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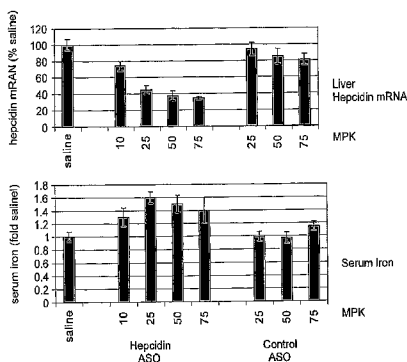
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(54) Title: COMPOSITIONS AND THEIR USES DIRECTED TO HEPCIDIN



(57) Abstract: Disclosed herein are compounds, compositions and methods for modulating the expression of hepcidin in a cell, tissue or animal or preventing, ameliorating or treating anemia. Also provided are methods for prevention, amelioration or treatment of anemia, and for increasing red blood cell count in an animal. Also provided are methods for the prevention, amelioration and/or treatment of low serum iron levels, low red blood cell count and other clinical endpoints of anemia in an animal. These methods may be achieved by administration of compounds or compositions including antisense compounds targeted to a nucleic acid that expresses hepcidin polypeptide combined with an erythropoiesis stimulating agent.

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## COMPOSITIONS AND THEIR USES DIRECTED TO HEPCIDIN

### BACKGROUND OF THE INVENTION

Anemia is characterized by a lower than normal number of red blood cells (erythrocytes) in the blood, usually measured by a decrease in the amount of hemoglobin. The cause of anemia can include chronic inflammation, chronic kidney disease, kidney dialysis treatment, genetic disorders, chronic infection, acute infection, cancer and cancer treatments. Altered iron homeostasis and/or erythropoiesis in these conditions can result in decreased erythrocyte (red blood cell) production. Anemia can limit the use of chemotherapeutic agents during cancer treatment. Symptoms of anemia include fatigue, pallor and poor exercise tolerance. Though rarely life threatening, anemia can be severely debilitating and difficult to treat. Clinical signs of anemia include low serum iron (hypoferremia), low hemoglobin levels, low hematocrit levels, decreased red blood cells, decreased reticulocytes, increased soluble transferrin receptor and iron restricted erythropoiesis.

In some cases, increasing dietary iron or intravenous iron delivery are used to treat anemia. Erythropoietin (EPO) stimulates erythrogenitors and promotes red blood cell formation. Recombinant erythropoietin and other erythropoiesis stimulating agents (ESAs) are used for treating anemia, although certain patients respond poorly to this treatment. EPO is well known and is commercially available through Amgen (Thousand Oaks, CA).

Anemia of chronic disease (ACD) is a highly prevalent, inflammatory-driven disorder that is poorly treated with currently available therapies. The mechanism underlying ACD is chronic inflammation, which results in changes in iron homeostasis and utilization, resulting in a blunting of erythroid progenitor cell proliferation and red cell function.

ACD is associated with increased production of inflammatory cytokines, including, for example, tumor necrosis factor-.alpha., IL-1 .beta., IL-6, and interferon-.gamma. (Means (1995) Stem cells 13:32-37 and Means (1999) Int J Hematol 70:7-12). In several *in vitro* and *in vivo* animal model systems, inflammatory cytokines negatively affected the ability to mediate erythropoietin (EPO) production, EPO responsiveness, and the coordinate regulation of iron metabolism (Roodman et al. (1989) Adv Exp Med Biol 271:185-196; Fuchs et al. (1991) Eur J Hematol 46:65-70; Jelkmann et al. (1994) Ann NY Acad Sci 718:300-311; Vannucchi et al. (1994) Br J Hematol 87:18-23; and Oldenburg et al. (2001) Aliment Pharmacol Ther 15:429-438). Administration of EPO failed to reverse anemia in mice continuously exposed to TNF-.alpha. (Clibon et al. (1990) Exp Hematol 18:438-441). Increased levels of inflammatory cytokines, such as TNF-.alpha., IL-1 .beta., and INF-.gamma., contribute to defective EPO production and EPO resistance observed in patients with anemia of chronic disease (Jelkmann et al. (1991) Ann NY Acad Sci 718:300-311 and Macdougall and Cooper (2002) Nephrol Dial Transplant 17(11):39-43.).

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Therefore, various cytokines, e.g., inflammatory cytokines and cytokines associated with inflammation, are involved in many aspects of the pathogenesis of anemia of chronic disease, including inhibition of erythroid progenitors, inhibition of EPO production, and impairment of iron release and iron availability for erythropoiesis.

5                   Hepcidin is an 8 kD polypeptide that is produced by hepatocytes in response to inflammation or to rising levels of iron in the blood. The primary role of hepcidin is to regulate blood iron levels by facilitating a decrease in these blood iron levels. Hepcidin binds with and down regulates ferroportin to reduce ferroportin mediated release of iron into the blood. Hepcidin expression is increased in conditions of acute and chronic inflammation resulting in decreased iron  
10 availability for erythropoiesis. Hepcidin is frequently measured in the urine or serum as a biomarker of anemia status. (Ganz *et al.* (2006) *Am J Physiol Gastrointest Liver Physiol* 290:G199-G203; and Ganz (2003) *Blood* 102(3):783-788). Moreover, hepcidin over expression has been strongly linked to ACD mechanistically as a mediator of this disorder in animal models and in humans.

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#### SUMMARY OF THE INVENTION

Provided herein are compounds, particularly oligomeric compounds, especially nucleic acid and nucleic acid-like oligomers, which are targeted to a nucleic acid encoding hepcidin. Preferably, the oligomeric compounds are antisense compounds targeted to a nucleic acid  
20 molecule encoding hepcidin, particularly human hepcidin (GenBank Accession Nos. BM719679.1, entered March 1, 2002; NM\_021175.2, entered July 23, 2004; and nucleotides 7819907 to 7825131 of NT\_011196.11, entered January 5, 2003; all herein incorporated by reference and assigned SEQ ID NOS: 1, 2 and 3, respectively), that modulate the expression of hepcidin. In a particular embodiment, the antisense compounds are antisense oligonucleotides. In another embodiment, the  
25 antisense compounds are siRNAs. In one embodiment, the compounds comprise at least an 8 nucleobase portion, preferably at least a 12 nucleobase portion, more preferably at least a 15 nucleobase portion, of the sequences listed in Table 3. In a further embodiment, the compounds are at least 80% identical to the sequences listed in or below Table 3.

Herein, active target segments are identified for SEQ ID NOS: 1, 2 and 3. A series  
30 of antisense oligonucleotide compounds was designed to target one or more of SEQ ID NOS: 1, 2, and 3. Active target segments were then identified as being regions of the hepcidin mRNA associated with the most active antisense oligonucleotides. Compounds are provided that are targeted to an active target segment of SEQ ID NO: 1, 2, or 3 and modulate the expression of hepcidin. In one embodiment, the compounds comprise at least an 8 nucleobase portion, preferably  
35 at least a 12 nucleobase portion, more preferably at least a 15 nucleobase portion, that is complementary to an active target segment. In a further embodiment, the compounds are at least

80% complementary to an active target segments. In another embodiment, the compounds are 13 to 30 nucleobases in length. In another embodiment, the compounds are at least about 80% complementary to at least a 20 nucleobase portion of the active target segment. In yet another embodiment, the compounds are complementary to at least an 8 nucleobase portion of the active target segment.

In another aspect, the compounds comprise at least one modified internucleoside linkage, modified sugar moiety, or modified nucleobase. In another aspect, the compounds comprise a chimeric oligonucleotide. In one aspect, the compounds comprise a phosphorothioate linkage. In another aspect, the compounds comprise a 2'-MOE modification. In another aspect, the compounds comprise a 5-methylcytosine modification.

Another embodiment provides for a composition comprising erythropoietin and an antisense compound targeted to a nucleic acid encoding hepcidin. In one aspect, the compound is an antisense oligonucleotide targeted to a nucleic acid molecule encoding hepcidin

A further embodiment provides methods for prevention, amelioration or treatment of anemia in an individual comprising administering to the individual erythropoietin and an antisense compound targeted to a nucleic acid encoding hepcidin. In one aspect, the compound is an antisense oligonucleotide targeted to a nucleic acid molecule encoding hepcidin.

In one embodiment, the antisense oligonucleotide used in this method causes an increase in serum iron levels, prevention of iron restriction of erythropoiesis, or a combination thereof. In yet another embodiment, the administration causes an increase in red blood cell counts, reticulocyte counts, hemoglobin levels, hematocrit levels, or a combination thereof.

In one aspect, the cause of anemia is chronic inflammation, chronic kidney disease, kidney dialysis treatment, genetic disorders, chronic infection, acute infection, cancer, or cancer treatments. In another aspect, the anemia is associated with inflammation. In another aspect, it is anemia of chronic disease (ACD).

In another embodiment, the individual receiving the administration has received or has been continuously receiving erythropoietin prior to treatment. Another embodiment provides methods for prevention, amelioration or treatment of anemia in an individual who is being treated with erythropoietin comprising administering to the individual erythropoietin and an antisense oligonucleotide targeted to a nucleic acid molecule encoding hepcidin.

In another embodiment, the administration comprises delivery of the antisense oligonucleotide and erythropoietin in a single formulation. In one aspect, the delivery of the single formulation is by injection. In another embodiment, the administration comprises delivery of the antisense oligonucleotide and erythropoietin in separate formulations. In one aspect delivery of

separate formulations is by injection. In another aspect, separate formulations are delivered at distinct timepoints. In another aspect, they are delivered simultaneously.

Another embodiment provides a method for increasing red blood cell count in an animal that is being treated with erythropoietin comprising administering to the animal an oligomeric compound targeted to a nucleic acid encoding hepcidin. In one aspect, the compound is an antisense oligonucleotide targeted to a nucleic acid molecule encoding hepcidin.

Another embodiment provides a method for increasing red blood cell count in an animal comprising the steps of delivering an erythropoietin therapy and delivering an antisense oligonucleotide therapy targeted to a nucleic acid molecule encoding hepcidin.

Another embodiment provides methods for prevention, amelioration or treatment of anemia in an individual comprising administering to the individual antisense compound targeted to a nucleic acid encoding hepcidin, wherein the individual is further receiving erythropoietin therapy. In one aspect, the erythropoietin therapy had occurred or was continuously occurring at the time of administration of the antisense oligonucleotide. In another aspect the individual is therapy naïve, meaning that the individual had not before received or was not receiving erythropoietin therapy at the initiation of the method. In one embodiment, the method further comprises administering to the individual erythropoietin. In one embodiment, the antisense compound and erythropoietin are administered in a single formulation. In another embodiment, they are administered in separate formulations. In one embodiment, the separate formulations are administered simultaneously. In another aspect the separate formulations are administered at distinct times. In one aspect, the formulations are administered by injection.

Another embodiment provides methods for increasing red blood cells in an individual antisense compound targeted to a nucleic acid encoding hepcidin, wherein the individual is further receiving erythropoietin therapy. In one aspect, the erythropoietin therapy had occurred or was continuously occurring at the time of administration of the antisense oligonucleotide. In another aspect the individual is therapy naïve, meaning that the individual had not before received or was not receiving erythropoietin therapy at the initiation of the method. In one embodiment, the method further comprises administering to the individual erythropoietin. In one embodiment, the antisense compound and erythropoietin are administered in a single formulation. In another embodiment, they are administered in separate formulations. In one embodiment, the separate formulations are administered simultaneously. In another aspect the separate formulations are administered at distinct times. In one aspect, the formulations are administered by injection.

Also provided herein are methods for providing a combination therapy for prevention, treatment or amelioration of anemia or increasing red blood cells in an animal

comprising the step of administering to the animal an antisense compound disclosed herein, wherein the animal is further receiving erythropoietin therapy. In one embodiment, the animal has been receiving erythropoietin therapy prior to the administration of the antisense compound. In another embodiment the animal begins erythropoietin therapy simultaneously with the  
5 administration of the antisense compound. In one embodiment, the combination therapy comprises receiving the antisense compound and an erythropoietin therapy compound in a single formulation. In another embodiment, the combination therapy comprises receiving the antisense compound and an erythropoietin therapy compound in separate formulations. In one embodiment, recombinant human erythropoietin is administered as the erythropoietin therapy.

10 Also provided herein is a use of an oligomeric compound targeted to a nucleic acid encoding hepcidin for the preparation of a medicament for the prevention, amelioration, and/or treatment of anemia. In one aspect, the compound is an antisense oligonucleotide targeted to a nucleic acid encoding hepcidin. Another embodiment provides for the use of an oligomeric composition targeted to a nucleic acid encoding hepcidin for the preparation of a medicament for  
15 the prevention, amelioration, and/or treatment of anemia. In one aspect the composition comprises an antisense oligonucleotide targeted to a nucleic acid encoding hepcidin and erythropoietin. In one aspect, the medicament is prepared for treatment of anemia in a patient being treated with erythropoietin. In one aspect, the cause of anemia is chronic inflammation, chronic kidney disease, kidney dialysis treatment, genetic disorders, chronic infection, acute infection, cancer or cancer  
20 treatments. In another embodiment, the anemia is anemia of chronic disease (ACD). In one embodiment, the medicament is formulated for delivery by injection.

#### **BRIEF DESCRIPTION OF THE FIGURES**

25 Figure 1. Western blot of liver lysate following treatment with antisense oligonucleotides targeting hepcidin mRNA and showing that the hepcidin polypeptide is reduced following treatment. Hepcidin was detected with hepcidin antibody (Alpha Diagnostics, HEPC11-A, 0.3 .micro.g/ml).

30 Figure 2. Graph illustrating that delivery of 10-75 mg/kg of antisense oligonucleotide targeting hepcidin mRNA reduces hepcidin expression and in turn leads to an increase in serum iron levels in normal mice.

Figure 3. Graph illustrating that antisense oligonucleotide reduction of hepcidin increases serum iron levels in both basal and LPS states in mice (N=4, SEM).

35 Figures 4a-d. Graphs illustrating responses to treatment with a compound that reduces the expression of mRNA encoding hepcidin for a number of clinical endpoints for anemia: a) serum levels; b) red blood cell count; c) hemoglobin levels; and d) hematocrit levels.

Figure 5 (a-c). Graphs illustrating the enhanced reticulocyte counts in turpentine-treated mice receiving erythropoietin and an antisense oligonucleotide targeted to hepcidin.

## DETAILED DESCRIPTION OF THE INVENTION

5 Anemia is a severely debilitating condition stemming from a lower than normal number of red blood cells (erythrocytes) in the blood that characterizes a number of diseases and conditions. Therapeutic interventions for these diseases or conditions are not completely satisfactory due to lack of efficacy and/or unwanted side effects of the compounds. Provided herein are methods, uses, compositions and compounds for the prevention, amelioration, and /or treatment  
10 of anemia. As used herein, the term "prevention" means to delay or forestall onset or development of a condition or disease for a period of time from hours to days, preferably weeks to months. As used herein, the term "amelioration" means a lessening of at least one indicator of the severity of a condition or disease. By way of example, some appropriate indicators include low serum iron (hypoferremia), low hemoglobin or hematocrit levels, decreased red blood cell or reticulocyte  
15 numbers, increased soluble transferrin receptor, iron restricted erythropoiesis; symptoms include fatigue, pallor and poor exercise tolerance. The severity of indicators may be determined by subjective or objective measures which are known to those skilled in the art. As used herein, "treatment" or "therapy" means to administer a composition of antisense compounds, erythropoietin (or other ESA), or of antisense compounds combined with erythropoietin (or other  
20 ESA) to effect an alteration or improvement of the disease or condition; the antisense compounds being targeted to a nucleic acid encoding hepcidin. Prevention, amelioration, and/or treatment may require administration of multiple doses at regular intervals, or prior to exposure to an agent (e.g., a chemotherapeutic) to alter the course of the condition or disease. Moreover, a single agent may be used in a single individual for each prevention, amelioration, and treatment of a condition or  
25 disease sequentially or concurrently. Moreover, the compounds and compositions disclosed herein may be administered or delivered to a patient who is receiving a particular therapy, compound, agent or composition. In this case, the receiving can occur prior to the method of administering or delivering, or it may occur simultaneously or following the administration or delivery of the compound or composition. Additionally, regardless of when the receiving begins relative to  
30 administration or delivery, it may continue after the administration or delivery.

Disclosed herein are antisense compounds, including antisense oligonucleotides, for use in modulating the expression of nucleic acid molecules encoding hepcidin. This modulation is accomplished by providing antisense compounds that are designed to target and hybridize with one or more target nucleic acid molecules encoding hepcidin (SEQ ID NOS: 1, 2 or 3.). As used  
35 herein, the terms "target nucleic acid" and "nucleic acid molecule encoding hepcidin" have been used for convenience to encompass RNA (including pre-mRNA and mRNA or portions thereof)

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transcribed from DNA encoding hepcidin and also cDNA derived from such RNA. In a preferred embodiment, the target nucleic acid is an mRNA encoding hepcidin.

### Target Nucleic Acids

5                   “Targeting” refers to the design and selection of antisense compounds capable of hybridizing to or complementary to a particular target nucleic acid molecule. Antisense compounds selected by this process are said to be “targeted to” the target nucleic acid molecule. Targeting can be a multistep process that usually begins with the identification of a target nucleic acid whose expression is to be modulated. For example, the target nucleic acid can be a cellular gene (or  
10 mRNA transcribed from the gene) whose expression is associated with a particular disorder or disease state, or a nucleic acid molecule from an infectious agent. As disclosed herein, the target nucleic acid encodes hepcidin.

### Variants

15                   It is also known in the art that alternative RNA transcripts can be produced from the same genomic region of DNA. These alternative transcripts are generally known as “variants.” More specifically, “pre-mRNA variants” are transcripts produced from the same genomic DNA that differ from other transcripts produced from the same genomic DNA in either their start or stop position and contain both intronic and exonic sequence. Variants can result in mRNA variants  
20 including, but not limited to, those with alternate splice junctions, or alternate initiation and termination codons. Variants in genomic and mRNA sequences can result in disease. Antisense compounds targeted to such variants are within the scope of the oligomeric compounds as described herein.

### 25 Target Names, Synonyms, Features

                  Accordingly, there are provided compositions and methods for modulating the expression of hepcidin. “Hepcidin” is also referred to as hepcidin antimicrobial peptide; HAMP; HAMP1; HEPC; HFE2; LEAP-1; LEAP1; and liver-expressed antimicrobial peptide. Herein the term “hepcidin” is used. Table 1 lists the GenBank accession numbers of sequences corresponding  
30 to nucleic acid molecules encoding hepcidin (nt = nucleotide), the date the version of the sequence was entered in GenBank, and the corresponding SEQ ID NO in the instant application, when assigned. Each sequence is incorporated herein by reference.

**Table 1**  
**Gene Targets**

| Species | Genbank #                                                       | Genbank Date      | SEQ ID NO |
|---------|-----------------------------------------------------------------|-------------------|-----------|
| Human   | BM719679.1                                                      | March 1, 2002     | 1         |
| Human   | NM_021175.2                                                     | July 23, 2004     | 2         |
| Human   | nucleotides 7819907 to 7825131 of NT_011196.11                  | January 5, 2003   | 3         |
| Mouse   | NM_032541.1                                                     | May 28, 2001      | 4         |
| Mouse   | the complement of nucleotides 3978217 to 3980665 of NT_039413.1 | February 24, 2003 | 5         |

### Modulation of Target Expression

- 5                   Modulation of expression of a target nucleic acid can be achieved through alteration of any number of nucleic acid functions. "Modulation" means a perturbation of function, for example, either an increase (stimulation or induction) or a decrease (inhibition or reduction) in expression. As another example, modulation of expression can include perturbing splice site selection of pre-mRNA processing. "Expression" includes all the functions by which a gene's
- 10                   coded information is converted into structures present and operating in a cell. These structures include the products of transcription and translation. "Modulation of expression" means the perturbation of such functions. The functions of RNA to be modulated can include translocation functions, which include, but are not limited to, translocation of the RNA to a site of protein translation, translocation of the RNA to sites within the cell which are distant from the site of RNA
- 15                   synthesis, and translation of protein from the RNA. RNA processing functions that can be modulated include, but are not limited to, splicing of the RNA to yield one or more RNA species, capping of the RNA, 3' maturation of the RNA and catalytic activity or complex formation involving the RNA which may be engaged in or facilitated by the RNA. Modulation of expression can result in the increased level of one or more nucleic acid species or the decreased level of one or
- 20                   more nucleic acid species, either temporally or by net steady state level. One result of such interference with target nucleic acid function is modulation of the expression of hepcidin. Thus, in one embodiment modulation of expression can mean increase or decrease in target RNA or protein levels. In another embodiment modulation of expression can mean an increase or decrease of one or more RNA splice products, or a change in the ratio of two or more splice products.
- 25                   The effect of antisense compounds on target nucleic acid expression can be tested in any of a variety of cell types provided that the target nucleic acid is present at measurable levels. The effect of antisense compounds on target nucleic acid expression can be routinely determined using, for example, PCR, Northern blot analysis or measurement of hepcidin polypeptide in the urine or serum of an animal (e.g., ELISA or Western blots). Cell lines are derived from both
- 30                   normal tissues and cell types and from cells associated with various disorders (e.g.

hyperproliferative disorders). Cell lines derived from multiple tissues and species can be obtained from American Type Culture Collection (ATCC, Manassas, VA) and other public sources, and are well known to those skilled in the art. Primary cells, or those cells which are isolated from an animal and not subjected to continuous culture, can be prepared according to methods known in the art, or obtained from various commercial suppliers. Additionally, primary cells include those obtained from donor human subjects in a clinical setting (i.e. blood donors, surgical patients). Primary cells are prepared by methods known in the art.

### Assaying Modulation of Expression

Modulation of hepcidin expression can be assayed in a variety of ways known in the art. Hepcidin mRNA levels can be quantitated by, e.g., Northern blot analysis, competitive polymerase chain reaction (PCR), or real-time PCR. RNA analysis can be performed on total cellular RNA or poly(A)<sup>+</sup> mRNA by methods known in the art. Methods of RNA isolation are taught in, for example, Ausubel, F.M. et al., *Current Protocols in Molecular Biology*, Volume 1, pp. 4.1.1-4.2.9 and 4.5.1-4.5.3, John Wiley & Sons, Inc., 1993.

Northern blot analysis is routine in the art and is taught in, for example, Ausubel, F.M. et al., *Current Protocols in Molecular Biology*, Volume 1, pp. 4.2.1-4.2.9, John Wiley & Sons, Inc., 1996. Real-time quantitative (PCR) can be conveniently accomplished using the commercially available ABI PRISM™ 7700 Sequence Detection System, available from PE-Applied Biosystems, Foster City, CA and used according to manufacturer's instructions. The method of analysis of modulation of RNA levels is not a limitation of the instant description.

Levels of a protein encoded by hepcidin can be quantitated in a variety of ways well known in the art, such as immunoprecipitation, Western blot analysis (immunoblotting), ELISA or fluorescence-activated cell sorting (FACS). Antibodies directed to a protein encoded by hepcidin can be identified and obtained from a variety of sources, such as the MSRS catalog of antibodies (Aerie Corporation, Birmingham, MI), or can be prepared via conventional antibody generation methods. Methods for preparation of polyclonal antisera are taught in, for example, Ausubel, F.M. et al., *Current Protocols in Molecular Biology*, Volume 2, pp. 11.12.1-11.12.9, John Wiley & Sons, Inc., 1997. Preparation of monoclonal antibodies is taught in, for example, Ausubel, F.M. et al., *Current Protocols in Molecular Biology*, Volume 2, pp. 11.4.1-11.11.5, John Wiley & Sons, Inc., 1997.

Immunoprecipitation methods are standard in the art and can be found at, for example, Ausubel, F.M. et al., *Current Protocols in Molecular Biology*, Volume 2, pp. 10.16.1-10.16.11, John Wiley & Sons, Inc., 1998. Western blot (immunoblot) analysis is standard in the art and can be found at, for example, Ausubel, F.M. et al., *Current Protocols in Molecular Biology*, Volume 2, pp. 10.8.1-10.8.21, John Wiley & Sons, Inc., 1997.

### Active Target Segments

The locations on the target nucleic acid defined by having one or more active antisense compounds targeted thereto are referred to as "active target segments." When an active target segment is validated by multiple antisense compounds, the compounds are preferably separated by no more than about 30 nucleotides on the active target segment, more preferably no more than about 10 nucleotides on the target sequence, even more preferably the compounds are contiguous, and most preferably the compounds are overlapping. In a preferred embodiment, at least 50%, preferably at least 70% of the oligonucleotides targeted to the active target segment modulate expression of their target RNA at least 40%. There may be substantial variation in activity (e.g., as defined by percent reduction or activity ranking) of each antisense compounds within an active target segment. Active antisense compounds are those that modulate the expression of their target RNA. Active antisense compounds reduce expression of their target RNA at least 10%, preferably at least 20%. In other embodiments at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or at least 99%. In a more preferred embodiment, the level of reduction required to define an active antisense compound is based on the results from the screen used to define the active target segments.

### Hybridization

As used herein, "hybridization" means the pairing of complementary strands of antisense compounds to their target sequence. While not limited to a particular mechanism, the most common mechanism of pairing involves hydrogen bonding, which may be Watson-Crick, Hoogsteen or reversed Hoogsteen hydrogen bonding, between complementary nucleoside or nucleotide bases (nucleobases). For example, the natural base adenine is complementary to the natural nucleobases thymidine and uracil which pair through the formation of hydrogen bonds. The natural base guanine is complementary to the natural base 5-methylcytosine and the artificial base known as a G-clamp. Hybridization can occur under varying circumstances.

An antisense compound is specifically hybridizable when there is a sufficient degree of complementarity to avoid non-specific binding of the antisense compound to non-target nucleic acid sequences under conditions in which specific binding is desired, i.e., under physiological conditions in the case of *in vivo* assays or therapeutic treatment, and under conditions in which assays are performed in the case of *in vitro* assays.

As used herein, "stringent hybridization conditions" or "stringent conditions" refers to conditions under which an antisense compound will hybridize to its target sequence, but to a minimal number of other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances, and "stringent conditions" under which antisense compounds

hybridize to a target sequence are determined by the nature and composition of the antisense compounds and the assays in which they are being investigated.

### Complementarity

5                   “Complementarity,” as used herein, refers to the capacity for precise pairing between two nucleobases on either two oligomeric compound strands or an antisense compound with its target nucleic acid. For example, if a nucleobase at a certain position of an antisense compound is capable of hydrogen bonding with a nucleobase at a certain position of a target nucleic acid, then the position of hydrogen bonding between the oligonucleotide and the target nucleic acid is considered to be a complementary position. The antisense compound and the further DNA or RNA are complementary to each other when a sufficient number of complementary positions in each molecule are occupied by nucleobases which can hydrogen bond with each other. Thus, “specifically hybridizable” and “complementary” are terms which are used to indicate a sufficient degree of precise pairing or complementarity over a sufficient number of nucleobases such that stable and specific binding occurs between the antisense compound and a target nucleic acid.

### Identity

                  Antisense compounds, or a portion thereof, may have a defined percent identity to a SEQ ID NO, or a compound having a specific CMPD number. As used herein, a sequence is identical to the sequence disclosed herein if it has the same nucleobase pairing ability. For example, an RNA which contains uracil in place of thymidine in the disclosed sequences would be considered identical as they both pair with adenine. Similarly, a G-clamp modified heterocyclic base would be considered identical to a cytosine or a 5-Me cytosine in the sequences of the instant application as it pairs with a guanine. This identity may be over the entire length of the oligomeric compound, or in a portion of the antisense compound (e.g., nucleobases 1-20 of a 27-mer may be compared to a 20-mer to determine percent identity of the antisense compound to the SEQ ID NO.) It is understood by those skilled in the art that an antisense compound need not have an identical sequence to those described herein to function similarly to the antisense compound described herein. Shortened versions of antisense compound taught herein, or non-identical versions of the antisense compound taught herein fall within the scope of the current disclosure. Non-identical versions are those wherein each base does not have the same pairing activity as the antisense compounds disclosed herein. In a preferred embodiment the antisense compounds can have about 3 mismatched base pairs. Bases do not have the same pairing activity by being shorter or having at least one abasic site. Alternatively, a non-identical version can include at least one base replaced with a different base with different pairing activity (e.g., G can be replaced by C, A, or T). Percent identity is calculated according to the number of bases that have identical base pairing

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corresponding to the SEQ ID NO or identical bases corresponding to the antisense compound to which it is being compared. The non-identical bases may be adjacent to each other, dispersed through out the oligonucleotide, or both.

5 For example, a 16-mer having the same sequence as nucleobases 2-17 of a 20-mer is 80% identical to the 20-mer. Alternatively, a 20-mer containing four nucleobases not identical to another 20-mer is also 80% identical to that other 20-mer. A 14-mer having the same sequence as nucleobases 1-14 of an 18-mer is 78% identical to the 18-mer. Such calculations are well within the ability of those skilled in the art.

10 The percent identity is based on the percent of nucleobases in the original sequence present in a portion of the modified sequence. Therefore, a 30 nucleobase antisense compound comprising the full sequence of the complement of a 20 nucleobase active target segment would have a portion of 100% identity with the complement of the 20 nucleobase active target segment, while further comprising an additional 10 nucleobase portion. Herein, the complement of an active target segment may constitute a single portion. In a preferred embodiment, the oligomeric  
15 compounds are at least about 80%, more preferably at least about 85%, even more preferably at least about 90%, most preferably at least 95% identical to at least a portion of the complement of the active target segments presented herein.

It is well known by those skilled in the art that it is possible to increase or decrease the length of an antisense compound and/or introduce mismatch bases without eliminating activity.  
20 For example, in Woolf et al. (Proc. Natl. Acad. Sci. USA 89:7305-7309, 1992, incorporated herein by reference), a series of ASOs 13-25 nucleobases in length were tested for their ability to induce cleavage of a target RNA in an oocyte injection model. ASOs 25 nucleobases in length with 8 or 11 mismatch bases near the ends of the ASOs were able to direct specific cleavage of the target mRNA, albeit to a lesser extent than the ASOs that contained no mismatches. Similarly, target  
25 specific cleavage was achieved using a 13 nucleobase ASOs, including those with 1 or 3 mismatches. Maher and Dolnick (Nuc. Acid. Res. 16:3341-3358, 1988, incorporated herein by reference) tested a series of tandem 14 nucleobase ASOs, and a 28 and 42 nucleobase ASOs comprised of the sequence of two or three of the tandem ASOs, respectively, for their ability to arrest translation of human DHFR in a rabbit reticulocyte assay. Each of the three 14 nucleobase  
30 ASOs alone were able to reduce translation, albeit at a more modest level than the 28 or 42 nucleobase ASOs.

### **Therapeutics**

35 The antisense compounds disclosed herein can be used to modulate the expression of hepcidin in an animal, such as a human. In one non-limiting embodiment, the methods comprise the step of administering to said animal in need of therapy for a disease or condition associated with

hepcidin an effective amount of an antisense compound that reduces expression of hepcidin. A disease or condition associated with hepcidin includes, but is not limited to, anemia. In one embodiment, the antisense compounds effectively reduce the levels or function of hepcidin RNA. Because reduction in hepcidin mRNA levels can lead to alteration in hepcidin protein products of expression as well, such resultant alterations can also be measured. Antisense compounds that effectively reduce the level or function of hepcidin RNA or protein products of expression are considered an active antisense compounds. In one embodiment, the antisense compounds reduce the expression of hepcidin causing a reduction of target RNA by at least about 10%, by at least about 20%, by at least about 25%, by at least about 30%, by at least about 40%, by at least about 50%, by at least about 60%, by at least about 70%, by at least about 75%, by at least about 80%, by at least about 85%, by at least about 90%, by at least about 95%, by at least about 98%, by at least about 99%, or by 100%.

For example, the reduction of the expression of hepcidin can be measured in a bodily fluid, tissue or organ of the animal. Methods of obtaining samples for analysis, such as body fluids (e.g., blood, serum or urine), tissues (e.g., biopsy), or organs, and methods of preparation of the samples to allow for analysis are well known to those skilled in the art. Methods for analysis of RNA and protein levels are discussed above and are well known to those skilled in the art. The effects of treatment can be assessed by measuring biomarkers associated with the hepcidin expression in the aforementioned fluids, tissues or organs, collected from an animal contacted with one or more oligomeric compounds targeted to a nucleic acid encoding hepcidin, by routine clinical methods known in the art. These biomarkers include but are not limited to: serum iron levels, hemoglobin levels, transferrin levels, iron restricted erythropoiesis, liver transaminases, bilirubin, albumin, blood urea nitrogen, creatine and other markers of kidney and liver function; interleukins, tumor necrosis factors, chemokines, cytokines and other markers of anemia.

The antisense compounds can be utilized in pharmaceutical compositions by adding an effective amount of a compound to a suitable pharmaceutically acceptable diluent or carrier. Acceptable carriers and dilutents are well known to those skilled in the art. Selection of a diluent or carrier is based on a number of factors, including, but not limited to, the solubility of the compound and the route of administration. Such considerations are well understood by those skilled in the art. In one aspect, the antisense compounds reduce the expression of hepcidin. The compounds can also be used in the manufacture of a medicament for the treatment of diseases and conditions related to hepcidin expression.

Methods whereby bodily fluids, organs or tissues are contacted with an effective amount of one or more of the antisense compounds or compositions are also contemplated. Bodily fluids, organs or tissues can be contacted with one or more of the antisense compounds resulting in modulation of hepcidin expression in the cells of bodily fluids, organs or tissues. An effective

amount can be determined by monitoring the modulatory effect of the antisense compound or compounds or compositions on target nucleic acids or their products by methods routine to the skilled artisan.

Thus, provided herein is the use of an isolated single- or double-stranded antisense  
5 compound targeted to hepcidin in the manufacture of a medicament for the treatment of a disease or disorder by means of the method described above. In a preferred embodiment, the antisense compound is a single stranded antisense compound. Also provided herein is the use of a composition comprising erythropoietin or other ESA and an antisense compound targeted to hepcidin in the manufacture of a medicament for the treatment of a disease or disorder by the  
10 means of the method described above.

#### **Kits, Research Reagents, and Diagnostics**

The antisense compounds can be utilized for diagnostics, and as research reagents and kits. Furthermore, antisense compounds, which are able to reduce gene expression with  
15 specificity, are often used by those of ordinary skill to elucidate the function of particular genes or to distinguish between functions of various members of a biological pathway.

For use in kits and diagnostics, the antisense compounds, either alone or in combination with other compounds or therapeutics, for example ESAs, can be used as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion or the entire  
20 complement of genes expressed within cells and tissues. Methods of gene expression analysis are well known to those skilled in the art.

#### **Compounds**

The term "oligomeric compound" refers to a polymeric structure capable of  
25 hybridizing to a region of a nucleic acid molecule. Generally, oligomeric compounds comprise a plurality of monomeric subunits linked together by internucleoside linking groups and/or internucleoside linkage mimetics. Each of the monomeric subunits comprises a sugar, abasic sugar, modified sugar, or a sugar mimetic, and except for the abasic sugar includes a nucleobase, modified nucleobase or a nucleobase mimetic. Preferred monomeric subunits comprise nucleosides and  
30 modified nucleosides.

An "antisense compound" or "antisense oligomeric compound" refers to an oligomeric compound that is at least partially complementary to the region of a target nucleic acid molecule to which it hybridizes and which modulates (increases or decreases) its expression. This term includes oligonucleotides, oligonucleosides, oligonucleotide analogs, oligonucleotide  
35 mimetics, antisense compounds, antisense oligomeric compounds, and chimeric combinations of these. Consequently, while all antisense compounds can be said to be oligomeric compounds, not

all oligomeric compounds are antisense compounds. An "antisense oligonucleotide" is an antisense compound that is a nucleic acid-based oligomer. An antisense oligonucleotide can, in some cases, include one or more chemical modifications to the sugar, base, and/or internucleoside linkages. Nonlimiting examples of antisense compounds include antisense compounds, antisense  
5 oligonucleotides, external guide sequence (EGS) oligonucleotides, alternate splicers, and siRNAs. As such, these compounds can be introduced in the form of single-stranded, double-stranded, circular, branched or hairpins and can contain structural elements such as internal or terminal bulges or loops. Antisense double-stranded compounds can be two strands hybridized to form double-stranded compounds or a single strand with sufficient self complementarity to allow for  
10 hybridization and formation of a fully or partially double-stranded compound. The oligomeric compounds are not auto-catalytic. As used herein, "auto-catalytic" means a compound has the ability to promote cleavage of the target RNA in the absence of accessory factors, e.g. proteins.

In one embodiment, the antisense compound comprises a single stranded oligonucleotide. In some embodiments the antisense compound contains chemical modifications.  
15 In a preferred embodiment, the antisense compound is a single stranded, chimeric oligonucleotide wherein the modifications of sugars, bases, and internucleoside linkages are independently selected.

The antisense compounds may comprise an antisense compound from about 12 to about 35 nucleobases (i.e. from about 12 to about 35 linked nucleosides). In other words, a single-stranded antisense compound comprises from about 12 to about 35 nucleobases, and a double-  
20 stranded antisense compound (such as a siRNA, for example) comprises two strands, each of which is independently from about 12 to about 35 nucleobases. This includes oligonucleotides 15 to 35 and 16 to 35 nucleobases in length. Contained within the antisense compounds (whether single or double stranded and on at least one strand) are antisense portions. The "antisense portion" is that part of the antisense compound that is designed to work by one of the aforementioned antisense  
25 mechanisms. One of ordinary skill in the art will appreciate that about 12 to about 35 nucleobases includes 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, or 35 nucleobases.

Antisense compounds about 12 to 35 nucleobases in length, preferably about 15 to 35 nucleobases in length, comprising a stretch of at least eight (8), preferably at least 12, more  
30 preferably at least 15 consecutive nucleobases selected from within the active target regions are considered to be suitable antisense compounds as well.

Modifications can be made to the antisense compounds and may include conjugate groups attached to one of the termini, selected nucleobase positions, sugar positions or to one of the internucleoside linkages. Possible modifications include, but are not limited to, 2'-fluoro (2'-F), 2'-  
35 OMethyl (2'-OMe), 2'-Methoxyethoxy (2'-MOE) sugar modifications, inverted abasic caps,

deoxynucleobases, and bicyclic nucleic acids such as locked nucleic acids (LNA) and ethylene nucleic acid (ENA).

In one embodiment, double-stranded antisense compounds encompass short interfering RNAs (siRNAs). As used herein, the term "siRNA" is defined as a double-stranded compound having a first and second strand, each strand having a central portion and two independent terminal portions. The central portion of the first strand is complementary to the central portion of the second strand, allowing hybridization of the strands. The terminal portions are independently, optionally complementary to the corresponding terminal portion of the complementary strand. The ends of the strands may be modified by the addition of one or more natural or modified nucleobases to form an overhang.

Each strand of the siRNA duplex may be from about 12 to about 35 nucleobases. In a preferred embodiment, each strand of the siRNA duplex is about 17 to about 25 nucleobases. The two strands may be fully complementary (i.e., form a blunt ended compound), or include a 5' or 3' overhang on one or both strands. Double-stranded compounds can be made to include chemical modifications as discussed herein.

### Chemical Modifications

As is known in the art, a nucleoside is a base-sugar combination. The base portion of the nucleoside is normally a heterocyclic base (sometimes referred to as a "nucleobase" or simply a "base"). The two most common classes of such heterocyclic bases are the purines and the pyrimidines. Nucleotides are nucleosides that further include a phosphate group covalently linked to the sugar portion of the nucleoside. For those nucleosides that include a pentofuranosyl sugar, the phosphate group can be linked to the 2', 3' or 5' hydroxyl moiety of the sugar. In forming oligonucleotides, the phosphate groups covalently link adjacent nucleosides to one another to form a linear polymeric compound. Within oligonucleotides, the phosphate groups are commonly referred to as forming the internucleoside backbone of the oligonucleotide. The normal linkage or backbone of RNA and DNA is a 3' to 5' phosphodiester linkage. It is often preferable to include chemical modifications in oligonucleotides to alter their activity. Chemical modifications can alter oligonucleotide activity by, for example: increasing affinity of an antisense oligonucleotide for its target RNA, increasing nuclease resistance, and/or altering the pharmacokinetics of the oligonucleotide. The use of chemistries that increase the affinity of an oligonucleotide for its target can allow for the use of shorter oligonucleotide compounds.

The term "nucleobase" or "heterocyclic base moiety" as used herein, refers to the heterocyclic base portion of a nucleoside. In general, a nucleobase is any group that contains one or more atom or groups of atoms capable of hydrogen bonding to a base of another nucleic acid. In addition to "unmodified" or "natural" nucleobases such as the purine nucleobases adenine (A) and

guanine (G), and the pyrimidine nucleobases thymine (T), cytosine (C) and uracil (U), many modified nucleobases or nucleobase mimetics known to those skilled in the art are amenable to the oligomeric compounds. The terms *modified nucleobase* and *nucleobase mimetic* can overlap but generally a modified nucleobase refers to a nucleobase that is fairly similar in structure to the parent nucleobase, such as for example a 7-deaza purine or a 5-methyl cytosine, whereas a nucleobase mimetic would include more complicated structures, such as for example a tricyclic phenoxazine nucleobase mimetic. Methods for preparation of the above noted modified nucleobases are well known to those skilled in the art.

Antisense compounds may also contain one or more nucleosides having modified sugar moieties. The furanosyl sugar ring of a nucleoside can be modified in a number of ways including, but not limited to, addition of a substituent group bridging two non-geminal ring atoms to form a bicyclic nucleic acid (BNA) and substitution of an atom or group such as -S-, -N(R)- or -C(R<sub>1</sub>)(R<sub>2</sub>) for the ring oxygen at the 4'-position. Modified sugar moieties are well known and can be used to alter, typically increase, the affinity of the antisense compound for its target and/or increase nuclease resistance. A representative list of preferred modified sugars includes but is not limited to bicyclic modified sugars (BNA's), including LNA and ENA (4'-(CH<sub>2</sub>)<sub>2</sub>-O-2' bridge); and substituted sugars, especially 2'-substituted sugars having a 2'-F, 2'-OCH<sub>2</sub> or a 2'-O(CH<sub>2</sub>)<sub>2</sub>-OCH<sub>3</sub> substituent group. Sugars can also be replaced with sugar mimetic groups among others. Methods for the preparations of modified sugars are well known to those skilled in the art.

Included herein are internucleoside linking groups that link the nucleosides or otherwise modified monomer units together thereby forming an antisense compound. The two main classes of internucleoside linking groups are defined by the presence or absence of a phosphorus atom. Representative phosphorus containing internucleoside linkages include, but are not limited to, phosphodiesters, phosphotriesters, methylphosphonates, phosphoramidate, and phosphorothioates. Representative non-phosphorus containing internucleoside linking groups include, but are not limited to, methylenemethylimino (-CH<sub>2</sub>-N(CH<sub>3</sub>)-O-CH<sub>2</sub>-), thiodiester (-O-C(O)-S-), thionocarbamate (-O-C(O)(NH)-S-); siloxane (-O-Si(H)<sub>2</sub>-O-); and N,N'-dimethylhydrazine (-CH<sub>2</sub>-N(CH<sub>3</sub>)-N(CH<sub>3</sub>)-). Antisense compounds having non-phosphorus internucleoside linking groups are referred to as oligonucleosides. Modified internucleoside linkages, compared to natural phosphodiester linkages, can be used to alter, typically increase, nuclease resistance of the antisense compound. Internucleoside linkages having a chiral atom can be prepared racemic, chiral, or as a mixture. Representative chiral internucleoside linkages include, but are not limited to, alkylphosphonates and phosphorothioates. Methods of preparation of phosphorous-containing and non-phosphorous-containing linkages are well known to those skilled in the art.

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As used herein the term "mimetic" refers to groups that are substituted for a sugar, a nucleobase, and/ or internucleoside linkage. Generally, a mimetic is used in place of the sugar or sugar-internucleoside linkage combination, and the nucleobase is maintained for hybridization to a selected target. Representative examples of a sugar mimetic include, but are not limited to, cyclohexenyl or morpholino. Representative examples of a mimetic for a sugar-internucleoside linkage combination include, but are not limited to, peptide nucleic acids (PNA) and morpholino groups linked by uncharged achiral linkages. In some instances a mimetic is used in place of the nucleobase. Representative nucleobase mimetics are well known in the art and include, but are not limited to, tricyclic phenoxazine analogs and universal bases (Berger et al., (2000) Nuc Acid Res., 28:2911-14, incorporated herein by reference). Methods of synthesis of sugar, nucleoside and nucleobase mimetics are well known to those skilled in the art.

As used herein the term "nucleoside" includes, nucleosides, abasic nucleosides, modified nucleosides, and nucleosides having mimetic bases and/or sugar groups.

As used herein, the term "oligonucleotide" refers to an oligomeric compound which is an oligomer or polymer of ribonucleic acid (RNA) or deoxyribonucleic acid (DNA). This term includes oligonucleotides composed of naturally- and non-naturally-occurring nucleobases, sugars and covalent internucleoside linkages, possibly further including non-nucleic acid conjugates.

Provided herein are compounds having reactive phosphorus groups useful for forming internucleoside linkages including for example phosphodiester and phosphorothioate internucleoside linkages. Methods of preparation and/or purification of precursors or antisense compounds are not a limitation of the compositions or methods described herein. Methods for synthesis and purification of DNA, RNA, and the antisense compounds are well known to those skilled in the art.

As used herein the term "chimeric antisense compound" refers to an antisense compound, having at least one sugar, nucleobase and/or internucleoside linkage that is differentially modified as compared to the other sugars, nucleobases and internucleoside linkages within the same oligomeric compound. The remainder of the sugars, nucleobases and internucleoside linkages can be independently modified or unmodified. In general a chimeric oligomeric compound will have modified nucleosides that can be in isolated positions or grouped together in regions that will define a particular motif. Any combination of modifications and or mimetic groups can comprise a chimeric oligomeric compound.

Chimeric oligomeric compounds typically contain at least one region modified so as to confer increased resistance to nuclease degradation, increased cellular uptake, and/or increased binding affinity for the target nucleic acid. An additional region of the oligomeric compound may serve as a substrate for enzymes capable of cleaving RNA:DNA or RNA:RNA

hybrids. By way of example, RNase H is a cellular endonuclease that cleaves the RNA strand of an RNA:DNA duplex. Activation of RNase H, therefore, results in cleavage of the RNA target, thereby greatly enhancing the efficiency of reduction of gene expression. Consequently, comparable results can often be obtained with shorter oligomeric compounds when chimeras are used, compared to for example phosphorothioate deoxyoligonucleotides hybridizing to the same target region. Cleavage of the RNA target can be routinely detected by gel electrophoresis and, if necessary, associated nucleic acid hybridization techniques known in the art.

Certain chimeric as well as non-chimeric oligomeric compounds can be further described as having a particular motif. As used in herein the term "motif" refers to the orientation of modified sugar moieties and/or sugar mimetic groups in an antisense compound relative to like or differentially modified or unmodified nucleosides. As used herein, the terms "sugars", "sugar moieties" and "sugar mimetic groups" are used interchangeably. Such motifs include, but are not limited to, gapped motifs, alternating motifs, fully modified motifs, hemimer motifs, blockmer motifs, and positionally modified motifs. The sequence and the structure of the nucleobases and type of internucleoside linkage is not a factor in determining the motif of an antisense compound.

As used herein the term "gapped motif" refers to an antisense compound comprising a contiguous sequence of nucleosides that is divided into 3 regions, an internal region (gap) flanked by two external regions (wings). The regions are differentiated from each other at least by having differentially modified sugar groups that comprise the nucleosides. In some embodiments, each modified region is uniformly modified (e.g. the modified sugar groups in a given region are identical); however, other motifs can be applied to regions. For example, the wings in a gapmer could have an alternating motif. The nucleosides located in the gap of a gapped antisense compound have sugar moieties that are different than the modified sugar moieties in each of the wings.

As used herein the term "alternating motif" refers to an antisense compound comprising a contiguous sequence of nucleosides comprising two differentially sugar modified nucleosides that alternate for essentially the entire sequence of the antisense compound, or for essentially the entire sequence of a region of an antisense compound.

As used herein the term "fully modified motif" refers to an antisense compound comprising a contiguous sequence of nucleosides wherein essentially each nucleoside is a sugar modified nucleoside having uniform modification.

As used herein the term "hemimer motif" refers to a sequence of nucleosides that have uniform sugar moieties (identical sugars, modified or unmodified) and wherein one of the 5'-end or the 3'-end has a sequence of from 2 to 12 nucleosides that are sugar modified nucleosides that are different from the other nucleosides in the hemimer modified antisense compound.

As used herein the term "blockmer motif" refers to a sequence of nucleosides that have uniform sugars (identical sugars, modified or unmodified) that is internally interrupted by a block of sugar modified nucleosides that are uniformly modified and wherein the modification is different from the other nucleosides. Methods of preparation of chimeric oligonucleotide compounds are well known to those skilled in the art.

As used herein the term "positionally modified motif" comprises all other motifs. Methods of preparation of positionally modified oligonucleotide compounds are well known to those skilled in the art.

The compounds described herein contain one or more asymmetric centers and thus give rise to enantiomers, diastereomers, and other stereoisomeric configurations that may be defined, in terms of absolute stereochemistry, as (R) or (S), alpha or beta, or as (D) or (L) such as for amino acids et al. The present description of oligomeric compounds is meant to include all such possible isomers, as well as their racemic and optically pure forms.

In one aspect, antisense compounds are modified by covalent attachment of one or more conjugate groups. Conjugate groups may be attached by reversible or irreversible attachments. Conjugate groups may be attached directly to antisense compounds or by use of a linker. Linkers may be mono- or bifunctional linkers. Such attachment methods and linkers are well known to those skilled in the art. In general, conjugate groups are attached to antisense compounds to modify one or more properties. Such considerations are well known to those skilled in the art.

### **Oligomer Synthesis**

Oligomerization of modified and unmodified nucleosides can be routinely performed according to literature procedures for DNA (*Protocols for Oligonucleotides and Analogs*, Ed. Agrawal (1993), Humana Press) and/or RNA (*Scaringe, Methods* (2001), 23, 206-217. Gait et al., *Applications of Chemically synthesized RNA in RNA: Protein Interactions*, Ed. Smith (1998), 1-36. Gallo et al., *Tetrahedron* (2001), 57, 5707-5713).

Antisense compounds can be conveniently and routinely made through the well-known technique of solid phase synthesis. Equipment for such synthesis is sold by several vendors including, for example, Applied Biosystems (Foster City, CA). Any other means for such synthesis known in the art may additionally or alternatively be employed. It is well known to use similar techniques to prepare oligonucleotides such as the phosphorothioates and alkylated derivatives. The current description is not limited by the method of antisense compound synthesis.

### **Oligomer Purification and Analysis**

Methods of oligonucleotide purification and analysis are known to those skilled in the art. Analysis methods include capillary electrophoresis (CE) and electrospray-mass spectroscopy. Such synthesis and analysis methods can be performed in multi-well plates. The methods described herein are not limited by the method of oligomer purification.

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#### **Salts, prodrugs and bioequivalents**

The antisense compounds comprise any pharmaceutically acceptable salts, esters, or salts of such esters, or any other functional chemical equivalent which, upon administration to an animal including a human, is capable of providing (directly or indirectly) the biologically active metabolite or residue thereof. Accordingly, for example, the disclosure is also drawn to prodrugs and pharmaceutically acceptable salts of the antisense compounds, pharmaceutically acceptable salts of such prodrugs, and other bioequivalents.

10

The term "prodrug" indicates a therapeutic agent that is prepared in an inactive or less active form that is converted to an active form (i.e., drug) within the body or cells thereof by the action of endogenous enzymes, chemicals, and/or conditions. In particular, prodrug versions of the oligonucleotides are prepared as SATE ((S-acetyl-2-thioethyl) phosphate) derivatives according to the methods disclosed in WO 93/24510 or WO 94/26764. Prodrugs can also include antisense compounds wherein one or both ends comprise nucleobases that are cleaved (e.g., phosphodiester backbone linkages) to produce the active compound.

15

The term "pharmaceutically acceptable salts" refers to physiologically and pharmaceutically acceptable salts of the compounds: i.e., salts that retain the desired biological activity of the parent compound and do not impart undesired toxicological effects thereto. Sodium salts of antisense oligonucleotides are useful and are well accepted for therapeutic administration to humans. In another embodiment, sodium salts of dsRNA compounds are also provided.

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#### **Combinations**

Compositions can contain two or more antisense compounds. In another related embodiment, compositions can contain one or more antisense compounds, particularly oligonucleotides, targeted to a first nucleic acid and one or more additional antisense compounds targeted to a second nucleic acid target. Alternatively, compositions can contain two or more antisense compounds targeted to different regions of the same nucleic acid target. Compositions can also include other non-antisense compound therapeutic agents. For example, disclosed herein are combinations comprising an antisense oligonucleotide targeted to hepcidin combined with erythropoietin. Two or more combined compounds may be used together or sequentially. Likewise, one or more compound and one or more therapeutic agent may be used together or sequentially. For example, disclosed herein are compounds and therapeutics and methods of use

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wherein the compounds are administered simultaneously, or at distinct timepoints. For example, an antisense oligonucleotide targeted to a nucleic acid encoding hepcidin can be administered either simultaneously with or at a distinct timepoint from erythropoietin.

## 5 Nonlimiting disclosure and incorporation by reference

While certain compounds, compositions and methods have been described with specificity in accordance with certain embodiments, the following examples serve only to illustrate the compounds and methods and are not intended to limit the same. Each of the references, GenBank accession numbers, and the like recited in the present application is incorporated herein  
10 by reference in its entirety.

### Example 1: Cell Types and Transfection Methods

The effect of oligomeric compounds on target nucleic acid expression was tested on the following cell types.

15 *Mouse Primary Hepatocytes:* Primary mouse hepatocytes were prepared from CD-1 mice purchased from Charles River Labs (Wilmington, MA). Primary mouse hepatocytes were routinely cultured in Hepatocyte Attachment Media supplemented with 10% fetal bovine serum, 1% penicillin/ streptomycin (both from Sigma-Aldrich, St. Louis, MO), 1% antibiotic-antimitotic (Invitrogen Life Technologies, Carlsbad, CA) and 10nM bovine insulin (Sigma-Aldrich, St. Louis,  
20 MO). Cells were seeded into 96-well plates (Falcon-Primaria #3872) coated with 0.1mg/ml collagen at a density of approximately 10,000 cells/well for use in oligomeric compound transfection experiments.

*HepG2:* The human hepatocarcinoma cell line was obtained from the American Type Culture Collection (Manassas, VA). HepG2 cells were routinely cultured in minimum  
25 essential medium (Eagle) with 2 mM L-glutamine and Earle's BSS (Cambrex, East Rutherford, NJ) adjusted to contain 1.5 g/L sodium bicarbonate, 0.1 mM non-essential amino acids, and 1.0 mM sodium pyruvate, 90%; fetal bovine serum, 10% (sigma-Aldrich, St. Louis, MO) at a temperature of 37.degrees.C. Cells were routinely passaged by trypsinization and dilution when they reached approximately 80% confluence. Cells were seeded into 96-well plates (Falcon-Primaria #3872) at a  
30 density of approximately 5000 cells/well for use in oligomeric compound transfection experiments.

When cells reached 65-75% confluency, they were treated with oligonucleotide. Oligonucleotide was mixed with LIPOFECTIN™ (Invitrogen Life Technologies, Carlsbad, CA) in OPTI-MEM™-1 reduced serum medium (Invitrogen Life Technologies, Carlsbad, CA) to achieve the desired concentration of oligonucleotide and a LIPOFECTIN™ concentration of 2.5 or 3  
35 .micro.g/mL per 100 nM oligonucleotide. This transfection mixture was incubated at room temperature for approximately 0.5 hours. For cells grown in 96-well plates, wells were washed

once with 100 .micro.L OPTI-MEM™-1 and then treated with 130 .micro.L of the transfection mixture. Cells were treated and data were obtained in duplicate or triplicate. After approximately 4-7 hours of treatment at 37.degrees.C, the medium containing the transfection mixture was replaced with fresh culture medium. Cells were harvested 16-24 hours after oligonucleotide treatment.

Control oligonucleotides were used to determine the optimal oligomeric compound concentration for a particular cell line. Furthermore, when oligomeric compounds were tested in oligomeric compound screening experiments or phenotypic assays, control oligonucleotides were tested in parallel.

The concentration of oligonucleotide used varied from cell line to cell line. To determine the optimal oligonucleotide concentration for a particular cell line, the cells were treated with a positive control oligonucleotide at a range of concentrations. The concentration of positive control oligonucleotide that resulted in about an 80% reduction of the target mRNA was then utilized as the screening concentration for new oligonucleotides in subsequent experiments for that cell line. If 80% reduction was not achieved, the lowest concentration of positive control oligonucleotide that resulted in a 60% reduction of the target mRNA was then utilized as the oligonucleotide screening concentration in subsequent experiments for that cell line. If 60% reduction was not achieved, that particular cell line was deemed as unsuitable for oligonucleotide transfection experiments.

#### **Example 2: Real-time Quantitative PCR Analysis of hepcidin mRNA Levels**

Quantitation of hepcidin mRNA levels was accomplished by real-time quantitative PCR using the ABI PRISM™ 7600, 7700, or 7900 Sequence Detection System (PE-Applied Biosystems, Foster City, CA) according to manufacturer's instructions.

Prior to quantitative PCR analysis, primer-probe sets specific to the hepcidin being measured were evaluated for their ability to be "multiplexed" with a GAPDH amplification reaction. After isolation the RNA was subjected to sequential reverse transcriptase (RT) reaction and real-time PCR, both of which were performed in the same well. RT and PCR reagents were obtained from Invitrogen Life Technologies (Carlsbad, CA). RT, real-time PCR was carried out in the same by adding 20 .micro.L PCR cocktail (2.5x PCR buffer minus MgCl.sub.2, 6.6 mM MgCl.sub.2, 375 .micro.M each of dATP, dCTP, dCTP and dGTP, 375 nM each of forward primer and reverse primer, 125 nM of probe, 4 Units RNase inhibitor, 1.25 Units PLATINUM® Taq, 5 Units MuLV reverse transcriptase, and 2.5x ROX dye) to 96-well plates containing 30 .micro.L total RNA solution (20-200 ng). The RT reaction was carried out by incubation for 30 minutes at 48.degrees.C. Following a 10 minute incubation at 95.degrees.C to activate the PLATINUM® Taq,

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40 cycles of a two-step PCR protocol were carried out: 95.degrees.C for 15 seconds (denaturation) followed by 60.degrees.C for 1.5 minutes (annealing/extension).

Gene target quantities obtained by RT, real-time PCR were normalized using either the expression level of GAPDH, a gene whose expression is constant, or by quantifying total RNA using RiboGreen™ (Molecular Probes, Inc. Eugene, OR). GAPDH expression was quantified by RT, real-time PCR, by being run simultaneously with the target, multiplexing, or separately. Total RNA was quantified using RiboGreen™ RNA quantification reagent (Molecular Probes, Inc. Eugene, OR).

170 .micro.L of RiboGreen™ working reagent (RiboGreen™ reagent diluted 1:350 in 10mM Tris-HCl, 1 mM EDTA, pH 7.5) was pipetted into a 96-well plate containing 30 .micro.L purified cellular RNA. The plate was read in a CytoFluor 4000 (PE Applied Biosystems) with excitation at 485nm and emission at 530nm.

The GAPDH PCR probes have JOE covalently linked to the 5' end and TAMRA or MGB covalently linked to the 3' end, where JOE is the fluorescent reporter dye and TAMRA or MGB is the quencher dye. In some cell types, primers and probe designed to a GAPDH sequence from a different species are used to measure GAPDH expression. For example, a human GAPDH primer and probe set is used to measure GAPDH expression in monkey-derived cells and cell lines.

Probes and primers for use in real-time PCR were designed to hybridize to target-specific sequences. The primers and probes and the target nucleic acid sequences to which they hybridize are presented in Table 2. The target-specific PCR probes have FAM covalently linked to the 5' end and TAMRA or MGB covalently linked to the 3' end, where FAM is the fluorescent dye and TAMRA or MGB is the quencher dye.

Table 2

## Hepcidin-specific primers and probes for use in real-time PCR

| Species | Target SEQ ID NO | Sequence Description | Sequence (5' to 3')          | SEQ ID NO |
|---------|------------------|----------------------|------------------------------|-----------|
| Human   | 2                | Forward Primer       | AGGAGGCGAGACACCCACTT         | 6         |
| Human   | 2                | Reverse Primer       | TCCCACACTTTGATCGATGACA       | 7         |
| Human   | 2                | Probe                | CATCTGCATTTTCTGCTGCGGCTG     | 8         |
| Mouse   | 4                | Forward Primer       | TGCAGAAGAGAAGGAAGAGAGACA     | 9         |
| Mouse   | 4                | Reverse Primer       | CACACTGGGAATTGTTACAGCATT     | 10        |
| Mouse   | 4                | Probe                | CAACTTCCCCATCTGCATCTTCTGCTGT | 11        |

**Example 3: Antisense reduction of human hepcidin expression by oligomeric compounds**

A series of antisense oligonucleotide compounds was designed to target different regions of human hepcidin RNA, using published sequences or portions of published sequences as

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cited in Table 1. The compounds are shown in Table 3. Methods for designing and testing antisense oligonucleotides for reduction of mRNA target expression are discussed herein and well known to those skilled in the art. Although an antisense oligonucleotide is reported in Table 3 as being targeted to a particular sequence, one ordinarily skilled in the art will know that these sequences may also target other sequences. For example, in Table 3 SEQ ID NO: 50 is reportedly designed to target nucleotides 261 to 280 of SEQ ID NO: 2. However, SEQ ID NO: 50 is also fully complementary to nucleotides 486 to 505 of SEQ ID NO: 1 and nucleotides 4662 to 4681 of SEQ ID NO: 3.

The compounds were analyzed for their effect on target mRNA levels by using quantitative real time RT-PCR as described above. The screen identified active target segments within these regions of the human hepcidin mRNA sequence and the genomic sequence encoding hepcidin mRNA, specifically GenBank numbers BM719679.1; NM\_021175.2; and nucleotides 7819907 to 7825131 of NT\_011196.11 (SEQ ID NOS: 1; 2; and 3, respectively). The activity of these antisense oligonucleotides to reduce hepcidin mRNA expression is ranked as follows: +++++ (reduction of target by greater than about 70%), ++++ (reduction of target by greater than about 70% to about 74%), +++ (reduction of target by greater than about 60% to about 69%), ++ (reduction of target by greater than about 55% to about 60%), + (reduction of target by greater than about 50% to about 55%) or bc (below cut-off or lesser than about 50%). Antisense compounds having an activity ranking of bc may have shown some reduction of hepcidin expression but fell below the cut-off level for this screening assay.

**Table 3**  
**Reduction of Human Hepcidin mRNA Levels by Antisense Oligonucleotides**

| CMPD # | Target SEQ ID NO | Target Start Site | Sequence (5' to 3')  | Activity Ranking | SEQ ID NO |
|--------|------------------|-------------------|----------------------|------------------|-----------|
| 392287 | 1                | 32                | AATGCACAGGCCCTGCCATC | +                | 12        |
| 392288 | 1                | 38                | CACAGAAATGCACAGGCCCT | bc               | 13        |
| 392289 | 1                | 43                | TCAAGCACAGAAATGCACAG | bc               | 14        |
| 392290 | 1                | 48                | CCCACTCAAGCACAGAAATG | bc               | 15        |
| 392291 | 1                | 53                | CAAGGCCCACTCAAGCACAG | +++              | 16        |
| 392292 | 1                | 58                | ACTTTCAAGGCCCACTCAAG | ++++             | 17        |
| 392280 | 1                | 66                | GCTGAACCACTTTCAAGGCC | bc               | 18        |
| 392281 | 1                | 71                | TGGTTGCTGAACCACTTTCA | bc               | 19        |
| 392282 | 1                | 91                | GAGGAATGAACACTTCTTCC | bc               | 20        |
| 392283 | 1                | 96                | TTGTCGAGGAATGAACACTT | ++               | 21        |
| 392284 | 1                | 101               | TGTTGTTGTCGAGGAATGAA | bc               | 22        |
| 392285 | 1                | 123               | CCAAGTCACCAGAGCCCGGG | +++++            | 23        |
| 392286 | 1                | 128               | GTCAGCCAAGTCACCAGAGC | +++++            | 24        |
| 392304 | 1                | 133               | CCAGTGTCAGCCAAGTCACC | bc               | 25        |

| CMPD # | Target SEQ ID NO | Target Start Site | Sequence (5' to 3')   | Activity Ranking | SEQ ID NO |
|--------|------------------|-------------------|-----------------------|------------------|-----------|
| 392305 | 1                | 138               | GCCATCCAGTGTCAGCCAAG  | +                | 26        |
| 392306 | 1                | 143               | CCAGGGCCATCCAGTGTCAG  | +++              | 27        |
| 392307 | 1                | 148               | TCATTCAGGGCCATCCAGT   | ++++             | 28        |
| 392308 | 1                | 153               | CTTTTCATTCAGGGCCAT    | ++               | 29        |
| 392309 | 1                | 179               | GGCCCTTGCACATTTTGCCT  | +                | 30        |
| 392293 | 1                | 186               | CCAGATGGGCCCTTGCACAT  | ++++             | 31        |
| 392294 | 1                | 191               | TGGTTCAGATGGGCCCTTG   | bc               | 32        |
| 392295 | 1                | 196               | GGCCTTGGTTCAGATGGGC   | +++              | 33        |
| 392296 | 1                | 215               | GTGACAGTCGCTTTTATGGG  | bc               | 34        |
| 392297 | 1                | 220               | ACCGAGTGACAGTCGCTTTT  | bc               | 35        |
| 392298 | 1                | 225               | CTGGGACCGAGTGACAGTCG  | +                | 36        |
| 392299 | 1                | 547               | CAGGGCAGGTAGGTTCTACG  | +++              | 37        |
| 392316 | 2                | 3                 | TGTCTGGGACCGAGTGACAG  | bc               | 38        |
| 392323 | 2                | 8                 | TCTGGTGTCTGGGACCGAGT  | +                | 39        |
| 392318 | 2                | 70                | CTGGGAGCTCAGTGCCATCG  | +++++            | 40        |
| 392319 | 2                | 75                | CAGATCTGGGAGCTCAGTGC  | bc               | 41        |
| 392300 | 2                | 127               | AGAGCCACTGGTCAGGCTGG  | +++++            | 42        |
| 392320 | 2                | 132               | AAAACAGAGCCACTGGTCAG  | bc               | 43        |
| 392302 | 2                | 137               | GTGGGAAAACAGAGCCACTG  | +++              | 44        |
| 392310 | 2                | 161               | GCTCTGCAAGTTGTCCCGTC  | +++              | 45        |
| 392311 | 2                | 166               | TTGCAGCTCTGCAAGTTGTC  | bc               | 46        |
| 392303 | 2                | 212               | GGAACATGGGCATCCAGCTG  | bc               | 47        |
| 392313 | 2                | 217               | CCTCTGGAACATGGGCATCC  | ++++             | 48        |
| 392314 | 2                | 242               | GGAAGTGGGTGTCTCGCCTC  | +++++            | 49        |
| 392315 | 2                | 261               | CAGCAGAAAATGCAGATGGG  | +++++            | 50        |
| 392326 | 2                | 268               | GCAGCCGCAGCAGAAAATGC  | +++++            | 51        |
| 392327 | 2                | 273               | TGACAGCAGCCGCAGCAGAA  | +++              | 52        |
| 392328 | 2                | 278               | ATCGATGACAGCAGCCGCAG  | +++++            | 53        |
| 392330 | 2                | 287               | CACACTTGTATCGATGACAG  | ++               | 54        |
| 392329 | 2                | 292               | CATCCACACTTTGATCGAT   | ++++             | 55        |
| 392321 | 2                | 297               | CAGCACATCCACACTTTGA   | ++               | 56        |
| 392322 | 2                | 302               | TCTTGCAGCACATCCACAC   | bc               | 57        |
| 392301 | 2                | 382               | TTATCCAAGACCTATGTTC   | ++               | 58        |
| 392317 | 2                | 390               | CAGCCATTTTATTCCAAGAC  | +++              | 59        |
| 392324 | 2                | 395               | AGAACCAGCCATTTTATTCC  | bc               | 60        |
| 392325 | 2                | 400               | ACAAAAGAACCAGCCATTTT  | bc               | 61        |
| 392340 | 3                | 2917              | CCTGACCAGGATGGAGAAAT  | +++              | 62        |
| 392341 | 3                | 2924              | CAAATTCCTGACCAGGATG   | +                | 63        |
| 392339 | 3                | 2929              | TTTAACAAATTCCTGACCA   | bc               | 64        |
| 392338 | 3                | 2934              | CAGTCTTTAACAAATTCCT   | bc               | 65        |
| 392344 | 3                | 2942              | GTTTTCATCAGTCTTTAACA  | +++              | 66        |
| 392343 | 3                | 2963              | TAGACACAATTATTTATTCA  | bc               | 67        |
| 392342 | 3                | 2968              | TGTA CTAGACACAATTATTT | ++               | 68        |
| 392332 | 3                | 2973              | TAGAATGTACTAGACACAAT  | +                | 69        |
| 392333 | 3                | 2982              | ATTCACGAATAGAATGTACT  | +++              | 70        |
| 392331 | 3                | 2987              | ATGAGATTCACGAATAGAAT  | bc               | 71        |
| 392337 | 3                | 3018              | ATGGGTCACGGTCACTCTAC  | ++               | 72        |
| 392336 | 3                | 3023              | GGCGAATGGGTCACGGTCAC  | +++              | 73        |
| 392335 | 3                | 3028              | TGTGTGGCGAATGGGTCACG  | bc               | 74        |

| CMPD # | Target SEQ ID NO | Target Start Site | Sequence (5' to 3')  | Activity Ranking | SEQ ID NO |
|--------|------------------|-------------------|----------------------|------------------|-----------|
| 392334 | 3                | 3227              | CAGCCCCTTGACCATGCCTG | ++++             | 75        |
| 392357 | 3                | 3260              | TGTCACCTTCTCATGAAACA | +++              | 76        |
| 392356 | 3                | 3278              | TCCAAGACGAAGGTCAACTG | bc               | 77        |
| 392355 | 3                | 3349              | TTGTTCAGCCTGACCCTGGG | +++++            | 78        |
| 392354 | 3                | 3375              | TTATCCCCAAGTCCCACCAT | bc               | 79        |
| 392353 | 3                | 3383              | CCTCAGCCTTATCCCCAAGT | bc               | 80        |
| 392352 | 3                | 3398              | TAGGGACTGCCACCCCTCA  | +++++            | 81        |
| 392348 | 3                | 3420              | CTGCATGGTTGCCACAAGA  | ++++             | 82        |
| 392347 | 3                | 3425              | AGTGCTGCATGGTTGCCCA  | +++++            | 83        |
| 392346 | 3                | 3430              | AAATCAGTGTCTGCATGGTT | +++++            | 84        |
| 392345 | 3                | 3435              | AGGAAAATCAGTGTCTGCA  | ++++             | 85        |
| 392351 | 3                | 3782              | TCCATTTTAAAAACCTACAG | bc               | 86        |
| 392350 | 3                | 3803              | GCCAGTGAGATTGTGGTTTT | bc               | 87        |
| 392349 | 3                | 3808              | ACATGGCCAGTGAGATTGTG | +++              | 88        |
| 392312 | 3                | 4516              | GGCATCCAGCTGGCCCTGGC | ++++             | 89        |

Each active target segment was targeted by multiple, active antisense oligonucleotides. This current example includes identification of active target segments identified on SEQ ID NO: 1, which active target segments are referred to as Regions A-E. The active target segments include nucleotides 456 to 527 for Region A, nucleotides 123 to 252 for Region B, nucleotides 352 to 405 for Region C, nucleotides 429 to 566 for Region D, and nucleotides 295 to 566 for Region E. Each of the oligonucleotides tested within Region A reduced expression of human hepcidin at least 55% (activity ranking ++). Four-fifths of the oligonucleotides tested in this region reduced expression by at least 75% (activity ranking +++++). Moreover, in Region D more than four-fifths of the oligonucleotides tested reduced expression by at least 55% (activity ranking ++) and more than one-half reduced expression by at least 70% (activity ranking +++++). In Region E, three-fourths of the oligonucleotides tested reduced expression by at least 50% (activity ranking +) and nearly one-half reduced expression by at least 70% (activity ranking +++++). Other active target segments on SEQ ID NO: 1 include Region C where three-fourths of the oligonucleotides tested reduced expression by at least 60% (activity ranking +++), and Region B where two-thirds of the oligonucleotides tested reduce expression by at least 50% (activity ranking +).

Active target segments were also identified on SEQ ID NO: 2 and SEQ ID NO: 3. The active target segments of SEQ ID NO: 2 are referred to as Regions F and G. Region F includes nucleotides 231 to 302. All of the nucleotides tested in Region F reduce expression by at least 55% (activity ranking ++), and two-thirds reduce at least 70% (activity ranking +++++). Region G includes nucleotides 204 to 341. More than four-fifths of the nucleotides tested in Region G reduce expression by at least 55% (activity ranking ++) and more than one-half reduce expression by at least 70% (activity ranking +++++).

The active target segments of SEQ ID NO: 3 are referred to as Regions H-K. Region H includes nucleotides 3398 to 3454 and all of the oligonucleotides tested in this region reduce expression by at least 70% (activity ranking ++++). Region I includes nucleotides 3249 to 3454. In Region I, three-fourths of the oligonucleotides tested reduced expression by at least 70% (activity ranking ++++) and one-half reduce by at least 75% (activity ranking +++++). Region J includes nucleotides 4643 to 4703. All of the oligonucleotides tested in this region reduce expression by at least 60% (activity ranking ++++) and four-fifths reduce expression by at least 75% (activity ranking +++++). Region K includes nucleotides 4643 to 4743 and at least one-half of the oligonucleotides tested in this region reduce expression by at least 70% (activity ranking ++++).

Thus, Applicant has discovered regions of the human hepcidin mRNA that are highly active in response to antisense reduction. Identification of these regions allows for the design of antisense oligonucleotides that will modulate the expression of hepcidin. Antisense oligonucleotides can be designed the active target segments with at least a + activity ranking, more preferably with at least a ++ activity ranking and most preferably with a +++ activity ranking. One skilled in the art will readily recognize that the percent reduction is referred to herein as a relative amount of reduction compared to other oligonucleotides tested against SEQ ID NOS: 1, 2 or 3. Assay to assay variations in conditions results in changes from the absolute data received, however, the general trends and relative reduction will be substantially the same.

#### **Example 4: Antisense reduction of mouse hepcidin expression by oligomeric compounds**

A series of antisense compounds was designed to target different regions of mouse hepcidin RNA, using published sequences or portions of published sequences as cited in Table 1. The compounds are shown in Table 4. The screen identified active target segments within these regions of the human hepcidin mRNA sequence and the genomic sequence encoding hepcidin mRNA, specifically GenBank numbers NM\_032541.1 and the complement of nucleotides 3978217 to 3980665 of NT\_039413.1 (SEQ ID NOS: 4 and 5, respectively). The activity of these antisense oligonucleotides are ranked based on measured percent reduction of the target from this study. The activity of these antisense oligonucleotides to reduce hepcidin mRNA expression is ranked as follows: +++++ (reduction of target by greater than about 70%), ++++ (reduction of target by greater than about 70% to about 74%), +++ (reduction of target by greater than about 60% to about 69%), ++ (reduction of target by greater than about 55% to about 60%), + (reduction of target by greater than about 50% to about 55%) or bc (below cut-off or lesser than about 50%). Antisense compounds having an activity ranking of bc may have shown some reduction of hepcidin expression but fell below the cut-off level for this screening assay.

**Table 4**  
**Reduction of Mouse Hepcidin mRNA Levels by Antisense Oligonucleotides**

| CMPD # | Target SEQ ID NO | Target Start Site | Sequence (5' to 3')   | Activity Ranking | SEQ ID NO |
|--------|------------------|-------------------|-----------------------|------------------|-----------|
| 326810 | 4                | 1                 | TGCTGTGCAGTCTAAGGACT  | +++              | 90        |
| 326811 | 4                | 6                 | TGTTCTGCTGTGCAGTCTAA  | bc               | 91        |
| 326812 | 4                | 10                | CTTCTGTTCTGCTGTGCAGT  | ++               | 92        |
| 326813 | 4                | 15                | CATGCCTTCTGTTCTGCTGT  | ++++             | 93        |
| 326814 | 4                | 17                | ATCATGCCTTCTGTTCTGCT  | +++              | 94        |
| 326815 | 4                | 22                | GTGCCATCATGCCTTCTGTT  | +++++            | 95        |
| 326816 | 4                | 24                | GAGTGCCATCATGCCTTCTG  | ++++             | 96        |
| 326817 | 4                | 27                | GCTGAGTGCCATCATGCCTT  | +++++            | 97        |
| 326818 | 4                | 29                | GTGCTGAGTGCCATCATGCC  | +++              | 98        |
| 326819 | 4                | 32                | CGAGTGCTGAGTGCCATCAT  | bc               | 99        |
| 326820 | 4                | 37                | GGGTCCGAGTGCTGAGTGCC  | +++              | 100       |
| 326821 | 4                | 41                | GCCTGGGTCCGAGTGCTGAG  | +++              | 101       |
| 326822 | 4                | 45                | GGCAGCCTGGGTCCGAGTGC  | +++++            | 102       |
| 326823 | 4                | 50                | AGACAGGCAGCCTGGGTCCG  | bc               | 103       |
| 326824 | 4                | 55                | GCAGGAGACAGGCAGCCTGG  | +++++            | 104       |
| 326825 | 4                | 71                | CTGGCAAGGAGGAGAAGCAG  | bc               | 105       |
| 326826 | 4                | 80                | CTGCTCAGGCTGGCAAGGAG  | bc               | 106       |
| 326827 | 4                | 84                | GGTGCTGCTCAGGCTGGCAA  | bc               | 107       |
| 326828 | 4                | 86                | GTGGTGCTGCTCAGGCTGGC  | bc               | 108       |
| 326829 | 4                | 88                | AGGTGGTGCTGCTCAGGCTG  | ++++             | 109       |
| 326830 | 4                | 89                | TAGGTGGTGCTGCTCAGGCT  | +++              | 110       |
| 326831 | 4                | 90                | ATAGGTGGTGCTGCTCAGGC  | +                | 111       |
| 326832 | 4                | 91                | GATAGGTGGTGCTGCTCAGG  | bc               | 112       |
| 326833 | 4                | 98                | TGATGGAGATAGGTGGTGCT  | bc               | 113       |
| 326834 | 4                | 99                | TTGATGGAGATAGGTGGTGCT | bc               | 114       |
| 326835 | 4                | 104               | ATCTGTTGATGGAGATAGGT  | bc               | 115       |
| 326836 | 4                | 105               | CATCTGTTGATGGAGATAGG  | bc               | 116       |
| 326837 | 4                | 112               | TCTGTCTCATCTGTTGATGG  | bc               | 117       |
| 326838 | 4                | 115               | TAGTCTGTCTCATCTGTTGA  | bc               | 118       |
| 326839 | 4                | 116               | GTAGTCTGTCTCATCTGTTG  | bc               | 119       |
| 326840 | 4                | 121               | GCTCTGTAGTCTGTCTCATC  | +                | 120       |
| 326841 | 4                | 124               | GCAGCTCTGTAGTCTGTCTC  | +++++            | 121       |
| 326842 | 4                | 127               | GCTGCAGCTCTGTAGTCTGT  | bc               | 122       |
| 326843 | 4                | 130               | AAGGCTGCAGCTCTGTAGTC  | +++              | 123       |
| 326844 | 4                | 135               | GTGCAAAGGCTGCAGCTCTG  | +++              | 124       |
| 326845 | 4                | 141               | TTCCCCGTGCAAAGGCTGCA  | bc               | 125       |
| 326846 | 4                | 145               | TTTCTTCCCCGTGCAAAGGC  | ++               | 126       |
| 326847 | 4                | 148               | TGCTTTCTTCCCCGTGCAAA  | bc               | 127       |
| 326848 | 4                | 158               | ATGTCTGCCCTGCTTTCTTC  | bc               | 128       |
| 326849 | 4                | 172               | GCATTGGTATCGCAATGTCT  | +                | 129       |
| 326850 | 4                | 176               | TTCTGCATTGGTATCGCAAT  | bc               | 130       |
| 326851 | 4                | 180               | TCTCTTCTGCATTGGTATCG  | bc               | 131       |
| 326852 | 4                | 200               | AAGTTGGTGTCTCTCTTCTT  | ++               | 132       |
| 326853 | 4                | 203               | GGGAAGTTGGTGTCTCTCTT  | +++++            | 133       |
| 326854 | 4                | 225               | TTACAGCAGAAGATGCAGA   | bc               | 134       |

| CMPD # | Target SEQ ID NO | Target Start Site | Sequence (5' to 3')   | Activity Ranking | SEQ ID NO |
|--------|------------------|-------------------|-----------------------|------------------|-----------|
| 326855 | 4                | 229               | AGCATTTACAGCAGAAGATG  | ++               | 135       |
| 326856 | 4                | 231               | ACAGCATTTACAGCAGAAGA  | +                | 136       |
| 326857 | 4                | 233               | TTACAGCATTTACAGCAGAA  | +++              | 137       |
| 326858 | 4                | 238               | AATTGTTACAGCATTTACAG  | bc               | 138       |
| 326859 | 4                | 242               | TGGGAATTGTTACAGCATTT  | bc               | 139       |
| 326860 | 4                | 245               | CACTGGGAATTGTTACAGCA  | bc               | 140       |
| 326861 | 4                | 252               | GATACCACACTGGGAATTGT  | bc               | 141       |
| 326862 | 4                | 256               | AACAGATACCACACTGGGAA  | bc               | 142       |
| 326863 | 4                | 258               | GCAACAGATACCACACTGGG  | ++++             | 143       |
| 326864 | 4                | 261               | TTTGCAACAGATACCACACT  | +++              | 144       |
| 326865 | 4                | 263               | GTTTGTGCAACAGATACCACA | +                | 145       |
| 326866 | 4                | 266               | TATGTTTTGCAACAGATACC  | bc               | 146       |
| 326867 | 4                | 275               | GCTCTAGGCTATGTTTTGCA  | ++++             | 147       |
| 326868 | 4                | 287               | GGTCAGGATGTGGCTCTAGG  | ++++             | 148       |
| 326869 | 4                | 291               | GAGAGGTCAGGATGTGGCTC  | ++++             | 149       |
| 326870 | 4                | 293               | TAGAGAGGTCAGGATGTGGC  | ++++             | 150       |
| 326871 | 4                | 296               | GTGTAGAGAGGTCAGGATGT  | ++++             | 151       |
| 326872 | 4                | 334               | AGGGCAGGAATAAATAATGG  | bc               | 152       |
| 326873 | 4                | 336               | GGAGGGCAGGAATAAATAAT  | bc               | 153       |
| 326874 | 4                | 355               | ATTTCAAGGTCATTGGTGGG  | bc               | 154       |
| 326875 | 4                | 357               | TTATTTCAAGGTCATTGGTG  | +++              | 155       |
| 326876 | 4                | 362               | CGTCTTTATTTCAAGGTCAT  | ++++             | 156       |
| 326877 | 4                | 367               | AAAATCGTCTTTATTTCAAG  | bc               | 157       |
| 326878 | 4                | 369               | ATAAAATCGTCTTTATTTCA  | bc               | 158       |
| 326879 | 4                | 371               | AAATAAAATCGTCTTTATTT  | bc               | 159       |
| 326880 | 5                | 512               | GGGTGCTCACCTGTTGATGG  | bc               | 160       |
| 326881 | 5                | 1239              | TGCTTACTGCTGACTGCCAT  | +                | 161       |
| 326882 | 5                | 1244              | ATGCATGCTTACTGCTGACT  | +                | 162       |
| 326883 | 5                | 1259              | GCCTATGTGTATCATATGCA  | ++               | 163       |
| 326884 | 5                | 1347              | CAGCAGAACCTCTACAGCCC  | bc               | 164       |
| 326885 | 5                | 1686              | TCTGTCTCATCTGTGAAAGC  | bc               | 165       |
| 326886 | 5                | 1746              | ATGCTCTTACCGCAATGTCT  | bc               | 166       |
| 326887 | 5                | 1829              | GCATTGGTATCTGTGTAAAG  | +                | 167       |

Each active target segment was targeted by multiple, active antisense oligonucleotides. This current example includes identification of active target segments identified on SEQ ID NO: 4, which active target segments are referred to as Regions L-O. The active target segments include nucleotides 287 to 315 for Region L, nucleotides 258 to 315 for Region M, nucleotides 1 to 74 for Region N, and nucleotides 80 to 199 for Region O. Each of the oligonucleotides tested within Region L reduced expression by at least 70% (++++) and three-fourths of them by at least 75% (+++++). Two-thirds of the oligonucleotides tested within Region M reduced expression by at least 70% (++++). About one-half of the oligonucleotides tested in Region N reduced expression by at least 70% (++++). This screen also identified regions with low activity when targeted with an antisense oligonucleotide. In Region O more than two-thirds of the

oligonucleotides tested reduced expression by less than 50% (bc) and more than three-fifths by less than 35% (bc).

The active target segments for SEQ ID NO: 5 are referred to as Regions P-R. Region P includes nucleotides 1942 to 1972 and all of the oligonucleotides tested in this region  
 5 reduce expression by at least 70% (+++). Region Q includes nucleotides 1991 to 2047 and three-fourths of the oligonucleotides tested in this region reduced expression by less than 50% (bc), and thus is considered a low-activity region. Similarly, for Region R, which includes nucleotides 474 to 531, more than two-thirds of the oligonucleotides tested in this region reduce expression by less than 50% (bc).

10 Thus, Applicant has discovered regions of the hepcidin mRNA that are highly responsive to antisense reduction and regions of the hepcidin mRNA that are less responsive to antisense reduction. Identification of these regions allows for the design of antisense oligonucleotides that will modulate the expression of hepcidin. One skilled in the art will readily recognize that the percent reduction is referred to herein as a relative amount of reduction compared  
 15 to other oligonucleotides tested against SEQ ID NOS: 4 or 5. Assay to assay variations in conditions will results in changes from the absolute data received, however, the general trends and relative reduction will be substantially the same.

**Example 5: Antisense Oligonucleotides from about 12 to about 35 Nucleobases.**

20 As stated above, antisense oligonucleotides directed to a target or more preferably to an active target segment can be from about 12 to about 35 linked nucleobases. The following Table 5a provides a non-limiting example of such antisense oligonucleotides targeting SEQ ID NO 4.

25 **Table 5a**  
**Antisense Oligonucleotides from about 12 to about 35 Nucleobases**

| Sequence                             | Length                          |
|--------------------------------------|---------------------------------|
| GGTCAGGATGTGGCTCTAGG                 | 20 nucleobases (SEQ ID NO: 148) |
| GGTCAGGATGTGGCT                      | 15 nucleobases (SEQ ID NO: 170) |
| CAGGATGTGGCTCTA                      | 15 nucleobases (SEQ ID NO: 171) |
| GTCAGGATGTGG                         | 12 nucleobases (SEQ ID NO: 172) |
| GAGAGGTCAGGATGTGGCTCTAGGCTATGTTTTGCA | 35 nucleobases (SEQ ID NO: 173) |
| GTCAGGATGTGGCTCTAGGCTATGTTTT         | 27 nucleobases (SEQ ID NO: 174) |
| TGTGGCTCTAGGCTATGTTTTGC              | 22 nucleobases (SEQ ID NO: 175) |

Antisense oligonucleotides directed to a target or more preferably to an active target segment can also contain mismatched nucleobases when compared to the target sequence. The following Table 5b provides a non-limiting example of such antisense oligonucleotides targeting nucleobases 287 to 306 of SEQ ID NO 4. Mismatched nucleobases are underlined.

5

**Table 5b****Antisense Oligonucleotides from about 1-3 Nucleobases Mismatched to the Target Sequence**

| Sequence                                               | Number of mismatches to SEQ ID NO: 4 |
|--------------------------------------------------------|--------------------------------------|
| GGTCAGGATGTGGCTCTAGG (SEQ ID NO: 148)                  | None                                 |
| GGTCAGGATGTGGCTCA <u>A</u> GG (SEQ ID NO: 176)         | One mismatch                         |
| GGTCAGGA <u>A</u> GTGGCTCTAGG (SEQ ID NO: 177)         | One mismatch                         |
| GGTCAG <u>TT</u> TGTGGCTCTAGG (SEQ ID NO: 178)         | Two mismatches                       |
| GGT <u>G</u> AGGATGTGGCTCCAGG (SEQ ID NO: 179)         | Two mismatches                       |
| GGT <u>CT</u> GATGTGC <u>CT</u> CTCGG (SEQ ID NO: 180) | Three mismatches                     |

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**Example 6: Effects of Antisense Oligonucleotides Targeted to Mouse Hepcidin mRNA: *In Vivo* Evaluation in Normal Mice.**

C57/Bl/6 mice were divided into treatment groups for injection with one of the following: antisense oligonucleotides targeting hepcidin mRNA (SEQ ID NOS: 4 and 5) at 50 mg/kg; antisense oligonucleotides that do not target hepcidin mRNA at 50 mg/kg; or saline. The animals received an initial dose and then were dosed twice per week for two weeks (5 doses total). The antisense oligonucleotides used in the study were all chimeric oligonucleotides ("gapmers") 20 nucleobases in length, composed of a central "gap" region consisting of 10 2'-deoxynucleotides, flanked on both the 5' and 3' ends by 5-nucleotide "wings." The wings are composed of 2'-methoxyethoxy nucleotides (2'-MOE). The internucleoside linkages are phosphorothioate (P=S) throughout the oligonucleotide. All cytidine residues are 5-methylcytidines. The sequences of the oligonucleotide are presented in Table 6.

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**Table 6**  
**Antisense oligonucleotides used in normal mouse *in vivo* screen assay**

| Sequence                      | SEQ ID NO: |
|-------------------------------|------------|
| Targeted to hepcidin mRNA     |            |
| GGTCAGGATGTGGCTCTAGG          | 148        |
| CGTCTTTATTTCAAGGTCAT          | 156        |
| GTGCCATCATGCCTTCTGTT          | 95         |
| Not targeted to hepcidin mRNA |            |
| CCTTCCCTGAAGGTTCTCC           | 168        |
| GTCATAGAACTGTCAGGCT           | 169        |

5                   At the end of the treatment period animals were sacrificed and tissues were harvested for assessment of levels of hepcidin mRNA in the liver, levels of hepcidin polypeptide in the liver and organ weight (specifically spleen and liver. Over the course of the study, data collected to evaluate overt toxicity, changes in body weight, changes in organ weight (specifically spleen and liver), changes in food intake, blood levels of aspartate aminotransferase (AST) and

10 blood levels of alanine aminotransferase (ALT). There were no signs of overt toxicity or in changes to organ or body weight. There was an increase in levels of AST and ALT in the mice receiving one of the antisense oligonucleotides (SEQ ID NO: 95); however, levels for the other hepcidin targeting antisense oligonucleotides remained comparable to the saline control. Liver hepcidin levels were reduced by 60-70 percent for the hepcidin targeting antisense oligonucleotides

15 compared to controls. A similar reduction was observed for liver hepcidin polypeptides. Hepcidin polypeptide levels were determined by Western blot of whole-liver lysates. Briefly, 50 .micro.g of whole-liver lysate was electrophoresed on a 16% TG-gel. Hepcidin was detected with hepcidin antibody (Alpha Diagnostics, HEPC11-A, 0.3 .micro.g/ml). FIG. 1. Thus, antisense oligonucleotides targeting hepcidin mRNA can result in a significant reduction in the levels of that

20 mRNA and in turn the expression thereof.

**Example 7: Dose-Response of Antisense Oligonucleotide Targeting Hepcidin mRNA in Normal Mice.**

25                   C57/Bl/6 mice were dosed with 10, 25, 50 or 75 .mg/kg of antisense oligonucleotide targeting hepcidin mRNA (SEQ ID NO: 145). C57/Bl/6 control mice received either saline or 10, 25, 50 or 75 mg/kg of an antisense oligonucleotide not targeted to hepcidin mRNA (SEQ ID NO: 168) The groups were given an initial dose and then were dosed twice per

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week for 2 weeks. Liver hepcidin mRNA and serum iron levels were measured at the end of the study. All antisense oligonucleotides used in this example were chimeric oligonucleotides (“gapmers”) 20 nucleobases in length, composed of a central “gap” region consisting of 10 2'-deoxynucleotides, flanked on both the 5' and 3' ends by 5-nucleotide “wings.” The wings are composed of 2'-methoxyethoxy nucleotides (2'-MOE). The internucleoside linkages are phosphorothioate (P=S) throughout the oligonucleotide. All cytidine residues are 5-methylcytidines.

There was a reduction in liver hepcidin mRNA for the group receiving the antisense oligonucleotide targeting hepcidin as compared to saline control. A reduction was not observed for the control antisense oligonucleotide group as shown in FIG. 2. Also observed was a corresponding increase in serum iron levels for the treatment groups compared to saline. This same increase was not seen in the control oligonucleotide group. These data demonstrate that antisense oligonucleotides targeting hepcidin mRNA will cause a decrease in liver hepcidin mRNA and a corresponding increase in serum iron levels.

**Example 8: Effects of Antisense Reduction of Hpcidin in Normal and LPS Stimulated Mice: Dose-Response.**

An ACD mouse model was prepared prior to treatment by injecting C57Bl/6 mice (Charles River Labs, Wilmington, MA) with lipopolysaccharide (LPS, Sigma-Aldrich, St. Louis, MO) for 6 hours (0.1 to 1 mg/kg intraperitoneal injection). (See, e.g. Ganz (2003) Blood, 102(3):783-785, and references therein). Injection of LPS caused an increase in cytokine production in these mice, which in turn resulted in a three fold increase in hepcidin production and an 80% reduction in serum iron levels.

A normal unstimulated mouse population and an LPS stimulated mouse population were each separated into treatment groups, antisense control groups and saline control groups. Mice in the LPS stimulated population were prepared using a 1 mg/kg intraperitoneal LPS injection for 6 hours. The treatment groups were treated with an antisense oligonucleotide targeted to mouse hepcidin mRNA (SEQ ID NOS: 4 and 5). The antisense control groups were treated with antisense oligonucleotide not targeted to mouse hepcidin. The saline control groups were injected with saline alone. The antisense oligonucleotide targeted to mouse hepcidin mRNA was (SEQ ID NO: 145). The control antisense oligonucleotide was SEQ ID NO 168. All mice were dosed at time point zero and then twice a week for two weeks using either 10, 25, 50 or 75 mg/kg of antisense oligonucleotide; 50 mg/kg of control oligonucleotide or using saline. All antisense oligonucleotides used in this example were chimeric oligonucleotides (“gapmers”) 20 nucleobases in length, composed of a central “gap” region consisting of 10 2'-deoxynucleotides, flanked on both the 5' and 3' ends by 5-nucleotide “wings.” The wings are composed of 2'-methoxyethoxy

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nucleotides (2'-MOE). The internucleoside linkages are phosphorothioate (P=S) throughout the oligonucleotide. All cytidine residues are 5-methylcytidines.

In both the normal mice and the LPS stimulated mice there was a reduction in levels of liver hepcidin mRNA for the 25, 50 and 75 mg/kg doses as compared to saline control. This same reduction was not seen in the antisense oligonucleotide control group. Additionally, there was a corresponding increase in serum iron levels for both the normal and LPS stimulated groups receiving antisense oligonucleotide targeting hepcidin as compared to saline. This same increase was not seen in the antisense oligonucleotide control group. This study shows that hepcidin increases serum iron levels in both normal and LPS stimulated mice. FIG. 3. Antisense oligonucleotides targeting hepcidin mRNA will reduce the levels of hepcidin mRNA in the liver, correlating with an increase in serum iron levels. This effect of the antisense oligonucleotide is observed in normal and LPS stimulated mice (ACD models). Thus, the antisense oligonucleotides are useful for treating subjects having low serum iron levels and disorders associated therewith.

**Example 9: Effects of Antisense Reduction of Hepcidin in Normal and Chronic Anemia Mice: Turpentine Mouse Model.**

The effect of antisense compound treatment on acute and chronic anemia was determined using a turpentine induced anemia mouse model. Male C57Bl/6 mice (Charles River Laboratories, Wilmington, MA) weighing approximately 25 g were separated into one of a control group, an oligonucleotide control group or a treatment group. The control group mice received either no treatment (n=5) or treatment with 100 microliters turpentine only (n=5). The oligonucleotide control group mice received 100 microliters turpentine and a dosing regimen comprising either 50 mg/kg/dose of control compound (n=5) or 75 mg/kg/dose of control compound (n=5). The control compound was an antisense compound that is not targeted to a nucleic acid encoding hepcidin (CCTTCCCTGAAGGTCCTCC, SEQ ID NO: 168). The treatment group mice received 100 microliters of turpentine and a dosing regimen comprising either 10 mg/kg/dose of treatment compound (n=5), 25 mg/kg/dose of treatment compound (n=5), 50 mg/kg/dose of treatment compound (n=5), or 75 mg/kg/dose of treatment compound (n=4). The treatment oligonucleotide is Cmpd 326868 (SEQ ID NO: 148). The turpentine injection stimulates an inflammatory response in the mice, and subsequently produces anemia. Turpentine mouse models of anemia are discussed in the literature. (Liuzzi, JP, Lichten, LA, Rivera, S, Blanchard, RK, Aydemir, TB, Knutson, MD, Ganz, T, and Cousins, RJ, *PNAS*, v.102, n.19, 6843-6848 (2005); Venihaki, M, Dikkes, P, Carrigan, A, and Karalis, KP, *J. Clin. Invest.*, 108:1159-1166 (2001)).

Mice in all groups were placed on a no-iron diet for two weeks, followed by a low-iron diet. At the same time the low-iron diet was started, the mice were subjected to the appropriate dosing regimen as described above. Briefly, the control group received no oligonucleotide, the

oligonucleotide control group received 50 or 75 mg/kg/dose of SEQ ID NO: 168 twice a week for two weeks, and the treatment group received 10, 25, 50 or 75 mg/kg/dose of SEQ ID NO: 148 twice a week for two weeks. After two weeks of the dosing regimen, all mice in the oligonucleotide group and in the treatment group received an injection comprising 100 microliters of turpentine (Sigma-Aldrich, St. Louis, MO). In the control group, only half of the mice population received an injection comprising 100 microliters of turpentine and the other half of the population received a saline injection only. The injections were delivered subcutaneously to the left hind limb of each mouse. To obtain acute anemia endpoints, blood was drawn at 16 hours post turpentine injection. For chronic anemia endpoints, the dosing regimen described above continued for another two weeks after turpentine injection. Blood was drawn at two weeks post-turpentine injection and at 24 hours after the final oligonucleotide injection was delivered. Mice were then sacrificed.

Analysis of the serum iron from acute blood draw showed that the turpentine injection produced a significant reduction in the serum iron levels at 16 hours post turpentine injection. The serum iron level reduction was reversed in a dose responsive manner for the treatment group. At two weeks post injection there was a dose dependent improvement in the clinical endpoints of anemia compared to the control group and the oligonucleotide control group. Table 7 and Figures 4a-d shows the dose dependent improvement in serum iron levels, red blood cell count, hematocrit levels and hemoglobin levels.

Table 7

The Effect of Hepcidin ASO in a Chronic Turpentine Model: Serum Iron, Red Blood Cell (RBC) Count, Hemoglobin Levels and Hematocrit Levels

|                                       | Control Group ~  |                  | Oligonucleotide Control Group |                    | Treatment Group    |                    |                    |                    |
|---------------------------------------|------------------|------------------|-------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
|                                       | 0                | 100              | 100                           | 100                | 100                | 100                | 100                | 100                |
| <b>Turpentine (.micro.l)</b>          | 0                | 100              | 100                           | 100                | 100                | 100                | 100                | 100                |
| <b>CMPD</b>                           | none             | none             | 50 mg/kg<br>141923            | 75 mg/kg<br>141923 | 10 mg/kg<br>326868 | 25 mg/kg<br>326868 | 50 mg/kg<br>326868 | 75 mg/kg<br>326868 |
| <b>Serum Iron (.micro.g/d L) (SD)</b> | 190.6<br>(±24.1) | 170.6<br>(±28.1) | 186.0<br>(±44.4)              | 208.2<br>(±40.0)   | 182.8<br>(±44.3)   | 260.8<br>(±22.9)   | 266.6<br>(±46.0)   | 325.5<br>(±55.7)   |
| <b>RBC (10.sup.6 / .micro.l)</b>      | 10.4<br>(±0.4)   | 9.4<br>(±1.0)    | 9.9<br>(±0.2)                 | 9.8<br>(±0.7)      | 9.4<br>(±0.5)      | 10.2<br>(±0.3)     | 10.2<br>(±0.3)     | 10.6<br>(±0.8)     |

|                               | Control Group – |                | Oligonucleotide Control Group |                | Treatment Group |                |                |                |
|-------------------------------|-----------------|----------------|-------------------------------|----------------|-----------------|----------------|----------------|----------------|
| (SD)                          |                 |                |                               |                |                 |                |                |                |
| <b>Hemoglobin (g/dL) (SD)</b> | 14.8<br>(±0.8)  | 13.0<br>(±1.2) | 13.3<br>(±0.4)                | 13.2<br>(±0.8) | 13.1<br>(±0.6)  | 14.0<br>(±0.5) | 14.0<br>(±0.3) | 14.3<br>(±0.9) |
| <b>Hematocrit (%) (SD)</b>    | 53.4<br>(±2.1)  | 47.6<br>(±2.6) | 49.8<br>(±1.1)                | 47.8<br>(±3.3) | 47.6<br>(±1.9)  | 51.2<br>(±1.9) | 51.0<br>(±1.7) | 51.5<br>(±3.5) |

The turpentine mouse model of anemia provides data for endpoints of chronic anemia, such as RBC count, hemoglobin levels and hematocrit levels, as well as serum iron levels. Treating these anemic mice with an antisense compound that targets and inhibits expression of nucleic acids encoding hepcidin polypeptide results in a dose dependent improvement in these endpoints.

**Example 10: Effects of Antisense Reduction of Hepcidin in Chronic Anemia (Turpentine Mouse Model) treated with erythropoietin.**

The effect of antisense compound treatment on chronic anemia, in combination with erythropoietin (EPO) treatment was determined using the chronic turpentine induced anemia mouse model. Male C57Bl/6 mice (Charles River Laboratories, Wilmington, MA) weighing approximately 25 g were fed a “no iron” diet (2.7 ppm iron) for 2 weeks and subsequently switched to a “low iron” diet (47 ppm iron) for the remainder of the study. Upon switch to the low iron diet, two weeks prior to sacrifice, mice were treated via subcutaneous injection with saline (vehicle) or a single 100 .micro. L dose of turpentine. Hepcidin antisense oligonucleotide (CMPD # 326868, 50 mg/kg, which is SEQ ID NO: 148) was administered via subcutaneous injection to the appropriate groups of animals (as indicated in Figure 5a-5c), two times per week, beginning 24 hours following turpentine treatment. EPO was administered daily, for the last four days of the study, by intraperitoneal injection to indicated animals at indicated doses (0-25 units/day). Thus, in this study, in indicated mice, regular treatment with antisense oligonucleotide targeted to hepcidin began prior to regular treatment with erythropoietin. After the first administration, each treatment was continued at regular intervals for the remainder of the study. At the end of the treatment period, animals were sacrificed and tissues and blood taken for assessment of levels hepcidin mRNA and phenotypic endpoints. Results from this study showed that hepcidin ASO in combination with EPO was well tolerated. Hepcidin mRNA levels in the liver, serum iron (.micro.g/mL) and % reticulocytes (immature red blood cells) were measured as endpoints. The results are shown in Figure 5a-5c.

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As shown in Figure 5, in this study using the turpentine mouse model of chronic anemia, erythropoietin treatment decreased liver hepcidin mRNA expression and serum iron levels and increased reticulocyte counts. Administration of the antisense oligonucleotide targeted to hepcidin caused decreased liver hepcidin mRNA, but an increase in serum iron. Administration of an antisense oligonucleotide targeted to hepcidin in addition to erythropoietin resulted in a further increase in reticulocyte counts compared to erythropoietin treatment alone. Thus the effects of erythropoietin and the antisense compound targeted to hepcidin were additive. These results show that treatment with both erythropoietin and an antisense compound targeted to hepcidin is effective in improving endpoints of chronic anemia in a mouse model for hypoferrremia and anemia associated with inflammation.

It is contemplated herein that a further experiment, evaluating the effectiveness of combination therapy for treating anemia or increasing red blood cells could be performed, according to the methods and using the mouse model described above, by evaluating multiple experimental mice groups.

In such an experiment, a control group would receive only saline. Experimental groups would all receive turpentine. A first experimental group would receive only turpentine (no treatment or therapy). A second experimental group would receive erythropoietin treatment continuously, meaning regularly, for over a week, prior to receiving antisense compound targeted to hepcidin, and would continue to receive erythropoietin treatment throughout the treatment period with antisense compound. Thus, this second experimental group will have been receiving erythropoietin therapy prior to administration of the antisense compound. Erythropoietin therapy treatment regimens are well known in the art. Thus, in the second experimental group, the antisense compound and the erythropoietin would be administered in separate formulations, at distinct timepoints. A third experimental group would have received erythropoietin therapy at some time prior to receiving antisense compound. A fourth experimental group would receive erythropoietin therapy and antisense compound treatment simultaneously. Thus, in this group, the group would begin erythropoietin therapy simultaneously with the administration of the antisense compound. In this case, the two treatments could be administered in separate formulations or in single formulations. A fifth experimental group would receive antisense compound prior to erythropoietin therapy. Thus, the second through fifth experimental groups would be receiving a combination therapy, wherein they would receive antisense compound and be further receiving erythropoietin. A sixth experimental group would receive only erythropoietin. A seventh experimental group would receive only antisense compound.

It is further contemplated that a combination therapy method could be used for preventing, treating or ameliorating anemia or for increasing red blood cell counts in a patient. It is contemplated that this combination method could include administration of an antisense compound

targeted to hepcidin and an ESA. It is contemplated that the ESA used in such a therapy could be erythropoietin, recombinant human erythropoietin, EPOGEN or PROCRIT. It is further contemplated that such a combination therapy method could comprise administration of the antisense compound and erythropoietin simultaneously. Alternatively, administration of the erythropoietin and antisense compound could be done at distinct timepoints.

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If administered simultaneously, the antisense compound and erythropoietin could be given in a single formulation, or in separate formulations. Also, this combination therapy could be used to treat a patient who is receiving erythropoietin. The patient could be receiving erythropoietin prior to initiation of the combination therapy, or the patient could begin receiving the erythropoietin at the same time the combination therapy is initiated.

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It is contemplated that an antisense compound used in this therapy could be an antisense oligonucleotide targeted to a nucleic acid molecule encoding hepcidin. Alternatively, the antisense compound could be double stranded. It is contemplated that the double stranded antisense compound could be an siRNA.

**CLAIMS**

What is claimed is:

1. A compound 15 to 35 nucleobases in length, wherein said compound specifically hybridizes with at least 8 contiguous nucleobases of nucleotides 123 to 566 of a nucleic acid molecule encoding hepcidin (SEQ ID NO: 1), and wherein said compound inhibits the expression of hepcidin.
2. The compound of claim 1 wherein said compound specifically hybridizes with at least 8 contiguous nucleobases of a nucleotide region wherein the nucleotide region is selected from the group consisting of nucleotides 123 to 252, 295 to 566, 352 to 405, 429 to 566, and 456 to 527 of a nucleic acid molecule encoding hepcidin (SEQ ID NO: 1).
3. The compound of claim 1 wherein said compound comprises at least 8 contiguous nucleobases of SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, or SEQ ID NO: 37.
4. The compound of claim 1 wherein said compound consists of SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, or SEQ ID NO: 37.
5. The compound of claim 1 wherein said compound is at least about 80% complementary to at least a 20 contiguous nucleobases of nucleotides 123 to 566 of a nucleic acid molecule encoding hepcidin (SEQ ID NO: 1).
6. The compound of claim 1 wherein said compound is at least about 100% complementary to at least a 20 contiguous nucleobases of nucleotides 123 to 566 of a nucleic acid molecule encoding hepcidin (SEQ ID NO: 1).
7. The compound of claim 1 wherein the compound is a single stranded compound.
8. The compound of claim 1 wherein the compound is an antisense oligonucleotide.

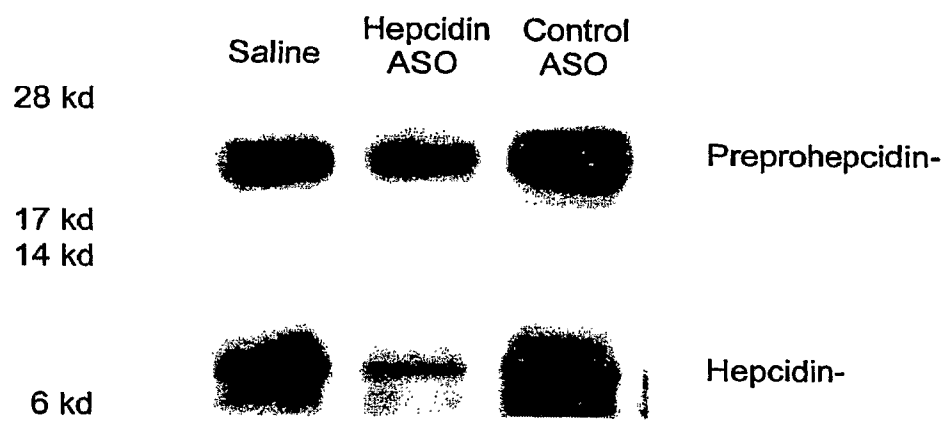
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9. The compound of claim 8 wherein the antisense oligonucleotide comprises at least one modified internucleoside linkage.
10. The compound of claim 9 wherein the modified internucleoside linkage is a phosphorothioate linkage.
11. The compound of claim 8 wherein the antisense oligonucleotide comprises at least one sugar moiety.
12. The compound of claim 11 wherein the modified sugar moiety is a 2'-O-methoxyethyl sugar moiety.
13. The compound of claim 8 wherein the antisense oligonucleotide comprises at least one modified nucleobase.
14. The compound of claim 13 wherein the modified nucleobase is a 5-methylcytosine.
15. The compound of claim 8 wherein the antisense oligonucleotide is a chimeric oligonucleotide.
16. The composition of claim 1 and a pharmaceutically acceptable carrier or diluent.
17. The composition of claim 16 further comprising a colloidal dispersion system.
18. The composition of claim 16 wherein the compound is an antisense oligonucleotide.
19. A compound 15 to 35 nucleobases in length, wherein said compound specifically hybridizes with at least 8 contiguous nucleobases of nucleotides 204 to 341 of a nucleic acid molecule encoding hepcidin (SEQ ID NO: 2), and wherein said compound inhibits the expression of hepcidin.
20. The compound of claim 18 wherein said compound specifically hybridizes with at least 8 contiguous nucleobases of nucleotides 231 to 302 of a nucleic acid molecule encoding hepcidin (SEQ ID NO: 2).
21. A compound 15 to 35 nucleobases in length, wherein said compound specifically hybridizes with at least 8 contiguous nucleobases of nucleotides 3249 to 4743 of a nucleic acid molecule encoding hepcidin (SEQ ID NO: 3), and wherein said compound inhibits the expression of hepcidin.

22. The compound of claim 21 wherein said compound specifically hybridizes with at least 8 contiguous nucleobases of a nucleotide region wherein the nucleotide region is selected from the group comprising nucleotides 3249 to 3454, 3398 to 3454, 4643 to 4703, and 4643 to 4743 of a nucleic acid molecule encoding hepcidin (SEQ ID NO: 3).
23. A method of inhibiting the expression of hepcidin in cells or tissues comprising contacting said cells or tissues with the compound of claim 1 so that expression of hepcidin is inhibited.
24. A method of treating an animal having a disease or condition associated with hepcidin comprising administering to said animal a therapeutically or prophylactically effective amount of the compound of claim 1 so that expression of hepcidin is inhibited.
25. The method of claim 24 wherein said disease or condition is selected from any of the group consisting of anemia and low serum iron levels.
26. The method of claim 24 wherein said compound modifies any of the group consisting of increasing serum iron levels, increasing red blood cell counts, increasing hemoglobin levels, increasing hematocrit levels, decreasing soluble transferrin receptor, and preventing iron restricted erythropoiesis.
27. The method of claim 24, wherein the compound of claim 1 is administered via an injection route selected from the group consisting of subcutaneous, intramuscular, intravenous and intraperitoneal.
28. The method of claim 24, wherein said animal is further receiving erythropoietin therapy.
29. The method of claim 28, wherein the compound of claim 1 and erythropoietin are administered in a single formulation.
30. The method of claim 29, wherein said single formulation is administered via an injection route selected from the group consisting of subcutaneous, intramuscular, intravenous and intraperitoneal.
31. The compound according to claim 1 for use in therapy.
32. Use of the compound of claim 1 in the preparation of a medicament for inhibiting the expression of hepcidin in cells or tissues.

33. Use of the compound of claim 1 in the preparation of a medicament for treating or preventing a disease or condition associated with hepcidin.
34. The use according to claim 33, wherein said disease or condition is selected from any of the group consisting of anemia and low serum iron levels.
35. The use according to any of claims 31-33, wherein said compound modifies any of the group consisting of increasing serum iron levels, increasing red blood cell counts, increasing hemoglobin levels, increasing hematocrit levels, decreasing soluble transferrin receptor, and preventing iron restricted erythropoiesis.
36. The use according to claim 33, wherein said disease or condition is in an animal that is further receiving erythropoietin therapy.
37. The use according to any of claims 32-36, wherein the medicament further comprises erythropoietin.
38. The use according to any of claims 32-37, wherein said compound is in a formulation suitable for administration via an injection route selected from the group consisting of subcutaneous, intramuscular, intravenous and intraperitoneal.

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*FIG. 1*

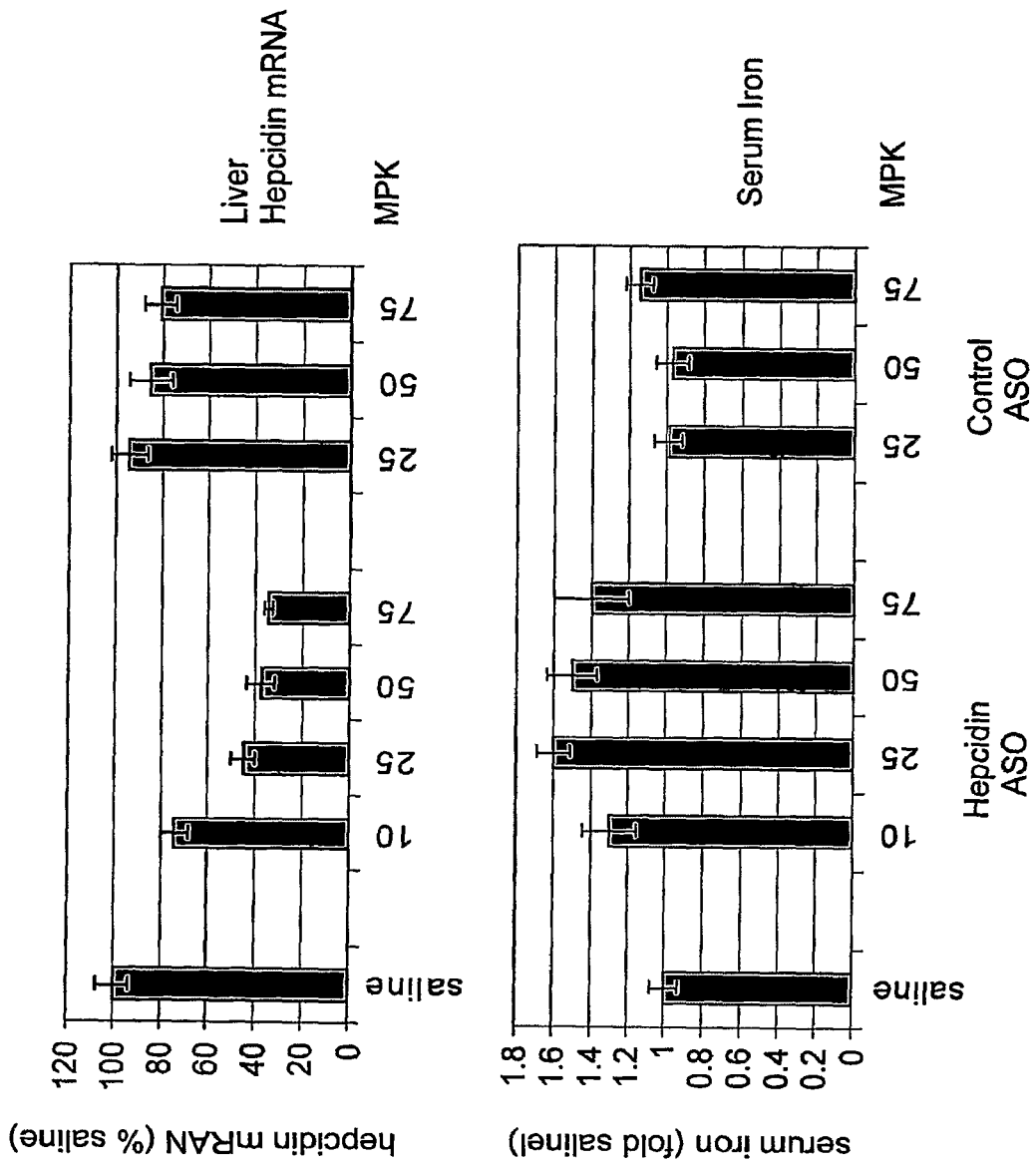


FIG. 2

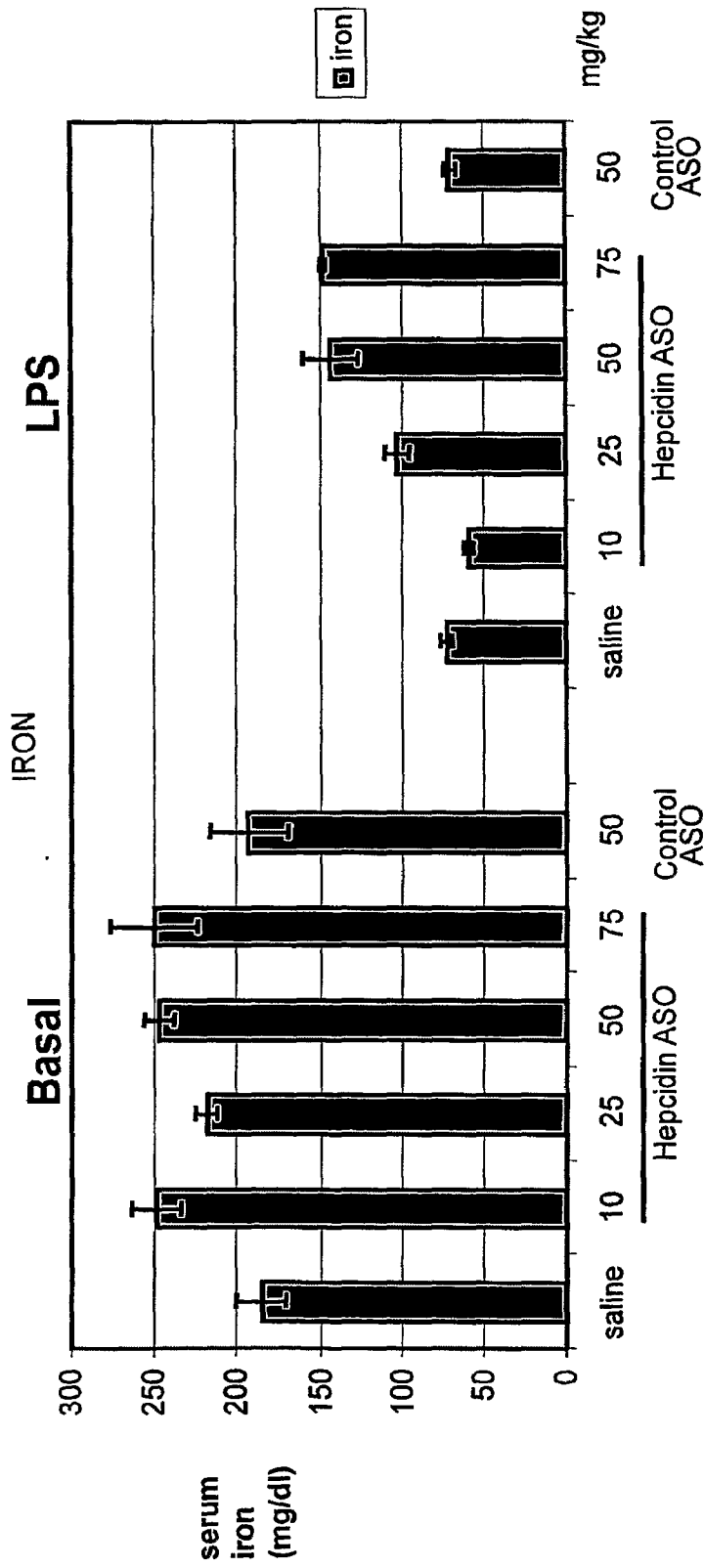
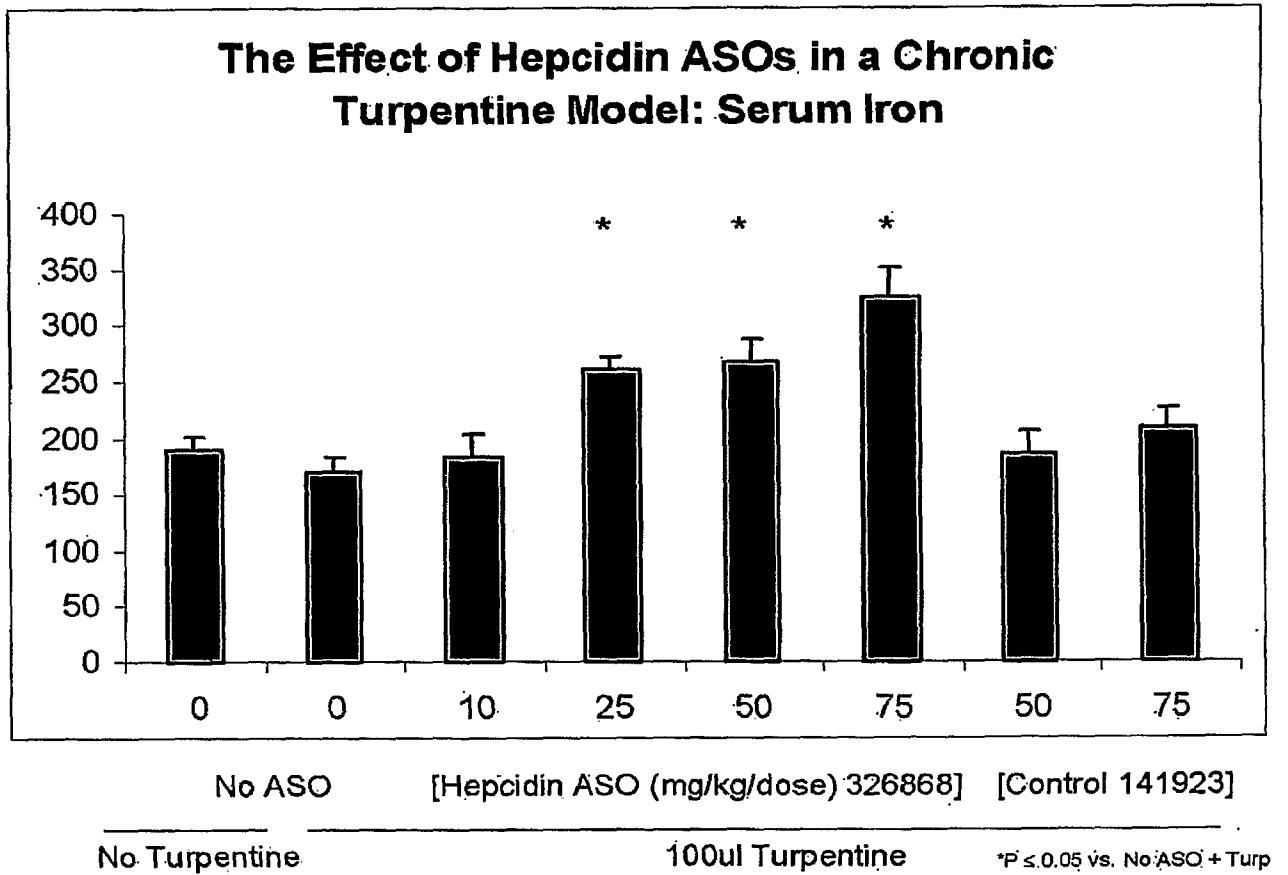


FIG. 3



**FIG. 4A**



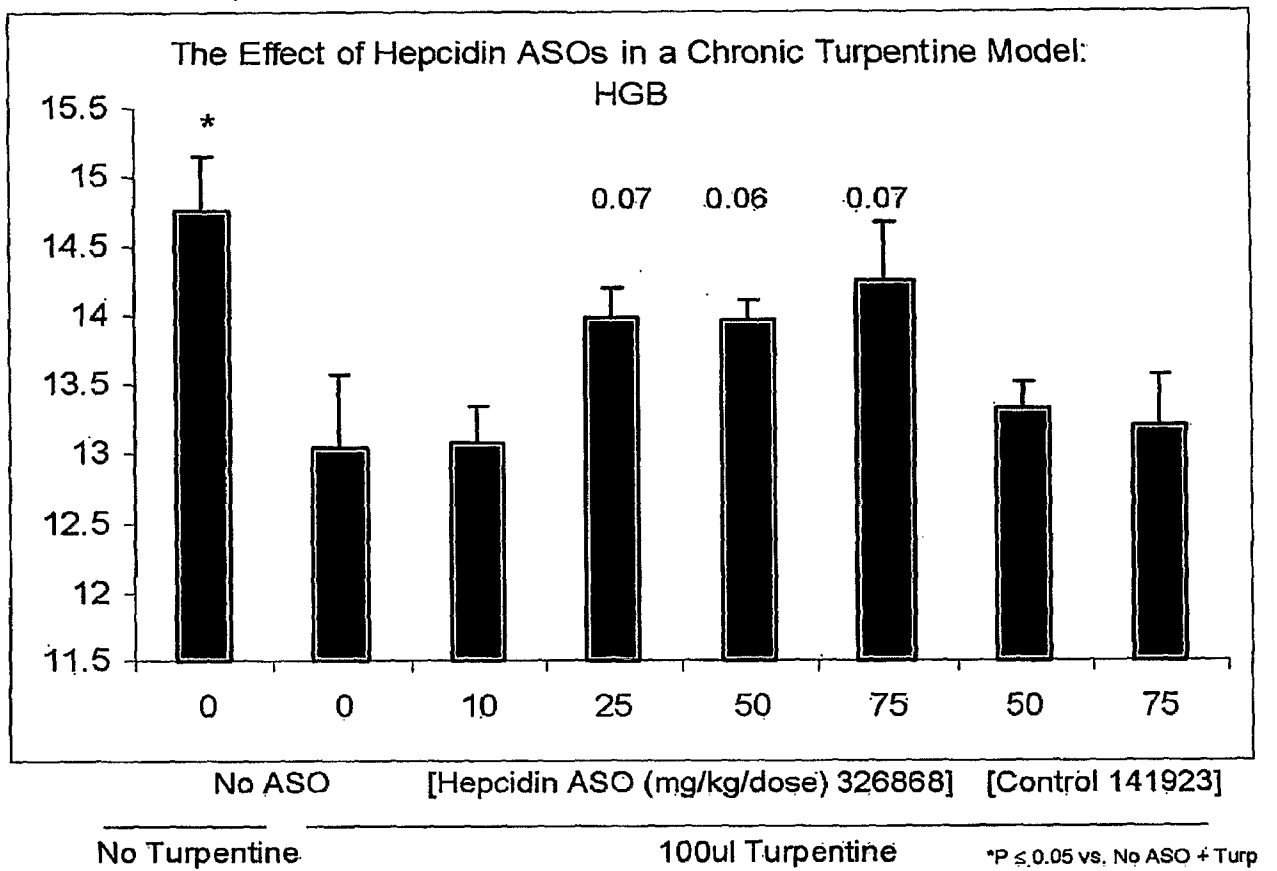


FIG. 4C

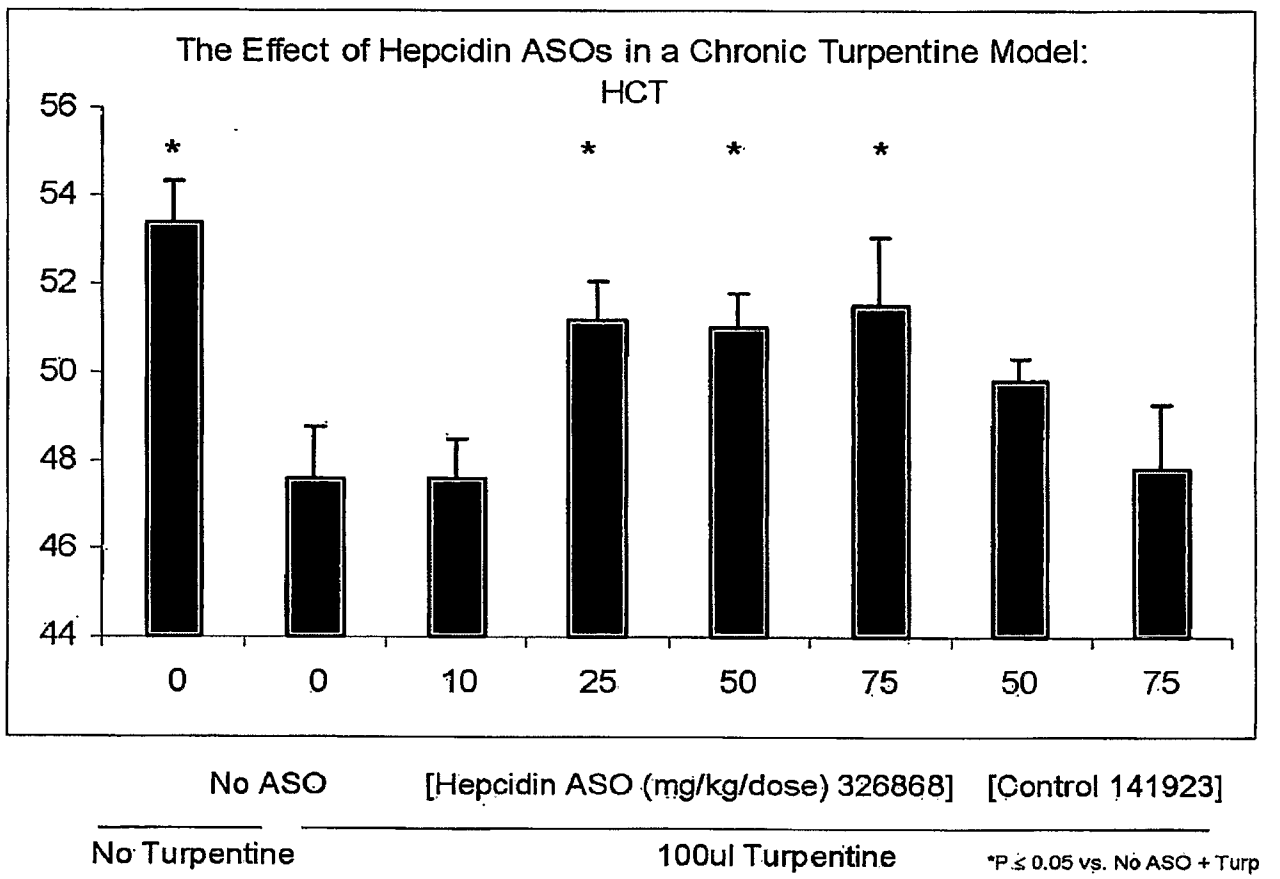


FIG. 4D

