present case SDF-1, is the so-called Kd value which as such as well as 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 Kd value. Preferably, the Kd value shown by the nucleic acids according to the present invention is below 1 μM. A Kd 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 Kd value of a group of compounds such as the nucleic acids according to the present invention are within a certain range. The above-mentioned Kd of about 1 μM is a preferred upper limit for the Kd value. The preferred lower limit for the Kd of target binding nucleic acids can be about 10 picomolar or higher. It is within the present invention that the Kd values of individual nucleic acids binding to ~~ghrelin~~ SDF-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 an 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 20 to 40 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

and off-rates and the K_D values of Spiegelmers 192-A10-008 and 192-A10-001 are listed;

Fig. 16 shows the efficacy of SDF-1 binding Spiegelmer 192-A10-008 in a chemotaxis assay; cells were allowed to migrate towards 0.3 nM human SDF-1 preincubated at 37°C with various amounts of Spiegelmer 192-A10-008, represented as percentage of control over concentration of Spiegelmer 192-A10-008;

Fig. 17 shows a Biacore 2000 sensorgram indicating the K_D value of Spiegelmer 193-G2-01 binding to human SDF-1 which was immobilized on a PioneerF1 sensor chip by amine coupling procedure, represented as response (RU) over time, additionally the on- and off-rates and the K_D values of Spiegelmers 193-G2-001 ~~and 193-C2-001~~ are listed;

Fig. 18 shows the result of a binding analysis of the human anti-SDF-1 aptamer 193-G2-012 to biotinylated human D-SDF-1 at 37°C, represented as binding of the aptamer over concentration of biotinylated human D-SDF-1;

Fig. 19 shows the result of a competitive binding analysis of the human SDF-1 binding aptamers 190-A3-001, 190-A3-003, 190-A3-004, 190-A3-007, 191-D5-001, 191-D5-002, 191-D5-003, 191-D5-004, 191-D5-005, 191-D5-006 and 191-D5-007 to biotinylated human D-SDF-1 at 37°C, represented as binding of the labeled aptamer 190-A3-001 or 191-D5-001 (used as reference that is displaced by the non-labeled aptamers) at 500 nM, 50 nM and 10 nM non-labeled aptamers 190-A3-001, 190-A3-003, 190-A3-004, 190-A3-007, 191-D5-001, 191-D5-002, 191-D5-003, 191-D5-004, 191-D5-005, 191-D5-006 and 191-D5-007;

Fig. 20 shows the result of a binding analysis of the human SDF-1 binding aptamers 190-A3-004 and 191-D5-007 to biotinylated human D-SDF-1 37°C, represented as binding of the aptamer over concentration of biotinylated human D-SDF-1;

Fig. 21 shows a Biacore 2000 sensorgram indicating the K_D value of Spiegelmer 191-D5-007 binding to human SDF-1 which was

immobilized on a PioneerF1 sensor chip by amine coupling procedure, represented as response (RU) over time, additionally the on- and off-rates and the K_D values of Spiegelmers ~~191-D5-001,~~ 191-D5-007, ~~190-A3-003 and 197-B2~~ are listed;

Fig. 22 shows the efficacy of SDF-1 binding Spiegelmer 190-A3-004 in a chemotaxis assay; cells were allowed to migrate towards 0.3 nM human SDF-1 preincubated at 37°C with various amounts of Spiegelmer 190-A3-004, represented as percentage of control over concentration of Spiegelmer 190-A3-004;

Fig. 23A shows the efficacy of SDF-1 binding Spiegelmers 193-G2-012-5'-PEG, 197-B2-006-5'-PEG, 191-D5-007-5'-PEG and 191-A10-008-5'-PEG in a chemotaxis assay; cells were allowed to migrate towards 0.3 nM human SDF-1 preincubated at 37°C with various amounts of Spiegelmers 193-G2-012-5'-PEG, 197-B2-006-5'-PEG, 191-D5-007-5'-PEG and 191-A10-008-5'-PEG, represented as percentage of control over concentration of Spiegelmers 193-G2-012-5'-PEG, 197-B2-006-5'-PEG, 191-D5-007-5'-PEG and 191-A10-008-5'-PEG;

Fig. 23B shows the efficacy of SDF-1 binding Spiegelmers 197-B2-006-5'PEG and 197-B2-006-31b-5'-PEG in a chemotaxis assay; cells were allowed to migrate towards 0.3 nM human SDF-1 preincubated at 37°C with various amounts of Spiegelmers 197-B2-006-5'PEG and 197-B2-006-31b-5'-PEG, represented as percentage of control over concentration of Spiegelmers 197-B2-006-5'PEG and 197-B2-006-31b-5'-PEG;

Fig. 24A shows a Biacore 2000 sensorgram indicating the K_D values of Spiegelmers 193-G2-012-5'-PEG, 191-A10-008-5'-PEG and 191-A10-001-5'-PEG binding to human SDF-1 which was immobilized on a PioneerF1 sensor chip by amine coupling procedure, represented as response (RU) over time;

Fig. 24B shows a Biacore 2000 sensorgram indicating the K_D values of Spiegelmers 197-B2-006-5'PEG, 197-B2-006-31b-5'-PEG and 191-D5-007-5'-PEG binding to human SDF-1 which was immobilized on a

Claims

1. A nucleic acid molecule capable of binding to SDF-1 and being an antagonist to SDF-1, comprising in 5'->3' direction a first stretch of nucleotides, a core nucleotide sequence, and a second stretch of nucleotides or a second stretch of nucleotides, a core nucleotide sequence, and a first stretch of nucleotides,

wherein the length of the nucleic acid molecule is 20 to 50 nucleotides,

wherein the nucleic acid molecule is selected from the group consisting of type A nucleic acid molecules, type B nucleic acid molecules, type C nucleic acid molecules and nucleic acid molecules having a nucleic acid sequence according to any one of SEQ.ID.No. 142, SEQ.ID.No. 143, SEQ.ID.No. 144;

whereby the type A nucleic acid molecules comprise the following core nucleotide sequence:

5' AAAGYRACAHGUMAAX$_A$UGAAAGGUARC 3' (SEQ.ID. 19)

whereby X_A is either absent or is A, and

whereby the first stretch of nucleotides of the type A nucleic acid molecules comprises a nucleotide sequence of 5' X_1X_2NNBV 3' (SEQ.ID.No. 44) and the second stretch of nucleotides of the type A nucleic acid molecules comprises a nucleotide sequence of 5' BNBNX_3X_4 3' (SEQ.ID.No. 45)

whereby X_1 is either absent or R, X_2 is S, X_3 is S and X_4 is either absent or Y,
or
X_1 is absent, X_2 is either absent or S, X_3 is either absent or S and X_4 is absent;

whereby the type B nucleic acid molecules comprise the following core nucleotide sequence:

5' GUGUGAUCUAGAUGUADWGGCUGWUCCUAGUYAGG 3' (SEQ.ID.No. 57), and

whereby the first stretch of nucleotides of the type B nucleic acid molecules comprises a nucleotide sequence of 5' X_1X_2SVNS 3' (SEQ.ID.No. 77) and the second stretch of nucleotides of the type B nucleic acid molecules comprises a nucleotide sequence of 5' BVBSX_3X_4 3' (SEQ.ID.No. 78), whereby

X_1 is either absent or is A, X_2 is G, X_3 is C and X_4 is either absent or is U;

or

X_1 is absent, X_2 is either absent or is G, X_3 is either absent or is C and X_4 is absent;

whereby the type C nucleic acid molecules comprise a core nucleotide sequence of GGUYAGGGCUHRX_AAGUCGG (SEQ.ID.No. 90),

whereby X_A is either absent or is A, and

whereby the first stretch of nucleotides of the type C nucleic acid molecules comprises a nucleotide sequence of 5' RKSBUSNVGR 3' (SEQ.ID.No. 120) and the second stretch of nucleotides of the type C nucleic acid molecules comprises a nucleotide sequence of 5' YYNRCASSMY 3' (SEQ.ID.No. 121),

or

whereby the first stretch of nucleotides of the type C nucleic acid molecules comprises a nucleotide sequence of 5' X_SSSSV 3' (SEQ.ID.No. 124) and the second stretch of nucleotides of the type C nucleic acid molecules comprises a nucleotide sequence of 5' BSSSX_S 3' (SEQ.ID.No. 125), whereby X_s is either absent or is S,

or

whereby the first stretch of nucleotides of the type C nucleic acid molecules comprises a nucleotide sequence of 5' UGAGAUAGG 3' and the second stretch of nucleotides of the type C nucleic acid molecules comprises a nucleotide sequence of 5' CUGAUUCUCA 3',

or

whereby the first stretch of nucleotides of the type C nucleic acid molecules comprises a nucleotide sequence of 5' GAGAUAGG 3' and the second stretch of nucleotides of the type C nucleic acid molecules comprises a nucleotide sequence of 5' CUGAUUCUC 3'.

2. The nucleic acid molecule according to claim 1, whereby the type A nucleic acid molecules comprise a core nucleotide sequence selected from the group comprising

5' AAAGYRACAHGUMAAUGAAAGGUARC 3' (SEQ.ID.No. 20),
5' AAAGYRACAHGUMAAAUGAAAGGUARC 3' (SEQ.ID.No. 21), and
5' AAAGYAACAHGUCAAUGAAAGGUARC 3' (SEQ.ID.No. 22), preferably the core nucleotide sequence comprises 5' AAAGYAACAHGUCAAUGAAAGGUARC 3' (SEQ. ID. No. 22).

3. The nucleic acid molecule according to claim 1 or 2, whereby said first and said second stretch of nucleotides of the type A nucleic acid molecules hybridize with each other, whereby upon hybridization a double-stranded structure is formed.

4. The nucleic acid molecule according to claim 3, whereby the double-stranded structure consists of four to six base pairs, preferably five base pairs.

5. The nucleic acid molecule according to any one of claims 1 to 4, whereby the first stretch of nucleotides of the type A nucleic acid molecules comprises a nucleotide sequence of 5' RSHRYR 3' (SEQ.ID.No. 23) and the second stretch of nucleotides of the type A nucleic acid molecules comprises a nucleotide sequence of 5' YRYDSY 3'(SEQ.ID.No. 24),

preferably the first stretch of nucleotides of the type A nucleic acid molecules comprises a nucleotide sequence of 5' GCUGUG 3' and the second stretch of nucleotides of the type A nucleic acid molecules comprises a nucleotide sequence of 5' CGCAGC 3'.

6. The nucleic acid molecule according to any one of claims 1 to 4, whereby the first stretch of nucleotides of the type A nucleic acid molecules comprises a nucleotide sequence

of 5' X_2BBBS 3' (SEQ.ID.No. 42) and the second stretch of nucleotides of the type A nucleic acid molecules comprises a nucleotide sequence of 5' SBBVX_3 3' (SEQ.ID.No. 43),

whereby X_2 is either absent or is S and X_3 is either absent or is S;

preferably the first stretch of nucleotides of the type A nucleic acid molecules comprises a nucleotide sequence of 5' CUGUG 3' and the second stretch of nucleotides of the type A nucleic acid molecules comprises a nucleotide sequence of 5' CGCAG 3',
or the first stretch of nucleotides of the type A nucleic acid molecules comprises a nucleotide sequence of 5' GCGUG 3'and the second stretch of nucleotides of the type A nucleic acid molecules comprises a nucleotide sequence of 5' CGCGC 3'.

7. The nucleic acid molecule according to any one of claims 1 to 6, whereby the type A nucleic acid molecule has a nucleic acid sequence according to any one of SEQ.ID.Nos. 5 to 18, 25 to 41, 133, 137, 139 to 141.

8. The nucleic acid molecule according to claim 1, whereby the type B nucleic acid molecules comprise a core nucleotide sequence of GUGUGAUCUAGAUGUADUGGCUGAUCCUAGUCAGG (SEQ.ID.No. 58).

9. The nucleic acid molecule according to claim 1 or 8, whereby said first and said second stretch of nucleotides of the type B nucleic acid molecules hybridize with each other, whereby upon hybridization a double-stranded structure is formed.

10. The nucleic acid molecule according to claim 9, whereby the double-stranded structure consists of four to six base pairs, preferably five base pairs.

11. The nucleic acid molecule according to any one of claims 1 and 8 to 10, whereby the first stretch of nucleotides of the type B nucleic acid molecules comprises a nucleotide sequence of 5' X_1GCRWG 3' (SEQ.ID.No. 59) and the second stretch of nucleotides of the type B nucleic acid molecules comprises a nucleotide sequence of 5'KRYSCX_4 3'(SEQ.ID.No. 60),

whereby X_1 is either absent or A, and X_4 is either absent or U.

12. The nucleic acid molecule according to any one of claims 1 and 8 to 11, whereby the first stretch of nucleotides of the type B nucleic acid molecules comprises a nucleotide sequence of 5' X_1GCGUG 3' (SEQ.ID.No. 75) and the second stretch of nucleotides of the type B nucleic acid molecules comprises a nucleotide sequence of 5' UACGCX_4 3' (SEQ.ID.No. 76),

whereby X_1 is either absent or A, and X_4 is either absent or U,

preferably the first stretch of nucleotides of the type B nucleic acid molecules comprises a nucleotide sequence of 5' AGCGUG 3' and the second stretch of nucleotides of the type B nucleic acid molecules comprises a nucleotide sequence of 5' UACGCU 3'.

13. The nucleic acid molecule according to any one of claims 1 and 8 to 10, whereby the first stretch of nucleotides of the type B nucleic acid molecules comprises a nucleotide sequence of 5' X_2SSBS 3' (SEQ.ID.No. 73) and the second stretch of nucleotides of the type B nucleic acid molecules comprises a nucleotide sequence of 5' BVSSX_3 3' (SEQ.ID.No. 74),

whereby X_2 is either absent or G, and X_3 is either absent or C,

preferably the first stretch of nucleotides of the type B nucleic acid molecules comprises a nucleotide sequence of 5' GCGUG 3' and the second stretch of nucleotides of the type B nucleic acid molecules comprises a nucleotide sequence of 5' UACGC 3'.

14. The nucleic acid molecule according to any one of claims 1 and 8 to 13, whereby the type B nucleic acid molecule has a nucleic acid sequence according to any one of SEQ.ID.Nos. 46 to 56, 61 to 72, 132.

15. The nucleic acid molecule according to claim 1, whereby the type C nucleic acid molecules comprise a core nucleotide sequence selected from the group comprising

5' GGUYAGGGCUHRAAGUCGG 3' (SEQ.ID.No. 91),

5' GGUYAGGGCUHRAGUCGG 3' (SEQ.ID.No. 92), and
5' GGUUAGGGCUHGAAGUCGG 3' (SEQ.ID.No. 93), preferably the core nucleotide sequence comprises 5' GGUUAGGGCUHGAAGUCGG 3' (SEQ. ID. No. 93).

16. The nucleic acid molecule according to claim 1 or 15, whereby at least a part of said first stretch and at least a part of said second stretch of nucleotides of the type C nucleic acid molecules hybridize with each other, whereby upon hybridization a double-stranded structure is formed.

17. The nucleic acid molecule according to claim 16, whereby the double-stranded structure comprises 4 to 10 base pairs, preferably 4 to 6 base pairs, more preferably 5 base pairs.

18. The nucleic acid molecule according to claim 17, whereby the double-stranded structure comprises 4 to 10 consecutive base pairs, preferably 4 to 6 consecutive base pairs, more preferably 5 consecutive base pairs.

19. The nucleic acid molecule according to any one of claims 1 and 15 to 18, whereby the first stretch of nucleotides of the type C nucleic acid molecules comprises a nucleotide sequence of 5' RKSBUGSVGR 3' (SEQ.ID.No. 122) and the second stretch of nucleotides of the type C nucleic acid molecules comprises a nucleotide sequence of 5' YCNRCASSMY 3' (SEQ.ID.No. 123).

20. The nucleic acid molecule according to any one of claims 1 and 15 to 18, whereby the first stretch of nucleotides of the type C nucleic acid molecules comprises a nucleotide sequence of 5' SSSSR 3' (SEQ.ID.No. 130) and the second stretch of nucleotides of the type C nucleic acid molecules comprise a nucleotide sequence of 5' YSBSS 3' (SEQ.ID.No. 131),

preferably the first stretch of nucleotides of the type C nucleic acid molecules comprises a nucleotide sequence of 5' SGGSR 3' (SEQ.ID.No. 126) and the second stretch of nucleotides of the type C nucleic acid molecules comprises a nucleotide sequence of 5' YSCCS 3' (SEQ.ID.No. 127).

21. The nucleic acid molecule according to any one of claims 1, 15 to 18 and 20, whereby the first stretch of nucleotides of the type C nucleic acid molecules comprises a nucleotide sequence of 5' GCSGG 3' (SEQ.ID.No. 128) and the second stretch of nucleotides of the type C nucleic acid molecules comprises a nucleotide sequence of 5' CCKGC 3' (SEQ.ID.No. 129),

preferably the first stretch of nucleotides of the type C nucleic acid molecules comprises a nucleotide sequence of 5' GCCGG 3' and the second stretch of nucleotides of the type C nucleic acid molecules comprises a nucleotide sequence of 5' CCGGC 3'.

22. The nucleic acid molecule according to any one of claims 1 and 15 to 21, whereby the type C nucleic acid molecule has a nucleic acid sequence according to any one of SEQ.ID.Nos. 79 to 89, 94 to 119, 134 to 136.

23. The nucleic acid molecule according to claim 1, whereby the nucleic acid molecule has a nucleic acid sequence according to any one of SEQ.ID.Nos. 142 to 144.

24. The nucleic acid molecule according to any one of claims 1 to 23, whereby the nucleic acid molecule is an antagonist of the SDF-1 receptor system, whereby preferably the SDF-1 receptor of the SDF-1 receptor system is the CXCR4 receptor.

25. The nucleic acid molecule according to any one of claims 1 to 24, whereby the SDF-1 is a human SDF-1 and/or the SDF-1 receptor of the SDF-1 receptor system is a human SDF-1 receptor.

26. The nucleic acid molecule according to any one of claims 1 to 25, whereby SDF-1 comprises an amino acid sequence according to SEQ ID No. 1.

27. The nucleic acid molecule according to any one of claims 1 to 26, wherein the nucleic acid molecule comprises a modification.

28. The nucleic acid molecule according to claim 27, whereby the modification is selected from the group comprising a HES moiety and a PEG moiety.

29. The nucleic acid molecule according to claim 28, 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 2 to 180 kD, more preferably from about 60 to 140 kD and most preferably about 40 kD.

30. The nucleic acid molecule according to claim 28, 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.

31. The nucleic acid molecule according to any one of claims 1 to 30, whereby the nucleotides of the nucleic acid molecule are L-nucleotides, preferably the nucleotides of the sequences according to any one of SEQ.ID:No. 19, 20, 21, 22, 57, 58, 90, 91, 92, or 93.

32. A pharmaceutical composition comprising a nucleic acid molecule according to any one of claims 1 to 31 and optionally a further constituent, whereby the further constituent is selected from the group comprising pharmaceutically acceptable excipients and pharmaceutically active agents.

33. The nucleic acid molecule according to any one of claims 1 to 31 for use in treating and/or preventing a disease or disorder.

34. The nucleic acid molecule according to claim 33 for use in treating and/or preventing a disease or disorder mediated by SDF-1

35. The nucleic acid molecule according to claim 33 or 34, for use in treating a disease or disorder selected from the group comprising back-of-the-eye diseases like diabetic retinopathy and age-related macular degeneration; cancer of breast, ovaries, prostate, pancreas, thyroid, nasopharynx, colon, lung, and stomach; osteosarcoma; melanoma; glioma; medullo- and neuroblastoma; leukemia; WHIM syndrome; immunologic deficiency syndromes; pathologic neovascularization; inflammation; multiple sclerosis; rheumatoid arthritis / osteoarthritis and nephritis.

36. Use of a nucleic acid molecule according to any one of claims 1 to 31 for the manufacture of a medicament for the treatment and/or prevention of a disease or disorder selected from the group comprising back-of-the-eye diseases like diabetic retinopathy and age-related macular degeneration; cancer of breast, ovaries, prostate, pancreas, thyroid, nasopharynx, colon, lung, and stomach; osteosarcoma; melanoma; glioma; medullo- and neuroblastoma; leukemia; WHIM syndrome; immunologic deficiency syndromes; pathologic neovascularization; inflammation; multiple sclerosis; rheumatoid arthritis / osteoarthritis and nephritis.

37. Use of a nucleic acid molecule according to any one of claims 1 to 31 for the manufacture of a medicament is for inhibiting angiogenesis, neovascularization, inflammation and metastasis.

38. The nucleic acid molecule according to any one of claims 1 to 31 for use in diagnosing a disease or disorder.

39. The nucleic acid molecule according to claim 38 for use in diagnosing a disease or disorder mediated by SDF-1.

40. The nucleic acid molecule according to claim 38 or 39 for use in diagnosing a disease or disorder selected from the group comprising back-of-the-eye diseases like diabetic retinopathy and age-related macular degeneration; cancer of breast, ovaries, prostate, pancreas, thyroid, nasopharynx, colon, lung, and stomach; osteosarcoma; melanoma; glioma; medullo- and neuroblastoma; leukemia; WHIM syndrome; immunologic deficiency syndromes; pathologic neovascularization; inflammation; multiple sclerosis; rheumatoid arthritis / osteoarthritis and nephritis.

41. Use of a nucleic acid molecule according to any one of claims 1 to 31 for the manufacture of a diagnostic means for the diagnosis of a disease or disorder selected from the group comprising back-of-the-eye diseases like diabetic retinopathy and age-related macular degeneration; cancer of breast, ovaries, prostate, pancreas, thyroid, nasopharynx, colon, lung, and stomach; osteosarcoma; melanoma; glioma; medullo- and neuroblastoma; leukemia;

WHIM syndrome; immunologic deficiency syndromes; pathologic neovascularization; inflammation; multiple sclerosis; rheumatoid arthritis / osteoarthritis and nephritis.

42. Use of a nucleic acid molecule according to any one of claims 1 to 31 for the manufacture of a diagnostic means is for diagnosing angiogenesis, neovascularization, inflammation and/or metastasis.

43. A complex comprising SDF-1 and a nucleic acid molecule according to any one of claims 1 to 31, whereby preferably the complex is a crystalline complex.

44. Use of a nucleic acid molecule according to any one of claims 1 to 31 for the *in vitro* detection of SDF-1.

45. A method for the screening of a SDF-1 antagonist or a SDF-1 agonist comprising the following steps:

- providing a candidate SDF-1 antagonist and/or a candidate SDF-1agonist,
- providing a nucleic acid molecule according to any one of claims 1 to 31,
- providing a test system which provides a signal in the presence of a SDF-1 antagonist and/or a SDF-1 agonist wherein the test system is a cell culture, and
- determining whether the candidate SDF-1 antagonist is a SDF-1 antagonist and/or whether the candidate SDF-1 agonist is a SDF-1 agonist.

46. A method for the screening of a SDF-1 agonist and/or a SDF-1 antagonist comprising the following steps:

- providing SDF-1 immobilised to a phase, preferably a solid phase,
- providing a nucleic acid molecule according to any one of claims 1 to 31, preferably a nucleic acid molecule according to any one of claims 1 to 31 which is labelled,

- adding a candidate SDF-1 agonist and/or a candidate SDF-1 antagonist, and

- determining whether the candidate SDF-1 agonist is a SDF-1 agonist and/or whether the candidate SDF-1 antagonist is a SDF-1 antagonist.

47. The method according to claim 46, characterized in that the determining is carried out such that it is assessed whether the nucleic acid molecule is replaced by the candidate SDF-1 agonist or by a candidate SDF-1 antagonist.

48. A kit for the detection of SDF-1, comprising a nucleic acid molecule according to any of claims 1 to 31.

Claims

1. An isolated L- nucleic acid molecule, capable of binding to SDF-1, selected from the group comprising type A nucleic acid molecules, type B nucleic acid molecules, type C nucleic acid molecules and nucleic acid molecules having a nucleic acid sequence according to any of SEQ.ID.No. 142, SEQ.ID.No. 143 and SEQ.ID.No. 144,

whereby the type A nucleic acid molecules comprise the following core nucleotide sequence:

5' AAAGYRACAHGUMAAX$_A$UGAAAGGUARC 3' (SEQ.ID. 19)

whereby X$_A$ is either absent or is A;

whereby the type B nucleic acid molecules comprise the following core nucleotide sequence:

5' GUGUGAUCUAGAUGUADWGGCUGWUCCUAGUYAGG 3' (SEQ.ID.No. 57); and

whereby the type C nucleic acid molecules comprise a core nucleotide sequence of GGUYAGGGCUHRX$_A$AGUCGG (SEQ.ID.No. 90),

whereby X$_A$ is either absent or is A.

2. The nucleic acid molecule according to claim 1, whereby the type A nucleic acid molecules comprise a core nucleotide sequence selected from the group comprising

5' AAAGYRACAHGUMAAUGAAAGGUARC 3' (SEQ.ID.No. 20),
5' AAAGYRACAHGUMAAAUGAAAGGUARC 3' (SEQ.ID.No. 21), and
5' AAAGYAACAHGUCAAUGAAAGGUARC 3' (SEQ.ID.No. 22), preferably the core nucleotide sequence comprises 5' AAAGYAACAHGUCAAUGAAAGGUARC 3' (SEQ. ID. No. 22).

3. The nucleic acid molecule according to any of claims 1 and 2, whereby the nucleic acid molecule comprises in 5'->3' direction a first stretch of nucleotides, the core nucleotide

sequence, and a second stretch of nucleotides or the nucleic acid molecule comprises in 5'->3' direction a second stretch of nucleotides, the core nucleotide sequence, and a first stretch of nucleotides.

4. The nucleic acid molecule according to claim 3, whereby said first and said second stretch of nucleotides optionally hybridize with each other, whereby upon hybridization a double-stranded structure is formed.

5. The nucleic acid molecule according to any of claims 3 to 4, whereby the double-stranded structure consists of four to six base pairs, preferably five base pairs.

6. The nucleic acid molecule according to any of claims 3 to 5, whereby the first stretch of nucleotides comprise a nucleotide sequence of 5' X_1X_2NNBV 3' (SEQ.ID.No. 44) and the second stretch of nucleotides comprises a nucleotide sequence of 5' BNBNX_3X_4 3' (SEQ.ID.No. 45)

whereby X_1 is either absent or R, X_2 is S, X_3 is S and X_4 is either absent or Y;
or
X_1 is absent, X_2 is either absent or S, X_3 is either absent or S and X_4 is absent.

7. The nucleic acid molecule according to any of claims 3 to 6, whereby the first stretch of nucleotides comprises a nucleotide sequence of 5' X_2BBBS 3' (SEQ.ID.No. 42) and the second stretch of nucleotides comprises a nucleotide sequence of 5' SBBVX_3 3' (SEQ.ID.No. 43),

whereby X_2 is either absent or is S and X_3 is either absent or is S;

preferably the first stretch of nucleotides comprises a nucleotide sequence of 5' CUGUG 3' and the second stretch of nucleotides comprises a nucleotide sequence of 5' CGCAG 3'; or the first stretch of nucleotides comprises a nucleotide sequence of 5' GCGUG 3'and the second stretch of nucleotides comprises a nucleotide sequence of 5' CGCGC 3'.

8. The nucleic acid molecule according to any of claims 1 to 7, whereby the nucleic acid molecule has a nucleic acid sequence according to any of SEQ.ID.Nos. 5 to 18, 25 to 41, 133, 137, 139 to 141.

9. The nucleic acid molecule according to claim 1, whereby the type B nucleic acid molecules comprise a core nucleotide sequence of GUGUGAUCUAGAUGUADUGGCUGAUCCUAGUCAGG (SEQ.ID.No. 58).

10. The nucleic acid molecule according to any of claims 1 and 9, whereby the nucleic acid molecule comprises in 5'->3' direction a first stretch of nucleotides, the core nucleotide sequence, and a second stretch of nucleotides or the nucleic acid molecule comprises in 5'->3' direction a second stretch of nucleotides, the core nucleotide sequence, and a first stretch of nucleotides.

11. The nucleic acid molecule according to claim 10, whereby said first and said second stretch of nucleotides optionally hybridize with each other, whereby upon hybridization a double-stranded structure is formed.

12. The nucleic acid molecule according to any of claims 10 to 11, whereby the double-stranded structure consists of four to six base pairs, preferably five base pairs.

13. The nucleic acid molecule according to any of claims 10 to 12, whereby the first stretch of nucleotides comprises a nucleotide sequence of 5' X_1X_2SVNS 3' (SEQ.ID.No. 77) and the second stretch of nucleotides comprises a nucleotide sequence of 5' BVBSX_3X_4 3' (SEQ.ID.No. 78), whereby

X_1 is either absent or is A, X_2 is G, X_3 is C and X_4 is either absent or is U;

or

X_1 is absent, X_2 is either absent or is G, X_3 is either absent or is C and X_4 is absent.

14. The nucleic acid molecule according to any of claims 10 to 13, whereby the first stretch of nucleotides comprises a nucleotide sequence of 5' X_2SSBS 3' (SEQ.ID.No. 73) and

the second stretch of nucleotides comprises a nucleotide sequence of 5' BVSSX$_3$ 3' (SEQ.ID.No. 74),

whereby X_2 is either absent or G, and X_3 is either absent or C,

preferably the first stretch of nucleotides comprises a nucleotide sequence of 5' GCGUG 3' and the second stretch of nucleotides comprises a nucleotide sequence of 5' UACGC 3'.

15. The nucleic acid molecule according to any of claims 1 and 9 to 14, whereby the nucleic acid molecule has a nucleic acid sequence according to any of SEQ.ID.Nos. 46 to 56, 61 to 72, and 132.

16. The nucleic acid molecule according to claim 1, whereby the type C nucleic acid molecules comprise a core nucleotide sequence selected from the group comprising

5' GGUYAGGGCUHRAAGUCGG 3' (SEQ.ID.No. 91),
5' GGUYAGGGCUHRAGUCGG 3' (SEQ.ID.No. 92), and
5' GGUUAGGGCUHGAAGUCGG 3' (SEQ.ID.No. 93), preferably the core nucleotide sequence comprises 5' GGUUAGGGCUHGAAGUCGG 3' (SEQ. ID. No. 93).

17. The nucleic acid molecule according to any of claims 1 and 16, whereby the nucleic acid molecule comprises in 5'->3' direction a first stretch of nucleotides, the core nucleotide sequence, and a second stretch of nucleotides or the nucleic acid molecule comprises in 5'->3' direction a second stretch of nucleotides, the core nucleotide sequence, and a first stretch of nucleotides.

18. The nucleic acid molecule according to claim 17, whereby at least a part of said first stretch and at least a part of said second stretch of nucleotides optionally hybridize with each other, whereby upon hybridization a double-stranded structure is formed.

19. The nucleic acid molecule according to any of claims 17 to 18, whereby the length of the first stretch and the length of the second stretch is individually and independently 0 to 17 nucleotides, preferably 4 to 10 nucleotides and more preferably 4 to 6 nucleotides.

20. The nucleic acid molecule according to any of claims 18 and 19, whereby the double-stranded structure comprises 4 to 10 base pairs, preferably 4 to 6 base pairs, more preferably 5 base pairs.

21. The nucleic acid molecule according to any of claims 17 to 20, whereby the first stretch of nucleotides comprises a nucleotide sequence of 5' RKSBUSNVGR 3' (SEQ.ID.No. 120) and the second stretch of nucleotides comprises a nucleotide sequence of 5' YYNRCASSMY 3' (SEQ.ID.No. 121),

preferably the first stretch of nucleotides comprises a nucleotide sequence of 5' RKSBUGSVGR 3' (SEQ.ID.No. 122) and the second stretch of nucleotides comprises a nucleotide sequence of 5' YCNRCASSMY 3' (SEQ.ID.No. 123).

22. The nucleic acid molecule according to any of claims 17 to 20, whereby the first stretch of nucleotides comprises a nucleotide sequence of 5' XsSSSV 3' (SEQ.ID.No. 124) and the second stretch of nucleotides comprises a nucleotide sequence of 5' BSSSXs 3' (SEQ.ID.No. 125), whereby X_s is either absent or is S.

23. The nucleic acid molecule according to any of claims 17 to 20, whereby the first stretch of nucleotides comprises a nucleotide sequence of 5' SSSSR 3' (SEQ.ID.No. 130) and the second stretch of nucleotides comprise a nucleotide sequence of 5' YSBSS 3' (SEQ.ID.No. 131).

24. The nucleic acid molecule according to any of claims 17 to 20, whereby the first stretch of nucleotides comprises a nucleotide sequence of 5' CGUGCGCUUGAGAUAGG 3' and the second stretch of nucleotides comprises a nucleotide sequence of 5' CUGAUUCUCACG 3'.

25. The nucleic acid molecule according to any of claims 17 to 20, whereby the first stretch of nucleotides comprises a nucleotide sequence of 5' UGAGAUAGG 3' and the second stretch of nucleotides comprises a nucleotide sequence of 5' CUGAUUCUCA 3'.

26. The nucleic acid molecule according to any of claims 17 to 20, whereby the first stretch of nucleotides comprises a nucleotide sequence of 5' GAGAUAGG 3' and the second stretch of nucleotides comprises a nucleotide sequence of 5' CUGAUUCUC 3'.

27. The nucleic acid molecule according to any of claims 1 and 16 to 26, whereby the nucleic acid molecule has a nucleic acid sequence according to any of SEQ.ID.Nos. 79 to 89, 94 to 119, and 134 to 136.

28. The nucleic acid molecule according to claim 1, whereby the nucleic acid molecule has a nucleic acid sequence according to any of SEQ.ID.Nos. 142 to 144.

29. The nucleic acid molecule according to any of claims 1 to 28, whereby the nucleic acid molecule is an antagonist to SDF-1.

30. The nucleic acid molecule according to any of claims 1 to 29, whereby the nucleic acid molecule is an antagonist of the SDF-1 receptor system, whereby preferably the SDF-1 receptor of the SDF-1 receptor system is the CXCR4 receptor.

31. The nucleic acid molecule according to any of claim 1 to 30, whereby the SDF-1 is a human SDF-1, whereby preferably SDF-1 comprises an amino acid sequence according to SEQ ID No. 1.

32. The nucleic acid molecule according to any of claims 1 to 31, wherein the nucleic acid molecule comprises a modification, preferably the modification is selected from the group comprising a HES moiety and a PEG moiety.

33. The nucleic acid molecule according to any of claims 1 to 32, whereby the nucleotides of the nucleic acid molecule are L-nucleotides, preferably the nucleotides of the sequences according to any of SEQ.ID.No. 19, 20, 21, 22, 57, 58, 90, 91, 92, and 93.

34. The nucleic acid molecule according to any of claims 1 to 33 for use in a method of treating a disease.

35. A pharmaceutical composition comprising a nucleic acid molecule according to any of claims 1 to 34 and optionally a further constituent, whereby the further constituent is selected from the group comprising pharmaceutically acceptable excipients and pharmaceutically active agents.

36. Use of a nucleic acid molecule according to any of claims 1 to 34 for the manufacture of a medicament.

37. The nucleic acid molecule according to claim 34, whereby the disease is mediated by SDF-1, preferably such disease or disorder is selected from the group comprising back-of-the-eye diseases like diabetic retinopathy and age-related macular degeneration; cancer of breast, ovaries, prostate, pancreas, thyroid, nasopharynx, colon, lung, and stomach; osteosarcoma; melanoma; glioma; medullo- and neuroblastoma; leukemia; WHIM syndrome; immunologic deficiency syndromes; pathologic neovascularization; inflammation; multiple sclerosis; rheumatoid arthritis / osteoarthritis and nephritis.

38. The nucleic acid molecule according to any one of claims 1 to 33 whereby the nucleic acid molecule is for use in inhibiting angiogenesis, neovascularizytion, inflammation and metastasis.

39. Use of a nucleic acid molecule according to any of claims 1 to 34 for the manufacture of a diagnostic means.

40. Use according to claim 39, whereby the diagnostic means is for the diagnosis of a disease, whereby the disease, whereby such disease is mediated by SDF-1, preferably such disease is selected from the group comprising back-of-the-eye diseases like diabetic retinopathy and age-related macular degeneration; cancer of breast, ovaries, prostate, pancreas, thyroid, nasopharynx, colon, lung, and stomach; osteosarcoma; melanoma; glioma; medullo- and neuroblastoma; leukemia; WHIM syndrome; immunologic deficiency syndromes; pathologic neovascularization; inflammation; multiple sclerosis; rheumatoid arthritis / osteoarthritis and nephritis.

41. Use according to claim 39, whereby the diagnostic means is for diagnosing angiogenesis, neovascularization, inflammation and/or metastasis.

42. A complex comprising SDF-1 and a nucleic acid molecule according to any of claims 1 to 34, whereby preferably the complex is a crystalline complex.

43. Use of a nucleic acid molecule according to any of claims 1 to 34 for the *in vitro* detection of SDF-1.

44. A method for the screening of a SDF-1 antagonist or a SDF-1 agonist comprising the following steps:

- providing a candidate SDF-1 antagonist and/or a candidate SDF-1 agonist,
- providing a nucleic acid molecule according to any of claims 1 to 34,
- providing a test system which provides a signal in the presence of a SDF-1 antagonist and/or a SDF-1 agonist wherein the test system is a cell culture, and
- determining whether the candidate SDF-1 antagonist is a SDF-1 antagonist and/or whether the candidate SDF-1 agonist is a SDF-1 agonist.

45. A method for the screening of a SDF-1 agonist and/or a SDF-1 antagonist comprising the following steps:

- providing SDF-1 immobilised to a phase, preferably a solid phase,
- providing a nucleic acid molecule according to any of claims 1 to 34, preferably a nucleic acid molecule according to any of claims 1 to 34 which is labelled,
- adding a candidate SDF-1 agonist and/or a candidate SDF-1 antagonist, and
- determining whether the candidate SDF-1 agonist is a SDF-1 agonist and/or whether the candidate SDF-1 antagonist is a SDF-1 antagonist.

46. Use according to claim 36, wherein the medicament is for treating a disease or disorder mediated by SDF-1.

47. Use according to claims 36 or 46, wherein the medicament is for treating a disease or disorder selected from the group comprising back-of-the-eye diseases like diabetic retinopathy and age-related macular degeneration; cancer of breast, ovaries, prostate, pancreas, thyroid, nasopharynx, colon, lung, and stomach; osteosarcoma; melanoma; glioma; medullo- and neuroblastoma; leukemia; WHIM syndrome; immunologic deficiency syndromes; pathologic neovascularization; inflammation; multiple sclerosis; rheumatoid arthritis/ osteoarthritis and nephritis.

48. Use according to claim 36, whereby the medicament is for inhibiting angiogenesis, neovascularization, inflammation and metastasis.