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(54) Benævnelse: **FREMGANGSMÅDER TIL BEHANDLING AF KRONISK NYRESYGDOM**

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DESCRIPTION

RELATED PATENTS

[0001] This application claims priority of United States Provisional Patent Applications Nos. 61/184937, filed 8 June 2009 and 61/235381, filed 20 August 2009.

[0002] Throughout this application various patents and publications are cited to more fully describe the state of the art to which this invention pertains.

FIELD OF THE INVENTION

[0003] The present invention relates to compounds for use in methods for treating chronic kidney disease (CKD) including methods for preventing or delaying onset of CKD and methods for preventing exacerbation and progression of CKD.

BACKGROUND OF THE INVENTION

Chronic Kidney Disease

[0004] Chronic kidney disease (CKD) is a worldwide public health problem and is recognized as a common condition that is associated with an increased risk of cardiovascular disease and end stage renal disease (ESRD).

[0005] The Kidney Disease Outcomes Quality Initiative (K/DOQI) of the National Kidney Foundation (NKF) defines chronic kidney disease as either kidney damage or a decreased kidney glomerular filtration rate (GFR) for three or more months. Other markers of CKD are also known and used for diagnosis. In general, the destruction of renal mass with irreversible sclerosis and loss of nephrons leads to a progressive decline in GFR and eventually ESRD.

[0006] Recently, the K/DOQI published a classification of the stages of CKD, as follows:

Stage 1: Kidney damage with normal or increased GFR (>90 mL/min/1.73 m^2)

Stage 2: Mild reduction in GFR (60-89 mL/min/1.73 m^2)

Stage 3: Moderate reduction in GFR (30-59 mL/min/1.73 m^2)

Stage 4: Severe reduction in GFR (15-29 mL/min/1.73 m^2)

Stage 5: Kidney failure (GFR <15 mL/min/1.73 m^2 or dialysis)

[0007] In stages 1 and 2 CKD, GFR alone does not confirm the diagnosis. Other markers of kidney damage, including abnormalities in the composition of blood or urine or abnormalities in imaging tests, should be relied upon.

Pathophysiology of CKD

[0008] Approximately 1 million nephrons are present in each kidney, each contributing to the total GFR. Irrespective of the etiology of renal injury, with progressive destruction of nephrons, the kidney is able to maintain GFR by hyperfiltration and compensatory hypertrophy of the remaining healthy nephrons. This nephron adaptability allows for continued normal clearance of plasma solutes so that substances such as urea and creatinine start to show significant increases in plasma levels only after total GFR has decreased to 50%, when the renal reserve has been exhausted. The plasma creatinine value will approximately double with a 50% reduction in GFR. Therefore, a doubling in plasma creatinine from a baseline value of 0.6 mg/dL to 1.2 mg/dL in a patient actually represents a loss of 50% of functioning nephron mass.

[0009] The residual nephron hyperfiltration and hypertrophy, although beneficial for the reasons noted, is thought to represent a major cause of progressive renal dysfunction. This is believed to occur because of increased glomerular capillary pressure, which damages the capillaries and leads initially to focal and segmental glomerulosclerosis and eventually to global glomerulosclerosis. This hypothesis has been based on studies of five-sixths nephrectomized rats, which develop lesions that are similar to those observed in humans with CKD.

[0010] The two most common causes of chronic kidney disease are diabetes and hypertension. Other factors include acute insults from nephrotoxins, including radiocontrast agents, or decreased perfusion (ischemia); sepsis; Proteinuria; Increased renal ammoniagenesis with interstitial injury; Hyperlipidemia; Hyperphosphatemia with calcium phosphate deposition; Decreased levels of nitrous oxide and smoking.

[0011] In the United States, the incidence and prevalence of CKD is rising, with poor outcomes and high cost to the health system. Kidney disease is the ninth leading cause of death in the US. The high rate of mortality has led the US Surgeon General's mandate for America's citizenry, Healthy People 2010, to contain a chapter focused on CKD. The objectives of this chapter are to articulate goals and to provide strategies to reduce the incidence, morbidity, mortality, and health costs of chronic kidney disease in the United States. The burden of chronic kidney disease can be assessed by multiple criteria, all of which underscore the need for improved detection, treatment, and monitoring of clinical and fiscal outcomes. Reducing renal failure will require additional public health efforts, including effective preventive strategies

and early detection and treatment of chronic kidney disease.

[0012] The incidence rates of end-stage renal disease (ESRD) have also increased steadily internationally since 1989. The United States has the highest incident rate of ESRD, followed by Japan. Japan has the highest prevalence per million population, followed by the US.

[0013] The mortality rates associated with hemodialysis are striking and indicate that the life expectancy of patients entering into hemodialysis is markedly shortened. At every age, patients with ESRD on dialysis have significantly increased mortality when compared with nondialysis patients and individuals without kidney disease. At age 60 years, a healthy person can expect to live for more than 20 years, whereas the life expectancy of a 60-year-old patient starting hemodialysis is closer to 4 years (Aurora and Verelli, May 21, 2009. Chronic Renal Failure: Treatment & Medication. Emedicine. http://emedicine.medscape.com/article/238798-treatment).

[0014] International Patent Publication Nos. WO 2006/035434, WO 2008/104978, WO 2008/106102, and WO 2009/001359 assigned to one of the assignees of the present invention relate to methods of treating acute kidney disease including acute renal failure following cardiac surgery.

[0015] Molitoris BA, et al ("siRNA targeted to p53 attenuates ischemic and cisplatin-induced acute kidney injury". J Am Soc Nephrol. 2009 Aug;20(8):1754-64) discloses the treatment of acute renal failure (ARF), also known as Acute Kidney Injury (AKI), in patients not suffering from established CKD.

[0016] Hiong LC, et al ("Effect of TGF-beta1 antisense oligodeoxynucleotide on renal function in chronic renal failure rats. Acta Pharmacol Sin. 2008 Apr;29(4):451-7) discloses an antisense compound which downregulates the expression of TGF-beta 1 and its use in the treatment of chronic renal failure (CRF), the increase in the glomerular filtration rate is however moderate.

[0017] Methods and compositions useful for treating CKD and for attenuating progression of CKD would be of great therapeutic value.

SUMMARY OF THE INVENTION

[0018] According to one aspect the present invention provides an oligonucleotide compound which down-regulates expression of the p53 gene, for use in treating chronic kidney disease (CKD) resulting from exposure to recurring renal insults in a subject suffering from CKD. The description also discloses a method of treating or preventing kidney damage in a subject at risk of chronic kidney disease (CKD) associated with exposure to a recurrence of renal insults comprising administering to the subject a therapeutically effective dose of a compound which inhibits a target gene associated with kidney damage wherein the oligonucleotide compound is administered to the subject within 24 hours of the renal insult. The compound is an

oligonucleotide compound which inhibits expression of a target gene, namely of the p53 gene.

[0019] According to another aspect the present invention provides an oligonucleotide compound for use in a method of attenuating progression of chronic kidney disease (CKD) in a subject at risk of CKD progression resulting from exposure to a recurrence of renal insults comprising administering to the subject a therapeutically effective dose of an oligonucleotide compound which down regulates expression of the p53 target gene associated with kidney injury wherein the oligonucleotide compound is administered to the subject within 24 hours of each renal insult. In some embodiments the kidney insult results in acute renal insult including acute kidney injury (AKI).

[0020] In various embodiments a subject at risk of chronic kidney disease (CKD) or CKD progression is a subject having any one or more of Type 1 or Type 2 diabetes mellitus, high blood pressure (hypertension), high cholesterol, heart disease, liver disease, amyloidosis, Sickle cell disease, Systemic Lupus erythematosus, glomerulonephritis, polycystic kidney disease, atherosclerosis, vascular diseases such as arteritis, vasculitis, or fibromuscular dysplasia or a subject that is about to undergo radiographical examination (i.e. administration of a radiocontrast agent) or a subject that uses nephrotoxic medications, including, without being limited to, analgesics such as acetaminophen (Tylenol®) and non-steroidal anti-inflammatory drugs (NSAIDs) (e.g. ibuprofen (Motrin®, Advil®)) that can cause analgesic nephropathy when used regularly over long durations of time.

[0021] Also disclosed herein is a method of attentuating the severity of kidney damage resulting from renal insult in a subject suffering from chronic kidney disease (CKD) comprising administering to the subject a therapeutically effective dose of an oligonucleotide compound which inhibits expression of the target gene associated with renal ischemia, thereby attenuating kidney damage. In some embodiments kidney damage is AKI.

[0022] Also disclosed herein is a method to prevent progression of CKD resulting from acute kidney injury or insult in a subject suffering from CKD comprising administering to the subject a therapeutically effective dose of an oligonucleotide compound which inhibits expression of the target gene associated with renal ischemia, thereby preventing progression of CKD.

[0023] In some embodiments the renal insult is selected from surgery including cardiovascular surgery, exposure to radiocontrast agent, myoglobinuria, ischemia/reperfusion injury, urinary tract obstruction exposure to nephrotoxins, including contrast agents including radiocontrast agents; decreased perfusion; proteinuria; increased renal ammoniagenesis with interstitial injury; hyperlipidemia; hyperphosphatemia with calcium phosphate deposition. In some embodiments the renal insult is selected from ischemia/reperfusion, sepsis and exposure to a radiocontrast agent. In certain embodiments ischemia/reperfusion injury ensues during or following cardiovascular surgery or cardiopulmonary surgery. Myoglobinurea results from myoglobin, which acts as an endogenous nephrotoxin by both direct proximal tubule cell (PTC) injury and renal vasoconstriction. A recurrence or plurality of renal insults refers to 2, 3, 4, 5 or more renal insults of the same or different types.

[0024] In some aspects the oligonucleotide is administered to the subject within (i.e. prior to, simultaneously with or post) 72 hours, within 48 hours, within 24 hours, within 16 hours, within 8 hours, within 4 hours pre or post renal insult and preferably at about 72 hours pre to about to about 8 hours post renal insult. In some aspects the oligonucleotide is administered 0 to 4 hours post renal insult. In some aspects the oligonucleotide is administered to the subject in proximity of the renal insult. in proximity refers to within one hour of renal insult, within 50, 45, 40, 35, 30, 25, 20, 15, 10, 5, 4, 3, 2 minutes or 1 minute post renal insult.

[0025] In an embodiment, the oligonucleotide is administered to the subject within 24 hours pre or post renal insult. According to another embodiment, the oligonucleotide is administered about 4 hours post renal insult.

[0026] In various embodiments the oligonucleotide compound is selected from the group consisting of unmodified or chemically modified siRNA, shRNA, an antisense molecule, miRNA, and a ribozyme. In the presently preferred embodiments the inhibitor is chemically modified siRNA.

[0027] In some aspects the target gene is a human gene whose expression is up regulated after renal insult. According to the invention, the target gene associated with kidney injury, kidney damage, renal ischemia is p53. Without being bound to theory, this gene is upregulated by renal insult and inhibition of this upregulation in the kidney protects the renal cells from damage including ischemic injury.

[0028] In another aspect the present description discloses a method of preventing the development of chronic kidney disease (CKD) in a subject at risk of developing CKD resulting from exposure to a plurality of renal insults comprising administering to the subject a therapeutically effective dose of an oligonucleotide compound which inhibits expression of a gene associated with renal ischemia wherein the oligonucleotide compound is administered to the subject within 16 hours of the renal insult.

[0029] In yet another aspect the present disclosure discloses a method of preventing chronic kidney disease (CKD) from occurring in a subject which may be predisposed or at risk of developing CKD resulting from exposure to a plurality of renal insults comprising administering to the subject a therapeutically effective dose of an oligonucleotide compound which inhibits expression of a gene associated with renal ischemia wherein the oligonucleotide compound is administered to the subject within 16 hours of the renal insult. Methods include sustained delivery and controlled delivery for local or systemic delivery including delivery of siRNA using for example a delivery vehicle including pump, a slow or sustained release composition or an implant comprising a siRNA depot. The delivery vehicle comprises natural and synthetic materials or a combination of natural and synthetic materials.

[0030] Kits for the treatment or prevention of chronic kidney disease (CKD) are also disclosed. In some aspects the description provides a kit for the treatment or prevention of chronic kidney

disease (CKD) associated with exposure to a radiocontrast agent. In some embodiments a kit includes a package containing a therapeutically effective dose of an oligonucleotide compound which inhibits expression of a gene associated with kidney damage in an amount effective to prevent radiocontrast agent induced kidney damage and a radiocontrast agent in an amount effective to perform a radiographical examination. In certain embodiments an oligonucleotide compound is included as a separate individual preparation and a radiocontrast agent as a separate individual preparation. In some embodiments, an oligonucleotide compound and a radiocontrast agent are combined as a single composition. In some embodiments, an oligonucleotide compound preparation and a radiocontrast agent preparation are provided in different forms (e.g. one preparation is a liquid and the other preparation is a freeze-dried preparation). In some embodiments, a kit further includes instructions for use.

[0031] In various aspects the present description discloses a double stranded oligoribonucleotide compound that inhibits expression of a target gene associated with AKI and progression to CKD for use in the methods as described. According to the invention, the target gene is p53, selected from the genes listed in Table 1, set forth hereinbelow. In particular embodiments the double stranded oligoribonucleotide compounds are chemically modified siRNA.

[0032] In some aspects the siRNA compound is chemically modified according to the following structure:

5'	$(N)_x$ - Z	3' (antisense strand)
3'	Z'-$(N')_y$-z''	5' (sense strand)

wherein each of N and N' is a ribonucleotide which may be unmodified or modified, or an unconventional moiety;

wherein each of (N)x and (N')y is an oligonucleotide in which each consecutive N or N' is joined to the next N or N' by a covalent bond;

wherein Z and Z' may be present or absent, but if present is independently 1-5 consecutive nucleotides covalently attached at the 3' terminus of the strand in which it is present;

wherein z'' may be present or absent, but if present is a capping moiety covalently attached at the 5' terminus of (N')y;

each of x and y is idependently an integer between 18 and 40;

wherein the sequence of (N')y is substantially complementary to the sequence of (N)x; and

wherein (N)x comprises an antisense sequence substantially complementary to from about 18 to about 40 consecutive ribonucleotides present in an mRNA of p53 shown in Table 1, set forth in any one of SEQ ID NOS:67-73.

[0033] In some embodiments the covalent bond joining each consecutive N or N' is a phosphodiester bond. In various embodiments all the covalent bonds are phosphodiester bonds.

[0034] In various embodiments the compound comprises ribonucleotides wherein x = y and each of x and y is 19, 20, 21, 22 or 23. In some embodiments x = y =23. In other embodiments x = y =19.

[0035] In some embodiments the compound is blunt ended, for example wherein both Z and Z' are absent. In an alternative embodiment, the compound comprises at least one 3' overhang, wherein at least one of Z or Z' is present. Z and Z' can independently comprise one or more covalently linked modified or non-modified nucleotides, for example inverted dT or dA; dT, LNA, mirror nucleotide and the like. In some embodiments each of Z and Z' are independently selected from dT and dTdT.

[0036] In some embodiments each of (N)x and (N')y consist of unmodified nucleotides.

[0037] In some embodiments N or N' comprises a modification in the sugar residue of one or more ribonucleotides. In other embodiments the compound comprises at least one ribonucleotide modified in the sugar residue. In some embodiments the compound comprises a modification at the 2' position of the sugar residue. In some embodiments the modification in the 2' position comprises the presence of an amino, a fluoro, an alkoxy or an alkyl moiety. In certain embodiments the 2' modification comprises a methoxy moiety (also known as 2'-O-methyl; 2'-O-Me; 2'-O-CH_3). In some embodiments in each of (N)x and (N')y the ribonucleotides alternate between modified ribonucleotides and unmodified ribonucleotides each modified ribonucleotide being modified so as to have a 2'-O-methyl on its sugar and the ribonucleotide located at the middle position of (N)x being unmodified and the ribonucleotide located at the middle position of (N')y being modified. In some embodiments the preferred compound is I5, which targets p53.

[0038] In some embodiments the siRNA compound comprises modified alternating ribonucleotides in one or both of the antisense and the sense strands. In other embodiments the compound comprises modified alternating ribonucleotides in the antisense strand (N)x only. In certain embodiments the middle ribonucleotide of the antisense strand is not modified; e.g. ribonucleotide in position 10 in a 19-mer strand or position 12 in a 23-mer strand.

[0039] In additional embodiments the compound comprises modified ribonucleotides in alternating positions wherein each N at the 5' and 3' termini of $(N)_x$ are modified in their sugar residues, and each N' at the 5' and 3' termini of $(N')_y$ are unmodified in their sugar residues. In some embodiments, neither $(N)_x$ nor $(N')_y$ are phosphorylated at the 3' and 5' termini. In other embodiments either or both $(N)_x$ and $(N')_y$ are phosphorylated at the 3' termini.

[0040] In some embodiments (N)x comprises modified and unmodified ribonucleotides, each

modified ribonucleotide having a 2'-O-methyl on its sugar, wherein N at the 3' terminus of (N)x is a modified ribonucleotide, (N)x comprises at least five alternating modified ribonucleotides beginning at the 3' end and at least nine modified ribonucleotides in total and each remaining N is an unmodified ribonucleotide. In some embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 8, 11, 13, 15, 17 and 19. In other embodiments (N)x comprises 2'O Me modified ribonucleotides at positions 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19.

[0041] In some embodiments the unconventional moiety is selected from a mirror nucleotide and a nucleotide joined to an adjacent nucleotide by a 2'-5' internucleotide phosphate bond. In some embodiments the mirror nucleotide is selected from an L-ribonucleotide (L-RNA) and an L-deoxyribonucleotide (L-DNA). In some embodiments (N')y comprises at least one unconventional moiety.

[0042] In one embodiment of the above structure, the compound comprises at least one mirror nucleotide at one or both termini in (N')y. In various embodiments the compound comprises two consecutive mirror nucleotides, one at the 3' penultimate position and one at the 3' terminus in (N')y. In one preferred embodiment x=y=19 and (N')y comprises an L-DNA at position 18.

[0043] In some embodiments x=y=19 and (N')y, consists of unmodified ribonucleotides at positions 1-17 and 19 and one L-DNA at the 3' penultimate position (position 18). In other embodiments x=y=19 and (N')y consists of unmodified ribonucleotides at position 1-16 and 19 and two consecutive L-DNA at the 3' penultimate position (positions 17 and 18).

[0044] In another embodiment of the above structure, (N')y further comprises one or more nucleotides containing an intra-sugar bridge at one or both termini.

BRIEF DESCRIPTION OF THE FIGURES

[0045]

Figure 1 provides a proposed vicious circle of mutual reinforcement between AKI and CKD in the development of ESRD (from: B. Molitoris (2008) "Contrast nephropathy: are short-term outcome measures adequate for quantification of long-term renal risk", Nat Clin Pract Nephrol. 2008 4:594-5.)

Figure 2 provides an outline of the study design as described in Example 2, hereinbelow.

Figure 3 shows the effect of p53 siRNA on kidney function following repetitive ischemic injury.

Figure 4 shows that siP53 protects GFR and minimizes proteinuria.

Figure 5. Effect of siP53 (12 mg/kg) on histology after five monthly cycles of ischemic injury.

Figure 6 provides the study design for a CKD model established by nephrectomy and multiple

AKI induction at bimonthly intervals. CKD was induced by subjecting rats to uninephrectomy and multiple AKI (3-4 over a period of 7-8 months) and feeding them with high salt (Na, sodium) diet.

Figure 7 shows pretreatment kidney function parameters after 7-8 months of feeding either a high or low Na diet. Serum creatinine, GFR and Urine protein were similar in rats treated with QM5 siRNA or carrier only. High Na diet resulted in more rapid progression of CKD, loss of GFR but not proteinuria.

Figure 8 shows the efficacy of QM5 (siP53) on prevention of AKI in CKD induced animals.

Figures 9A-9H show the histopatholgy evaluation at termination of the CKD study outlined in Figure 6 and described in Example 2.2. Figures 9A-9C relate to acute injury parameters tubular necrosis (9A), tubular dialation (9B) and casts (9C). Figures 9D-9H relate to chronic injury parameters glomerular damage (9D), interstitial cellular infiltrate (9E); interstitial fibrosis (9F), tubular atrophy or dilation (9G) and vasculopathy (9H).

Figure 10 shows results of histopathogy evaluation at termination and records the average acute and chronic injury scores in treated vs untreated group.

DETAILED DESCRIPTION OF THE INVENTION

[0046] The present disclosure relates in general to a compounds for use in a method of attenuating the progression of chronic kidney disease or preventing exacerbation of CKD progression in a subject at risk thereof. The method employs generally compounds which down-regulate expression of p53 target gene associated with acute kidney injury and in particular with ischemic reperfusion injury. The method employs chemically modified small interfering RNA oligonucleotides (siRNAs), possessing structures and modifications which may increase activity, increase stability, and or minimize toxicity, reduce off target effect or reduce innate immune response when compared to the unmodified compound.

[0047] Table 1, below, sets forth the gene identification number (gi) with an NCBI accession number for non-limiting examples of target genes. The table sets forth the respective mRNA sequences, the gi number (gene identifier number) and the sequence identifier number (SEQ ID NO) for the corresponding mRNA.

Table 1: Non-limiting list of target genes

Gene	Full name and Human Gene ID
REDD1	DDIT4,DNA-damage-inducible transcript 4
	gi|56676369|ref|NM_019058 (SEQ ID NO:1)
REDD2	DNA-damage-inducible transcript 4-like
	gi|34222182|ref|NM_145244 (SEQ ID NO:2)

Gene	Full name and Human Gene ID
TP53BP2 (ASPP2)	tumor protein p53 binding protein, 2
	gi|112799848|ref|NM_001031685.2 (SEQ ID NO:3)
	gi|112799845|ref|NM_005426.2 (SEQ ID NO:4):
LRDD	leucine-rich repeats and death domain containing
	gi|61742781|ref|NM_018494.3 (SEQ ID NO:5)
	gi|61742783|ref|NM_145886.2 (SEQ ID NO:6)
	gi|61742785|ref|NM_145887.2 (SEQ ID NO:7)
CYBA	cytochrome b-245, alpha polypeptide
	gi|68509913|ref|NM_000101.2|(SEQ ID NO:8)
ATF3	activating transcription factor 3
	gi|95102484|ref|NM_001030287.2| v.3 (SEQ ID NO:9)
	gi|71902534|ref|NM_001674.2|v. 1 (SEQ ID NO:10)
	gi|95102482|ref|NM_001040619.1| (SEQ ID NO:11)
CASP2	caspase 2, apoptosis-related cysteine peptidase
	gi|39995058|ref|NM_032982.2 (SEQ ID NO:12)
	gi|39995060|ref|NM_032983.2 (SEQ ID NO:13)
NOX3	NADPH oxidase 3
	Gi|11136625|ref|NM_015718.1 (SEQ ID NO:14)
HRK	harakiri
	gi|4504492|ref|NM_003806.1 (SEQ ID NO:15)
C1QBP	complement component 1, q subcomponent binding protein
	gi|28872801|ref|NM_001212.3 (SEQ ID NO:16)
BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3
	Gi|7669480|ref|NM_004052.2 (SEQ ID NO:17)
MAPK8	mitogen-activated protein kinase 8
	gi|20986493|ref|NM_002750.2 v.2 (SEQ ID NO:18)
	gi|20986522|ref|NM_139049.1 v. 1 (SEQ ID NO:19)
	gi|20986518|ref|NM_139046.1 v.3 (SEQ ID NO:20)
	gi|20986520|ref|NM_139047.1 v.4 (SEQ ID NO:21)
MAPK14	mitogen-activated protein kinase 14
	gi|20986511|ref|NM_139012.1 v.2 (SEQ ID NO:22)
	gi|20986515|ref|NM_139014.1 v. 4 (SEQ ID NO:23)
	gi|4503068|ref|NM_001315.1 v.1 (SEQ ID NO:24)
	gi|20986513|ref|NM_139013.1 v.3 (SEQ ID NO:25)
Rac1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP

Gene	Full name and Human Gene ID
	binding protein)
	gi|156071511|ref|NM_018890.3(SEQ ID NO:26)
	gi|156071503|ref|NM_006908.4(SEQ ID NO:27)
GSK3B	glycogen synthase kinase 3 beta
	gi|21361339|ref|NM_002093.2(SEQ ID NO:28)
	gi|225903436|ref|NM_001146156.1 (SEQ ID NO:29)
P2RX7	purinergic receptor P2X, ligand-gated ion channel, 7
	gi|34335273|ref|NM_002562.4 (SEQ ID NO:30)
TRPM2	transient receptor potential cation channel, subfamily M, member 2
	gi|67906812|ref|NM_003307.3 v. L (SEQ ID NO:31)
PARG	poly (ADP-ribose) glycohydrolase
	gi|70610135|ref|NM_003631.2 (SEQ ID NO:32)
CD38	CD38 molecule
	Gi|38454325|ref|NM_001775.2 (SEQ ID NO:33)
STEAP4	STEAP family member 4
	Gi|13375867|ref|NM_024636.1 (SEQ ID NO:34)
BMP2	bone morphogenetic protein 2
	gi|80861484|ref|NM_001200.2(SEQ ID NO:35)
GJA1	gap junction protein, alpha 1, 43kDa
	gi|4755136|ref|NM_000165.2(SEQ ID NO:36)
TYROBP	TYRO protein tyrosine kinase binding protein
	gi|291045273|ref|NM_001173515.1 variant 4 (SEQ ID NO:37)
	gi|291045270|ref|NM_198125.2| variant 2 (SEQ ID NO:38)
	gi|291045269|ref|NM_003332.3| variant 1 (SEQ ID NO:39)
	gi|291045271|ref|NM_001173514.1 variant 3 (SEQ ID NO:40)
CTGF	connective tissue growth factor
	gi|4503122|ref|NM_001901.1 (SEQ ID NO:41)
SPP1	secreted phosphoprotein 1
	gi|91206461|ref|NM_001040058.1 (SEQ ID NO:42)
	gi|38146097|ref|NM_000582.2 (SEQ ID NO:43)
	gi|91598938|ref|NM_001040060.1 (SEQ ID NO:44)
RHOA	ras homolog gene family member A
	gi|50593005|ref|NM_001664.2(SEQ ID NO:45)
DUOX1	dual oxidase 1

Gene	Full name and Human Gene ID
	gi|28872749|ref|NM_017434.3 (SEQ ID NO:46)
	gi|28872750|ref|NM_175940.1 (SEQ ID NO:47)
NOX4	NADPH oxidase 4
	gi|219842344|ref|NM_016931.3| v. 1 (SEQ ID NO:48)
	gi|219842345|ref|NM_001143836.1| v. 1 (SEQ ID NO:49)
	gi|219842347|ref|NM_001143837.1| v. 1 (SEQ ID NO:50)
NOX1	NADPH oxidase 1
	(gi:21614529, NM_007052 isoform 1L; SEQ ID NO:51)
	(gi:7669509, NM_013955 isoform 1Lv; SEQ ID NO:52)
NOX2 (gp91pho, CYBB)	NADPH oxidase 2
	(gi:6996020, NM_000397; SEQ ID NO:53)
NOX5	NADPH oxidase 5
	(gi:20127623, NM_024505; SEQ ID NO:54)
DUOX2	Dual oxidase 2
	(gi:132566531, NM_014080; SEQ ID NO:55)
NOXO1	NADPH oxidase organizer 1
	(gi:34222190, variant a, NM_144603, SEQ ID NO:56)
	(gi:41281810, variant b, NM_172167; SEQ ID NO:57)
	(gi:41281827, variant c, NM_172168; SEQ ID NO:58)
NCF1 (p47phox, NOXO2)	NADPH oxidase organizer 2
	(gi:115298671, NM_000265; SEQ ID NO:59)
NOXA1	NADPH oxidase activator 1
	(gi:41393186, NM_006647; SEQ ID NO:60)
NCF2 (p67phox, NOXA2)	NADPH oxidase activator 2
	(gi:67189969, NM_000433; SEQ ID NO:61)
	(gi|189083741|ref|NM_001127651.1| v.2 (SEQ ID NO:62)
ASPP1	protein phosphatase 1, regulatory (inhibitor) subunit 13B (PPP1R13B)
	gi|121114286|ref|NM_015316.2| (SEQ ID NO:63)
CTSD	Cathepsin D
	gi|23110949|ref|NM_001909.3| (SEQ ID NO:64)
CAPNS1	Calpain small subunit 1
	gi|51599152|ref|NM_001749.2| Variant 1 (SEQ ID NO:65)
	gi|51599150|ref|NM_001003962.1| variant 2 (SEQ ID NO:66)
p53 (TP53)	tumor protein p53

Gene	Full name and Human Gene ID
	gi|187830767|ref|NM_000546.4| variant 1 (SEQ ID NO:67)
	gi|187830776|ref|NM_001126112.1| variant 2(SEQ ID NO:68)
	gi|187830854|ref|NM_001126114.1| variant 3(SEQ ID NO:69)
	gi|187830822|ref|NM_001126113.1| variant 4(SEQ ID NO:70)
	gi|187830893|ref|NM_001126115.1| variant 5(SEQ ID NO:71)
	gi|187830900|ref|NM_001126116.1| variant 6(SEQ ID NO:72)
	gi|187830908|ref|NM_001126117.1 variant 7(SEQ ID NO:73)
HTRA2	Htra serine peptidase 2
	var 1 gi:73747817, NM_013247 (SEQ ID NO:74)
	var 2 gi:73747818, NM_145074 (SEQ ID NO:75)
KEAP1	Kelch-like ECH-associated protein 1
	var 1 gi:45269144 NM_203500 (SEQ ID NO:76)
	var 2 gi:45269143 NM_012289 (SEQ ID NO:77)
SHC1	Src homology 2 domain containing) transforming prot. 1
	gi|194239661|ref|NM_183001.4| (SEQ ID NO:78
	gi|194239660|ref|NM_003029.4| (SEQ ID NO:79)
	gi|194239663|ref|NM_001130040.1| (SEQ ID NO:80)
	gi|194239667|ref|NM_001130041.1| (SEQ ID NO:81)
ZNHIT 1	Zn finger HIT type 1
	gi:37594439|; NM_006349 (SEQ ID NO:82)
LGALS3	lectin galactoside-binding soluble 3
	var 1 gi:115430222 NM_002306 (SEQ ID NO:83)
	var 2 gi:115430224 NR_003225 (SEQ ID NO:84)
	var 3 gi|294345474|ref|NM_001177388.1| (SEQ ID NO:85)
HI95	Sestrin2
	gi:32454742 NM_031459 (SEQ ID NO:86)
TGFb-1	transforming growth factor beta-1
	gi: 63025221 NM_000660 (SEQ ID NO:87)
ACE	angiotensin-converting enzyme
	transcript variant 2: gi|23238213|ref|NM_152830.1| (SEQ ID NO:88)
	transcript variant 1, gi|23238217|ref|NM_000789.2| (SEQ ID NO:89)
CCL2	Homo sapiens chemokine (C-C motif) ligand 2 (CCL2), mRNA
	gi|56119169|ref|NM_002982.3| (SEQ ID NO:90)

Gene	Full name and Human Gene ID
CDK1 (CDC2)	Homo sapiens cell division cycle 2, G1 to S and G2 to M (CDC2),
	gi|195927038|ref|NM_001786.3| v.1 (SEQ ID NO:91)
	gi|195927039|ref|NM_033379.3| v.2 (SEQ ID NO:92)
	gi|195927040|ref|NM_001130829.1| v.3 (SEQ ID NO:93)
MIF	macrophage inhibitory factor
	gi: 4505184 NM_002415 (SEQ ID NO:94)
ECE-1	endothelin converting enzyme
	gi|164519130|ref|NM_001397.2| variant 1, (SEQ ID NO:95)
	gi|164519139|ref|NM_001113349.1| (SEQ ID NO:96)
	gi|164519135|ref|NM_001113347.1| (SEQ ID NO:97)
	gi|164519137|ref|NM_001113348.1| (SEQ ID NO:98)
ET-1 (EDN1)	Homo sapiens endothelin 1, mRNA
	gi|154800436|ref|NM_001955.3| (SEQ ID NO:99)
TSA (LY6E)	(Thymic shared antigen1)
	Homo sapiens lymphocyte antigen 6 complex, locus E (LY6E), mRNA
	variant 1, gi|187827163|ref|NM_002346.2| (SEQ ID NO:100)
	variant 2, gi|187761330|ref|NM_001127213.1| (SEQ ID NO:101)
Smad2	Homo sapiens SMAD family member 2 (SMAD2), mRNA
	variant 1, gi|118572580|ref|NM_005901.4| (SEQ ID NO:102)
	variant 2, gi|118572581|ref|NM_001003652.2 (SEQ ID NO:103)
	gi|209693425|ref|NM_001135937.1| var 3 (SEQ ID NO:104)
Smad3	Homo sapiens SMAD family member 3 (SMAD3), mRNA
	variant 1, gi|52352808|ref|NM_005902.3 (SEQ ID NO:105)
	gi|223029439|ref|NM_001145102.1| v.2 (SEQ ID NO:106)
	gi|223029441|ref|NM_001145103.1| v.3 (SEQ ID NO:107)
	gi|223029443|ref|NM_001145104.1| v.4 (SEQ ID NO:108)
TGFBR1	Homo sapiens transforming growth factor, beta receptor 1 , mRNA
	(ALK5, activin-receptor like kinase)
	transcript variant 1, gi|66346739|ref|NM_004612.2| (SEQ ID NO:109)
	ranscript variant 2, gi|195963411|ref|NM_001130916.1| (SEQ ID
	NO:110)
STAT3	Homo sapiens signal transducer and activator of transcription 3

Gene	Full name and Human Gene ID
	(acute-phase response factor) (STAT3), mRNA
	transcript variant 1, gi|47080104|ref|NM_139276.2| (SEQ ID NO:111)
	transcript variant 2 gi|47080105|ref|NM_003150.3| (SEQ ID NO:112)
	transcript variant 3 gi|47458819|ref|NM_213662.1| (SEQ ID NO:113)
PTGDS	Homo sapiens prostaglandin D2 synthase 21kDa (brain) (PTGDS),
	mRNA gi|38505192|ref|NM_000954.5| (SEQ ID NO:114)
TLR2	Homo sapiens toll-like receptor 2 (TLR2), mRNA
	gi|68160956|ref|NM_003264.3| (SEQ ID NO:115)

Definitions

[0048] For convenience certain terms employed in the specification, examples and claims are described herein.

[0049] It is to be noted that, as used herein, the singular forms "a", "an" and "the" include plural forms unless the content clearly dictates otherwise.

[0050] Where aspects or embodiments of the invention are described in terms of Markush groups or other grouping of alternatives, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the group.

[0051] An "inhibitor" is a compound, which is capable of reducing (partially or fully) or down regulating the expression of a gene or the activity of the product of such gene to an extent sufficient to achieve a desired biological or physiological effect. The term "inhibitor" as used herein refers to one or more of an oligonucleotide inhibitor, including siRNA, shRNA, synthetic shRNA; miRNA, antisense RNA and DNA and ribozymes.

[0052] A "siRNA inhibitor" is a compound which is capable of reducing the expression of a gene or the activity of the product of such gene to an extent sufficient to achieve a desired biological or physiological effect. The term "siRNA inhibitor" as used herein refers to one or more of a siRNA, shRNA, synthetic shRNA; miRNA. Inhibition may also be referred to as down-regulation or, for RNAi, silencing.

[0053] The term "inhibit" or "down regulate" as used herein refers to reducing the expression

of a gene or the activity of the product of such gene to an extent sufficient to achieve a desired biological or physiological effect. Inhibition or down regulation may be complete or partial.

[0054] As used herein, the term "inhibition" or "down-regulation" of a target gene means reduction of the gene expression (transcription or translation) or polypeptide activity of a gene selected from the group consisiting of any one of SEQ ID NO:67-73 or an SNP (single nucleotide polymorphism) or other variants thereof. The gi number for the mRNA of each target gene is set forth in Table 1. The polynucleotide sequence of the target mRNA sequence, refers to the mRNA sequences set forth herein, or any homologous sequences thereof preferably having at least 70% identity, more preferably 80% identity, even more preferably 90% or 95% identity to any one of mRNA set forth herein. Therefore, polynucleotide which have undergone mutations, alterations or modifications as described herein are encompassed in the present invention. The terms "mRNA polynucleotide sequence" and "mRNA" are used interchangeably.

[0055] As used herein, the terms "polynucleotide" and "nucleic acid" may be used interchangeably and refer to nucleotide sequences comprising deoxyribonucleic acid (DNA), and ribonucleic acid (RNA). The terms should also be understood to include, as equivalents, analogs of either RNA or DNA made from nucleotide analogs. Throughout this application, mRNA sequences are set forth as representing the corresponding genes. "Oligonucleotide" or "oligomer" refers to a deoxyribonucleotide or ribonucleotide sequence from about 2 to about 50 nucleotides. Each DNA or RNA nucleotide may be independently natural or synthetic, and or modified or unmodified. Modifications include changes to the sugar moiety, the base moiety and or the linkages between nucleotides in the oligonucleotide. The compounds for use according to the present invention encompass molecules comprising deoxyribonucleotides, ribonucleotides, modified deoxyribonucleotides, modified ribonucleotides and combinations thereof.

[0056] "Nucleotide" is meant to encompass deoxyribonucleotides and ribonucleotides, which may be natural or synthetic, and or modified or unmodified. Modifications include changes to the sugar moiety, the base moiety and or the linkages between ribonucleotides in the oligoribonucleotide. As used herein, the term "ribonucleotide" encompasses natural and synthetic, unmodified and modified ribonucleotides. Modifications include changes to the sugar moiety, to the base moiety and/ or to the linkages between ribonucleotides in the oligonucleotide.

[0057] Analogs of, or modifications to, a nucleotide / oligonucleotide are preferably employed with the present invention, provided that said analog or modification does not substantially adversely affect the function of the nucleotide / oligonucleotide. In some embodiments a chemical modification results in an increase in activity or stability or a reduction in off-target effects or induction of innate immune responses. Acceptable modifications include modifications of the sugar moiety, modifications of the base moiety, modifications in the internucleotide linkages and combinations thereof.

[0058] The nucleotides can be selected from naturally occurring or synthetic modified bases. Naturally occurring bases include adenine, guanine, cytosine, thymine and uracil. Modified bases of nucleotides include inosine, xanthine, hypoxanthine, 2- aminoadenine, 6-methyl, 2-propyl and other alkyl adenines, 5-halo uracil, 5-halo cytosine, 6-aza cytosine and 6-aza thymine, pseudo uracil, 4- thiouracil, 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.

[0059] In addition, compounds comprising nucleotide analogs can be prepared wherein the structure of one or more nucleotide is fundamentally altered and 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 which is similar to that found in peptides. PNA analogs have been shown to be resistant to enzymatic degradation and to have extended lives *in vivo* and *in vitro.*

[0060] Possible modifications to the sugar residue are manifold and include 2'-O alkyl, locked nucleic acid (LNA), glycol nucleic acid (GNA), threose nucleic acid (TNA), arabinoside, altritol (ANA) and other, 6-membered sugars including morpholinos, and cyclohexinyls. LNA compounds are disclosed in International Patent Publication Nos. WO 00/47599, WO 99/14226, and WO 98/39352. Examples of siRNA compounds comprising LNA nucleotides are disclosed in Elmen et al., (NAR 2005. 33(1):439-447) and in International Patent Publication No. WO 2004/083430.

[0061] Backbone modifications, such as ethyl (resulting in a phospho-ethyl triester); propyl (resulting in a phospho-propyl triester); and butyl (resulting in a phospho-butyl triester) are also possible. Other backbone modifications include polymer backbones, cyclic backbones, acyclic backbones, thiophosphate-D-ribose backbones, amidates, phosphonoacetate derivatives. Certain structures include siRNA compounds having one or a plurality of 2'-5' internucleotide linkages (bridges or backbone).

[0062] Additional modifications which may be present in the molecules for use according to the present invention include nucleoside modifications such as artificial nucleic acids, peptide nucleic acid (PNA), morpholino and locked nucleic acid (LNA), glycol nucleic acid (GNA), threose nucleic acid (TNA), arabinoside, and mirror nucleoside (for example, beta-L-deoxynucleoside instead of beta-D-deoxynucleoside). Further, said molecules may additionally contain modifications on the sugar, such as 2'-alkyl, 2'-fluoro, 2'-deoxy-2'-fluoro, 2'O-allyl, 2'-amine and 2'-alkoxy. Additional sugar modifications are discussed herein.

[0063] Further, the inhibitory nucleic acid molecules for use according to the present invention may comprise one or more gaps and/or one or more nicks and/or one ore more mismatches. Without wishing to be bound by theory, gaps, nicks and mismatches have the advantage of partially destabilizing the nucleic acid / siRNA, so that it may be more easily processed by

endogenous cellular machinery such as DICER, DROSHA or RISC into its inhibitory components.

[0064] In the context of the present invention, a gap in a nucleic acid refers to the absence of one or more internal nucleotides in one strand, while a nick in a nucleic acid refers to the absence of an internucleotide linkage between two adjacent nucleotides in one strand. Any of the molecules for use according to the present invention may contain one or more gaps and/or one or more nicks.

siRNAs and RNA interference

[0065] RNA interference (RNAi) is a phenomenon involving double-stranded (ds) RNA-dependent gene specific posttranscriptional 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 (Gil et al. Apoptosis, 2000. 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 defense mechanisms (see Elbashir et al. Nature 2001, 411:494-498 and Caplen et al. PNAS USA 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 function. 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, Nature 1998. 391, 806) or microRNAs (miRNA; Ambros, Nature 2004 431:7006,350-55; and Bartel, Cell. 2004. 116(2):281-97). The corresponding process in plants is commonly referred to as specific post transcriptional gene silencing or RNA silencing and is referred to as quelling in fungi.

[0066] A siRNA is a double-stranded RNA molecule which inhibits or down regulates, either partially or fully, a gene or the expression of a gene/ mRNA of its endogenous or cellular counterpart, or of an exogenous gene such as a viral nucleic acid. The mechanism of RNA interference is detailed *infra.*

[0067] Several studies have revealed that siRNA therapeutics are effective *in vivo* in both mammals and in humans. Bitko et al., have shown that specific siRNA molecules directed against the respiratory syncytial virus (RSV) nucleocapsid N gene are effective in treating mice when administered intranasally (Bitko et al., Nat. Med. 2005, 11(1):50-55). siRNA has recently been successfully used for inhibition in primates (Tolentino et al., Retina 2004. 24(1):132-138). For a review of the use of siRNA as therapeutics, see for example Barik (J. Mol. Med. 2005. 83: 764-773) or Dykxhoorn et al (2006. Gene Ther. 13:541-552).

siRNA Structures

[0068] The selection and synthesis of siRNA corresponding to known genes has been widely reported; (see for example Ui-Tei et al., J Biomed Biotech. 2006; 2006: 65052; Chalk et al., BBRC. 2004, 319(1): 264-74; Sioud & Leirdal, Met. Mol Biol.; 2004, 252:457-69; Levenkova et al., Bioinform. 2004, 20(3):430-2; Ui-Tei et al., NAR. 2004, 32(3):936-48). For examples of the use of, and production of, modified siRNA see, for example, Braasch et al., Biochem. 2003, 42(26):7967-75; Chiu et al., RNA, 2003, 9(9):1034-48; PCT publications WO 2004/015107 (atugen AG) and WO 02/44321 (Tuschl et al). US Patent Nos. 5,898,031 and 6,107,094, teach chemically modified oligomers. US Patent Publication Nos. 2005/0080246 and 2005/0042647 relate to oligomeric compounds having an alternating motif and dsRNA compounds having chemically modified internucleoside linkages, respectively.

[0069] Other modifications have been disclosed. The inclusion of a 5'-phosphate moiety was shown to enhance activity of siRNAs in Drosophila embryos (Boutla, et al., Curr. Biol. 2001, 11:1776-1780) and is required for siRNA function in human HeLa cells (Schwarz et al., Mol. Cell, 2002, 10:537-48). Amarzguioui et al., (NAR, 2003, 31(2):589-95) showed that siRNA activity depended on the positioning of the 2'-O-methyl modifications. Holen et al (NAR. 2003, 31(9):2401-07) report that an siRNA having small numbers of 2'-O-methyl modified nucleosides gave good activity compared to wild type but that the activity decreased as the numbers of 2'-O-methyl modified nucleosides was increased. Chiu and Rana (RNA. 2003, 9:1034-48) teach that incorporation of 2'-O-methyl modified nucleosides in the sense or antisense strand (fully modified strands) severely reduced siRNA activity relative to unmodified siRNA. The placement of a 2'-O-methyl group at the 5'-terminus on the antisense strand was reported to severely limit activity whereas placement at the 3'-terminus of the antisense and at both termini of the sense strand was tolerated (Czauderna et al., NAR. 2003, 31(11):2705-16; WO 2004/015107). The molecules described herein offer an advantage in that they are non-toxic and may be formulated as pharmaceutical compositions for treatment of various diseases.

[0070] International Patent Publication No. WO 2008/050329 to the assignee of the present invention relates to siRNA compounds, compositions comprising same and to methods of use thereof for treating diseases and disorders related to expression of proapoptotic genes. US Ser. No. 11/ 655610 relates to methods of treating hearing impairment by inhibiting a pro-apoptotic gene in general and p53 in particular.

Oligonucleotides

[0071] The present description discloses methods employing oligonucleotide inhibitors including double-stranded oligonucleotides (e.g. siRNA), which down-regulate the expression of a desired gene. A siRNA is a duplex oligoribonucleotide in which the sense strand is derived from the mRNA sequence of the desired gene, 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., NAR. 2003, 31(11):2705-

2716). Without being bound by theory, an siRNA for use according to the invention inhibits gene expression on a post-transcriptional level with or without destroying the mRNA; siRNA may target the mRNA for specific cleavage and degradation and/ or may inhibit translation from the targeted message.

[0072] In various embodiments the siRNA comprises an RNA duplex comprising a first strand and a second strand, whereby the first strand comprises a ribonucleotide sequence at least partially complementary to about 18 to about 40 consecutive nucleotides of a target nucleic acid which is mRNA transcribed from the p53 target gene, and the second strand comprises a ribonucleotide sequence at least partially complementary to the first strand and wherein said first strand and or said second strand comprises a one or more chemically modified ribonucleotides and or unconventional moieties.

[0073] In one embodiment the siRNA compound comprises at least one ribonucleotide comprising a 2' modification on the sugar moiety ("2' sugar modification"). In certain embodiments the compound comprises 2'O-alkyl or 2'-fluoro or 2'O-allyl or any other 2' modification, optionally on alternate positions. Other stabilizing modifications are also possible (e.g. terminal modifications). In some embodiments a preferred 2'O-alkyl is 2'O-methyl (methoxy, 2'OMe) sugar modification.

[0074] In some embodiments the backbone of the oligonucleotides is modified and comprises phosphate-D-ribose entities but may also contain thiophosphate-D-ribose entities, triester, thioate, 2'-5' bridged backbone (also may be referred to as 5'-2'), PACE and the like.

[0075] As used herein, the terms "non-pairing nucleotide analog" means a nucleotide analog which comprises a non-base pairing moiety including but not limited to: 6 des amino adenosine (Nebularine), 4-Me-indole, 3-nitropyrrole, 5-nitroindole, Ds, Pa, N3-Me riboU, N3-Me riboT, N3-Me-dC, N3-Me-dT, N1-Me-dG, N1-Me-dA, N3-ethyl-dC, N3-Me-dC. In some embodiments the non-base pairing nucleotide analog is a ribonucleotide. In other embodiments it is a deoxyribonucleotide. In addition, analogues of polynucleotides may be prepared wherein the structure of one or more nucleotide is fundamentally altered and better suited as therapeutic or experimental reagents. An example of a nucleotide analogue is a peptide nucleic acid (PNA) wherein the deoxyribose (or ribose) phosphate backbone in DNA (or RNA) is replaced with a polyamide backbone which is similar to that found in peptides. PNA analogues have been shown to be resistant to enzymatic degradation and to enhance stability *in vivo* and *in vitro.* Other useful modifications include polymer backbones, cyclic backbones, acyclic backbones, thiophosphate-D-ribose backbones, triester backbones, thioate backbones, 2'-5' bridged backbone, artificial nucleic acids, morpholino nucleic acids, glycol nucleic acid (GNA), threose nucleic acid (TNA), arabinoside, and mirror nucleoside (for example, beta-L-deoxyribonucleoside instead of beta-D-deoxyribonucleoside). The compounds for use according to the present invention can be synthesized using one or more inverted nucleotides, for example inverted thymidine or inverted adenine (see, for example, Takei, et al., 2002, JBC 277(26):23800-06).

[0076] Additional modifications include terminal modifications on the 5' and/or 3' part of the oligonucleotides and are also known as capping moieties. Such terminal modifications are selected from a nucleotide, a modified nucleotide, a lipid, a peptide, a sugar and an inverted abasic moiety.

[0077] What is sometimes referred to in the present invention as an "abasic nucleotide" or "abasic nucleotide analog" is more properly referred to as a pseudo-nucleotide or an unconventional moiety. A nucleotide is a monomeric unit of nucleic acid, consisting of a ribose or deoxyribose sugar, a phosphate, and a base (adenine, guanine, thymine, or cytosine in DNA; adenine, guanine, uracil, or cytosine in RNA). A modified nucleotide comprises a modification in one or more of the sugar, phosphate and or base. The abasic pseudo-nucleotide lacks a base, and thus is not strictly a nucleotide.

[0078] The term "unconventional moiety" as used herein refers to abasic ribose moiety, an abasic deoxyribose moiety, a deoxyribonucleotide, a modified deoxyribonucleotide, a mirror nucleotide, a non-base pairing nucleotide analog and a nucleotide joined to an adjacent nucleotide by a 2'-5' internucleotide phosphate bond; bridged nucleic acids including LNA and ethylene bridged nucleic acids. In some embodiments of the present invention a preferred unconventional moiety is an abasic ribose moiety, an abasic deoxyribose moiety, a deoxyribonucleotide, a mirror nucleotide, and a nucleotide joined to an adjacent nucleotide by a 2'-5' internucleotide phosphate bond.

[0079] Abasic deoxyribose moiety includes for example abasic deoxyribose-3'-phosphate; 1,2-dideoxy-D-ribofuranose-3-phosphate; 1,4-anhydro-2-deoxy-D-ribitol-3-phosphate. Inverted abasic deoxyribose moiety includes inverted deoxyriboabasic; 3',5' inverted deoxyabasic 5' -phosphate.

[0080] A "mirror" nucleotide is a nucleotide with reversed chirality to the naturally occurring or commonly employed nucleotide, i.e., a mirror image (L-nucleotide) of the naturally occurring (D-nucleotide), also referred to as L-RNA in the case of a mirror ribonucleotide, and "spiegelmer". The nucleotide can be a ribonucleotide or a deoxyribonucleotide and may further comprise at least one sugar, base and or backbone modification. See US Patent No. 6,586,238. Also, US Patent No. 6,602,858 discloses nucleic acid catalysts comprising at least one L-nucleotide substitution. Mirror nucleotide includes for example L-DNA (L-deoxyriboadenosine-3'-phosphate (mirror dA); L-deoxyribocytidine-3'-phosphate (mirror dC); L-deoxyriboguanosine-3'-phosphate (mirror dG); L-deoxyribothymidine-3'-phosphate (mirror image dT)) and L-RNA (L-riboadenosine-3'-phosphate (mirror rA); L-ribocytidine-3'-phosphate (mirror rC); L-riboguanosine-3'-phosphate (mirror rG); L-ribouracil-3'-phosphate (mirror dU)).

[0081] The term "capping moiety" as used herein includes abasic ribose moiety, abasic deoxyribose moiety, modifications to abasic ribose and abasic deoxyribose moieties including 2' O alkyl modifications; inverted abasic ribose and abasic deoxyribose moieties and modifications thereof; C6-imino-Pi; a mirror nucleotide including L-DNA and L-RNA; 5'O-Me nucleotide; and nucleotide analogs including 4',5'-methylene nucleotide; 1-(β-D-

erythrofuranosyl)nucleotide; 4'-thio nucleotide, carbocyclic nucleotide; 5'-amino-alkyl phosphate; 1,3-diamino-2-propyl phosphate, 3-aminopropyl phosphate; 6-aminohexyl phosphate; 12-aminododecyl phosphate; hydroxypropyl phosphate; 1,5-anhydrohexitol nucleotide; alpha-nucleotide; threo-pentofuranosyl nucleotide; acyclic 3',4'-seco nucleotide; 3,4-dihydroxybutyl nucleotide; 3,5-dihydroxypentyl nucleotide, 5'-5'-inverted abasic moiety; 1,4-butanediol phosphate; 5'-amino; and bridging or non bridging methylphosphonate and 5'-mercapto moieties.

[0082] Certain preferred capping moieties are abasic ribose or abasic deoxyribose moieties; inverted abasic ribose or abasic deoxyribose moieties; C6-amino-Pi; a mirror nucleotide including L-DNA and L-RNA.

[0083] A further end modification is a biotin group. Such biotin group may preferably be attached to either the most 5' or the most 3' nucleotide of the first and/or second strand or to both ends. In a more preferred embodiment the biotin group is coupled to a polypeptide or a protein. The polypeptide or protein may be attached through any of the other aforementioned end modifications.

[0084] The various end modifications as disclosed herein are preferably located at the ribose moiety of a nucleotide of the nucleic acid for use according to the present invention. More particularly, the end modification may be attached to or replace any of the OH-groups of the ribose moiety, including but not limited to the 2'OH, 3'OH and 5'OH position, provided that the nucleotide thus modified is a terminal nucleotide. Inverted abasic or abasic are nucleotides, either deoxyribonucleotides or ribonucleotides which do not have a nucleobase moiety (for example see Sternberger, et al., (2002). Antisense Nucleic Acid Drug Dev, 12, 131-43).

[0085] Modified deoxyribonucleotide includes, for example 5'OMe DNA (5-methyl-deoxyriboguanosine-3'-phosphate) which may be useful as a nucleotide in the 5' terminal position (position number 1); PACE (deoxyriboadenine 3' phosphonoacetate, deoxyribocytidine 3' phosphonoacetate, deoxyriboguanosine 3' phosphonoacetate, deoxyribothymidine 3' phosphonoacetate.

[0086] Bridged nucleic acids include LNA (2'-O, 4'-C-methylene bridged Nucleic Acid adenosine 3' monophosphate, 2'-O,4'-C-methylene bridged Nucleic Acid 5-methyl-cytidine 3' monophosphate, 2'-O,4'-C-methylene bridged Nucleic Acid guanosine 3' monophosphate, 5-methyl-uridine (or thymidine) 3' monophosphate); and ENA (2'-O,4'-C-ethylene bridged nucleic acid adenosine 3' monophosphate, 2'-O,4'-C-ethylene bridged nucleic acid 5-methyl-cytidine 3' monophosphate, 2'-O,4'-C-ethylene bridged nucleic acid guanosine 3' monophosphate, 5-methyl-uridine (or thymidine) 3' monophosphate).

[0087] In certain embodiments the complementarity between said first strand and the target nucleic acid is perfect. In some embodiments, the strands are substantially complementary, i.e. having one, two or up to three mismatches between said first strand and the target nucleic acid. Substantially complementary refers to complementarity of greater than about 84%, to

another sequence. For example in a duplex region consisting of 19 base pairs one mismatch results in 94.7% complementarity, two mismatches results in about 89.5% complementarity and 3 mismatches results in about 84.2% complementarity, rendering the duplex region substantially complementary. Accordingly substantially identical refers to identity of greater than about 84%, to another sequence.

[0088] In some embodiments the first strand and the second strand of the compound are linked by a loop structure, which is comprised of a non-nucleic acid polymer such as, *inter alia,* polyethylene glycol. Alternatively, the loop structure is comprised of a nucleic acid, including modified and non-modified ribonucleotides and modified and non-modified deoxyribonucleotides.

[0089] In further embodiments, the 5'-terminus of the first strand of the siRNA is linked to the 3'-terminus of the second strand, or the 3'-terminus of the first strand is linked to the 5'-terminus of the second strand, said linkage being via a nucleic acid linker typically having a length between 2-100 nucleobases, preferably about 2 to about 30 nucleobases.

[0090] Preferably the methods disclosed herein employ oligonucleotide compounds having alternating ribonucleotides modified in at least one of the antisense and the sense strands of the compound, for 19 mer and 23 mer oligomers 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. For 21 mer oligomers the ribonucleotides at the 5' and 3' termini of the sense strand are modified in their sugar residues, and the ribonucleotides at the 5' and 3' termini of the antisense strand are unmodified in their sugar residues, or may have an optional additional modification at the 3' terminus. As mentioned above, it is preferred that the middle nucleotide of the antisense strand is unmodified.

[0091] According to one preferred embodiment of the invention, the antisense and the sense strands of the oligonucleotide / siRNA are phosphorylated at the 3'-terminus and not at the 5'-terminus. According to another preferred embodiment of the invention, the antisense and the sense strands are non-phosphorylated. According to yet another preferred embodiment of the invention, the 5' most ribonucleotide in the sense strand is modified to abolish any possibility of *in vivo* 5'-phosphorylation.

[0092] Any siRNA sequence can be prepared having any of the modifications / structures disclosed herein. The compound comprising a combination of sequence plus structure is useful in the treatment of the conditions disclosed herein.

Structural motifs

[0093] In a preferred embodiment of the invention, the oligonucleotide for use according to the invention is the I5 siRNA compound, having the structure:

Sense sequence	5'	GaGaAuAuUuCaCcCuUcA 3' (SEQ ID NO:118)
Antisense sequence	3'	cUcUuAuAaAgUgGgAaGu 5' (SEQ ID NO:119),

wherein upper case letters represent unmodified nucleotides and lower case letters represent 2'-methoxy sugar modified ribonucleotides.

[0094] In some aspects of the present description the oligonucleotide inhibitor is chemically modified siRNA according to one of the following modifications set forth in Structures (A)-(P) or as tandem siRNA or RNAstar.

[0095] In one aspect the present description provides a compound set forth as Structure (A):

(A)	5'	$(N)_x$ - Z	3' (antisense strand)
	3'	Z'-$(N')_y$	5' (sense strand)

wherein each of N and N' is a nucleotide selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide and a modified deoxyribonucleotide;

wherein each of $(N)_x$ and $(N')_y$ is an oligonucleotide 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 18 and 40;

wherein each of Z and Z' may be present or absent, but if present is 1-5 consecutive nucleotides covalently attached at the 3' terminus of the strand in which it is present;

wherein the sequence of $(N')_y$ is a sequence substantially complementary to (N)x; and

wherein the sequence of $(N)_x$ comprises an antisense sequence substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of the target gene associated with acute kidney injury.

[0096] In certain embodiments the present description provides a compound having structure (B)

(B)	5'	$(N)_x$ - Z	3' (antisense strand)
	3'	Z'-$(N')_y$	5' (sense strand)

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

wherein each of Z and Z' may be present or absent, but if present is 1-5 consecutive nucleotides covalently attached at the 3' terminus of the strand in which it is present;

wherein each of x and y =19, 21 or 23 and $(N)_x$ and $(N')_y$ are fully complementary

wherein alternating ribonucleotides in each of $(N)_x$ and $(N')_y$ are modified to result in a 2'-O-methyl modification in the sugar residue of the ribonucleotides;

wherein the sequence of $(N')_y$ is a sequence substantially complementary to (N)x; and

wherein the sequence of $(N)_x$ comprises an antisense sequence substantially complementary to the substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of the target gene associated with acute kidney injury.

[0097] In some embodiments each of $(N)_x$ and $(N')_y$ is independently phosphorylated or non-phosphorylated at the 3' and 5' termini.

[0098] In certain embodiments wherein each of x and y =19 or 23, each N at the 5' and 3' termini of $(N)_x$ is modified; and each N' at the 5' and 3' termini of $(N')_y$ is unmodified.

[0099] In certain embodiments wherein each of x and y =21, each N at the 5' and 3' termini of $(N)_x$ is unmodified; and each N' at the 5' and 3' termini of $(N')_y$ is modified.

[0100] In particular embodiments, when x and y =19, the siRNA is modified such that a 2'-O-methyl (2'-OMe) group is present on the first, third, fifth, seventh, ninth, eleventh, thirteenth, fifteenth, seventeenth and nineteenth nucleotide of the antisense strand $(N)_x$, and whereby the very same modification, i. e. a 2'-OMe group, is present at the second, fourth, sixth, eighth, tenth, twelfth, fourteenth, sixteenth and eighteenth nucleotide of the sense strand $(N')_y$. In various embodiments these particular siRNA compounds are blunt ended at both termini.

[0101] In some embodiments, the present description provides a compound having Structure (C):

(C)	5'	(N)x-Z	3' antisense strand
	3'	Z'-(N')y	5' sense strand

wherein each of N and N' is a nucleotide independently selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide and a modified deoxyribonucleotide;

wherein each of (N)x and (N')y is an oligomer in which each consecutive nucleotide is joined to the next nucleotide by a covalent bond and each of x and y is an integer between 18 and 40;

wherein in (N)x the nucleotides are unmodified or (N)x comprises alternating modified ribonucleotides and unmodified ribonucleotides; each modified ribonucleotide being modified so as to have a 2'-O-methyl on its sugar and the ribonucleotide located at the middle position

of (N)x being modified or unmodified preferably unmodified;

wherein (N')y comprises unmodified ribonucleotides further comprising one modified nucleotide at a terminal or penultimate position, wherein the modified nucleotide is selected from the group consisting of a mirror nucleotide, a bicyclic nucleotide, a 2'-sugar modified nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage;

wherein if more than one nucleotide is modified in (N')y, the modified nucleotides may be consecutive;

wherein each of Z and Z' may be present or absent, but if present is 1-5 deoxyribonucleotides covalently attached at the 3' terminus of any oligomer to which it is attached;

wherein the sequence of $(N')_y$ comprises a sequence substantially complementary to (N)x; and wherein $(N)_x$ comprises an antisense sequence substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of the target gene associated with acute kidney injury.

[0102] In particular embodiments, x=y=19 and in (N)x each modified ribonucleotide is modified so as to have a 2'-O-methyl on its sugar and the ribonucleotide located at the middle of (N)x is unmodified. Accordingly, in a compound wherein x=19, (N)x comprises 2'-O-methyl sugar modified ribonucleotides at positions 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 8, 11, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 5. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 8, 11, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 6. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 8, 11, 13, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 15. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 8, 11, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 14. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 1, 2, 3, 7, 9, 11, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 5. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 1, 2, 3, 5, 7, 9, 11, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 6. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 1, 2, 3, 5, 7, 9, 11, 13, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 15. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 1, 2, 3, 5, 7, 9, 11, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 14. In other embodiments, (N)x

comprises 2'OMe modified ribonucleotides at positions 2, 4, 6, 7, 9, 11, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 5. In other embodiments, (N)x comprises 2'OMe modified ribonucleotides at positions 1, 2, 4, 6, 7, 9, 11, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 5. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 8, 11, 13, 14, 16, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 15. In other embodiments, (N)x comprises 2'OMe modified ribonucleotides at positions 1, 2, 3, 5, 7, 9, 11, 13, 14, 16, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 15. In other embodiments, (N)x comprises 2'OMe modified ribonucleotides at positions 2, 4, 6, 8, 11, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 7. In other embodiments, (N)x comprises 2'OMe modified ribonucleotides at positions 2, 4, 6, 11, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 8.

[0103] In yet other embodiments (N)x comprises at least one nucleotide mismatch relative to the one of the genes. In certain preferred embodiments, (N)x comprises a single nucleotide mismatch on position 5, 6, or 14. In one embodiment of Structure (C), at least two nucleotides at either or both the 5' and 3' termini of (N')y are joined by a 2'-5' phosphodiester bond. In certain preferred embodiments x=y=19 or x=y=23; in (N)x the nucleotides alternate between modified ribonucleotides and unmodified ribonucleotides, each modified ribonucleotide being modified so as to have a 2'-O-methyl on its sugar and the ribonucleotide located at the middle of (N)x being unmodified; and three nucleotides at the 3' terminus of (N')y are joined by two 2'-5' phosphodiester bonds (set forth herein as Structure I). In other preferred embodiments, x=y=19 or x=y=23; in (N)x the nucleotides alternate between modified ribonucleotides and unmodified ribonucleotides, each modified ribonucleotide being modified so as to have a 2'-O-methyl on its sugar and the ribonucleotide located at the middle of (N)x being unmodified; and four consecutive nucleotides at the 5' terminus of (N')y are joined by three 2'-5' phosphodiester bonds. In a further embodiment, an additional nucleotide located in the middle position of (N)y may be modified with 2'-O-methyl on its sugar. In another preferred embodiment, in (N)x the nucleotides alternate between 2'-O-methyl modified ribonucleotides and unmodified ribonucleotides, and in (N')y four consecutive nucleotides at the 5' terminus are joined by three 2'-5' phosphodiester bonds and the 5' terminal nucleotide or two or three consecutive nucleotides at the 5' terminus comprise 3'-O-methyl modifications.

[0104] In certain preferred embodiments of Structure C, x=y=19 and in (N')y the nucleotide in at least one position comprises a mirror nucleotide, a deoxyribonucleotide and a nucleotide joined to an adjacent nucleotide by a 2'-5' internucleotide bond;.

[0105] In certain preferred embodiments of Structure C, x=y=19 and (N')y comprises a mirror nucleotide. In various embodiments the mirror nucleotide is an L-DNA nucleotide. In certain embodiments the L-DNA is L-deoxyribocytidine. In some embodiments (N')y comprises L-DNA at position 18. In other embodiments (N')y comprises L-DNA at positions 17 and 18. In certain

embodiments (N')y comprises L-DNA substitutions at positions 2 and at one or both of positions 17 and 18. In certain embodiments (N')y further comprises a 5' terminal cap nucleotide such as 5'-O-methyl DNA or an abasic or inverted abasic moiety as an overhang.

[0106] In yet other embodiments (N')y comprises a DNA at position 15 and L-DNA at one or both of positions 17 and 18. In that structure, position 2 may further comprise an L-DNA or an abasic unconventional moiety.

[0107] Other embodiments of Structure C are envisaged wherein x=y=21 or wherein x=y=23; in these embodiments the modifications for (N')y discussed above instead of being on positions 15, 16, 17, 18 are on positions 17, 18, 19, 20 for 21 mer and on positions 19, 20, 21, 22 for 23 mer ; similarly the modifications at one or both of positions 17 and 18 are on one or both of positions 19 or 20 for the 21 mer and one or both of positions 21 and 22 for the 23 mer. All modifications in the 19 mer are similarly adjusted for the 21 and 23 mer.

[0108] According to various embodiments of Structure (C), in (N')y 2, 3, 4, 5, 6, 7, 8 , 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides at the 3' terminus are linked by 2'-5' internucleotide linkages. In one preferred embodiment, four consecutive nucleotides at the 3' terminus of (N')y are joined by three 2'-5' phosphodiester bonds, wherein one or more of the 2'-5' nucleotides which form the 2'-5' phosphodiester bonds further comprises a 3'-O-methyl sugar modification. Preferably the 3' terminal nucleotide of (N')y comprises a 2'-O-methyl sugar modification. In certain preferred embodiments of Structure C, x=y=19 and in (N')y two or more consecutive nucleotides at positions 15, 16, 17, 18 and 19 comprise a nucleotide joined to an adjacent nucleotide by a 2'-5' internucleotide bond. In various embodiments the nucleotide forming the 2'-5' internucleotide bond comprises a 3' deoxyribose nucleotide or a 3' methoxy nucleotide. In some embodiments the nucleotides at positions 17 and 18 in (N')y are joined by a 2'-5' internucleotide bond. In other embodiments the nucleotides at positions 16, 17, 18, 16-17, 17-18, or 16-18 in (N')y are joined by a 2'-5' internucleotide bond.

[0109] In certain embodiments (N')y comprises an L-DNA at position 2 and 2'-5' internucleotide bonds at positions 16-17, 17-18, or 16-18. In certain embodiments (N')y comprises 2'-5' internucleotide bonds at positions 16-17, 17-18, or 16-18 and a 5' terminal cap nucleotide.

[0110] According to various embodiments of Structure (C), in (N')y 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive nucleotides at either terminus or 2-8 modified nucleotides at each of the 5' and 3' termini are independently mirror nucleotides. In some embodiments the mirror nucleotide is an L-ribonucleotide. In other embodiments the mirror nucleotide is an L-deoxyribonucleotide. The mirror nucleotide may further be modified at the sugar or base moiety or in an internucleotide linkage.

[0111] In one preferred embodiment of Structure (C), the 3' terminal nucleotide or two or three consecutive nucleotides at the 3' terminus of (N')y are L-deoxyribonucleotides.

[0112] In other embodiments of Structure (C), in (N')y 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14

consecutive ribonucleotides at either terminus or 2-8 modified nucleotides at each of the 5' and 3' termini are independently 2' sugar modified nucleotides. In some embodiments the 2' sugar modification comprises the presence of an amino, a fluoro, an alkoxy or an alkyl moiety. In certain embodiments the 2' sugar modification comprises a methoxy moiety (2'-OMe). In one series of preferred embodiments, three, four or five consecutive nucleotides at the 5' terminus of (N')y comprise the 2'-OMe modification. In another preferred embodiment, three consecutive nucleotides at the 3' terminus of (N')y comprise the 2'-O-methyl modification.

[0113] In some embodiments of Structure (C), in (N')y 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides at either or 2-8 modified nucleotides at each of the 5' and 3' termini are independently bicyclic nucleotide. In various embodiments the bicyclic nucleotide is a locked nucleic acid (LNA). A 2-O, 4'-C-ethylene-bridged nucleic acid (ENA) is a species of LNA (see below).

[0114] In various embodiments (N')y comprises modified nucleotides at the 5' terminus or at both the 3' and 5' termini.

[0115] In some embodiments of Structure (C), at least two nucleotides at either or both the 5' and 3' termini of (N')y are joined by P-ethoxy backbone modifications. In certain preferred embodiments x=y=19 or x=y=23; in (N)x the nucleotides alternate between modified ribonucleotides and unmodified ribonucleotides, each modified ribonucleotide being modified so as to have a 2'-O-methyl on its sugar and the ribonucleotide located at the middle position of (N)x being unmodified; and four consecutive nucleotides at the 3' terminus or at the 5' terminus of (N')y are joined by three P-ethoxy backbone modifications. In another preferred embodiment, three consecutive nucleotides at the 3' terminus or at the 5' terminus of (N')y are joined by two P-ethoxy backbone modifications.

[0116] In some embodiments of Structure (C), in (N')y 2, 3, 4, 5, 6, 7 or 8, consecutive ribonucleotides at each of the 5' and 3' termini are independently mirror nucleotides, nucleotides joined by 2'-5' phosphodiester bond, 2' sugar modified nucleotides or bicyclic nucleotide. In one embodiment, the modification at the 5' and 3' termini of (N')y is identical. In one preferred embodiment, four consecutive nucleotides at the 5' terminus of (N')y are joined by three 2'-5' phosphodiester bonds and three consecutive nucleotides at the 3' terminus of (N')y are joined by two 2'-5' phosphodiester bonds. In another embodiment, the modification at the 5' terminus of (N')y is different from the modification at the 3' terminus of (N')y. In one specific embodiment, the modified nucleotides at the 5' terminus of (N')y are mirror nucleotides and the modified nucleotides at the 3' terminus of (N')y are joined by 2'-5' phosphodiester bond. In another specific embodiment, three consecutive nucleotides at the 5' terminus of (N')y are LNA nucleotides and three consecutive nucleotides at the 3' terminus of (N')y are joined by two 2'-5' phosphodiester bonds. In (N)x the nucleotides alternate between modified ribonucleotides and unmodified ribonucleotides, each modified ribonucleotide being modified so as to have a 2'-O-methyl on its sugar and the ribonucleotide located at the middle of (N)x being unmodified, or the ribonucleotides in (N)x being unmodified.

[0117] In another embodiment of Structure (C), the present invention provides a compound wherein x=y=19 or x=y=23; in (N)x the nucleotides alternate between modified ribonucleotides and unmodified ribonucleotides, each modified ribonucleotide being modified so as to have a 2'-O-methyl on its sugar and the ribonucleotide located at the middle of (N)x being unmodified; three nucleotides at the 3' terminus of (N')y are joined by two 2'-5' phosphodiester bonds and three nucleotides at the 5' terminus of (N')y are LNA such as ENA.

[0118] In another embodiment of Structure (C), five consecutive nucleotides at the 5' terminus of (N')y comprise the 2'-O-methyl sugar modification and two consecutive nucleotides at the 3' terminus of (N')y are L-DNA.

[0119] In yet another embodiment, the present invention provides a compound wherein x=y=19 or x=y=23; (N)x consists of unmodified ribonucleotides; three consecutive nucleotides at the 3' terminus of (N')y are joined by two 2'-5' phosphodiester bonds and three consecutive nucleotides at the 5' terminus of (N')y are LNA such as ENA.

[0120] According to other embodiments of Structure (C), in (N')y the 5' or 3' terminal nucleotide, or 2, 3, 4, 5 or 6 consecutive nucleotides at either termini or 1-4 modified nucleotides at each of the 5' and 3' termini are independently phosphonocarboxylate or phosphinocarboxylate nucleotides (PACE nucleotides). In some embodiments the PACE nucleotides are deoxyribonucleotides. In some preferred embodiments in (N')y, 1 or 2 consecutive nucleotides at each of the 5' and 3' termini are PACE nucleotides.

[0121] In some embodiments, the present description provides a compound having Structure (D):

(D)	5'	(N)x -Z	3' antisense strand
	3'	Z'-(N')$_y$	5' sense strand

wherein each of N and N' is a nucleotide selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide or a modified deoxyribonucleotide;

wherein each of (N)x and (N')y is an oligomer in which each consecutive nucleotide is joined to the next nucleotide by a covalent bond and each of x and y is an integer between 18 and 40;

wherein (N)x comprises unmodified ribonucleotides further comprising one modified nucleotide at the 3' terminal or penultimate position, wherein the modified nucleotide is selected from the group consisting of a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage;

wherein (N')y comprises unmodified ribonucleotides further comprising one modified nucleotide at the 5' terminal or penultimate position, wherein the modified nucleotide is selected from the group consisting of a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage;

wherein in each of (N)x and (N')y modified and unmodified nucleotides are not alternating;

wherein each of Z and Z' may be present or absent, but if present is 1-5 deoxyribonucleotides covalently attached at the 3' terminus of any oligomer to which it is attached;

wherein the sequence of $(N')_y$ is a sequence substantially complementary to (N)x; and

wherein $(N)_x$ comprises an antisense sequence substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of the target gene associated with acute kidney injury.

[0122] In one embodiment of Structure (D), x=y=19 or x=y=23; (N)x comprises unmodified ribonucleotides in which two consecutive nucleotides linked by one 2'-5' internucleotide linkage at the 3' terminus; and (N')y comprises unmodified ribonucleotides in which two consecutive nucleotides linked by one 2'-5' internucleotide linkage at the 5' terminus.

[0123] In some embodiments, x=y=19 or x=y=23; (N)x comprises unmodified ribonucleotides in which three consecutive nucleotides at the 3' terminus are joined together by two 2'-5' phosphodiester bonds; and (N')y comprises unmodified ribonucleotides in which four consecutive nucleotides at the 5' terminus are joined together by three 2'-5' phosphodiester bonds (set forth herein as Structure II).

[0124] According to various embodiments of Structure (D) 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 3' terminus of (N)x and 2, 3, 4, 5, 6, 7, 8 , 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 5' terminus of (N')y are linked by 2'-5' internucleotide linkages.

[0125] According to one preferred embodiment of Structure (D), four consecutive nucleotides at the 5' terminus of (N')y are joined by three 2'-5' phosphodiester bonds and three consecutive nucleotides at the 3' terminus of (N')x are joined by two 2'-5' phosphodiester bonds. Three nucleotides at the 5' terminus of (N')y and two nucleotides at the 3' terminus of (N')x may also comprise 3'-O-methyl modifications.

[0126] According to various embodiments of Structure (D), 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive nucleotides starting at the ultimate or penultimate position of the 3' terminus of (N)x and 2, 3, 4, 5, 6, 7, 8 , 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 5' terminus of (N')y are independently mirror nucleotides. In some embodiments the mirror is an L-ribonucleotide. In other embodiments the mirror nucleotide is L-deoxyribonucleotide.

[0127] In other embodiments of Structure (D), 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14

consecutive ribonucleotides starting at the ultimate or penultimate position of the 3' terminus of (N)x and 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 5' terminus of (N')y are independently 2' sugar modified nucleotides. In some embodiments the 2' sugar modification comprises the presence of an amino, a fluoro, an alkoxy or an alkyl moiety. In certain embodiments the 2' sugar modification comprises a methoxy moiety (2'-OMe).

[0128] In one preferred embodiment of Structure (D), five consecutive nucleotides at the 5' terminus of (N')y comprise a 2'OMe sugar modification and five consecutive nucleotides at the 3' terminus of (N')x comprise the 2'OMe sugar modification. In another preferred embodiment of Structure (D), ten consecutive nucleotides at the 5' terminus of (N')y comprise the 2'OMe sugar modification and five consecutive nucleotides at the 3' terminus of (N')x comprise the 2'OMe sugar modification. In another preferred embodiment of Structure (D), thirteen consecutive nucleotides at the 5' terminus of (N')y comprise the 2'OMe sugar modification and five consecutive nucleotides at the 3' terminus of (N')x comprise the 2'-O-methyl modification.

[0129] In some embodiments of Structure (D), in (N')y 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 3' terminus of (N)x and 2, 3, 4, 5, 6, 7, 8 , 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 5' terminus of (N')y are independently a bicyclic nucleotide. In various embodiments the bicyclic nucleotide is a locked nucleic acid (LNA) such as a 2-O, 4'-C-ethylene-bridged nucleic acid (ENA).

[0130] In various embodiments of Structure (D), (N')y comprises a modified nucleotide selected from a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage;

[0131] In various embodiments of Structure (D), (N)x comprises a modified nucleotide selected from a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage;

[0132] In embodiments wherein each of the 3' and 5' termini of the same strand comprises a modified nucleotide, the modification at the 5' and 3' termini is identical. In another embodiment, the modification at the 5' terminus is different from the modification at the 3' terminus of the same strand. In one specific embodiment, the modified nucleotides at the 5' terminus are mirror nucleotides and the modified nucleotides at the 3' terminus of the same strand are joined by 2'-5' phosphodiester bond.

[0133] In one specific embodiment of Structure (D), five consecutive nucleotides at the 5' terminus of (N')y comprise the 2'OMe sugar modification and two consecutive nucleotides at the 3' terminus of (N')y are L-DNA. In addition, the compound may further comprise five consecutive 2'OMe sugar modified nucleotides at the 3' terminus of (N')x.

[0134] In various embodiments of Structure (D), the modified nucleotides in (N)x are different from the modified nucleotides in (N')y. For example, the modified nucleotides in (N)x are 2' sugar modified nucleotides and the modified nucleotides in (N')y are nucleotides linked by 2'-5' internucleotide linkages. In another example, the modified nucleotides in (N)x are mirror nucleotides and the modified nucleotides in (N')y are nucleotides linked by 2'-5' internucleotide linkages. In another example, the modified nucleotides in (N)x are nucleotides linked by 2'-5' internucleotide linkages and the modified nucleotides in (N')y are mirror nucleotides.

[0135] In additional embodiments, the present description provides a compound having Structure (E):

(E)	5'	(N)x -Z	3' antisense strand
	3'	Z'-(N')y	5' sense strand

wherein each of N and N' is a nucleotide selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide or a modified deoxyribonucleotide;

wherein each of (N)x and (N')y is an oligomer in which each consecutive nucleotide is joined to the next nucleotide by a covalent bond and each of x and y is an integer between 18 and 40;

wherein (N)x comprises unmodified ribonucleotides further comprising one modified nucleotide at the 5' terminal or penultimate position, wherein the modified nucleotide is selected from the group consisting of a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage;

wherein (N')y comprises unmodified ribonucleotides further comprising one modified nucleotide at the 3' terminal or penultimate position, wherein the modified nucleotide is selected from the group consisting of a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage;

wherein in each of (N)x and (N')y modified and unmodified nucleotides are not alternating;

wherein each of Z and Z' may be present or absent, but if present is 1-5 deoxyribonucleotides covalently attached at the 3' terminus of any oligomer to which it is attached;

wherein the sequence of $(N')_y$ is a sequence substantially complementary to (N)x; and

wherein the sequence of $(N)_x$ comprises an antisense sequence substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of the target gene associated with acute kidney injury.

[0136] In certain preferred embodiments the ultimate nucleotide at the 5' terminus of (N)x is

unmodified.

[0137] According to various embodiments of Structure (E) 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 5' terminus of (N)x, preferably starting at the 5' penultimate position, and 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 3' terminus of (N')y are linked by 2'-5' internucleotide linkages.

[0138] According to various embodiments of Structure (E), 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive nucleotides starting at the ultimate or penultimate position of the 5' terminus of (N)x, preferably starting at the 5' penultimate position, and 2, 3, 4, 5, 6, 7, 8 , 9, 10, 11, 12, 13 or 14 consecutive nucleotides starting at the ultimate or penultimate position of the 3' terminus of (N')y are independently mirror nucleotides. In some embodiments the mirror is an L-ribonucleotide. In other embodiments the mirror nucleotide is L-deoxyribonucleotide.

[0139] In other embodiments of Structure (E), 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 5' terminus of (N)x, preferably starting at the 5' penultimate position, and 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 3' terminus of (N')y are independently 2' sugar modified nucleotides. In some embodiments the 2' sugar modification comprises the presence of an amino, a fluoro, an alkoxy or an alkyl moiety. In certain embodiments the 2' sugar modification comprises a methoxy moiety (2'-OMe).

[0140] In some embodiments of Structure (E), in (N')y 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 5' terminus of (N)x, preferably starting at the 5' penultimate position, and 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 3' terminus of (N')y are independently a bicyclic nucleotide. In various embodiments the bicyclic nucleotide is a locked nucleic acid (LNA) such as a 2-O, 4'-C-ethylene-bridged nucleic acid (ENA).

[0141] In various embodiments of Structure (E), (N')y comprises modified nucleotides selected from a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, a nucleotide joined to an adjacent nucleotide by a P-alkoxy backbone modification or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage at the 3' terminus or at each of the 3' and 5' termini.

[0142] In various embodiments of Structure (E), (N)x comprises a modified nucleotide selected from a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage at the 5' terminus or at each of the 3' and 5' termini.

[0143] In one embodiment where both 3' and 5' termini of the same strand comprise a modified nucleotide, the modification at the 5' and 3' termini is identical. In another embodiment, the modification at the 5' terminus is different from the modification at the 3' terminus of the same strand. In one specific embodiment, the modified nucleotides at the 5' terminus are mirror nucleotides and the modified nucleotides at the 3' terminus of the same strand are joined by 2'-5' phosphodiester bond.

[0144] In various embodiments of Structure (E), the modified nucleotides in (N)x are different from the modified nucleotides in (N')y. For example, the modified nucleotides in (N)x are 2' sugar modified nucleotides and the modified nucleotides in (N')y are nucleotides linked by 2'-5' internucleotide linkages. In another example, the modified nucleotides in (N)x are mirror nucleotides and the modified nucleotides in (N')y are nucleotides linked by 2'-5' internucleotide linkages. In another example, the modified nucleotides in (N)x are nucleotides linked by 2'-5' internucleotide linkages and the modified nucleotides in (N')y are mirror nucleotides.

[0145] In additional embodiments, the present description provides a compound having Structure (F):

(F)	5'	(N)x -Z	3' antisense strand
	3'	Z'-(N')y	5' sense strand

wherein each of N and N' is a nucleotide selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide or a modified deoxyribonucleotide;

wherein each of (N)x and (N')y is an oligomer in which each consecutive nucleotide is joined to the next nucleotide by a covalent bond and each of x and y is an integer between 18 and 40;

wherein each of (N)x and (N')y comprise unmodified ribonucleotides in which each of (N)x and (N')y independently comprise one modified nucleotide at the 3' terminal or penultimate position wherein the modified nucleotide is selected from the group consisting of a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, a nucleotide joined to an adjacent nucleotide by a P-alkoxy backbone modification or a nucleotide joined to an adjacent nucleotide by a 2'-5' phosphodiester bond;

wherein in each of (N)x and (N')y modified and unmodified nucleotides are not alternating;

wherein each of Z and Z' may be present or absent, but if present is 1-5 deoxyribonucleotides covalently attached at the 3' terminus of any oligomer to which it is attached;

wherein the sequence of $(N')_y$ is a sequence substantially complementary to (N)x; and

wherein the sequence of $(N)_x$ comprises an antisense sequence substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of the target gene associated with acute kidney injury.

[0146] In some embodiments of Structure (F), x=y=19 or x=y=23; (N')y comprises unmodified ribonucleotides in which two consecutive nucleotides at the 3' terminus comprises two consecutive mirror deoxyribonucleotides; and (N)x comprises unmodified ribonucleotides in which one nucleotide at the 3' terminus comprises a mirror deoxyribonucleotide (set forth as Structure III).

[0147] According to various embodiments of Structure (F) 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides independently beginning at the ultimate or penultimate position of the 3' termini of (N)x and (N')y are linked by 2'-5' internucleotide linkages.

[0148] According to one preferred embodiment of Structure (F), three consecutive nucleotides at the 3' terminus of (N')y are joined by two 2'-5' phosphodiester bonds and three consecutive nucleotides at the 3' terminus of (N')x are joined by two 2'-5' phosphodiester bonds.

[0149] According to various embodiments of Structure (F), 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive nucleotides independently beginning at the ultimate or penultimate position of the 3' termini of (N)x and (N')y are independently mirror nucleotides. In some embodiments the mirror nucleotide is an L-ribonucleotide. In other embodiments the mirror nucleotide is an L-deoxyribonucleotide.

[0150] In other embodiments of Structure (F), 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides independently beginning at the ultimate or penultimate position of the 3' termini of (N)x and (N')y are independently 2' sugar modified nucleotides. In some embodiments the 2' sugar modification comprises the presence of an amino, a fluoro, an alkoxy or an alkyl moiety. In certain embodiments the 2' sugar modification comprises a methoxy moiety (2'-OMe).

[0151] In some embodiments of Structure (F), 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides independently beginning at the ultimate or penultimate position of the 3' termini of (N)x and (N')y are independently a bicyclic nucleotide. In various embodiments the bicyclic nucleotide is a locked nucleic acid (LNA) such as a 2-O, 4'-C-ethylene-bridged nucleic acid (ENA).

[0152] In various embodiments of Structure (F), (N')y comprises a modified nucleotide selected from a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage at the 3' terminus or at both the 3' and 5' termini.

[0153] In various embodiments of Structure (F), (N)x comprises a modified nucleotide selected from a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage at the 3' terminus or at each of the 3' and 5' termini.

[0154] In one embodiment where each of 3' and 5' termini of the same strand comprise a modified nucleotide, the modification at the 5' and 3' termini is identical. In another embodiment, the modification at the 5' terminus is different from the modification at the 3' terminus of the same strand. In one specific embodiment, the modified nucleotides at the 5' terminus are mirror nucleotides and the modified nucleotides at the 3' terminus of the same strand are joined by 2'-5' phosphodiester bond.

[0155] In various embodiments of Structure (F), the modified nucleotides in (N)x are different from the modified nucleotides in (N')y. For example, the modified nucleotides in (N)x are 2' sugar modified nucleotides and the modified nucleotides in (N')y are nucleotides linked by 2'-5' internucleotide linkages. In another example, the modified nucleotides in (N)x are mirror nucleotides and the modified nucleotides in (N')y are nucleotides linked by 2'-5' internucleotide linkages. In another example, the modified nucleotides in (N)x are nucleotides linked by 2'-5' internucleotide linkages and the modified nucleotides in (N')y are mirror nucleotides.

[0156] In additional embodiments, the present description provides a compound having Structure (G):

(G)	5'	(N)x -Z	3' antisense strand
	3'	Z'-(N')y	5' sense strand

wherein each of N and N' is a nucleotide selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide or a modified deoxyribonucleotide;

wherein each of (N)x and (N')y is an oligomer in which each consecutive nucleotide is joined to the next nucleotide by a covalent bond and each of x and y is an integer between 18 and 40;

wherein each of (N)x and (N')y comprise unmodified ribonucleotides in which each of (N)x and (N')y independently comprise one modified nucleotide at the 5' terminal or penultimate position wherein the modified nucleotide is selected from the group consisting of a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, a nucleotide joined to an adjacent nucleotide by a P-alkoxy backbone modification or a nucleotide joined to an adjacent nucleotide by a 2'-5' phosphodiester bond;

wherein for (N)x the modified nucleotide is preferably at penultimate position of the 5' terminal;

wherein in each of (N)x and (N')y modified and unmodified nucleotides are not alternating;

wherein each of Z and Z' may be present or absent, but if present is 1-5 deoxyribonucleotides covalently attached at the 3' terminus of any oligomer to which it is attached;

wherein the sequence of $(N')_y$ is a sequence substantially complementary to (N)x; and

wherein the sequence of $(N)_x$ comprises an antisense sequence substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of the target gene associated with acute kidney injury.

[0157] In some embodiments of Structure (G), x=y=19 or x=y=23.

[0158] According to various embodiments of Structure (G) 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides independently beginning at the ultimate or penultimate position of the 5' termini of (N)x and (N')y are linked by 2'-5' internucleotide linkages. For (N)x the modified nucleotides preferably starting at the penultimate position of the 5' terminal.

[0159] According to various embodiments of Structure (G), 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive nucleotides independently beginning at the ultimate or penultimate position of the 5' termini of (N)x and (N')y are independently mirror nucleotides. In some embodiments the mirror nucleotide is an L-ribonucleotide. In other embodiments the mirror nucleotide is an L-deoxyribonucleotide. For (N)x the modified nucleotides preferably starting at the penultimate position of the 5' terminal.

[0160] In other embodiments of Structure (G), 2, 3, 4, 5, 6, 7, 8 , 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides independently beginning at the ultimate or penultimate position of the 5' termini of (N)x and (N')y are independently 2' sugar modified nucleotides. In some embodiments the 2' sugar modification comprises the presence of an amino, a fluoro, an alkoxy or an alkyl moiety. In certain embodiments the 2' sugar modification comprises a methoxy moiety (2'-OMe). In some preferred embodiments the consecutive modified nucleotides preferably begin at the penultimate position of the 5' terminus of (N)x.

[0161] In one preferred embodiment of Structure (G), five consecutive ribonucleotides at the 5' terminus of (N')y comprise a 2'OMe sugar modification and one ribonucleotide at the 5' penultimate position of (N')x comprises a 2'OMe sugar modification. In another preferred embodiment of Structure (G), five consecutive ribonucleotides at the 5' terminus of (N')y comprise 2'OMe sugar modification and two consecutive ribonucleotides at the 5' terminal position of (N')x comprise a 2'OMe sugar modification.

[0162] In some embodiments of Structure (G), 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides independently beginning at the ultimate or penultimate position of the 5' termini of (N)x and (N')y are bicyclic nucleotides. In various embodiments the bicyclic nucleotide is a locked nucleic acid (LNA) such as a 2-O, 4'-C-ethylene-bridged nucleic acid (ENA). In some preferred embodiments the consecutive modified nucleotides preferably begin at the penultimate position of the 5' terminus of (N)x.

[0163] In various embodiments of Structure (G), (N')y comprises a modified nucleotide selected from a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage at the 5' terminus or at each of the 3' and 5' termini.

[0164] In various embodiments of Structure (G), (N)x comprises a modified nucleotide selected from a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage at the 5' terminus or at each of the 3' and 5' termini.

[0165] In one embodiment where each of 3' and 5' termini of the same strand comprise a modified nucleotide, the modification at the 5' and 3' termini is identical. In another embodiment, the modification at the 5' terminus is different from the modification at the 3' terminus of the same strand. In one specific embodiment, the modified nucleotides at the 5' terminus are mirror nucleotides and the modified nucleotides at the 3' terminus of the same strand are joined by 2'-5' phosphodiester bond. In various embodiments of Structure (G), the modified nucleotides in (N)x are different from the modified nucleotides in (N')y. For example, the modified nucleotides in (N)x are 2' sugar modified nucleotides and the modified nucleotides in (N')y are nucleotides linked by 2'-5' internucleotide linkages. In another example, the modified nucleotides in (N)x are mirror nucleotides and the modified nucleotides in (N')y are nucleotides linked by 2'-5' internucleotide linkages. In another example, the modified nucleotides in (N)x are nucleotides linked by 2'-5' internucleotide linkages and the modified nucleotides in (N')y are mirror nucleotides.

[0166] In additional embodiments, the present description provides a compound having Structure (H):

(H)	5'	(N)x -Z	3' antisense strand
	3'	Z'-(N')y	5' sense strand

wherein each of N and N' is a nucleotide selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide or a modified deoxyribonucleotide;

wherein each of (N)x and (N')y is an oligomer in which each consecutive nucleotide is joined to the next nucleotide by a covalent bond and each of x and y is an integer between 18 and 40;

wherein (N)x comprises unmodified ribonucleotides further comprising one modified nucleotide at the 3' terminal or penultimate position or the 5' terminal or penultimate position, wherein the modified nucleotide is selected from the group consisting of a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage;

wherein (N')y comprises unmodified ribonucleotides further comprising one modified nucleotide at an internal position, wherein the modified nucleotide is selected from the group consisting of a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage;

wherein in each of (N)x and (N')y modified and unmodified nucleotides are not alternating;

wherein each of Z and Z' may be present or absent, but if present is 1-5 deoxyribonucleotides covalently attached at the 3' terminus of any oligomer to which it is attached;

wherein the sequence of $(N')_y$ is a sequence substantially complementary to (N)x; and

wherein the sequence of $(N)_x$ comprises an antisense sequence substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of the target gene associated with acute kidney injury.

[0167] In one embodiment of Structure (H), 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides independently beginning at the ultimate or penultimate position of the 3' terminus or the 5' terminus or both termini of (N)x are independently 2' sugar modified nucleotides, bicyclic nucleotides, mirror nucleotides, altritol nucleotides or nucleotides joined to an adjacent nucleotide by a 2'-5' phosphodiester bond and 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive internal ribonucleotides in (N')y are independently 2' sugar modified nucleotides, bicyclic nucleotides, mirror nucleotides, altritol nucleotides or nucleotides joined to an adjacent nucleotide by a 2'-5' phosphodiester bond. In some embodiments the 2' sugar modification comprises the presence of an amino, a fluoro, an alkoxy or an alkyl moiety. In certain embodiments the 2' sugar modification comprises a methoxy moiety (2'-OMe).

[0168] In another embodiment of Structure (H), 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides independently beginning at the ultimate or penultimate position of the 3' terminus or the 5' terminus or 2-8 consecutive nucleotides at each of 5' and 3' termini of (N')y are independently 2' sugar modified nucleotides, bicyclic nucleotides, mirror nucleotides, altritol nucleotides or nucleotides joined to an adjacent nucleotide by a 2'-5' phosphodiester bond, and 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive internal ribonucleotides in (N)x are independently 2' sugar modified nucleotides, bicyclic nucleotides, mirror nucleotides, altritol nucleotides or nucleotides joined to an adjacent nucleotide by a 2'-5' phosphodiester bond.

[0169] In one embodiment wherein each of 3' and 5' termini of the same strand comprises a modified nucleotide, the modification at the 5' and 3' termini is identical. In another embodiment, the modification at the 5' terminus is different from the modification at the 3' terminus of the same strand. In one specific embodiment, the modified nucleotides at the 5' terminus are mirror nucleotides and the modified nucleotides at the 3' terminus of the same strand are joined by 2'-5' phosphodiester bond.

[0170] In various embodiments of Structure (H), the modified nucleotides in (N)x are different from the modified nucleotides in (N')y. For example, the modified nucleotides in (N)x are 2' sugar modified nucleotides and the modified nucleotides in (N')y are nucleotides linked by 2'-5' internucleotide linkages. In another example, the modified nucleotides in (N)x are mirror nucleotides and the modified nucleotides in (N')y are nucleotides linked by 2'-5' internucleotide linkages. In another example, the modified nucleotides in (N)x are nucleotides linked by 2'-5'

internucleotide linkages and the modified nucleotides in (N')y are mirror nucleotides.

[0171] In one preferred embodiment of Structure (H), x=y=19; three consecutive ribonucleotides at the 9-11 nucleotide positions 9-11 of (N')y comprise 2'OMe sugar modification and five consecutive ribonucleotides at the 3' terminal position of (N')x comprise 2'OMe sugar modification.

[0172] For all the above Structures (A)-(H), in various embodiments x = y and each of x and y is 19, 20, 21, 22 or 23. In certain embodiments, x=y=19. In yet other embodiments x=y=23. In additional embodiments the compound comprises modified ribonucleotides in alternating positions wherein each N at the 5' and 3' termini of (N)x are modified in their sugar residues and the middle ribonucleotide is not modified, e.g. ribonucleotide in position 10 in a 19-mer strand, position 11 in a 21 mer and position 12 in a 23-mer strand.

[0173] In some embodiments where x = y =21 or x = y =23 the position of modifications in the 19 mer are adjusted for the 21 and 23 mers with the proviso that the middle nucleotide of the antisense strand is preferably not modified.

[0174] In some embodiments, neither (N)x nor (N')y are phosphorylated at the 3' and 5' termini. In other embodiments either or both (N)x and (N')y are phosphorylated at the 3' termini. In yet another embodiment, either or both (N)x and (N')y are phosphorylated at the 3' termini using non-cleavable phosphate groups. In yet another embodiment, either or both (N)x and (N')y are phosphorylated at the terminal 2' termini position using cleavable or non-cleavable phosphate groups. These particular siRNA compounds are also blunt ended and are non-phosphorylated at the termini; however, comparative experiments have shown that siRNA compounds phosphorylated at one or both of the 3'-termini have similar activity *in vivo* compared to the non-phosphorylated compounds.

[0175] In certain embodiments for all the above-mentioned Structures, the compound is blunt ended, for example wherein both Z and Z' are absent. In an alternative embodiment, the compound comprises at least one 3' overhang, wherein at least one of Z or Z' is present. Z and Z' independently comprises one or more covalently linked modified or non-modified nucleotides, for example inverted dT or dA; dT, LNA, mirror nucleotide and the like. In some embodiments each of Z and Z' are independently selected from dT and dTdT. siRNA in which Z and/or Z' is present have similar activity and stability as siRNA in which Z and Z' are absent.

[0176] In certain embodiments for all the above-mentioned Structures, the compound comprises one or more phosphonocarboxylate and /or phosphinocarboxylate nucleotides (PACE nucleotides). In some embodiments the PACE nucleotides are deoxyribonucleotides and the phosphinocarboxylate nucleotides are phosphinoacetate nucleotides. Examples of PACE nucleotides and analogs are disclosed in US Patent Nos. 6,693,187 and 7,067,641.

[0177] In certain embodiments for all the above-mentioned Structures, the compound comprises one or more locked nucleic acids (LNA) also defined as bridged nucleic acids or

bicyclic nucleotides. Preferred locked nucleic acids are 2'-*O*, 4'-*C*-ethylene nucleosides (ENA) or 2'-O, 4'-*C*-methylene nucleosides. Other examples of LNA and ENA nucleotides are disclosed in WO 98/39352, WO 00/47599 and WO 99/14226.

[0178] In certain embodiments for all the above-mentioned Structures, the compound comprises one or more altritol monomers (nucleotides), also defined as 1,5 anhydro-2-deoxy-D-altrito-hexitol (see for example, Allart, et al., 1998. Nucleosides & Nucleotides 17:1523-1526; Herdewijn et al., 1999. Nucleosides & Nucleotides 18:1371-1376*;* Fisher et al., 2007, NAR 35(4):1064-1074*).*

[0179] The present invention explicitly excludes compounds in which each of N and /or N' is a deoxyribonucleotide (D-A, D-C, D-G, D-T). In certain embodiments (N)x and (N')y may comprise independently 1, 2, 3, 4, 5, 6, 7, 8, 9 or more deoxyribonucleotides. In certain aspect, the present description discloses a compound wherein each of N is an unmodified ribonucleotide and the 3' terminal nucleotide or 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive nucleotides at the 3' terminus of (N')y are deoxyribonucleotides. In yet other embodiments each of N is an unmodified ribonucleotide and the 5' terminal nucleotide or 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive nucleotides at the 5' terminus of (N')y are deoxyribonucleotides. In further embodiments the 5' terminal nucleotide or 2, 3, 4, 5, 6, 7, 8, or 9 consecutive nucleotides at the 5' terminus and 1, 2, 3, 4, 5, or 6 consecutive nucleotides at the 3' termini of (N)x are deoxyribonucleotides and each of N' is an unmodified ribonucleotide. In yet further embodiments (N)x comprises unmodified ribonucleotides and 1 or 2, 3 or 4 consecutive deoxyribonucleotides independently at each of the 5' and 3' termini and 1 or 2, 3, 4, 5 or 6 consecutive deoxyribonucleotides in internal positions; and each of N' is an unmodified ribonucleotide. In certain embodiments the 3' terminal nucleotide or 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 13 or 14 consecutive nucleotides at the 3' terminus of (N')y and the terminal 5' nucleotide or 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 13 or 14 consecutive nucleotides at the 5' terminus of (N)x are deoxyribonucleotides. The present invention excludes compounds in which each of N and/or N' is a deoxyribonucleotide. In some embodiments the 5' terminal nucleotide of N or 2 or 3 consecutive of N and 1, 2, or 3 of N' is a deoxyribonucleotide. Certain examples of active DNA/RNA siRNA chimeras are disclosed in US patent publication 2005/0004064, and Ui-Tei, 2008 (NAR 36(7):2136-2151).

[0180] Unless otherwise indicated, in preferred embodiments of the structures discussed herein the covalent bond between each consecutive N or N' is a phosphodiester bond.

[0181] An additional novel molecule provided by the present description is an oligonucleotide comprising consecutive nucleotides wherein a first segment of such nucleotides encode a first inhibitory RNA molecule, a second segment of such nucleotides encode a second inhibitory RNA molecule, and a third segment of such nucleotides encode a third inhibitory RNA molecule. Each of the first, the second and the third segment may comprise one strand of a double stranded RNA and the first, second and third segments may be joined together by a linker. Further, the oligonucleotide may comprise three double stranded segments joined together by one or more linker.

[0182] Thus, one molecule provided by the present description is an oligonucleotide comprising consecutive nucleotides which encode three inhibitory RNA molecules; said oligonucleotide may possess a triple stranded structure, such that three double stranded arms are linked together by one or more linker, such as any of the linkers presented hereinabove. This molecule forms a "star"-like structure, and may also be referred to herein as RNAstar. Such structures are disclosed in PCT patent publication WO 2007/091269, assigned to the assignee of the present invention.

[0183] A covalent bond refers to an internucleotide linkage linking one nucleotide monomer to an adjacent nucleotide monomer. A covalent bond includes for example, a phosphodiester bond, a phosphorothioate bond, a P-alkoxy bond, a P-carboxy bond and the like. The normal internucleoside linkage of RNA and DNA is a 3' to 5' phosphodiester linkage. In certain preferred embodiments a covalent bond is a phosphodiester bond. Covalent bond encompasses non-phosphorous-containing internucleoside linkages, such as those disclosed in WO 2004/041924 *inter alia.* Unless otherwise indicated, in preferred embodiments of the structures discussed herein the covalent bond between each consecutive N or N' is a phosphodiester bond.

[0184] For all of the structures above, in some embodiments the oligonucleotide sequence of (N)x is fully complementary to the oligonucleotide sequence of (N')y. In other embodiments (N)x and (N')y are substantially complementary. In certain embodiments (N)x is fully complementary to a target sequence. In other embodiments (N)x is substantially complementary to a target sequence.

[0185] In some embodiments, neither (N)x nor (N')y are phosphorylated at the 3' and 5' termini. In other embodiments either or both (N)x and (N')y are phosphorylated at the 3' termini (3' Pi). In yet another embodiment, either or both (N)x and (N')y are phosphorylated at the 3' termini with non-cleavable phosphate groups. In yet another embodiment, either or both (N)x and (N')y are phosphorylated at the terminal 2' termini position using cleavable or non-cleavable phosphate groups. Further, the inhibitory nucleic acid molecules of the present invention may comprise one or more gaps and/or one or more nicks and/or one or more mismatches. Without wishing to be bound by theory, gaps, nicks and mismatches have the advantage of partially destabilizing the nucleic acid / siRNA, so that it may be more easily processed by endogenous cellular machinery such as DICER, DROSHA or RISC into its inhibitory components.

[0186] In the context of the present invention, a gap in a nucleic acid refers to the absence of one or more internal nucleotides in one strand, while a nick in a nucleic acid refers to the absence of an internucleotide linkage between two adjacent nucleotides in one strand. Any of the molecules of the present invention may contain one or more gaps and/or one or more nicks.

[0187] In one aspect the present description provides a compound having Structure (I):

(I)	5'	(N)x - Z	3' (antisense strand)
	3'	Z'-(N')y- z''	5' (sense strand)

wherein each of N and N' is a ribonucleotide which may be unmodified or modified, or an unconventional moiety;

wherein each of (N)x and (N')y is an oligonucleotide in which each consecutive N or N' is joined to the next N or N' by a covalent bond;

wherein Z and Z' may be present or absent, but if present is independently 1-5 consecutive nucleotides or non-nucleotide moieties covalently attached at the 3' terminus of the strand in which it is present;

wherein z'' may be present or absent, but if present is a capping moiety covalently attached at the 5' terminus of (N')y;

wherein x =18 to 27;

wherein y =18 to 27;

wherein (N)x comprises modified and unmodified ribonucleotides, each modified ribonucleotide having a 2'-O-methyl on its sugar, wherein N at the 3' terminus of (N)x is a modified ribonucleotide, (N)x comprises at least five alternating modified ribonucleotides beginning at the 3' end and at least nine modified ribonucleotides in total and each remaining N is an unmodified ribonucleotide;

wherein in (N')y at least one unconventional moiety is present, which unconventional moiety may be an abasic ribose moiety, an abasic deoxyribose moiety, a modified or unmodified deoxyribonucleotide, a mirror nucleotide, and a nucleotide joined to an adjacent nucleotide by a 2'-5' internucleotide phosphate bond; and

wherein the sequence of $(N')_y$ is a sequence having complementarity to (N)x; and wherein the sequence of $(N)_x$ comprises an antisense sequence having complementarity to from about 18 to about 27 consecutive ribonucleotides in an mRNA of the target gene associated with acute kidney injury.

[0188] In some embodiments x =y=19. In other embodiments x =y=23. In some embodiments the at least one unconventional moiety is present at positions 15, 16, 17, or 18 in (N')y. In some embodiments the unconventional moiety is selected from a mirror nucleotide, an abasic ribose moiety and an abasic deoxyribose moiety. In some preferred embodiments the unconventional moiety is a mirror nucleotide, preferably an L-DNA moiety. In some embodiments an L-DNA moiety is present at position 17, position 18 or positions 17 and 18.

[0189] In other embodiments the unconventional moiety is an abasic moiety. In various embodiments (N')y comprises at least five abasic ribose moieties or abasic deoxyribose

moieties.

[0190] In yet other embodiments (N')y comprises at least five abasic ribose moieties or abasic deoxyribose moieties and at least one of N' is an LNA.

[0191] In some embodiments (N)x comprises nine alternating modified ribonucleotides. In other embodiments of Structure (I) (N)x comprises nine alternating modified ribonucleotides further comprising a 2'O modified nucleotide at position 2. In some embodiments (N)x comprises 2'O Me modified ribonucleotides at the odd numbered positions 1, 3, 5, 7, 9, 11, 13, 15, 17, 19. In other embodiments (N)x further comprises a 2'O Me modified ribonucleotide at one or both of positions 2 and 18. In yet other embodiments (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 8, 11, 13, 15, 17, 19.

[0192] In various embodiments z'' is present and is selected from an abasic ribose moiety, a deoxyribose moiety; an inverted abasic ribose moiety, a deoxyribose moiety; C6-amino-Pi; a mirror nucleotide.

[0193] In another aspect the present description provides a compound having Structure (J) set forth below:

(J)	5'	(N)x - Z	3' (antisense strand)
	3'	Z'-(N')y-z''	5' (sense strand)

wherein each of N and N' is a ribonucleotide which may be unmodified or modified, or an unconventional moiety;

wherein each of (N)x and (N')y is an oligonucleotide in which each consecutive N or N' is joined to the next N or N' by a covalent bond;

wherein Z and Z' may be present or absent, but if present is independently 1-5 consecutive nucleotides covalently attached at the 3' terminus of the strand in which it is present;

wherein z'' may be present or absent but if present is a capping moiety covalently attached at the 5' terminus of (N')y;

wherein x =18 to 27;

wherein y =18 to 27;

wherein (N)x comprises modified or unmodified ribonucleotides, and optionally at least one unconventional moiety;

wherein in (N')y at least one unconventional moiety is present, which unconventional moiety may be an abasic ribose moiety, an abasic deoxyribose moiety, a modified or unmodified deoxyribonucleotide, a mirror nucleotide, a non-base pairing nucleotide analog or a nucleotide joined to an adjacent nucleotide by a 2'-5' internucleotide phosphate bond; and

wherein the sequence of $(N')_y$ is a sequence having complementarity to (N)x; and wherein the sequence of $(N)_x$ comprises an antisense sequence having complementarity to from about 18 to about 27 consecutive ribonucleotides in an mRNA of the target gene associated with acute kidney injury.

[0194] In some embodiments x =y=19. In other embodiments x =y=23. In some preferred embodiments (N)x comprises modified and unmodified ribonucleotides, and at least one unconventional moiety.

[0195] In some embodiments in (N)x the N at the 3' terminus is a modified ribonucleotide and (N)x comprises at least 8 modified ribonucleotides. In other embodiments at least 5 of the at least 8 modified ribonucleotides are alternating beginning at the 3' end. In some embodiments (N)x comprises an abasic moiety in one of positions 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15.

[0196] In some embodiments the at least one unconventional moiety in (N')y is present at positions 15, 16, 17, or 18. In some embodiments the unconventional moiety is selected from a mirror nucleotide, an abasic ribose moiety and an abasic deoxyribose moiety. In some preferred embodiments the unconventional moiety is a mirror nucleotide, preferably an L-DNA moiety. In some embodiments an L-DNA moiety is present at position 17, position 18 or positions 17 and 18. In other embodiments the at least one unconventional moiety in (N')y is an abasic ribose moiety or an abasic deoxyribose moiety.

[0197] In yet another aspect the present description provides a compound having Structure (K) set forth below:

(K)	5'	$(N)_x$ -Z	3' (antisense strand)
	3'	Z'-$(N')_y$-z''	5' (sense strand)

wherein each of N and N' is a ribonucleotide which may be unmodified or modified, or an unconventional moiety;

wherein each of (N)x and (N')y is an oligonucleotide in which each consecutive N or N' is joined to the next N or N' by a covalent bond;

wherein Z and Z' may be present or absent, but if present is independently 1-5 consecutive nucleotides covalently attached at the 3' terminus of the strand in which it is present;

wherein z'' may be present or absent but if present is a capping moiety covalently attached at the 5' terminus of (N')y;

wherein x =18 to 27;

wherein y =18 to 27;

wherein (N)x comprises a combination of modified or unmodified ribonucleotides and

unconventional moieties, any modified ribonucleotide having a 2'-O-methyl on its sugar;

wherein (N')y comprises modified or unmodified ribonucleotides and optionally an unconventional moiety, any modified ribonucleotide having a 2'OMe on its sugar;

wherein the sequence of $(N')_y$ is a sequence having complementarity to (N)x; and wherein the sequence of $(N)_x$ comprises an antisense sequence having complementarity to from about 18 to about 27 consecutive ribonucleotides in an mRNA of the target gene associated with acute kidney injury.

[0198] In some embodiments x =y=19. In other embodiments x =y=23. In some preferred embodiments the at least one unconventional moiety is present in (N)x and is an abasic ribose moiety or an abasic deoxyribose moiety. In other embodiments the at least one unconventional moiety is present in (N)x and is a non-base pairing nucleotide analog. In various embodiments (N')y comprises unmodified ribonucleotides. In some embodiments (N)x comprises at least five abasic ribose moieties or abasic deoxyribose moieties or a combination thereof. In certain embodiments (N)x and/or (N')y comprise modified ribonucleotides which do not base pair with corresponding modified or unmodified ribonucleotides in (N')y and/or (N)x.

[0199] In various embodiments the present description provides an siRNA set forth in Structure (L):

(L)	5'	$(N)_x$ - Z	3' (antisense strand)
	3'	Z'-$(N')_y$	5' (sense strand)

wherein each of N and N' is a nucleotide selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide and a modified deoxyribonucleotide;

wherein each of $(N)_x$ and $(N')_y$ is an oligonucleotide in which each consecutive N or N' is joined to the next N or N' by a covalent bond;

wherein Z and Z' are absent;

wherein x=y=19;

wherein in (N')y the nucleotide in at least one of positions 15, 16, 17, 18 and 19 comprises a nucleotide selected from an abasic unconventional moiety, a mirror nucleotide, a deoxyribonucleotide and a nucleotide joined to an adjacent nucleotide by a 2'-5' internucleotide bond;

wherein (N)x comprises alternating 2'OMe sugar modified ribonucleotides and unmodified ribonucleotides so as to have 2'OMe sugar modified ribonucleotide at the middle position of (N)x; and

wherein the sequence of $(N')_y$ is a sequence having complementarity to (N)x; and wherein the sequence of $(N)_x$ comprises an antisense having complementarity to from about 18 to about 40 consecutive ribonucleotides in an mRNA of the target gene associated with acute kidney injury.

[0200] In some embodiments of Structure (L), in (N')y the nucleotide in one or both of positions 17 and 18 comprises a modified nucleotide selected from an abasic unconventional moiety, a mirror nucleotide and a nucleotide joined to an adjacent nucleotide by a 2'-5' internucleotide bond. In some embodiments the mirror nucleotide is selected from L-DNA and L-RNA. In various embodiments the mirror nucleotide is L-DNA.

[0201] In various embodiments (N')y comprises a modified nucleotide at position 15 wherein the modified nucleotide is selected from a mirror nucleotide and a deoxyribonucleotide.

[0202] In certain embodiments (N')y further comprises a modified nucleotide or pseudo nucleotide at position 2 wherein the pseudo nucleotide may be an abasic unconventional moiety and the modified nucleotide is optionally a mirror nucleotide.

[0203] In various embodiments the antisense strand (N)x comprises 2'O-Me modified ribonucleotides at the odd numbered positions (5' to 3'; positions 1, 3, 5, 7, 9, 11, 13, 15, 17, 19). In some embodiments (N)x further comprises 2'O-Me modified ribonucleotides at one or both positions 2 and 18. In other embodiments (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 8, 11, 13, 15, 17, 19.

[0204] Other embodiments of Structures (L) are envisaged wherein x=y=21 or wherein x=y=23; in these embodiments the modifications for (N')y discussed above instead of being in positions 17 and 18 are in positions 19 and 20 for 21-mer oligonucleotide and 21 and 22 for 23-mer oligonucleotide; similarly the modifications in positions 15, 16, 17, 18 or 19 are in positions 17, 18, 19, 20 or 21 for the 21-mer oligonucleotide and positions 19, 20, 21, 22, or 23 for the 23-mer oligonucleotide. The 2'O Me modifications on the antisense strand are similarly adjusted. In some embodiments (N)x comprises 2'O Me modified ribonucleotides at the odd numbered positions (5' to 3'; positions 1, 3, 5, 7, 9, 12, 14, 16, 18, 20 for the 21-mer oligonucleotide [nucleotide at position 11 unmodified] and 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23 for the 23-mer oligonucleotide [nucleotide at position 12 unmodified]. In other embodiments (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 8, 10, 12, 14, 16, 18, 20 [nucleotide at position 11 unmodified for the 21-mer oligonucleotide and at positions 2, 4, 6, 8, 10, 13, 15, 17, 19, 21, 23 for the 23-mer oligonucleotide [nucleotide at position 12 unmodified].

[0205] In some embodiments (N')y further comprises a 5' terminal cap nucleotide. In various embodiments the terminal cap moiety is selected from an abasic unconventional moiety, an inverted abasic unconventional moiety, an L-DNA nucleotide, and a C6-imine phosphate (C6 amino linker with phosphate at terminus).

[0206] In other embodiments the present description provides a compound having Structure (M) set forth below:

(M)	5'	$(N)_x$ - Z	3' (antisense strand)
	3'	Z'-$(N')_y$	5' (sense strand)

wherein each of N and N' is selected from a pseudo-nucleotide and a nucleotide;

wherein each nucleotide is selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide and a modified deoxyribonucleotide;

wherein each of $(N)_x$ and $(N')_y$ is an oligonucleotide in which each consecutive N or N' is joined to the next N or N' by a covalent bond;

wherein Z and Z' are absent;

wherein x =18 to 27;

wherein y =18 to 27;

wherein the sequence of $(N')_y$ is a sequence having complementarity to (N)x; and wherein the sequence of $(N)_x$ comprises an antisense sequence having complementarity to from about 18 to about 27 consecutive ribonucleotides in an mRNA of the target gene associated with acute kidney injury.

[0207] In other embodiments the present description provides a double stranded compound having Structure (N) set forth below:

(N)	5'	$(N)_x$ - Z	3' (antisense strand)
	3'	Z'-$(N')_y$	5' (sense strand)

wherein each of N and N' is a nucleotide selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide and a modified deoxyribonucleotide;

wherein each of $(N)_x$ and $(N')_y$ is an oligonucleotide in which each consecutive N or N' is joined to the next N or N' by a covalent bond;

wherein Z and Z' are absent;

wherein each of x and y is an integer between 18 and 40;

wherein the sequence of $(N')_y$ is a sequence having complementarity to (N)x; and wherein the sequence of $(N)_x$ comprises an antisense sequence having complementarity to from about 18 to about 40 consecutive ribonucleotides in an antisense sequence to the mRNA of the target

gene associated with acute kidney injury;

wherein (N)x, (N')y or (N)x and (N')y comprise non base-pairing modified nucleotides such that (N)x and (N')y form less than 15 base pairs in the double stranded compound.

[0208] In other embodiments the present description provides a compound having Structure (O) set forth below:

(O)	5'	$(N)_x$ - Z	3' (antisense strand)
	3'	Z'-$(N')_y$	5' (sense strand)

wherein each of N is a nucleotide selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide and a modified deoxyribonucleotide;

wherein each of N' is a nucleotide analog selected from a six membered sugar nucleotide, seven membered sugar nucleotide, morpholino moiety, peptide nucleic acid and combinations thereof;

wherein each of $(N)_x$ and $(N')_y$ is an oligonucleotide in which each consecutive N or N' is joined to the next N or N' by a covalent bond;

wherein Z and Z' are absent;

wherein each of x and y is an integer between 18 and 40;

wherein the sequence of $(N')_y$ is a sequence having complementarity to (N)x; and wherein the sequence of $(N)_x$ comprises an antisense sequence having complementarity to from about 18 to about 40 consecutive ribonucleotides in an mRNA of the target gene associated with acute kidney injury.

[0209] In other embodiments the present description provides a compound having Structure (P) set forth below:

(P)	5'	$(N)_x$ - Z	3' (antisense strand)
	3'	Z'-$(N')_y$	5' (sense strand)

wherein each of N and N' is a nucleotide selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide and a modified deoxyribonucleotide;

wherein each of $(N)_x$ and $(N')_y$ is an oligonucleotide in which each consecutive N or N' is joined to the next N or N' by a covalent bond;

wherein Z and Z' are absent;

wherein each of x and y is an integer between 18 and 40;

wherein one of N or N' in an internal position of (N)x or (N')y or one or more of N or N' at a terminal position of (N)x or (N')y comprises an abasic moiety or a 2' modified nucleotide;

wherein the sequence of $(N')_y$ is a sequence having complementarity to (N)x; and wherein the sequence of $(N)_x$ comprises an antisense sequence having complementarity to from about 18 to about 40 consecutive ribonucleotides in an mRNA of the target gene associated with acute kidney injury.

[0210] In various embodiments (N')y comprises a modified nucleotide at position 15 wherein the modified nucleotide is selected from a mirror nucleotide and a deoxyribonucleotide.

[0211] In certain embodiments (N')y further comprises a modified nucleotide at position 2 wherein the modified nucleotide is selected from a mirror nucleotide and an abasic unconventional moiety.

[0212] In various embodiments the antisense strand (N)x comprises 2'O-Me modified ribonucleotides at the odd numbered positions (5' to 3'; positions 1, 3, 5, 7, 9, 11, 13, 15, 17, 19). In some embodiments (N)x further comprises 2'O-Me modified ribonucleotides at one or both positions 2 and 18. In other embodiments (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 8, 11, 13, 15, 17, 19.

[0213] An additional novel molecule disclosed herein is an oligonucleotide comprising consecutive nucleotides wherein a first segment of such nucleotides encode a first inhibitory RNA molecule, a second segment of such nucleotides encode a second inhibitory RNA molecule, and a third segment of such nucleotides encode a third inhibitory RNA molecule. Each of the first, the second and the third segment may comprise one strand of a double stranded RNA and the first, second and third segments may be joined together by a linker. Further, the oligonucleotide may comprise three double stranded segments joined together by one or more linker.

[0214] Thus, one molecule employed in the methods of the present description is an oligonucleotide comprising consecutive nucleotides which encode three inhibitory RNA molecules; said oligonucleotide may possess a triple stranded structure, such that three double stranded arms are linked together by one or more linker, such as any of the linkers presented hereinabove. This molecule forms a "star"-like structure, and may also be referred to herein as RNAstar and described in PCT Patent Publication WO 2007/091269 assigned to one of the assignees of the present application.

[0215] Said triple-stranded oligonucleotide may be an oligoribonucleotide having the general structure:

5'	Oligo1 (sense)	LINKER A	Oligo2 (sense)	3'
3'	Oligo1 (antisense)	LINKER B	Oligo3 (sense)	5'
3'	Oligo3 (antisense)	LINKER C	Oligo2 (antisense)	5'
	or			
5'	Oligo1 (sense)	LINKER A	Oligo2 (antisense)	3'
3'	Oligo1 (antisense)	LINKER B	Oligo3 (sense)	5'
3'	Oligo3 (antisense)	LINKER C	Oligo2 (sense)	5'
or				
5'	Oligo1 (sense)	LINKER A	Oligo3 (antisense)	3'
3'	Oligo1 (antisense)	LINKER B	Oligo2 (sense)	5'
5'	Oligo3 (sense)	LINKER C	Oligo2 (antisense)	3'

wherein one or more of linker A, linker B or linker C is present; any combination of two or more oligonucleotides and one or more of linkers A-C is possible, so long as the polarity of the strands and the general structure of the molecule remains. Further, if two or more of linkers A-C are present, they may be identical or different.

[0216] Thus, a triple-armed structure is formed, wherein each arm comprises a sense strand and complementary antisense strand (i.e. Oligo1 antisense base pairs to Oligo1 sense etc.). The triple armed structure may be triple stranded, whereby each arm possesses base pairing.

[0217] Further, the above triple stranded structure may have a gap instead of a linker in one or more of the strands. Such a molecule with one gap is technically quadruple stranded and not triple stranded; inserting additional gaps or nicks will lead to the molecule having additional strands. Preliminary results obtained by the inventors of the present invention indicate that said gapped molecules are more active in inhibiting certain target genes than the similar but non-gapped molecules. This may also be the case for nicked molecules. According to one preferred embodiment of the invention, the antisense and the sense strands of the siRNA are phosphorylated only at the 3'-terminus and not at the 5'-terminus. According to another preferred embodiment of the invention, the antisense and the sense strands are non-phosphorylated. According to yet another preferred embodiment of the invention, the 5' most ribonucleotide in the sense strand is modified to abolish any possibility of *in vivo* 5'-phosphorylation.

[0218] Further disclosed herein is a vector capable of expressing any of the aforementioned oligoribonucleotides in a cell after which appropriate modification may be made. In preferred embodiment the cell is a mammalian cell, preferably a human cell.

Methods of Treatment

[0219] Disclosed herein is an oligonucleotide inhibitor for use in a method for the treatment of

a subject in need of treatment for attenuation of CKD progression which is associated with expression of the p53 gene, comprising administering to the subject an amount of said oligonucleotide inhibitor, which reduces, down regulates or inhibits expression or upregulation of the p53 gene.

[0220] A number of conditions can cause permanent damage to the kidneys and/or affect the function of the kidneys and lead to CKD. The most common causes of CKD in adults are:

1. a) Diabetes. Diabetic nephropathy (DN) is a common complication of diabetes;
2. b) High blood pressure. Untreated or poorly treated high blood pressure is a major cause of CKD;
3. c) Aging kidneys. There appears to be an age-related decline in kidney function;
4. d) Acute or chronic kidney ischemia (this is the model we used in rats and you are using in humans);
5. e) sepsis.

[0221] Other less common conditions that can lead to CKD include diseases of the glomeruli, such as glomerulonephritis (inflammation of the glomeruli in the kidneys); renal artery stenosis (narrowing), haemolytic-uraemic syndrome, polycystic kidney disease, blockages to the flow of urine, drug and toxin-induced kidney damage, and repeated kidney infections.

[0222] Disclosed herein is an oligonucleotide inhibitor for use in a method for the treatment of a subject in need of treating chronic kidney disease (CKD) which is associated with expression of the p53 gene, comprising administering to the subject an amount of said oligonucleotide inhibitor, which prevents upregulation or overexpression of the p53 gene in a kidney of the subject. In certain embodiments the upregulation or overexpression of the p53 gene is in response to renal insult or injury. In some embodiments the renal insult is an acute renal insult including acute kidney injury (AKI). In various embodiments of the invention treatment includes preventing exacerbation and progression of CKD.

[0223] In preferred embodiments the subject being treated is a warm-blooded animal and, in particular, mammals including non-human primate and human.

[0224] The methods disclosed herein comprise administering to the subject one or more inhibitory compounds which down-regulate expression of the target p53 gene of Table 1; and in particular siRNA in a therapeutically effective dose so as to thereby treat the subject.

[0225] In various embodiments the inhibitor is selected from the group consisting of siRNA, shRNA, an antisense molecule, miRNA, and a ribozyme. In the presently preferred embodiments the inhibitor is siRNA. In preferred embodiments the siRNA is a chemically synthesized, modified compound.

[0226] The term "treatment" refers to both therapeutic treatment and prophylactic or

preventative measures, wherein the object is to attenuate, prevent or slow down CKD or progression or severity of CKD as listed above. Those in need of treatment include those already experiencing the disease or condition, those prone to CKD, and those in which CKD is to be prevented; for example in a subject exposed to repetitive renal insults, including renal insults due to nephrotoxic drugs, such as, without being limited to, antibiotics (e.g. aminoglycosides), chemotherapeutic drugs (e.g. Cisplatin), immunosuppressant drugs (e.g. Cyclosporin A, Tacrolimus (also FK-506 or Fujimycin)) and radiocontrast agents, or ischemia-reperfusion injury (IRI). According to various embodiments of the present invention the oligonucleotide inhibitor is administered before, during or subsequent to the exposure to the renal insult, preferably subsequent to the insult. In some embodiments the oligonucleotide inhibitor is a siRNA compound. In some embodiments CKD develops in response to repetitive renal insults including repetitive acute kidney injury (AKI).

[0227] Acute renal failure (ARF), also known as acute kidney injury (AKI), is a rapid loss of renal function due to kidney damage and resulting in retention of nitrogenous (urea and creatinine) and non-nitrogenous waste products in the blood. Depending on the severity and duration of the renal dysfunction, this accumulation is accompanied by metabolic disturbances, such as metabolic acidosis (acidification of the blood) and hyperkalaemia (elevated serum potassium levels), changes in body fluid balance, and effects on many other organ systems. It can be characterized by oliguria or anuria (decrease or cessation of urine production).

[0228] Glomerular filtration rate "GFR" describes the flow rate of filtered fluid across the glomeruli. The assessment of GFR is the most commonly used test of renal function. In some embodiments the method of attenuating progression of CKD or preventing exacerbation of CKD is measured as an increase of about 5%, 10%, 20%, 30%, 40% or more in GFR in a treated subject when compared to the untreated subject.

[0229] Creatinine clearance rate (CCr, mL/min/1.73 m^2) is the volume of blood plasma that is cleared of creatinine per unit time and is a useful measure for approximating the true GFR.

[0230] SCr (mg/dL) relates to serum creatinine levels. In some embodiments the method of attenuating progression of CKD or preventing exacerbation of CKD is measured as an decrease of about 5%, 10%, 20%, 30%, 40% or more in SCr in a treated subject when compared to the untreated subject.

[0231] The method disclosed herein relates to a method of treating CKD induced by repetitive acute kidney injury (AKI) insults, in particular acute renal failure due to ischemia in post surgical patients, acute renal failure due to chemotherapy treatment such as cisplatin administration, sepsis-associated acute renal failure, nephrotoxin induced AKI including radiocontrast media induced AKI. Contrast induced AKI (CIAKI) (also known as contrast-induced nephropathy) relates to the induction of AKI by intravascular administration of iodinated contrast media, for example in patients undergoing angiography, and in particular coronary angiography. Alternatively, the method relates to the prevention of CKD in high-risk patients undergoing major cardiac surgery or vascular surgery. The patients are at risk of developing acute renal

failure which in some cases progresses to CKD. Those patients are identified using various scoring methods such as the Cleveland Clinic algorithm or that developed by US Academic Hospitals (QMMI) and by Veterans' Administration (CICSS).

[0232] Preferably the methods relate to treating or preventing CKD in a subject induced by treatment of the subject with a nephrotoxin including a diuretic, a β-blocker, a vasodilator agent, an ACE inhibitor, an immunosuppressant (e.g. cyclosporin), an aminoglycoside antibiotic (e.g. gentamicin), an antifungal (e.g. amphotericin B), a chemotherapeutic agent (e.g. cisplatin), radiocontrast media, an antibody (e.g. immunoglobulin), mannitol, a NSAID (e.g. aspirin, ibuprofen, diclofenac), cyclophosphamide, methotrexate, aciclovir, polyethylene glycol, β-lactam antibiotics, vancomycin, rifampicin, sulphonamides, ciprofloxacin, ranitidine, cimetidine, furosemide, thiazides, phenytoin, penicillamine, lithium salts, fluoride, demeclocycline, foscarnet, aristolochic acid, an anti-oxidant, a calcium channel blocker, a vasoactive substance, a growth factors, an anti-inflammatory agents and more.

[0233] In the majority of hospitalized ARF patients, ARF is caused by acute tubular necrosis (ATN), which results from ischemic, septic and/or nephrotoxic insults. Renal hypoperfusion is caused by hypovolemic, cardiogenic and septic shock, by administration of vasoconstrictive drugs or renovascular injury. Nephrotoxins include exogenous toxins, such as radiocontrast media, aminoglycosides and cisplatin and cisplatin-like compounds, as well as endogenous toxins, such as myoglobin. Without wishing to be bound to theory, recent studies support the theory that apoptosis in renal tissues is prominent in most human cases of ARF. The principal site of apoptotic cell death is the distal nephron. During the initial phase of ischemic injury, loss of integrity of the actin cytoskeleton leads to flattening of the epithelium, with loss of the brush border, loss of focal cell contacts, and subsequent disengagement of the cell from the underlying substratum. It has been suggested that apoptotic tubule cell death may be more predictive of functional changes than necrotic cell death (Komarov et al., Science 1999, 10;285(5434):1733-7); Supavekin et al., Kidney Int. 2003, 63(5):1714-24).

[0234] A "contrast agent," as used herein, refers to a compound employed to improve the visibility of internal body structures in an image, such as an X-ray image or a scanning image (e.g., CAT (Computerized Axial Tomography) scan, MRI (Magnetic Resonance Imaging) scan). The term contrast agent is also referred to herein as a radiocontrast agent. Contrast agents are employed in various diagnostic (e.g. embolism; cardiac catheterization) and therapeutic procedures. Contrast-induced nephropathy (CIN) remains the primary risk factor in the use of contrast agents. Patients with pre-existing renal failure and diabetes are at particularly high risk. Moreover, CIN is associated with significant in-hospital and long-term morbidity and mortality.

[0235] Additional mechanisms that contribute to the development of AKI: ischemia, vasoconstriction, toxic injury related to selected endogenous substances (e.g. myoglobin in rhabdomyolysis due to crush injury and extensive blunt trauma), radiocontrast (iodinated and IV contrast for radiological examination including CT angiography, cardiac arteriography), phosphate nephropathy due to bowel preparation for colonoscopy with sodium phosphate,

nephrotoxic drugs (e.g., NSAIDs, aminoglycoside antibiotics, gentamycin and penicillin, amphotericin B), microcirculatory changes, as observed with sepsis and other inflammatory states, hemolysis, diagnostic cardiac catheterization, femoral arteriography especially in aged or diabetic patients, percutaneous coronary intervention (PCI), coronary artery bypass grafting (CABG), sepsis, thoracoabdominal aortic surgery, aortic aneurysim repair for example for infra-renal aortic abdominal surgery or thoracic or thoracoabdominal aortic surgery.

[0236] Preexisting conditions predicting severity and long term outcome of AKI patients with coronary arthery disease (CAD), heart failure, diabetes, vascular complications (e.g. atheroembolic disease and renal vein thrombosis), HIV-infected patients, gender, older age (>60), pre-existing chronic kidney disease or underlying renal insufficiency, volume depletion, hepatitis co-infection, liver disease, hepatorenal syndrome, cancer patients, patients with serious water and electrolyte metabolism disturbances, patients with hematological and non-hematological malignancies, cirrhosis, COPD, severe burns, pericarditis and pancreatitis.

[0237] Intrinsic damage to the kidney:

toxins or medication (e.g. some NSAIDs, aminoglycoside antibiotics, iodinated contrast, lithium, phosphate nephropathy due to bowel preparation for colonoscopy with sodium phosphates)

rhabdomyolysis (breakdown of muscle tissue) - the resultant release of myoglobin in the blood affects the kidney; it can be caused by injury (especially crush injury and extensive blunt trauma), statins, stimulants and some other drugs

hemolysis (breakdown of red blood cells) - the hemoglobin damages the tubules; it may be caused by various conditions such as sickle-cell disease, and lupus erythematosus

multiple myeloma, either due to hypercalcemia or "cast nephropathy" (multiple myeloma can also cause chronic renal failure by a different mechanism)

acute glomerulonephritis which may be due to a variety of causes, such as anti glomerular basement membrane disease/Goodpasture's syndrome, Wegener's granulomatosis or acute lupus nephritis with systemic lupus erythematosus

Post-renal (obstructive causes in the urinary tract) due to medication interfering with normal emptying of bladder (e.g. anticholinergics), benign prostatic hypertrophy or prostate cancer, kidney stones, abdominal malignancy (e.g. ovarian cancer, colorectal cancer), obstructed urinary catheter, drugs that can cause crystalluria and drugs that can lead to myoglobinuria & cystitis.

[0238] In conclusion, currently there is no satisfactory mode of therapy for the prevention and/or treatment of CKD induced by recurring acute insults to the kidney, and there is a need therefore to develop novel compounds for this purpose.

Pharmaceutical Compositions

[0239] While it may be possible for the compounds for use according to the present invention to be administered as the raw chemical, it is preferable to present them as a pharmaceutical composition. Accordingly disclosed herein is a method employing a pharmaceutical composition comprising one or more of the oligonucleotide compounds for use according to the invention; and a pharmaceutically acceptable carrier. This composition may comprise a mixture of two or more different siRNA compounds.

[0240] In some embodiments the pharmaceutical composition comprises at least one siRNA compound for use according to the invention covalently or non-covalently bound to one or more siRNA compounds for use according to the invention in an amount effective to inhibit the p53 target gene; and a pharmaceutically acceptable carrier. The compound may be processed intracellularly by endogenous cellular complexes to produce one or more oligoribonucleotides for use according to the invention.

[0241] Further disclosed herein is a pharmaceutical composition comprising a pharmaceutically acceptable carrier and one or more of the compounds for use according to the invention in an amount effective to inhibit expression in a cell of the human p53 target gene, the compound comprising a sequence $(N)_X$ which is substantially complementary to the sequence of a target nucleic acid.

[0242] "Having complementarity" or "substantially complementary" refers to complementarity of greater than about 84%, to another sequence. For example in a duplex region consisting of 19 base pairs one mismatch results in 94.7% complementarity, two mismatches results in about 89.5% complementarity and 3 mismatches results in about 84.2% complementarity, rendering the duplex region substantially complementary. Accordingly substantially identical refers to identity of greater than about 84%, to another sequence.

[0243] Additionally, disclosed herein is a method of inhibiting the expression of the p53 target gene by at least 40%, preferably by 50%, 60% or 70%, more preferably by 75%, 80% or 90% as compared to a control comprising contacting an mRNA transcript of the p53 target gene with one or more of the compounds for use according to the invention.

[0244] In one embodiment the oligoribonucleotide is inhibiting the p53 target gene, whereby the inhibition is selected from the group comprising inhibition of gene function, inhibition of polypeptide and inhibition of mRNA expression. In one embodiment the compound inhibits the target polypeptide, whereby the inhibition is selected from the group comprising inhibition of function (which may be examined by an enzymatic assay or a binding assay with a known interactor of the native gene / polypeptide, *inter alia*), inhibition of protein (which may be examined by Western blotting, ELISA or immuno-precipitation, *inter alia*) and inhibition of mRNA expression (which may be examined by Northern blotting, quantitative RT-PCR, in-situ hybridisation or microarray hybridisation, *inter alia*).

Delivery

[0245] The siRNA compound for use according to the invention is administered as the compound *per se* (i.e. as naked siRNA) or as pharmaceutically acceptable salt and is administered alone or as an active ingredient in combination with one or more pharmaceutically acceptable carrier, solvent, diluent, excipient, adjuvant and vehicle. In some embodiments, the siRNA molecules for use according to the present invention are delivered to the target tissue by direct application of the naked molecules prepared with a carrier or a diluent. The term "naked siRNA" refers to siRNA molecules that are free from any delivery vehicle that acts to assist, promote or facilitate entry into the cell, including viral sequences, viral particles, liposome formulations, lipofectin or precipitating agents and the like. For example, siRNA in PBS is "naked siRNA".

[0246] However, in some embodiments the siRNA molecules for use according to the invention are delivered in liposome formulations and lipofectin formulations and the like and can be prepared by methods well known to those skilled in the art. Such methods are described, for example, in US Patent Nos. 5,593,972, 5,589,466, and 5,580,859.

[0247] 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 Let. 2003, 539:111-115; Xia et al., Nat. Biotech. 2002, 20:1006-1010; Reich et al., Mol. Vision 2003, 9: 210-216; Sorensen et al., J. Mol. Biol. 2003. 327: 761-766; Lewis et al., Nat. Gen. 2002, 32: 107-108 and Simeoni et al., NAR 2003, 31,11: 2717-2724). siRNA has recently been successfully used for inhibition of gene expression in primates (see for example, Tolentino et al., Retina 24(4):660).

[0248] 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. Patent 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. Other such implants, delivery systems, and modules are well known to those skilled in the art. The siRNAs or pharmaceutical compositions for use according to the present invention are administered and dosed in accordance with good medical practice, taking into account the clinical condition of the individual subject, 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.

[0249] 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.

[0250] 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 a single dose or multiple doses, e.g. or two doses or three or more doses, administered within 24 hours of each renal insult. The siRNA compounds for use according to the present invention can be administered by any of the conventional routes of administration. The compounds are 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 are 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 co-solvents, aqueous or oil suspensions, emulsions with edible oils, as well as similar pharmaceutical vehicles. In a particular embodiment, the administration comprises intravenous administration.

[0251] Pharmaceutical compositions that include the nucleic acid molecule disclosed herein may be administered once daily, qid, tid, bid, QD, or at any interval and for any duration that is medically appropriate. However, the composition may also be dosed in dosage units containing two, three, four, five, six or more sub-doses administered at appropriate intervals throughout the day.

[0252] In some embodiments the dosage unit is compounded for a single dose over several days, e.g., using a conventional sustained release formulation which provides sustained and consistent release of the dsRNA over a several day period. Sustained release formulations are well known in the art. In certain embodiments the methods disclosed herein include administering one or more siRNA compound or compounds to the subject for sustained or controlled delivery. The methods disclosed herein rely primarily on parenteral administration routes and more specifically on implant depots or depot injections, which provide for prolonged release of the biological agent into the circulatory system. Devices for use in these parenteral delivery systems include non-injectable and injectable devices. Non-injectable devices include an implant such as a siRNA depot implant, or similar device. Known depot implants include, but are not limited to, synthetic and natural materials including solid biodegradable and non-biodegradable polymer devices including foams, gels, matrices, and the like comprising one or more of dextran, fibrin, hyaluronate, chitosan and the like as well as a pump and micropump systems also known in the art. Injectable devices include bolus injections (release and dissipation of the compound subsequent to injection), and repository or depot injections, which provide a storage reservoir or depot at the site of injection, allowing for sustained release of the biological agent over time.

[0253] The present description also provides for a process of preparing a pharmaceutical composition for use according to present invention, which comprises:

providing one or more double stranded compound for use according to the invention ; and

admixing said compound with a pharmaceutically acceptable carrier.

[0254] The present description also provides for a process of preparing a pharmaceutical composition, for use according to present invention, which comprises admixing one or more siRNA compounds for use according to present invention with a pharmaceutically acceptable carrier.

[0255] In a preferred embodiment, the siRNA compound used in the preparation of a pharmaceutical composition, for use according to present invention, is admixed with a carrier in a pharmaceutically effective dose. In a particular embodiment the siRNA compound, for use according to the present invention is conjugated to a steroid, vitamin or to a lipid or to another suitable molecule e.g. to cholesterol.

[0256] The present invention is illustrated in detail below with reference to examples, but is not to be construed as being limited thereto.

[0257] Citation of any document herein is not intended as an admission that such document is pertinent prior art, or considered material to the patentability of any claim of the present application. Any statement as to content or a date of any document is based on the information available to applicant at the time of filing and does not constitute an admission as to the correctness of such a statement.

EXAMPLES

General methods in molecular biology

[0258] 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, Maryland (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 US Patents 4,666,828; 4,683,202; 4,801,531; 5,192,659 and 5,272,057. Polymerase chain reaction (PCR) was carried out generally as in PCR Protocols: A Guide To Methods And Applications, Academic Press, San Diego, CA (1990). In situ (In cell) PCR in combination with Flow Cytometry can be used for detection of cells containing specific DNA and mRNA sequences (Testoni et al., 1996, Blood

87:3822.) Methods of performing RT-PCR are also well known in the art.

EXAMPLE 1: Generation of sequences for active siRNA compounds to target genes and production of the siRNAs

[0259] Using proprietary algorithms and the known sequence of the target genes, the sequences of many potential siRNAs were generated. In addition to the algorithm, some of the 23-mer oligomer sequences were generated by 5' and/or 3' extension of the 19-mer sequences. The sequences that have been generated using this method are fully complementary to the corresponding mRNA sequence.

[0260] Sequence listing: The sequence listing for this application (SEQ ID NO:1 - SEQ ID NO:119) has been submitted electronically as sequence listing file entitled "209-PCT1_ST25.txt" created Jun. 7, 2010, 459 kb. Applicants hereby incorporate by reference the sequence listing into the instant specification.

EXAMPLE 2: in vitro Testing of siRNA Compounds

1. General

[0261] About 1.5-2x10^5 test cells (HEPG2 or PC3 cells for siRNA targeting the human gene) were seeded per well in 6 wells plate (70-80% confluent).

[0262] After 24h cells were transfected with siRNA oligomers using Lipofectamine™ 2000 reagent (Invitrogene) at final concentration of 500pM, 5nM, 20nM or 40nM. The cells were incubated at 37°C in a CO_2 incubator for 72h.

[0263] As positive control for cells transfection PTEN-Cy3 labeled siRNA oligos were used. As negative control for siRNA activity GFP siRNA oligos were used.

[0264] About 72h after transfection cells were harvested and RNA was extracted from cells. Transfection efficiency was tested by fluorescent microscopy.

[0265] The percent of inhibition of gene expression using specific siRNAs was determined using qPCR analysis of target gene in cells expressing the endogenous gene.

[0266] The inhibitory activity of the compounds of the present invention on the p53 target gene or binding of the compounds for use according to the present invention to the p53 target gene may be used to determine the interaction of an additional compound with the target polypeptide, e.g., if the additional compound competes with the oligonucleotides for use

according to the present invention for inhibition of the target gene, or if the additional compound rescues said inhibition. The inhibition or activation is tested by various means, such as, *inter alia,* assaying for the product of the activity of the target polypeptide or displacement of binding compound from the target polypeptide in radioactive or fluorescent competition assays.

EXAMPLE 3: siP53 compounds

[0267] QM5 is a chemically modified siRNA compound which targets rat and mouse p53 and is the disclosed of International Patent Publication WO 2006/035434, assigned to one of the assignees of the present invention. QM5 . The compound has two separate strands, sense (SEN; passenger) and antisense (AS; guide), each comprising alternating unmodified ribonucleotides (upper case letters) and 2'-methoxy (2'-O-Me; 2'-O-CH_3) sugar modified ribonucleotides (lower case letters) on both strands forming a specific pattern as shown herein below:

Sense (passenger) sequence 5'	GaAgAaAaUuUcCgCaAaA 3' (SEQ ID NO:1 16
Antisense (guide) sequence 3'	cUuCuUuUaAaGgCgUuUu 5' (SEQ ID NO:1 17)

[0268] The 15 compound is a 19-mer blunt-ended nucleic acid duplex that targets human p53, a gene that plays a pivotal role in the stress-response apoptotic pathway. The compound has two separate strands, sense (SEN) and antisense (AS), each comprising alternating unmodified ribonucleotides (upper case letters) and 2'-methoxy (2'OMe) sugar modified ribonucleotides (lower case letters) on both strands forming a specific pattern as shown herein below :

Sense (passenger) sequence 5'	GaGaAuAuUuCaCcCuUcA 3' (SEQ ID NO:118)
Antisense (guide) sequence 3'	cUcUuAuAaAgUgGgAaGu 5' (SEQ ID NO:119)

[0269] For treating or preventing kidney damage in a human subject at risk of chronic kidney disease (CKD) associated with exposure to a recurrence of renal insults a therapeutically effective dose of 15 is administered to the subject within 24 hours of each renal insult thereby treating CKD. 15 is the subject of WO 2006/035434, assigned to one of the assignees of the present invention.

EXAMPLE 4: Model systems of CKD

[0270] The following animal models were implemented to support the methods disclosed herein

1. (1) preventing CKD development in a subject at risk of CKD due to multiple renal insults (supported by example 4-1;
2. (2) preventing acceleration/progression of CKD development by AKI episodes in a subject with a CKD background (supported by Example 4-2); and
3. (3) attenuating the severity of AKI on the background of CKD (supported by Example 4-2).

Example 4-1. Bilateral kidney arterial clamp CKD model

[0271] This animal model is useful in assessing the test compounds for prevention of CKD or attenuation of CKD progression resulting from repetitive AKI/ARF insults.

[0272] Repetitive AKI/ARF insults often results in the exacerbation of chronic kidney disease (CKD), progression of CKD or development of CKD (see Figure 1). ARF is a clinical syndrome characterized by rapid deterioration of renal function that occurs within days. Without being bound by theory the acute kidney injury may be the result of renal ischemia-reperfusion injury such as renal ischemia-reperfusion injury in patients undergoing major surgery such as major cardiac surgery. The principal feature of ARF is an abrupt decline in glomerular filtration rate (GFR), resulting in the retention of nitrogenous wastes (urea, creatinine) in the blood. Recent studies, support that apoptosis in renal tissues is prominent in most human cases of ARF. The principal site of apoptotic cell death is the distal nephron. During the initial phase of ischemic injury, loss of integrity of the actin cytoskeleton leads to flattening of the epithelium, with loss of the brush border, loss of focal cell contacts, and subsequent disengagement of the cell from the underlying substratum.

[0273] The rat model for CKD comprises repetitive (5 times) ischemia-reperfusion-induced ARF as follows and as shown in Figure 2:
Ischemia-reperfusion injury was induced in rats following 45 minutes bilateral kidney arterial clamp and subsequent release of the clamp to allow 24 hours of reperfusion. PBS or QM5 (rat siP53) (12 mg/kg) were injected i.v. into individual experimental animals 4 hours post clamp. ARF progression was monitored by measurement of serum creatinine (SCr) levels before (baseline) and 24 hrs, 2 days and 7 days post surgery. The treatment (I/R injury, QM5, SCr measurement) was repeated for four more cycles at 30-day intervals, for a total of five cycles. At 7 days post 5^{th} cycle 24 hour creatinine clearance (CrCl) metabolic cage and urine protein were measured. The right kidneys were surgically removed 2 days after metabolic cage (day 10 post 5^{th} cycle) and the kidney was histologically analyzed for CKD. At 3 weeks post right nephrectomy the left kidney was exteriorized and studied *in vivo* using intravital two-photon microscopy (for Cy3-siRNa uptake and retention).

Results

[0274]

Age-matched untreated rats had much more uniform uptake and distribution of the Cy3 labeled siRNA. Twenty-four hours after the initial injection, reduction in cellular levels of the siRNA was visible. Also tubular lumens were generally more open with only a few collapsed lumens visible.

Saline treated CKD rats had much more heterogeneous distribution (patchy) and uptake of the siRNA. Tubules could be seen with thin epithelia and the lumen greatly distended. Uptake in tubular cells did occur, but at a lower level than surrounding tubular cells with more normal morphology. Degradation of the labeled siRNA appeared slower in these rats as there appeared to be greater residual fluorescence than in age-matched untreated rats at 24 hours.

QM5 treated CKD rats displayed uptake and distribution characteristics that were intermediary between the control age-matched untreated and saline treated CKD groups. Overall uptake was more homogeneous when viewing individual fields. Cystic tubules were still present on occasion. Overall, QM5 aided in the uniform delivery of the Cy3-labeled siRNA to the tubular epithelia, this was more readily apparent in Rat #4. Metabolism of siRNA at 24 hr was also intermediate between age-matched untreated rats and saline treated ischemic rats. Under physiological conditions, in age-matched untreated rats Cy3-labeled siRNA, following intravenous injection, was rapidly filtered across the glomerulus and taken up selectively by proximal tubule cells (PTC). Total cellular and cytosolic accumulation in proximal tubule cells was quantified using threshold analysis and revealed a maximum at 120 minutes with a rapid decay over the next four hours. The biological activity of the siRNA correlated closely to the fluorescent half life.

[0275] Figure 3 shows the effect of p53 siRNA on kidney function following repetitive ischemic injury. Serum creatinine levels prior to each ischemia (AKI) cycle, and at days 1, 2, and 7 post each ischemia cycle in rats treated with PBS or siP53 (QM5) (12 mg/kg) given i.v. at 4 hrs post each ischemia (AKI). Data represent the mean + SD (n=10/group).

[0276] Figure 4 shows that siP53 protects GFR and minimizes proteinuria. Measurements from PBS treated animals are shown by hatched columns, while QM5 treated animals are solid coumns.

[0277] Table 2 hereinbelow shows the effect of siP53 on kidney function following five monthly cycles of ischemic injury: siP53 protects glomerular filtration rate and minimizes proteinuria. Glomerular filtration rate (GFR) and proteinuria (Uprot) were measured at 7 days following last (5th) AKI cycle by 24 hrs urine collection and tail blood collection. Groups: PBS - rats were treated with PBS given i.v. at 4 hrs post each ischemic injury; QM5 - siP53 (12 mg/kg) given i.v. at 4 hrs post each ischemic injury. Data represent means + SD (n=10/group)
Table 2:

	Injury score, mean/group (n=10) ± SD		
Histopatholgy scoring parameters	**PBS**	**QM5**	**p-value**
Glomerular Damage	0.1+ 0.3	0.1+0.3	1
Interstitial Cellular Infiltrate	1.2+ 0.4	0.5+ 0.5	0.008
Interstitial fibrosis	1.3+ 0.5	0.9+ 0.6	0.12
Tubular status	1.4+ 0.5	0.8+ 0.6	0.04
Vasculopathy	0.1+0.3	0	0.37
Total Chronic injury score	**4.1+ 0.7**	**2.3+ 1.2**	**0.02**
Tubular necrosis	0.1+0.3	0	0.37
Tubular dilation	1.4+ 0.5	0.8+ 0.6	0.04
Casts	1.3+ 1.3	0.5+ 0.5	0.16
Total Acute injury score	**2.8+ 1.8**	**1.3+ 0.9**	**0.05**
Total pathology score Chronic + acute	***6.9+ 3.3***	***3.6+ 1.8***	***0.02***

[0278] Figure 5 shows histopathology scoring of right kidney procured 10 days post fifth AKI cycle. At 10 days post last (5th) ischemic injury, the rats (treated with PBS or siP53 at 4 hrs post each monthly ischemic injury) were subjected to right nephrectomy. Harvested right kidney sections were blindly analyzed by board-certified pathologist. At least two representative kidney sections were analyzed for each rat. The parameters of acute (tubular necrosis, tubular dilation, casts) and chronic (glomerular damage, interstitial cellular infiltrate, interstitial fibrosis, tubular status and vasculopathy) damage were analyzed. Total acute and total chronic injury scores are a sums of all chronic or acute damage parameters respectively. Total pathology score is a sum of acute and chronic injury scores for each rat. Grading of pathological changes was performed according to the following scoring system:
Grade 0 - no pathological changes; Grade 1 - feature involves 1 to 10 % of the area (mild and focal); Grade 2 - feature involves 10 to 25% of the area (moderate and multifocal); Grade 3 - feature involves 25 to 75 % of the area (diffuse damage without damage of normal architecture); Grade 4 - feature involves more than 75% of the area (diffuse damage with prominent damage of normal kidney architecture). Data represent the mean + SD (n=10/group).

Example 4-2. Uninephrectomy and high salt diet

[0279] This animal model is useful in assessing the test compounds for reduction/attenuation of AKI/ARF in a CKD background thereby providing a model for preventing exacerbation or progression of CKD by recurring AKI /ARF insults in CKD patients and in attenuating the severity of AKI in patients suffereing from CKD who undergo a proceedure or event likely to cause AKI.

[0280] Figure 6 shows the study design used to establish CKD. In summary, SD rats were subjected to right nephrectomy, followed by 3 or 4 repetitive bimonthly cycles of AKI (until SCr and GFR rates were at CKD levels). The first AKI cycle comprised a left pedicle clamp for a period of 45 minutes, whereas all following AKIs comprised a 30 minute clamp. Throughout the entire period, the rats were fed a high salt diet. After 3 or 4 cycles, the following kidney function parameters were evaluated: serum creatinine (SCr), GFR and urine protein.

[0281] Animal was considered to have moderate to severe CKD when serum creatinine (SCr) levels were above 0.8 mg/ml and glomerular filtration rate (GFR) was less than 0.60 ml/min/100 gr. In addition, 3 rats were uninephrectomized and fed with regular diet for the same total period of time as above (7-8 months). At the end of this period, their SCr, GFR and Uprot were evaluated. Results are shown in Table 3, hereinbelow:

Table 3

	SCr, mg/ml	GFR, ml/min/100g BW	Uprot, mg/24h
Normal rats (historical and published data)	0.2-0.3	0.8-0.9*	
Uninephr rats after 3 AKI cycles (N=3), HS diet	1.13± 0.05	0.16 ± 0.03	221 ± 21
Uninephr rats after 4 AKI cycles (N=4), HS diet	0.98± 0.17	0.19 ± 0.03	646 ± 160
*Zaladek-Gil et al (1999), Braz J Med Biol Res, 32:107-113 ; Chamberlain et al, (2007) Exp Physiol, 92:251-262			

[0282] Figure 7 shows kidney function parameters in group sorted animals prior to AKI/ARF insults and prior to siP53 treatment). The results show that uninephrectomized animals exposed to a high salt diet exhibit more severe CKD than uninephrectomized animals exposed to a normal diet as measured by SCr, GFR and urine protein (Uprot) levels. CKD and control animals received siP53 or siGFP (12 mg/kg) or vehicle by i.v. injection at 4 hours post last AKI insult. Figure 8 shows the effect of siP53 (QM5) on prevention of AKI insult in animals with CKD.

[0283] Figures 9A-9H show histopathological parameters for acute injury (9A-9C) and chronic injury (9D-9H). The scoring system for histopathology was as follows: 0: none; 1: mild and focal; 2: moderate and multifocal; 3: diffuse without damage of normal architecture; 4: diffuse with prominent damage of normal architecture. All acute parameters, tubular necrosis, tubular dilation and urinary casts were improved in siP53 treated animals. The chromic injury parameters glomerular damage, interstitial infitrate, interstitial fibrosis and tubular atrophy were reduced in treated animals.

[0284] Average histopathology scores for acute and chronic injury in treated and untreated

animals are shown in Figure 10.

[0285] While certain embodiments of the invention have been illustrated and described, it will be clear that the invention is not limited to the embodiments described herein. Modifications, changes, variations, substitutions and equivalents will be apparent to those skilled in the art without departing from scope of the present invention as described by the claims, which follow.

SEQUENCE LISTING

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The United States of America as represented by the
Department of Veterans Affairs (Washington, DC)

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cuccaaggac cgucgguggg cgauggcugc aacgguggag gggccagagc uggaggcagc 180

ugcugccgca ggagaugcuu cagaggauuc ggacgcaggg uccagggcgc ugccuuuccu 240

gggcggcaac cggcugagcu uggaccugua ccccgggggc ugccagcagc ugcugcaccu 300

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cucccugguc cucaaaggag ggcaacgccg ggacacacug ggugccuguc uccggggugc 480

ccugaccaac cugcccgcug gucugagugg ccuggcccau cuggcccacc uggaccugag 540

cuucaacagc cuggagacac ugccggccug uguccugcag augcgagguc ugggugcgcu 600

cuugcugucu cacaacugcc ucucugagcu gccugaggcu cuggggccc ucccccgccu 660

caccuuccuc acagugacac acaaccgccu gcagacgcug ccccccagcac ugggggcccu 720

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cgcaggagau gcuucagagg auucggacgc aggguccagg gcgcugccuu uccugggcgg 180

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gguccucaaa ggagggcaac gccgggacac acugggugcc ugucuccggg gugcccugac 420

caaccugccc gcuggucuga guggccuggc ccaucuggcc caccuggacc ugagcuucaa 480

cagccuggag acacugccgg ccuguguccu gcagaugcga ggucugggug cgcucuugcu 540

gucucacaac ugccucucug agcugccuga ggcucugggg gcccucccca cccucaccuu 600

ccucacagug acacacaacc gccugcagac gcugccccca gcacuggggg cccuauccac 660

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ucuggcggga cuucgguccu ugcggcuccu uguccugcac agcaaccucc uggccucugu 840

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aagucucucc agugugуggg gacgggуccc ugugagcaac aaaacugcac uguuucuuuc 2880

accucaaaaa aaaaaaaaaa aa 2902

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<211> 743

<212> RNA

<213> HUMAN

<400> 8

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acagcugggc gcuucaccca gugguacuuu ggugccuacu ccauuguggc gggcguguuu 180

gugugccugc uggaguaccc ccgggggaag aggaagaagg gcuccaccau ggagcgcugg 240

ggacagaagu acaugaccgc cguggugaag cuguucgggc ccuuuaccag gaauuacuau 300

guucgggccg uccugcaucu ccugcucucg gugcccgccg gcuuccugcu ggccaccauc 360

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gagcagugga cgcccaucga gcccaagccc cgggagcggc cgcagaucgg aggcaccauc 480

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gaggaggagg cugcgguggc ggcgggggga cccccgggag gucccccaggu caaccccauc 600

ccggugaccg acgaggucgu gugaccucgc cccggaccug cccucccgcc aggugcaccc 660

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aaaaaaaaaa aaaaaaaaaa aaa 743

<210> 9

<211> 1914

<212> RNA

<213> HUMAN

<400> 9

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ccccaaaauc aaaaugaugc uucaacaccc aggccagguc ucugccucgg aagugagugc 180

uucugccauc gucccugccc ugucccccucc ugggucacug guguuugagg auuuugcuaa 240

ccugacgccc uuugucaagg aagagcugag guuugccauc cagaacaagc accucugcca 300

ccggaugucc ucugcgcugg aaucagucac ugucagcgac agaccccucg ggguguccau 360

cacaaaagcc gagguagccc cugaagaaga ugaaaggaaa aagaggcgac gagaaagaaa 420

uaagauugca gcugcaaagu gccgaaacaa gaagaaggag aagacggagu gccugcagaa 480

agagucggag aagcuggaaa gugugaaugc ugaacugaag gcucagauug aggagcucaa 540

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ggcucagaau gggaggacuc cagaagauga gagaaaccuc uuuauccaac agauaaaaga 660

aggaacauug cagagcuaag cagucguggu auggggcga cuggggaguc cucauugaau 720

ccucauuuua uacccaaaac ccugaagcca uuggagagcu gucuuccugu guaccucuag 780

aaucccagca gcagagaacc aucaaggcgg gagggccugc agugauucag caggcccuuc 840

ccauucugcc ccagaguggg ucuuggacca gggcaagugc aucuuugccu caacuccagg 900

auuuaggccu uaacacacug gccauucuua uguuccagau ggccccccagc ugguguccug 960

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uacugucuau uaaaauucug auguuucugu gaaauucuca gaguguuuaa uuguacucaa 1800

ugguaucauu acaauuuucu guaagagaaa auauuacuua uuuauccuag uauuccuaac 1860

cugucagaau aauaaauauu ggaaccaaga caugguaaaa aaaaaaaaaa aaaa 1914

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<212> RNA
<213> HUMAN

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cagccaggcg cgcacugcac agcucucuuc ucucgccgcc gcccgagcgc acccuucagc 180

ccgcgcgccg gccgugaguc cucggugcuc gcccgccggc cagacaaaca gcccgcccga 240

ccccgucccg acccuggccg ccccgagcgg agccuggagc aaaaugaugc uucaacaccc 300

aggccagguc ucugccucgg aagugagugc uucugccauc guccccugcc ugucccccucc 360

ugggucacug guguuuugagg auuuugcuaa ccugacgccc uuugucaagg aagagcugag 420

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ugaacugaag gcucagauug aggagcucaa gaacgagaag cagcauuuga uauacaugcu 720

caaccuucau cggcccacgu guauuguccg ggcucagaau gggaggacuc cagaagauga 780

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gaaauucuca gaguguuuaa uuguacucaa ugguaucauu acaauuuucu guaagagaaa 1980

auauuacuua uuuauccuag uauuccuaac cugucagaau aauaaauauu ggaaccaaga 2040

caugguaaa 2049

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<212> RNA
<213> HUMAN

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cagccaggcg cgcacugcac agcucucuuc ucucgccgcc gcccgagcgc acccuucagc 180

ccgcgcgccg gccgugaguc cucggugcuc gcccgccggc cagacaaaca gcccgcccga 240

ccccgucccg acccuggccg ccccgagcgg agccuggagc aaaaugaugc uucaacaccc 300

aggccagguc ucugccucgg aagugagugc uucugccauc guccccugcc ugucccccucc 360

ugggucacug guguuugagg auuuugcuaa ccugacgccc uuugucaagg aagagcugag 420

guuugccauc cagaacaagc accucugcca ccggaugucc ucugcgcugg aaucagucac 480

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ugaaaggaaa aagaggcgac gagaaagaaa uaagauugca gcugcaaagu gccgaaacaa 600

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cugcauaugg gcuguugacu caugcaaaug agguaucuga acugcagcuu caguauuagc 720

agagccacag gccgccucug uggcaucacc aggguuucuc ugaagaagag ggucugcauu 780

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gauauacaug cucaaccuuc aucggcccac guguauuguc cgggcucaga augggaggac 1080

uccagaagau gagagaaacc ucuuuaucca acagauaaaa gaaggaacau ugcagagcua 1140

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uugucagcaa gaggaggaca gaauucuccc agcguuaaca caaaauccau gggcaguaug 1860

auggcagguc cucuguugca aacucaguuc caaagucaca ggaagaaagc agaaaguuca 1920

acuuccaaag gguuaggacu cuccacucaa ugucuuaggu caggaguugu gucuaggcug 1980

gaagagccaa agaauauucc auuuuccuuu ccuuugugguu gaaaaccaca gucaguggag 2040

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augucaauag cauuguuuuu gucauguagc uguuuuaaga aaucuggccc aggguguuug 2160

cagcugugag aagucacuca cacuggccac aaggacgcug gcuacugucu auuaaaauuc 2220

ugauguuucu gugaaauucu cagaguguuu aauuguacuc aaugguauca uuacaauuuu 2280

cuguaagaga aaauauuacu uauuuauccu aguauuccua accugucaga auaauaaaua 2340

uuggaaccaa gacaugguaa a 2361

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<211> 4145

<212> RNA

<213> HUMAN

<400> 12

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cagcggagag cccgggaaaa gcgggaaaug gcggcgccga gcgcgggguc uugguccacc 180

uuccagcaca aggagcugau ggccgcugac aggggacgca ggauauuggg aguguguggc 240

augcauccuc aucaucagga aacucuaaaa aagaaccgag uggugcuagc caaacagcug 300

uuguugagcg aauuguuaga acaucuucug gagaaggaca ucaucaccuu ggaaaugagg 360

gaggcugaug agggcaaagu gggcaguuug agcgagaaug uggaaguggu gaaguuggug 420

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cuuugggucg acauaguaug gaaguauuug agagagagaa ccuuuccacu cccacugcca 4080

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<211> 2044

<212> RNA

<213> HUMAN

<400> 14

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guuuauugac acguucuacu gguaugaaga ggaggagucu uuccauuaca cacgaguuau 240

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cuaugggaua gcuguuaaug caaccaucca caucguggcg cauuucuuca accuggaacg 480

cuaccacugg agccaguccg aggaggccca gggacuucug gccgcacuuu ccaagcuggg 540

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acaccauguu uucaucgucu ucuuucucag ccuggccauc caugggacgg gucggauugu 780

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cggagccgag acccagccgg agcgagcaac agguugguga aaacccugug uccuuggaga 480

aagcugguuc ccguuuuucca gaggggggagc ccagagcuug aaaggccgcg guuggcacuu 540

cgagaaggaa guggagagua aagacagcgc cuggagcgau cguagaaaca cagaauggga 600

cuggggaagc ccuuuggaaa uccagcugca gaaacagaca ccccaaugcu auuuacauac 660

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<211> 1163
<212> RNA
<213> HUMAN

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guugaagaac aggagccuga acugacauca acucccaauu ucgugguuga aguuauaaag 600

aaugaugaug gcaagaaggc ccuuguguug gacugucauu auccagagga ugagguugga 660

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gagcuggugg agcucagcac agcccuggag caccaggagu acauuacuuu ucuugaagac 900

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ucauccuaau aucaugggggg aaaaaauacc aaauuuaaau uauauguuuu guguucucau 1080

uuauuaucau uuuuuucugu acaaaucuau uauuucuaga uuuuuguaua acaugauaga 1140

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<213> HUMAN

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ggcgccaugu cgcagaacgg agcgcccggg augcaggagg agagccugca gggcuccugg 180

guagaacugc acuucagcaa uaaugggaac gggggcagcg uuccagccuc gguuucuauu 240

uauaauggag acauggaaaa aauacugcug gacgcacagc augagucugg acggaguagc 300

uccaagagcu cucacuguga cagcccaccu cgcucgcaga caccacaaga uaccaacagg 360

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gauuggucaa gucggccgga aaauauuccc cccaaggagu uccucuuuaa acacccgaag 540

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<212> RNA
<213> HUMAN

<400> 18

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gagcucaagg aauaguaugc gcagcuuaug augccauucu ugaaagaaau guugcaauca 180

agaagcuaag ccgaccauuu cagaaucaga cucaugccaa gcgggccuac agagagcuag 240

uucuuaugaa auguguuaau cacaaaaaua uaauuggccu uuugaauguu uucacaccac 300

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uugaacaaug cauagaugau cgaaaauuac ggaaaaucau agggcagaga ggugugaaga 2580

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cuucuuuacu gcugauaugu uuccuguauu cuagaaaaau uuuuacacuu ucacauuauu 4380

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<213> HUMAN

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gagccgcggu gcuuucaacu ggcgagcgcg aaugggggug cacuggagua aggcagagug 180

augcgggggg gcaacucgcc uggcaccgag aucgccgccg ugcccuuccc uggacccggc 240

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cccucgaccc ccgagucccg gagccggccc cgcgcggggc cacgcguccc ucgggcgcug 360

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cuccuccccc ugcucgcugu uguugugugu cagcacuugg cuggggacuu cuugaacuug 480

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gaguuuuaaa cuuuaaauag acaggucuga gugccugaac uugccuuuuc auuuuacuuc 180

auccuccaag gaguucaauc acuuggcgug acuucacuac uuuuaagcaa aagaguggug 240

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cucaacugcu ggagggaagg uguggcuguc aguacuuuuc auuuuccgaa uccugcugcu 360

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cuaugugaug cgaaaggaag agaaacugaa caagaaagag gaagaacuca agguugccca 600

aacugauggu gucaaugugg acaugcacuu gaagcagauu gagauaaaga aguucaagua 660

cgguauugaa gagcauggua aggugaaaau gcgagggggg uugcugcgaa ccuacaucau 720

caguauccuc uucaagucua ucuuugaggu ggccuucuug cugauccagu gguacaucua 780

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cuuggugucc cuggccuuga auaucauuga acucuucuau guuuucuuca agggcguuaa 960

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ccucuccugc uggcuguaag ugauugcagu ugcucuacgg ugagcccggg cgugcuggca 180

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gagaccgagu cgccuuauca ggagcuccag ggucagaggu cggaugucua cagcgaccuc 360

aacacacaga ggccguauua caaaugagcc cgaaucauga cagucagcaa caugauaccu 420

ggauccagcc auuccugaag cccacccugc accucauucc aacuccuacc gcgauacaga 480

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<212> RNA

<213> HUMAN

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gcugcggagg cgacccggaa acagcguauc acugagaccg agucgccuua ucaggagcuc 360

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gcccgaauca ugacagucag caacaugaua ccuggaucca gccauuccug aagcccaccc 480

ugcaccucau uccaacuccu accgcgauac agacccacag agugccaucc cugagagacc 540

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gcugcggagg cagcgacccg gaaacagcgu aucacugaga ccgagucgcc uuaucaggag 360

cuccagggcc agaggucgga ugucuacagc gaccucaaca cacagaggcc guauuacaaa 420

ugagcccgaa ucaugacagu cagcaacaug auaccuggau ccagccauuc cugaagccca 480

cccugcaccu cauuccaacu ccuaccgcga uacagaccca cagagugcca ucccugagag 540

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aaaaaaaa 608

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<400> 40
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cucaacacac agaggccgua uuacaaauga gcccgaauca ugacagucag caacaugaua 420

ccuggaucca gccauuccug aagcccaccc ugcaccucau uccaacuccu accgcgauac 480

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ggcaagugaa uuugccugua acaagccaga uuuuuuaaaa uuuauauugu aaauauugug 1860

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gaacaccaua gguagaaugu aaagcuuguc ugaucguuca aagcaugaaa uggauacuua 2040

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<212> RNA
<213> HUMAN

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uugcagccuu cucagccaaa cgccgaccaa ggaaaacuca cuaccaugag aauugcagug 180

auuugcuuuu gccuccuagg caucaccugu gccauaccag uuaaacaggc ugauucugga 240

aguucugagg aaaagcagcu uuacaacaaa uacccagaug cuguggccac auggcuaaac 300

ccugacccau cucagaagca gaaucuccua gccccacaga augcuguguc cucugaagaa 360

accaaugacu uuaaacaaga gacccuucca aguaagucca acgaaagcca ugaccacaug 420

gaugauaugg augaugaaga ugaugaugac cauguggaca gccaggacuc cauugacucg 480

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uucacuccag uuguccccac aguagacaca uaugauggcc gaggugauag ugugguuuau 660

ggacugaggu caaaaucuaa gaaguuucgc agaccugaca uccaguaccc ugaugcuaca 720

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gaaacgaguc agcuggauga ccagagugcu gaaacccaca gccacaagca guccagauua 900

uauaagcgga aagccaauga ugagagcaau gagcauuccg augugauuga uagucaggaa 960

cuuuccaaag ucagccguga auuccacagc caugaauuuc acagccauga agauaugcug 1020

guuguagacc ccaaaaguaa ggaagaagau aaacaccuga aauuucguau uucucaugaa 1080

uuagauagug caucuucuga ggucaauuaa aaggagaaaa aauacaauuu cucacuuugc 1140

auuuagucaa aagaaaaaau gcuuuauagc aaaaugaaag agaacaugaa augcuucuuu 1200

cucaguuuau uggauugaaug uguaucuauu ugagucugga aauaacuaau guguuugaua 1260

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cuauguucau ucuauagaag aaaugcaaac uaucacugua uuuuaauauu uguuauucuc 1380

ucaugaauag aaauuuaugu agaagcaaac aaaauacuuu uacccacuua aaaagagaau 1440

auaacauuuu augucacuau aaucuuuugu uuuuuaaguu aguguauauu uuguugugau 1500

uaucuuuuug uggugugaau aaaucuuuua ucuugaaugu aauaagaauu uggugguguc 1560

aauugcuuau uuguuuuccc acgguugucc agcaauuaau aaaacauaac cuuuuuuacu 1620

gccuaaaaaa aaaaaaaaaa a 1641

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<211> 1616
<212> RNA
<213> HUMAN

<400> 43
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uugcagccuu cucagccaaa cgccgaccaa ggaaaacuca cuaccaugag aauugcagug 180

auuugcuuuu gccuccuagg caucaccugu gccauaccag uuaaacaggc ugauucugga 240

aguucugagg aaaagcagcu uuacaacaaa uacccagaug cuguggccac auggcuaaac 300

ccugacccau cucagaagca gaaucuccua gccccacaga cccuuccaag uaaguccaac 360

gaaagccaug accacaugga ugauauggau gaugaagaug augaugacca uguggacagc 420

caggacucca uugacucgaa cgacucugau gauguagaug acacugauga uucucaccag 480

ucugaugagu cucaccauuc ugaugaaucu gaugaacugg ucacugauuu ucccacggac 540

cugccagcaa ccgaaguuuu cacuccaguu gucccccacag uagacacaua ugauggccga 600

ggugauagug ugguuuaugg acugagguca aaaucuaaga aguuucgcag accugacauc 660

caguacccug augcuacaga cgaggacauc accucacaca uggaaagcga ggaguugaau 720

ggugcauaca aggccauccc cguugcccag gaccugaacg cgccuucuga uugggacagc 780

cgugggaagg acaguuauga aacgagucag cuggaugacc agagugcuga aacccacagc 840

cacaagcagu ccagauuaua uaagcggaaa gccaaugaug agagcaauga gcauuccgau 900

gugauugaua gucaggaacu uuccaaaguc agccgugaau uccacagcca ugaauuucac 960

agccaugaag auaugcuggu uguagacccc aaaaguaagg aagaagauaa acaccugaaa 1020

uuucguauuu cucaugaauu agauagugca ucuucugagg ucaauuaaaa ggagaaaaaa 1080

uacaauuucu cacuuugcau uuagucaaaa gaaaaaaugc uuuauagcaa aaugaaagag 1140

aacaugaaau gcuucuuucu caguuuauug guugaaugug uaucuauuug agucuggaaa 1200

uaacuaaugu guuugauaau uaguuuaguu uguggcuuca uggaaacucc cuguaaacua 1260

aaagcuucag gguuaugucu auguucauuc uauagaagaa augcaaacua ucacuguauu 1320

uuaauauuug uuauucucuc augaauagaa auuuauguag aagcaaacaa aauacuuuua 1380

cccacuuaaa aagagaauau aacauuuuau gucacuauaa ucuuuuguuu uuuaaguuag 1440

uguauauuuu guugugauua ucuuuuugug gugugaauaa aucuuuuauc uugaauguaa 1500

uaagaauuug guggugucaa uugcuuauuu guuuucccac gguuguccag caauuaauaa 1560

aacauaaccu uuuuuacugc cuaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1616

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<211> 1560
<212> RNA
<213> HUMAN

<400> 44
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uugcagccuu cucagccaaa cgccgaccaa ggaaaacuca cuaccaugag aauugcagug 180

auuugcuuuu gccuccuagg caucaccugu gccauaccag uuaaacaggc ugauucugga 240

aguucugagg aaaagcagaa ugcugugucc ucugaagaaa ccaaugacuu uaaacaagag 300

acccuuccaa guaaguccaa cgaaagccau gaccacaugg augauaugga ugaugaagau 360

gaugaugacc auguggacag ccaggacucc auugacucga acgacucuga ugauguagau 420

gacacugaug auucucacca gucugaugag ucucaccauu cugaugaauc ugaugaacug 480

gucacugauu uucccacgga ccugccagca accgaaguuu ucacuccagu ugucccccaca 540

guagacacau augauggccg aggugauagu gugguuuaug gacugagguc aaaaucuaag 600

aaguuucgca gaccugacau ccaguacccu gaugcuacag acgaggacau caccucacac 660

auggaaagcg aggaguugaa uggugcauac aaggccaucc ccguugccca ggaccugaac 720

gcgccuucug auugggacag ccgugggaag gacaguuaug aaacgaguca gcuggaugac 780

cagagugcug aaacccacag ccacaagcag uccagauuau auaagcggaa agccaaugau 840

gagagcaaug agcauuccga ugugauugau agucaggaac uuuccaaagu cagccgugaa 900

uuccacagcc augaauuuca cagccaugaa gauaugcugg uuguagaccc caaaaguaag 960

gaagaagaua aacaccugaa auuucguauu ucucaugaau uagauagugc aucuucugag 1020

gucaauuaaa aggagaaaaa auacaauuuc ucacuuugca uuuagucaaa agaaaaaaug 1080

cuuuauagca aaaugaaaga gaacaugaaa ugcuucuuuc ucaguuuauu gguugaaugu 1140

guaucuauuu gagucuggaa auaacuaaug uguuugauaa uuaguuuagu uuguggcuuc 1200

auggaaacuc ccuguaaacu aaaagcuuca ggguuauguc uauguucauu cuauagaaga 1260

aaugcaaacu aucacuguau uuuaauauuu guuauucucu caugaauaga aauuuaugua 1320

gaagcaaaca aaauacuuuu acccacuuaa aaagagaaua uaacauuuua ugucacuaua 1380

aucuuuuguu uuuuaaguua guguauauuu uguugugauu aucuuuuugu ggugugaaua 1440

aaucuuuuau cuugaaugua auaagaauuu ggugguguca auugcuuauu uguuuuccca 1500

cgguugucca gcaauuaaua aaacauaacc uuuuuuacug ccuaaaaaaa aaaaaaaaaa 1560

<210> 45
<211> 1926

<212> RNA
<213> HUMAN

<400> 45

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cgcgaagagg cuggacucgg auucguugcc ugagcaaugg cugccauccg gaagaaacug 300

gugauuguug gugauggagc cuguggaaag acaugcuugc ucauagucuu cagcaaggac 360

caguucccag agguguaugu gcccacagug uuugagaacu auguggcaga uaucgaggug 420

gauggaaagc agguagaguu ggcuuugugg gacacagcug ggcaggaaga uuaugaucgc 480

cugaggcccc ucuccuaccc agauaccgau guuauacuga uguguuuuuc caucgacagc 540

ccugauaguu uagaaaacau cccagaaaag uggaccccag aagucaagca uuucugucccc 600

aacgugccca ucauccuggu ugggaauaag aaggaucuuc ggaaugauga gcacacaagg 660

cgggagcuag ccaagaugaa gcaggagccg gugaaaccug aagaaggcag agauauggca 720

aacaggauug gcgcuuuugg guacauggag uguucagcaa agaccaaaga uggagugaga 780

gagguuuuug aaauggcuac gagagcugcu cugcaagcua gacgugggaa gaaaaaaucu 840

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ugcuguuuau uaaucuuagu guaugauuac uggccuuuuu cauuuaucua uaauuuaccu 960

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cgauguccaa cccgucuggc ccaccagggu ccuuuugaca cugcucuaac agcccuccuc 1080

ugcacuccca ccugacacac caggcgcuaa uucaaggaau uucuuaacuu cuugcuucuu 1140

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cauguccugc cuauuaucug ucagcugcaa gguacucugg ugagucacca cuucagggcu 1260

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uccucaaaga aaguguauug guuuuuuaaa aaagaaagug uauuuggaaa uaaagucaga 1560

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cccagaggag ccaccaguuc ucaugggugg cacucagucu cucuucucuc cagcugacua 1860

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aaaaaa 1926

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<211> 5693
<212> RNA
<213> HUMAN

<400> 46

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aaggaucaga uuggagaagu gauuuaucua agaucccaca guggacuggc agcagcacug 180

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cuccauuuug ggacauucua aucccugagc cccuauuauu uucaucaugg gcuucugccu 360

ggcucuagca uggacacuuc ugguuggggc auggaccccu cugggagcuc agaaccccau 420

uucgugggag gugcagcgau uugaugggug guacaacaac cucauggagc acagaugggg 480

cagcaaaggc ucccggcugc agcgccuggu cccagccagc uaugcagaug gcguguacca 540

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uuagaacccu cccuacuccc auaccuccuc cucuucuggg cuccccacug ucagacgggc 5460

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aucagacccu ggcccaauac cuauguaugc aaugcuccuc agcccucuuc ucccugcucc 5640

aguagucucc cuuccaaaua aaucacuuuu cugccuuaaa aaaaaaaaaa aaa 5693

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<213> HUMAN

<400> 47

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acauucuaau cccugagccc cuauuauuuu caucaugggc uucugccugg cucuagcaug 180

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gggucaauuu cuuuuuucuu uuuuuuuuuu uuuuuucuuu uucuuugaga cugggucucg 1860

cuuuguugcc caggcuggag uggaguggcg ugaucuuggc uuacugcagc cuuugccucc 1920

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gucucaaacu ccugggcuca ggcgauccac cugucucagc cucccagagu gcugggauua 2100

caauugugag ccaccacguc cagcuggaag ggucaacauc uuuuacauuc ugcaagcaca 2160

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uugcugccgu cuuccaguug cuuuaucugu ucacuugugc ccugacuuuc aacucugucu 240

ccuuccucuu ccuacaguac uccccugccc ucaacaagau guuuugccaa cuggccaaga 300

ccugcccugu gcagcugugg guugauucca cacccccgcc cggcacccgc guccgcgcca 360

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ccaugugguaa ucuacuggga cggaacagcu uugaggugcg uguuugugcc uguccuggga 720

gagaccggcg cacagaggaa gagaaucucc gcaagaaagg ggagccucac cacgagcugc 780

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auuguuaaag agagcaugaa aaugguucua ugacuuugcc ugauacagau gcuacuugac 960

uuacgauggu guuacuuccu gauaaacucg ucguaaguug aaaauauuau ccgugggcgu 1020

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uuccauuugc uuugucccgg ggcuccacug aacaaguugg ccugcacugg uguuuuguug 1380

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ccaucccaca cccuggagga uuucaucucu uguauaugau gaucuggauc caccaagacu 1920

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agacuggguc ucgcuuuguu gcccaggcug gaguggagug gcgugaucuu ggcuuacugc 2040

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gguucaugcc accauggcca gccaacuuuu gcauguuuug uagagauggg gucucacagu 2160

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agugcuggga uuacaauugu gagccaccac guccagcugg aagggucaac aucuuuuaca 2280

uucugcaagc acaucugcau uuucacccca cccuuccccu ccuucucccu uuuuauaucc 2340

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<213> HUMAN

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uugcugccgu cuuccaguug cuuuaucugu ucacuugugc ccugacuuuc aacucugucu 240

ccuuccucuu ccuacaguac uccccugccc ucaacaagau guuuugccaa cuggccaaga 300

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<213> HUMAN

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aagccucugc ccugccuccc uuucugggag ggcggggugg gggugacuga auuugggccu 2520

cuuguacagu uaacucuccc agguggauuu uguggaggug agaaaagggg cauugagacu 2580

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uuuuauaugc auauauuuua gggcuguaga cuuacuuucc uauuuucuuu uccauugcuu 2700

auucuugagc acaaaaugau aaucaauuau uacauuuaua caucaccuuu uugacuuuuc 2760

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uggaggggaa acgcaaaacc ugcaguuccu gaguaccuuc uacaggcccg gcccagccua 3000

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gagaguugac cguuuucauc cuggccuccu uuugcuguuu ggauguuucc acgggucuca 3120

cuuauaccaa agggaaaacu cuucauuaaa guccguauuu cuucuaaaaa aaaaaaaaaa 3180

aaaaaaaaaa aa 3192

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<211> 1208

<212> RNA

<213> HUMAN

<400> 82

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cacuuucuuu gacaguccag cccaccuccu cuucugcccg gagaagcucc aggggcugcc 180

uuugugauca cagcaucuuc acaaggacca aaggaaaaua agauuucuug uaagaacacc 240

gugaccacau cuuuaaaaug acccauuucg uggcucccac aagauuuaca ccuccacacu 300

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aacgccacgu aaugagucaa agcuguggcg cacgcgcaga aguacaagcu accggaagug 420

auggcgcccc uacuaaagcc uuggggguag uacgcgugcg cagcaguuuc uuccgacagu 480

uguguugugc caauggugga gaagaaaacu ucgguucgcu cccaggaccc cgggcagcgg 540

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caguuugaug acgaugcgga cacuggaaag aaaaagaaga aaacccgagg ugaucauuuu 720

aaacuucgcu uccgaaaaaa cuuucaggcc cuguuggagg agcagaacuu gaguguggcc 780

gagggcccua acuaccugac ggccugugcg ggacccccau cgcggcccca gcgccccuuc 840

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acaaaacugu gucuuaucug ccaggaaaga ccagccucac uccugggaac ugucuggcag 1140

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aaaaaaaa 1208

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<213> HUMAN

<400> 83
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aucugggucu ggaaacccaa acccucaagg auggccuggc gcaugggggа accagccugc 180

uggggcaggg ggcuacccag gggcuuccua uccuggggcc uaccccgggc aggcaccccc 240

aggggcuuau ccuggacagg caccuccagg cgccuacccu ggagcaccug gagcuuaucc 300

cggagcaccu gcaccuggag ucuacccagg gccacccagc ggcccugggg ccuacccauc 360

uucuggacag ccaagugcca ccggagccua cccugccacu ggccccuaug gcgccccugc 420

ugggccacug auugugccuu auaaccugcc uuugccuggg ggaguggugc cucgcaugcu 480

gauaacaauu cugggcacgg ugaagcccaa ugcaaacaga auugcuuuag auuuccaaag 540

agggaaugau guugccuucc acuuuaaccc acgcuucaau gagaacaaca ggagagucau 600

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auuugaaagu gggaaaccau ucaaaauaca aguacugguu gaaccugacc acuucaaggu 720

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cagcaaacug ggaauuucug gugacauaga ccucaccagu gcuucauaua ccaugauaua 840

aucugaaagg ggcagauuaa aaaaaaaaaa agaaucuaaa ccuuacaugu guaaagguuu 900

cauguucacu gugagugaaa auuuuuacau ucaucaauau cccucuugua agucaucuac 960

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<211> 1973
<212> RNA
<213> HUMAN

<400> 84

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guuaguggggg acagagggca gaugggguaag auucagagca caggcuagug ugacggaagu 180

uuaaacuugu gaguuaaaua ggguuuggca aucuagcugg auagcauccc ugccccuuga 240

agagauguuu uuguggcgcc acacuacuga cuuaggcaua augccuagag auggauuaga 300

acugcacaau gaacuagugg ugagguucag uuuaauggaa auuggugaaa gcuuuuagga 360

uaaaaugaua aucuuuguuu cuuucaggaa aauggcagac aauuuuucgg uaaguguuuu 420

augccuguuu cuuccccuug aucagcucca caugguugag gguuggggggu uuuguuuuua 480

ccaugacuuu cccuuuucac ucucccacug cguggcuucc ccuggacuca uuuguccaau 540

gagggcuugc aagcuggagc cuuguuuuuc cagcagcaga uuugggaaga aagccaggca 600

gagcgaggcc ugggacucac ucacaguaac ccuuucacca aaaggcccag ggcggaaggg 660

aguggacucu gccggcagga gcugagaaau ccucugagua gcgggaagug cgguacaguc 720

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uagaggagcg cuaacuccug acuugagcua auuaugaaaa ugcagcccuc ccugaucuga 840

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cuuagaaacu caaacuauua auaaguggaa aaaguuuaau gauaugcaug uaaugccuuu 960

gccauauucc ucuccuucuu agaucacaua uuccuauuuu ccugaaaauu cugcuuuuga 1020

gaaugcuuuc ugucccguaa uuguguaugu cuuucuuucc agcuccauga ugcguuaucu 1080

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gcaggggcu acccaggggc uuccuauccu ggggccuacc ccgggcaggc acccccaggg 1200

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acaauucugg gcacggugaa gcccaaugca aacagaauug cuuuagauuu ccaaagaggg 1500

aaugauguug ccuuccacuu uaacccacgc uucaaugaga acaacaggag agucauuguu 1560

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gugaaugaug cucacuuguu gcaguacaau caucggguua aaaaacucaa ugaaaucagc 1740

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gaaaggggca gauuaaaaaa aaaaaaagaa ucuaaaccuu acauguguaa agguuucaug 1860

uucacuguga gugaaaauuu uuacauucau caauaucccu cuuguaaguc aucuacuuaa 1920

uaaauauuac agugaauuac cugucucaau augucaaaaa aaaaaaaaaa aaa 1973

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<211> 744
<212> RNA
<213> HUMAN

<400> 85
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gauaacaauu cugggcacgg ugaagcccaa ugcaaacaga auugcuuuag auuuccaaag 540

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uguuugcacu uacaugugua aagguuucau guucacugug agugaaaauu uuuacauuca 660

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<212> RNA
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<400> 86
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auacccgugc aggcgcggag aagcaaccgg caccccccuuc cggccugaaa gcccucccug 3300

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ugaugacugu aaauguucac ugggugggua gggaguggua uccaguguuc aagugcagaa 3420

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<213> HUMAN

<400> 87
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agcagccuga ggccccagag ucugagacga gccgccgccg cccccgccac ugcggggagg 240

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<213> HUMAN

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cuaccagucc aaggaggccg ggcagcgccu ggcgaccgcc augaagcugg gcuucaguag 1860

gccguggccg gaagccaugc agcugaucac gggccagccc aacaugagcg ccucggccau 1920

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gaagcugggc uggccgcagu acaacuggac gccgaacucc gcucgcucag aagggccccu 2040

cccagacagc ggccgcguca gcuuccuggg ccuggaccug gaugcgcagc aggcccgcgu 2100

gggccagugg cugcugcucu uccugggcau cgcccugcug guagccaccc ugggccucag 2160

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accaccagcc gccccagccc cuucucccag cacacggcug ccugacacug agccccaccu 2460

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<211> 4195

<212> RNA

<213> HUMAN

<400> 89

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gcugcagccc ggcaacuuuu cugcugacga ggccgggggcg cagcucuucg cgcagagcua 180

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caacaucacc gcggagaaug caaggcgcca ggaggaagca gcccugcuca gccaggaguu 300

ugcggaggcc uggggccaga aggccaagga gcuguaugaa ccgaucuggc agaacuucac 360

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ccuggcuaag cggcagcagu acaacgcccu gcuaagcaac augagcagga ucuacuccac 480

cgccaagguc ugccucccca acaagacugc caccugcugg ucccuggacc cagaucucac 540

caacauccug gcuuccucgc gaagcuacgc caugcuccug uuugccuggg agggcuggca 600

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ccccaccuuc gaggacgauc uggaacaccu cuaccaacag cuagagcccc ucuaccugaa 780

ccuccaugcc uucguccgcc gcgcacugca ucgccgauac ggagacagau acaucaaccu 840

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cuacgacaug guggugccuu ucccagacaa gcccaaccuc gaugucacca guacuaugcu 960

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<211> 760
<212> RNA
<213> HUMAN

<400> 90
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cuucauuccc caagggcucg cucagccaga ugcaaucaau gccccaguca ccugcuguua 180

uaacuucacc aauaggaaga ucucagugca gaggcucgcg agcuauagaa gaaucaccag 240

cagcaagugu cccaaagaag cugugaucuu caagaccauu guggccaagg agaucugugc 300

ugaccccaag cagaaguggg uucaggauuc cauggaccac cuggacaagc aaacccaaac 360

uccgaagacu ugaacacuca cuccacaacc caagaaucug cagcuaacuu auuuuccccu 420

agcuuucccc agacacccug uuuuauuuua uuauaaugaa uuuuguuugu ugaugugaaa 480

cauuaugccu uaaguaaugu uaauucuuau uuaaguuauu gauguuuuaa guuuaucuuu 540

caugguacua guguuuuuua gauacagaga cuuggggaaa uugcuuuucc ucuugaacca 600

caguucuacc ccugggaugu uuugaggguc uuugcaagaa ucauuaauac aaagaauuuu 660

uuuuaacauu ccaaugcauu gcuaaaauau uauuguggaa augaauauuu uguaacuauu 720

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<211> 1916

<212> RNA

<213> HUMAN

<400> 91

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cccauugacu aacuauggaa gauuauacca aaauagagaa aauuggagaa gguaccuaug 180

gaguugugua uaaggguaga cacaaaacua caggucaagu gguagccaug aaaaaaauca 240

gacuagaaag ugaagaggaa gggguuccua guacugcaau ucgggaaauu ucucuauuaa 300

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uauaucucau cuuugaguuu cuuuccaugg aucugaagaa auacuuggau ucuaucccuc 420

cuggucagua cauggauucu ucacuuguua agaguuauuu auaccaaauc cuacagggga 480

uuguguuuug ucacucuaga agaguucuuc acagagacuu aaaaccucaa aaucucuuga 540

uugaugacaa aggaacaauu aaacuggcug auuuuggccu ugccagagcu uuuggaauac 600

cuaucagagu auauacacau gagguaguaa cacucuggua cagaucucca gaaguauugc 660

uggggucagc ucguuacuca acuccaguug acauuuggag uauaggcacc auauuugcug 720

aacuagcaac uaagaaacca cuuuuccaug gggauucaga aauugaucaa cucuucagga 780

uuuucagagc uuugggcacu cccaauaaug aaguguggcc agaaguggaa ucuuuacagg 840

acuauaagaa uacauuuccc aaauggaaac caggaagccu agcaucccau gucaaaaacu 900

uggaugaaaa uggcuuggau uugcucucga aaauguuaau cuaugaucca gccaaacgaa 960

uuucuggcaa aauggcacug aaucauccau auuuuaauga uuuggacaau cagauuaaga 1020

agauguagcu uucugacaaa aaguuuccau auguuauauc aacagauagu uguguuuuua 1080

uuguuaacuc uugucuauuu uugucuuaua uauauuucuu uguuaucaaa cuucagcugu 1140

acuucgucuu cuaauuucaa aaauauaacu uaaaaaugua aauauucuau augaauuuaa 1200

auauaauucu guaaaugugu guaggucuca cuguaacaac uauuuguuac uauaauaaaa 1260

cuauaauauu gaugucagga aucaggaaaa aauuugaguu ggcuuaaauc aucucagucc 1320

uuauggcagu uuuauuuucc uguaguugga acuacuaaaa uuuaggaaaa ugcuaaguuc 1380

aaguuucgua augcuuugaa guauuuuuau gcucugaaug uuuaaauguu cucaucaguu 1440

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uaauuuuuga ccuaaauguu uaagcauucg gaaugagaaa acuauacaga uuugagaaau 1560

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aacuacacau uuugacauag uguuuauuag cagccaucua aaaaggcucu aauguauauu 1860

uaacuaaaau uacuagcuuu gggaauuaaa cuguuuaaca aauaaaaaaa aaaaaa 1916

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<212> RNA
<213> HUMAN

<400> 92
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gaaaaaaauc agacuagaaa gugaagagga agggguuccu aguacugcaa uucgggaaau 180

uucucuauua aaggaacuuc gucauccaaa uauagucagu cuucaggaug ugcuuaugca 240

ggauuccagg uuauaucuca ucuuugaguu ucuuuccaug gaucugaaga aauacuugga 300

uucuaucccu ccuggucagu acauggauuc uucacuuguu aagguaguaa cacucuggua 360

cagaucucca gaaguauugc uggggucagc ucguuacuca acuccaguug acauuuggag 420

uauaggcacc auauuugcug aacuagcaac uaagaaacca cuuuuccaug gggauucaga 480

aauugaucaa cucuucagga uuuucagagc uuugggcacu cccaauaaug aaguguggcc 540

agaaguggaa ucuuuacagg acuauaagaa uacauuuccc aaauggaaac caggaagccu 600

agcaucccau gucaaaaacu uggaugaaaa uggcuuggau uugcucucga aaauguuaau 660

cuaugaucca gccaaacgaa uuucuggcaa aauggcacug aaucauccau auuuuaauga 720

uuuggacaau cagauuaaga agauguagcu uucugacaaa aaguuuccau auguuauauc 780

aacagauagu uguguuuuua uuguuaacuc uugucuauuu uugucuuaua uauauuucuu 840

uguuaucaaa cuucagcugu acuucgucuu cuaauuucaa aaauauaacu uaaaaaugua 900

aauauucuau augaauuuaa auauaauucu guaaaugugu guaggucuca cuguaacaac 960

uauuuguuac uauaauaaaa cuauaauauu gaugucagga aucaggaaaa aauuugaguu 1020

ggcuuaaauc aucucagucc uuauggcagu uuuauuuucc uguaguugga acuacuaaaa 1080

uuuaggaaaa ugcuaaguuc aaguuucgua augcuuugaa guauuuuuau gcucugaaug 1140

uuuaaauguu cucaucaguu ucuugccaug uuguuaacua uacaaccugg cuaaagauga 1200

auauuuuucu acugguauuu uaauuuuuga ccuaaauguu uaagcauucg gaaugagaaa 1260

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aacaugagag caugccaaaa uuugcuaagu cuuacaaaga ucaagggcug uccgcaacag 1380

ggaagaacag uuuugaaaau uuaugaacua ucuuauuuuu agguagguuu ugaaagcuuu 1440

uugucuaagu gaauucuuau gccuugguca gaguaauaac ugaaggaguu gcuuaucuug 1500

gcuuucgagu cugaguuuaa aacuacacau uuugacauag uguuuauuag cagccaucua 1560

aaaaggcucu aauguauauu uaacuaaaau uacuagcuuu gggaauuaaa cuguuuaaca 1620

aauaaaaaaa aaaaaa 1636

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<211> 1943
<212> RNA
<213> HUMAN

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gaaggccgga cuggaggauc uaccauaccc auugacuaac uauggaagau uauaccaaaa 180

uagagaaaau uggagaaggu accuauggag uuguguauaa ggguagacac aaaacuacag 240

gucaaguggu agccaugaaa aaaaucagac uagaaaguga agaggaaggg guuccuagua 300

cugcaauucg ggaaauuucu cuauuaaagg aacuucguca uccaaauaua gucagucuuc 360

aggaugugcu uaugcaggau uccagguuau aucucaucuu ugaguuucuu uccauggauc 420

ugaagaaaua cuuggauucu aucccuccug gucaguacau ggauucuuca cuuguuaaga 480

guuauuuaua ccaaauccua caggggauug uguuuuguca cucuagaaga guucuucaca 540

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ucugguacag aucuccagaa guauugcugg ggucagcucg uuacucaacu ccaguugaca 720

uuuggaguau aggcaccaua uuugcugaac uagcaacuaa gaaaccacuu uuccaugggg 780

auucagaaau ugaucaacuc uucaggauuu ucagagcuuu gggcacuccc aauaaugaag 840

uguggccaga aguggaaucu uuacaggacu auaagaauac auuucccaaa uggaaaccag 900

gaagccuagc aucccauguc aaaaacuugg augaaaaugg cuuggauuug cucucgaaaa 960

uguuaaucua ugauccagcc aaacgaauuu cuggcaaaau ggcacugaau cauccauauu 1020

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acuaaaauuu aggaaaaugc uaaguucaag uuucguaaug cuuugaagua uuuuuaugcu 1440

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uaucuuggcu uucgagucug aguuuaaaac uacacauuuu gacauagugu uuauuagcag 1860

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<400> 94
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cggcggcgcg cagaaccgcu ccuacagcaa gcugcugugc ggccugcugg ccgagcgccu 360

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cuggaacaac uccaccuucg ccuaagagcc gcagggaccc acgcugucug cgcuggcucc 480

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gccaaaccuc uaauggaguu gauugagagg cucgggggcu ggaacaucac aggucccugg 720

gccaaggaca acuuccagga cacccugcag guggucaccg cccacuaccg caccucaccc 780

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aaggugcuga ccggauaucu gaacuacaug guccagcugg ggaagcugcu gggcggcggg 960

gacgaggagg ccauccggcc ccagaugcag cagaucuugg acuuugagac ggcacuggcc 1020

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gagcagaucu ccacucucau caacaccacc gacagaugcc ugcucaacaa cuacaugauc 1260

uggaaccugg ugcggaaaac aagcuccuuc cuugaccagc gcuuucagga cgccgaugag 1320

aaguucaugg aagucaugua cgggaccaag aagaccuguc uuccucgcug gaaguuuugc 1380

gugagugaca cagaaaacaa ccugggcuuu gcguugggcc ccauguuugu caaagcaacc 1440

uucgccgagg acagcaagag cauagccacc gagaucaucc uggagauuaa gaaggcauuu 1500

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auuguguuuc cggccgggau ccugcaggca ccauucuaca cacgcuccuc acccaaggcc 1860

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REFERENCES CITED IN THE DESCRIPTION

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PATENTKRAV

1. Oligonukleotidforbindelse, der nedregulerer ekspression af p53-genet, til anvendelse i behandling af kronisk nyresygdom (CKD) efter eksponering for tilbagevendende nyreanfald hos et individ, der lider af CKD.

2. Oligonukleotidforbindelse til anvendelse ifølge krav 1, hvor behandlingen er dæmpning af progressionen af kronisk nyresygdom (CKD) hos individet.

3. Oligonukleotidforbindelse til anvendelse ifølge krav 1, hvor oligonukleotidforbindelsen skal administreres til individet inden for 24 timer før eller efter nyreanfald.

4. Oligonukleotidforbindelse til anvendelse ifølge krav 3, hvor oligonukleotidforbindelsen skal administreres til individet ca. 4 timer efter nyreanfald.

5. Oligonukleotidforbindelse til anvendelse ifølge krav 1, hvor nyreanfaldet resulterer i akut nyrelæsion (AKI).

6. Oligonukleotidforbindelse til anvendelse ifølge krav 1, hvor nyreanfaldet er forbundet med én eller flere af: kirurgi indbefattende kardiovaskulær kirurgi; myoglobinuri, iskæmi/reperfusionslæsion; sepsis; urinvejsobstruktion; eksponering for et nephrotoksin indbefattende et nephrotoksin røntgenkontrastmiddel eller et antibiotikum; proteinuri; øget renal ammoniagenese med interstitiel læsion; hyperlipidæmi; hyperphosphatæmi med calciumphosphataflejring.

7. Oligonukleotidforbindelse til anvendelse ifølge krav 6, hvor nyreanfaldet er forbundet med iskæmi/reperfusionslæsion eller eksponering for et nephrotoksin.

8. Oligonukleotidforbindelse til anvendelse ifølge krav 7, hvor iskæmi/reperfusionslæsionen indtræder under eller efter kardiovaskulær eller kardiopulmonal kirurgi.

9. Oligonukleotidforbindelse til anvendelse ifølge krav 6, hvor nyreanfaldet er forbundet med myoglobinuri.

10. Oligonukleotidforbindelse til anvendelse ifølge krav 1, hvor oligonukleotidforbindelsen er udvalgt fra gruppen bestående af et ikke-modificeret siRNA, et kemisk modificeret siRNA, shRNA, et antisense-molekyle, miRNA og et ribozym.

11. Oligonukleotidforbindelse til anvendelse ifølge krav 10, hvor oligonukleotidforbindelsen er et ikke-modificeret siRNA eller et kemisk modificeret siRNA.

12. Oligonukleotidforbindelse til anvendelse ifølge krav 1, hvor forbindelsen er I5 siRNA-forbindelsen med strukturen:

sense-sekvens 5' GaGaAuAuUuCaCcCuUcA 3' (SEQ ID NO: 118)

antisense-sekvens 3' cUcUuAuAaAgUgGgAaGu 5' (SEQ ID NO: 119),

hvor store bogstaver repræsenterer ikke-modificerede nukleotider og små bogstaver repræsenterer 2'-methoxy-sukkermodificerede ribonukleotider.

DRAWINGS

FIGURE 1

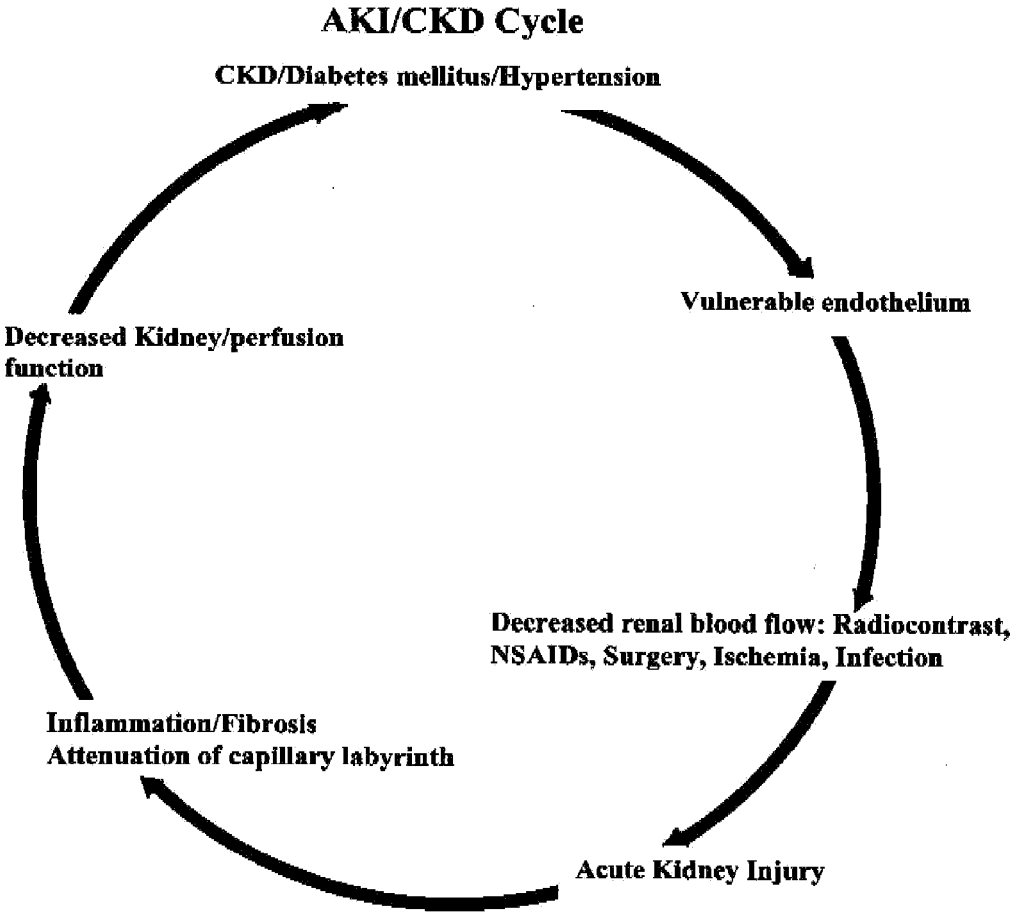


FIGURE 2

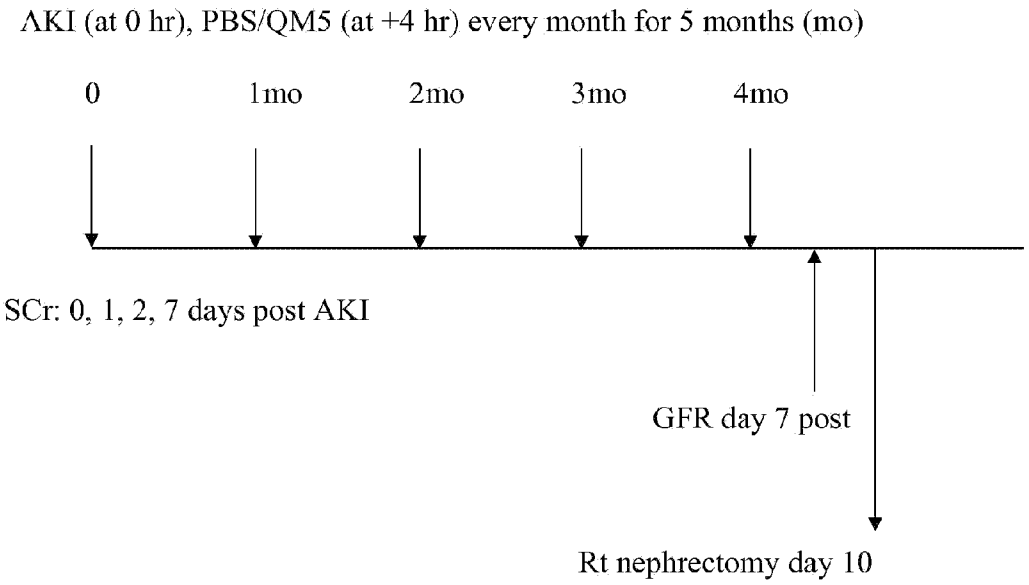


FIGURE 3

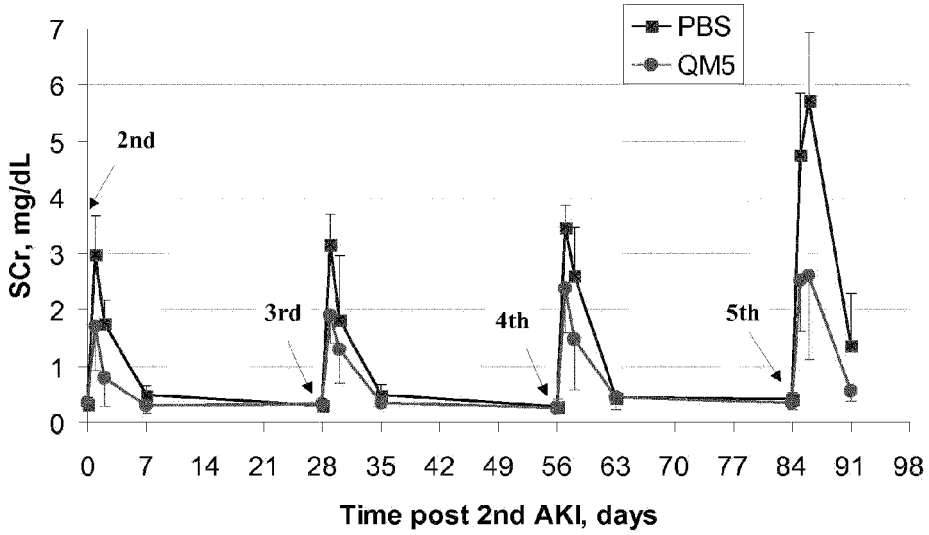


FIGURE 4

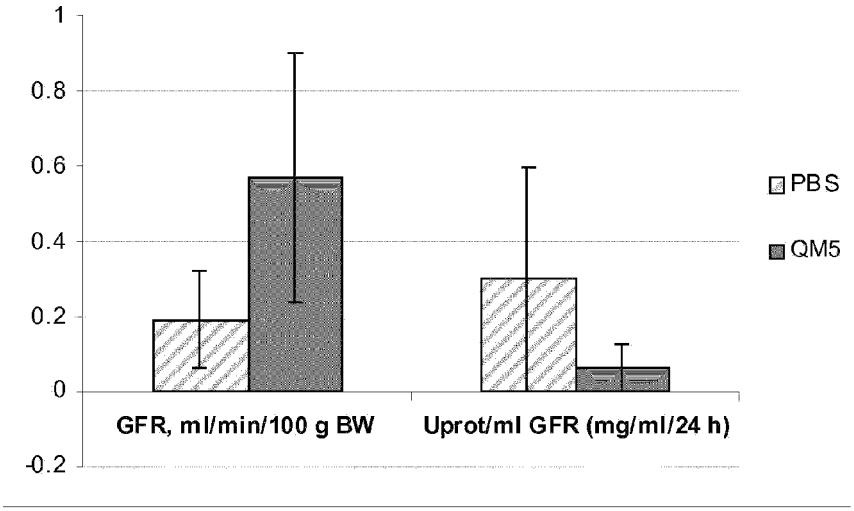


FIGURE 5

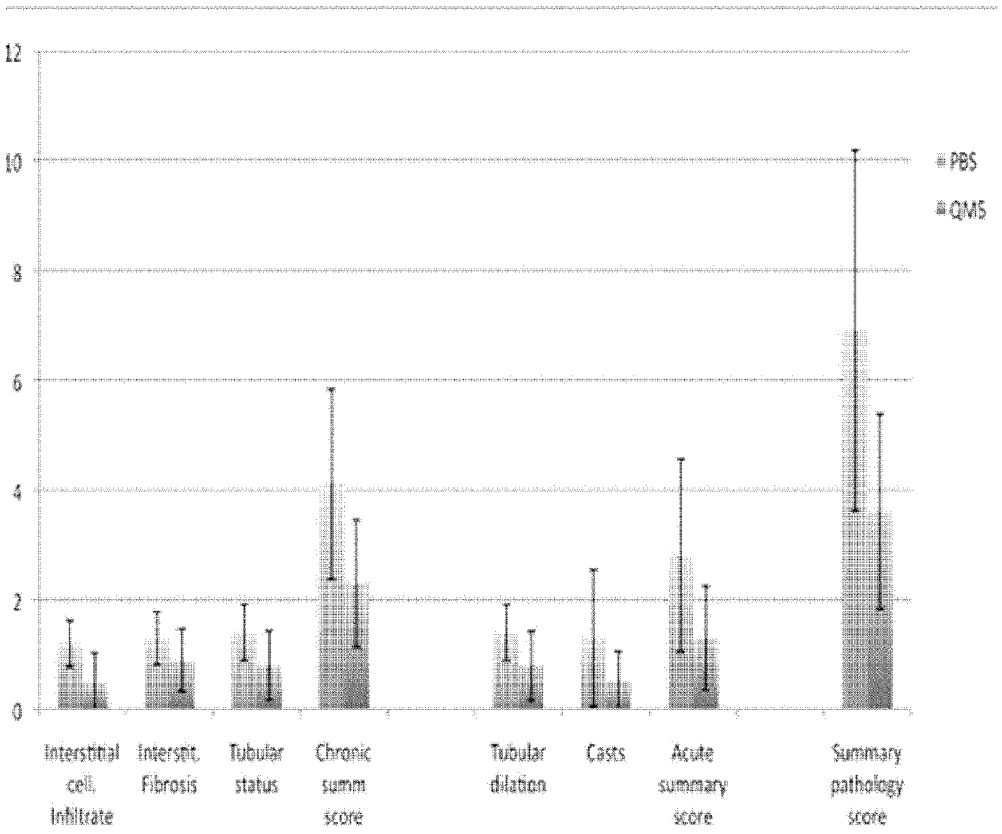

12
10
8
6
4
2
0
PBS
QM5
Interstitial cell. Infiltrate
Interstit. Fibrosis
Tubular status
Chronic summ score
Tubular dilation
Casts
Acute summary score
Summary pathology score

FIGURE 6

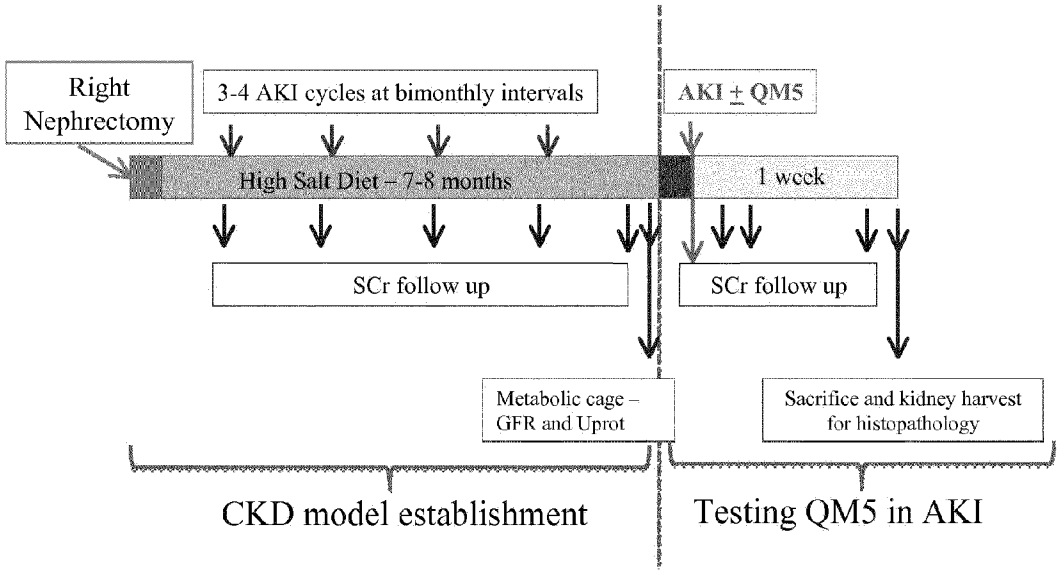
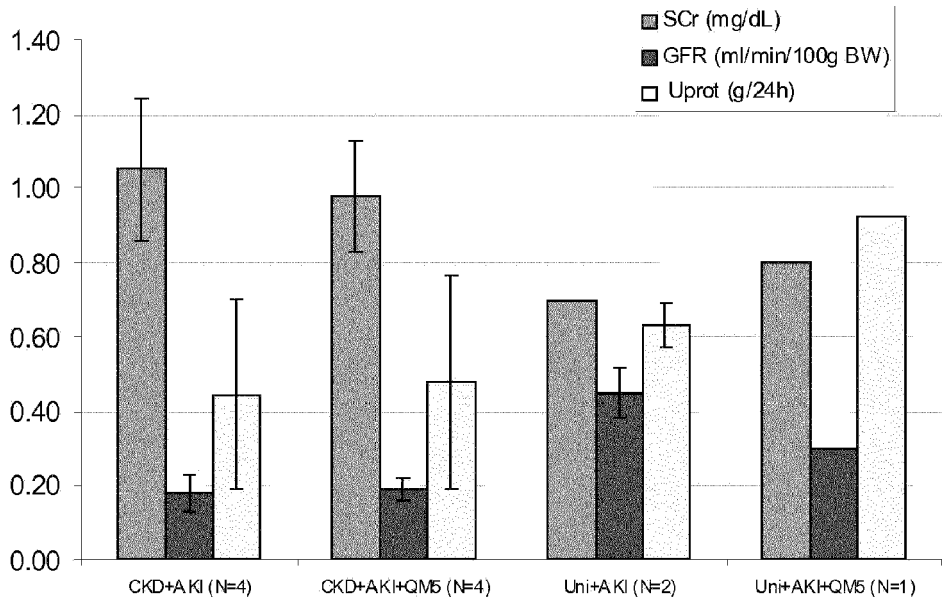

Right Nephrectomy
3-4 AKI cycles at bimonthly intervals
AKI ± QM5
High Salt Diet – 7-8 months
1 week
SCr follow up
SCr follow up
Metabolic cage – GFR and Uprot
Sacrifice and kidney harvest for histopathology
CKD model establishment
Testing QM5 in AKI

FIGURE 7



high salt diet | regular diet

FIGURE 8

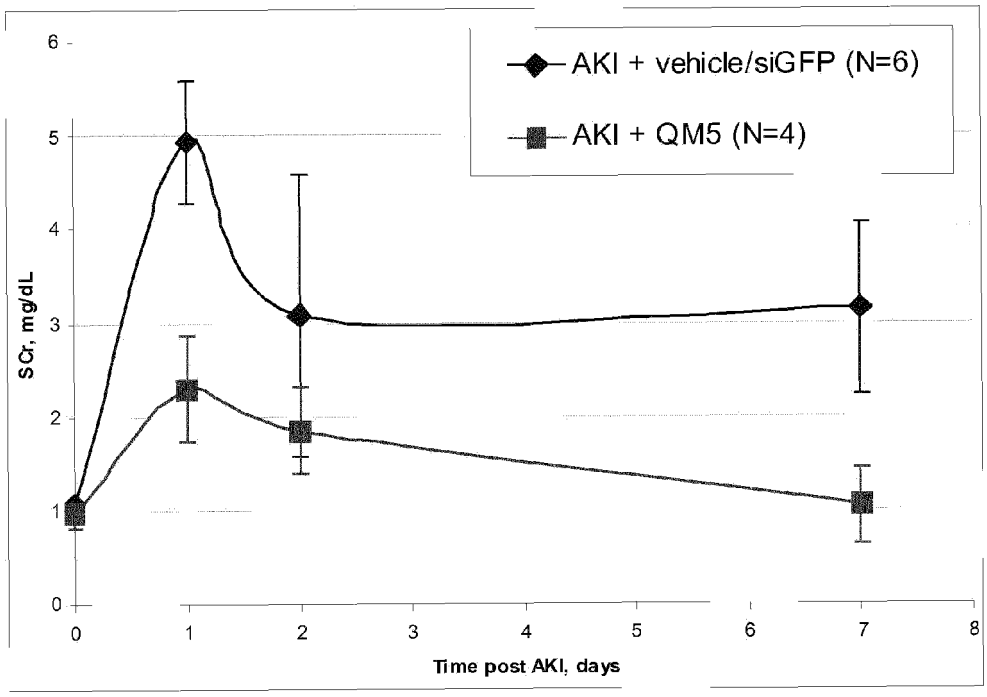

AKI + vehicle/siGFP (N=6)
AKI + QM5 (N=4)
SCr, mg/dL
Time post AKI, days
0
1
2
3
4
5
6
7
8

FIGURE 9A

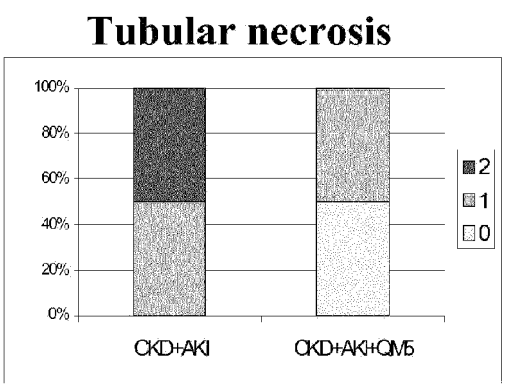


FIGURE 9B

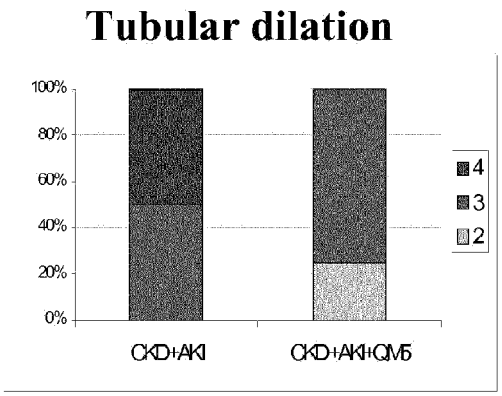


FIGURE 9C

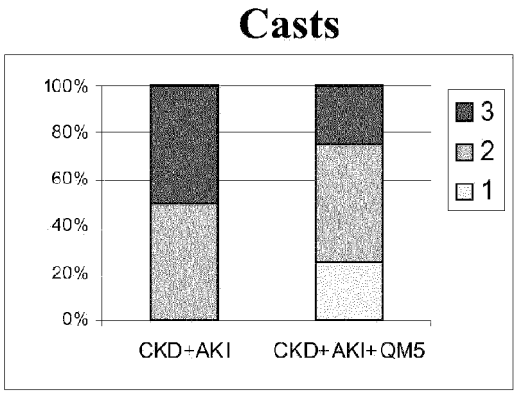


FIGURE 9D

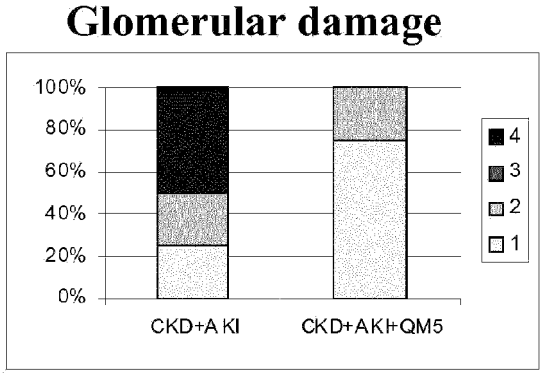


FIGURE 9E

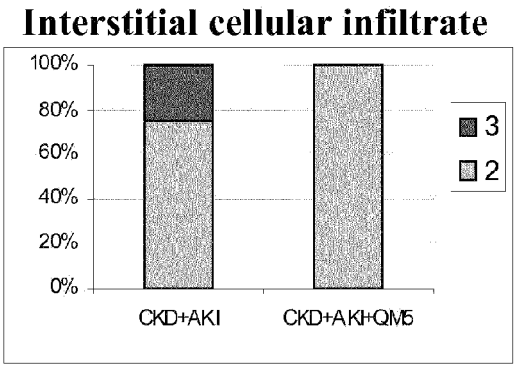


FIGURE 9F

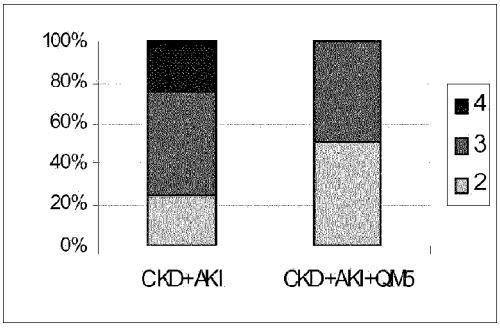


FIGURE 9G

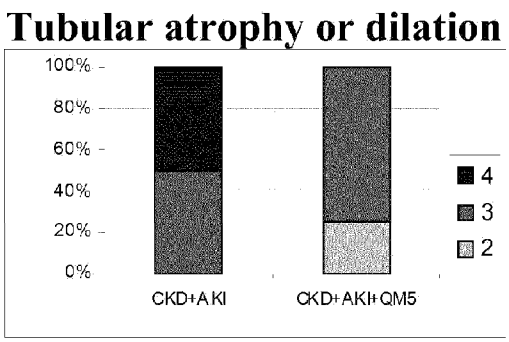


FIGURE 9H

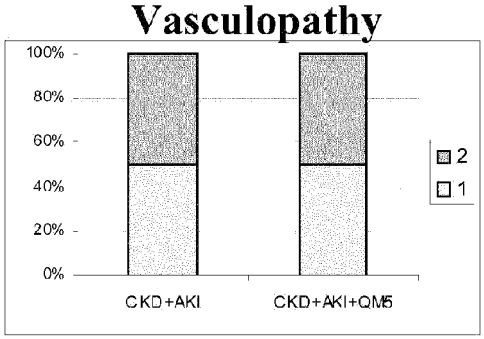


FIGURE 10

