MCP-1 binding nucleic acids

The present invention is related to nucleic acids binding to MCP-1, and the use thereof for the manufacture of a medicament and a diagnostic agent, respectively.

Human MCP-1 (monocyte chemoattractant protein-1; alternative names, MCAF [monocyte chemoattracting and activating factor]; CCL2; SMC-CF [smooth muscle cell-colony simulating factor]; HC-11; LDCF; GDCF; TSG-8; SCYA2; A2; SwissProt accession code, P13500) was characterized by three groups independently (Matsushima 1988; Rollins 1989; Yoshimura 1989). It consists of 76 amino acids and features a heparin binding site like all chemokines. The two intramolecular disulfide bonds confer a stable, rigid structure to the molecule. Furthermore, MCP-1 carries a pyroglutamate at its amino terminus. At Thr 71, a potential O-linked glycosylation site is located. Additional MCP family members exist both in humans (MCP-2, -3, -4) and mice (MCP-2, -3, -5). The human proteins are approximately 70% homologous to human MCP-1.

The structure of MCP-1 has been solved by NMR (Handel 1996) and X-ray (Lubkowski 1997). The MCP-1 monomer has the typical chemokine fold in which the amino-terminal cysteines are followed by a long loop that leads into three antiparallel β-pleated sheets in a Greek key motif. The protein terminates in an α helix that overlies the three β sheets (PDB data accession code 1DOK).

Although the three-dimensional structure of MCP-1 forms from different mammalian species has generally been maintained, the amino acid sequence has not particularly well been conserved during evolution. Sequence alignment results demonstrate 55% overall sequence similarity between human and murine MCP-1 (also called JE) within the first 76 amino acids. Apart from the amino acid sequence, murine MCP-1 differs from human MCP-1 in molecular size (125 amino acids) and the extent of glycosylation. Murine MCP-1 contains a 49-amino acid carboxyterminal domain that is not present in human MCP-1 and is not required for *in vitro* bioactivity. Human MCP-1 shares the following percentage of identical amino acids with MCP-1 from:

- *Macaca mulatta* (Rhesus monkey) MCP-1 97%
- *Sus scrofa* (Pig) MCP-1 79%
- *Equus caballus* (Horse) 78%
- *Canis familiaris* (Dog) MCP-1 76%
- *Oryctolagus cuniculus* (Rabbit) MCP-1 75%
- *Bos Taurus* (Bovine) 72%
- *Homo sapiens* MCP-3 71%
- *Homo sapiens* Eotaxin 64%
- *Homo sapiens* MCP-2 62%
- *Mus musculus* (Mouse) MCP-1 55%
- *Rattus norvegicus* (Rat) MCP-1 55%

Given this high degree of divergence it may be necessary to generate antagonists of rodent MCP-1 for successful performance of pharmacological studies in rodent models.

MCP-1 is a potent attractor of monocytes/macrophages, basophils, activated T cells, and NK cells. A wide variety of cell types, such as endothelial cells, epithelial cells, fibroblasts, keratinocytes, synovial cells, mesangial cells, osteoblasts, smooth muscle cells, as well as a multitude of tumor cells express MCP-1 (Baggiolini 1994). Its expression is stimulated by several types of proinflammatory agents such as IL-1β, TNF-α, IFN-γ, LPS (lipopolysaccharide), and GM-CSF.

Rather unusual in the promiscuous chemokine network, MCP-1 is highly specific in its receptor usage, binding only to the chemokine receptor CCR2 with high affinity. Like all chemokine receptors, CCR2 is a GPCR (Dawson 2003). CCR2 seems to be expressed in two slightly different forms due to alternative splicing of the mRNA encoding the carboxyterminal region, CCR2a and CCR2b (Charo 1994). These receptors are expressed in monocytes, myeloid precursor cells and activated T cells (Myers 1995; Qin 1996). The dissociation constant of MCP-1 to the receptor transfected into HEK-293 cells is 260 pM which is in agreement with values measured on monoytes (Myers 1995; Van Riper 1993). Activation of CCR2b on transfected HEK-293 cells with MCP-1 inhibits adenylyl cyclase at a concentration of 90 pM, and mobilizes intracellular calcium at slightly higher concentrations, seemingly independent of phosphatidyl inositol hydrolysis. The effects on adenylyl cyclase and intracellular calcium release are strongly inhibited by pertussis toxin, implying the involvement of G_i type heterotrimeric G-proteins in signal transduction (Myers 1995).

MCP-1 is involved in monocyte recruitment into inflamed tissues. There, resident macrophages release chemokines such as MCP-1 and others, and cytokines like TNF, IL-1β and others, which activate endothelial cells to express a battery of adhesion molecules. The resulting "sticky" endothelium causes monocytes in the blood vessel to roll along its surface. Here, the monocytes encounter MCP-1 presented on the endothelial surface, which binds to CCR2 on monocytes and activates them. This finally leads to firm arrest, spreading of monocytes along the endothelium, and transmigration into the surrounding tissue, where the monocytes differentiate into macrophages and migrate towards the site of maximal MCP-1 concentration.

MCP-1 is a member of the chemokine family which is a family of small (ca. 8-14 kDa) heparin-binding, mostly basic and structurally related molecules. They are formed predominantly in inflamed tissues and regulate the recruitment, activation, and proliferation of white blood cells (leukocytes) (Baggiolini 1994; Springer 1995; Schall 1994). Chemokines selectively induce chemotaxis of neutrophils, eosinophils, basophils, monocytes, macrophages, mast cells, T and B cells. In addition to their chemotactic effect, they can selectively exert other effects in responsive cells like changes in cell shape, transient increase in the concentration of free intracellular calcium ions, degranulation, upregulation of integrins, formation of bioactive lipids such as leukotrienes, prostaglandins, thromboxans, or respiratory burst (release of reactive oxygen species for destruction of pathogenic organisms or tumor cells). Thus, by provoking the release of further proinflammatory mediators, chemotaxis and extravasation of leukocytes towards sites of infection or inflammation, chemokines trigger escalation of the inflammatory response.

Based on the arrangement of the first two of four conserved cystein residues, the chemokines are divided into four classes: CC or β-chemokines in which the cysteins are in tandem, CXC or α-chemokines, where they are separated by one additional amino acid residue, XC or γ chemokines with lymphotactin as only representant to date, that possess only one disulfide bridge, and CX3C-chemokines which feature three amino acid residues between the cysteins, with membrane-bound fractalkin as only class member known to date (Bazan 1997).

The CXC chemokines act primarily on neutrophils, in particular those CXC chemokines that carry the amino acid sequence ELR on their amino terminus. Examples of CXC chemokines that are active on neutrophils are IL-8, GROα, -β, and –γ, NAP-2, ENA-78 and GCP-2. The CC

chemokines act on a larger variety of leukocytes, such as monocytes, macrophages, eosinophils, basophils, as well as T and B lymphocytes (Oppenheim 1991; Baggiolini 1994; Miller 1992; Jose 1994; Ponath 1996a). Examples of these are I-309; MCP-1, -2, -3, -4, MIP-1α and –β, RANTES, and eotaxin.

Chemokines act through receptors that belong to a superfamily of seven transmembrane-spanning G protein-coupled receptors (GPCRs; Murphy 2000). Generally speaking, chemokine and chemokine receptor interactions tend to be promiscuous in that one chemokine can bind many chemokine receptors and conversely a single chemokine receptor can interact with several chemokines. Some known receptors for the CC chemokines include CCR1, which binds MIP-1α and RANTES (Neote 1993; Gao 1993); CCR2, which binds chemokines including MCP-1, -2, -3, and –4 (Charo 1994; Myers 1995; Gong 1997; Garcia-Zepeda 1996); CCR3, which binds chemokines including eotaxin, RANTES, and MCP-3 (Ponath 1996b); CCR4, which has been found to signal in response to MCP-1, MIP-1α, and RANTES (Power 1995); and CCR5, which has been shown to signal in response to MIP-1α and –β, and RANTES (Boring 1996; Raport 1996; Samson 1996).

As mentioned above, all four members of the MCP family (1-4) bind to CCR2, whereas MCP-2, MCP-3, and MCP-4 can also interact with CCR1 and CCR3 (Gong 1997; Heath 1997; Uguccioni 1997) and, in the case of MCP-2, CCR5 (Ruffing 1998). Another CC chemokine showing high homology with the MCP family is eotaxin, which was originally isolated from the bronchoalveolar lavage fluid taken from allergen-challenged, sensitized guinea pigs (Jose 1994). It has been shown that eotaxin is also able to activate CCR2 (Martinelli 2001).

The problem underlying the present invention is to provide a means which specifically interacts with MCP-1. More specifically, the problem underlying the present invention is to provide for a nucleic acid based means which specifically interacts with MCP-1.

A further problem underlying the present invention is to provide a means for the manufacture of a medicament for the treatment of a human or non-human diseases, whereby the disease is characterized by MCP-1 being either directly or indirectly involved in the pathogenetic mechanism of such disease.

A still further problem underlying the present invention is to provide a means for the manufacture of a diagnostic agent for the treatment of a disease, whereby the disease is characterized by MCP-1 being either directly or indirectly involved in the pathogenetic mechanism of such disease.

These and other problems underlying the present invention are solved by the subject matter of the attached independent claims. Preferred embodiments may be taken from the dependent claims.

The problem underlying the present invention is also solved in a first aspect by a nucleic acid, preferably binding to MCP-1, selected from the group comprising type 1A nucleic acids, type 1B nucleic acids, type 2 nucleic acids, type 3 nucleic acids, type 4 nucleic acids and nucleic acids having a nucleic acid sequence according to any of SEQ.ID.No. 87 to 115.

In a first subaspect of the first aspect the type 1A nucleic acid comprises in 5'->3' direction a first stretch Box B1A, a second stretch Box B2, a third stretch Box B3, a fourth stretch Box B4, a fifth stretch Box B5, a sixth stretch Box B6 and a seventh stretch Box B1B, whereby

the first stretch Box B1A and the seventh stretch Box B1B optionally hybridize with each other, whereby upon hybridization a double-stranded structure is formed,

the first stretch Box B1A comprises a nucleotide sequence of AGCRUG,

the second stretch Box B2 comprises a nucleotide sequence of CCCGGW,

the third stretch Box B3 comprises a nucleotide sequence of GUR,

the fourth stretch Box B4 comprises a nucleotide sequence of RYA,

the fifth stretch Box B5 comprises a nucleotide sequence of GGGGGRCGCGAYC

the sixth stretch Box B6 comprises a nucleotide sequence of UGCAAUAAUG or URYAWUUG, and

the seventh stretch Box B1B comprises a nucleotide sequence of CRYGCU.

In a preferred embodiment of the first subaspect

the first stretch Box B1A comprises a nucleotide sequence of AGCGUG.

In an embodiment of the first subaspect

the second stretch Box B2 comprises a nucleotide sequence of CCCGGU.

In an embodiment of the first subaspect

the third stretch Box B3 comprises a nucleotide sequence of GUG.

In an embodiment of the first subaspect

the fourth stretch Box B4 comprises a nucleotide sequence of GUA.

In an embodiment of the first subaspect

the fifth stretch Box B5 comprises a nucleotide sequence of GGGGGGCGCGACC.

In an embodiment of the first subaspect

the sixth stretch Box B6 comprises a nucleotide sequence of UACAUUUG.

In an embodiment of the first subaspect

the seventh stretch Box B1B comprises a nucleotide sequence of CACGCU.

In an embodiment of the first subaspect the nucleic acid comprises a nucleic acid sequence according to SEQ.ID.No 21.

In a second subaspect of the first aspect the type 1B nucleic acid comprises in 5'->3' direction a first stretch Box B1A, a second stretch Box B2, a third stretch Box B3, a fourth stretch Box B4, a fifth stretch Box B5, a sixth stretch Box B6 and a seventh stretch Box B1B, whereby

the first stretch Box B1A and the seventh stretch Box B1B optionally hybridize with each other, whereby upon hybridization a double-stranded structure is formed,

the first stretch Box B1A comprises a nucleotide sequence of AGYRUG,

the second stretch Box B2 comprises a nucleotide sequence of CCAGCU or CCAGY,

the third stretch Box B3 comprises a nucleotide sequence of GUG,

the fourth stretch Box B4 comprises a nucleotide sequence of AUG,

the fifth stretch Box B5 comprises a nucleotide sequence of GGGGGGCGCGACC

the sixth stretch Box B6 comprises a nucleotide sequence of CAUUUUA or CAUUUA, and

the seventh stretch Box B1B comprises a nucleotide sequence of CAYRCU.

In an embodiment of the second subaspect

the first stretch Box B1A comprises a nucleotide sequence of AGCGUG.

In an embodiment of the second subaspect

the second stretch Box B2 comprises a nucleotide sequence of CCAGU.

In an embodiment of the second subaspect

the sixth stretch Box B6 comprises a nucleotide sequence of CAUUUUA.

In an embodiment of the second subaspect

the seventh stretch Box B1B comprises a nucleotide sequence of CACGCU.

In an embodiment of the second subaspect the nucleic acid comprises a nucleic acid sequence according to SEQ.ID.No 28 and SEQ.ID.No 27.

In a third subaspect of the first aspect the type 2 nucleic acid comprises in 5'->3' direction a first stretch Box B1A, a second stretch Box B2, and a third stretch Box B1B, whereby

the first stretch Box B1A and the third stretch Box B1B optionally hybridize with each other, whereby upon hybridization a double-stranded structure is formed,

the first stretch Box B1A comprises a nucleotide sequence selected from the group comprising ACGCA, CGCA and GCA,

the second stretch Box B2 comprises a nucleotide sequence of CSUCCCUCACCGGUGCAAGUGAAGCCGYGGCUC, and

the third stretch Box B1B comprises a nucleotide sequence selected from the group comprising UGCGU, UGCG and UGC.

In an embodiment of the third subaspect

the second stretch Box B2 comprises a nucleotide sequence of CGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUC.

In an embodiment of the third subaspect

a) the first stretch Box B1A comprises a nucleotide sequence of ACGCA,
and
the third stretch Box B1B comprises a nucleotide sequence of UGCGU; or

b) the first stretch Box B1A comprises a nucleotide sequence of CGCA,

and

the third stretch Box B1B comprises a nucleotide sequence of UGCG; or

c) the first stretch Box B1A comprises a nucleotide sequence of GCA,
and
the third stretch Box B1B comprises a nucleotide sequence of UGC or UGCG.

In an embodiment of the third subaspect

the first stretch Box B1A comprises a nucleotide sequence of GCA.

In a preferred embodiment of the third subaspect

the third stretch Box B1B comprises a nucleotide sequence of UGCG.

In an embodiment of the third subaspect the nucleic acid comprises a nucleic acid sequence according to SEQ.ID.No 37. , SEQ.ID.No 116, SEQ.ID.No 117 and SEQ.ID.No 278.

In a fourth subaspect of the first aspect the type 3 nucleic acid comprises in 5'->3' direction a first stretch Box B1A, a second stretch Box B2A, a third stretch Box B3, a fourth stretch Box B2B, a fifth stretch Box B4, a sixth stretch Box B5A, a seventh stretch Box B6, an eighth stretch Box B5B and a ninth stretch Box B1B, whereby

the first stretch Box B1A and the ninth stretch Box B1B optionally hybridize with each other, whereby upon hybridization a double-stranded structure is formed,

the second stretch Box B2A and the fourth Box B2B optionally hybridize with each other, whereby upon hybridization a double-stranded structure is formed,

the sixth stretch Box B5A and the eighth Box B5B optionally hybridize with each other, whereby upon hybridization a double-stranded structure is formed,

the first stretch Box B1A comprises a nucleotide sequence which is selected from the group comprising GURCUGC, GKSYGC, KBBSC and BNGC,

the second stretch Box B2A comprises a nucleotide sequence of GKMGU,

the third stretch Box B3 comprises a nucleotide sequence of KRRAR,

the fourth stretch Box B2B comprises a nucleotide sequence of ACKMC,

the fifth stretch Box B4 comprises a nucleotide sequence selected from the group comprising CURYGA, CUWAUGA, CWRMGACW and UGCCAGUG,

the sixth stretch Box B5A comprises a nucleotide sequence selected from the group comprising GGY and CWGC,

the seventh stretch Box B6 comprises a nucleotide sequence selected from the group comprising YAGA, CKAAU and CCUUUAU,

the eighth stretch Box B5B comprises a nucleotide sequence selected from the group comprising GCYR and GCWG, and

the ninth stretch Box B1B comprises a nucleotide sequence selected from the groupc comprising GCAGCAC, GCRSMC, GSVVM and GCNV.

In an embodiment of the fourth subaspect

the third stretch Box B3 comprises a nucleotide sequence of GAGAA or UAAAA

In an embodiment of the fourth subaspect

the fifth stretch Box B4 comprises a nucleotide sequence of CAGCGACU or CAACGACU.

In an embodiment of the fourth subaspect

the fifth stretch Box B4 comprises a nucleotide sequence of CAGCGACU and Box B3 comprises a nucleotide sequence of UAAAA.

In an embodiment of the fourth subaspect

the fifth stretch Box B4 comprises a nucleotide sequence of CAACGACU and Box B3 comprises a nucleotide sequence of GAGAA.

In an embodiment of the fourth subaspect

the seventh stretch Box B6 comprises a nucleotide sequence of UAGA.

In an embodiment of the fourth subaspect

a) the first stretch Box B1A comprises a nucleotide sequence of GURCUGC,
and
the ninth stretch Box B1B comprises a nucleotide sequence of GCAGCAC; or

b) the first stretch Box B1A comprises a nucleotide sequence of GKSYGC,
and
the ninth stretch Box B1B comprises a nucleotide sequence of GCRSMC; or

c) the first stretch Box B1A comprises a nucleotide sequence of KBBSC,
and
the ninth stretch Box B1B comprises a nucleotide sequence of GSVVM; or

d) the first stretch Box B1A comprises a nucleotide sequence of BNGC,
and
the ninth stretch Box B1B comprises a nucleotide sequence of GCNV.

In a preferred embodiment of the fourth subaspect

a) the first stretch Box B1A comprises a nucleotide sequence of GUGCUGC,
and

the ninth stretch Box B1B comprises a nucleotide sequence of GCAGCAC; or

b) the first stretch Box B1A comprises a nucleotide sequence of GUGCGC,
and
the ninth stretch Box B1B comprises a nucleotide sequence of GCGCAC; or

c) the first stretch Box B1A comprises a nucleotide sequence of KKSSC,
and
the ninth stretch Box B1B comprises a nucleotide sequence of GSSMM; or

d) the first stretch Box B1A comprises a nucleotide sequence of SNGC,
and
the ninth stretch Box B1B comprises a nucleotide sequence of GCNS.

In a further preferred embodiment of the fourth subaspect

the first stretch Box B1A comprises a nucleotide sequence of GGGC,
and
the ninth stretch Box B1B comprises a nucleotide sequence of GCCC.

In an embodiment of the fourth subaspect the second stretch Box B2A comprises a nucleotide sequence of GKMGU and the fourth stretch Box B2B comprises a nucleotide sequence of ACKMC.

In a preferred embodiment of the fourth subaspect the second stretch Box B2A comprises a nucleotide sequence of GUAGU and the fourth stretch Box B2B comprises a nucleotide sequence of ACUAC.

In an embodiment of the fourth subaspect

a) the sixth stretch Box B5A comprises a nucleotide sequence of GGY,
and
the eighth stretch Box B5B comprises a nucleotide sequence of GCYR; or

b) the sixth stretch Box B5A comprises a nucleotide sequence of CWGC, and
the eighth stretch Box B5B comprises a nucleotide sequence of GCWG.

In a preferred embodiment of the fourth subaspect

the sixth stretch Box B5A comprises a nucleotide sequence of GGC,

and

the eighth stretch Box B5B comprises a nucleotide sequence of GCCG.

In a more preferred embodiment of the fourth subaspect the sixth stretch Box B5A hybridizes with the nucleotides GCY of the eighth stretch Box B5B.

In an embodiment of the fourth subaspect the nucleic acid comprises a nucleic acid sequence according to SEQ.ID.No 56.

In an embodiment of the fourth subaspect the nucleic acid comprises a nucleic acid sequence selected from the group comprising the nucleic acid sequences according to SEQ.ID.No 57 to 61, SEQ.ID.No 67 to 71 and SEQ.ID.No 73.

In a fifth subaspect of the first aspect the type 4 nucleic acid comprises in 5'->3' direction a first stretch Box B1A, a second stretch Box B2, a third stretch Box B1B whereby

the first stretch Box B1A and the third stretch Box B1B optionally hybridize with each other, whereby upon hybridization a double-stranded structure is formed,

the first stretch Box B1A comprises a nucleotide sequence selected from the group comprising AGCGUGDU, GCGCGAG, CSKSUU, GUGUU, and UGUU;

the second stretch Box B2 comprises a nucleotide sequence selected from the group comprising AGNDRDGBKGGURGYARGUAAAG,

AGGUGGGUGGUAGUAAGUAAAG and CAGGUGGGUGGUAGAAUGUAAAGA, and

the third stretch Box B1B comprises a nucleotide sequence selected from the group comprising GNCASGCU, CUCGCGUC, GRSMSG, GRCAC, and GGCA.

In an embodiment of the fifth subaspect

a) the first stretch Box B1A comprises a nucleotide sequence of GUGUU,
and
the third stretch Box B1B comprises a nucleotide sequence of GRCAC;

b) the first stretch Box B1A comprises a nucleotide sequence of GCGCGAG,
and
the third stretch Box B1B comprises a nucleotide sequence of CUCGCGUC; or

c) the first stretch Box B1A comprises a nucleotide sequence of CSKSUU,
and
the third stretch Box B1B comprises a nucleotide sequence of GRSMSG, or

d) the first stretch Box B1A comprises a nucleotide sequence of UGUU,
and
the third stretch Box B1B comprises a nucleotide sequence of GGCA, or

e) the first stretch Box B1A comprises a nucleotide sequence of AGCGUGDU,
and
the third stretch Box B1B comprises a nucleotide sequence of GNCASGCU.

In a preferred embodiment of the fifth subaspect the first stretch Box B1A comprises a nucleotide sequence of CSKSUU and the third stretch Box B1B comprises a nucleotide sequence of GRSMSG.

In a more preferred embodiment of the fifth subaspect the first stretch Box B1A comprises a nucleotide sequence of CCGCUU and the third stretch Box B1B comprises a nucleotide sequence of GGGCGG.

In an embodiment of the fifth subaspect

the second stretch Box B2 comprises a nucleotide sequence of AGGUGGGUGGUAGUAAGUAAAG.

In an embodiment of the fifth subaspect the nucleic acid comprises a nucleic acid sequence according to SEQ.ID.No 80.

In an embodiment of the first to the fifth subaspect the nucleic acid is capable of binding MCP-1, preferably human MCP-1.

In an embodiment of the first to the fifth subaspect the nucleic acid is capable of binding a chemokine, whereby the chemokine is selected from the group comprising eotaxin, MCP-1, MCP-2 and MCP-3.

In an embodiment of the first to the fifth subaspect the nucleic acid is capable of binding a chemokine, whereby the chemokine is selected from the group comprising human eotaxin, human MCP-1, human MCP-2 and human MCP-3.

In an embodiment of the first to the fifth subaspect the nucleic acid is capable of binding MCP-1, whereby MCP-1 is preferably selected from the group comprising monkey MCP-1, horse MCP-1, rabbit MCP-1, bovine MCP-1, canine MCP-1, porcine MCP-1 and human MCP-1.

In an embodiment of the first to the fifth subaspect the nucleic acid is capable of binding human MCP-1.

In a preferred embodiment of the first to the fifth subaspect the MCP-1 has an amino acid sequence according to SEQ ID No. 1.

The problem underlying the present invention is solved in a second aspect by a nucleic acid, preferably binding to murine MCP-1, whereby the nucleic acid comprises a nucleic acid sequence according to SEQ.ID.No. 122, SEQ.ID.No. 253 and SEQ.ID.No. 254.

The problem underlying the present invention is solved in a third aspect by a nucleic acid, preferably binding to murine MCP-1, whereby the nucleic acid comprises a nucleic acid sequence according to SEQ.ID.No. 127.

In an embodiment of the second and third aspect the murine MCP-1 comprises an amino acid sequence according to SEQ ID No. 2.

In an embodiment of the first to the third aspect the nucleic acid comprises a modification, whereby the modification is preferably a high molecular weight moiety and/or whereby the modification preferably allows to modify the characteristics of the nucleic acid according to any of the first, second and third aspect in terms of residence time in the animal or human body, preferably the human body.

In a preferred embodiment of the first to the third aspect the modification is selected from the group comprising a HES moiety and a PEG moiety.

In a more preferred embodiment of the first to the third aspect the modification is a PEG moiety consisting of a straight or branched PEG, whereby the molecular weight of the PEG moiety is preferably from about 20 to 120 kD, more preferably from about 30 to 80 kD and most preferably about 40 kD.

In an alternative more preferred embodiment of the first to the third aspect the modification is a HES moiety, whereby preferably the molecular weight of the HES moiety is from about 10 to 130 kD, more preferably from about 30 to 130 kD and most preferably about 100 kD.

In an embodiment of the first to the third aspect the modification is coupled to the nucleic acid via a linker.

In an embodiment of the first to the third aspect the modification is coupled to the nucleic acid at its 5'-terminal nucleotide and/or its 3'-terminal nucleotide and/or to a nucleotide of the nucleic acid between the 5'-terminal nucleotide and the 3'-terminal nucleotide.

In an embodiment of the first to the third aspect the nucleotides of or the nucleotides forming the nucleic acid are L-nucleotides.

In an embodiment of the first to the third aspect the nucleic acid is an L-nucleic acid.

In an embodiment of the first to the third aspect the moiety of the nucleic acid capable of binding MCP-1 consists of L-nucleotides.

The problem underlying the present invention is solved in a fourth aspect by a pharmaceutical composition comprising a nucleic acid according to the first, second and third aspect and optionally a further constituent, whereby the further constituent is selected from the group comprising pharmaceutically acceptable excipients, pharmaceutically acceptable carriers and pharmaceutically active agents.

In an embodiment of the fourth aspect the pharmaceutical composition comprises a nucleic acid according to any of the first to third aspect and a pharmaceutically acceptable carrier.

The problem underlying the present invention is solved in a fifth aspect by the use of a nucleic acid according to the first, second and third aspect for the manufacture of a medicament.

In an embodiment of the fifth aspect the medicament is for use in human medicine or for use in veterinary medicine.

The problem underlying the present invention is solved in a sixth aspect by the use of a nucleic acid according to the first, second and third aspect for the manufacture of a diagnostic means.

In an embodiment of the fifth aspect and in an embodiment of the sixth aspect the medicament and diagnostic means, respectively, is for the treatment and/or prevention and diagnosis, respectively, of a disease or disorder selected from the group comprising inflammatory diseases, autoimmune diseases, autoimmune encephalomyelitis, stroke, acute and chronic multiple sclerosis, chronic inflammation, rheumatoid arthritis, renal diseases, restenosis, restenosis after angioplasty, acute and chronic allergic reactions, primary and secondary immunologic or allergic reactions, asthma, conjunctivitis, bronchitis, cancer, atherosclerosis, artheriosclerotic cardiovasular heart failure or stroke, psoriasis, psoriatic arthritis, inflammation of the nervous system, atopic dermatitis, colitis, endometriosis, uveitis, retinal disorders including macular degeneration, retinal detachment, diabetic retinopathy, retinopathy of prematurity, retinitis

pigmentosa, proliferative vitreoretinopathy, and central serous chorioretinopathy; idiopathic pulmonary fibrosis, sarcoidosis, polymyositis, dermatomyositis, avoidance of immunosuppression, reducing the risk of infection, sepsis, renal inflammation, glomerulonephritis, rapid progressive glomerulonephritis, proliferative glomerulonephritis, diabetic nephropathy, obstructive nephropathy, acute tubular necrosis, and diffuse glomerulosclerosis, systemic lupus erythematosus, chronic bronchitis, Behçet's disease, amyotrophic lateral sclerosis (ALS), premature atherosclerosis after Kawasaki's disease, myocardial infarction, obesity, chronic liver disease, peyronie's disease, acute spinal chord injury, lung or kidney transplantation, myocarditis, Alzheimer's disease and neuropathy, breast carcinoma, gastric carcinoma, bladder cancer, ovarian cancer, hamartoma, colorectal carcinoma, colonic adenoma, pancreatitis, chronic obstructiv pulmonary disesase (COPD) and inflammatory bowel diseases such as Crohn's disease or ulcerative colitis.

Without wishing to be bound be any theory, the suitability of the nucleic acids of the present invention for diagnostic purposes is mostly based on an increased or decreased chemokine level, whereby such chemokine is selected from the group comprising eotaxin, MCP-1, MCP-2 and MCP-3, more specifically MCP-1. It will be acknowledged by the person skilled in the art that most of the aforementioned diseases show such increased or decreased chemokine level.

The problem underlying the present invention is solved in a seventh aspect by a complex comprising a chemokine and a nucleic acid according to the first, second and third aspect, whereby the chemokine is selected from the group comprising eotaxin, MCP-1, MCP-2 and MCP-3, whereby preferably the complex is a crystalline complex.

In an embodiment of the seventh aspect the chemokine is selected from the group comprising human eotaxin, human MCP-1, human MCP-2 and human MCP-3.

In an embodiment of the seventh aspect the chemokine is MCP-1, whereby MCP-1 is preferably selected from the group comprising human MCP-1, monkey MCP-1, horse MCP-1, rabbit MCP-1, bovine MCP-1, canine MCP-1 and porcine MCP-1, more preferably MCP-1 is human MCP-1.

The problem underlying the present invention is solved in an eighth aspect by the use of a nucleic acid according to the first, second and third aspect for the detection of a chemokine,

whereby the chemokine is selected from the group comprising eotaxin, MCP-1, MCP-2 and MCP-3.

In an embodiment of the eighth aspect the chemokine is selected from the group comprising human eotaxin, human MCP-1, human MCP-2 and human MCP-3.

In an embodiment of the eighth aspect the chemokine is MCP-1, whereby MCP-1 is preferably selected from the group comprising human MCP-1, monkey MCP-1, horse MCP-1, rabbit MCP-1, bovine MCP-1, canine MCP-1 and porcine MCP-1, more preferably MCP-1 is human MCP-1.

The problem underlying the present invention is solved in a ninth aspect by a method for the screening of a chemokine antagonist or a chemokine agonist comprising the following steps:

- providing a candidate chemokine antagonist and/or a candidate chemokine agonist,

- providing a nucleic acid according to the first, second or third aspect,

- providing a test system which provides a signal in the presence of a chemokine antagonist and/or a chemokine agonist, and

- determining whether the candidate chemokine antagonist is a chemokine antagonist and/or whether the candidate chemokine agonist is a chemokine agonist,

whereby the chemokine is selected from the group comprising eotaxin, MCP-1, MCP-2 and MCP-3.

In an embodiment of the nineth aspect the chemokine is selected from the group comprising human eotaxin, human MCP-1, human MCP-2 and human MCP-3.

In an embodiment of the nineth aspect the chemokine is MCP-1, whereby MCP-1 is preferably selected from the group comprising human MCP-1, monkey MCP-1, horse MCP-1, rabbit MCP-1, bovine MCP-1, canine MCP-1 and porcine MCP-1, more preferably MCP-1 is human MCP-1.

The problem underlying the present invention is solved in a tenth aspect by a method for the screening of a chemokine agonist and/or a chemokine antagonist comprising the following steps:

- providing a chemokine immobilised to a phase, preferably a solid phase,
- providing a nucleic acid according to the first, second or third aspect, preferably a nucleic acid according to the first aspect which is labelled,
- adding a candidate chemokine agonist and/or a candidate chemokine antagonist, and
- determining whether the candidate chemokine agonist is a chemokine agonist and/or whether the candidate chemokine antagonist is a chemokine antagonist,

whereby the chemokine is selected from the group comprising eotaxin, MCP-1, MCP-2 and MCP-3.

In an embodiment of the tenth aspect the determining is carried out such that it is assessed whether the nucleic acid is replaced by the candidate chemokine_agonist or by a candidate chemokine antagonist.

In an embodiment of the tenth aspect the chemokine is selected from the group comprising human eotaxin, human MCP-1, human MCP-2 and human MCP-3.

In an embodiment of the tenth aspect the chemokine is MCP-1, whereby MCP-1 is preferably selected from the group comprising human MCP-1, monkey MCP-1, horse MCP-1, rabbit MCP-1, bovine MCP-1, canine MCP-1 and porcine MCP-1, more preferably MCP-1 is human MCP-1.

The problem underlying the present invention is solved in an eleventh aspect by a kit for the detection of a chemokine, comprising a nucleic acid according to the first, second and third aspect, whereby the chemokine is selected from the group comprising eotaxin, MCP-1, MCP-2 and MCP-3.

In an embodiment of the eleventh aspect the chemokine is selected from the group comprising human eotaxin, human MCP-1, human MCP-2 and human MCP-3.

In an embodiment of the eleventh aspect the chemokine is MCP-1, whereby MCP-1 is preferably selected from the group comprising human MCP-1, monkey MCP-1, horse MCP-1, rabbit MCP-1, bovine MCP-1, canine MCP-1 and porcine MCP-1, more preferably MCP-1 is human MCP-1.

The problem underlying the present invention is solved in a twelfth aspect by a chemokine antagonist obtainable by the method according to the tenth aspect or the ninth aspect, whereby the chemokine is selected from the group comprising eotaxin, MCP-1, MCP-2 and MCP-3.

In an embodiment of the twelfth aspect the chemokine is selected from the group comprising human eotaxin, human MCP-1, human MCP-2 and human MCP-3.

In an embodiment of the twelfth aspect the chemokine is MCP-1, whereby MCP-1 is preferably selected from the group comprising human MCP-1, monkey MCP-1, horse MCP-1, rabbit MCP-1, bovine MCP-1, canine MCP-1 and porcine MCP-1, more preferably MCP-1 is human MCP-1.

The problem underlying the present invention is solved in a thirteenth aspect by a chemokine agonist obtainable by the method according to the tenth aspect or the ninth aspect, whereby the chemokine is selected from the group comprising eotaxin, MCP-1, MCP-2 and MCP-3.

In an embodiment of the thirteenth aspect the chemokine is selected from the group comprising human eotaxin, human MCP-1, human MCP-2 and human MCP-3.

In an embodiment of the thirteenth aspect the chemokine is MCP-1, whereby MCP-1 is preferably selected from the group comprising human MCP-1, monkey MCP-1, horse MCP-1, rabbit MCP-1, bovine MCP-1, canine MCP-1 and porcine MCP-1, more preferably MCP-1 is human MCP-1.

It will be acknowledged by the person skilled in the art that a chemokine agonist and/or a chemokine antagonist is preferably an agonist and antagonist, respectively, addressing the respective chemokine as specified herein. Accordingly, the chemokine agonist and chemokine antagonist is, for example, an MCP-1 agonist and MCP-1 antagonist, respectively.

The problem underlying the present invention is solved in a fourteenth aspect by a method for the detection of the nucleic acid according to any of the first, second and third aspect in a sample, whereby the method comprises the steps of:

a) providing a sample containing the nucleic acid according to the present invention;
b) providing a capture probe, whereby the capture probe is at least partially complementary to a first part of the nucleic acid according to any of the first, second and third aspect, and a detection probe, whereby the detection probe is at least partially complementary to a second part of the nucleic acid according to any of the first, second and third aspect, or, alternatively, the capture probe is at least partially complementary to a second part of the nucleic acid according to any of the first, second and third aspect and the detection probe is at least partially complementary to the first part of the nucleic acid according to any of the first, second and third aspect;
c) allowing the capture probe and the detection probe to react either simultaneously or in any order sequentially with the nucleic acid according to any of the first, second and third aspect or part thereof;
d) optionally detecting whether or not the capture probe is hybridized to the nucleic acid according to the nucleic acid according to any of the first, second and third aspect provided in step a); and
e) detecting the complex formed in step c) consisting of the nucleic acid according to any of the first, second and third aspect, and the capture probe and the detection probe.

In an embodiment of the fourteenth aspect the detection probe comprises a detection means, and/or whereby the capture probe can be immobilized to a support, preferably a solid support.

In an embodiment of the fourteenth aspect any detection probe which is not part of the complex is removed from the reaction so that in step e) only a detection probe which is part of the complex, is detected.

In an embodiment of the fourteenth aspect step e) comprises the step of comparing the signal generated by the detection means when the capture probe and the detection probe are hybridized

in the presence of the nucleic acid according to any of the first, second or third aspect or part thereof, and in the absence of said nucleic acid or part thereof.

In an embodiment of the fourteenth aspect the nucleic acid to be detected is the nucleic acid having a nucleic acid sequence according to SEQ. ID. NOs. 37, 116, 117 or 278, and the capture probe or detection probe comprises a nucleic acid sequence according to SEQ .ID. NO. 255 or SEQ. ID. NO. 256.

In an embodiment of the fourteenth aspect the nucleic acid to be detected is the nucleic acid having a nucleic acid sequence according to SEQ. ID. NOs. 122, 253 or 254 and the capture probe or detection probe comprises a nucleic acid sequence according to SEQ. ID. NO. 281 and SEQ. ID. NO. 282.

The problem underlying the present invention is also solved by the subject matter of the independent claims attached hereto. Preferred embodiment may be taken from the attached dependent claims.

The features of the nucleic acid according to the present invention as described herein can be realised in any aspect of the present invention where the nucleic acid is used, either alone or in any combination.

Human as well as murine MCP-1 are basic proteins having the amino acid sequence according to SEQ. ID. Nos. 1 and 2, respectively.

The finding that short high affinity binding nucleic acids to MCP-1 could be identified, is insofar surprising as Eaton et al. (1997) observed that the generation of aptamers, i.e. D-nucleic acids binding to a target molecule, directed to a basic protein is in general very difficult because this kind of target produces a high but non-specific signal-to-noise ratio. This high signal-to-noise ratio results from the high non-specific affinity shown by nucleic acids for basic targets such as MCP-1.

As outlined in more detail in the claims and example 1, the present inventors could more surprisingly identify a number of different MCP-1 binding nucleic acid molecules, whereby most of the nucleic acids could be characterised in terms of stretches of nucleotide which are also

referred to herein as Boxes. The various MCP-1 binding nucleic acid molecules can be categorised based on said Boxes and some structural features and elements, respectively. The various categories thus defined are also referred to herein as types and more specifically as type 1A, type 1B, type 2, type 3 and type 4.

The nucleic acids according to the present invention shall also comprise nucleic acids which are essentially homologous to the particular sequences disclosed herein. The term substantially homologous shall be understood such that the homology is at least 75%, preferably 85%, more preferably 90% and most preferably more than 95 %, 96 %, 97 %, 98 % or 99%.

The actual percentage of homologous nucleotides present in the nucleic acid according to the present invention will depend on the total number of nucleotides present in the nucleic acid. The percent modification can be based upon the total number of nucleotides present in the nucleic acid.

The homology can be determined as known to the person skilled in the art. More specifically, a sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters. The test sequence is preferably the sequence or nucleic acid molecule which is said to be or to be tested whether it is homologous, and if so, to what extent, to another nucleic acid molecule, whereby such another nucleic acid molecule is also referred to as the reference sequence. In an embodiment, the reference sequence is a nucleic acid molecule as described herein, more preferably a nucleic acid molecule having a sequence according to any of SEQ. ID. NOs. 10 to 129, 132 to 256 and 278 – 282. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman (Smith & Waterman, 1981) by the homology alignment algorithm of Needleman & Wunsch (Needleman & Wunsch, 1970) by the search for similarity method of Pearson & Lipman (Pearson & Lipman, 1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis.), or by visual inspection.

One example of an algorithm that is suitable for determining percent sequence identity is the algorithm used in the basic local alignment search tool (hereinafter "BLAST "), see, e.g. Altschul

et al (Altschul et al. 1990 and Altschul et al, 1997). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (hereinafter "NCBI"). The default parameters used in determining sequence identity using the software available from NCBI, e.g., BLASTN (for nucleotide sequences) and BLASTP (for amino acid sequences) are described in McGinnis et al (McGinnis et al , 2004).

The term inventive nucleic acid or nucleic acid according to the present invention shall also comprise those nucleic acids comprising the nucleic acids sequences disclosed herein or part thereof, preferably to the extent that the nucleic acids or said parts are involved in the binding to MCP-1. The term inventive nucleic acid as preferably used herein, shall also comprise in an embodiment a nucleic acid which is suitable to bind to any molecule selected from the group comprising MCP-2, MCP-3, MCP-4, and eotaxin. It will be acknowledged by the ones skilled in the art that the individual nucleic acids according to the present invention will bind to one or several of such molecules. Such nucleic acid is, in an embodiment, one of the nucleic acid molecules described herein, or a derivative and/ or a metabolite thereof, whereby such derivative and/ or metabolite are preferably a truncated nucleic acid compared to the nucleic acid molecules described herein. Truncation may be related to either or both of the ends of the nucleic acids as disclosed herein. Also, truncation may be related to the inner sequence of nucleotides of the nucleic acid, i.e. it may be related to the nucleotide(s) between the 5' and the 3' terminal nucleotide, respectively. Moreover, truncation shall comprise the deletion of as little as a single nucleotide from the sequence of the nucleic acids disclosed herein. Truncation may also be related to more than one stretch of the inventive nucleic acid(s), whereby the stretch can be as little as one nucleotide long. The binding of a nucleic acid according to the present invention, preferably to a molecule selected from the group comprising MCP-1, MCP-2, MCP-3, MCP-4 and eotaxin, can be determined by the ones skilled in the art using routine experiments or by using or adopting a method as described herein, preferably as described herein in the example part. It is within an embodiment of the present invention, unless explicitly indicated to the contrary, that whenever it is referred herein to the binding of the nucleic acids according to the present invention to or with MCP-1, this applies also to the binding of the nucleic acids according to the present invention to or with any molecule selected from the group comprising MCP-2, MCP-3, MCP-4 and eotaxin.

The nucleic acids according to the present invention may be either D-nucleic acids or L-nucleic acids. Preferably, the inventive nucleic acids are L-nucleic acids. In addition it is possible that

one or several parts of the nucleic acid are present as D-nucleic acids or at least one or several parts of the nucleic acids are L-nucleic acids. The term "part" of the nucleic acids shall mean as little as one nucleotide. Such nucleic acids are generally referred to herein as D- and L-nucleic acids, respectively. Therefore, in a particularly preferred embodiment, the nucleic acids according to the present invention consist of L-nucleotides and comprise at least one D-nucleotide. Such D-nucleotide is preferably attached to a part different from the stretches defining the nucleic acids according to the present invention, preferably those parts thereof, where an interaction with other parts of the nucleic acid is involved. Preferably, such D-nucleotide is attached at a terminus of any of the stretches and of any nucleic acid according to the present invention, respectively. In a further preferred embodiment, such D-nucleotides may act as a spacer or a linker, preferably attaching modifications such as PEG and HES to the nucleic acids according to the present invention.

It is also within an embodiment of the present invention that each and any of the nucleic acid molecules described herein in their entirety in terms of their nucleic acid sequence(s) are limited to the particular nucleotide sequence(s). In other words, the terms "comprising" or "comprise(s)" shall be interpreted in such embodiment in the meaning of containing or consisting of.

It is also within the present invention that the nucleic acids according to the present invention are part of a longer nucleic acid whereby this longer nucleic acid comprises several parts whereby at least one such part is a nucleic acid according to the present invention, or a part thereof. The other part(s) of these longer nucleic acids can be either one or several D-nucleic acid(s) or one or several L-nucleic acid(s). Any combination may be used in connection with the present invention. These other part(s) of the longer nucleic acid either alone or taken together, either in their entirety or in a particular combination, can exhibit a function which is different from binding, preferably from binding to MCP-1. One possible function is to allow interaction with other molecules, whereby such other molecules preferably are different from MCP-1, such as, e.g., for immobilization, cross-linking, detection or amplification. In a further embodiment of the present invention the nucleic acids according to the invention comprise, as individual or combined moieties, several of the nucleic acids of the present invention. Such nucleic acid comprising several of the nucleic acids of the present invention is also encompassed by the term longer nucleic acid.

L-nucleic acids as used herein are nucleic acids consisting of L-nucleotides, preferably consisting completely of L-nucleotides.

D-nucleic acids as used herein are nucleic acids consisting of D-nucleotides, preferably consisting completely of D-nucleotides.

The terms nucleic acid and nucleic acid molecule are used herein in an interchangeable manner if not explicitly indicated to the contrary.

Also, if not indicated to the contrary, any nucleotide sequence is set forth herein in 5' → 3' direction.

Irrespective of whether the inventive nucleic acid consists of D-nucleotides, L-nucleotides or a combination of both with the combination being e.g. a random combination or a defined sequence of stretches consisting of at least one L-nucleotide and at least one D-nucleic acid, the nucleic acid may consist of desoxyribonucleotide(s), ribonucleotide(s) or combinations thereof.

Designing the inventive nucleic acids as L-nucleic acid is advantageous for several reasons. L-nucleic acids are enantiomers of naturally occurring nucleic acids. D-nucleic acids, however, are not very stable in aqueous solutions and particularly in biological systems or biological samples due to the widespread presence of nucleases. Naturally occurring nucleases, particularly nucleases from animal cells are not capable of degrading L-nucleic acids. Because of this the biological half-life of the L-nucleic acid is significantly increased in such a system, including the animal and human body. Due to the lacking degradability of L-nucleic acid no nuclease degradation products are generated and thus no side effects arising therefrom observed. This aspect delimits the L-nucleic acid of factually all other compounds which are used in the therapy of diseases and/or disorders involving the presence of MCP-1. L-nucleic acids which specifically bind to a target molecule through a mechanism different from Watson Crick base pairing, or aptamers which consists partially or completely of L-nucleotides, particularly with those parts of the aptamer being involved in the binding of the aptamer to the target molecule, are also called spiegelmers.

It is also within the present invention that the inventive nucleic acids, also referred to herein as nucleic acids according to the invention, regardless whether they are present as D-nucleic acids,

L-nucleic acids or D, L-nucleic acids or whether they are DNA or RNA, may be present as single-stranded or double-stranded nucleic acids. Typically, the inventive nucleic acids are single-stranded nucleic acids which exhibit defined secondary structures due to the primary sequence and may thus also form tertiary structures. The inventive nucleic acids, however, may also be double-stranded in the meaning that two strands which are complementary or partially complementary to each other are hybridised to each other. This confers stability to the nucleic acid which, in particular, will be advantageous if the nucleic acid is present in the naturally occurring D-form rather than the L-form.

The inventive nucleic acids may be modified. Such modifications may be related to the single nucleotide of the nucleic acid and are well known in the art. Examples for such modification are described in, among others, Venkatesan (2003); Kusser (2000); Aurup (1994); Cummins (1995); Eaton (1995); Green (1995); Kawasaki (1993); Lesnik (1993); and Miller (1993). Such modification can be a H atom, a F atom or O-CH3 group or NH2-group at the 2' position of the individual nucleotide of which the nucleic acid consists. Also, the nucleic acid according to the present invention can comprises at least one LNA nucleotide. In an embodiment the nucleic acid according to the present invention consists of LNA nucleotides.

In an embodiment, the nucleic acids according to the present invention may be a multipartite nucleic acid. A multipartite nucleic acid as used herein, is a nucleic acid which consists of at least two nucleic acid strands. These at least two nucleic acid strands form a functional unit whereby the functional unit is a ligand to a target molecule. The at least two nucleic acid strands may be derived from any of the inventive nucleic acids by either cleaving the nucleic acid to generate two strands or by synthesising one nucleic acid corresponding to a first part of the inventive, i.e. overall nucleic acid and another nucleic acid corresponding to the second part of the overall nucleic acid. It is to be acknowledged that both the cleavage and the synthesis may be applied to generate a multipartite nucleic acid where there are more than two strands as exemplified above. In other words, the at least two nucleic acid strands are typically different from two strands being complementary and hybridising to each other although a certain extent of complementarity between the various nucleic acid parts may exist.

Finally it is also within the present invention that a fully closed, i.e. circular structure for the nucleic acids according to the present invention is realized, i.e. that the nucleic acids according to the present invention are closed, preferably through a covalent linkage, whereby more

preferably such covalent linkage is made between the 5' end and the 3' end of the nucleic acid sequences as disclosed herein.

The present inventors have discovered that the nucleic acids according to the present invention exhibit a very favourable K_D value range.

A possibility to determine the binding constant is the use of the so called biacore device, which is also known to the one skilled in the art. Affinity as used herein was also measured by the use of the "pull-down assay" as described in the examples. An appropriate measure in order to express the intensity of the binding between the nucleic acid according to the target which is in the present case MCP-1, is the so-called K_D value which as such as well the method for its determination are known to the one skilled in the art.

The nucleic acids according to the present invention are characterized by a certain K_D value. Preferably, the K_D value shown by the nucleic acids according to the present invention is below 1 μM. A K_D value of about 1 μM is said to be characteristic for a non-specific binding of a nucleic acid to a target. As will be acknowledged by the ones in the art, the K_D value of a group of compounds such as the nucleic acids according to the present invention are within a certain range. The above-mentioned K_D of about 1 μM is a preferred upper limit for the K_D value. The preferred lower limit for the K_D of target binding nucleic acids can be about 10 picomolar or higher. It is within the present invention that the K_D values of individual nucleic acids binding to MCP-1 is preferably within this range. Preferred ranges can be defined by choosing any first number within this range and any second number within this range. Preferred upper values are 250 nM and 100 nM, preferred lower values are 50 nM, 10 nM, 1 nM, 100 pM and 10 pM.

The nucleic acid molecules according to the present invention may have any length provided that they are still able to bind to the target molecule. It will be acknowledged in the art that there are preferred lengths of the nucleic acids according to the present inventions. Typically, the length is between 15 and 120 nucleotides. It will be acknowledged by the ones skilled in the art that any integer between 15 and 120 is a possible length for the nucleic acids according to the present invention. More preferred ranges for the length of the nucleic acids according to the present invention are lengths of about 20 to 100 nucleotides, about 20 to 80 nucleotides, about 20 to 60 nucleotides, about 20 to 50 nucleotides and about 30 to 50 nucleotides.

It is within the present invention that the nucleic acids disclosed herein comprise a moiety which preferably is a high molecular weight moiety and/or which preferably allows to modify the characteristics of the nucleic acid in terms of, among others, residence time in the animal body, preferably the human body. A particularly preferred embodiment of such modification is PEGylation and HESylation of the nucleic acids according to the present invention. As used herein PEG stands for poly(ethylene glycole) and HES for hydroxyethly starch. PEGylation as preferably used herein is the modification of a nucleic acid according to the present invention whereby such modification consists of a PEG moiety which is attached to a nucleic acid according to the present invention. HESylation as preferably used herein is the modification of a nucleic acid according to the present invention whereby such modification consists of a HES moiety which is attached to a nucleic acid according to the present invention. These modifications as well as the process of modifying a nucleic acid using such modifications, is described in European patent application EP 1 306 382, the disclosure of which is herewith incorporated in its entirety by reference.

Preferably, the molecular weight of a modification consisting of or comprising a high molecular weight moiety is about from 2,000 to 200,000 Da, preferably 20,000 to 120,000 Da, particularly in case of PEG being such high molecular weight moiety, and is preferably about from 3,000 to 180,000 Da, more preferably from 5,000 to 130,000 Da, particularly in case of HES being such high molecular weight moiety. The process of HES modification is, e.g., described in German patent application DE 1 2004 006 249.8 the disclosure of which is herewith incorporated in its entirety by reference.

It is within the present invention that either of PEG and HES may be used as either a linear or branched from as further described in the patent applications WO2005074993 and PCT/EP02/11950. Such modification can, in principle, be made to the nucleic acid molecules of the present invention at any position thereof. Preferably such modification is made either to the 5' –terminal nucleotide, the 3'-terminal nucleotide and/or any nucleotide between the 5' nucleotide and the 3' nucleotide of the nucleic acid molecule.

The modification and preferably the PEG and/or HES moiety can be attached to the nucleic acid molecule of the present invention either directly or through a linker. It is also within the present invention that the nucleic acid molecule according to the present invention comprises one or more modifications, preferably one or more PEG and/or HES moiety. In an embodiment the

individual linker molecule attaches more than one PEG moiety or HES moiety to a nucleic acid molecule according to the present invention. The linker used in connection with the present invention can itself be either linear or branched. This kind of linkers are known to the ones skilled in the art and are further described in the patent applications WO2005074993 and PCT/EP02/11950.

Without wishing to be bound by any theory, it seems that by modifying the nucleic acids according to the present invention with high molecular weight moiety such as a polymer and more particularly the polymers disclosed herein, which are preferably physiologically acceptable, the excretion kinetic is changed. More particularly, it seems that due to the increased molecular weight of such modified inventive nucleic acids and due to the nucleic acids not being subject to metabolism particularly when in the L form, excretion from an animal body, preferably from a mammalian body and more preferably from a human body is decreased. As excretion typically occurs via the kidneys, the present inventors assume that the glomerular filtration rate of the thus modified nucleic acid is significantly reduced compared to the nucleic acids not having this kind of high molecular weight modification which results in an increase in the residence time in the body. In connection therewith it is particularly noteworthy that, despite such high molecular weight modification the specificity of the nucleic acid according to the present invention is not affected in a detrimental manner. Insofar, the nucleic acids according to the present invention have surprising characteristics - which normally cannot be expected from pharmaceutically active compounds - such that a pharmaceutical formulation providing for a sustained release is not necessarily required to provide for a sustained release. Rather the nucleic acids according to the present invention in their modified form comprising a high molecular weight moiety, can as such already be used as a sustained release-formulation. Insofar, the modification(s) of the nucleic acid molecules as disclosed herein and the thus modified nucleic acid molecules and any composition comprising the same may provide for a distinct, preferably controlled pharmacokinetics and biodistribution thereof. This also includes residence time in circulation and distribution to tissues. Such modifications are further described in the patent application PCT/EP02/11950.

However, it is also within the present invention that the nucleic acids disclosed herein do not comprise any modification and particularly no high molecular weight modification such as PEGylation or HESylation. Such embodiment is particularly preferred when the nucleic acid shows preferential distribution to any target organ or tissue in the body. Nucleic acid agents with

such a distributive profile would allow establishment of effective local concentrations in the target tissue while keeping systemic concentration low. This would allow the use of low doses which is not only beneficial from an economic point of view, but also reduces unnecessary exposure of other tissues to the nucleic acid agent, thus reducing the potential risk of side effects.

The inventive nucleic acids, which are also referred to herein as the nucleic acids according to the present invention, and/or the antagonists according to the present invention may be used for the generation or manufacture of a medicament. Such medicament or a pharmaceutical composition according to the present invention contains at least one of the inventive nucleic acids, optionally together with further pharmaceutically active compounds, whereby the inventive nucleic acid preferably acts as pharmaceutically active compound itself. Such medicaments comprise in preferred embodiments at least a pharmaceutically acceptable carrier. Such carrier may be, e.g., water, buffer, PBS, glucose solution, preferably a 5% glucose salt balanced solution, starch, sugar, gelatine or any other acceptable carrier substance. Such carriers are generally known to the one skilled in the art. It will be acknowledged by the person skilled in the art that any embodiments, use and aspects of or related to the medicament of the present invention is also applicable to the pharmaceutical composition of the present invention and vice versa.

The indication, diseases and disorders for the treatment and/or prevention of which the nucleic acids, the pharmaceutical compositions and medicaments in accordance with or prepared in accordance with the present invention result from the involvement, either direct or indirect, of MCP-1 in the respective pathogenetic mechanism. However, also those indications, diseases and disorders can be treated and prevented in the pathogenetic mechanism of which MCP-2, MCP-3, MCP-4 and/or eotaxin are either directly or indirectly involved. It is obvious for the ones skilled in the art that particularly those nucleic acids according to the present invention can be used insofar, i.e. for the diseases involving in the broader sense MCP-2, MCP-3, MCP-4 and eotaxin, which interact and bind, respectively, to or with MCP-2, MCP-3, MCP-4 and eotaxin, respectively.

More specifically, such uses arise, among others, from the expression pattern of MCP-1 which suggests that it plays important roles in human diseases that are characterized by mononuclear cell infiltration. Such cell infiltration is present in many inflammatory and autoimmune diseases.

In animal models, MCP-1 has been shown to be expressed in the brain after focal ischemia (Kim 1995; Wang 1995) and during experimental autoimmune encephalomyelitis (Hulkower 1993; Ransohoff 1993; Banisor 2005). MCP-1 may be an important chemokine that targets mononuclear cells in the disease process illustrated by these animal models, such as stroke and multiple sclerosis.

A large body of evidence argues in favor of a unique role of the MCP-1/CCR2 axis in monocyte chemoattraction and thus chronic inflammation: (i) MCP-1- or CCR2-deficient mice show markedly reduced macrophage chemotactic response while otherwise appearing normal (Kuziel 1997; Kurihara 1997; Boring 1997; Lu 1998). (ii), despite functional redundancy with other chemokines in vitro, loss of MCP-1 effector function alone is sufficient to impair monocytic trafficking in several inflammatory models (Lloyd 1997; Furuichi 2003; Egashira 2002; Galasso 2000; Ogata 1997; Kennedy 1998; Gonzalo 1998; Kitamoto 2003). (iii), MCP-1 levels are elevated in many inflammatory diseases. In fact, MCP-1 is thought to play a role in many diseases with and without an obvious inflammatory component such as rheumatoid arthritis (Koch 1992; Hosaka 1994; Akahoshi 1993; Harigai 1993; Rollins 1996), renal disease (Wada 1996; Viedt 2002), restenosis after angioplasty (Economou 2001), allergy and asthma (Alam 1996; Holgate 1997; Gonzalo 1998), cancer (Salcedo 2000; Gordillo 2004), atherosclerosis (Nelken 1991; Yla-Herttuala 1991; Schwartz 1993; Takeya 1993; Boring 1998), psoriasis (Vestergaard 2004), inflammation of the nervous system (Huang 2001), atopic dermatitis (Kaburagi 2001), colitis (Okuno 2002), endometriosis (Jolicoeur 2001), uveitis (Tuaillon 2002), retinal disorders (Nakazawa 2007), idiopathic pulmonary fibrosis and sarcoidosis (Iyonaga 1994) and polymyositis/dermatomyositis (De Bleecker 2002).

Therapeutic intervention with anti-MCP-1 agents – or CCR2 antagonists – would affect the excess inflammatory monocyte trafficking but may spare basal trafficking of phagocytes, thereby avoiding general immunosuppression and increased risk of infections (Dawson 2003).

Additionally, based on the increasing knowledge on the molecular mechanisms of the inflammatory process and the interplay of locally secreted mediators of inflammation, new targets for the therapy of kidney diseases have been identified (Holdsworth 2000; Segerer 2000).

One of those targets, for which robust data on expression and interventional studies with specific antagonists in appropriate animal models exist is MCP-1. This protein has a widely non-redundant role for immune-cell recruitment to sites of renal inflammation. Infiltration of immune cells to the kidney is thought to be a major mechanism of structural renal damage and decline of renal function in the development of various forms of kidney disease.

All types of renal cells can express chemokines including MCP-1 upon stimulation *in vitro* (Segerer 2000); there is a long list of stimuli that trigger MCP-1 expression *in vitro* including cytokines, oxygen radicals, immune complexes, and lipid mediators.

In healthy kidneys of rats and mice, MCP-1 is not expressed, but is readily upregulated during the course of acute and chronic rodent models of renal inflammation including immune complex glomerulonephritis, rapid progressive glomerulonephritis, proliferative glomerulonephritis, diabetic nephropathy, obstructive nephropathy, or acute tubular necrosis (Segerer 2000; Anders 2003). The expression data for MCP-1 in rodents do correlate well with the respective expression found in human renal biopsies (Rovin 1994; Cockwell 1998; Wada 1999). Furthermore, renal expression in human kidneys is associated with disease activity and declines when appropriate therapy induced disease remission (Amann 2003).

Glomerular mononuclear cell infiltration is associated with the development of a diffuse glomerulosclerosis in patients with diabetic nephropathy. MCP-1 plays an important role in the recruitment and accumulation of monocytes and lymphocytes within the glomerulus (Banba 2000; Morii 2003).

Locally produced MCP-1 seems to be particularly involved in the initiation and progression of tubulointerstitial damage, as documented in experiments using transgenic mice with nephrotoxic serum-induced nephritis (NSN). MCP-1 was mainly detected in vascular endothelial cells, tubular epithelial cells and infiltrated mononuclear cells in the interstitial lesions. The MCP-1 mediated activation of tubular epithelial cells is consistent with the notion that MCP-1 contributes to tubulointerstitial inflammation, a hallmark of progressive renal disease (Wada 2001; Viedt 2002)

Due to the homology between MCP-1 on the one hand and MCP-2, MCP-3, MCP-4 and eotaxin on the other hand, the nucleic acids according to the present invention, at least those of them which interact with or bind to MCP-2, MCP-3, MCP-4 and eotaxin, respectively, can typically be used for the treatment, prevention and/or diagnosis of any disease where MCP-2, MCP-3, MCP-4 and eotaxin, respectively, is either directly or indirectly involved. Involved as preferably used herein, means that if the respective molecule which is involved in the disease, is prevented from exerting one, several or all of its functions in connection with the pathogenetic mechanism underlying the disease, the disease will be cured or the extent thereof decreased or the outbreak thereof prevented; at least the symptoms or any indicator of such disease will be relieved and improved, respectively, such that the symptoms and indicator, respectively, is identical or closer to the one(s) observed in a subject not suffering from the disease or not being at risk to develop such disease.

Of course, because the MCP-1 binding nucleic acids according to the present invention interact with or bind to human or murine MCP-1, a skilled person will generally understand that the MCP-1 binding nucleic acids according to the present invention can easily be used for the treatment, prevention and/or diagnosis of any disease as described herein of humans and animals.

These members of the monocyte chemoattractant protein (MCP) family, i.e. MCP-2, MCP-3, MCP-4 and eotaxin thus share a high degree of sequence similarity with MCP-1. Although not exclusively, eotaxin, MCP-2, -3, and –4 interact via CCR3, the characteristic chemokine receptor on human eosinophils (Heath 1997). The CCR3 receptor is upregulated in neoplastic conditions, such as cutaneous T-cell lymphoma (Kleinhans 2003), glioblastoma (Kouno 2004), or renal cell carcinoma (Johrer 2005).

More specifically, increased levels of eotaxin are directly associated with asthma diagnosis and compromised lung function (Nakamura 1999). Elevated expression of eotaxin at sites of allergic inflammation has been observed in both atopic and nonatopic asthmatics (Ying 1997; Ying 1999). Also, mRNAs coding for MCP-2 and –4 are constitutively expressed in a variety of tissues; their physiological functions in these contexts, however, are unknown. Plasma MCP-2 levels are elevated in sepsis together with MCP-1 (Bossink 1995); MCP-3 expression occurs in

asthmatics (Humbert 1997). Finally, MCP-4 can be found at the luminal surface of atherosclerotic vessels (Berkhout 1997).

Accordingly, disease and/or disorders and/or diseased conditions for the treatment and/or prevention of which the medicament according to the present invention may be used include, but are not limited to inflammatory diseases, autoimmune diseases, autoimmune encephalomyelitis, stroke, acute and chronic multiple sclerosis, chronic inflammation, rheumatoid arthritis, renal diseases, restenosis, restenosis after angioplasty, acute and chronic allergic reactions, primary and secondary immunologic or allergic reactions, asthma, conjunctivitis, bronchitis, cancer, atherosclerosis, artheriosclerotic cardiovasular heart failure or stroke, psoriasis, psoriatic arthritis, inflammation of the nervous system, atopic dermatitis, colitis, endometriosis, uveitis, retinal disorders including macular degeneration, retinal detachment, diabetic retinopathy, retinopathy of prematurity, retinitis pigmentosa, proliferative vitreoretinopathy, and central serous chorioretinopathy; idiopathic pulmonary fibrosis, sarcoidosis, polymyositis, dermatomyositis, avoidance of immunosuppression, reducing the risk of infection, sepsis, renal inflammation, glomerulonephritis, rapid progressive glomerulonephritis, proliferative glomerulonephritis, diabetic nephropathy, obstructive nephropathy, acute tubular necrosis, and diffuse glomerulosclerosis, systemic lupus erythematosus, chronic bronchitis, Behçet's disease, amyotrophic lateral sclerosis (ALS), premature atherosclerosis after Kawasaki's disease, myocardial infarction, obesity, chronic liver disease, peyronie's disease, acute spinal chord injury, lung or kidney transplantation, myocarditis, Alzheimer's disease, and neuropathy, breast carcinoma, gastric carcinoma, bladder cancer, ovarian cancer, hamartoma, colorectal carcinoma, colonic adenoma, pancreatitis, chronic obstructiv pulmonary disesase (COPD) and inflammatory bowel diseases such as Crohn's disease or ulcerative colitis.

In a further embodiment, the medicament comprises a further pharmaceutically active agent. Such further pharmaceutically active compounds are, among others but not limited thereto, those known to control blood pressure and diabetes such as angiotensin converting enzyme (ACE) inhibitors and angiotensin receptor blockers. The further pharmaceutically active compound can be, in a further embodiment, also one of those compounds which reduce infiltration of immune cells to sites of chronic inflammation or generally suppress the exuberant immune response that is present in chronic inflammatory settings and that leads to tissue damage. Such compounds can be, but are not limited to, steroids or immune suppressants and are preferably selected from the group comprising corticosteroids like prednisone, methylprednisolone, hydrocortisone,

dexamethasone and general immunosuppressants such as cyclophosphamide, cyclosporine, chlorambucil, azathioprine, tacrolimus or mycophenolate mofetil. Additionally, more specific blockers of T-cell costimulation, e.g. blockers of CD154 or CD40 or CD28 or CD86 or CD80; or T- and/or B-cell depleting agents like an anti-CD20 agent are useful in further embodiments. Finally, the further pharmaceutically active agent may be a modulator of the activity of any other chemokine which can be a chemokine agonist or antagonist or a chemokine receptor agonist or antagonist. Alternatively, or additionally, such further pharmaceutically active agent is a further nucleic acid according to the present invention. Alternatively, the medicament comprises at least one more nucleic acid which binds to a target molecule different from MCP-1 or exhibits a function which is different from the one of the nucleic acids according to the present invention.

It is within the present invention that the medicament is alternatively or additionally used, in principle, for the prevention of any of the diseases disclosed in connection with the use of the medicament for the treatment of said diseases. Respective markers therefore, i.e. for the respective diseases are known to the ones skilled in the art. Preferably, the respective marker is MCP-1. Alternatively and/or additionally, the respective marker is selected from the group comprising MCP-2, MCP-3, MCP-4 and eotaxin. A still further group of markers is selected from the group comprising autoreactive antibodies in the plasma, such as, for example, anti-dsDNA antibodies or rheumatoid factor.

In one embodiment of the medicament of the present invention, such medicament is for use in combination with other treatments for any of the diseases disclosed herein, particularly those for which the medicament of the present invention is to be used.

"Combination therapy" (or "co-therapy") includes the administration of a medicament of the invention and at least a second agent as part of a specific treatment regimen intended to provide the beneficial effect from the co-action of these therapeutic agents, i. e. the medicament of the present invention and said second agent. The beneficial effect of the combination includes, but is not limited to, pharmacokinetic or pharmacodynamic co-action resulting from the combination of therapeutic agents. Administration of these therapeutic agents in combination typically is carried out over a defined time period (usually minutes, hours, days or weeks depending upon the combination selected).

"Combination therapy" may, but generally is not, intended to encompass the administration of two or more of these therapeutic agents as part of separate monotherapy regimens that incidentally and arbitrarily result in the combinations of the present invention. "Combination therapy" is intended to embrace administration of these therapeutic agents in a sequential manner, that is, wherein each therapeutic agent is administered at a different time, as well as administration of these therapeutic agents, or at least two of the therapeutic agents, in a substantially simultaneous manner. Substantially simultaneous administration can be accomplished, for example, by administering to a subject a single capsule having a fixed ratio of each therapeutic agent or in multiple, single capsules for each of the therapeutic agents.

Sequential or substantially simultaneous administration of each therapeutic agent can be effected by any appropriate route including, but not limited to, topical routes, oral routes, intravenous routes, intramuscular routes, and direct absorption through mucous membrane tissues. The therapeutic agents can be administered by the same route or by different routes. For example, a first therapeutic agent of the combination selected may be administered by injection while the other therapeutic agents of the combination may be administered topically.

Alternatively, for example, all therapeutic agents may be administered topically or all therapeutic agents may be administered by injection. The sequence in which the therapeutic agents are administered is not narrowly critical unless noted otherwise. "Combination therapy" also can embrace the administration of the therapeutic agents as described above in further combination with other biologically active ingredients. Where the combination therapy further comprises a non-drug treatment, the non-drug treatment may be conducted at any suitable time so long as a beneficial effect from the co-action of the combination of the therapeutic agents and non-drug treatment is achieved. For example, in appropriate cases, the beneficial effect is still achieved when the non-drug treatment is temporally removed from the administration of the therapeutic agents, perhaps by days or even weeks.

As outlined in general terms above, the medicament according to the present invention can be administered, in principle, in any form known to the ones skilled in the art. A preferred route of administration is systemic administration, more preferably by parenteral administration, preferably by injuction.. Alternatively, the medicament may be administered locally. Other routes of administration comprise intramuscular, intraperitoneal, and subcutaneous, per orum,

intranasal, intratracheal or pulmonary with preference given to the route of administration that is the least invasive, while ensuring efficiancy.

Parenteral administration is generally used for subcutaneous, intramuscular or intravenous injections and infusions. Additionally, one approach for parenteral administration employs the implantation of a slow-release or sustained-released systems, which assures that a constant level of dosage is maintained, that are well known to the ordinary skill in the art.

Furthermore, preferred medicaments of the present invention can be administered in intranasal form via topical use of suitable intranasal vehicles, inhalants, or via transdermal routes, using those forms of transdermal skin patches well known to those of ordinary skill in that art. To be administered in the form of a transdermal delivery system, the dosage administration will, of course, be continuous rather than intermittent throughout the dosage regimen. Other preferred topical preparations include creams, ointments, lotions, aerosol sprays and gels, wherein the concentration of active ingredient would typically range from 0.01% to 15%, w/w or w/v.

The medicament of the present invention will generally comprise an effective amount of the active component(s) of the therapy, including, but not limited to, a nucleic acid molecule of the present invention, dissolved or dispersed in a pharmaceutically acceptable medium. Pharmaceutically acceptable media or carriers include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Supplementary active ingredients can also be incorporated into the medicament of the present invention.

In a further aspect the present invention is related to a pharmaceutical composition. Such pharmaceutical composition comprises at least one of the nucleic acids according to the present invention and preferably a pharmaceutically acceptable vehicle. Such vehicle can be any vehicle or any binder used and/or known in the art. More particularly such binder or vehicle is any binder or vehicle as discussed in connection with the manufacture of the medicament disclosed herein. In a further embodiment, the pharmaceutical composition comprises a further pharmaceutically active agent.

The preparation of a medicament and a pharmaceutical composition will be known to those of skill in the art in light of the present disclosure. Typically, such compositions may be prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid prior to injection; as tablets or other solids for oral administration; as time release capsules; or in any other form currently used, including eye drops, creams, lotions, salves, inhalants and the like. The use of sterile formulations, such as saline-based washes, by surgeons, physicians or health care workers to treat a particular area in the operating field may also be particularly useful. Compositions may also be delivered via microdevice, microparticle or sponge.

Upon formulation, a medicament will be administered in a manner compatible with the dosage formulation, and in such amount as is pharmacologically effective. The formulations are easily administered in a variety of dosage forms, such as the type of injectable solutions described above, but drug release capsules and the like can also be employed.

In this context, the quantity of active ingredient and volume of composition to be administered depends on the individual or the subject to be treated. Specific amounts of active compound required for administration depend on the judgment of the practitioner and are peculiar to each individual.

A minimal volume of a medicament required to disperse the active compounds is typically utilized. Suitable regimes for administration are also variable, but would be typified by initially administering the compound and monitoring the results and then giving further controlled doses at further intervals.

For instance, for oral administration in the form of a tablet or capsule (e.g., a gelatin capsule), the active drug component, i. e. a nucleic acid molecule of the present invention and/or any further pharmaceutically active agent, also referred to herein as therapeutic agent(s) or active compound(s) can be combined with an oral, non-toxic, pharmaceutically acceptable inert carrier such as ethanol, glycerol, water and the like. Moreover, when desired or necessary, suitable binders, lubricants, disintegrating agents, and coloring agents can also be incorporated into the mixture. Suitable binders include starch, magnesium aluminum silicate, starch paste, gelatin, methylcellulose, sodium carboxymethylcellulose and/or polyvinylpyrrolidone, natural sugars such as glucose or beta-lactose, corn sweeteners, natural and synthetic gums such as acacia, tragacanth or sodium alginate, polyethylene glycol, waxes, and the like. Lubricants used in these

dosage forms include sodium oleate, sodium stearate, magnesium stearate, sodium benzoate, sodium acetate, sodium chloride, silica, talcum, stearic acid, its magnesium or calcium salt and/or polyethyleneglycol, and the like. Disintegrators include, without limitation, starch, methyl cellulose, agar, bentonite, xanthan gum starches, agar, alginic acid or its sodium salt, or effervescent mixtures, and the like. Diluents, include, e.g., lactose, dextrose, sucrose, mannitol, sorbitol, cellulose and/or glycine.

The medicament of the invention can also be administered in such oral dosage forms as timed release and sustained release tablets or capsules, pills, powders, granules, elixirs, tinctures, suspensions, syrups and emulsions. Suppositories are advantageously prepared from fatty emulsions or suspensions.

The pharmaceutical composition or medicament may be sterilized and/or contain adjuvants, such as preserving, stabilizing, wetting or emulsifying agents, solution promoters, salts for regulating the osmotic pressure and/or buffers. In addition, they may also contain other therapeutically valuable substances. The compositions are prepared according to conventional mixing, granulating, or coating methods, and typically contain about 0.1% to 75%, preferably about 1% to 50%, of the active ingredient.

Liquid, particularly injectable compositions can, for example, be prepared by dissolving, dispersing, etc. The active compound is dissolved in or mixed with a pharmaceutically pure solvent such as, for example, water, saline, aqueous dextrose, glycerol, ethanol, and the like, to thereby form the injectable solution or suspension. Additionally, solid forms suitable for dissolving in liquid prior to injection can be formulated.

For solid compositions, excipients include pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like. The active compound defined above, may be also formulated as suppositories, using for example, polyalkylene glycols, for example, propylene glycol, as the carrier. In some embodiments, suppositories are advantageously prepared from fatty emulsions or suspensions.

The medicaments and nucleic acid molecules, respectively, of the present invention can also be administered in the form of liposome delivery systems, such as small unilamellar vesicles, large unilamellar vesicles and multilamellar vesicles. Liposomes can be formed from a variety of

phospholipids, containing cholesterol, stearylamine or phosphatidylcholines. In some embodiments, a film of lipid components is hydrated with an aqueous solution of drug to a form lipid layer encapsulating the drug, what is well known to the ordinary skill in the art. For example, the nucleic acid molecules described herein can be provided as a complex with a lipophilic compound or non-immunogenic, high molecular weight compound constructed using methods known in the art. Additionally, liposomes may bear such nucleic acid molecules on their surface for targeting and carrying cytotoxic agents internally to mediate cell killing. An example of nucleic-acid associated complexes is provided in U.S. Patent No. 6,011,020.

The medicaments and nucleic acid molecules, respectively, of the present invention may also be coupled with soluble polymers as targetable drug carriers. Such polymers can include polyvinylpyrrolidone, pyran copolymer, polyhydroxypropyl-methacrylamide-phenol, polyhydroxyethylaspanamidephenol, or polyethyleneoxidepolylysine substituted with palmitoyl residues. Furthermore, the medicaments and nucleic acid molecules, respectively, of the present invention may be coupled to a class of biodegradable polymers useful in achieving controlled release of a drag, for example, polylactic acid, polyepsilon capro lactone, polyhydroxy butyric acid, polyorthoesters, polyacetals, polydihydropyrans, polycyanoacrylates and cross- linked or amphipathic block copolymers of hydrogels.

If desired, the pharmaceutical composition and medicament, respectively, to be administered may also contain minor amounts of non-toxic auxiliary substances such as wetting or emulsifying agents, pH buffering agents, and other substances such as for example, sodium acetate, and triethanolamine oleate.

The dosage regimen utilizing the nucleic acid molecules and medicaments, respectively, of the present invention is selected in accordance with a variety of factors including type, species, age, weight, sex and medical condition of the patient; the severity of the condition to be treated; the route of administration; the renal and hepatic function of the patient; and the particular aptamer or salt thereof employed. An ordinarily skilled physician or veterinarian can readily determine and prescribe the effective amount of the drug required to prevent, counter or arrest the progress of the condition.

Effective plasma levels of the nucleic acid according to the present invention preferably range from 500 fM to 500 μM in the treatment of any of the diseases disclosed herein.

The nucleic acid molecules and medicaments, respectively, of the present invention may preferably be administered in a single daily dose, every second or third day, weekly, every second week, in a single monthly dose or every third month.

It is within the present invention that the medicament as described herein constitutes the pharmaceutical composition disclosed herein.

In a further aspect the present invention is related to a method for the treatment of a subject who is need of such treatment, whereby the method comprises the administration of a pharmaceutically active amount of at least one of the nucleic acids according to the present invention. In an embodiment, the subject suffers from a disease or is at risk to develop such disease, whereby the disease is any of those disclosed herein, particularly any of those diseases disclosed in connection with the use of any of the nucleic acids according to the present invention for the manufacture of a medicament.

It is to be understood that the nucleic acid as well as the antagonists according to the present invention can be used not only as a medicament or for the manufacture of a medicament, but also for cosmetic purposes, particularly with regard to the involvement of MCP-1 in inflamed regional skin lesions. Therefore, a further condition or disease for the treatment or prevention of which the nucleic acid, the medicament and/or the pharmaceutical composition according to the present invention can be used, is inflamed regional skin lesions.

As preferably used herein a diagnostic or diagostic agent or diagnostic means is suitable to detect, either directly or indirectly MCP-1, preferably MCP-1 as described herein and more preferably MCP-1 as described herein in connection with the various disorders and diseases described herein. However, to the extent that the nucleic acid molecules according to the present invention are also binding to any, some or all of MCP-2, MCP-3, MCP-4 and eotaxin, such nucleic acid molecules can also be used for the diagnosis of diseases and disorders, respectively, the pathogenetic mechanism is either directly or indirectly linked or associated with the over-expression or over-activity with MCP-2, MCP-3, MCP-4 and/or eotaxin. The diagnostic is suitable for the detection and/or follow-up of any of the disorders and diseases, respectively, described herein. Such detection is possible through the binding of the nucleic acids according to the present invention to MCP-1. Such binding can be either directly or indirectly be detected.

The respective methods and means are known to the ones skilled in the art. Among others, the nucleic acids according to the present invention may comprise a label which allows the detection of the nucleic acids according to the present invention, preferably the nucleic acid bound to MCP-1. Such a label is preferably selected from the group comprising radioactive, enzymatic and fluorescent labels. In principle, all known assays developed for antibodies can be adopted for the nucleic acids according to the present invention whereas the target-binding antibody is substituted to a target-binding nucleic acid. In antibody-assays using unlabeled target-binding antibodies the detection is preferably done by a secondary antibody which is modified with radioactive, enzymatic and fluorescent labels and bind to the target-binding antibody at its Fc-fragment. In the case of a nucleic acid, preferably a nucleic acid according to the present invention, the nucleic acid is modified with such a label, whereby preferably such a label is selected from the group comprising biotin, Cy-3 and Cy-5, and such label is detected by an antibody directed against such label, e.g. an anti-biotin antibody, an anti-Cy3 antibody or an anti-Cy5 antibody, or - in the case that the label is biotin – the label is detected by streptavidin or avidin which naturally bind to biotin. Such antibody, streptavidin or avidin in turn is preferably modified with a respective label, e.g. a radioactive, enzymatic or fluorescent label (like an secondary antibody).

In a further embodiment the nucleic acid molecules according to the invention are detected or analysed by a second detection means, wherein the said detection means is a molecular beacon. The methodology of molecular beacon is known to persons skilled in the art. In brief, nucleic acids probes which are also referred to as molecular beacons, are a reverse complement to the nucleic acids sample to be detected and hybridise because of this to a part of the nucleic acid sample to be detected. Upon binding to the nucleic acid sample the fluorophoric groups of the molecular beacon are separated which results in a change of the fluorescence signal, preferably a change in intensity. This change correlates with the amount of nucleic acids sample present.

It will be acknowledged that the detection of MCP-1 using the nucleic acids according to the present invention will particularly allow the detection of MCP-1 as defined herein.

In connection with the detection of the MCP-1 a preferred method comprises the following steps:

(a) providing a sample which is to be tested for the presence of MCP-1,

(b) providing a nucleic acid according to the present invention,

(c) reacting the sample with the nucleic acid, preferably in a reaction vessel

whereby step (a) can be performed prior to step (b), or step (b) can be preformed prior to step (a).

In a preferred embodiment a further step d) is provided, which consists in the detection of the reaction of the sample with the nucleic acid. Preferably, the nucleic acid of step b) is immobilised to a surface. The surface may be the surface of a reaction vessel such as a reaction tube, a well of a plate, or the surface of a device contained in such reaction vessel such as, for example, a bead. The immobilisation of the nucleic acid to the surface can be made by any means known to the ones skilled in the art including, but not limited to, non-covalent or covalent linkages. Preferably, the linkage is established via a covalent chemical bond between the surface and the nucleic acid. However, it is also within the present invention that the nucleic acid is indirectly immobilised to a surface, whereby such indirect immobilisation involves the use of a further component or a pair of interaction partners. Such further component is preferably a compound which specifically interacts with the nucleic acid to be immobilised which is also referred to as interaction partner, and thus mediates the attachment of the nucleic acid to the surface. The interaction partner is preferably selected from the group comprising nucleic acids, polypeptides, proteins and antibodies. Preferably, the interaction partner is an antibody, more preferably a monoclonal antibody. Alternatively, the interaction partner is a nucleic acid, preferably a functional nucleic acid. More preferably such functional nucleic acid is selected from the group comprising aptamers, spiegelmers, and nucleic acids which are at least partially complementary to the nucleic acid. In a further alternative embodiment, the binding of the nucleic acid to the surface is mediated by a multi-partite interaction partner. Such multi-partite interaction partner is preferably a pair of interaction partners or an interaction partner consisting of a first member and a second member, whereby the first member is comprised by or attached to the nucleic acid and the second member is attached to or comprised by the surface. The multi-partite interaction partner is preferably selected from the group of pairs of interaction partners comprising biotin and avidin, biotin and streptavidin, and biotin and neutravidin. Preferably, the first member of the pair of interaction partners is biotin.

A preferred result of such method is the formation of an immobilised complex of MCP-1 and the nucleic acid, whereby more preferably said complex is detected. It is within an embodiment that from the complex the MCP-1 is detected.

A respective detection means which is in compliance with this requirement is, for example, any detection means which is specific for that/those part(s) of the MCP-1. A particularly preferred detection means is a detection means which is selected from the group comprising nucleic acids, polypeptides, proteins and antibodies, the generation of which is known to the ones skilled in the art.

The method for the detection of MCP-1 also comprises that the sample is removed from the reaction vessel which has preferably been used to perform step c).

The method comprises in a further embodiment also the step of immobilising an interaction partner of MCP-1 on a surface, preferably a surface as defined above, whereby the interaction partner is defined as herein and preferably as above in connection with the respective method and more preferably comprises nucleic acids, polypeptides, proteins and antibodies in their various embodiments. In this embodiment, a particularly preferred detection means is a nucleic acid according to the present invention, whereby such nucleic acid may preferably be labelled or non-labelled. In case such nucleic acid is labelled it can directly or indirectly be detected. Such detection may also involve the use of a second detection means which is, preferably, also selected from the group comprising nucleic acids, polypeptides, proteins and embodiments in the various embodiments described herein. Such detection means are preferably specific for the nucleic acid according to the present invention. In a more preferred embodiment, the second detection means is a molecular beacon. Either the nucleic acid or the second detection means or both may comprise in a preferred embodiment a detection label. The detection label is preferably selected from the group comprising biotin, a bromo-desoxyuridine label, a digoxigenin label, a fluorescence label, a UV-label, a radio-label, and a chelator molecule. Alternatively, the second detection means interacts with the detection label which is preferably contained by, comprised by or attached to the nucleic acid. Particularly preferred combinations are as follows:

the detection label is biotin and the second detection means is an antibody directed against biotin, or wherein

the detection label is biotin and the second detection means is an avidin or an avidin carrrying molecule, or wherein

the detection label is biotin and the second detection means is a streptavidin or a stretavidin carrying molecule, or wherein

the detection label is biotin and the second detection means is a neutravidin or a neutravidin carrying molecule, or

wherein the detection label is a bromo-desoxyuridine and the second detection means is an antibody directed against bromo-desoxyuridine, or wherein

the detection label is a digoxigenin and the second detection means is an antibody directed against digoxigenin, or wherein

the detection label is a chelator and the second detection means is a radio-nuclide, whereby it is preferred that said detection label is attached to the nucleic acid. It is to be acknowledged that this kind of combination is also applicable to the embodiment where the nucleic acid is attached to the surface. In such embodiment it is preferred that the detection label is attached to the interaction partner.

Finally, it is also within the present invention that the second detection means is detected using a third detection means, preferably the third detection means is an enzyme, more preferably showing an enzymatic reaction upon detection of the second detection means, or the third detection means is a means for detecting radiation, more preferably radiation emitted by a radio-nuclide. Preferably, the third detection means is specifically detecting and/or interacting with the second detection means.

Also in the embodiment with an interaction partner of MCP-1 being immobilised on a surface and the nucleic acid according to the present invention is preferably added to the complex formed between the interaction partner and the MCP-1, the sample can be removed from the reaction, more preferably from the reaction vessel where step c) and/or d) are preformed.

In an embodiment the nucleic acid according to the present invention comprises a fluorescence moiety and whereby the fluorescence of the fluorescence moiety is different upon complex formation between the nucleic acid and MCP-1 and free MCP-1.

In a further embodiment the nucleic acid is a derivative of the nucleic acid according to the present invention, whereby the derivative of the nucleic acid comprises at least one fluorescent derivative of adenosine replacing adenosine. In a preferred embodiment the fluorescent derivative of adenosine is ethenoadenosine.

In a further embodiment the complex consisting of the derivative of the nucleic acid according to the present invention and the MCP-1 is detected using fluorescence.

In an embodiment of the method a signal is created in step (c) or step (d) and preferably the signal is correlated with the concentration of MCP-1 in the sample.

In a preferred aspect, the assays may be performed in 96-well plates, where components are immobilized in the reaction vessels as described above and the wells acting as reaction vessels.

It will be acknowledged by the ones skilled in the art that what has been said above also applies to MCP-2, MCP-3, MCP-4 and/or eotaxin, at least to the extent that the nucleic acids according to the present invention are also binding to or with MCP-2, MCP-3, MCP-4 and/or eotaxin.

The inventive nucleic acid may further be used as starting material for drug design. Basically there are two possible approaches. One approach is the screening of compound libraries whereas such compound libraries are preferably low molecular weight compound libraries. In an embodiment, the screening is a high throughput screening. Preferably, high throughput screening is the fast, efficient, trial-and-error evaluation of compounds in a target based assay. In best case the analysis are carried by a colorimetric measurement. Libraries as used in connection therewith are known to the one skilled in the art.

Alternatively, the nucleic acid according to the present invention may be used for rational design of drugs. Preferably, rational drug design is the design of a pharmaceutical lead structure. Starting from the 3-dimensional structure of the target which is typically identified by methods such as X-ray crystallography or nuclear magnetic resonance spectroscopy, computer programs are used to search through databases containing structures of many different chemical compounds. The selection is done by a computer, the identified compounds can subsequently be tested in the laboratory.

The rational design of drugs may start from any of the nucleic acid according to the present invention and involves a structure, preferably a three dimensional structure, which is similar to the structure of the inventive nucleic acids or identical to the binding mediating parts of the structure of the inventive nucleic acids. In any case such structure still shows the same or a similar binding characteristic as the inventive nucleic acids. In either a further step or as an

alternative step in the rational design of drugs the preferably three dimensional structure of those parts of the nucleic acids binding to the neurotransmitter are mimicked by chemical groups which are different from nucleotides and nucleic acids. By this mimicry a compound different from the nucleic acids can be designed. Such compound is preferably a small molecule or a peptide.

In case of screening of compound libraries, such as by using a competitive assay which are known to the one skilled in the arts, appropriate MCP-1 analogues, MCP-1 agonists or MCP-1 antagonists may be found. Such competitive assays may be set up as follows. The inventive nucleic acid, preferably a spiegelmer which is a target binding L-nucleic acid, is coupled to a solid phase. In order to identify MCP-1 analogues labelled MCP-1 may be added to the assay. A potential analogue would compete with the MCP-1 molecules binding to the spiegelmer which would go along with a decrease in the signal obtained by the respective label. Screening for agonists or antagonists may involve the use of a cell culture assay as known to the ones skilled in the art.

The kit according to the present invention may comprise at least one or several of the inventive nucleic acids. Additionally, the kit may comprise at least one or several positive or negative controls. A positive control may, for example, be MCP-1, particularly the one against which the inventive nucleic acid is selected or to which it binds, preferably, in liquid form. A negative control may, e.g., be a peptide which is defined in terms of biophysical properties similar to MCP-1, but which is not recognized by the inventive nucleic acids. Furthermore, said kit may comprise one or several buffers. The various ingredients may be contained in the kit in dried or lyophilised form or solved in a liquid. The kit may comprise one or several containers which in turn may contain one or several ingredients of the kit. In a further embodiment, the kit comprises an instruction or instruction leaflet which provides to the user information on how to use the kit and its various ingredients.

The pharmaceutical and bioanalytical determination of the nucleic acid according to the present invention is elementarily for the assessment of its pharmacokinetic and biodynamic profile in several humours, tissues and organs of the human and non-human body. For such purpose, any of the detection methods disclosed herein or known to a person skilled in the art may be used. In a further aspect of the present invention a sandwich hybridisation assay for the detection of the nucleic acid according to the present invention is provided. Within the detection assay a capture

probe and a detection probe are used. The capture probe is complementary to the first part and the detection probe to the second part of the nucleic acid according to the present invention. Both, capture and detection probe, can be formed by DNA nucleotides, modified DNA nucleotides, modified RNA nucleotides, RNA nucleotides, LNA nucleotides and/or PNA nucleotides.

Hence, the capture probe comprise a sequence stretch complementary to the 5'-end of the nucleic acid according to the present invention and the detection probe comprise a sequence stretch complementary to the 3'-end of the nucleic acid according to the present invention. In this case the capture probe is immobilised to a surface or matrix via its 5'-end whereby the capture probe can be immobilised directly at its 5'-end or via a linker between of its 5'-end and the surface or matrix. However, in principle the linker can be linked to each nucleotide of the capture probe. The linker can be formed by hydrophilic linkers of skilled in the art or by D-DNA nucleotides, modified D-DNA nucleotides, D-RNA nucleotides, modified D-RNA nucleotides, D-LNA nucleotides, PNA nucleotides, L-RNA nucleotides, L-DNA nucleotides, modified L-RNA nucleotides, modified L-DNA nucleotides and/or L-LNA nucleotides.

Alternatively, the capture probe comprises a sequence stretch complementary to the 3'-end of the nucleic acid according to the present invention and the detection probe comprise a sequence stretch complementary to the 5'-end of the nucleic acid according to the present invention. In this case the capture probe is immobilised to a surface or matrix via its 3'-end whereby the capture probe can be immobilised directly at its 3'-end or via a linker between of its 3'-end and the surface or matrix. However, in principle, the linker can be linked to each nucleotide of the sequence stretch that is complementary to the nucleic acid according to the present invention. The linker can be formed by hydrophilic linkers of skilled in the art or by D-DNA nucleotides, modified D-DNA nucleotides, D-RNA nucleotides, modified D-RNA nucleotides, D-LNA nucleotides, PNA nucleotides, L-RNA nucleotides, L-DNA nucleotides, modified L-RNA nucleotides, modified L-DNA nucleotides and/or L-LNA nucleotides.

The number of nucleotides of the capture and detection probe that may hybridise to the nucleic acid according to the present invention is variable and can be dependant from the number of nucleotides of the capture and/or the detection probe and/or the nucleic acid according to the present invention itself. The total number of nucleotides of the capture and the detection probe that may hybridise to the nucleic acid according to the present invention should be maximal the

number of nucleotides that are comprised by the nucleic acid according to the present invention. The minimal number of nucleotides (2 to 10 nucleotides) of the detection and capture probe should allow hybridisation to the 5'-end or 3'-end, respectively, of the nucleic acid according to the present invention. In order to realize high specificity and selectivity between the nucleic acid according to the present invention and other nucleic acids occurring in samples that are analyzed the total number of nucleotides of the capture and detection probe should be or maximal the number of nucleotides that are comprised by the nucleic acid according to the present invention.

Moreover the detection probe preferably carries a marker molecule or label that can be detected as previously described herein. The label or marker molecule can in principle be linked to each nucleotide of the detection probe. Preferably, the label or marker is located at the 5'-end or 3'-end of the detection probe, whereby between the nucleotides within the detection probe that are complementary to the nucleic acid according to the present invention, and the label a linker can be inserted. The linker can be formed by hydrophilic linkers of skilled in the art or by D-DNA nucleotides, modified D-DNA nucleotides, D-RNA nucleotides, modified D-RNA nucleotides, D-LNA nucleotides, PNA nucleotides, L-RNA nucleotides, L-DNA nucleotides, modified L-RNA nucleotides, modified L-DNA nucleotides and/or L-LNA nucleotides.

The detection of the nucleic acid according to the present invention can be carried out as follows: The nucleic acid according to the present invention hybridises with one of its ends to the capture probe and with the other end to the detection probe. Afterwards unbound detection probe is removed by, e. g., one or several washing steps. The amount of bound detection probe which preferably carries a label or marker molecule, can be measured subsequently.

As preferably used herein, the term treatment comprises in a preferred embodiment additionally or alternatively prevention and/or follow-up.

As preferably used herein, the terms disease and disorder shall be used in an interchangeable manner, if not indicated to the contrary.

As used herein, the term comprise is preferably not intended to limit the subject matter followed or described by such term. However, in an alternative embodiment the term comprises shall be understood in the meaning of containing and thus as limiting the subject matter followed or described by such term.

The various SEQ.ID. Nos., the chemical nature of the nucleic acid molecules according to the present invention and the target molecules MCP-1 as used herein, the actual sequence thereof and the internal reference number is summarized in the following table.

Seq.-ID	RNA/Peptide	Sequence	Internal Reference
1	L-protein	QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV QDSMDHLDKQTQTPKT	human MCP-1, huMCP-1 CCL2
2	L-protein	QPDAVNAPLTCCYSFTSKMIPMSRLESYKRITSSRCPKEAVVFVTKLKREVCADPKKEWV QTYIKNLDRNQMRSEPTTLFKTASALRSSAPLNVKLTRKSEANASTTFSTTTSSTSVGVT SVTVN	mouse MCP-1, mCCL2, mMCP-1, murine MCP-1 (Mus musculus)
3	L-protein	QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV QDSMDHLDKQIQTPKP	monkey MCP-1 (Macaca mulatta)
4	L-protein	QPDAINSPVTCCYTLTSKKISMQRLMSYRRVTSSKCPKEAVIFKTIAGKEICAEPKQKWV QDSISHLDKKNQTPKP	pig MCP-1 (Sus scrof
5	L-protein	QPDAIISPVTCCYTLTNKKISIQRLASYKRVTSSKCPKEAVIFKTVLNKEICADPKQKWV QDSMAHLDKKSQTQTA	dog MCP-1 (Canis familiaris)
6	L-protein	QPDAVNSPVTCCYTFTNKTISVKRLMSYRRINSTKCPKEAVIFMTKLAKGICADPKQKWV QDAIANLDKKMQTPKTLTSYSTTQEHTTNLSSTRTPSTTTSL	rabbit MCP-1 (Oryctolagus cuniculus)
7	L-protein	QPVGINTSTTCCYRFINKKIPKQRLESYRRTTSSHCPREAVIFKTKLDKEICADPTQKWV QDFMKHLDKKTQTPKL	human MCP-3, CCL7, huMCP-3
8	L-protein	GPASVPTTCCFNLANRKIPLQRLESYRRITSGKCPQKAVIFKTKLAKDICADPKKKWVQD SMKYLDQKSPTPKP	human eotaxin/CCL11
9	L-protein	QPDSVSIPITCCFNVINRKIPIQRLESYTRITNIQCPKEAVIFKTKRGKEVCADPKERWV RDSMKHLDQIFQNLKP	human MCP-2, CCL8, huMCP-2
10	L-RNA	AGCGUGCCCGGAGUGGCAGGGGGACGCGACCUGCAAUAAUGCACGCU	169-B1trc
11	L-RNA	AGCGUGCCCGGAGUGGCAGGGGGACGCGACCUGCAAUUGCACGCU	169-F3trc
12	L-RNA	AGCGUGCCCGGAGUGGCAGGGGGACGCGACCUGUAAUAAUGCACGCU	169-C1trc
13	L-RNA	AGCGUGCCCGGUGUGGCAGGGGGACGCGACCUGCAAUAAUGCGCGCU	169-A3trc
14	L-RNA	AGCGUGCCCGGAGUAGCAGGGGGGCGCGACCUGCAAUAAUGCACGCU	169-B2trc
15	L-RNA	AGCGUGCCCGGUGUGGUAGGGGGGCGCGAUCUACAAUUGCACGCU	176-B12trc
16	L-RNA	AGCGUGCCCGGUGUGACAGGGGGGCGCGACCUGCAUUUGCACGCU	176-D9trc

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Seq.-ID	RNA/Peptide	Sequence	Internal Reference
17	L-RNA	AGCGUGCCCGGUGUGGCAGGGGGGCGCGACCUGUAUUUGCACGCU	176-B10trc
18	L-RNA	AGCGUGCCCGGAGUGGCAGGGGGGCGCGACCUGCAAUAAUGCACGCU	169-F2trc
19	L-RNA	AGCGUGCCCGGUGUGGCAGGGGGGCGCGACCUGCAAUUGCACGCU	176-B9trc
20	L-RNA	AGCAUGCCCGGUGUGGCAGGGGGGCGCGACCUGCAUUUGCAUGCU	176-H9trc
21	L-RNA	AGCGUGCCCGGUGUGGUAGGGGGGCGCGACCUACAUUUGCACGCU	176-E10trc
22	L-RNA	AGUGUGCCAGCUGUGAUGGGGGGGCGCGACCCAUUUUACACACU	176-G9trc
23	L-RNA	AGUGUGCCAGCGUGAUGGGGGGGCGCGACCCAUUUUACACACU	176-F9trc
24	L-RNA	AGUGUGCGAGCGUGAUGGGGGGGCGCGACCCAUUUUACAUACU	176-C11trc
25	L-RNA	AGUGUGCCAGCGUGAUGGGGGGGCGCGACCCAUUUUACAUACU	176-E11trc
26	L-RNA	AGUAUGCCAGCGUGAUGGGGGGGCGCGACCCAUUUACAUACU	176-D10trc
27	L-RNA	AGUGUGCCAGUGUGAUGGGGGGGCGCGACCCAUUUUACACACU	176-H10trc
28	L-RNA	AGCGUGCCAGUGUGAUGGGGGGGCGCGACCCAUUUUACACGCU	176-C9trc
29	L-RNA	ACGCACGUCCCUCACCGGUGCAAGUGAAGCCGCGGCUCUGCGU	180-B1-001
30	L-RNA	ACGCACCUCCCUCACCGGUGCAAGUGAAGCCGUGGCUCUGCGC	180-A4-002
31	L-RNA	ACGCACGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUCUGCGU	180-D1-002
32	L-RNA	GCACGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUCUGCGU	180-D1-011
33	L-RNA	ACGCACGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUCUGC	180-D1-012
34	L-RNA	GCACGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUCUGC	180-D1-018
35	L-RNA	CGCACGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUCUGCGU	180-D1-034
36	L-RNA	CGCACGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUCUGCG	180-D1-035

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37	L-RNA	GCACGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUCUGCG	180-D1-036 = NOX-E3
Seq.-ID	**RNA/Peptide**	**Sequence**	**Internal Reference**
38	L-RNA	GUGCUGCGUAGUGGAAGACUACCUAAUGACAGCCGAAUGCUGGCAGCAC	178-A8
39	L-RNA	GUGCUGCGUAGUGGAAGACUACCUAAUGACAGCCUAAUGCUGGCAGCAC	178-F7
40	L-RNA	GUGCUGCGUAGUGGAAGACUACCUUAUGACAGCCGAAUGCUGGCAGCAC	178-G7
41	L-RNA	GUGCUGCGUAGUGAAAAACUACUGCCAGUGGGUCAGAGCUAGCAGCAC	178-C6
42	L-RNA	GUGCUGCGGAGUUAAAAACUCCCUAAGACAGGCCAGAGCCGGCAGCAC	178-E7
43	L-RNA	GUGCUGCGGAGUUGAAAACUCCCUAAGACAGGCCAGAGCCGGCAGCAC	178-G6
44	L-RNA	GUGCUGCGUAGUGGAAGACUACCUAUGACAGCCUAAUGCUGGCAGCAC	178-A7
45	L-RNA	GUGCUGCGGAGUUAAAAACUCCCUAAGACAGGCUAGAGCCGGCAGCAC	178-C7
46	L-RNA	GUGCUGCGGCGUGAAAAACGCCCUGCGACUGCCCUUUAUGCAGGCAGCAC	178-E5
47	L-RNA	GUGCUGCGUAGUGAAAAACUACCAACGACUGGCUAGAGCCGGCAGCAC	181-F1
48	L-RNA	GUGCUGCGUAGUGAAAGACUACCUGUGACAGCCGAAUGCUGGCAGCAC	181-B2
49	L-RNA	GUACUGCGUAGUUAAAAACUACCAACGACUGGCUAGAGCCGGCAGCAC	181-C2
50	L-RNA	GUGCUGCGUAGUUAAAAACUACCAACGACUGGCUAGAGCCGGCAGCAC	178-A6
51	L-RNA	GUGCUGCGUAGUUAAAAACUACCAGCGACAGGCUAGAGCCGGCAGCAC	178-D6
52	L-RNA	GUGCUGCGUAGUUAAAAACUACCAGCGACUGGCUAGAGCCGGCAGCAC	178-D5
53	L-RNA	GUGCUGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCAGCAC	181-A2
54	L-RNA	GGCUGCGUAGUUAAAAACUACCAGCGACUGGCUAGAGCCGGCAGCC	178-D5-020
55	L-RNA	GGCGCGUAGUUAAAAACUACCAGCGACUGGCUAGAGCCGGCGCC	178-D5-027
56	L-RNA	GUGCGCGUAGUUAAAAACUACCAGCGACUGGCUAGAGCCGGCGCAC	178-D5-030

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57	L-RNA	GUGCGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCGCAC	181-A2-002
58	L-RNA	GUGCCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGGCAC	181-A2-004
Seq.-ID	**RNA/Peptide**	**Sequence**	**Internal Reference**
59	L-RNA	GUGGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCCAC	181-A2-005
60	L-RNA	GUCGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCGAC	181-A2-006
61	L-RNA	UGCGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCGCA	181-A2-007
62	L-RNA	GCUGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCAGC	181-A2-008
63	L-RNA	GCUGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCAGC	181-A2-011
64	L-RNA	GGUGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCACC	181-A2-012
65	L-RNA	UGGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGC—CA	181-A2-015
66	L-RNA	GCGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCGC	181-A2-016
67	L-RNA	GUGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCAC	181-A2-017
68	L-RNA	GG—GCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCCC	181-A2-018
69	L-RNA	GAGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCUC	181-A2-019
70	L-RNA	CGGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCCG	181-A2-020
71	L-RNA	CCGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCGG	181-A2-021
72	L-RNA	CAGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCUG	181-A2-022
73	L-RNA	CUGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCAG	181-A2-023
74	L-RNA	AGCGUGUUAGUGAAGUGGGUGGCAGGUAAAGGACACGCU	184-B8trc
75	L-RNA	AGCGUGGUAGCGGUGUGGGUGGUAGGUAAAGGCCACGCU	184-C6trc
76	L-RNA	AGCGUGAUAGAAGAGCGGGUGGUAGGUAAAGGUCAGGCU	184-H5trc

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77	L-RNA	AGCGUGUUAGGUAGGGUGGUAGUAAGUAAAGGACACGCU	184-A7trc
78	L-RNA	AGCGUGUUAGGUGGGUGGUAGUAAGUAAAGGACACGCU	187-A5trc
79	L-RNA	AGCGUGUUAGGUGGGUGGUAGUAAGUAAAGGGCACGCU	187-H5trc
Seq.-ID	**RNA/Peptide**	**Sequence**	**Internal Reference**
80	L-RNA	CCGCUUAGGUGGGUGGUAGUAAGUAAAGGGGCGG	174-D4-004
81	L-RNA	GCGCGAGCAGGUGGGUGGUAGAAUGUAAAGACUCGCGUC	166-A4-002
82	L-RNA	CGUGUUAGGUGGGUGGUAGUAAGUAAAGGACACG	187-A5trc-001
83	L-RNA	GUGUUAGGUGGGUGGUAGUAAGUAAAGGACAC	187-A5trc-002
84	L-RNA	CGUGUUAGGUGGGUGGUAGUAAGUAAAGGGCACG	187-H5trc-002
85	L-RNA	GUGUUAGGUGGGUGGUAGUAAGUAAAGGGCAC	187-H5trc-003
86	L-RNA	UGUUAGGUGGGUGGUAGUAAGUAAAGGGCA	187-H5trc-004
87	L-RNA	GGACGAGAGUGACAAAUGAUAUAACCUCCUGACUAACGCUGCGGGCGACAGG	177-B3
88	L-RNA	GGACCUAUCGCUAAGACAACGCGCAGUCUACGGGACAUUCUCCGCGGACAGG	177-C1
89	L-RNA	GGACAAUUGUUACCCCCGAGAGAGACAAAUGAGACAACCUCCUGAAGACAGG	177-C2
90	L-RNA	GGACGAAAGUGAGAAAUGAUACAACCUCCUGUUGCUGCGAAUCCGGACAGG	177-E3
91	L-RNA	GGACGUAAAAGACGCUACCCGAAAGAAUGUCAGGAGGGUAGACCGACAGG	177-D1
92	L-RNA	GGACUAGAAACUACAAUAGCGGCCAGUUGCACCGCGUUAUCAACGACAGG	177-E1
93	L-RNA	GGACUAGUCAGCCAGUGUGUAUAUCGGACGCGGGUUUAUUUACUGACAGG	177-A1
94	L-RNA	GGACUGUCCGGAGUGUGAAACUCCCCGAGACCGCCAGAAGCGGGGACAGG	177-G3
95	L-RNA	GGACUUCUAUCCAGGUGGGUGGUAGUAUGUAAAGAGAUAGAAGUGACAGG	177-C3
96	L-RNA	GGACGAGAGCGAACAAUGAUAUAACCUCCUGACGGAAAGAGAUCGACAGG	177-A2

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97	L-RNA	CCUGUGCUACACGCAGUAAGAAGUGAACGUUCAGUAUGUGUGCACAGG	170-E4trc
98	L-RNA	CGUGAGCCAGGCACCGAGGGCGUUAACUGGCUGAUUGGACACGACACG	166-D2trc
99	L-RNA	CGUGAACAUGCAAGCUAAGCGGGGCUGUUGGUUGCUUGGCCCGCCACG	174-A2trc
100	L-RNA	CGUGCAGAGAGAGACCAACCACGUAAAAUCAACCUAAUGGGCCGCACG	174-E2trc
Seq.-ID	**RNA/Peptide**	**Sequence**	**Internal Reference**
101	L-RNA	CGUGCAGAGAGAGACCAACCACGUAAAAUCAACCUAAUGGGCCGCACG	183-G3trc
102	L-RNA	CGUGAACAUUCAAGCUAAGCGGGGCUGUUGGUUGCUUGGCCCGCCACG	183-B2trc
103	L-RNA	CGUGCCGAGGCGGCGACCAGCGUUACUUAGAGAGGCUUUGGCACCACG	166-B2trc
104	L-RNA	CGUGAUAACAGCCGUCGGUCAAGAAAACAAAGUUCGGGCGGCGCACG	166-G3trc
105	L-RNA	CGUGGGUGGCGCACCGAGGGCGAAAAGCCACCAGUAAAGAUAGACCG	166-D1trc
106	L-RNA	CGUGUGAUCUCCUUUGGGGUGAUUAGCUUAGAGACUUCCCACACG	183-H2trc
107	L-RNA	GCACCUUCGCCUAAUACACGUGCCGGCUAGCUAAUACUCGUCCGC	167-A7trc
108	L-RNA	GCACGACUUGGGCGACCAGUGAUACUUAGAGAGCAAGUCGUCGGC	167-C7trc
109	L-RNA	GCGCGCGCUCAGUAAGAAAUUGAAAGUUCAGAAUGUCGUCGCGC	167-B5trc
110	L-RNA	AGUGUGUGGCAGGCUAAGGAGAUAUUCCGAGACCACGCU	184-D7trc
111	L-RNA	AGUGUGUGGCAGACUAUGGAUAGACUCCGAGACCACGCU	184-D6trc
112	L-RNA	AGCGUGAGGCGACCAGCGGAUUACUUAGAGAGUCACGCU	184-E5trc
113	L-RNA	AGCGUGAAGGGGACCAGCGUUACUUACAGAGUUCACGCU	184-G6trc
114	L-RNA	AGCGUGUGAUGUAUGUAGCACCGUAUCAGAGGACACGCU	184-B7trc
115	L-RNA	AGCGUGAGGCGACCCGUGUUUCGUAGAGAGUCACGCU	184-B6trc
116	L-RNA	5′PEG-GCACGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUCUGCG	NOX-E36-5′PEG

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117	L-RNA	GCACGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUCUGCG-3'PEG	NOX-E36-3'PEG
118	L-RNA	GAGAUGGCGACAUUGGUUGGGCAUGAGGCGAGGCCCUUUGAUGAAUCCGCGGCCAUUC	188-A3-001
119	L-RNA	GAUGGCGACAUUGGUUGGGCAUGAGGCGAGGCCCUUUGAUGAAUCCGCGGCCAUUC	188-A3-004
120	L-RNA	GGCGACAUUGGUUGGGCAUGAGGCGAGGCCCUUUGAUGAAUCCGCGGCCAUUC	188-A3-005
121	L-RNA	GGCGACAUUGGUUGGGCAUGAGGCGAGGCCCUUUGAUGAAUCCGCGGCCAUU	188-A3-006
Seq.-ID	**RNA/Peptide**	**Sequence**	**Internal Reference**
122	L-RNA	GGCGACAUUGGUUGGGCAUGAGGCGAGGCCCUUUGAUGAAUCCGCGGCCA	188-A3-007 = mNOX-E3
123	L-RNA	GCUGGUUACCGAGGGGGCGUCGUUGGAGUUUGGUUGGUUGUCACCAGC	189-G7-001
124	L-RNA	CUGGUUACCGAGGGGGCGUCGUUGGAGUUUGGUUGGUUGUCACCAG	189-G7-002
125	L-RNA	UGGUUACCGAGGGGGCGUCGUUGGAGUUUGGUUGGUUGUCACCA	189-G7-003
126	L-RNA	GCCGGUUACCGAGGGGGCGUCGUUGGAGUUUGGUUGGUUGUCACCGGC	189-G7-007
127	L-RNA	GCCGGCUACCGAGGGGGCGUCGUUGGAGUUUGGUUGGUUGUCGCCGGC	189-G7-008
128	L-RNA	GCGCGUACCGAGGGGGCGUCGUUGGAGUUUGGUUGGUUGUCCGCGC	189-G7-010
129	L-RNA	GGGCCUACCGAGGGGGCGUCGUUGGAGUUUGGUUGGUUGUCGGCCC	189-G7-012
130	D-protein	Biotin-QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWVQDSMDHLDKQTQTPKT	biotinylated human D-MCP-1
131	D-protein	Biotin-QPDAVNAPLTCCYSFTSKMIPMSRLESYKRITSSRCPKEAVVFVTKLKREVCADPKKEWVQTYIKNLDRNQMRSEP-Biotin	biotinylated mouse D-MCP-1
132	D-RNA	AGCGUGCCCGGAGUGGCAGGGGGACGCGACCUGCAAUAAUGCACGCU	169-B1trc
133	D-RNA	AGCGUGCCCGGAGUGGCAGGGGGACGCGACCUGCAAUUGCACGCU	169-F3trc
134	D-RNA	AGCGUGCCCGGAGUGGCAGGGGGACGCGACCUGUAAUAAUGCACGCU	169-C1trc

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135	D-RNA	AGCGUGCCCGGUGUGGCAGGGGGACGCGACCUGCAAUAAUGCGCGCU	169-A3trc
136	D-RNA	AGCGUGCCCGGAGUAGCAGGGGGGCGCGACCUGCAAUAAUGCACGCU	169-B2trc
137	D-RNA	AGCGUGCCCGGUGUGGUAGGGGGGCGCGAUCUACAAUUGCACGCU	176-B12trc
138	D-RNA	AGCGUGCCCGGUGUGACAGGGGGGCGCGACCUGCAUUUGCACGCU	176-D9trc
139	D-RNA	AGCGUGCCCGGUGUGGCAGGGGGGCGCGACCUGUAUUUGCACGCU	176-B10trc

Seq.-ID	RNA/Peptide	Sequence	Internal Reference
140	D-RNA	AGCGUGCCCGGAGUGGCAGGGGGGCGCGACCUGCAAUAAUGCACGCU	169-F2trc
141	D-RNA	AGCGUGCCCGGUGUGGCAGGGGGGCGCGACCUGCAAUUGCACGCU	176-B9trc
142	D-RNA	AGCAUGCCCGGUGUGGCAGGGGGGCGCGACCUGCAUUUGCAUGCU	176-H9trc
143	D-RNA	AGCGUGCCCGGUGUGGUAGGGGGGCGCGACCUACAUUUGCACGCU	176-E10trc
144	D-RNA	AGUGUGCCAGCUGUGAUGGGGGGGCGCGACCCAUUUUACACACU	176-G9trc
145	D-RNA	AGUGUGCCAGCGUGAUGGGGGGGCGCGACCCAUUUUACACACU	176-F9trc
146	D-RNA	AGUGUGCGAGCGUGAUGGGGGGGCGCGACCCAUUUUACAUACU	176-C11trc
147	D-RNA	AGUGUGCCAGCGUGAUGGGGGGGCGCGACCCAUUUUACAUACU	176-E11trc
148	D-RNA	AGUAUGCCAGCGUGAUGGGGGGGCGCGACCCAUUUACAUACU	176-D10trc
149	D-RNA	AGUGUGCCAGUGUGAUGGGGGGGCGCGACCCAUUUUACACACU	176-H10trc
150	D-RNA	AGCGUGCCAGUGUGAUGGGGGGGCGCGACCCAUUUUACACGCU	176-C9trc
151	D-RNA	ACGCACGUCCCUCACCGGUGCAAGUGAAGCCGCGGCUCUGCGU	180-B1-001
152	D-RNA	ACGCACCUCCCUCACCGGUGCAAGUGAAGCCGUGGCUCUGCGC	180-A4-002
153	D-RNA	ACGCACGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUCUGCGU	180-D1-002
154	D-RNA	GCACGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUCUGCGU	180-D1-011

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Seq.-ID	RNA/Peptide	Sequence	Internal Reference
155	D-RNA	ACGCACGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUCUGC	180-D1-012
156	D-RNA	GCACGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUCUGC	180-D1-018
157	D-RNA	CGCACGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUCUGCGU	180-D1-034
158	D-RNA	CGCACGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUCUGCG	180-D1-035
159	D-RNA	GCACGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUCUGCG	(D-)180-D1-036, (D-)NOX-E36
160	D-RNA	GUGCUGCGUAGUGGAAGACUACCUAAUGACAGCCGAAUGCUGGCAGCAC	178-A8
161	D-RNA	GUGCUGCGUAGUGGAAGACUACCUAAUGACAGCCUAAUGCUGGCAGCAC	178-F7
162	D-RNA	GUGCUGCGUAGUGGAAGACUACCUUAUGACAGCCGAAUGCUGGCAGCAC	178-G7
163	D-RNA	GUGCUGCGUAGUGAAAAACUACUGCCAGUGGGUCAGAGCUAGCAGCAC	178-C6
164	D-RNA	GUGCUGCGGAGUUAAAAACUCCCUAAGACAGGCCAGAGCCGGCAGCAC	178-E7
165	D-RNA	GUGCUGCGGAGUUGAAAACUCCCUAAGACAGGCCAGAGCCGGCAGCAC	178-G6
166	D-RNA	GUGCUGCGUAGUGGAAGACUACCUAUGACAGCCUAAUGCUGGCAGCAC	178-A7
167	D-RNA	GUGCUGCGGAGUUAAAAACUCCCUAAGACAGGCUAGAGCCGGCAGCAC	178-C7
168	D-RNA	GUGCUGCGGCGUGAAAAACGCCCUGCGACUGCCCUUUAUGCAGGCAGCAC	178-E5
169	D-RNA	GUGCUGCGUAGUGAAAAACUACCAACGACUGGCUAGAGCCGGCAGCAC	181-F1
170	D-RNA	GUGCUGCGUAGUGAAAGACUACCUGUGACAGCCGAAUGCUGGCAGCAC	181-B2
171	D-RNA	GUACUGCGUAGUUAAAAACUACCAACGACUGGCUAGAGCCGGCAGCAC	181-C2
172	D-RNA	GUGCUGCGUAGUUAAAAACUACCAACGACUGGCUAGAGCCGGCAGCAC	178-A6
173	D-RNA	GUGCUGCGUAGUUAAAAACUACCAGCGACAGGCUAGAGCCGGCAGCAC	178-D6

Seq.-ID	RNA/Peptide	Sequence	Internal Reference
174	D-RNA	GUGCUGCGUAGUUAAAAACUACCAGCGACUGGCUAGAGCCGGCAGCAC	178-D5
175	D-RNA	GUGCUGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCAGCAC	181-A2
176	D-RNA	GGCUGCGUAGUUAAAAACUACCAGCGACUGGCUAGAGCCGGCAGCC	178-D5-020
177	D-RNA	GGCGCGUAGUUAAAAACUACCAGCGACUGGCUAGAGCCGGCGCC	178-D5-027
178	D-RNA	GUGCGCGUAGUUAAAAACUACCAGCGACUGGCUAGAGCCGGCGCAC	178-D5-030
179	D-RNA	GUGCGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCGCAC	181-A2-002
180	D-RNA	GUGCCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGGCAC	181-A2-004
181	D-RNA	GUGGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCCAC	181-A2-005
182	D-RNA	GUCGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCGAC	181-A2-006
183	D-RNA	UGCGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCGCA	181-A2-007
184	D-RNA	GCUGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCAGC	181-A2-008
185	D-RNA	GCUGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCAGC	181-A2-011
186	D-RNA	GGUGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCACC	181-A2-012
187	D-RNA	UGGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGC–CA	181-A2-015
188	D-RNA	GCGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCGC	181-A2-016
189	D-RNA	GUGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCAC	181-A2-017
190	D-RNA	GG–GCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCCC	181-A2-018
191	D-RNA	GAGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCUC	181-A2-019
192	D-RNA	CGGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCCG	181-A2-020

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Seq.-ID	RNA/Peptide	Sequence	Internal Reference
193	D-RNA	CCGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCGG	181-A2-021
194	D-RNA	CAGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCUG	181-A2-022
195	D-RNA	CUGCGUAGUGAGAAACUACCAACGACUGGCUAGAGCCGGCAG	181-A2-023
196	D-RNA	AGCGUGUUAGUGAAGUGGGUGGCAGGUAAAGGACACGCU	184-B8trc
197	D-RNA	AGCGUGGUAGCGGUGUGGGUGGUAGGUAAAGGCCACGCU	184-C6trc
198	D-RNA	AGCGUGAUAGAAGAGCGGGUGGUAGGUAAAGGUCAGGCU	184-H5trc
199	D-RNA	AGCGUGUUAGGUAGGGUGGUAGUAAGUAAAGGACACGCU	184-A7trc
200	D-RNA	AGCGUGUUAGGUGGGUGGUAGUAAGUAAAGGACACGCU	187-A5trc
201	D-RNA	AGCGUGUUAGGUGGGUGGUAGUAAGUAAAGGGCACGCU	187-H5trc
202	D-RNA	CCGCUUAGGUGGGUGGUAGUAAGUAAAGGGGCGG	174-D4-004
203	D-RNA	GCGCGAGCAGGUGGGUGGUAGAAUGUAAAGACUCGCGUC	166-A4-002
204	D-RNA	CGUGUUAGGUGGGUGGUAGUAAGUAAAGGACACG	187-A5trc-001
205	D-RNA	GUGUUAGGUGGGUGGUAGUAAGUAAAGGACAC	187-A5trc-002
206	D-RNA	CGUGUUAGGUGGGUGGUAGUAAGUAAAGGGCACG	187-H5trc-002
207	D-RNA	GUGUUAGGUGGGUGGUAGUAAGUAAAGGGCAC	187-H5trc-003
208	D-RNA	UGUUAGGUGGGUGGUAGUAAGUAAAGGGCA	187-H5trc-004
209	D-RNA	GGACGAGAGUGACAAAUGAUAUAACCUCCUGACUAACGCUGCGGGCGACAGG	177-B3
210	D-RNA	GGACCUAUCGCUAAGACAACGCGCAGUCUACGGGACAUUCUCCGCGGACAGG	177-C1
211	D-RNA	GGACAAUUGUUACCCCCGAGAGAGACAAAUGAGACAACCUCCUGAAGACAGG	177-C2
212	D-RNA	GGACGAAAGUGAGAAAUGAUACAACCUCCUGUUGCUGCGAAUCCGGACAGG	177-E3

Seq.-ID	RNA/Peptide	Sequence	Internal Reference
213	D-RNA	GGACGUAAAAGACGCUACCCGAAAGAAUGUCAGGAGGGUAGACCGACAGG	177-D1
214	D-RNA	GGACUAGAAACUACAAUAGCGGCCAGUUGCACCGCGUUAUCAACGACAGG	177-E1
215	D-RNA	GGACUAGUCAGCCAGUGUGUAUAUCGGACGCGGGUUUAUUUACUGACAGG	177-A1
216	D-RNA	GGACUGUCCGGAGUGUGAAACUCCCCGAGACCGCCAGAAGCGGGGACAGG	177-G3
217	D-RNA	GGACUUCUAUCCAGGUGGGUGGUAGUAUGUAAAGAGAUAGAAGUGACAGG	177-C3
218	D-RNA	GGACGAGAGCGAACAAUGAUAUAACCUCCUGACGGAAAGAGAUCGACAGG	177-A2
219	D-RNA	CCUGUGCUACACGCAGUAAGAAGUGAACGUUCAGUAUGUGUGCACAGG	170-E4trc
220	D-RNA	CGUGAGCCAGGCACCGAGGGCGUUAACUGGCUGAUUGGACACGACACG	166-D2trc
221	D-RNA	CGUGAACAUGCAAGCUAAGCGGGGCUGUUGGUUGCUUGGCCCGCCACG	174-A2trc
222	D-RNA	CGUGCAGAGAGAGACCAACCACGUAAAAUCAACCUAAUGGGCCGCACG	174-E2trc
223	D-RNA	CGUGCAGAGAGAGACCAACCACGUAAAAUCAACCUAAUGGGCCGCACG	183-G3trc
224	D-RNA	CGUGAACAUUCAAGCUAAGCGGGGCUGUUGGUUGCUUGGCCCGCCACG	183-B2trc
225	D-RNA	CGUGCCGAGGCGGCGACCAGCGUUACUUAGAGAGGCUUUGGCACCACG	166-B2trc
226	D-RNA	CGUGAUAACAGCCGUCGGUCAAGAAAACAAAGUUCGGGCGGCGCACG	166-G3trc
227	D-RNA	CGUGGGUGGCGCACCGAGGGCGAAAAGCCACCAGUAAAGAUAGACCG	166-D1trc
228	D-RNA	CGUGUGAUCUCCUUUGGGGUGAUUAGCUUAGAGACUUCCCACACG	183-H2trc
229	D-RNA	GCACCUUCGCCUAAUACACGUGCCGGCUAGCUAAUACUCGUCCGC	167-A7trc
230	D-RNA	GCACGACUUGGGCGACCAGUGAUACUUAGAGAGCAAGUCGUCGGC	167-C7trc
231	D-RNA	GCGCGCGCUCAGUAAGAAAUUGAAAGUUCAGAAUGUCGUCGCGC	167-B5trc
232	D-RNA	AGUGUGUGGCAGGCUAAGGAGAUAUUCCGAGACCACGCU	184-D7trc

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Seq.-ID	RNA/Peptide	Sequence	Internal Reference
233	D-RNA	AGUGUGUGGCAGACUAUGGAUAGACUCCGAGACCACGCU	184-D6trc
234	D-RNA	AGCGUGAGGCGACCAGCGGAUUACUUAGAGAGUCACGCU	184-E5trc
235	D-RNA	AGCGUGAAGGGGACCAGCGUUACUUACAGAGUUCACGCU	184-G6trc
236	D-RNA	AGCGUGUGAUGUAUGUAGCACCGUAUCAGAGGACACGCU	184-B7trc
237	D-RNA	AGCGUGAGGCGACCCGUGUUUCGUAGAGAGUCACGCU	184-B6trc
238	D-RNA	5'PEG-GCACGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUCUGCG	NOX-E36-5'PEG
239	D-RNA	GCACGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUCUGCG-3'PEG	NOX-E36-3'PEG
240	D-RNA	GAGAUGGCGACAUUGGUUGGGCAUGAGGCGAGGCCCUUUGAUGAAUCCGCGGCCAUUC	188-A3-001
241	D-RNA	GAUGGCGACAUUGGUUGGGCAUGAGGCGAGGCCCUUUGAUGAAUCCGCGGCCAUUC	188-A3-004
242	D-RNA	GGCGACAUUGGUUGGGCAUGAGGCGAGGCCCUUUGAUGAAUCCGCGGCCAUUC	188-A3-005
243	D-RNA	GGCGACAUUGGUUGGGCAUGAGGCGAGGCCCUUUGAUGAAUCCGCGGCCAUU	188-A3-006
244	D-RNA	GGCGACAUUGGUUGGGCAUGAGGCGAGGCCCUUUGAUGAAUCCGCGGCCA	(D-)188-A3-007 = (D-mNOX-E36
245	D-RNA	GCUGGUUACCGAGGGGGCGUCGUUGGAGUUUGGUUGGUUGUCACCAGC	189-G7-001
246	D-RNA	CUGGUUACCGAGGGGGCGUCGUUGGAGUUUGGUUGGUUGUCACCAG	189-G7-002
247	D-RNA	UGGUUACCGAGGGGGCGUCGUUGGAGUUUGGUUGGUUGUCACCA	189-G7-003
248	D-RNA	GCCGGUUACCGAGGGGGCGUCGUUGGAGUUUGGUUGGUUGUCACCGGC	189-G7-007
249	D-RNA	GCCGGCUACCGAGGGGGCGUCGUUGGAGUUUGGUUGGUUGUCGCCGGC	189-G7-008
250	D-RNA	GCGCGUACCGAGGGGGCGUCGUUGGAGUUUGGUUGGUUGUCCGCGC	189-G7-010
251	D-RNA	GGGCCUACCGAGGGGGCGUCGUUGGAGUUUGGUUGGUUGUCGGCCC	189-G7-012
252	L-protein	QPDAVNAPLTCCYSFTGKMIPMSRLENYKRITSSRCPKEAVVFVTKLKREICADPNKEWVQ	rat MCP-1

		KYIRKLDQNQVRSET	

Seq.-ID	RNA/Peptide	Sequence	Internal Reference
253	L-RNA	5'PEG-GGCGACAUUGGUUGGGCAUGAGGCGAGGCCCUUUGAUGAAUCCGCGGCCA	mNOX-E36-5'PEG
254	L-RNA	GGCGACAUUGGUUGGGCAUGAGGCGAGGCCCUUUGAUGAAUCCGCGGCCA-3'PEG	mNOX-E36-3'PEG
255	L-DNA	5'-GAGGGACGTGC-(Spacer18)$_2$-NH4$^+$ -3'	NOX-E36 Capture probe
256	L-DNA	5'- Biotin-(Spacer18)$_2$-CGCAGAGCC	NOX-E36 Detect (-ion) probe
257	L-Protein	KSMQVPFSRCCFSFAEQEIPLRAILCYRNTSSICSNEGLIFKLKRGKEACALDTVGWVQRHRKM LRHCPSKRK	CCL1/I-309
258	L-Protein	SLAADTPTACCFSYTSRQIPQNFIADYFETSSQCSKPGVIFLTKRSRQVCADPSEEWVQKYVSD LELSA	CCL3/MIP-1α
259	L-Protein	APMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQPAVVFQTKRSKQVCADPSESWVQEYVY DLELN	CCL4/MIP-1β
260	L-Protein	SPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNPAVVFVTRKNRQVCANPEKKWVREYINS LEMS	CCL5/RANTES
261	L-Protein	FNPQGLAQPDALNVPSTCCFTFSSKKISLQRLKSYVITTSRCPQKAVIFRTKLGKEICADPKEK WVQNYMKHLGRKAHTLKT	CCL13/MCP-4
262	L-Protein	TKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCSKPGIVFITKRGHSVCTNPSDKWV QDYIKDMKEN	CCL14/HCC-1
263	L-Protein	ASVATELRCQCLQTLQGIHPKNIQSVNVKSPGPHCAQTEVIATLKNGRKACLNPASPIVKKIIE KMLNSDKSN	CXCL1/GROα
264	L-Protein	APLATELRCQCLQTLQGIHLKNIQSVKVKSPGPHCAQTEVIATLKNGQKACLNPASPMVKKIIE KMLKNGKSN	CXCL2/GROβ
265	L-Protein	ASVVTELRCQCLQTLQGIHLKNIQSVNVRSPGPHCAQTEVIATLKNGKKACLNPASPMVQKIIE KILNKGSTN	CXCL3/GROγ

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266	L-Protein	EAEEDGDLQCLCVKTTSQVRPRHITSLEVIKAGPHCPTAQLIATLKNGRKICLDLQAPLYKKII KKLLES	CXCL4/PF4

Seq.-ID	RNA/Peptide	Sequence	Internal Reference
267	L-Protein	GPAAAVLRELRCVCLQTTQGVHPKMISNLQVFAIGPQCSKVEVVASLKNGKEICLDPEA PFLKKVIQKILDGGNKEN	CXCL5/ENA-78
268	L-Protein	GPVSAVLTELRCTCLRVTLRVNPKTIGKLQVFPAGPQCSKVEVVASLKNGKQVCLDPEA PFLKKVIQKILDSGNKKN	CXCL6/GCP-2
269	L-Protein	SSTKGQTKRNLAKGKEESLDSDLYAELRCMCIKTTSGIHPKNIQSLEVIGKGTHCNQVE VIATLKDGRKICLDPDAPRIKKIVQKKLAGDESAD	CXCL7/NAP-2
270	L-Protein	EGAVLPRSAKELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRELCLD PKENWVQRVVEKFLKRAENS	CXCL8/IL-8
271	L-Protein	TPVVRKGRCSCISTNQGTIHLQSLKDLKQFAPSPSCEKIEIIATLKNGVQTCLNPDSAD VKELIKKWEKQVSQKKKQKNGKKHQKKKVLKVRKSQRSRQKKTT	CXCL9/MIG
272	L-Protein	VPLSRTVRCTCISISNQPVNPRSLEKLEIIPASQFCPRVEIIATMKKKGEKRCLNPESK AIKNLLKAVSKERSKRSP	CXCL10/IP-10
273	L-Protein	FPMFKRGRCLCIGPGVKAVKVADIEKASIMYPSNNCDKIEVIITLKENKGQRCLNPKSK QARLIIKKVERKNF	CXCL11/I-TAC
274	L-Protein	KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQ EYLEKALNKRFKM	CXCL12α/SDF-1α
275	L-Protein	KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQ EYLEKALNKRFKM	CXCL12β/SDF-1β
276	L-Protein	QHHGVTKCNITCSKMTSKIPVALLIHYQQNQASCGKRAIILETRQHRLFCADPKEQWVK	CX_3CL1/Fractalkine

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		DAMQHLDRQAAALTRNG	
277	L-Protein	VGSEVSDKRTCVSLTTQRLPVSRIKTYTITEGSLRAVIFITKRGLKVCADPQATWVRDV VRSMDRKSNTRNNMIQTKPTGTQQSTNTAVTLTG	XCL1/Lymphotactin

Seq.-ID	RNA/Peptide	Sequence	Internal Reference
278	L-RNA	5′-Biotin-GCACGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUCUGCG	biotinylated NOX-E36
279	L-RNA	5′-UAAGGAAACUCGGUCUGAUGCGGU AGCGCUGUGCAGAGCU	POC
280	L-RNA	5′-PEG-UAAGGAAACUCGGUCUGAUGCGGU AGCGCUGUGCAGAGCU-3′	POC-PEG
281	L-DNA	5'-CCAATGTCGCC-$(Spacer18)_2$-$NH4^+$ -3'	mNOX-E36 Capture probe
282	L-DNA	5'- Biotin-$(Spacer18)_2$-CGCAGAGCC	mNOX-E36 Detect (-ion) probe
283	L-protein	QPDAINSPVTCCYTFTGKKISSQRLGSYKRVTSSKCPKEAVIFKTILAKEIC ADPEQKWVQDAVKQLDKKAQTPKP	horse MCP-1 (Equus caballus)
284	L-protein	QPDAINSQVACCYTFNSKKISMQRLMNYRRVTSSKCPKEAVIFKTILGKELC ADPKQKWVQDSINYLNKKNQTPKP	bovine MCP-1 (Bos Taurus)
285	L-protein	QPDAVNAPLTCCYSFTGKMIPMSRLENYKRITSSRCPKEAVVFVTKLKREIC ADPNKEWVQKYIRKLDQNQVRSETTVFYKIASTLRTSAPLNVNLTHKSEANA STLFSTTTSSTSVEVTSMTEN	rat MCP-1 (Rattus norvegicus)

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The present invention is further illustrated by the figures, examples and the sequence listing from which further features, embodiments and advantages may be taken, wherein

Fig. 1 shows an alignment of sequences of related RNA ligands binding to human MCP-1 indicating the sequence motif ("Type 1A") that is in a preferred embodiment in its entirety essential for binding to human MCP-1;

Fig. 2 shows an alignment of sequences of related RNA ligands binding to human MCP-1 indicating the sequence motif ("Type 1B") that is in a preferred embodiment in its entirety essential for binding to human MCP-1 and derivatives of RNA ligands 180-D1-002;

Fig. 3 shows an alignment of sequences of related RNA ligands binding to human MCP-1 indicating the sequence motif ("Type 2") that is in a preferred embodiment in its entirety essential for binding to human MCP-1;

Fig. 4 shows an alignment of sequences of related RNA ligands binding to human MCP-1 indicating the sequence motif ("Type 3") that is in a preferred embodiment in its entirety essential for binding to human MCP-1;

Fig. 5 shows derivatives of RNA ligands 178-D5 and 181-A2 (human MCP-1 RNA ligands of sequence motif "Type 3");

Fig. 6 shows an alignment of sequences of related RNA ligands binding to human MCP-1 indicating the sequence motif ("Type 4") that is in a preferred embodiment in its entirety essential for binding to human MCP-1 (other sequences);

Fig. 7 shows a table of sequences of several different RNA ligands binding to human MCP-1 which can not be related to the MCP-1 binding sequence motifs "Type 1A", "Type 1B"; "Type 2", "Type 3" or "Type 4";

Fig. 8 shows alignments of derivatives of RNA ligand 188-A3-001 and of 189-G7-001 that bind to murine MCP-1;

Fig. 9 shows the result of a binding analysis of the aptamer D-NOX-E36 to biotinylated human D-MCP-1 at room temperature and 37°C, represented as binding of the aptamer over concentration of biotinylated human D-MCP-1 ;

Fig. 10 shows the result of a binding analysis of the aptamer D-mNOX-E36 to biotinylated murine D-MCP-1 at 37°C, represented as binding of the aptamer over concentration of biotinylated murine D-MCP-1;

Fig. 11 shows MCP-1-induced Ca^{++}-release in THP-1 cells, whereas a dose-response curve for human MCP-1 was obtained, indicating a half effective concentration (EC_{50}) of approximately 3 nM, represented as difference in fluorescence to blank over concentration of human MCP-1;

Fig. 12 shows the efficacy of Spiegelmer NOX-E36 in a calcium release assay; cells were stimulated with 3 nM human MCP-1 preincubated at 37°C with various amounts of Spiegelmer NOX-E36, represented as percentage of control over concentration of NOX-E36;

Fig. 13 shows the efficacy of Spiegelmer mNOX-E36 in a calcium release assay; cells were stimulated with 5 nM murine MCP-1 preincubated at 37°C with various amounts of Spiegelmer mNOX-E36, represented as percentage of control over concentration of mNOX-E36;

Fig. 14 shows the human MCP-1-induced chemotaxis of THP-1 cells whereas after 3 hours migration of THP-1 cells towards various MCP-1 concentrations a dose-response curve for MCP-1 was obtained, represented as X-fold increase compared to control over concentration of human MCP-1;

Fig. 15 shows the efficacy of Spiegelmer NOX-E36 in a chemotaxis assay; cells were allowed to migrate towards 0.5 nM human MCP-1 preincubated at 37°C with various amounts of Spiegelmer NOX-E36, represented as percentage of control over concentration of Spiegelmer NOX-E36;

Fig. 16 shows the efficacy of Spiegelmer mNOX-E36 in a chemotaxis assay; cells were allowed to migrate towards 0.5 nM murine MCP-1 preincubated at 37°C with various amounts of Spiegelmer NOX-E36, represented as percentage of control over concentration of Spiegelmer mNOX-E36;

Fig. 17 shows the Biacore 2000 sensorgram indicating the K_D value of Spiegelmer NOX-E-36 binding to human MCP-1 which was immobilized on a PioneerF1 sensor chip by amine coupling procedure, represented as response (RU) over time;

Fig. 18 shows the Biacore 2000 sensorgram indicating binding of Spiegelmer NOX-E36 to human MCP-family proteins (huMCP-1, huMCP-2, huMCP-

3) and human eotaxin, which were immobilized by amine coupling procedure on a PioneerF1 and a CM4 sensor chip, respectively, represented as response (RU) over time;

Fig. 19 shows the Biacore 2000 sensorgram indicating binding of Spiegelmer NOX-E36 to MCP-1 from different species (canine MCP-1, monkey MCP-1, human MCP-1, porcine MCP-1, rabbit MCP-1, mouse MCP-1, rat MCP-1) whereas different forms of MCP-1 were immobilized by amine coupling procedure on PioneerF1 and a CM4 sensor chips, respectively, represented as response (RU) over time;

Fig. 20 shows the Biacore 2000 sensorgram indicating the K_D value of Spiegelmer 181-A2-018 binding to to human MCP-1 which was immobilized on a CM4 sensor Chip by amine coupling procedure, represented as response (RU) over time;

Fig. 21 shows the Biacore 2000 sensorgram indicating binding of Spiegelmer 181-A2-018 to human MCP-family proteins (huMCP-1, huMCP-2, huMCP-3) and human eotaxin which were immobilized by amine coupling procedure on a PioneerF1 and a CM4 sensor chip, respectively, represented as response (RU) over time;

Fig. 22 shows the Biacore 2000 sensorgram indicating binding of Spiegelmer 181-A2-018 to MCP-1 from different species (canine MCP-1, monkey MCP-1, human MCP-1, porcine MCP-1, rabbit MCP-1, mouse MCP-1, rat MCP-1) whereas different forms of MCP-1 were immobilized by amine coupling procedure on PioneerF1 and a CM4 sensor chips, respectively, represented as response (RU) over time;

Fig. 23 shows a Clustal W alignment of MCP-1 from different mammalian species as well as human MCP-2, MCP-3, and eotaxin (Positions 1-76 only);

Fig. 24A shows a table summarizing the binding specificity of NOX-E36 and 181-A2-018 regarding MCP-1 from different mammalian species as well as human MCP-2, MCP-3, and eotaxin;

Fig. 24B shows a table summarizing the selectivity of NOX-E36 as determined by Biacore analysis whereby biotinylated NOX-E36 was immobilized on a sensor chip surface and binding of a panel of various CC and CXC chemokines to NOX-E36 was analyzed;

Fig. 24C shows the kinetic analysis of NOX-E36 interacting with chemokines as determined by Biacore analysis whereby the chemokines were immobilized covalently on a CM5 sensor chip surface and various concentrations of the NOX-E36 were injected and NOX-E36s binding behaviour was analyzed using the BiaEvaluation software;

Fig. 24D shows the chemotaxis dose-response curve of THP-1 cell stimulation with MIP-1α with a half- effective concentration of about 0.2 nM;

Fig. 24E shows the Inhibition of MIP-1α induced chemotaxis by NOX-E36. NOX-E36 had no influence on the MIP1a induced chemotaxis of THP-1 cells;

Fig. 25 shows the efficacy of Spiegelmer NOX-E36-3'-PEG in a calcium release assay; cells were stimulated with 3 nM human MCP-1 preincubated at 37°C with various amounts of Spiegelmer NOX-E36-3'-PEG, represented as percentage of control over concentration of Spiegelmer NOX-E36-3'-PEG;

Fig. 26 shows the efficacy of Spiegelmer NOX-E36-3'-PEG in a chemotaxis assay; cells were allowed to migrate towards 0.5 nM human MCP-1 preincubated at 37°C with various amounts of Spiegelmer NOX-E36-3'-PEG, represented as percentage of control over concentration of NOX-E36-3'-PEG;

Fig. 27A shows the efficacy of Spiegelmer NOX-E36-5'-PEG in a calcium release assay; cells were stimulated with 3 nM human MCP-1 preincubated at 37°C with various amounts of Spiegelmer NOX-E36-5'-PEG, represented as percentage of control over concentration of Spiegelmer NOX-E36-5'-PEG;

Fig. 27B shows the efficacy of Spiegelmer NOX-E36-5'-PEG in a chemotaxis assay; cells were allowed to migrate towards 0.5 nM human MCP-1 preincubated at 37°C with various amounts of Spiegelmer NOX-E36-5'-PEG, represented as percentage of control over concentration of Spiegelmer NOX-E36-5'-PEG;

Fig. 28 shows murine MCP-1-induced Ca^{++}-release in THP-1 cells, whereas a dose-response curve for murine MCP-1 was obtained, indicating a half effective concentration (EC_{50}) of approximately 5 nM, represented as difference in fluorescence to blank over concentration of murine MCP-1;

Fig. 29 shows the efficacy of anti-murine MCP-1 Spiegelmer mNOX-E36-3'-PEG in a calcium release assay; cells were stimulated with 3 nM murine MCP-1 preincubated at 37°C with various amounts of Spiegelmer mNOX-E36-3'-PEG, represented as percentage of control over concentration of Spiegelmer mNOX-E36-3'-PEG;

Fig. 30 shows the murine MCP-1-induced chemotaxis of THP-1 cells whereas after 3 hours migration of THP-1 cells towards various mMCP-1 concentrations a dose-response curve for mMCP-1 was obtained, represented as X-fold increase compared to control over concentration of murine MCP-1;

Fig. 31 shows the efficacy of anti-murine MCP-1 Spiegelmer mNOX-E36-3'-PEG in a chemotaxis assay; cells were allowed to migrate towards 0.5 nM murine MCP-1 preincubated at 37°C with various amounts of Spiegelmer mNOX-E36-3'-PEG, represented as percentage of control over concentration of anti-murine Spiegelmer mNOX-E36-3'-PEG;

Fig. 32 shows the Biacore 2000 sensorgram indicating the K_D value of aptamer D-mNOX-E36 binding to murine D-MCP-1 which was immobilized on a PioneerF1 sensor chip by amine coupling procedure, represented as response (RU) over time;

Fig. 33 shows the Biacore 2000 sensorgram indicating binding of aptamer D-mNOX-E36 to human D-MCP-1 and murine D-MCP-1 whereas the two different forms of D-MCP-1 were immobilized by amine coupling procedure on PioneerF1 and a CM4 sensor chips, respectively, represented as response (RU) over time;

Fig. 34 shows renal sections of 24-week old $MRL^{lpr/lpr}$ mice, stained with periodic acid Schiff (PAS), antibodies for Mac-2 (macrophages) and CD3 (T cells) as indicated; images are representative for 7-12 mice in each group (original magnification PAS: x 100, PAS inserts: x 400, Mac2: x 400, CD3: x 100;

Fig. 35 shows a table illustrating renal function parameters and histological findings in the different groups of 24-week old $MRL^{lpr/lpr}$ mice;

Fig. 36 shows the quantification of histological changes by morphometry performed on silver stained sections of mice from all groups; A, interstitial volume index; B, tubular dilation index, and C, tubular cell damage index

were calculated as percentage of high power field and are expressed as means ± SEM;

Fig. 37 shows the survival of $MRL^{lpr/lpr}$ mice of the various treatment groups as calculated by Kaplan-Meier analysis;

Fig. 38 shows renal mRNA expression for the CC-chemokines CCL2 and CCL5 as determined by real-time RT-PCR using total renal RNA pooled from 5 mice of each group whereby RNA levels for each group of mice are expressed per respective 18S rRNA expression;

Fig. 39 shows reduction of lung pathology by treatment with mNOX-E36-3'PEG; lung tissue was prepared from of all groups at age 24 weeks and scored semiquantitatively; treatment with mNOX-E36 and mNOX-E36-3'PEG reduced peribronchiolar inflammation in $MRL^{lpr/lpr}$ mice; images are representative for 7-11 mice in each group; original magnification x 100;

Fig. 40 shows cutaneous lupus manifestations of $MRL^{lpr/lpr}$ mice at age 24 weeks which typically occur at the facial or neck area (left mouse) which were less common in anti-mCCL2 Spiegelmer-treated mice (right mouse);

Fig. 41 shows serum and histological findings in $MRL^{lpr/lpr}$ mice at age 24 weeks;

Fig. 42 shows the pharmacokinetics of pegylated and unpegylated anti-mCCL2 Spiegelmers in plasma during the study, indicated as plasma concentration of Spiegelmer mNOX-E36 as a function of time;

Fig. 43 shows flow cytometry for CCR2 on bone marrow and peripheral blood in 24 week old vehicle- or mNOX-E36-3'PEG-treated $MRL^{lpr/lpr}$ mice; data are shown as mean percentage of CCR2 positive cells ± SEM in either bone marrow or peripheral blood in 5 mice of each group;

Fig. 44 shows serum CCL2 levels in PoC-PEG- (white bars) and mNOX-E36-3'PEG (mNOX-E36-P)-treated (black bars) 1K db/db mice as determined by ELISA at different time points as indicated; data are means ± SEM; *, $p < 0.05$ mNOX-E36-3'PEG (mNOX-E36-P) vs. PoC-PEG;

Fig. 45 shows the infiltrated number of Mac-2 and Ki-67 positive cells in the glomeruli and the interstitium of untreated or POC-PEG or rather mNOX-E36-3'PEG treated db/db mice;

Fig. 46 shows the diabetic glomerulosclerosis in 6 months old db/db mice; renal sections from mice of the different groups were stained with periodic acid Schiff and 15 glomeruli from each renal section were scored for the extent

of glomerulosclerosis; images show representative glomeruli graded to the respective scores as indicated, original magnification 400 x; the graph illustrates the mean percentage of each score ± SEM from all mice in each group (n = 7 – 10); *, $p < 0.05$ for mNOX-E36-3'PEG (mNOX-E36-P) vs. PoC-PEG (PoC-P)-treated 1K db/db mice;

Fig. 47 shows the glomerular filtration rate (GFR) in 6 months old mNOX-E36-3'PEG (mNOX-E36-P)- and PoC-PEG(PoC-P)-treated 1K db/db mice; GFR was determined by FITC-inulin clearance kinetics in the groups of PoC-PEG- and mNOX-E36-3'PEG-treated 1K db/db mice at the end of the study;

Fig. 48 shows tubular atrophy and interstitial volume of 6 months old db/db mice; images of silver-stained renal sections illustrate representative kidneys from the respective groups (original magnification 100x); values represent means ± SEM of the respective morphometric analysis index from 7 – 10 mice in each group; *, $p < 0.05$ 2K db/db vs. BKS wild-type mice; $^{\#}$, $p < 0.05$ 1K vs. 2K db/db mice; †, $p < 0.05$ mNOX-E36-3'PEG (mNOX-E36-PEG) - vs. PoC-PEG-treated 1K db/db mice;

Fig. 49 shows renal CCL2 mRNA expression db/db mice as determined by real-time RT-PCR using total renal RNA pooled from 6 – 10 mice of each group; mRNA levels for each group of mice are expressed per respective 18 S rRNA expression; and

Fig. 50 shows spatial CCL2 expression in kidneys of db/db mice as determined by immunostaining; images illustrate representative sections of kidneys from 6 months old mice of the respective groups as indicated (original magnification, 200 x).

Example 1: Nucleic acids that bind human MCP-1

Using biotinylated human D-MCP-1 as a target, several nucleic acids that bind to human MCP-1 could be generated the nucleotide sequences of which are depicted in Figures 1 through 7. The nucleic acids were characterized on the aptamer, i. e. D-nucleic acid level using competitive or direct pull-down assays with biotinylated human D-MCP-1 (Example 4) or on the Spiegelmer level, i. e. L-nucleic acid with the natural configuration of MCP-1 (L-MCP) by surface plasmon

resonance measurement using a Biacore 2000 instrument (Example 7), an *in vitro* cell culture Ca^{++}-release assay (Example 5), or an *in vitro* chemotaxis assay (Example 6).

The nucleic acid molecules thus generated exhibit different sequence motifs, four main types are defined in Figs. 1 and 2 (Type 1A / 1B), Fig. 3 (Type 2), Figs. 4 and 5 (Type 3), and Fig. 6 (Type 4). Additional MCP-1 binding nucleic acids which can not be related to each other and to the differerent sequence motifs decribed herein, are listed in Fig. 7. For definition of nucleotide sequence motifs, the IUPAC abbreviations for ambiguous nucleotides is used:

S	strong	G or C;
W	weak	A or U;
R	purine	G or A;
Y	pyrimidine	C or U;
K	keto	G or U;
M	imino	A or C;
B	not A	C or U or G;
D	not C	A or G or U;
H	not G	A or C or U;
V	not U	A or C or G;
N	all	A or G or C or U

If not indicated to the contrary, any nucleic acid sequence or sequence of stretches and boxes, respectively, is indicated in the 5' → 3' direction.

Type 1A MCP-1 binding nucleic acids (Fig. 1)

As depicted in Fig. 1 all sequences of MCP-1 binding nucleic acids of Type 1A comprise several sequences stretches or boxes whereby boxes B1A and B1B are the 5'- and 3' terminal stretches that can hybridize with each other. However, such hybridization is not necessarily given in the molecule as actually present under physiological conditions. Boxes B2, *B3*, B4, B5 and box **B6** are flanked by box B1A and box B1B.

The nucleic acids were characterized on the aptamer level using direct and competitive pull-down assays with biotinylated human D-MCP-1 in order to rank them with respect to their

binding behaviour (Example 4). Selected sequences were synthesized as Spiegelmer (Example 3) and were tested using the natural configuration of MCP-1 (L-MCP) in an *in vitro* cell culture Ca^{++}-release assay (Example 5).

The sequences of the defined boxes may be different between the MCP-1 binding nucleic acids of Type 1A which influences the binding affinity to MCP-1. Based on binding analysis of the different MCP-1 binding nucleic acids summarized as ***Type 1A MCP-1 binding nucleic acids,*** the boxes B1A, B2, *B3*, B4, B5, **B6** and B1B and their nucleotide sequences as described in the following are individually and more preferably in their entirety essential for binding to MCP-1:

- boxes B1A and B1B are the 5'- and 3' terminal stretches can hybridize with each other; where B1A is AGCRUG, preferably AGCGUG; and where B1B is CRYGCU, preferably CACGCU;
- box B2, which is CCCGGW, preferably CCCGGU;
- box *B3*, which is *GUR*, preferably *GUG*;
- box B4, which is RYA, preferably GUA;
- box B5, which is GGGGGRCGCGAYC, preferably GGGGGGCGCGACC;
- box **B6**, which is **UGCAAUAAUG** or **URYAWUUG**, preferably **UACAUUUG**;

As depicted in Fig. 1, the nucleic acid molecule referred to as 176-E10trc has the best binding affinity to MCP-1 (as aptamer in the pull-assay with a K_D of 5 nM as well as as Spiegelmer with an IC_{50} of 4 – 5 nM in *in vitro* cell culture Ca^{++}-release assay) and therefore may constitute the optimal sequence and the optimal combination of sequence elements B1A, B2, *B3*, B4, B5, **B6** and B1B.

Type 1B MCP-1 binding nucleic acids (Fig. 2)

As depicted in Fig. 2, all sequences of Type 1B comprise several sequences stretches or boxes whereby boxes B1A and B1B are the 5'- and 3' terminal stretches that can hybridize with each other and boxes B2, *B3*, B4, B5 and box **B6** are flanked by box B1A and box B1B. However, such hybridization is not necessarily given in the molecule as actually present under physiological conditions.

The nucleic acids were characterized on the aptamer level using using direct and competitive pull-down assays with biotinylated human D-MCP-1 in order to rank them with respect to their binding behaviour (Example 4). Selected sequences were synthesized as Spiegelmer (Example 3) and were tested using the natural configuration of MCP-1 (L-MCP) in an *in vitro* cell culture Ca^{++}-release assay (Example 5).

The sequences of the defined boxes may be different between the MCP-1 binding nucleic acids of Type 1B which influences the binding affinity to MCP-1. Based on binding analysis of the different MCP-1 binding nucleic acids summarized as ***Type 1B MCP-1 binding nucleic acids,*** the boxes B1A, B2, *B3*, B4, B5, **B6** and B1B and their nucleotide sequences as described in the following are individually and more preferably in their entirety essential for binding to MCP-1:

- boxes B1A and B1B that can hybridize with each other; where B1A is AGYRUG, preferably AGCGUG; and where B1B is CAYRCU, preferably CACGCU;
- box B2, which is CCAGCU or CCAGY, preferably CCAGU;
- box *B3*, which is *GUG*;
- box B4, which is AUG;
- box B5, which is GGGGGGCGCGACC;
- box **B6**, which is **CAUUUUA** or **CAUUUA,** preferably **CAUUUUA**;

As depicted in Fig. 2, the nucleic acid referred to as 176-C9trc has the best binding affinity to MCP-1 (as aptamer in the pull-down assay with a K_D of 5 nM as well as as Spiegelmer with an IC_{50} of 4 – 5 nM in *in vitro* cell culture Ca^{++}-release assay) and therefore may constitute the optimal sequence and the optimal combination of sequence elements B1A, B2, *B3*, B4, B5, **B6** and B1B.

Type 2 MCP-1 binding nucleic acids (Fig. 3)

As depicted in Fig. 3, all sequences of Type 2 comprise several sequences stretches or boxes whereby boxes B1A and B1B are the 5'- and 3' terminal stretches that can hybridize with each other and box B2 is the central sequence element. However, such hybridization is not necessarily given in the molecule as actually present under physiological conditions.

The nucleic acids were characterized on the aptamer level using direct and competitive pull-down assays with biotinylated human D-MCP-1 in order to rank them with respect to their binding behaviour (Example 4). Selected sequences were synthesized as Spiegelmer (Example 3) and were tested tested using the natural configuration of MCP-1 (L-MCP) in *in vitro* cell culture Ca^{++}-release (Example 5) or *in vitro* chemotaxis assays (Example 6).

The sequences of the defined boxes may be different between the MCP-1 binding nucleic acids of Type 3 which influences the binding affinity to MCP-1. Based on binding analysis of the different MCP-1 binding nucleic acids summarized as ***Type 2 MCP-1 binding nucleic acids,*** the boxes B1A, B2, and B1B and their nucleotide sequences as described in the following are individually and more preferably in their entirety essential for binding to MCP-1:

- boxes B1A and B1B, 5'- and 3' terminal stretches that can hybridize with each other; where B1A is ACGCA and B1B is UGCGU, or B1A is CGCA and B1B is UGCG, or B1A is GCA and B1B is UGCG or UGC; preferably B1A is GCA and B1B is UGCG;
- box B2, CSUCCCUCACCGGUGCAAGUGAAGCCGYGGCUC, preferably CGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUC

As depicted in Fig. 3, the nucleic acid referred to as 180-D1-002 as well as the derivatives of 180-D1-002 like 180-D1-011, 180-D1-012, 180-D1-035, and 180-D1-036 (= NOX-E36) have the best binding affinity to MCP-1 as aptamer in the pull-down or competitive pull-down assay with an K_D of < 1 nM and therefore may constitute the optimal sequence and the optimal combination of sequence elements B1A, B2, and B1B.

For nucleic acid molecule D-NOX-E36 (D-180-D1-036; SEQ.ID No. 159), a dissociation constant (K_D) of 890 ± 65 pM at room temperature (RT) and of 146 ± 13 pM at 37°C was determined (Example 4; Fig. 9). The respective Spiegelmer NOX-E36 (180-D1-036; SEQ.ID No. 37) exhibited an inhibitory concentration (IC_{50}) of 3 – 4 nM in an *in vitro* Ca^{++}-release assay (Example 5; Fig. 12) and of ca. 0.5 nM in an *in vitro* chemotaxis assay (Example 6; Fig. 15). For the PEGylated derivatives of NOX-E36, NOX-E36-3'PEG and NOX-E36-5'PEG, IC_{50}s of ca. 3 nM were determined in the Ca^{++}-release assay (Example 5, Fig. 25 and Fig.27A) and < 1 nM in the chemotaxis assay (Example 6; Fig. 26 and Fig. 27B).

Type 3 MCP-1 binding nucleic acids (Figs. 4+5)

As depicted in Figs. 4 and 5, all sequences of Type 3 comprise several sequence stretches or boxes whereby three pairs of boxes are characteristic for ***Type 3 MCP-1 binding nucleic acids.*** Both boxes B1A and B1B as well as boxes B2A and B2B as well as boxes **B5A** and **B5B** bear the ability to hybridize with each other. However, such hybridization is not necessarily given in the molecule as actually present under physiological conditions. Between these potentially hybridized sequence elements, non-hybridizing nucleotides are located, defined as box *B3*, box B4 and box B6.

The nucleic acids were characterized on the aptamer level using direct and competitive pull-down assays with biotinylated human D-MCP-1 in order to rank them with respect to their binding behavior (Example 4). Selected sequences were synthesized as Spiegelmer (Example 3) and were tested using the natural configuration of MCP-1 (L-MCP) in *in vitro* chemotaxis assays (Example 6) or via Biacore measurements (Example 7).

The sequences of the defined boxes may be different between the MCP-1 binding nucleic acids of Type 3 which influences the binding affinity to MCP-1. Based on binding analysis of the different MCP-1 binding nucleic acids summarized as ***Type 3 MCP-1 binding nucleic acids,*** the boxes B1A, B2A, *B3*, B2B, B4, **B5A,** B6, **B5B,** B1B and their nucleotide sequences as described in the following are individually and more preferably in their entirety essential for binding to MCP-1:

- boxes B1A and B1B, 5'- and 3' terminal stretches that can hybridize with each other; where B1A is GURCUGC and B1B is GCAGCAC; preferably B1A is GUGCUGC and B1B is GCAGCAC;
  or B1A is GKSYGC and B1B is GCRSMC; preferably B1A is GUGCGC and B1B is GCGCAC;
  or B1A is KBBSC and B1B is GSVVM; preferably B1A is KKSSC and B1B is GSSMM;
  or B1A is BNGC and B1B is GCNV; preferably B1A is SNGC and B1B is GCNS; most preferably B1A is GGGC and B1B is GCCC;
- boxes B2A and B2B, stretches that can hybridize with each other; where B2A is GKMGU and B2B is ACKMC; preferably B2A is GUAGU and B2B is ACUAC;

- box *B3*, which is *KRRAR*, preferably *UAAAA* or *GAGAA*;
- box B4, which is CURYGA or CUWAUGA or CWRMGACW or UGCCAGUG, preferably CAGCGACU or CAACGACU;
- **B5A** and **B5B,** stretches that can hybridize with each other; where **B5A** is **GGY** and **B5B** is **GCYR** whereas **GCY** can hybridize with the nucleotides of **B5A**; or **B5A** is **CWGC** and **B5B** is **GCWG**; preferably **B5A** is **GGC** and **B5B** is **GCCG**;
- box B6, which is: YAGA or CKAAU or CCUUUAU, preferably UAGA.

As depicted in Figs. 4 and 5, the nucleic acid referred to as 178-D5 and its derivative 178-D5-030 as well as 181-A2 with its derivatives 181-A2-002, 181-A2-004, 181-A2-005, 181-A2-006, 181-A2-007, 181-A2-017, 181-A2-018, 181-A2-019, 181-A2-020, 181-A2-021, and 181-A2-023 have the best binding affinity to MCP-1. 178-D5 and 178-D5-030 were evaluated as aptamers in direct or competitive pull-down assays (Example 4) with an K_D of approx. 500 pM. In the same experimental set-up, 181-A2 was determined with an K_D of approx. 100 pM. By Biacore analysis (Example 7), the K_D of 181-A2 and its derivatives towards MCP-1 was determined to be 200 – 300 pM. In Ca^{++} release and chemotaxis assays with cultured cells (Example 5 and 6, respectively), for both 178-D5 and 181-A2, an IC_{50} of approx. 500 pM was measured. Therefore, 178-D5 as well as 181-A2 and their derivatives may constitute the optimal sequence and the optimal combination of sequence elements B1A, B2A, *B3*, B2B, B4, **B5A,** B6, **B5B** and B1B.

Type 4 MCP-1 binding nucleic acids (Fig. 6)

As depicted in Fig. 6, all sequences of Type 4 comprise several sequences, stretches or boxes whereby boxes B1A and B1B are the 5'- and 3' terminal stretches that can hybridize with each other and box B2 is the central sequence element.

The nucleic acids were characterized on the aptamer level using direct pull-down assays with biotinylated human D-MCP-1 in order to rank them with respect to their binding behavior (Example 4). Selected sequences were synthesized as Spiegelmer (Example 3) and were tested using the natural configuration of MCP-1 (L-MCP) in an *in vitro* cell culture Ca^{++}-release (Example 5) and/or chemotaxis assay (Example 6).

The sequences of the defined boxes may differ among the MCP-1 binding nucleic acids of Type 4 which influences the binding affinity to MCP-1. Based on binding analysis of the different

MCP-1 binding nucleic acids summarized as ***Type 4 MCP-1 binding nucleic acids,*** the boxes B1A, B2, and B1B and their nucleotide sequences as described in the following are individually and more preferably in their entirety essential for binding to MCP-1:

- boxes B1A and B1B, 5'- and 3' terminal stretches that can hybridize with each other; where B1A is AGCGUGDU and B1B is GNCASGCU; or B1A is GCGCGAG and B1B is CUCGCGUC; or B1A is CSKSUU and B1B is GRSMSG; or B1A is GUGUU and B1B is GRCAC; or B1A is UGUU and B1B is GGCA; preferably B1A is CSKSUU and B1B is GRSMSG; mostly preferred B1A is CCGCUU and B1B is GGGCGG; and
- box B2, which is AGNDRDGBKGGURGYARGUAAAG or AGGUGGGUGGUAGUAAGUAAAG or CAGGUGGGUGGUAGAAUGUAAAGA, preferably AGGUGGGUGGUAGUAAGUAAAG

As depicted in Fig. 6, the nucleic acid referred to as 174-D4-004 and 166-A4-002 have the best binding affinity to MCP-1 (as Spiegelmer with an IC_{50} of 2 – 5 nM in *in vitro* cell culture Ca^{++} release assay) and may, therefore, constitute the optimal sequence and the optimal combination of sequence elements B1A, B2, and B1B.

Additionally, 29 other MCP-1 binding nucleic acids were identified which cannot be described by a combination of nucleotide sequence elements as has been shown for Types 1 - 4 of MCP-1 binding nucleic acids. These sequences are listed in Fig. 7.

It is to be understood that any of the sequences shown in Figs. 1 through 7 are nucleic acids according to the present invention, including those truncated forms thereof but also including those extended forms thereof under the proviso, however, that the thus truncated and extended, respectively, nucleic acid molecules are still capable of binding to the target.

Example 2: Nucleic acids that bind murine MCP-1

Using biotinylated murine D-MCP-1 as a target, several nucleic acid molecules binding thereto could be generated. The result of a sequence analysis of these nucleic acid molecules can be taken from Fig. 8.

The nucleic acids were characterized on the aptamer level using a pull-down assay using biotinylated murine D-MCP-1 in order to in order to rank them with respect to their binding behavior (Example 4). Selected sequences were synthesized as Spiegelmer (Example 3) and were tested using the natural configuration of MCP-1 (L-MCP) in an *in vitro* cell culture Ca^{++}-release (Example 5) and chemotaxis assay (Example 6).

As depicted in Fig. 8, D-188-A3-001 and D-189-G7-001 and their derivatives bind D-MCP-1 with subnanomolar K_D in the pull-down assay (Fig. 8).

For D-mNOX-E36 (= D-188-A3-007; SEQ.ID No. 244), a dissociation constant (K_D) of 0.1 – 0.2 nM at 37°C was determined (Example 4; Fig. 10). The respective Spiegelmer mNOX-E36 (188-A3-007; SEQ.ID No. 122) exhibited an inhibitory concentration (IC_{50}) of approx. 12 nM in an *in vitro* Ca^{++}-release assay (Example 5; Fig. 13) and of approx. 7 nM in an *in vitro* chemotaxis assay (Example 6; Fig. 16). For the PEGylated derivative of mNOX-E36, mNOX-E36-3'PEG (SEQ.ID No. 254), IC_{50}'s of approx. 8 nM were determined in the Ca^{++}-release assay (Example 5, Fig. 29) and approx. 3 nM in the chemotaxis assay (Example 6; Fig. 31).

It is to be understood that any of the sequences shown in Figs. 1 through 7 are nucleic acids according to the present invention, including those truncated forms thereof but also including those extended forms thereof under the proviso, however, that the thus truncated and extended, respectively, nucleic aicd molecules are still capable of binding to the target.

Example 3: Synthesis and derivatization of Aptamers and Spiegelmers

Small scale synthesis

Aptamers and Spiegelmers were produced by solid-phase synthesis with an ABI 394 synthesizer (Applied Biosystems, Foster City, CA, USA) using 2'TBDMS RNA phosphoramidite chemistry (M.J. Damha, K.K. Ogilvie, Methods in Molecular Biology, Vol. 20 Protocols for oligonucleotides and analogs, ed. S. Agrawal, p. 81-114, Humana Press Inc. 1993). rA(N-Bz)-, rC(Ac)-, rG(N-ibu)-, and rU- phosphoramidites in the D- and L-configuration were purchased from ChemGenes, Wilmington, MA. Aptamers and Spiegelmers were purified by gel electrophoresis.

Large scale synthesis plus modification

Spiegelmer NOX-E36 was produced by solid-phase synthesis with an ÄktaPilot100 synthesizer (Amersham Biosciences; General Electric Healthcare, Freiburg) using 2'TBDMS RNA phosphoramidite chemistry (M.J. Damha, K.K. Ogilvie, Methods in Molecular Biology, Vol. 20 Protocols for oligonucleotides and analogs, ed. S. Agrawal, p. 81-114, Humana Press Inc. 1993). L-rA(N-Bz)-, L-rC(Ac)-, L-rG(N-ibu)-, and L-rU- phosphoramidites were purchased from ChemGenes, Wilmington, MA. The 5'-amino-modifier was purchased from American International Chemicals Inc. (Framingham, MA, USA). Synthesis of the unmodified Spiegelmer was started on L-riboG modified CPG pore size 1000 Å (Link Technology, Glasgow, UK); for the 3'-NH_2-modified Spiegelmer, 3'-Aminomodifier-CPG, 1000 Å (ChemGenes, Wilmington, MA) was used. For coupling (15 min per cycle), 0.3 M benzylthiotetrazole (CMS-Chemicals, Abingdon, UK) in acetonitrile, and 3.5 equivalents of the respective 0.1 M phosphoramidite solution in acetonitrile was used. An oxidation-capping cycle was used. Further standard solvents and reagents for oligonucleotide synthesis were purchased from Biosolve (Valkenswaard, NL). The Spiegelmer was synthesized DMT-ON; after deprotection, it was purified via preparative RP-HPLC (Wincott F. *et al.* (1995) *Nucleic Acids Res* **23**:2677) using Source15RPC medium (Amersham). The 5'DMT-group was removed with 80% acetic acid (30 min at RT). Subsequently, aqueous 2 M NaOAc solution was added and the Spiegelmer was desalted by tangential-flow filtration using a 5 K regenerated cellulose membrane (Millipore, Bedford, MA).

PEGylation of NOX-E36

In order to prolong the Spiegelmer's plasma residence time *in vivo*, Spiegelmer NOX-E36 was covalently coupled to a 40 kDa polyethylene glycol (PEG) moiety at the 3'-end or 5'-end.

3'-PEGylation of NOX-E36

For PEGylation (for technical details of the method for PEGylation see European patent application EP 1 306 382), the purified 3'-amino modified Spiegelmer was dissolved in a mixture of H_2O (2.5 ml), DMF (5 ml), and buffer A (5 ml; prepared by mixing citric acid • H_2O [7 g], boric acid [3.54 g], phosphoric acid [2.26 ml], and 1 M NaOH [343 ml] and adding H2O to a final volume of 1 l; pH = 8.4 was adjusted with 1 M HCl).

The pH of the Spiegelmer solution was brought to 8.4 with 1 M NaOH. Then, 40 kDa PEG-NHS ester (Nektar Therapeutics, Huntsville, AL) was added at 37°C every 30 min in four portions of 0.6 equivalents until a maximal yield of 75 to 85% was reached. The pH of the reaction mixture was kept at 8 – 8.5 with 1 M NaOH during addition of the PEG-NHS ester.

The reaction mixture was blended with 4 ml urea solution (8 M), 4 ml buffer A, and 4 ml buffer B (0.1 M triethylammonium acetate in H_2O) and heated to 95°C for 15 min. The PEGylated Spiegelmer was then purified by RP-HPLC with Source 15RPC medium (Amersham), using an acetonitrile gradient (buffer B; buffer C: 0.1 M triethylammonium acetate in acetonitrile). Excess PEG eluted at 5% buffer C, PEGylated Spiegelmer at 10 – 15% buffer C. Product fractions with a purity of >95% (as assessed by HPLC) were combined and mixed with 40 ml 3 M NaOAC. The PEGylated Spiegelmer was desalted by tangential-flow filtration (5 K regenerated cellulose membrane, Millipore, Bedford MA).

5'-PEGylation of NOX-E36

For PEGylation (for technical details of the method for PEGylation see European patent application EP 1 306 382), the purified 5'-amino modified Spiegelmer was dissolved in a mixture of H_2O (2.5 ml), DMF (5 ml), and buffer A (5 ml; prepared by mixing citric acid • H_2O [7 g], boric acid [3.54 g], phosphoric acid [2.26 ml], and 1 M NaOH [343 ml] and adding water to a final volume of 1 l; pH = 8.4 was adjusted with 1 M HCl).

The pH of the Spiegelmer solution was brought to 8.4 with 1 M NaOH. Then, 40 kDa PEG-NHS ester (Nektar Therapeutics, Huntsville, AL) was added at 37°C every 30 min in six portions of 0.25 equivalents until a maximal yield of 75 to 85% was reached. The pH of the reaction mixture was kept at 8 – 8.5 with 1 M NaOH during addition of the PEG-NHS ester.

The reaction mixture was blended with 4 ml urea solution (8 M), , and 4 ml buffer B (0.1 M triethylammonium acetate in H_2O) and heated to 95°C for 15 min. The PEGylated Spiegelmer was then purified by RP-HPLC with Source 15RPC medium (Amersham), using an acetonitrile gradient (buffer B; buffer C: 0.1 M triethylammonium acetate in acetonitrile). Excess PEG eluted at 5% buffer C, PEGylated Spiegelmer at 10 – 15% buffer C. Product fractions with a purity of >95% (as assessed by HPLC) were combined and mixed with 40 ml 3 M NaOAC. The PEGylated Spiegelmer was desalted by tangential-flow filtration (5 K regenerated cellulose membrane, Millipore, Bedford MA).

Example 4: Determination of Binding Constants (Pull-Down Assay)

Direct pull-down assay

The affinity of aptamers to D-MCP-1 was measured in a pull down assay format at 20 or 37°C, respectively. Aptamers were 5'-phosphate labeled by T4 polynucleotide kinase (Invitrogen, Karlsruhe, Germany) using [γ-^{32}P]-labeled ATP (Hartmann Analytic, Braunschweig, Germany). The specific radioactivity of labeled aptamers was 200,000 – 800,000 cpm/pmol. Aptamers were incubated after de- and renaturation at 20 pM concentration at 37°C in selection buffer (20 mM Tris-HCl pH 7.4; 137 mM NaCl; 5 mM KCl; 1 mM $MgCl_2$; 1 mM $CaCl_2$; 0.1% [w/vol] Tween-20) together with varying amounts of biotinylated D-MCP-1 for 4 - 12 hours in order to reach equilibrium at low concentrations. Selection buffer was supplemented with 10 µg/ml human serum albumin (Sigma-Aldrich, Steinheim, Germany), and 10 µg/ml yeast RNA (Ambion, Austin, USA) in order to prevent adsorption of binding partners with surfaces of used plasticware or the immobilization matrix. The concentration range of biotinylated D-MCP-1 was set from 8 pM to 100 nM; total reaction volume was 1 ml. Peptide and peptide-aptamer complexes were immobilized on 1.5 µl Streptavidin Ultralink Plus particles (Pierce

Biotechnology, Rockford, USA) which had been preequilibrated with selection buffer and resuspended in a total volume of 6 µl. Particles were kept in suspension for 30 min at the respective temperature in a thermomixer. Immobilized radioactivity was quantitated in a scintillation counter after detaching the supernatant and appropriate washing. The percentage of binding was plotted against the concentration of biotinylated D-MCP-1 and dissociation constants were obtained by using software algorithms (GRAFIT; Erithacus Software; Surrey U.K.) assuming a 1:1 stoichiometry.

Competitive pull-down assay

In order to compare different D-MCP-1 binding aptamers, a competitive ranking assay was performed. For this purpose the most affine aptamer available was radioactively labeled (see above) and served as reference. After de- and renaturation it was incubated at 37°C with biotinylated D-MCP-1 in 1 ml selection buffer at conditions that resulted in around 5 - 10 % binding to the peptide after immobilization and washing on NeutrAvidin agarose or Streptavidin Ultralink Plus (both from Pierce) without competition. An excess of de- and renatured non-labeled D-RNA aptamer variants was added to different concentrations (e.g. 2, 10, and 50 nM) with the labeled reference aptamer to parallel binding reactions. The aptamers to be tested competed with the reference aptamer for target binding, thus decreasing the binding signal in dependence of their binding characteristics. The aptamer that was found most active in this assay could then serve as a new reference for comparative analysis of further aptamer variants.

Example 5: Determination of Inhibitory Concentration in a Ca^{++}-Release Assay

THP-1-cells (DSMZ, Braunschweig) were cultivated overnight at a cell density of 0.3 x 10^6/ml at 37°C and 5% CO_2 in RPMI 1640 medium with GlutaMAX (Invitrogen) which contained in addition 10% fetal calf serum, 50 units/ml penicillin, 50 µg/ml streptomycin and 50 µM β-mercaptoethanol.

The Spiegelmers were incubated together with recombinant human MCP-1 (Bachem) in Hanks balanced salt solution (HBSS), containing 1 mg/ml bovine serum albumin, 5 mM probenecid and 20 mM HEPES (HBSS+) for 15 to 60 min at 37°C in a 0.2 ml low profile 96-tube plate ("stimulation solution").

For loading with the calcium indicator dye, cells were centrifuged at 300 x *g* for 5 min, resuspended in 4 ml indicator dye solution (10 µM fluo-4 [Molecular Probes], 0.08% pluronic 127 [Molecular Probes] in HBSS+) and incubated for 60 min at 37°C. Thereafter, 11 ml HBSS+ were added and the cells were centrifuged as above, washed once with 15 ml HBSS+ and then resuspended in HBSS+ to give a cell density of 1.1 x 10^6/ml. 90 µl of this cell suspension were added to each well of a black 96-well plate.

Measurement of fluorescence signals was done at an excitation wavelength of 485 nm and an emission wavelength of 520 nm in a Fluostar Optima multidetection plate reader (BMG). For parallel measurement of several samples, wells of one (perpendicular) row of a 96-well plate were recorded together. First three readings with a time lag of 4 sec were done for determination of the base line. Then the recording was interrupted and the plate was moved from the instrument. Using a multi-channel pipette, 10 µl of the stimulation solution was added to the wells, then the plate was moved into the instrument again and the measurement was continued. In total, 20 recordings with time intervals of 4 seconds were performed.

For each well the difference between maximal fluorescence and base line value was determined and plotted against MCP-1 concentration or, in the experiments on the inhibition of calcium release by Spiegelmers, against concentration of Spiegelmer.

Determination of half-maximal effective concentration (EC_{50}) for human MCP-1

After stimulation of THP-1 cells with various hMCP-1 concentrations and plotting the difference between the maximal and the baseline signals, a dose-response curve for human MCP-1 was obtained, indicating a half effective concentration (EC_{50}) of about 2 – 4 nM (Fig. 11). This concentration was used for the further experiments on inhibition of Ca^{++}-release by Spiegelmers.

Determination of half-maximal effective concentration (EC_{50}) for murine MCP-1

After stimulation of THP-1 cells with various mMCP-1 concentrations and plotting the difference between the maximal and the baseline signals, a dose-response curve for murine MCP-1 was obtained, indicating a half effective concentration (EC_{50}) of about 5 nM (Fig. 28).

This concentration was used for the further experiments on inhibition of Ca^{++}-release by Spiegelmers.

Example 6: Determination of Inhibitory Concentration in a Chemotaxis Assay

THP-1 cells grown as described above were centrifuged, washed once in HBH (HBSS, containing 1 mg/ml bovine serum albumin and 20 mM HEPES) and resuspended at 3 x 10^6 cells/ml. 100 µl of this suspension were added to Transwell inserts with 5 µm pores (Corning, #3421). In the lower compartments MCP-1 was preincubated together with Spiegelmers in various concentrations in 600 µl HBH at 37°C for 20 to 30 min prior to addition of cells. Cells were allowed to migrate at 37°C for 3 hours. Thereafter the inserts were removed and 60 µl of 440 µM resazurin (Sigma) in phosphate buffered saline was added to the lower compartments. After incubation at 37°C for 2.5 hours, fluorescence was measured at an excitation wavelength of 544 nm and an emission wavelength of 590 nm in a Fluostar Optima multidetection plate reader (BMG).

Determination of half-maximal effective concentration (EC_{50}) for human MCP-1

After 3 hours migration of THP-1 cells towards various human MCP-1 concentrations, a dose-response curve for human MCP-1 was obtained, indicating a maximal effective concentration of about 1 nM and reduced activation at higher concentrations (Fig. 14). For the further experiments on inhibition of chemotaxis by Spiegelmers a MCP-1 concentration of 0.5 nM was used.

Determination of half-maximal effective concentration (EC_{50}) for murine MCP-1

After 3 hours migration of THP-1 cells towards various murine MCP-1 concentrations, a dose-response curve for murine MCP-1 was obtained, indicating a maximal effective concentration of about 1 – 3 nM and reduced activation at higher concentrations (Fig. 30). For the further experiments on inhibition of chemotaxis by Spiegelmers a murine MCP-1 concentration of 0.5 nM was used.

Example 7: Binding Analysis by Surface Plasmon Resonance Measurement

7.1 Specificity assessment of NOX-E36, 181-A2-018 and mNOX-E36

The Biacore 2000 instrument (Biacore AB, Uppsala, Sweden) was used to analyze binding of nucleic acids to human MCP-1 and related proteins. When coupling was to be achieved via amine groups, the proteins were dialyzed against water for 1 – 2 h (Millipore VSWP mixed cellulose esters; pore size, 0.025 µM) to remove interfering amines. PioneerF1 or CM4 sensor chips (Biacore AB) were activated before protein coupling by a 35-µl injection of a 1:1 dilution of 0.4 M NHS and 0.1 M EDC at a flow of 5 µl/min. Chemokine was then injected in concentrations of 0.1 – 1.5 µg/ml at a flow of 2 µl/min until the instrument's response was in the range of 1000 – 2000 RU (relative units). Unreacted NHS esters were deactivated by injection of 35 µl ethanolamine hydrochloride solution (pH 8.5) at a flow of 5 µl/min. The sensor chip was primed twice with binding buffer and equilibrated at 10 µl/min for 1 – 2 hours until the baseline appeared stable. For all proteins, kinetic parameters and dissociation constants were evaluated by a series of Spiegelmer injections at concentrations of 1000, 500, 250, 125, 62.5, 31.25, and 0 nM in selection buffer (Tris-HCl, 20 mM; NaCl, 137 mM; KCl, 5 mM; $CaCl_2$, 1 mM; $MgCl_2$, 1 mM; Tween20, 0.1% [w/v]; pH 7.4). In all experiments, the analysis was performed at 37°C using the Kinject command defining an association time of 180 and a dissociation time of 360 seconds at a flow of 10 µl/min. Data analysis and calculation of dissociation constants (K_D) was done with the BIAevaluation 3.0 software (BIACORE AB, Uppsala, Sweden) using the Langmuir 1:1 stochiometric fitting algorithm.

7.1.1 NOX-E36 and 181-A2-018 (human-MCP-1 specific nucleic acids)

Only for human MCP-1 all sensorgrams are depicted (Figs 17 and 20, respectively); for the other proteins, only the sensorgram obtained with 125 nM Spiegelmer concentration is shown for sake of clarity (Figs. 18/19 and 21/22).

Analysis of the NOX-E36•hMCP-1 interaction: recombinant human MCP-1 was immobilized on a PioneerF1 sensor chip following the manufacturer's recommendations (amine coupling procedure) until an instrument response of 1381 RU (relative units) was established. The determined dissociation constant (K_D) for NOX-E36 binding to human MCP-1 was ca. 890 pM (Fig. 17).

Analysis of the 181-A2-018•hMCP-1 interaction: recombinant human MCP-1 was immobilized on a CM4 sensor chip following the manufacturer's recommendations (amine coupling procedure) until an instrument response of 3111 RU (relative units) was established. The determined dissociation constant (K_D) for 181-A2-018 binding to human MCP-1 was ca. 370 pM (Fig. 20).

To determine the specificity of NOX-E36 and 181-A2-018, various human MCP-1 family proteins as well as human eotaxin were immobilized on a PioneerF1 and a CM4 sensor chip (hMCP-1, 1754 RU; hMCP-2, 1558 RU; hMCP-3, 1290 RU; eotaxin, 1523 RU). Kinetic analysis revealed that NOX-E36 binds to eotaxin and hMCP-2 with dissociation constants (K_D) of 5 - 10 nM; hMCP-3 was not recognized (Figs. 18 and 24A). 181-A2-018, in contrast, binds eotaxin, hMCP-2 and hMCP-3, but with slightly lower affinity (10 – 20 nM; Figs. 21 and 24A).

Interspecies cross-reactivity of NOX-E36 and 181-A2-018 was assessed using amino-coupling immobilized MCP-1 from human (1460 RU), monkey (1218 RU), pig (1428 RU), dog (1224 RU), rabbit (1244 RU), rat (1267 RU), and mouse (1361 RU) on a PioneerF1 and a CM4 sensor chip. Kinetic analysis revealed that NOX-E36 binds to human, monkey, porcine, and canine MCP-1 with comparable dissociation constants (K_D) of 0.89 – 1.2 nM whereas MCP-1 from mouse, rat and rabbit were not recognized (Figs. 19 and 24A). 181-A2-018 binds to human and monkey MCP-1 with comparable dissociation constants (K_D) of 0.5-0.6 nM, whereas porcine, rabbit and canine MCP-1 are bound with much lower affinity. Rat and mouse MCP-1 were not recognized by NOX-A2-018 (Figs. 22 and 24A).

Sequences as well as degree of homology in percent identical amino acids between the MCP-1 protein from different species and closely related human proteins are depicted in Fig. 23; calculated KD values for NOX-E36 and 181-A2-018 are displayed in tabular format in Fig. 24A.

7.1.2 mNOX-E36 (murine MCP-1 specific nucleic acid)

To analyze the binding behaviour of mNOX-E36, 3759 RU of synthetic biotinylated murine D-MCP-1 (flow cell 3) and 3326 RU of biotinylated human D-MCP-1 (flow cell 4) were immobilized on a Streptavidin conjugated sensor chip (Biacore AB, Freiburg, Germany), respectively. mNOX-E36 aptamer (D-RNA) solutions of 500, 250, 125, 62.5, 31.25, and 0 nM were injected using the Kinject command defining an association time of 180 sec and a dissociation time of 360 sec. Flow cell 1 was used as buffer and dextran matrix control (Biacore

SA-Chip surface) whereas on flow cell 2, an unspecific D-peptide was immobilized to determine unspecific binding of the aptamer. Fig. 32 shows a sensorgram of the D-NOX-E36 kinetic for binding to murine D-MCP-1 with a calculated dissociation constant (K_D) of 200 – 300 pM. mNOX-E36 does not bind human D-MCP-1 (Fig. 33); for sake of clarity, only the sensorgram obtained with 125 nM Spiegelmer is shown.

7.2 Selectivity assessment of NOX-E36

Selectivity of NOX-E36 was assessed by surface plasmon resonance analysis by immobilizing 5'biotinylated NOX-E36 on a Streptavidin (SA-Chip). 352 RU of NOX-E36 on flowcell (FC) 1 and equal amount of 5'-terminal biotinylated non-functional control Spiegelmer (POC) on FC 2 were immobilized by streptavidin/biotin binding. FC3 was used as surface control to determine unspecific binding to the dextran-SA sensor surface.

100 nM of a panel of human chemokines from all four subgroups (CC, CXC, CX_3C, and XC) were injected for 360s and complexes were allowed to dissociate for 360s at a flow of 10µl/min and 37°C. Response units after association (Resp.1; degree of interaction) and after dissociation (Resp.2, affinity of interaction) were plotted. After each injection the chip surface was regenerated with a 240s of 1 M sodium chloride with 0,1% Tween; immobilized Spiegelmers were subsequently allowed to refold for 2 minutes at physiological conditions (running buffer). Injection of each chemokine was repeated 3 times. CXCL1, CXCL2, CXCL6 and CXCL9 showed unspecific binding to ribonucleic acids and chip dextran surface. Specific high-affinity binding to immobilized NOX-E36 could only be detected for CCL2/MCP-1, CCL8/MCP-2, CCL11/eotaxin, CCL3/MIP1α, and CXCL7/NAP-2 (Fig. 24B). The finding that MCP-2 and eotaxin are bound by NOX-E36 is not surprising due to the relatively high homology between these chemokines and MCP-1 of 62 and 70 %, for the unexpected positives CCL3/MIP-1α and CXCL7/NAP-2, *in vitro* tests for functional inhibition have been performed or are currently being established, respectively.

Finally, the kinetic parameters of interaction between NOX-E36 and CCL2/MCP-1, CCL8/MCP-2, CCL11/eotaxin, CCL3/MIP1α, CXCL7/NAP-2, CCL7/MCP-3 and CCL13/MCP-4 were determined in the "inverted" system. Here, the chemokines were immobilized and free NOX-E36 was injected (for the detailed protocol, see 7.1). Kinetic data are summarized in Fig. 24C.

7.3 Assessment of anti-MIP-1α Functionality *in vitro*

Biacore measurements had shown cross reactivity of NOX-E36 with MIP-1α. By employing a functional, cell culture-based *in vitro* assay it should be checked if mere Biacore binding of NOX-E36 to MIP-1α also translates to functionality, e.g. antagonism.

To achieve this, chemotaxis experiments with THP-1 cells were performed that can be stimulated by MIP-1 α. THP-1 cells grown as described above were centrifuged, washed once in HBH (HBSS, containing 1 mg/ml bovine serum albumin and 20 mM HEPES) and resuspended at 3 x 10^6 cells/ml. 100 µl of this suspension were added to Transwell inserts with 5 µm pores (Corning, #3421). In the lower compartments MIP-1α was preincubated together with Spiegelmers in various concentrations in 600 µl HBH at 37°C for 20 to 30 min prior to addition of cells. Cells were allowed to migrate at 37°C for 3 hours. Thereafter the inserts were removed and 60 µl of 440 µM resazurin (Sigma) in phosphate buffered saline was added to the lower compartments. After incubation at 37°C for 2.5 hours, fluorescence was measured at an excitation wavelength of 544 nm and an emission wavelength of 590 nm in a Fluostar Optima multidetection plate reader (BMG).

After 3 hours migration of THP-1 cells towards various human MIP-1α concentrations, a dose-response curve for human MIP-1α was obtained, indicating a half-maximal effective concentration of about 1 nM and reduced activation at higher concentrations (Fig. 24D). For the further experiments on inhibition of chemotaxis by Spiegelmers a MIP-1α concentration of 0.5 nM was used.

Experiments for determination of chemotaxis inhibition by NOX-E36 were performed with a stimulus of 0.5 nM MIP-1α. It could be clearly shown that NOX-E36 does not inhibit MIP-1α induced chemotaxis up to the highest tested concentration of 1 µM MIP-1α. As positive control, the respective experiment with MCP-1 as stimulus was performed in parallel (Fig. 24E).

Example 8: Therapy of lupus-like disease in MRL$^{lpr/lpr}$ mice with anti-mMCP-1 Spiegelmer

Blocking proinflammatory mediators has become a successful approach for the treatment of chronic inflammation (Steinman 2004). In addition to TNF and interleukins, CC-chemokines are important candidates for specific antagonism because CC-chemokines mediate leukocyte recruitment from the intravascular space to sites of inflammation (Baggiolini 1998, Luster 2005). There is very strong evidence that MCP-1 (= CCL2) and its respective chemokine receptor CCR2 play a crucial role in autoimmune tissue injury such as the clinical manifestations of systemic lupus erythematosus (Gerard & Rollins 2001). For example, MRL$^{lpr/lpr}$ mice deficient either for the *Ccl2* or the *Ccr2* gene are protected from lupus-like autoimmunity (Perez de Lema 2005, Tesch 1999). Hence, the CCL2/CCR2 axis may represent a promising therapeutic target, e.g. for lupus nephritis. In fact, delayed gene therapy or transfer of transfected cells, both resulting in *in situ* production of an NH_2-truncated MCP-1, markedly reduced autoimmune tissue injury in MRL$^{lpr/lpr}$ mice. However, such experimental approaches cannot be used in humans because of irrepressible antagonist production and tumor formation (Hasegawa 2003, Shimizu 2004). Therefore, it remains necessary to develop novel CCL2 antagonists with favorable pharmacokinetic profiles *in vivo.* In this example it is shown that blockade of murine CCL2 with the anti-mCCL2 Spiegelmer mNOX-E36 or mNOX-E36-3'PEG would be suitable for the treatment of lupus nephritis and other disease manifestations of systemic lupus erythematosus. Late onset of mCCL2 Spiegelmer therapy effectively improves lupus nephritis, autoimmune peribronchitis, and lupus-like skin disease in MRL$^{lpr/lpr}$ mice, independent of any previous problem associated with therapeutic CCL2/CCR2 blockade.

Animals and Experimental Protocol

Ten week old female MRL$^{lpr/lpr}$ mice were obtained from Harlan Winkelmann (Borchen, Germany) and kept under normal housing conditions in a 12 hour light and dark cycle. Water and standard chow (Ssniff, Soest, Germany) were available *ad libitum.* At age 14 weeks, groups of 12 mice received subcutaneous injections of Spiegelmers in 5 % glucose (injection volume, 4 ml/kg) three times per week as follows: mNOX-E36, 1.5 µmol/kg; mNOX-E36-3'PEG, 0.9 µmol/kg; nonfunctional control Spiegelmer PoC (5'-UAAGGAAACUCGGUCUGAUGCGGU AGCGCUGUGCAGAGCU-3'), 1.9 µmol/kg; PoC-PEG, 0.9 µmol/kg; vehicle (5 % glucose). The plasma levels of mNOX-E36 and mNOX-E36-3'PEG were determined from blood samples taken weekly from the retroorbital sinus 3 or 24 hours after injection, respectively. Spiegelmer

levels in plasma samples were determined by a modification of the sandwich hybridization method as described in Example 8. Mice were sacrificed by cervical dislocation at the end of week 24 of age.

Evaluation of systemic lupus

Skin lesions were recorded by a semiquantitative score (Schwarting 2005). The weight ratio of spleen and the bulk of mesenterial lymphnodes to total body weight were calculated as markers of the lupus-associated lymphoproliferative syndrome. Blood and urine samples were collected from each animal at the end of the study period by bleeding from the retro-orbital venous plexus under general anesthesia with inhaled ether. Blood and urine samples were collected from each animal at the end of the study and urine albumin/creatinine ratio and serum dsDNA autoantibody IgG isotype titers were determined as previously described (Pawar 2006). Glomerular filtration rate (GFR) was determined at 24 weeks by clearance kinetics of plasma FITC-inulin (Sigma-Aldrich, Steinheim, Germany) 5, 10, 15, 20, 35, 60, and 90 minutes after a single bolus injection (Qi 2004). Fluorescence was determined with 485 nm excitation and read at 535 nm emission. GFR was calculated based on a two-compartment model using a non-linear regression curve-fitting software (GraphPad Prism, GraphPad Software Inc., San Diego, CA). Serum cytokine levels were determined using commercial ELISA kits for IL-6, IL-12p40 (OptEiA, BD Pharmingen), and IFN-α (PBL Biomedical Labs, USA). From all mice, kidneys and lungs were fixed in 10 % buffered formalin, processed, and embedded in paraffin. 5-µm sections for silver and periodic acid-Schiff stains were prepared following routine protocols (Anders 2002). The severity of the renal lesions was graded using the indices for activity and chronicity as described for human lupus nephritis (Austin 1984), and morphometry of renal interstitial injury was conducted as previously described (Anders 2002). The severity of the peribronchial inflammation was graded semiquantitatively from 0-4. For immunostaining, sections of formalin-fixed and paraffin-embedded tissues were dewaxed and rehydrated. Endogenous peroxidase was blocked by 3 % hydrogen peroxide and antigen retrieval was performed in Antigen Retrieval Solution (Vector, Burlingame, CA) in an autoclave oven. Biotin was blocked using the Avidin/Biotin blocking Kit (Vector). Slides were incubated with the primary antibodies for one hour, followed by biotinylated secondary antibodies (anti-rat IgG, Vector), and the ABC reagent (Vector). Slides were washed in phosphate buffered saline between the incubation steps. 3'3'Diaminobenzidine (DAB, Sigma, Taufkirchen, Germany) with metal enhancement was used as detection system, resulting in a black colour product. Methyl green was used as counterstain, slides were dehydrated and mounted in Histomount (Zymed Laboratories, San Francisco, CA).

The following primary antibodies were used: rat anti-Mac2 (macrophages, Cederlane, Ontario, Canada, 1:50), anti-mouse CD3 (1:100, clone 500A2, BD), anti-mouse IgG_1 (1:100, M32015, Caltag Laboratories, Burlingame, CA, USA), anti-mouse IgG_{2a} (1:100, M32215, Caltag), anti-mouse C3 (1:200, GAM/C3c/FITC, Nordic Immunological Laboratories, Tilburg, Netherlands). Negative controls included incubation with a respective isotype antibody. For quantitative analysis glomerular cells were counted in 15 cortical glomeruli per section. Glomerular Ig and C3c deposits were scored from 0-3 on 15 cortical glomerular sections.

RNA preparation and real-time quantitative (TaqMan) RT-PCR

Renal tissue from each mouse was snap frozen in liquid nitrogen and stored at -80°C. From each animal, total renal RNA preparation and reverse transcription were performed as described (Anders 2002). Primers and probes were from PE Biosystems, Weiterstadt, Germany. The used primers (300 nM) used for detection of *Ccl2, Ccl5 and18S rRNA* , predeveloped TaqMan assay reagent from PE Biosystems.

Flow cytometry

Total blood and bone marrow samples were obtained from mice of all groups at the end of the study. Flow cytometry was performed using a FACScalibur machine and the previously characterized MC21 anti-mCCR2 antibody (Mack 2001). A biotinylated anti-rat IgG antibody (BD Biosciences) was used for detection. A rat IgG_{2b} (BD Biosciences) was used as isotype control.

Statistical analysis

Data were expressed as mean ± standard error of the mean (SEM). Comparison between groups were performed using univariate ANOVA. Posthoc Bonferroni's correction was used for multiple comparisons. A value of $p < 0.05$ was considered to indicate statistical significance.

Sandwich Hybridisation Assay

Amount of Spiegelmer in the samples was quantified by a sandwich hybridisation assay based on an assay as described by Drolet *et al.* 2000 (*Pharm Res* **17**:1503). Blood samples were collected in parallel to follow the plasma clearance of NOX-E36. Selected tissues were prepared to determine Spiegelmer concentrations.

Hybridisation plate preparation

Spiegelmer mNOX-E36 was quantified by using a non-validated sandwich hybridisation assay. Briefly, the mNOX-E36 capture probe (Seq.ID.: 281) was immobilized to white DNA-BIND 96well plates (Corning Costar, Wiesbaden, Germany) at 0.75 mM in 0.5 M sodium phosphate, 1 mM EDTA, pH 8.5 over night at 4°C. Wells were washed twice and blocked with 0.5% w/v BSA in 0.25 M sodium phosphate, 1 mM EDTA, pH 8.5 for 3 h at 37°C, washed again and stored at 4°C until use. Prior to hybridisation, wells were pre-warmed to 37°C and washed twice with pre-warmed wash buffer (3×SSC, 0.5% [w/v] sodium dodecyl sarcosinate, pH 7.0; in advance a 20x stock [3 M NaCl, 0,3 M Na_3Citrate) is prepared without sodium lauroylsarcosine and diluted accordingly).

Sample preparation

All samples were assayed in duplicates. Plasma samples were thawed on ice, vortexed and spun down briefly in a cooled tabletop centrifuge. Tissue homogenates were thawed at RT and centrifuged 5 min at maximum speed and RT. Only 5 µl each sample were removed for the assay, and afterwards returned to the freezer for storage. Samples were diluted with hybridisation buffer (8 nM mNOX-E36 detection probe [Seq.ID:282] in wash buffer) at RT according to the following scheme:

1:30	5 µl sample	+ 145 µl hybridisation buffer
1:300	20 µl 1:30	+ 180 µl hybridisation buffer
1:3000	20 µl 1:300	+ 180 µl hybridisation buffer
1:30000	20 µl 1:3000	+ 180 µl hybridisation buffer

All sample dilutions were assayed. mNOX-E36 standard was serial diluted to a 8-point calibration curve spanning the 0-4 nM range. No QC samples were prepared and assayed. Calibration standard was identical to that of the in-study samples.

Hybridisation and detection

Samples were heated for 10 min at 95°C and cooled to 37°C. Spiegelmer/detection probe complexes were annealed to immobilized capture probes for 30 min at 37°C. Unbound spiegelmers were removed by washing twice with wash buffer and 1× TBST (20 mM Tris-Cl, 137 mM NaCl, 0.1% Tween 20, pH 7.5), respectively. Hybridized complexes were detected by

streptavidin alkaline phosphatase diluted 1:5000 in 1× TBST for 1 h at room temperature. To remove unbound conjugate, wells were washed again with 1× TBST and 20 mM Tris-Cl, 1 mM MgCl2, pH 9.8 (twice each). Wells were finally filled with 100 ml CSDP substrate (Applied Biosystems, Darmstadt, Germany) and incubated for 45 min at room temperature. Chemiluminescence was measured on a FLUOstar Optima microplate reader (BMG Labtechnologies, Offenburg, Germany).

Data analysis

The following assayed sample dilutions were used for quantitative data analysis:

rat EDTA plasma 1:2000

The data obatained from the vehicle group (no Spiegelmer was adminstered) was subtracted as background signal.

The sandwich hybridisation assay as described herein also works in similar fashion for Spiegelmer NOX-36, NOX-E36-5'-PEG and NOX-E36-3'-PEG whereby the respective NOX-E36 capture probe (Seq.ID:255) and the respective NOX-E36 detection probe (Seq.ID:256) has to be used (data not shown).

Results

mNOX-E36-3'PEG improves survival and kidney disease of MRL$^{lpr/lpr}$ mice

Female MRL$^{lpr/lpr}$ mice develop and subsequentially die from proliferative immune complex glomerulonephritis with striking similarities to diffuse proliferative lupus nephritis in humans. In this therapeutic study design, treated MRL$^{lpr/lpr}$ mice were treated with pegylated and unpegylated anti-mCCL2 Spiegelmer, pegylated and unpegylated control ("PoC")-Spiegelmer or vehicle from week 14 to 24 of age. At this time point vehicle, PoC or PoC-PEG-treated MRL$^{lpr/lpr}$ mice showed diffuse proliferative glomerulonephritis characterized by glomerular macrophage infiltration and a mixed periglomerular and interstitial inflammatory cell infiltrate consting of glomerular and interstitial Mac2-positive macrophages and interstitial CD3-positive lymphocytes (Figs. 34 and 35). mNOX-E36-3'PEG improved the activity and chronicity index of lupus nephritis as well as the forementioned markers of renal inflammation (Fig. 35). The unpegylated molecule mNOX-E36 was less effective on the chronicity index and interstitial macrophage and T cell counts (Fig. 35). Advanced chronic kidney disease was further illustrated

by tubular atrophy and confluent areas of interstitial fibrosis in vehicle-, PoC-, and PoC-PEG-treated mice (Fig. 34). Applying morphometry to quantify these changes, it was found that pegylated and unpegylated mNOX-E36 reduced interstitial volume, tubular cell damage, and tubular dilation, all being markers of the severity and prognosis of chronic kidney disease (Fig. 36). mNOX-E36-3'PEG but not unpegylated mNOX-E36 improved 50% mortality (Fig. 37). Thus, mNOX-E36-3'PEG can reduce the number of renal macrophage and T cell infiltrates and improve lupus nephritis and (renal) survival of $MRL^{lpr/lpr}$ mice. In order to study whether treatment with mNOX-E36 and mNOX-E36-3'PEG affects intrarenal inflammation in $MRL^{lpr/lpr}$ mice, real-time RT-PCR was performed to assess the expression levels of the proinflammatory chemokines CCL2 and CCL5 which were previously shown to be progressively upregulated in kidneys of $MRL^{lpr/lpr}$ mice during progression of renal disease (Perez de Lema 2001). Treatment with mNOX-E36 and mNOX-E36-3'PEG from week 14 to 24 of age reduced renal expression of CCL2 and CCL5 mRNA compared to vehicle-treated controls (Fig. 38).

Anti-CCL2 Spiegelmers reduce extrarenal autoimmune tissue injury in $MRL^{lpr/lpr}$ mice

Skin and lungs are also commonly affected from autoimmune tissue injury in $MRL^{lpr/lpr}$ mice. In vehicle-treated mice autoimmune lung disease was characterized by moderate peribronchiolar and perivascular inflammatory cell infiltrates and skin lesions were observed in 60% of mice (Figs. 39, 40 and 35). mNOX-E36 and mNOX-E36-3'PEG both reduced peribronchial inflammation and skin disease as compared to vehicle-, PoC-, and PoC-PEG-treated $MRL^{lpr/lpr}$ mice, respectively (Figs. 39, 40 and 35). Hence, the effects of CCL2-specific Spiegelmers are not limited to lupus nephritis but extend to other manifestations of autoimmune tissue injury in $MRL^{lpr/lpr}$ mice.

mNOX-E36 and the lymphoproliferative syndrome, dsDNA autoantibodies, and serum cytokine levels in $MRL^{lpr/lpr}$ mice

Female $MRL^{lpr/lpr}$ mice develop a lymphoproliferative syndrome characterized by massive splenomegaly and bulks of cervical, axillary, inguinal, and mesenterial lymph nodes. mNOX-E36 and mNOX-E36-3'PEG both had no effect on the weight of spleens and lymph nodes in $MRL^{lpr/lpr}$ mice (Fig. 41). Autoimmunity in $MRL^{lpr/lpr}$ mice is characterized by the production of autoantibodies against multiple nuclear antigens including dsDNA. In 24 week old $MRL^{lpr/lpr}$ mice serum dsDNA IgG, IgG_1, IgG_{2a}, IgG_{2b} autoantibodies were present at high levels. mNOX-E36 and mNOX-E36-3'PEG both had no effect on either of these DNA autoantibodies (Fig. 41). Lupus-like disease in vehicle-treated $MRL^{lpr/lpr}$ mice was characterized by elevated serum levels

of IFN-α, IL-12p40, and IL-6. mNOX-E36 and mNOX-E36-3'PEG both had no effect on either of these inflammatory mediators (Fig. 41). Thus, both mNOX-E36 variants do not affect lymphoproliferation, anti-dsDNA IgG production, and serum cytokine levels in $MRL^{lpr/lpr}$ mice.

Plasma levels of mNOX-E36 and mNOX-E36-3'PEG in $MRL^{lpr/lpr}$ mice

mNOX-E36 and mNOX-E36-3'PEG plasma levels were determined at weekly intervals in order to monitor drug exposure during progressive kidney disease of $MRL^{lpr/lpr}$ mice. The median plasma levels of mNOX-E36 3 h after injection and mNOX-E36-3'PEG 24 h after injection were approximately 300 nM and 1 μM throughout the study, respectively (Fig. 42). Thus, pegylation increased the plasma levels of mNOX-E36 and the progressive kidney disease of $MRL^{lpr/lpr}$ mice did not modulate the pharmacokinetics of both Spiegelmers.

mNOX-E36-3'PEG blocks the emigration of monocytes from the bone marrow

Monocyte emigration from bone marrow during bacterial infection was shown to involve chemokine receptor CCR2 (Serbina 2006), but the role of CCL2 in the context of autoimmunity remains hypothetical. Therefore, the CCR2-positive monocyte population in peripheral blood and bone marrows in mice of mNOX-E36-3'PEG- and vehicle-treated groups of 24 week old $MRL^{lpr/lpr}$ mice was examined. Treatment with mNOX-E36-3'PEG increased the percentage of CCR2 positive cells in the bone marrow from 13 % to 26 % whereas it reduced this population in the peripheral blood from 26 % to 11 % (Fig. 43). These data support a role of CCL2 for the evasion of CCR2 positive cells from the bone marrow during autoimmune disease of $MRL^{lpr/lpr}$ mice.

Summary

Applying the Spiegelmer technology, a novel and specific mCCL2 antagonist was created which potently blocks mCCL2 *in vitro* and *in vivo*. In fact, late onset of treatment with the CCL2 Spiegelmer markedly improved advanced lupus-like autoimmune tissue injury in $MRL^{lpr/lpr}$ mice. These data support a central role for CCL2 in chronic inflammatory tissue damage and identify CCL2 Spiegelmers as a novel therapeutic for autoimmune tissue injury.

Example 9: Therapy of diabetic nephropathy in unilaterally nephrectomized diabetic mice with anti-mMCP-1 Spiegelmer

Diabetic nephropathy remains a leading cause of end-stage renal disease because targeting the angiotensin-dependent pathomechanisms does not always prevent disease progression (Zimmet 2001; Ritz 1999; United States Renal Data System 2004; Svensson 2003). Hence, other treatment strategies are required to add on to the therapeutic armament for diabetic nephropathy.

Data from recent experimental studies relate the progression of diabetic nephropathy to intrarenal inflammation (Galkina 2006; Mora 2005; Meyer 2003; Tuttle 2005). For example, mycophenolate mofetil, methotrexate or irradiation reduce urinary albumin excretion, and glomerulosclerosis in rats with streptozotocin-induced diabetic nephropathy (Yozai 2005; Utimura 2003). Yet, the molecular and cellular mechanisms of intrarenal inflammation in diabetic nephropathy remain poorly characterized. Patients with diabetic nephropathy have increased serum levels of acute phase markers of inflammation but this may not represent intrarenal inflammation (Dalla Vestra 2005; Navarro 2003). Patients with diabetic nephropathy excrete high levels of the CC-chemokine monocyte chemoattractant protein 1 (MCP-1/CCL2) in the urine which may be more specific for intrarenal inflammation (Morii 2003; Tashiro 2002; Takebayashi 2006). In fact, MCP-1/CCL2 is expressed by human mesangial cells exposed to either high glucose concentrations or advanced glycation end products (Ihm 1998; Yamagishi 2002). CCL2 is involved in the complex multistep process of leukocyte recruitment from intravascular to extravascular compartments, i.e. glomeruli and the renal interstitium (Baggiolini 1998). In fact, macrophage infiltrates are a common finding in human and experimental diabetic glomerulosclerosis and tubulointerstitial injury (Bohle 1991; Furuta 1993; Chow 2007). *Ccl2*-deficient type 1 or type 2 diabetic mice have lower glomerular macrophage counts which is associated with less glomerular injury (Chow 2004; Chow 2006). In these studies the functional role of CCL2 for glomerular pathology of type 1 and type 2 diabetic nephropathy was also demonstrated. Hence, CCL2 may represent a potential therapeutic target for diabetic nephropathy, and suitable CCL2 antagonists with favourable pharmacokinetic profiles should be validated in this disease context. In this example we report the effects of the PEGylated anti-CCL2 Spiegelmer mNOX-E36-3'PEG in type 2 diabetic db/db mice with advanced diabetic nephropathy. We shown that an anti-CCL2-Spiegelmer would be suitable for the treatment of diabetic nephropathy.

Animals and Experimental Protocol

Male 5 week old C57BLKS db/db or C57BLKS wild-type mice were obtained from Taconic (Ry, Denmark) and housed in filter top cages with a 12 hour dark/light cycle and unlimited access to food and water for the duration of the study. Cages, bedding, nestlets, food, and water were sterilized by autoclaving before use. At the age of 6 weeks uninephrectomy ("1K" mice) or sham surgery ("2K" mice) was performed through a 1 cm flank incision as previously described in db/db and wild-type mice (Bower 1980). In mice of the sham surgery groups the kidney was left in situ. 10 weeks later, at the age of 4 months, 1K db/db mice were divided in two groups that received three times per week subcutaneous injections with either mNOX-E36-3'PEG or PoC-PEG in 5% glucose (dose, 0.9 µmol/kg; injection volume, 1 ml/kg). Treatment was continued for 8 weeks (until the age 6 months) when the animals were sacrificed and the tissues were obtained for histopathological evaluation. All experimental procedures had been approved by the local government authorities.

Evaluation of diabetic nephropathy

All immunohistological studies were performed on paraffin-embedded sections as described (Anders 2002). The following antibodies were used as primary antibodies: rat anti-Mac2 (glomerular macrophages, Cederlane, Ontario, Canada, 1:50), anti-Ki-67 (cell proliferation, Dianova, Hamburg, Germany, 1:25). For histopathological evaluation, from each mouse parts of the kidneys were fixed in 10 % formalin in phosphate-buffered saline and embedded in paraffin. 3 µm-sections were stained with periodic acid-Schiff reagent or silver following the instructions of the supplier (Bio-Optica, Milano, Italy). Glomerular sclerotic lesions were assessed using a semiquantitative score by a blinded observer as follows: 0 = no lesion, 1 = < 25 % sclerotic, 2 = 25-49 % sclerotic, 3 = 50-74 % sclerotic, 4 = 75-100 % sclerotic, respectively. 15 glomeruli were analysed per section. The indices for interstitial volume and tubular dilatation were determined by superimposing a grid of 100 points on 10 non-overlapping cortical fields as described previously (Anders 2002). Interstitial cell counts were determined in 15 high power fields (hpf, 400 x) by a blinded observer. RNA preparation and real-time quantitative (TaqMan) RT-PCR was done from deparaffinized glomeruli. After incubation in lysing buffer (10 mM Tris-HCl, 0.1 mM EDTA, 2 % SDS and 20 µg/ml proteinase K) for 16 h at 60°C, phenol-chloroform-based RNA extraction was performed. Glomerular RNA was dissolved in 10 µl RNAse free water. Reverse transcription and real time RT-PCR from total organ and glomerular RNA was performed as described (Anders 2002, Cohen 2002). Controls consisting of ddH_2O were negative

for target and housekeeper genes. Oligonucleotide primer (300 nM) and probes (100 nM) for mCcl2, Gapdh, and 18 S rRNA were predeveloped TaqMan assay reagents from PE. Primers and probes were from ABI Biosystems, Weiterstadt, Germany. Glomerular filtration rate (GFR) was determined by clearance kinetics of plasma FITC-inulin (Sigma-Aldrich, Steinheim, Germany) 5, 10, 15, 20, 35, 60, and 90 minutes after a single bolus injection (Qi 2004). Fluorescence was determined with 485 nm excitation and read at 535 nm emission. GFR was calculated based on a two-compartment model using a non-linear regression curve-fitting software (GraphPad Prism, GraphPad Software Inc., San Diego, CA). All data are presented as mean ± SEM. Comparison of groups was performed using ANOVA and post-hoc Bonferroni's correction was used for multiple comparisons. A value of $p < 0.05$ was considered to indicate statistical significance.

Results

mNOX-E36-3'PEG reduces glomerular macrophage counts and global glomerulosclerosis in unilaterally nephrectomized db/db mice

When lack of functional CCL2 is associated with decreased glomerular macrophage recruitment in db/db mice (Chow 2007) and mNOX-E36-3'PEG is able to block CCL2-mediated macrophage recruitment *in vitro* and *in vivo,* mNOX-E36-3'PEG should impair renal macrophage recruitment in db/db mice with advanced type 2 diabetic nephropathy. To test this hypothesis, we initiated subcutaneous injections with mNOX-E36-3'PEG or PoC-PEG at age of 4 months in unilaterally nephrectomized ("1K") db/db mice. Treatment was continued for 8 weeks when tissues were collected for the assessment of diabetic nephropathy. During that period, mNOX-E36-3'PEG treatment did not significantly affect white blood or platelet counts, blood glucose levels or body weight which were both markedly elevated in all groups of db/db mice as compared to non-diabetic BLKS mice (data not shown). Interestingly, mNOX-E36-3'PEG increased the serum levels of CCL2 in 1K db/db mice, indicating that the CCL2 antagonist retains CCL2 in the circulation (Fig. 44). Consistent with our hypothesis mNOX-E36-3'PEG significantly reduced the number of glomerular macrophages by 40 % as compared to PoC-PEG- or vehicle-treated db/db mice, associated with lower numbers of Ki-67 positive proliferating cells within the glomerulus in mNOX-E36-3'PEG-treated db/db mice (Fig. 45). These findings were associated with a significant improvement of global diabetic glomerulosclerosis in 1K db/db mice (Fig. 46). In fact, mNOX-E36-3'PEG treatment reduced diabetic glomerulosclerosis in 1K db/db mice to the extent of glomerulosclerosis present in age-

matched non-nephrectomized ("2K") db/db mice (Fig. 46). These findings show that delayed blockade of CCL2-dependent glomerular macrophage recruitment with mNOX-E36-3'PEG prevents global diabetic glomerulosclerosis in type 2 diabetic db/db mice.

mNOX-E36-3'PEG improves GFR in 1K db/db mice

The beneficial effects of mNOX-E36-3'PEG treatment on diabetic glomerulosclerosis in 1K db/db mice should be associated with a better GFR. We analyzed FITC-inulin clearance kinetics as a marker of GFR in db/db mice (Qi 2004). As compared to a normal GFR of about 250 ml/min in db/db mice (Qi 2004), we found a reduced GFR of was 112 ± 23 ml/min in 6 months old 1K db/db mice injected with PoC-PEG (Fig. 47). mNOX-E36-3'PEG treatment significantly improved the GFR to 231 ± 30 ml/min in 1K db/db mice ($p < 0.001$) suggesting that blocking CCL2-dependent glomerular macrophage recruitment can also improve renal function in type 2 diabetic mice.

mNOX-E36-3'PEG reduces interstitial macrophage counts and tubulointerstitial injury in 1K db/db mice

Advanced diabetic nephropathy in humans is associated with significant numbers of interstitial macrophages and tubulointerstitial injury (Bohle 1991). In 2K db/db mice interstitial macrophage infiltrates and significant tubulointerstitial injury does not occur before 8 months of age (Chow 2007). Early uninephrectomy accelerates the development of tubulointerstitial pathology in db/db mice (Ninichuk 2005), thus we quantified interstitial macrophages, tubular dilatation and interstitial volume as markers of tubulointerstitial damage in mice of all groups at 6 months of age. At this time point 1K db/db mice revealed increased numbers of interstitial macrophages and significant elevations of tubular dilatation and interstitial volume as compared to 2K db/db mice (Fig. 45, Fig. 48). mNOX-E36-3'PEG treatment reduced the numbers of interstitial macrophages by 53 % as well as tubular dilatation and interstitial volume in 1K db/db mice (Fig. 45, Fig. 48). Thus, blocking CCL2-dependent renal macrophage recruitment also prevents tubulointerstitial injury in type 2 diabetic db/db mice.

mNOX-E36-3'PEG reduces renal expression of Ccl2 in 1K db/db mice

Macrophage infiltrates amplify inflammatory responses in tissue injury, e.g. local CCL2 expression. We therefore hypothesized that the mNOX-E36-3'PEG-related decrease in renal macrophages would be associated with less renal CCL2 expression. We used real-time RT-PCR to quantify the mRNA expression of CCL2 in db/db mice. mNOX-E36-3'PEG reduced the mRNA levels of CCL2 in kidneys of 6 months old 1K db/db mice as compared to age-matched PoC-PEG-treated mice (Fig. 49). To further assess the spatial expression of CCL2 we performed immunostaining for CCL2 protein on renal sections. In 1K db/db mice the expression of CCL2 was markedly enhanced in glomeruli, tubuli, and interstitial cells as compared to 2K db/db or 2K wild-type mice (Fig. 50). mNOX-E36-3'PEG markedly reduced the staining for CCL2 in all these compartments as compared to vehicle- or PoC-PEG-treated 1K db/db mice. These data indicate that blocking CCL2-dependent renal macrophage recruitment with mNOX-E36-3'PEG reduces the local expression of CCL2 in 1K db/db mice.

Summary

The concept that inflammation contributies to the progression of human diabetic nephropathy becomes increasingly accepted (Tuttle 2005), bringing MCP-1/CCL2 as a potential target to treat this disease into the focus. In this example, we have shown that treatment of unilaterally nephrectomized diabetic mice with mNOX-E36-3'PEG reduced the numbers of glomerular (and interstitial) macrophages at 6 months of age, associated with less proliferating glomerular cells. In addition, renal/glomerular expression of CCL2 mRNA was markedly reduced with mNOX-E36-3'PEG treatment. Furthermore, lower numbers of glomerular macrophages and glomerular proliferating cells in the therapy group were associated with protection from global glomerulosclerosis and with a significant improvement of the glomerular filtraton rate. The beneficial effects of mNOX-E36-3'PEG on glomerular pathology and renal function in diabetic mice are consistent with those studies that have used other CCL2 antagonists in other models of glomerular injury (Lloyd 1997, Hasegawa 2003, Tang 1996, Wenzel 1997, Fujinaka 1997, Schneider 1999). Remarkably, delayed onset of CCL2 blockade also reduced the numbers of interstitial macrophages being associated with less tubulointerstitial pathology in 1K db/db mice.

Together, these data validate CCL2 as a promising therapeutic target for diabetic nephropathy and suggest that initiating CCL2 blockade with a Spiegelmer – even at an advanced stage of the disease – may still be protective.

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The features of the present invention disclosed in the specification, the claims and/or the drawings may both separately and in any combination thereof be material for realizing the invention in various forms thereof.

Claims

1. A nucleic acid, preferably binding to MCP-1, selected from the group comprising type 1A nucleic acids, type 1B nucleic acids, type 2 nucleic acids, type 3 nucleic acids, type 4 nucleic acids and nucleic acids having a nucleic acid sequence according to any of SEQ.ID.No. 87 to 115.

2. The nucleic acid according to claim 1, whereby the type 1A nucleic acid comprises in 5'->3' direction a first stretch Box B1A, a second stretch Box B2, a third stretch Box B3, a fourth stretch Box B4, a fifth stretch Box B5, a sixth stretch Box B6 and a seventh stretch Box B1B, whereby

the first stretch Box B1A and the seventh stretch Box B1B optionally hybridize with each other, whereby upon hybridization a double-stranded structure is formed,

the first stretch Box B1A comprises a nucleotide sequence of AGCRUG,

the second stretch Box B2 comprises a nucleotide sequence of CCCGGW,

the third stretch Box B3 comprises a nucleotide sequence of GUR,

the fourth stretch Box B4 comprises a nucleotide sequence of RYA,

the fifth stretch Box B5 comprises a nucleotide sequence of GGGGGRCGCGAYC

the sixth stretch Box B6 comprises a nucleotide sequence of UGCAAUAAUG or URYAWUUG, and

the seventh stretch Box B1B comprises a nucleotide sequence of CRYGCU.

3. The nucleic acid according to claim 2, whereby

the first stretch Box B1A comprises a nucleotide sequence of AGCGUG.

4. The nucleic acid according to claims 2 or 3, whereby

the second stretch Box B2 comprises a nucleotide sequence of CCCGGU.

5. The nucleic acid according to any of claims 2 to 4, whereby

the third stretch Box B3 comprises a nucleotide sequence of GUG.

6. The nucleic acid according to any of claims 2 to 5, whereby

the fourth stretch Box B4 comprises a nucleotide sequence of GUA.

7. The nucleic acid according to any of claims 2 to 6, whereby

the fifth stretch Box B5 comprises a nucleotide sequence of GGGGGGCGCGACC.

8. The nucleic acid according to any of claims 2 to 7, whereby

the sixth stretch Box B6 comprises a nucleotide sequence of UACAUUUG.

9. The nucleic acid according to any of claims 2 to 8, whereby

the seventh stretch Box B1B comprises a nucleotide sequence of CACGCU.

10. The nucleic acid according to any of claims 2 to 9, whereby the nucleic acid comprises a nucleic acid sequence according to SEQ.ID. No 21.

11. The nucleic acid according to claim 1, whereby the type 1B nucleic acid comprises in 5'->3' direction a first stretch Box B1A, a second stretch Box B2, a third stretch Box B3, a fourth stretch Box B4, a fifth stretch Box B5, a sixth stretch Box B6 and a seventh stretch Box B1B, whereby

the first stretch Box B1A and the seventh stretch Box B1B optionally hybridize with each other, whereby upon hybridization a double-stranded structure is formed,

the first stretch Box B1A comprises a nucleotide sequence of AGYRUG,

the second stretch Box B2 comprises a nucleotide sequence of CCAGCU or CCAGY,

the third stretch Box B3 comprises a nucleotide sequence of GUG,

the fourth stretch Box B4 comprises a nucleotide sequence of AUG,

the fifth stretch Box B5 comprises a nucleotide sequence of GGGGGGCGCGACC

the sixth stretch Box B6 comprises a nucleotide sequence of CAUUUUA or CAUUUA, and

the seventh stretch Box B1B comprises a nucleotide sequence of CAYRCU.

12. The nucleic acid according to claim 11, whereby

the first stretch Box B1A comprises a nucleotide sequence of AGCGUG.

13. The nucleic acid according to claims 11 or 12, whereby

the second stretch Box B2 comprises a nucleotide sequence of CCAGU.

14. The nucleic acid according to any of claims 11 to 13, whereby

the sixth stretch Box B6 comprises a nucleotide sequence of CAUUUUA.

15. The nucleic acid according to any of claims 11 to 14, whereby

the seventh stretch Box B1B comprises a nucleotide sequence of CACGCU.

16. The nucleic acid according to any of claims 11 to 15, whereby the nucleic acid comprises a nucleic acid sequence according to SEQ.ID.No 28 and SEQ.ID.No 27.

17. The nucleic acid according to claim 1, whereby the type 2 nucleic acid comprises in 5'->3' direction a first stretch Box B1A, a second stretch Box B2, and a third stretch Box B1B, whereby

the first stretch Box B1A and the third stretch Box B1B optionally hybridize with each other, whereby upon hybridization a double-stranded structure is formed,

the first stretch Box B1A comprises a nucleotide sequence selected from the group comprising ACGCA, CGCA and GCA,

the second stretch Box B2 comprises a nucleotide sequence of CSUCCCUCACCGGUGCAAGUGAAGCCGYGGCUC, and

the third stretch Box B1B comprises a nucleotide sequence selected from the group comprising UGCGU, UGCG and UGC.

18. The nucleic acid according to claim 17, whereby

the second stretch Box B2 comprises a nucleotide sequence of CGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUC.

19. The nucleic acid according to any of claims 17 to 18, whereby

a) the first stretch Box B1A comprises a nucleotide sequence of ACGCA,
and
the third stretch Box B1B comprises a nucleotide sequence of UGCGU; or

b) the first stretch Box B1A comprises a nucleotide sequence of CGCA,
and
the third stretch Box B1B comprises a nucleotide sequence of UGCG; or

c) the first stretch Box B1A comprises a nucleotide sequence of GCA,
and
the third stretch Box B1B comprises a nucleotide sequence of UGC or UGCG.

20. The nucleic acid according to any of claims 17 to 19, whereby

the first stretch Box B1A comprises a nucleotide sequence of GCA.

21. The nucleic acid according to any of claims 17 to 20 and preferably claim 20, whereby

the third stretch Box B1B comprises a nucleotide sequence of UGCG.

22. The nucleic acid according to any of claims 17 to 21, whereby the nucleic acid comprises a nucleic acid sequence according to SEQ.ID.No 37, SEQ.ID.No 116, SEQ.ID.No 117 and SEQ.ID.No 278.

23. The nucleic acid according to claim 1, whereby the type 3 nucleic acid comprises in 5'->3' direction a first stretch Box B1A, a second stretch Box B2A, a third stretch Box B3, a fourth stretch Box B2B, a fifth stretch Box B4, a sixth stretch Box B5A, a seventh stretch Box B6, an eighth stretch Box B5B and a ninth stretch Box B1B, whereby

the first stretch Box B1A and the ninth stretch Box B1B optionally hybridize with each other, whereby upon hybridization a double-stranded structure is formed,

the second stretch Box B2A and the fourth Box B2B optionally hybridize with each other, whereby upon hybridization a double-stranded structure is formed,

the sixth stretch Box B5A and the eighth Box B5B optionally hybridize with each other, whereby upon hybridization a double-stranded structure is formed,

the first stretch Box B1A comprises a nucleotide sequence which is selected from the group comprising GURCUGC, GKSYGC, KBBSC and BNGC,

the second stretch Box B2A comprises a nucleotide sequence of GKMGU,

the third stretch Box B3 comprises a nucleotide sequence of KRRAR,

the fourth stretch Box B2B comprises a nucleotide sequence of ACKMC,

the fifth stretch Box B4 comprises a nucleotide sequence selected from the group comprising CURYGA, CUWAUGA, CWRMGACW and UGCCAGUG,

the sixth stretch Box B5A comprises a nucleotide sequence selected from the group comprising GGY and CWGC,

the seventh stretch Box B6 comprises a nucleotide sequence selected from the group comprising YAGA, CKAAU and CCUUUAU,

the eighth stretch Box B5B comprises a nucleotide sequence selected from the group comprising GCYR and GCWG, and

the ninth stretch Box B1B comprises a nucleotide sequence selected from the groupc comprising GCAGCAC, GCRSMC, GSVVM and GCNV.

24. The nucleic acid according to claim 23, whereby

the third stretch Box B3 comprises a nucleotide sequence of GAGAA or UAAAA

25. The nucleic acid according to claims 23 or 24, whereby

the fifth stretch Box B4 comprises a nucleotide sequence of CAGCGACU or CAACGACU.

26. The nucleic acid according to any of claims 23 to 25, whereby

the fifth stretch Box B4 comprises a nucleotide sequence of CAGCGACU and Box B3 comprises a nucleotide sequence of UAAAA.

27. The nucleic acid according to any of claims 23 to 25, whereby

the fifth stretch Box B4 comprises a nucleotide sequence of CAACGACU and the third stretch Box B3 comprises a nucleotide sequence of GAGAA.

28. The nucleic acid according to any of claims 23 to 27, whereby

the seventh stretch Box B6 comprises a nucleotide sequence of UAGA.

29. The nucleic acid according to any of claims 23 to 28, whereby

a) the first stretch Box B1A comprises a nucleotide sequence of GURCUGC,
and
the ninth stretch Box B1B comprises a nucleotide sequence of GCAGCAC; or

b) the first stretch Box B1A comprises a nucleotide sequence of GKSYGC,
and
the ninth stretch Box B1B comprises a nucleotide sequence of GCRSMC; or

c) the first stretch Box B1A comprises a nucleotide sequence of KBBSC,
and
the ninth stretch Box B1B comprises a nucleotide sequence of GSVVM; or

d) the first stretch Box B1A comprises a nucleotide sequence of BNGC,
and
the ninth stretch Box B1B comprises a nucleotide sequence of GCNV.

30. The nucleic acid according to claim 29, whereby

a) the first stretch Box B1A comprises a nucleotide sequence of GUGCUGC,
and
the ninth stretch Box B1B comprises a nucleotide sequence of GCAGCAC; or

b) the first stretch Box B1A comprises a nucleotide sequence of GUGCGC, and
the ninth stretch Box B1B comprises a nucleotide sequence of GCGCAC; or

c) the first stretch Box B1A comprises a nucleotide sequence of KKSSC, and
the ninth stretch Box B1B comprises a nucleotide sequence of GSSMM; or

d) the first stretch Box B1A comprises a nucleotide sequence of SNGC, and
the ninth stretch Box B1B comprises a nucleotide sequence of GCNS.

31. The nucleic acid according to claim 30, whereby

the first stretch Box B1A comprises a nucleotide sequence of GGGC, and
the ninth stretch Box B1B comprises a nucleotide sequence of GCCC.

32. The nucleic acid according to any of claims 23 to 31, whereby the second stretch Box B2A comprises a nucleotide sequence of GKMGU and the fourth stretch Box B2B comprises a nucleotide sequence of ACKMC.

33. The nucleic acid according to claim 32, whereby the second stretch Box B2A comprises a nucleotide sequence of GUAGU and the fourth stretch Box B2B comprises a nucleotide sequence of ACUAC.

34. The nucleic acid according to any of claims 23 to 33, whereby

a) the sixth stretch Box B5A comprises a nucleotide sequence of GGY, and
the eighth stretch Box B5B comprises a nucleotide sequence of GCYR; or

b) the sixth stretch Box B5A comprises a nucleotide sequence of CWGC, and

the eighth stretch Box B5B comprises a nucleotide sequence of GCWG.

35. The nucleic acid according to claim 34, whereby

the sixth stretch Box B5A comprises a nucleotide sequence of GGC,

and

the eighth stretch Box B5B comprises a nucleotide sequence of GCCG.

36. The nucleic acid according to any of claims 23 to 35, preferably 34 to 35, whereby the sixth stretch Box B5A hybridizes with the nucleotides GCY of the eighth stretch Box B5B.

37. The nucleic acid according to any of claims 23 to 26 and 28 to 36, whereby the nucleic acid comprises a nucleic acid sequence according to SEQ.ID.No 56.

38. The nucleic acid according to any of claims 23 to 25 and 27 to 36 , whereby the nucleic acid comprises a nucleic acid sequence selected from the group comprising the nucleic acid sequences according to SEQ.ID.No 57 to 61, SEQ.ID.No 67 to 71 and SEQ.ID.No 73.

39. The nucleic acid according to claim 1, whereby the type 4 nucleic acid comprises in 5'->3' direction a first stretch Box B1A, a second stretch Box B2, a third stretch Box B1B whereby

the first stretch Box B1A and the third stretch Box B1B optionally hybridize with each other, whereby upon hybridization a double-stranded structure is formed,

the first stretch Box B1A comprises a nucleotide sequence selected from the group comprising AGCGUGDU, GCGCGAG, CSKSUU, GUGUU, and UGUU;

the second stretch Box B2 comprises a nucleotide sequence selected from the group comprising AGNDRDGBKGGURGYARGUAAAG, AGGUGGGUGGUAGUAAGUAAAG and CAGGUGGGUGGUAGAAUGUAAAGA, and

the third stretch Box B1B comprises a nucleotide sequence selected from the group comprising GNCASGCU, CUCGCGUC, GRSMSG, GRCAC, and GGCA.

40. The nucleic acid according to claim 39, whereby

a) the first stretch Box B1A comprises a nucleotide sequence of GUGUU,
and
the third stretch Box B1B comprises a nucleotide sequence of GRCAC;

b) the first stretch Box B1A comprises a nucleotide sequence of GCGCGAG,
and
the third stretch Box B1B comprises a nucleotide sequence of CUCGCGUC; or

c) the first stretch Box B1A comprises a nucleotide sequence of CSKSUU,
and
the third stretch Box B1B comprises a nucleotide sequence of GRSMSG, or

d) the first stretch Box B1A comprises a nucleotide sequence of UGUU,
and
the third stretch Box B1B comprises a nucleotide sequence of GGCA, or

e) the first stretch Box B1A comprises a nucleotide sequence of AGCGUGDU,
and
the third stretch Box B1B comprises a nucleotide sequence of GNCASGCU.

41. The nucleic acid according to claim 40, whereby the first stretch Box B1A comprises a nucleotide sequence of CSKSUU and the third stretch Box B1B comprises a nucleotide sequence of GRSMSG.

42. The nucleic acid according to claims 41, whereby the first stretch Box B1A comprises a nucleotide sequence of CCGCUU and the third stretch Box B1B comprises a nucleotide sequence of GGGCGG.

43. The nucleic acid according to any of claims 39 to 42, whereby

the second stretch Box B2 comprises a nucleotide sequence of AGGUGGGUGGUAGUAAGUAAAG.

44. The nucleic acid according to any of claims 39 to 43, whereby the nucleic acid comprises a nucleic acid sequence according to SEQ.ID.No 80.

45. The nucleic acid according to any of claims 1 to 44, whereby the nucleic acid is capable of binding a chemokine, whereby the chemokine is selected from the group comprising eotaxin, MCP-1, MCP-2 and MCP-3.

46. The nucleic acid according to any of claims 1 to 45, whereby the nucleic acid is capable of binding a chemokine, whereby the chemokine is selected from the group comprising human eotaxin, human MCP-1, human MCP-2 and human MCP-3.

47. The nucleic acid according to any of claims 1 to 46, whereby the nucleic acid is capable of binding MCP-1, whereby MCP-1 is preferably selected from the group comprising monkey MCP-1, horse MCP-1, rabbit MCP-1, bovine MCP-1, canine MCP-1, porcine MCP-1 and human MCP-1.

48. The nucleic acid according to any of claims 1 to 47, whereby the nucleic acid is capable of binding human MCP-1.

49. The nucleic acid according to any of claims 1 to 48, preferably claim 48, whereby the MCP-1 has an amino acid sequence according to SEQ ID No. 1.

50. A nucleic acid, preferably binding to murine MCP-1, whereby the nucleic acid comprises a nucleic acid sequence according to SEQ.ID.No. 122, SEQ.ID.No. 253 and SEQ.ID.No. 254.

51. A nucleic acid, preferably binding to murine MCP-1, whereby the nucleic acid comprises a nucleic acid sequence according to SEQ.ID.No. 127.

52. The nucleic acid according to claim 50 or 51, whereby the murine MCP-1 comprises an amino acid sequence according to SEQ ID No. 2.

53. The nucleic acid according to any of claims 1 to 52, wherein the nucleic acid comprises a modification, whereby the modification is preferably a high molecular weight moiety and/or whereby the modification preferably allows to modify the characteristics of the nucleic acid according to any of claims 1 to 52 in terms of residence time in the animal or human body, preferably the human body.

54. The nucleic acid according to claim 53, whereby the modification is selected from the group comprising a HES moiety and a PEG moiety.

55. The nucleic acid according to claim 54, whereby the modification is a PEG moiety consisting of a straight or branched PEG, whereby the molecular weight of the PEG moiety is preferably from about 20 to 120 kD, more preferably from about 30 to 80 kD and most preferably about 40 kD.

56. The nucleic acid according to claim 54, whereby the modification is a HES moiety, whereby preferably the molecular weight of the HES moiety is from about 10 to 130 kD, more preferably from about 30 to 130 kD and most preferably about 100 kD.

57. The nucleic acid according to any of claims of 53 to 56, whereby the modification is coupled to the nucleic acid via a linker.

58. The nucleic acid according to any of claims of 53 to 57, whereby the modification is coupled to the nucleic acid at its 5'-terminal nucleotide and/or its 3'-terminal nucleotide and/or to a nucleotide of the nucleic acid between the 5'-terminal nucleotide and the 3'-terminal nucleotide.

59. The nucleic acid according to any of claims 1 to 58, whereby the nucleotides of or the nucleotides forming the nucleic acid are L-nucleotides.

60. The nucleic acid according to any of claims 1 to 59, whereby the nucleic acid is an L-nucleic acid.

61. The nucleic acid according to any of claims 1 to 59, whereby the moiety of the nucleic acid capable of binding MCP-1 consists of L-nucleotides.

62. A pharmaceutical composition comprising a nucleic acid according to any of claims 1 to 61 and optionally a further constituent, whereby the further constituent is selected from the group comprising pharmaceutically acceptable excipients, pharmaceutically acceptable carriers and pharmaceutically active agents.

63. The pharmaceutical composition according to claim 62, whereby the pharmaceutical composition comprises a nucleic acid according to any of claims 1 to 61 and a pharmaceutically acceptable carrier.

64. Use of a nucleic acid according to any of claims 1 to 61 for the manufacture of a medicament.

65. Use according to claim 64, whereby the medicament is for use in human medicine or for use in veterinary medicine.

66. Use of a nucleic acid according to any of claims 1 to 61 for the manufacture of a diagnostic means.

67. Use according to claim 64 or 65, whereby the medicament is for the treatment and/or prevention of a disease or disorder selected from the group comprising inflammatory diseases, autoimmune diseases, autoimmune encephalomyelitis, stroke, acute and chronic multiple sclerosis, chronic inflammation, rheumatoid arthritis, renal diseases, restenosis, restenosis after angioplasty, acute and chronic allergic reactions, primary and secondary immunologic or allergic reactions, asthma, conjunctivitis, bronchitis, cancer, atherosclerosis, artheriosclerotic cardiovasular heart failure or stroke, psoriasis, psoriatic arthritis, inflammation of the nervous system, atopic dermatitis, colitis, endometriosis, uveitis, retinal disorders including macular degeneration, retinal detachment, diabetic retinopathy, retinopathy of prematurity, retinitis pigmentosa, proliferative vitreoretinopathy, and central serous chorioretinopathy; idiopathic pulmonary fibrosis, sarcoidosis, polymyositis, dermatomyositis, avoidance of immunosuppression, reducing the risk of infection, sepsis, renal inflammation, glomerulonephritis, rapid progressive glomerulonephritis, proliferative glomerulonephritis, diabetic nephropathy, obstructive nephropathy, acute tubular necrosis, and diffuse glomerulosclerosis, systemic lupus erythematosus, chronic bronchitis, Behçet's disease,

amyotrophic lateral sclerosis (ALS), premature atherosclerosis after Kawasaki's disease, myocardial infarction, obesity, chronic liver disease, peyronie's disease, acute spinal chord injury, lung or kidney transplantation, myocarditis, Alzheimer's disease and neuropathy, breast carcinoma, gastric carcinoma, bladder cancer, ovarian cancer, hamartoma, colorectal carcinoma, colonic adenoma, pancreatitis, chronic obstructiv pulmonary disesase (COPD) and inflammatory bowel diseases such as Crohn's disease or ulcerative colitis.

68. A complex comprising a chemokine and a nucleic acid according to any of claims 1 to 61, whereby the chemokine is selected from the group comprising eotaxin, MCP-1, MCP-2 and MCP-3, whereby preferably the complex is a crystalline complex.

69. The complex according to claim 68, whereby the chemokine is selected from the group comprising human eotaxin, human MCP-1, human MCP-2 and human MCP-3.

70. The complex according to claim 68 or 69, whereby the chemokine is MCP-1, whereby MCP-1 is preferably selected from the group comprising human MCP-1, monkey MCP-1, horse MCP-1, rabbit MCP-1, bovine MCP-1, canine MCP-1 and porcine MCP-1, more preferably MCP-1 is human MCP-1.

71. Use of a nucleic acid according to any of claims 1 to 61 for the detection of a chemokine, whereby the chemokine is selected from the group comprising eotaxin, MCP-1, MCP-2 and MCP-3.

72. Use according to claim 71, whereby the chemokine is selected from the group comprising human eotaxin, human MCP-1, human MCP-2 and human MCP-3.

73. Use according to claim 71 or 72, whereby the chemokine is MCP-1, whereby MCP-1 is preferably selected from the group comprising human MCP-1, monkey MCP-1, horse MCP-1, rabbit MCP-1, bovine MCP-1, canine MCP-1 and porcine MCP-1, more preferably MCP-1 is human MCP-1.

74. A method for the screening of a chemokine antagonist or a chemokine agonist comprising the following steps:

- providing a candidate chemokine antagonist and/or a candidate chemokine agonist,

- providing a nucleic acid according to any of claims 1 to 61,

- providing a test system which provides a signal in the presence of a chemokine antagonist and/or a chemokine agonist, and

- determining whether the candidate chemokine antagonist is a chemokine antagonist and/or whether the candidate chemokine agonist is a chemokine agonist,

whereby the chemokine is selected from the group comprising eotaxin, MCP-1, MCP-2 and MCP-3.

75. The method according to claim 74, whereby the chemokine is selected from the group comprising human eotaxin, human MCP-1, human MCP-2 and human MCP-3.

76. The method according to claim 74 or 75, whereby the chemokine is MCP-1, whereby MCP-1 is preferably selected from the group comprising human MCP-1, monkey MCP-1, horse MCP-1, rabbit MCP-1, bovine MCP-1, canine MCP-1 and porcine MCP-1, more preferably MCP-1 is human MCP-1.

77. A method for the screening of a chemokine agonist and/or a chemokine antagonist comprising the following steps:

- providing a chemokine immobilised to a phase, preferably a solid phase,

- providing a nucleic acid according to any of claims 1 to 61, preferably a nucleic acid according to any of claims 1 to 52 which is labelled,

- adding a candidate chemokine agonist and/or a candidate chemokine antagonist, and

- determining whether the candidate chemokine agonist is a chemokine agonist and/or whether the candidate chemokine antagonist is a chemokine antagonist,

whereby the chemokine is selected from the group comprising eotaxin, MCP-1, MCP-2 and MCP-3.

78. The method according to claim 77, characterised in that the determining is carried out such that it is assessed whether the nucleic acid is replaced by the candidate chemokine agonist or by a candidate chemokine antagonist.

79. The method according to claim 77 or 78, whereby the chemokine is selected from the group comprising human eotaxin, human MCP-1, human MCP-2 and human MCP-3.

80. The method according to any of claims 77 to 79, whereby the chemokine is MCP-1, whereby MCP-1 is preferably selected from the group comprising human MCP-1, monkey MCP-1, horse MCP-1, rabbit MCP-1, bovine MCP-1, canine MCP-1 and porcine MCP-1, more preferably MCP-1 is human MCP-1.

81. A kit for the detection of a chemokine comprising a nucleic acid according to any of claims 1 to 61, whereby the chemokine is selected from the group comprising eotaxin, MCP-1, MCP-2 and MCP-3.

82. The kit according to claim 81, whereby the chemokine is selected from the group comprising human eotaxin, human MCP-1, human MCP-2 and human MCP-3.

83. The kit according to claim 81 or 82, whereby the chemokine is MCP-1, whereby MCP-1 is preferably selected from the group comprising human MCP-1, monkey MCP-1, horse MCP-1, rabbit MCP-1, bovine MCP-1, canine MCP-1 and porcine MCP-1, more preferably MCP-1 is human MCP-1.

84. A chemokine antagonist obtainable by the method according to any of claims 74 to 80, whereby the chemokine is selected from the group comprising eotaxin, MCP-1, MCP-2 and MCP-3.

85. The chemokine antagonist according to claim 84, whereby the chemokine is selected from the group comprising human eotaxin, human MCP-1, human MCP-2 and human MCP-3.

86. The chemokine antagonist according to claim 84 or 85, whereby the chemokine is MCP-1, whereby MCP-1 is preferably selected from the group comprising human MCP-1, monkey MCP-1, horse MCP-1, rabbit MCP-1, bovine MCP-1, canine MCP-1 and porcine MCP-1, more preferably MCP-1 is human MCP-1.

87. A chemokine agonist obtainable by the method according to any of claims 74 to 80, whereby the chemokine is selected from the group comprising eotaxin, MCP-1, MCP-2 and MCP-3.

88. The chemokine agonist according to claim 87, whereby the chemokine is selected from the group comprising human eotaxin, human MCP-1, human MCP-2 and human MCP-3.

89. The chemokine agonist according to claim 87 or 88, whereby the chemokine is MCP-1, whereby MCP-1 is preferably selected from the group comprising human MCP-1, monkey MCP-1, horse MCP-1, rabbit MCP-1, bovine MCP-1, canine MCP-1 and porcine MCP-1, more preferably MCP-1 is human MCP-1.

90. A method for the detection of the nucleic acid according to any of claims 1 to 61 in a sample, whereby the method comprises the steps of:

f) providing a sample containing the nucleic acid according to the present invention;

g) providing a capture probe, whereby the capture probe is at least partially complementary to a first part of the nucleic acid according to any of claims 1 to 61, and a detection probe, whereby the detection probe is at least partially complementary to a second part of the nucleic acid according to any of claims 1 to 61, or, alternatively, the capture probe is at least partially complementary to a second part of the nucleic acid according to any of claims 1 to 61 and the detection probe is at least partially complementary to the first part of the nucleic acid according to any of claims 1 to 61;

h) allowing the capture probe and the detection probe to react either simultaneously or in any order sequentially with the nucleic acid according to any of claims 1 to 61 or part thereof;

i) optionally detecting whether or not the capture probe is hybridized to the nucleic acid according to the nucleic acid according to any of claims 1 to 61 provided in step a); and

j) detecting the complex formed in step c) consisting of the nucleic acid according to any of claims 1 to 61, and the capture probe and the detection probe.

91. The method according to claim 90, whereby the detection probe comprises a detection means, and/or whereby the capture probe can be immobilized to a support, preferably a solid support.

92. The method according to claim 90 or 91, wherein any detection probe which is not part of the complex is removed from the reaction so that in step e) only a detection probe which is part of the complex, is detected.

93. The method according to any of claims 90 to 92, wherein step e) comprises the step of comparing the signal generated by the detection means when the capture probe and the detection probe are hybridized in the presence of the nucleic acid according to any of claims 1 to 61 or part thereof, and in the absence of said nucleic acid or part thereof.

94. The method according to any of claims 90 to 93, wherein the nucleic acid to be detected is the nucleic acid having a nucleic acid sequence according to SEQ. ID. NOs. 37, 116, 117 or 278, and the capture probe or detection probe comprises a nucleic acid sequence according to SEQ .ID. NO. 255 or SEQ. ID. NO. 256.

95. The method according to any of claims 90 to 93, wherein the nucleic acid to be detected is the nucleic acid having a nucleic acid sequence according to SEQ. ID. NOs. 122, 253 or 254 and the capture probe or detection probe comprises a nucleic acid sequence according to SEQ. ID. NO. 281 and SEQ. ID. NO. 282.