCAGAU	1091-1109	1083-1101	-	1059-1077	1037-1055	hm
18	Cross	Sp AGCUUUGUGCUGGGCCACU	AGUGGCCAGCACAAAGCU	485-503	477-495	-	-	-	hm
19	Cross	Sp AACCCCAAGUUCUGAAGA	UCUUCAGGAACUUGGGGU	698-716	690-708	654-671	666-684	644-659	hm
20	Cross	Sp CAGGAGAAGAGCGAAGGGA	UCCCUUCGCUCUUCUCCUG	1184-1202	1176-1194	1140-1156	1152-1170	1130-1148	hm
21	Cross	Sp UUGUGCUGGGCCACUUCAU	AUGAAGUGGCCAGCACAA	489-507	481-499	-	462-475	-	hm
22	Cross	Sp GAACUUCACUGCUGGGUG	CACCCAGCAGUGGAAGUUC	1096-1114	1088-1106	1056-1070	1064-1082	1042-1060	hm
23	Cross	Sp GGAACUUCACUGCUGGGU	ACCCAGCAGUGGAAGUCC	1095-1113	1087-1105	1051-1069	1063-1081	1041-1059	hm
24	Cross	Sp ACUUCACUGCUGGGUGGA	UCCACCCAGCAGUGGAAGU	1098-1116	1090-1108	1056-1072	1066-1084	1044-1062	hm
25	Cross	Sp CGAGAUGAUCUGGAACUUC	GAAGUCCAGAUCAUCUCG	1084-1102	1076-1094	1040-1054	1052-1070	1030-1048	hm
26	Cross	Sp AUGAUCUGGAACUCCACU	AGUGGAAGUCCAGAUCAU	1088-1106	1080-1098	1044-1062	1056-1074	1034-1052	hm
27	Cross	Sp UUUGUGCUGGGCCACUUCA	UGAAGUGGCCAGCACAAA	488-506	480-498	-	462-474	-	hm
28	Cross	Sp GAUGAUCUGGAACUCCAC	GUGGAAGUCCAGAUCAUC	1087-1105	1079-1097	1043-1061	1055-1073	1033-1051	hm
29	Cross	Sp UGGAAGUCCACUGCUGGG	CCCAGCAGUGGAAGUCCA	1094-1112	1086-1104	1050-1068	1062-1080	1040-1058	hm
30	Cross	Sp CUUUGUGCUGGGCCACUUC	GAAGUGGCCAGCACAAAG	487-505	479-497	-	462-473	-	hm
31	Cross	Sp GCUUUGUGCUGGGCCACUU	AAGUGGCCAGCACAAAGC	486-504	478-496	-	462-472	-	hm
32	Cross	Sp UCAGCACUAAGAGCGUGGG	CCCACGCUCUUAGUGCUGA	1377-1395	1369-1387	1333-1351	-	-	hr

TABLE B-continued

No.	Method	Sense siRNA	AntiSense siRNA	human GI	Mouse GI	Rat GI	Guinea-	Cow GI	species
				39777598	31543859	42476286	387604	31343554	
33	Cross	Sp AGAUCAGCACUAAGAGCGU	ACGCUCUUAGUGCUGAUCU	1374-1392	1366-1381	1330-1348	-	-	hr
34	Cross	Sp GAAGAUCAGCACUAAGAGC	GCUCUUAGUGCUGAUCUUC	1372-1390	1364-1381	1328-1346	-	1318-1329	hr
35	Cross	Sp GAUCAGCACUAAGAGCGUG	CACGCUCUUAGUGCUGAUC	1375-1393	1367-1381	1331-1349	-	-	hr
36	Cross	Sp AGUAUGGCCAGUGCUGGGU	ACCCAGCACUGGCCAUACU	918-936	918-928	874-892	886-904	864-882	hr
37	Cross	Sp AAGUAUGGCCAGUGCUGGG	CCCAGCACUGGCCAUACUU	917-935	-	873-891	885-903	863-881	hr
38	Cross	Sp AUCAGCACUAAGAGCGUGG	CCACGCUCUUAGUGCUGAU	1376-1394	1368-1386	1332-1350	-	-	hr
39	Cross	Sp AAGAUCAGCACUAAGAGCG	CCCUCUUAGUGCUGAUCUU	1373-1391	1365-1381	1329-1347	-	1319-1329	hr
40	Cross	Sp GGAUCCUAGACAUCUGCCU	AGGCAGAUGUCUAGGAUCC	663-681	-	-	-	609-627	hc
41	Cross	Sp CGCUGGGACAACAACUACG	CGUAGUUGUUGCCAGCG	818-836	810-826	774-787	786-803	764-782	hc
42	Cross	Sp CUUGGAAUUUUGGGCAGUU	AACUGCCCAAAAUCCAAG	636-654	628-646	592-610	-	582-600	hc
43	Cross	Sp GUCAACUGCAACGAUGACC	GGUCAUCGUUGCAGUUGAC	782-800	774-792	738-756	750-760	728-746	hc
44	Cross	Sp CAAGAACAUAACCUUGGAAU	AUCCAAGUAUGUUCUUG	625-643	-	-	599-610	571-589	hc
45	Cross	Sp CUCAUCGAGUACUCCGCA	UGCGGAAGUACUGAUGAG	1034-1052	1026-1042	990-1006	1002-1018	980-998	hc
46	Cross	Sp GCAUGGUCAACUGCAACGA	UCGUUGCAGUUGACCAUGC	777-795	770-784	733-748	746-760	723-741	hc
47	Cross	Sp CGGAUGCUGUGUACCUGGA	UCCAGGUACACAGCAUCCG	534-552	-	-	-	480-498	hc
48	Cross	Sp CCAUGACCAGAACAGCAAC	GUUGCUGUUCUGGUCAUGG	1012-1030	1008-1022	972-986	984-998	958-976	hc
49	Cross	Sp ACAUACCUUGGAAUUUUGG	CCAAAAUCCAAGGUAUGU	630-648	-	-	599-610	576-594	hc
50	Cross	Sp UCGAGUACUCCGCAAUGA	UCAUUGCGGAAGUACUCGA	1038-1056	1030-1048	994-1006	1006-1018	984-1002	hc
51	Cross	Sp AUGGUCAACUGCAACGAUG	CAUCGUUGCAGUUGACCAU	779-797	771-789	735-753	747-760	725-743	hc
52	Cross	Sp ACCUUGGAAUUUUGGGCAG	CUGCCCAAAAUCCAAGGU	634-652	-	-	-	580-598	hc
53	Cross	Sp CAAGUUAUCAAGAACAUA	UAUGUUCUUGAUAACUUG	616-634	608-621	572-585	584-595	562-580	hc
54	Cross	Sp UUCAUCAAGAACAUAACUU	AAGUAUGUUCUUGAUGAA	620-638	-	-	-	566-584	hc
55	Cross	Sp AUACCUUGGAAUUUUGGGC	GCCCAAAAUCCAAGGUAU	632-650	-	-	600-610	578-596	hc
56	Cross	Sp AGUACUCCGCAAUGAGUU	AACUCAUUGCGGAAGUACU	1041-1059	-	-	-	987-1005	hc
57	Cross	Sp UGGUGGAGUCUGGGAUGA	UCAUCCACGACUCCACCCA	1109-1127	1101-1119	1065-1083	1077-1095	1055-1073	hc
58	Cross	Sp CCAUGACCAGAACAGCAA	UUGCUGUUCUGGUCAUGGG	1011-1029	1003-1021	967-985	979-997	957-975	hc
59	Cross	Sp CCAAGUUAUCAAGAACAUA	AUGUUCUUAUGAACUUGG	615-633	608-621	572-585	583-595	561-579	hc
60	Cross	Sp GUCAACCCCAAGUCCUGA	UCAGGAACUUGGGUUGAC	695-713	690-705	654-669	665-681	641-659	hc
61	Cross	Sp AUCAAGAACAUAACCUUGGA	UCCAAGGUAUGUUCUUGAU	623-641	-	-	599-609	569-587	hc
62	Cross	Sp UGGUCAACUGCAACGAUGA	UCAUGGUUGCAGUUGACCA	780-798	772-790	736-754	748-760	726-744	hc
63	Cross	Sp CAUGGUCAACUGCAACGAU	AUCGUUGCAGUUGACCAUG	778-796	770-784	734-748	746-760	724-742	hc

TABLE B-continued

No.	Method	Sense siRNA	AntiSense siRNA	human GI	Mouse GI	Rat GI	Guinea-	Cow GI	species
				39777598	31543859	42476286	387604	31343554	
64	Cross	Sp UGGAAUUUUUGGCAGUUUG	CAAACUGCCCAAAAUCCA	638-656	630-646	594-612	-	584-602	hc
65	Cross	Sp ACUGCAACGAUGACCAGGG	CCCUGGUCAUCGUUGCAGU	786-804	778-796	742-760	-	732-750	hc
66	Cross	Sp AUCCUAGACAUCUGCCUGA	UCAGGCAGAUUCUAGGAU	665-683	-	-	-	611-629	hc
67	Cross	Sp CAACUGCAACGAUGACCAG	CUGGUCAUCGUUGCAGUUG	784-802	-	-	-	730-748	hc
68	Cross	Sp GGAAUUUUUGGCAGUUUGA	UCAAACUGCCCAAAAUUCC	639-657	631-646	595-613	615-625	585-603	hc
69	Cross	Sp AGCGGAUGCUGUGUACCUG	CAGGUACACAGCAUCCGCU	532-550	-	-	500-511	478-496	hc
70	Cross	Sp UUUCCCCACAUCACCAACA	UGUUGGUGAUGUGGGCAA	1574- 1592	1566- 1577	1530- 1541	-	1520- 1538	hc
71	Cross	Sp AAGAACAUAACCUUGGAAUU	AAUCCAAGGUAUGUUCUU	626-644	-	-	599-610	572-590	hc
72	Cross	Sp UCCUAGACAUCUGCCUGAU	AUCAGGCAGAUUCUAGGA	666-684	-	-	-	612-630	hc
73	Cross	Sp CGAGUACUUCGCA AUGAG	CUCAUUGCGGAAGUACUCG	1039- 1057	1031- 1049	995- 1006	1007- 1018	985- 1003	hc
74	Cross	Sp UGUCAACCCCAAGUUCUG	CAGGAACUUGGGGUUGACA	694-712	690-704	654-668	665-680	640-658	hc
75	Cross	Sp GACGUCUUUGCCCAUCA	UGAUGUGGGCAAGACGUC	1568- 1586	1560- 1577	1524- 1541	-	1514- 1532	hc
76	Cross	Sp GAUGCUGUGUACCGGACU	AGUCCAGGUACACCAUC	536-554	-	-	-482-500	hc	
77	Cross	Sp AGAACAUAACCUUGGAAUUU	AAAUCCAAGGUAUGUUCU	627-645	-	-	599-610	573-591	hc
78	Cross	Sp ACGUCUUUGCCCAUCAC	GUGAUGUGGGCAAGACGU	1569- 1587	1561- 1577	1525- 1541	-	1515- 1533	hc
79	Cross	Sp AUCGAGUACUUCGCAAUG	CAUUGCGGAAGUACUCGAU	1037- 1055	1029- 1047	993- 1006	1005- 1018	983- 1001	hc
80	Cross	Sp AAGUUCAUCAAGAACAUC	GUAUGUUCUUGAUGAACUU	617-635	609-621	573-585	585-595	563-581	hc
81	Cross	Sp UGGAGUCGUGGAUGACCAG	CUGGUCAUCCACGACUCCA	1113- 1131	1105- 1123	1069- 1087	1081- 1099	1059- 1077	hc
82	Cross	Sp GUGACAAGAGCGAGAUGAU	AUCAUCUCGCUCUUGUCAC	1074- 1092	1069- 1084	1033- 1048	1045- 1060	1020- 1038	hc
83	Cross	Sp UCAUCGAGUACUUCGCAA	UUGCGGAAGUACUCGAUGA	1035- 1053	1027- 1042	991- 1006	1003- 1018	981-999	hc
84	Cross	Sp GUUCGUGCCAUCAAGGAGG	CCUCCUUGAUGGCACGAAC	1226- 1244	1224- 1236	1188- 1200	1194- 1212	1172- 1190	hc
85	Cross	Sp CAUCAAGAACAUAACCUUGG	CCAAGGUAUGUUCUUGAUG	622-640	-	-	-	568-586	hc
86	Cross	Sp UACCUUGGAAUUUUGGGCA	UGCCCAAAAUCCAAGGUA	633-651	-	-	-	579-597	hc
87	Cross	Sp GACAAGAGCGAGAUGAUCU	AGAUCAUCUCGCUCUUGUC	1076- 1094	1069- 1086	1033- 1050	1045- 1062	1022- 1040	hc
88	Cross	Sp CGUCUUUGCCCAUCACG	GGUGAUGUGGGCAAAGACG	1570- 1588	1566- 1577	1530- 1541	-	1516- 1534	hc
89	Cross	Sp AUGCUGUGUACCGGACUC	GAGUCCAGGUACACAGCAU	537-555	-	-	-	483-501	hc
90	Cross	Sp UUGGAAUUUUGGCAGUUU	AAACUGCCCAAAAUCCA	637-655	629-646	593-611	-	583-601	hc
91	Cross	Sp GCCAAGUUCAUCAAGAACA	UGUUCUUGAUGAACUUGGC	614-632	608-621	572-585	582-595	560-578	hc
92	Cross	Sp AGUUCAUCAAGAACAUAAC	GGUAUGUUCUUGAUGAACU	618-636	610-621	574-585	-	564-582	hc
93	Cross	Sp GUCUUUGCCCAUCACCA	UGGUGAUGUGGGCAAAGAC	1571- 1589	1566- 1577	1530- 1541	-	1517- 1535	hc

TABLE B-continued

No.	Method	Sense siRNA	AntiSense siRNA	human GI	Mouse GI	Rat GI	Guinea-	Cow GI	species
				39777598	31543859	42476286	387604	31343554	
94	Cross	Sp GGGAUCCUAGACAUCUGCC	GGCAGAUGUCUAGGAUCCC	662-680	-	-	-	608-626	hc
95	Cross	Sp GAUCCUAGACAUCUGCCUG	CAGGCAGAUGUCUAGGAUC	664-682	-	-	-	610-628	hc
96	Cross	Sp AUGUCAACCCCAAGUCCU	AGGAACUUGGGGUUGACAU	693-711	690-703	649-667	665-679	639-657	hc
97	Cross	Sp UCAUCAAGAACAUAACCUUG	CAAGGUAUGUUCUUGAUGA	621-639	-	-	-	567-585	hc
98	Cross	Sp UCAAGAACAUAACCUUGGAA	UUCCAAGGUAUGUUCUUGA	624-642	-	-	599-610	570-588	hc
99	Cross	Sp CAUCGAGUACUUCGCAAU	AUUGCGGAAGUACUCGAUG	1036-1054	1028-1042	992-1005	1004-1018	982-1000	hc
100	Cross	Sp GGAUGCUGUGUACCGGAC	GUCCAGGUACACAGGAUCC	535-553	-	-	-	481-499	hc
101	Cross	Sp GAUGUCAACCCCAAGUCC	GGAACUUGGGGUUGACAUC	692-710	690-702	648-666	665-678	638-656	hc
102	Cross	Sp CAUGACCAGAACAGCAACC	GGUUGCUGUUCUGGUAUG	1013-1031	1008-1023	972-987	984-999	959-977	hc
103	Cross	Sp GCCCAUGACCAGAACAGCA	UGCUGUUCUGGUAUGGGC	1010-1028	1002-1020	966-984	978-996	956-974	hc
104	Cross	Sp GAACAUACCUUGGAAUUUU	AAAAUCCAAGGUAUGUUC	628-646	-	-	599-610	574-592	hc
105	Cross	Sp GUGGAGUCGUGGAUGACCA	UGGUCAUCCACGACUCCAC	1112-1130	-	-	1080-1098	1058-1076	hc
106	Cross	Sp UCAACUGCAACGAUGACCA	UGGUCAUCGUUGCAGUUGA	783-801	-	-	-	729-747	hc
107	Cross	Sp AUUUUGGCAGUUUUGAAGA	UCUCAAACUGCCCAAAAU	642-660	636-646	600-613	615-628	588-606	hc
108	Cross	Sp AACAUACCUUGGAAUUUUUG	CAAAAUCCAAGGUAUGUU	629-647	-	-	599-610	575-593	hc
109	Cross	Sp UGACAAGAGCGAGAUGAUC	GAUCAUCUCGCUCUUGUCA	1075-1093	1069-1085	1033-1049	1045-1061	1021-1039	hc
110	Cross	Sp UUCGUGCCAUCAAGGAGGG	CCCUCUUGAUGGCACGAA	1227-1245	1224-1237	1188-1201	1195-1213	1173-1191	hc
111	Cross	Sp UCAGCCCAUGUCCUGGAU	AUCCAGGACAUGGGCUGA	846-864	-	-	814-832	792-810	hc
112	Cross	Sp GGUCAAACUGCAACGAUGAC	GUCAUCGUUGCAGUUGACC	781-799	773-791	737-755	749-760	727-745	hc
113	Cross	Sp AAUUUUGGGCAGUUUGAAG	CUUCAAAACUGCCCAAAAU	641-659	636-646	600-613	615-627	587-605	hc
114	Cross	Sp CAGCGGAUCGUGUACCU	AGGUACACAGCAUCCGUG	531-549	-	-	499-511	477-495	hc
115	Cross	Sp AACUGCAACGAUGACCAGG	CCUGGUCAUCGUUGCAGUU	785-803	-	-	-	731-749	hc
116	Cross	Sp AUGACCAGAACAGCAACCU	AGGUUGCUGUUCUGGUCAU	1014-1032	1008-1024	972-988	984-1000	960-978	hc
117	Cross	Sp CAUACCUUGGAAUUUUGGG	CCCAAAAUCCAAGGUAUG	631-649	-	-	599-610	577-595	hc
118	Cross	Sp CUUUGCCCAUCAACCAAC	GUUGGUGAUGUGGGCAAAG	1573-1591	1566-1577	1530-1541	-	1519-1537	hc
119	Cross	Sp GAGUACUUCGCAAUGAGU	ACUCAUUGCGGAAGUACUC	1040-1058	1032-1050	996-1006	1008-1018	986-1004	hc
120	Cross	Sp GGCAUGGUCAACUGCAACG	CGUUGCAGUUGACCAUGCC	776-794	770-784	732-748	746-760	722-740	hc
121	Cross	Sp UCUUUGCCCAUCAACCAA	UUGGUGAUGUGGGCAAAGA	1572-1590	1566-1577	1530-1541	-	1518-1536	hc
122	Cross	Sp GAAUUUUGGGCAGUUUGAA	UUCAAAACUGCCCAAAAUUC	640-658	636-646	600-613	615-626	586-604	hc
123	Cross	Sp CCUUGGAAUUUUGGGCAGU	ACUGCCCAAAAUCCAAGG	635-653	-	-	-	581-599	hc
124	Cross	Sp GUUCAUCAAGAACAUAACCU	AGGUAUGUUCUUGAUGAAC	619-637	611-621	575-585	-	565-583	hc

TABLE B-continued

No.	Method	Sense siRNA	AntiSense siRNA	human	GI	Mouse	GI	Rat	GI	Guinea-	Cow	species
				39777598	31543859	42476286	387604	31343554				
125	Cross	Sp	UGUAUCGCCUCAGCCUGGA	UCCAGGCUGAGGCGAUACA	441-459	-		402-415	409-427	3571-3582		hg
126	Cross	Sp	GCUCGGCCAAGUUAUCA	UUGAUGAACUUGGCCGAGC	609-627	608-619	572-583	577-595	555-573			hg
127	Cross	Sp	GGCUCGGCCAAGUUAUCA	UGAUGAACUUGGCCGAGCC	608-626	608-618	572-582	576-594	554-572			hg
128	Cross	Sp	GGACGCUGGGACAACAACU	AGUUGUUGUCCAGCGUCC	815-833	810-825	774-787	783-801	764-779			hg
129	Cross	Sp	GGCAGUUUGAAGAUGGGAU	AUCCCAUCUCAAACUGCC	648-666	-		616-634	594-612			hg
130	Cross	Sp	AGUUUGAAGAUGGGAUCCU	AGGAUCCCAUCUCAAACU	651-669	-		607-625	619-637			hg
131	Cross	Sp	CAGUUUGAAGAUGGGAUCC	GGAUCCCAUCUCAAACUG	650-668	-		618-636	596-614			hg
132	Cross	Sp	AGGGCUCGGCCAAGUUAUC	AUGAACUUGGCCGAGCCCU	606-624	-		574-592	552-570			hg
133	Cross	Sp	GCAGUUUGAAGAUGGGAUCC	GAUCCCAUCUCAAACUGC	649-667	-		617-635	595-613			hg
134	Cross	Sp	CAACCCCAAGUUCUGAAG	CUUCAGGAACUUGGGUUG	697-715	690-707	654-671	665-683	643-659			hg
135	Cross	Sp	GGGCAGUUUGAAGAUGGG	UCCCAUCUCAAACUGCCC	647-665	-		603-621	615-633	593-611		hg
136	Cross	Sp	ACGCUGGGACAACAACUAC	GUAGUUGUUGUCCAGCGU	817-835	810-826	774-787	785-803	764-781			hg
137	Cross	Sp	UACUGCUGUGGCCAGUUC	GAACUGGGCCACAGCAGUA	1205-1223	1197-1213	1161-1177	1173-1191	1151-1169			hg
138	Single	Sp	UUGCCCAUACACCAACAA	UUGUUGGUGAUGUGGGCAA	1575-1593	1567-1577	1531-1541	-	1521-1538			h
139	Single	Sp	CCAAGUACCUGCUCACACCU	AGGUUGAGCAGGUACUUGG	1677-1695	-	-	1660-1672	-			h
140	Single	Sp	CGGCCAAGUUAUCAAGAA	UUCUUGAUGAACUUGGCCG	612-630	608-621	572-585	580-595	560-576			h
141	Single	Sp	CGAUGGGUCUGUGCACAAA	UUUGUGCACAGACCCCAUCG	1324-1342	1317-1334	1281-1298	-	-			h
142	Single	Sp	CAGUGACUUUGACGUCUUU	AAAGACGUCAAAGUCACUG	1558-1576	-	1517-1528	1535-1553	-			h
143	Single	Sp	GCAUGAACAUUGGGCAGUGA	UCACUGCCCAUGUUC AUGC	1545-1563	-	-	1530-1540	1540			h
144	Single	Sp	CAACUACGAGGCCAGUGUA	UACACUGGCCUCGUAGUUG	244-262	239-250	-	-	-			h
145	Single	Sp	CAUGGGCAGUGACUUUGAC	GUCAAAGUCACUGCCCAUG	1552-1570	-	-	1530-1547	-			h
146	Single	Sp	GCCCAUACACCAACAACA	UGUUGUUGGUGAUGUGGGC	1577-1595	-	-	-	1523-1538			h
147	Single	Sp	CGAACCACCUGAACAAACU	AGUUUGUUCAGGUGGUUCG	1476-1494	1470-1486	1434-1450	-	1424-1440			h
148	Single	Sp	GGCCGUUUUCCACUAAGA	UCUUAGUGGAAAACGGGCC	322-340	-	-	-	-			h
149	Single	Sp	UGACGUCUUUGCCCAUAC	GAUGUGGGCAAAGACGUCA	1567-1585	1560-1577	1523-1541	-	1514-1531			h
150	Single	Sp	GAACAUUGGGCAGUGACUUU	AAAGUCACUGCCCAUGUUC	1549-1567	-	-	1530-1544	-			h
151	Single	Sp	GCAGUGACUUUGACGUCUU	AAGACGUCAAAGUCACUGC	1557-1575	-	1517-1528	1534-1552	-			h

TABLE B-continued

No.Method	Sense siRNA	AntiSense siRNA	human GI	Mouse GI	Rat GI	Guinea-	Cow GI	species
			39777598	31543859	42476286	pig GI	31343554	
152 Single Sp	CUGUGUCCUGGAGCAUUU	AAAUGCUCACGACACAG	1724-1742	-	-	-	-	h
153 Single Sp	CAACCUGGAGCCUUUCUCU	AGAGAAAGGCUCAGGUUG	1696-1714	-	-	1105-1115	-	h

[0205]

TABLE C

No Method	Sense siRNA	AntiSense siRNA	human	mouse	rat	Guinea-	Cow	file
			39777598	31543859	42476286	pig	31343554	
1 Single Sp	CUAGACAUCUGCCUGAUCCUU	AAGGAUCAGGCAGAUGUCUAG	668-688	-	-	-	614-630	hmrgc
2 Single Sp	CAACUGACAACAUGCUAGGUA	UACCUAGCAUGUUGUCAGUUG	1752-1172	-	-	-	-	hmrgc
3 Single Sp	CCAAGUUCAUCAAGAACAUAUC	GUAUGUUCUUGAUGAACUUGG	615-635	608-621	572-585	583-595	561-581	hmrgc
4 Single Sp	CCUGAUCCUUCUAGAUUGCAA	UUCACAUCUAGAAGGAUCAGG	679-699	-	-	-	-	hmrgc
5 Cross Sp	ACAAGAGCGAGAUGAUCUGGA	UCCAGAUAUCUCGCUCUUGU	1077-1097	1069-1089	1033-1053	1045-1065	1023-1043	hmrgc
6 Single Sp	CAAGAACAUAACCUUGGAAUUU	AAAUCCAAGGUAGUUCUUG	625-645	-	-	599-610	571-591	hmrgc
7 Single Sp	CGGCCAAGUUCAUCAAGAACA	UGUUCUUGAUGAACUUGGCCG	612-632	608-621	572-585	580-595	560-578	hmrgc
8 Single Sp	CUGUGUCCUGGAGCAUUUGU	ACAAAUGCUCAGGAACACAG	1724-1744	-	-	-	-	hmrgc
9 Cross Sp	CAAGAGCGAGAUGAUCUGGAA	UCCAGAUAUCUCGCUCUUG						hmrgc
10 Single Sp	CAACUACGAGGCCAGUGUAGA	UCUACACUGGCCUCGUAGUUG	244-264	239-250	-	-	-	hmrgc
11 Single Sp	GGCCCGUUUCCACUAAGAGA	UCUCUUAGUGGAAAACGGGCC	322-342	-	-	-	-	hmrgc
12 Single Sp	GCAACCUUCUACUCGAGUACU	AGUACUCGAGAGAAGGUUGC	1026-1046	1018-1038	982-1002	994-1014	972-992	hmrgc
13 Cross Sp	CGAGAUGAUCUGGAACUCCA	UGGAAGUCCAGAUCAUCUCG	1084-1104	1076-1096	1040-1060	1052-1072	1030-1050	hm
14 Cross Sp	ACUCCACUCUGGGUGGAGU	ACUCCACCCAGCAGUGGAAGU	1098-1118	1090-1110	1056-1074	1066-1086	1044-1064	hm
15 Cross Sp	AACCCCAAGUCCUGAAGAAC	GUUCUUCAGGAACUUGGGUU	698-718	690-710	654-671	666-685	644-659	hm
16 Cross Sp	AUGAUCUGGAACUCCACUCG	GCAGUGGAAGUCCAGAUCAU	1088-1108	1080-1100	1044-1064	1056-1076	1034-1054	hm
17 Cross Sp	GAACUCCACUCUGGGUGGA	UCCACCCAGCAGUGGAAGUUC	1096-1116	1088-1108	1056-1072	1064-1084	1042-1062	hm
18 Cross Sp	UGGAACUCCACUCUGGGUG	CACCCAGCAGUGGAAGUCCA	1094-1114	1086-1106	1050-1070	1062-1082	1040-1060	hm
19 Cross Sp	AGCGAGAUGAUCUGCAACUUC	GAAGUCCAGAUCAUCUCGCU	1082-1102	1074-1094	1038-1054	1050-1070	1028-1048	hm
20 Cross Sp	GAUGAUCUGGAACUCCACUCG	CAGUGGAAGUCCAGAUCAUC	1087-1107	1079-1099	1043-1063	1055-1075	1033-1053	hm
21 Cross Sp	AGAGCGAGAUGAUCUGGAACU	AGUCCAGAUCAUCUCGCUCU	1080-1100	1072-1092	1036-1054	1048-1068	1026-1046	hm

TABLE C-continued

No Method	Sense siRNA	AntiSense siRNA	human 39777598	mouse 31543859	rat 42476286	Guinea- pig 387604	Cow 31343554	file
22 Cross Sp	CUGGAACUCCACUGCUGGGU	ACCCAGCAGUGGAAGUCCAG	1093-1113	1085-1105	1049-1069	1061-1081	1039-1059	hm
23 Cross Sp	UGAUCUGGAACUCCACUGCUCU	AGCAGUGGAAGUCCAGAUA	1089-1109	1081-1101	—	1057-1077	1035-1055	hm
24 Cross Sp	AAGAGCGAGAUGAUCUGGAAC	GUCCAGAUAUCUCGCUCUU	1079-1099	1071-1091	1035-2054	1047-1067	1025-1045	hm
25 Cross Sp	CAGCUUGUGCUGGGCCACUU	AAGUGGCCAGCACAAAGCUG	484-504	476-496	—	452-472	—	hm
26 Cross Sp	GCUUUGUGCUGGGCCACUUCA	UGAAGUGGCCAGCACAAAGC	486-506	478-498	—	462-474	—	hm
27 Cross Sp	AGAUGAUCUGGAACUCCACU	AGUGGAAGUCCAGAUAUCU	1086-1106	1078-1098	1042-1062	1054-1074	1032-1052	hm
28 Cross Sp	CUUUGUGCUGGGCCACUUCAU	AUGAAGUGGCCAGCACAAAG	487-507	479-499	—	462-475	—	hm
29 Cross Sp	GCGAGAUGAUCUGGAACUCC	GGAAGUCCAGAUAUCUCGC	1083-1103	1075-1095	1039-1059	1051-1071	1029-1049	hm
30 Cross Sp	AUCUGGAACUCCACUGCUGG	CCAGCAGUGGAAGUCCAGAU	1091-1111	1083-1103	1047-1067	1059-1079	1037-1057	hm
31 Cross Sp	UCUGGAACUCCACUGCUGGG	CCCAGCAGUGGAAGUCCAGA	1092-1112	1084-1104	1048-1068	1060-1080	1038-1058	hm
32 Cross Sp	GAUCUGGAACUCCACUGCUG	CAGCAGUGGAAGUCCAGAUC	1090-1110	1082-1102	1046-1066	1058-1078	1036-1056	hm
33 Cross Sp	GAGAUGAUCUGGAACUCCAC	GUGGAAGUCCAGAUAUCUC	1085-1105	1077-1097	1041-1061	1053-1073	1031-1051	hm
34 Cross Sp	AGCUUUGUGCUGGGCCACUUC	GAAGUGGCCAGCACAAAGCU	485-505	477-497	—	453-473	—	hm
35 Cross Sp	GAGCGAGAUGAUCUGGAACUU	AAGUCCAGAUAUCUCGCUC	1081-1101	1073-1093	1037-1054	1049-1069	1027-1047	hm
36 Cross Sp	AACUCCACUGCUGGGUGGAG	CUCCACCCAGCAGUGGAAGUU	1097-1117	1089-1109	1056-1073	1065-1085	1043-1063	hm

Example 2

[0206] Testing the siRNA Compounds for Anti-TGaseII Activity

[0207] 1. Preparation of working solutions of siRNAs (double-stranded oligonucleotides)

[0208] Lyophilized oligonucleotides were dissolved in RNase-free double-distilled water to produce a final concentration of 100 uM. The diluted oligonucleotides were kept at room temperature for 15 min and immediately frozen in liquid nitrogen. The oligonucleotides were stored at -80° C. and diluted before use with PBS.

[0209] II. Establishment of NRK49 cell line stably over-expressing rat TGaseII

[0210] The full length cDNA of rat TGaseII cloned in PLXSN vector (CLONTECH) was used for transfection into a Rat1 fibroblast cell line. Lipofectamine reagent (Invitrogen) was used as the transfection reagent using the protocol described below. 48 hr following transfection, selection of stable clones was performed using G418 antibiotic (neomycin). The stable overexpression of TGaseII in this polyclonal population was verified by Western blotting and TGaseII activity assay. The cells were designated as NRK49-TGaseII (TGase-OE®).

[0211] III Activity assay for TGaseII in NRK49

[0212] 4x10³NRK49-rat TGase-OE cells were seeded per well in a 96 well plate. TGaseII activity was measured using a cell-based assay for TGaseII activity. Briefly, the growth medium was replaced with cell labeling medium (DMEM in 0.1% BSA, 25 uM BC, 10 uM Calcimycin, 16.2 mM CaCl₂) for 45 min at 37° C. 45 min later, the cells were fixed with 4% formaldehyde, treated with 0.6% H₂O₂ and stained with Netravidin-HRP Ab in order to test the cross-linking of biotin-labeled cadaverin. The absorbance was read at λ=450 nm. For normalization, the cells were stained with Hoechst dye solution. The activity of TGaseII is 75 fold higher in NRK49-TGaseII cells compared to NRK49 control cells.

[0213] IV. Transfection by siRNA oligonucleotides using Lipofectamine2000 reagent

[0214] 2x10⁵ cells were seeded per well in 6 well-plates. After 24 hrs, the cells were transfected with TGaseII specific siRNA oligonucleotides using Lipofectamine2000 reagent (Invitrogen) according to the following procedure:

[0215] 1. Before transfection, the cell medium was replaced with 1500 ul of fresh medium without antibiotics.

[0216] 2. In a sterile plastic tube, Lipofectamine2000 reagent (the amount is calculated according to 5 ul per well) was added to 250 ul of serum-free medium, and incubated for 5 min at room temperature.

[0217] 3. In another tube, the siRNA oligonucleotides (varying amounts to fit the desired final concentration per well) were added to 250 ul of serum-free medium.

[0218] 4. Lipofectamine2000 complex was combined with the siRNA solution and incubated for 20 min at room temperature.

[0219] 5. The resulting mixture was added dropwise to the cells, and the cells were incubated at 37° C. until analysis of siRNA activity.

[0220] V. Testing the activity of anti TGaseII siRNAs in transfected human, mouse and rat cells

[0221] The activity of TGaseII siRNAs listed in Table A was tested in 3 different cell lines originating from different species:

[0222] 1. Mouse-specific TGaseII siRNAs were tested in mouse cells, which express mouse TGaseII-NMUMG cells.

[0223] 2. Human-specific TGaseII siRNA were tested in human HeLa cells which express human TgaseII; see FIG. 3.

[0224] 3. Rat-specific TGaseII siRNAs were tested in NRK49 overexpressing rat TGaseII (TGASE-OE® cells).

[0225] 48 h to 6 days after transfection of siRNAs, the cells were harvested and expression of TGaseII protein was examined by Western blot analysis with specific antibodies. The decrease in TGaseII polypeptide expression in the cells transfected with siRNA oligonucleotides specific to TGaseII as compared to controls indicated that siRNAs elicited inhibitory effect on TGaseII protein expression, which can be quantified.

[0226] Table D below summarizes the information about TGaseII inhibitory activity of each siRNA oligonucleotide. The names of oligonucleotides in Table D correspond to the names used in Table A. Note that the comparison is to the activity in each cell line transfected by different siRNAs, and not between cell lines. The presently most preferred human siRNA is TG_HMRG1, which elicited high TGaseII inhibitory effect and also inhibited mouse, rat and guinea pig TGaseII. Other preferred human siRNAs are TG_HMG1 and TG_HM1.

TABLE D

name	Species	Human TGII	Mouse TGII	Rat TGII
TG_HMR1	hum_mus_rat	+	-	+
TG_HMRG1	hum_mus_rat_GP	++++	+++	++++
TG_HMG1	hum_mus_GP	++++	+	ND
TG_HMG2	hum_mus_GP	++++ (toxic)	++++ (toxic)	ND
TG_HM1	hum_mus	++++	+	ND
TG_M1	Mus	+	+++	ND
TG_M2	Mus	-	+++	ND
TG_M3	Mus	+++	++++	ND

TABLE D-continued

name	Species	Human TGII	Mouse TGII	Rat TGII
TG_M4	mus_rat	ND	++	++
TG_M5	mus_rat	+++	+++	+++
TG_M6	mus_rat	ND	++	+++
TG_M7	mus_rat	ND	++	++++
TG_M8	mus_rat	ND	++	++
TG_M9	mus_rat	+++	+++	+++
TG_M10	mus_rat	ND	+	+++
TG_H1	Hum	-	ND	ND
TG_H2	Hum	-	ND	ND
TG_HG1	hum_GP	++	ND	ND

Example 3

[0227] Animal Models of Kidney Fibrosis

[0228] Testing of the in vivo therapeutic activity of anti-TGaseII siRNAs, or of neutralizing antibodies against TGaseII or of other TGaseII inhibitors may be done in the following animal models of kidney fibrosis in which disease-associated overexpression of TGaseII was found (as detected by in situ hybridization; see below).

[0229] A. Rat Diabetic and Aging Models of Kidney Fibrosis

[0230] A1. ZDF Rats

[0231] Kidney samples of 9-month-old ZDF rats (Zucker diabetic fatty rats) presented hydronephrotic changes with dilated calyces. Microscopically these samples displayed the features of glomerulosclerosis and tubulointerstitial fibrosis. In accordance with these morphological changes, the expression of fibrosis marker genes (osteopontin (OPN), transforming growth factor β 1 (TGF- β 1) and procollagen α 1(1) (Coll)), as measured by in situ hybridization, was significantly increased compared to normal kidneys. Strong OPN expression was detectable in all tubular structures in both kidney cortex and medulla. TGF- β 1 expression was widespread throughout interstitial cells. Some epithelial cells also showed TGF- β 1 expression. Coll expression was detectable by in situ hybridization in most interstitial cells within the medulla, while cortical expression was "focal".

[0232] A2. Aged fa/fa (Obese Zucker) Rats

[0233] Fa/fa rats are genetically deficient for leptin receptor; and, as a result, develop insulin resistant diabetes (type II diabetes) with progressive diabetic nephropathy. Kidney samples of 12-month-old fa/fa rats presented with high degree glomerulosclerosis and diffuse tubulointerstitial fibrosis throughout both the cortex and the medulla. The pattern of fibrosis marker gene expression corresponded to the morphological changes. OPN was expressed in tubular structures in the cortex and in the medulla. Multiple interstitial cells expressed TGF- β 1. Significantly, multiple foci and single interstitial cells showed strong Coll expression in both cortex and medulla so that the number of Coll-expressing cells appeared to be higher in fa/fa kidney samples than in ZDF samples.

[0234] A3. Aged Sprague-Dawley (SD) (Normal) Rats

[0235] Kidney samples of aged SD rats also showed increased accumulation of collagen in glomeruli and inter-

stitial space and increased expression of fibrosis marker genes. Significantly, the intensity of fibrotic changes varied among samples. Thus, one of the four samples studied displayed very few changes compared with young animals; in the second sample, fibrotic changes were confined only to "polar" regions, and the remaining two samples displayed uniform accumulation of collagen and elevated expression of marker genes throughout the sections

[0236] A4. Goto Kakizaki (GK)48-week-old Rats

[0237] GK rats are an inbred strain derived from Wistar rats, selected for spontaneous development of NIDDM (diabetes type II). Kidney samples from both GK and control Wistar 48-week-old rats showed accumulation of collagen in glomeruli and interstitial space. This accumulation was more pronounced in the GK samples.

[0238] TGaseII Hybridization Pattern

[0239] TGaseII-specific hybridization signal was associated with fibrotic phenotype (diffuse or focal) in kidneys of both healthy and diabetic rats. Non-fibrotic kidney samples demonstrate a diffuse, low but detectable TGaseII-specific hybridisation signal over proximal tubules. By 12 months of age, a stronger signal is concentrated over interstitial cells and epithelial lining of distended tubules that show clear signs of atrophy. In chronic renal failure sample (kidney from two years old rat), a strong TGaseII expression is visible in tubular profiles lined by atrophic or proliferating epithelium cells within surrounding interstitium. Similarly, ZDF samples showed intensification of the hybridization signal along with the progression of the fibrosis (or aging).

[0240] B. Induced Models of Kidney Fibrosis

[0241] B. Permanent Unilateral Ureteral Obstruction (UUO) Model

[0242] Unilateral ureteral obstruction (UUO) is a model of acute interstitial fibrosis occurring in healthy non-diabetic animals. Renal fibrosis develops within days following the obstruction.

[0243] To produce the model, rats were anaesthetized with Ketamin/Xylazine and the abdominal cavity was opened. After exposure, the right ureter was ligated with a suture at the level of the lower kidney pole. In sham-operated rats, the ureter was exposed but not ligated. The study was terminated at different timepoints following ureteral obstruction (e.g., at 24 hr, 5 days, 10 days, 15 days, 20 days and 25 days), and the kidneys were removed and examined.

[0244] Histological examination revealed that permanent UUO results in a rapid activation of collagen synthesis by interstitial cells in both medulla and cortex. By 20-25 days of UUO, significant amounts of interstitial collagen were deposited in the interstitial space, whereas glomerular accumulation of collagen was confined to the outer capsule.

[0245] situ hybridization analysis of obstructed kidney samples indicated rapid and significant changes in the pattern of TGaseII expression dependent on the duration of UUO. After 24 hours of UUO, a very strong hybridization signal was detected over cortical tubular epithelium, whereas medullar epithelial cells showed much weaker signal. At 5 and 10 days of UUO, the "foci" of strong hybridization signal were associated with the areas of developing tubulointerstitial fibrosis where the signal was located to both epithelial and interstitial cells. Similar results were observed in mice exposed to the same UUO model.

[0246] B2. 5/6 Nephrectomy

[0247] 5/6 nephrectomy is another useful animal model for chronic renal insufficiency (CRI) in which fibrosis is evident.

[0248] In summary, the results suggest that an increase in TGaseII expression and activity level accompanies fibrotic changes in the kidneys.

Example 4

[0249] Establishment of TGaseII Role in Renal Fibrosis Employing the UUO Model Using TGaseII Knock-out Mice

[0250] TgaseII knock-out mice were obtained from Dr. Melino (De Laurenzi V, Melino G., *Gene disruption of tissue transglutaminase*, *Mol Cell Biol.* 2001 January;21(1):148-55). The mice appeared phenotypically normal. Also no morphological changes were observed in kidneys obtained from these mice. TGaseII KO mice were then used for the analysis of the development of kidney fibrosis following induction of UUO by assessing kidney collagen accumulation compared to normal mice. The results clearly demonstrated that disruption of TGaseII results in statistically significant reduced collagen accumulation following both three (3) and seven (7) days of obstruction, as compared to collagen accumulation in obstructed kidneys of wild type mice, thus implicating TGaseII as a functionally important factor in kidney fibrosis. It is thus suggested that inhibition of TGaseII activity may have an anti-fibrotic therapeutic effect.

Example 5

[0251] Inhibition of TGaseII Activity Using Monoclonal Neutralizing Antibodies

[0252] Recombinant monoclonal human-anti-human antibodies against TGaseII were obtained by screening of a phage display library. 720 clones were screened for binding human TGaseII. Seven (7) clones were selected which showed intense binding to the enzyme. The activity assay demonstrated that these antibodies inhibited the crosslinking activity of human TGaseII enzyme at a range of concentrations (1-5 nM).

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Asn Ile Pro Trp Asn Phe Gly Gln Phe Glu Asp Gly Ile Leu Asp Ile
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Cys Leu Ile Leu Leu Asp Val Asn Pro Lys Phe Leu Lys Asn Ala Gly
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Arg Asp Cys Ser Arg Arg Ser Ser Pro Val Tyr Val Gly Arg Val Val

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Lys	Tyr	Gly	Gln	Cys	Trp	Val	Phe	Ala	Ala	Val	Ala	Cys	Thr	Val	Leu
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Arg	Cys	Leu	Gly	Ile	Pro	Thr	Arg	Val	Val	Thr	Asn	Tyr	Asn	Ser	Ala
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His	Asp	Gln	Asn	Ser	Asn	Leu	Leu	Ile	Glu	Tyr	Phe	Arg	Asn	Glu	Phe
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Gly	Glu	Ile	Gln	Gly	Asp	Lys	Ser	Glu	Met	Ile	Trp	Asn	Phe	His	Cys
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Trp	Val	Glu	Ser	Trp	Met	Thr	Arg	Pro	Asp	Leu	Gln	Pro	Gly	Tyr	Glu
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Tyr	Cys	Cys	Gly	Pro	Val	Pro	Val	Arg	Ala	Ile	Lys	Glu	Gly	Asp	Leu
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Arg	Asp	Glu	Arg	Glu	Asp	Ile	Thr	His	Thr	Tyr	Lys	Tyr	Pro	Glu	Gly
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Leu	Ala	Glu	Lys	Glu	Glu	Thr	Gly	Met	Ala	Met	Arg	Ile	Arg	Val	Gly
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Gln	Ser	Met	Asn	Met	Gly	Ser	Asp	Phe	Asp	Val	Phe	Ala	His	Ile	Thr
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Cys	Ile	Leu	Tyr	Glu	Lys	Tyr	Arg	Asp	Cys	Leu	Thr	Glu	Ser	Asn	Leu
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acuccacca gcaguggaag u 21

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<400> SEQUENCE: 410
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<210> SEQ ID NO 411
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cccagcagug gaaguuccag a 21

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cuccaccag caguggaagu u                21

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1. A compound having the structure:5'(N)_x-Z 3' (antisense strand)3'Z'-(N')_y5' (sense strand)

wherein each N and N' is a ribonucleotide which may be modified or unmodified in its sugar residue and (N)_x and (N')_y is an oligomer in which each consecutive N or N' is joined to the next N or N' by a covalent bond;

wherein each of x and y is an integer between 19 and 40;

wherein each of Z and Z' may be present or absent, but if present is dTdT and is covalently attached at the 3' terminus of the strand in which it is present; and wherein the sequence of (N)_x comprises any one of the sequences set forth in SEQ ID NOS: 21-38, 192-344 and 381-416.

2. The compound of claim 1, wherein the covalent bond is a phosphodiester bond.

3. The compound of claim 2, wherein x=y.

4. The compound of claim 3, wherein x=y=19.

5. The compound of claim 1 wherein Z and Z' are both absent.

6. The compound of claim 1 wherein one of Z or Z' is present.

7. The compound of claim 1 wherein all of the ribonucleotides are unmodified in their sugar residues.

8. The compound of claim 1 wherein at least one ribonucleotide is modified in its sugar residue.

9. The compound of claim 8, wherein the modification of the sugar residue comprises a modification at the 2' position.

10. The compound of claim 9, wherein the modification at the 2' position results in the presence of a moiety selected from the group comprising amino, fluoro, methoxy, alkoxy and alkyl groups.

11. The compound of claim 10, wherein the moiety at the 2' position is methoxy (2'-O-methyl).

12. The compound of claim 1 wherein alternating ribonucleotides are modified in both the antisense and the sense strands.

13. The compound of claim 1 wherein the ribonucleotides at the 5' and 3' termini of the antisense strand are modified

in their sugar residues, and the ribonucleotides at the 5' and 3' termini of the sense strand are unmodified in their sugar residues.

14. The compound of claim 1 wherein the antisense strand is phosphorylated at the 5' terminus, and may or may not be phosphorylated at the 3' terminus; and

wherein the sense strand may or may not be phosphorylated at the 5' terminus and at the 3' terminus.

15. A vector capable of expressing the compound of claim 1.

16. A composition comprising the compound of claim 1 in an amount effective to inhibit human TGaseII and a carrier.

17. A method of treating a patient suffering from a disorder comprising administering to the patient an inhibitor of human TGaseII in a therapeutically effective dose so as to thereby treat the patient.

18. The method of claim 17, where the inhibitor is an siRNA.

19. The method of claim 17, where the inhibitor is an antibody.

20. (canceled)

21. The method of claim 17, wherein the disorder is a fibrosis-related pathology.

22. The method of claim 21, wherein the fibrosis-related pathology is kidney fibrosis, liver fibrosis, pulmonary fibrosis or ocular scarring.

23. The method of claim 17, wherein the disorder is any one of an ocular disease especially cataract, a cardiovascular disease especially cardiac hypertrophy, atherosclerosis/retinosis, a neurological disease, including polyglutamine disease, spinobulbar muscular atrophy, dentatorubral-pallidoluysian atrophy, spinocerebellar ataxias (SCAs) 1, 2, 3, 6, 7 and 17, Alzheimer's disease or Parkinson's disease.

24. A composition comprising the vector of claim 15 in an amount effective to inhibit human TGaseII and a carrier.

25. A method of treating a patient suffering from a disorder comprising administering to the patient the compounds of claim 1 in a therapeutically effective dose so as to thereby treat the patient.

26. A method of treating a patient suffering from a disorder comprising administering to the patient the vector of claim 15 in a therapeutically effective dose so as to thereby treat the patient.

* * * * *