Type A SDF-1 binding nucleic acids

Name	nt.	Sequence: 5′-3′	Comp.
192-A10-001	38	**GCUGUG**AAAGCAACAUGUCAA-UGAAAGGUAGC**CGCAGC**	
192-G10	38	**GCUGUG**AAAGUAACAUGUCAA-UGAAAGGUAAC**CACAGC**	<
192-F10	38	**GCUGUG**AAAGUAACACGUCAA-UGAAAGGUAAC**CGCAGC**	<
192-B11	38	**GCUGUG**AAAGUAACACGUCAA-UGAAAGGUAAC**CACAGC**	=
192-C9	38	**GCUGUA**AAAGUAACAUGUCAA-UGAAAGGUAAC**UACAGC**	<
192-E10	38	**GCUGUA**AAAGUAACAAGUCAA-UGAAAGGUAAC**UACAGC**	<
192-C10	38	**GCUGUG**AAAGUAACAAGUCAA-UGAAAGGUAAC**CACAGC**	=
192-D11	38	**GCAGUG**AAAGUAACAUGUCAA-UGAAAGGUAAC**CACAGC**	<
192-G11	38	**GCUGUG**AAAGUAACAUGUCAA-UGAAAGGUAAC**CACUGC**	<
192-H11	38	**GCUAUG**AAAGUAACAUGUCAA-UGAAAGGUAAC**CAUAGC**	<
192-D10	38	**GCUGCG**AAAGCGACAUGUCAA-UGAAAGGUAGC**CGCAGC**	<<
192-E9	38	**GCUGUG**AAAGCAACAUGUCAA-UGAAAGGUAGC**CACAGC**	<<
192-H9	38	**GCUGUG**AAAGUAACAUGUCAA-UGAAAGGUAGC**CGCAGC**	<<
191-A6	39	**AGCGUG**AAAGUAACACGUAAAAUGAAAGGUAAC**CACGCU**	<

terminal nucleotides that may hybridize to each other (bold)

nucleotides which may mainly comprise a SDF-binding motif

nt.:= nucleotides [Geben Sie ein Zitat aus dem Dokument oder die Zusammenfassung eines interessanten Punkts ein. Sie können das Textfeld an einer beliebigen Stelle im Dokument positionieren. Verwenden Sie die Registerkarte 'Zeichentools', wenn Sie das Format des Textfelds 'Textzitat' ändern möchten.]

Comp.:= Clones were tested as aptamers in a competition binding assay vs. 192-A10-001

=:= equal binding affinity as 192-A10-001; <:= weaker binding affinity than 192-A1-001

<<:= much weaker binding affinity than 192-A10-001

Fig. 1

Derivatives of Type A SDF Binding Nucleic Acid 192-A10-001

Name	nt.	Sequence: 5′-3′	Comp.	PD: K_D [nM]	TAX IC_{50} [nM]
192-A10-001	38	**GCUGUG**AAAGCAACAUGUCAAUGAAAGGUAGC**CGCAGC**		1.5	0.1 - 0.2
192-A10-002	36	**CUGUG**AAAGCAACAUGUCAAUGAAAGGUAGC**CGCAG**	=		=
192-A10-003	34	**UGUG**AAAGCAACAUGUCAAUGAAAGGUAGC**CGCA**	<		<
192-A10-004	32	**GUG**AAAGCAACAUGUCAAUGAAAGGUAGC**CGC**	<<		<<
192-A10-005	30	**UG**AAAGCAACAUGUCAAUGAAAGGUAGC**CG**	<<		<<
192-A10-006	28	**G**AAAGCAACAUGUCAAUGAAAGGUAGC**C**	<<<		
192-A10-007	26	AAAGCAACAUGUCAAUGAAAGGUAGC	i.a.		

terminal nucleotides at the 5′- and the 3′-end that may hybridize to each other (bold) **nt.:=** nucleotides

nucleotides which may mainly comprise a SDF-binding motif **i.a.:=** inactive **=:=** equal binding affinity as 192-A10-001

</<</<<<:= weaker (<), much weaker (<<) or very much weaker (<<<) binding affinity than 192-A1-001

Comp.:= Clones were tested as aptamers in a competition binding assay vs. 193-A10-001

PD.:= Clones were tested as aptamers in a pull-down binding assay

TAX:= Clones were tested as Spiegelmers in a cell culture *in vitro* chemotaxis assay

Fig. 2A

Derivatives of Type A SDF Binding Nucleic Acid 192-A10-001

Name	nt.	Sequence: 5′-3′	Comp.	PD: K_D [nM]	TAX IC_{50} [nM]
192-A10-001	38	**GCUGUG**AAAGCAACAUGUCAAUGAAAGGUAGC**CGCAGC**		1.5	0.1 - 0.2
192-A10-002	36	**CUGUG**AAAGCAACAUGUCAAUGAAAGGUAGC**CGCAG**	=		=
192-A10-008	36	**GCGUG**AAAGCAACAUGUCAAUGAAAGGUAGC**CGCGC**	=	1.5	=
192-A10-015	36	**GCGCG**AAAGCAACAUGUCAAUGAAAGGUAGC**CGCGC**	<	4.6	
192-A10-014	34	**GCGG**AAAGCAACAUGUCAAUGAAAGGUAGC**CCGC**	<	8.0	=
192-A10-016	34	**CGUG**AAAGCAACAUGUCAAUGAAAGGUAGC**CGCG**	<		
192-A10-017	34	**GCGC**AAAGCAACAUGUCAAUGAAAGGUAGC**GUGC**	i.a.		
192-A10-018	34	**GUGC**AAAGCAACAUGUCAAUGAAAGGUAGC**GCGC**	<<<		
192-A10-019	34	**CGCG**AAAGCAACAUGUCAAUGAAAGGUAGC**CGUG**	<<		
192-A10-020	34	**GGGC**AAAGCAACAUGUCAAUGAAAGGUAGC**GCCC**	<<*		
192-A10-021	34	**GGCC**AAAGCAACAUGUCAAUGAAAGGUAGC**GGCC**	<<*		
192-A10-022	34	**GCCC**AAAGCAACAUGUCAAUGAAAGGUAGC**GGGC**	<<*		
192-A10-023	34	**CCCC**AAAGCAACAUGUCAAUGAAAGGUAGC**GGGG**	<<*		

terminal nucleotides at the 5′- and the 3′-end that may hybridize to each other (bold) **nt.:=** nucleotides

nucleotides which may mainly comprise a SDF-binding motif **i.a.:=** inactive **=:=** equal binding affinity as 192-A10-001/ -008

</<</<<:= weaker (<), much weaker (<<) or very much weaker (<<<) binding affinity than 192-A1-001/ -008

Comp.:= Clones were tested as aptamers in a competition binding assay vs. 192-A10-001 (* = except from 192-A10-020, -021, -022, and –023 which were tested vs. 193-A10-008 that has the identical binding affinity to SDF-1 as 192-A10-001)

PD.:= Clones were tested as aptamers in a pull-down binding assay

TAX:= Clones were tested as Spiegelmers in a cell culture *in vitro* chemotaxis assay

Fig. 2B

Type B SDF-1 binding nucleic acids

Name	nt.	Sequence: 5′-3′	C.
193-C2-001	47	**AGCGUG**GUGUGAUCUAGAUGUAGUGGCUGAUCCUAGUCAGG**UACGCU**	+
193-G2-001	47	**AGCGUG**GUGUGAUCUAGAUGUAUUGGCUGAUCCUAGUCAGG**UACGCU**	+
193-F2-001	47	**AGCGUG**GUGUGAUCUAGAUGUAAUGGCUGAUCCUAGUCAGG**UGCGCU**	+
193-G1-002	45	**GCGAG**GUGUGAUCUAGAUGUAGUGGCUGAUCCUAGUCAGG**UGCGC**	<<
193-D2-002	45	**GCGUG**GUGUGAUCUAGAUGUAGUGGCUGAUCCUAGUCAGG**UGCGC**	<
193-A1-002	45	GCA**UG**GUGUGAUCUAGAUGUAGUGGCUGAUCCUAGUCAGG**UG**CCC	<<<
193-D3-002	45	**GCGUG**GUGUGAUCUAGAUGUAAUGGCUGAUCCUAGUCAGG**GACGC**	<
193-B3-002	45	**GCGUG**GUGUGAUCUAGAUGUAGAGGCUGAUCCUAGUCAGG**UACGC**	<<
193-H3-002	45	**GCGUG**GUGUGAUCUAGAUGUAAAGGCUGAUCCUAGUCAGG**UACGC**	<
193-E3-002	45	**GCGUG**GUGUGAUCUAGAUGUAGUGGCUGUUCCUAGUCAGG**UAUGC**	<<
193-D1-002	45	**GCGUG**GUGUGAUCUAGAUGUAGUGGCUGAUCCUAGUUAGG**UACGC**	<<<

terminal nucleotides that may hybridize to each other (bold)

nucleotides which may mainly comprise a SDF-binding motif **nt.:=** nucleotides

C.:= Clones C2, G2, and F2 were tested as aptamers in a competition binding assay vs. 192-A10-001; all other clones were tested as aptamers in a competition binding assay vs. 193-G2-012 that has the identical binding affinity to SDF-1 as 193-G2-001 (see Fig. 4B)

+:= better binding affinity than 192-A10-001

</<</<<:= weaker (<), much weaker (<<) or very much weaker (<<<) binding affinity than 193-G2-001/ -012

Fig. 3

Derivatives of Type B SDF Binding Nucleic Acids 193-C2/G2-001

Name	nt.	Sequence: 5'-3'	Comp.	PD K_D [nM]	Biacore K_D [nM]
193-G2-001	47	**AGCGUG**GUGUGAUCUAGAUGUAUUGGCUGAUCCUAGUCAGG**UACGCU**		0.3	0.5
193-C2-001	47	**AGCGUG**GUGUGAUCUAGAUGUAGUGGCUGAUCCUAGUCAGG**UACGCU**	=		0.6
193-C2-002	45	**GCGUG**GUGUGAUCUAGAUGUAGUGGCUGAUCCUAGUCAGG**UACGC**	=		0.8
193-C2-003	43	**CGUG**GUGUGAUCUAGAUGUAGUGGCUGAUCCUAGUCAGG**UACG**	<		
193-C2-004	41	**GUG**GUGUGAUCUAGAUGUAGUGGCUGAUCCUAGUCAGG**UAC**	<<		
193-C2-005	39	**UG**GUGUGAUCUAGAUGUAGUGGCUGAUCCUAGUCAGG**UA**	<<<		
193-C2-006	37	**G**GUGUGAUCUAGAUGUAGUGGCUGAUCCUAGUCAGG**U**	<<<		
193-C2-007	35	GUGUGAUCUAGAUGUAGUGGCUGAUCCUAGUCAGG	i.a.		

terminal nucleotides at the 5'- and the 3'-end that may hybridize to each other (bold) **nt.:=** nucleotides

nucleotides which may mainly comprise a SDF-binding motif **i.a.:=** inactive **=:=** equal binding affinity as 193-G2-001

</<</<<<:= weaker (<), much weaker (<<) or very much weaker (<<<) binding affinity than 193-G2-001

Comp.:= Clones were tested as aptamers in a competition binding assay vs. 193-G2-001

PD.:= Clones were tested as aptamers in a pull-down binding assay

Fig. 4A

Derivatives of Type B SDF Binding Nucleic Acid 193-C2/G2-001

Name	nt.	Sequence: 5'-3'	Comp.	PD K_D [nM]	Biacore K_D [nM]
193-G2-001	47	**AGCGUG**GUGUGAUCUAGAUGUAUUGGCUGAUCCUAGUCAGG**UACGCU**		0.3	0.5
193-G2-012	45	**GCGUG**GUGUGAUCUAGAUGUAUUGGCUGAUCCUAGUCAGG**UACGC**	=	0.3	
193-G2-013	45	**GCGCG**GUGUGAUCUAGAUGUAUUGGCUGAUCCUAGUCAGG**CGCGC**	<<	5.3	
193-G2-014	43	**GCGC**GUGUGAUCUAGAUGUAUUGGCUGAUCCUAGUCAGG**GCGC**	<<	4.7	
193-G2-015	43	**GGGC**GUGUGAUCUAGAUGUAUUGGCUGAUCCUAGUCAGG**GCCC**	<<*	4.5	
193-G2-016	43	**GGCC**GUGUGAUCUAGAUGUAUUGGCUGAUCCUAGUCAGG**GGCC**	<<*	4.2	
193-G2-017	43	**GCCC**GUGUGAUCUAGAUGUAUUGGCUGAUCCUAGUCAGG**GGGC**	<<*	4.2	

terminal nucleotides at the 5'- and the 3'-end that may hybridize to each other (bold) **nt.:=** nucleotides

nucleotides which may mainly comprise a SDF-binding motif **=:=** equal binding affinity as 193-G2-001/ -012

</<</<<<:= weaker (<), much weaker (<<) or very much weaker (<<<) binding affinity than 193-G2-001 and 193-G2-012, respectively

Comp.:= Clones were tested as aptamers in a competition binding assay vs. 193-G2-001 (* = except from 193-G2-015, -016, -017 which were tested in a competition binding assay vs. 193-G2-012 that has the identical binding affinity to SDF-1 as 193-G2-001)

PD.:= Clones were tested as aptamers in a pull-down binding assay

Fig. 4B

Type C SDF-1 binding nucleic acids

Name	nt.	Sequence: 5'-3'	Comp.
197-B2	39	**GUGCUGCGGG**GGUUAGGGCUAGAAGUCGG**CCUGCAGCAC**	<
191-D5-001	39	**AGCGUGGCGA**GGUUAGGGCUAGAAGUCGG**UCGACACGCU**	<
197-H1	39	**GUGUUGCGGA**GGUUAGGGCUAGAAGUCGG**UCAGCAGCAC**	<
190-D3	48	**CGUGCGGCCUAAGA**GGUUAGGGCUUAAAGUCGG**UCUUUGGCCAACACG**	<<
190-A3-001	48	**CGUG**CGCUUGAGAUAGGGGUUAGGGCUUAAAGUCGGCUGAUUCU**CACG**	<
190-A3-001*	48	CGUGCGCU**UGAGA**UAGGGGUUAGGGCUUAAAGUCGGCUGAU**UCUCA**CG	<
190-A2	48	**CGUGAUUGGU**GAGGGGUUAGGGCUUGAAGUCGG**CCUUGUCCAGUCACG**	<<
191-A5	39	**AGCGUGAAGG**GGUUAGGGCUCGAAGUCGG**CUGACACGCU**	<<
197-H3	39	**GUGCUGCGGG**GGUUAGGGCUCGAAGUCGG**CCCGCAGCAC**	<
197-B1	39	**GUGUU**CCCGGGGUUAGGGCUUGAAGUCGG**CCGGCAGCAC**	<<
197-E3	39	**GUGUUGCAGG**GGUUAGGGCUUGAAGUCGG**CCUGCAGCAC**	<
197-H2	39	**GUGCUGCGGG**GGUUAGGGCUCAAAGUCGG**CCUGCAGCAC**	<<
197-D1	38	**GUGCUGCCGG**GGUUAGGGCUAA-AGUCGG**CCGACAGCAC**	<<
197-D2	39	**GUGCUGUGGG**GGUCAGGGCUAGAAGUCGG**CCUGCAGCAC**	<<

terminal nucleotides that may hybridize to each other (bold)

nucleotides which may mainly comprise a SDF-binding motif

nt.:= nucleotides **Comp.:=** Clones were tested as aptamers in a competition binding assay vs. 192-A10-001

=:= equal binding affinity as 192-A10; <:= weaker binding affinity than 192-A10 <<:= much weaker binding affinity than 192-A10

*:= alternative hybridization

Fig. 5

Derivatives of Type C SDF Binding Nucleic Acid 190-A3-001

Name	nt.	Sequence: 5'-3'	Comp.
190-A3-001	48	**CGUG**CGCUUGAGAUAGG GGUUAGGGCUUAAAGUCGG CUGAUUCU**CACG**	
190-A3-001*	48	CGUGCGCU**UGAGA**UA**GG** GGUUAGGGCUUAAAGUCGG **CU**GAU**UCUCA**CG	
190-A3-003	38	**UGAGA**UA**GG** GGUUAGGGCUUAAAGUCGG CUGAU**UCUCA**	=
190-A3-004	36	**GAGA**UA**GG** GGUUAGGGCUUAAAGUCGG **CU**GAU**UCUC**	=
190-A3-007	29	**GG** GGUUAGGGCUUAAAGUCGG **CU**GAUUCU	<<<

terminal nucleotides at the 5'- and the 3'-end that may hybridize to each other (bold) **nt.:=** nucleotides

nucleotides which may mainly comprise a SDF-binding motif **=:=** equal binding affinity as 190-A3-001

</<</<<<:= weaker (<), much weaker (<<) or very much weaker (<<<) binding affinity than 190-A3-001

Comp.:= Clones were tested as aptamers in a competition binding assay vs. 190-A3-001

*:= alternative hybridization of the terminal nucleotides

Fig. 6

Derivatives of Type C SDF Binding Nucleic Acid 191-D5-001

Name	nt.	Sequence: 5′-3′	Comp. vs. 191-D5-001	Comp. vs. 191-D5-007	Biacore K_D [nM]
191-D5-001	39	**AGCGUGGCGA**GGUUAGGGCUAGAAGUCGG**UCGACACGCU**		<	0.73
191-D5-002	37	**GCGUGGCGA**GGUUAGGGCUAGAAGUCGG**UCGACACGC**	=		
191-D5-003	35	**CGUGGCGA**GGUUAGGGCUAGAAGUCGG**UCGACACG**	=		
191-D5-004	33	**CG-GGCGA**GGUUAGGGCUAGAAGUCGG**UCGAC-CG**	<		
191-D5-005	33	**CG-GGCGA**GGUUAGGGCUAGAAGUCGG**UCGCC-CG**	=		
191-D5-006	31	**CG--GCGA**GGUUAGGGCUAGAAGUCGG**UCGC--CG**	=		
191-D5-007	29	**CG--G-GA**GGUUAGGGCUAGAAGUCGG**UC-C--CG**	+		0.75
191-D5-010	27	**G--G-GA**GGUUAGGGCUAGAAGUCGG**UC-C--C**		<	

terminal nucleotides at the 5′- and the 3′-end that may hybridize to each other (bold) **nt.:=** nucleotides

nucleotides which may mainly comprise a SDF-binding motif **=:=** equal binding affinity as 191-D5-001/ -007

</<</<<:= weaker (<), much weaker (<<) or very much weaker (<<<) binding affinity than 191-D5-001/ -007

Comp.:= Clones were tested as aptamers in a competition binding assay vs. 191-D5-001 or 191-D5-007 whereas both clones have the identical binding affinity to SDF-1 as 191-D5-001

Fig. 7A

Derivatives of Type C SDF Binding Nucleic Acid 191-D5-001

Name	nt.	Sequence: 5′-3′	Comp. vs. 191-D5-007
191-D5-007	29	**CG--G-GA**GGUUAGGGCUAGAAGUCGG**UC-C--CG**	
191-D5-010	27	**G--G-GA**GGUUAGGGCUAGAAGUCGG**UC-C--C**	<
191-D5-017	27	**CCGC**GGUUAGGGCUAGAAGUCGG**GCGG**	<
191-D5-029	27	**CCCG**GGUUAGGGCUAGAAGUCGG**CGGG**	<
191-D5-024	27	**GGCG**GGUUAGGGCUAGAAGUCGG**CGCC**	<
191-D5-017-29a	29	**CCCGC**GGUUAGGGCUAGAAGUCGG**GCGGG**	<
191-D5-017-29b	29	**GCCGC**GGUUAGGGCUAGAAGUCGG**GCGGC**	<
191-D5-019-29a	29	**CCCCG**GGUUAGGGCUAGAAGUCGG**CGGGG**	<
191-D5-024-29a	29	**CGGCG**GGUUAGGGCUAGAAGUCGG**CGCCG**	=
191-D5-024-29b	29	**GGGCG**GGUUAGGGCUAGAAGUCGG**CGCCC**	=

terminal nucleotides at the 5′- and the 3′-end that may hybridize to each other (bold) **nt.:=** nucleotides

nucleotides which may mainly comprise a SDF-binding motif

=:= equal binding affinity as 191-D5-007

</<</<<:= weaker (<), much weaker (<<) or very much weaker (<<<) binding affinity than 191-D5-007

Comp.:= Clones were tested as aptamers in a competition binding assay vs. 191-D5-007

Fig. 7B

Derivatives of Type C SDF Binding Nucleic Acid 197-B2

Name	nt.	Sequence: 5′-3′	Comp.vs. 197-B2	Comp. vs. 191-D5-007	TAX IC_{50} [nM]
197-B2	39	**GUGCUGCGGG**GGUUAGGGCUAGAAGUCGG**CCUGCAGCAC**		=	0.1-0.2
197-B2-001	37	**UGCUGCGGG**GGUUAGGGCUAGAAGUCGG**CCUGCAGCA**	=		
197-B2-002	35	**GCUGCGGG**GGUUAGGGCUAGAAGUCGG**CCUGCAGC**	=		
197-B2-003	33	**CUGCGGG**GGUUAGGGCUAGAAGUCGG**CCUGCAG**	=		
197-B2-004	31	**UGCGGG**GGUUAGGGCUAGAAGUCGG**CCUGCA**	=		
197-B2-005	29	**GCGGG**GGUUAGGGCUAGAAGUCGG**CCUGC**	=		
197-B2-006	29	**GCCGG**GGUUAGGGCUAGAAGUCGG**CCGGC**	=	=	0.1-0.2
197-B2-006-31a	31	**GGCCGG**GGUUAGGGCUAGAAGUCGG**CCGGCC**		=	
197-B2-006-31b	31	**CGCCGG**GGUUAGGGCUAGAAGUCGG**CCGGCG**		=	

terminal nucleotides at the 5′- and the 3′-end that may hybridize to each other (bold) **nt.:=** nucleotides

nucleotides which may mainly comprise a SDF-binding motif **i.a.:=** inactive

=:= equal binding affinity as 197-B2 or 191-D5-007

</<</<<<:= weaker (<), much weaker (<<) or very much weaker (<<<) binding affinity than as 197-B2 or 191-D5-007

Comp.:= Clones were tested as aptamers in a competition binding assay vs. 197-B2 or 191-D5-007 whereas both clones have the identical binding affinity to SDF-1

TAX:= Clones were tested as Spiegelmers in a cell culture *in vitro* chemotaxis assay

Fig. 8

Other SDF-1 Binding Nucleic Acids (Type D SDF-1 Binding Nucleic Acids)

Name	nt.	Sequence: 5′-3′	PD K_D [nM]
194-A2-001	48	**CGUGG**UCCGUUGUGUCAGGUCUAUUCGCCCCGGUGCAGGGCAU**CCGCG**	12.0
196-B12-003	49	GCAGUGUGACGCGGACGUGAUAGGACAGAGCUGAUCCCGCUCAGGUGAG	7.6
196-B12-004	49	CAACAGCAGUGUGACGCGGACGUGAUAGGACAGAGCUGAUCCCGCUCAG	5.3

terminal nucleotides at the 5′- and the 3′-end that may hybridize to each other (bold) **nt.:=** nucleotides

PD.:= Clones were tested as aptamers in a pull-down binding assay

Fig. 9

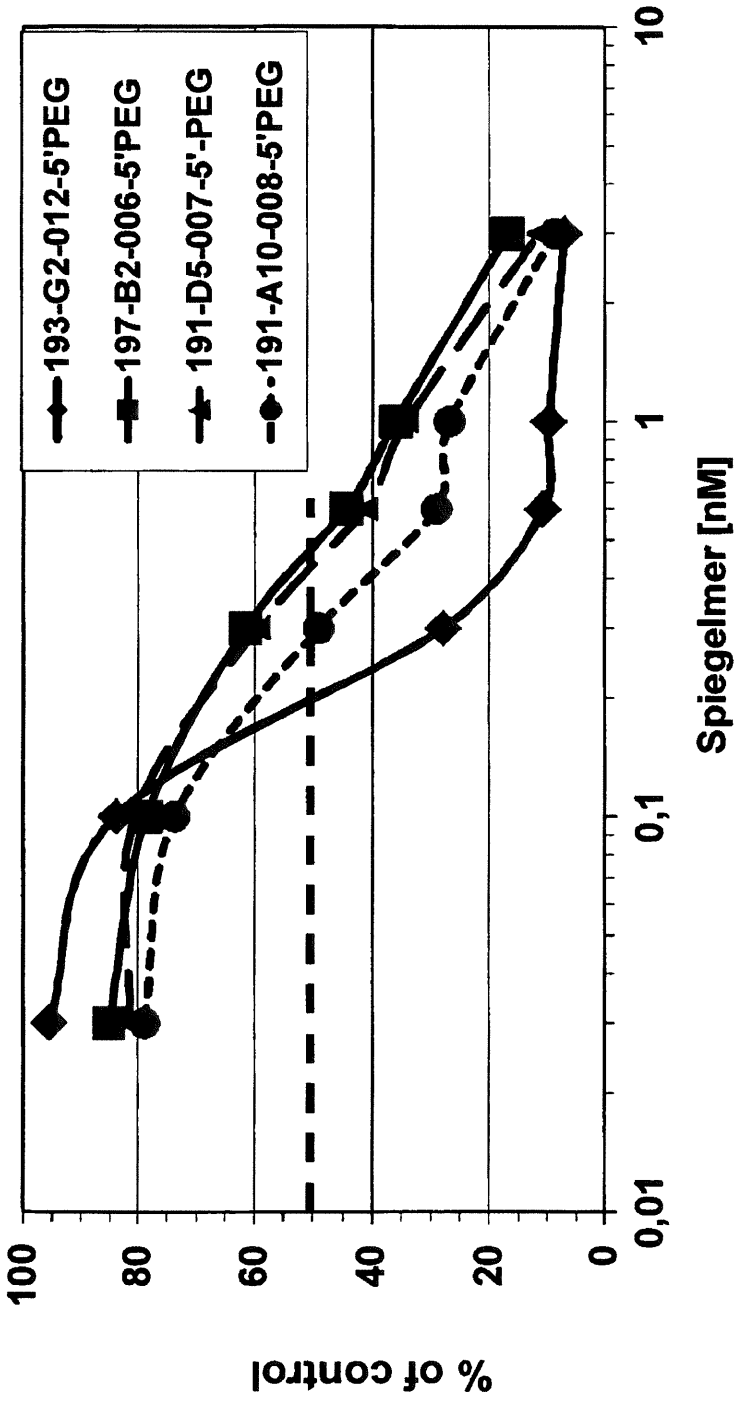
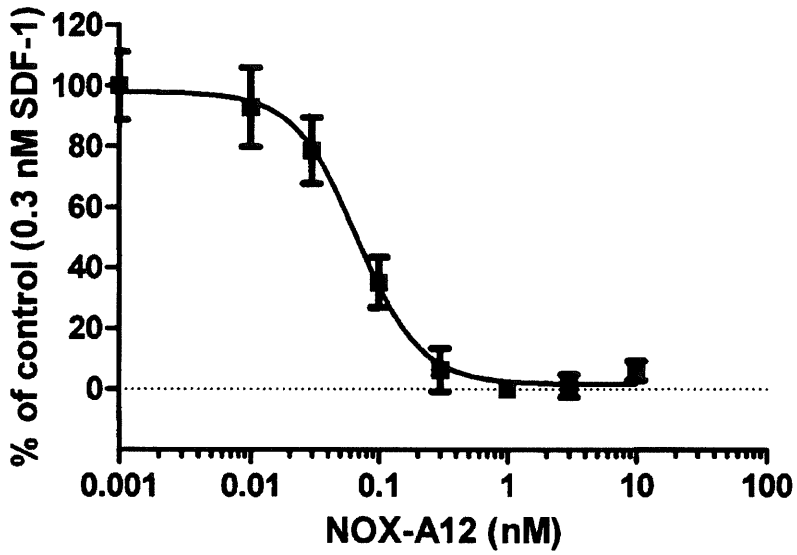

193-G2-012-5'PEG
197-B2-006-5'PEG
191-D5-007-5'-PEG
191-A10-008-5'PEG
% of control
100
80
60
40
20
0
0,01
0,1
1
10
Spiegelmer [nM]

Fig. 10

A


% of control (0.3 nM SDF-1)
120
100
80
60
40
20
0
0.001
0.01
0.1
1
10
100
NOX-A12 (nM)

B

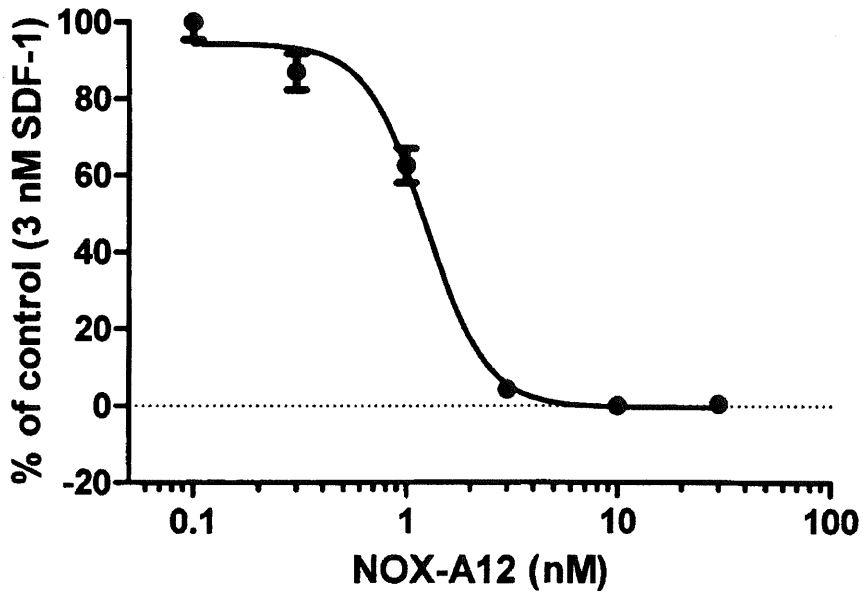

% of control (3 nM SDF-1)
100
80
60
40
20
0
-20
0.1
1
10
100
NOX-A12 (nM)

Fig. 11

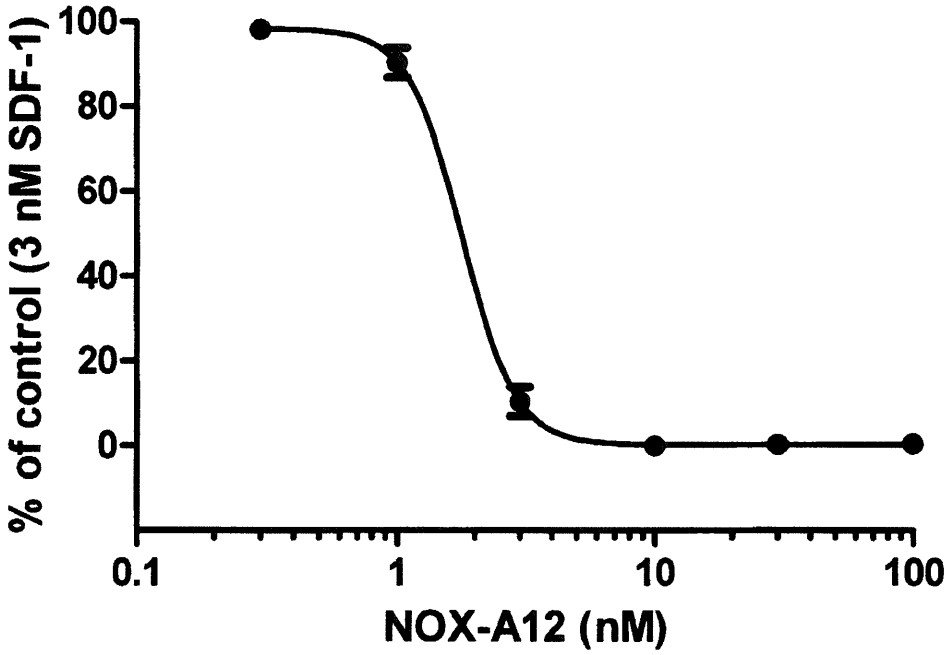


Fig. 12

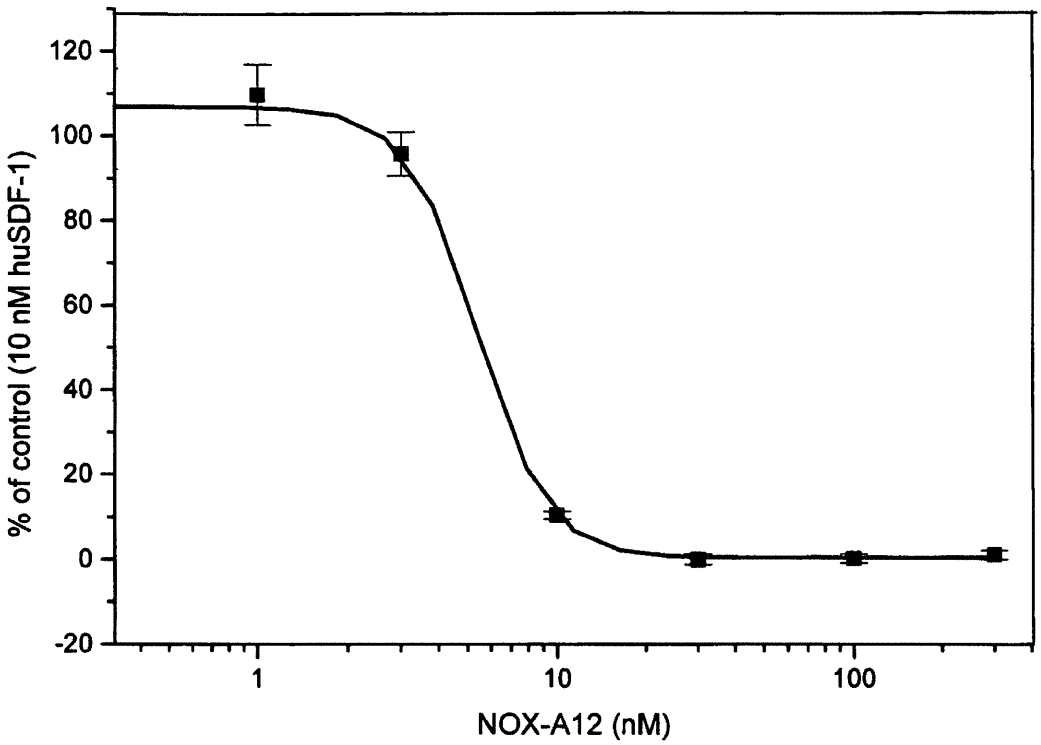

120
100
80
60
40
20
0
-20
% of control (10 nM huSDF-1)
1
10
100
NOX-A12 (nM)

Fig. 13

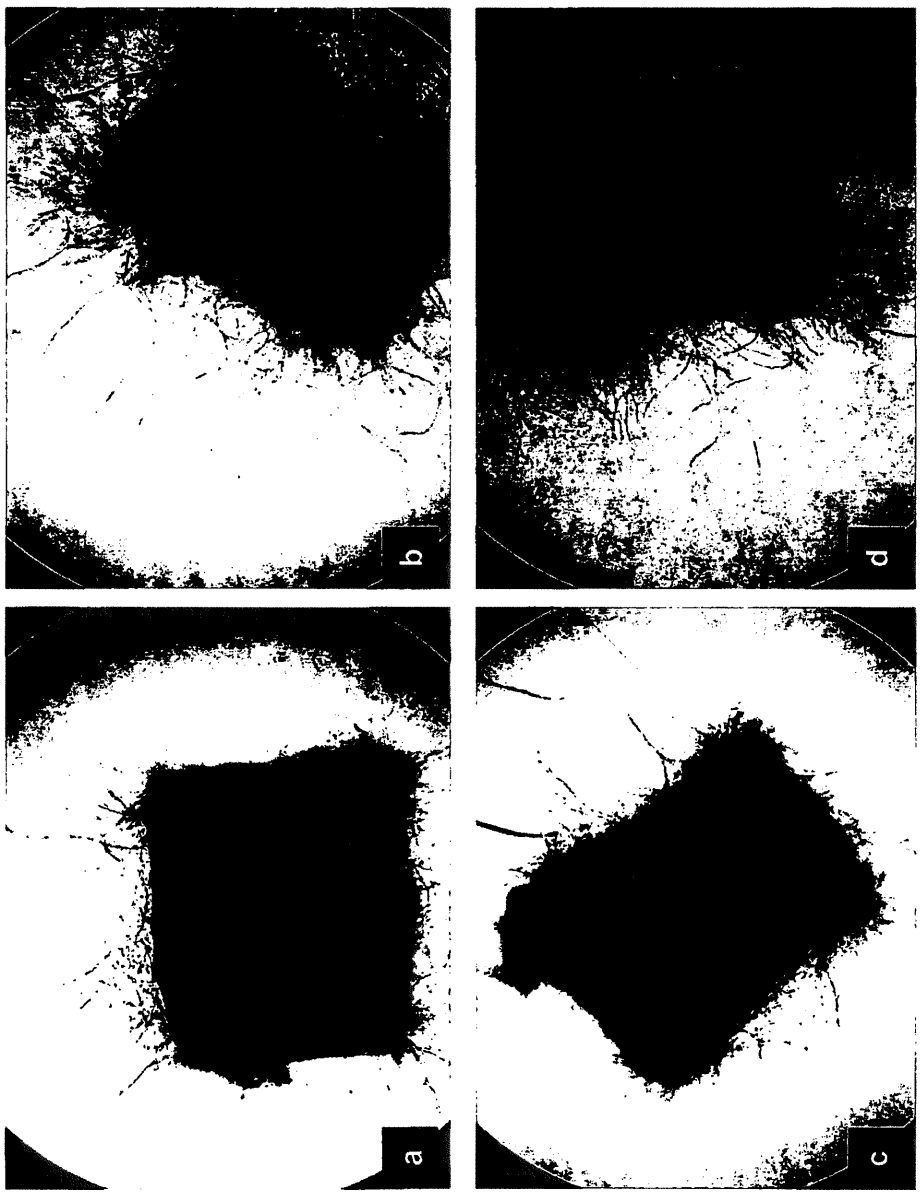


Fig. 14

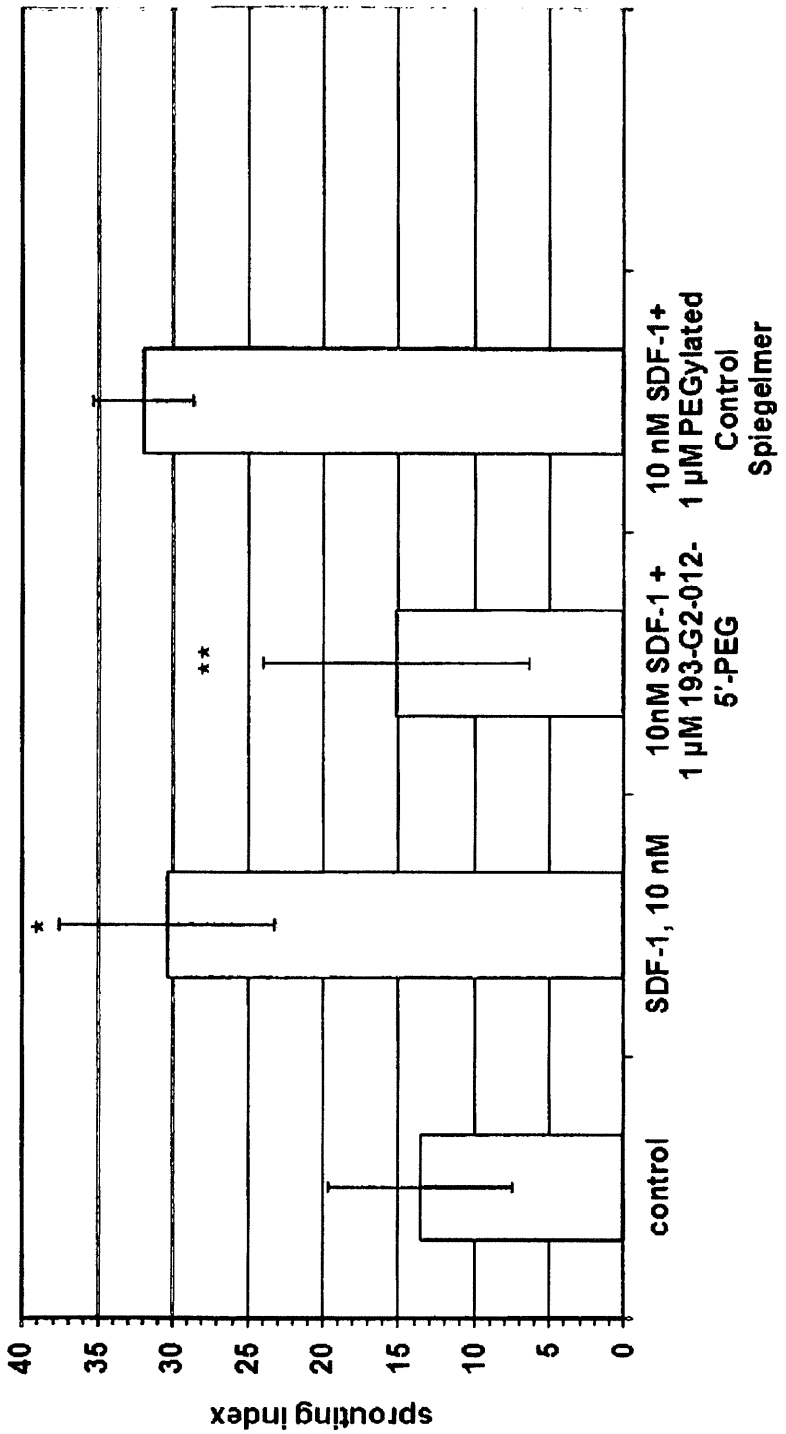

sprouting index
40
35
30
25
20
15
10
5
0
*
**
control
SDF-1, 10 nM
10nM SDF-1 + 1 µM 193-G2-012-5'-PEG
10 nM SDF-1+ 1 µM PEGylated Control Spiegelmer

Fig. 15

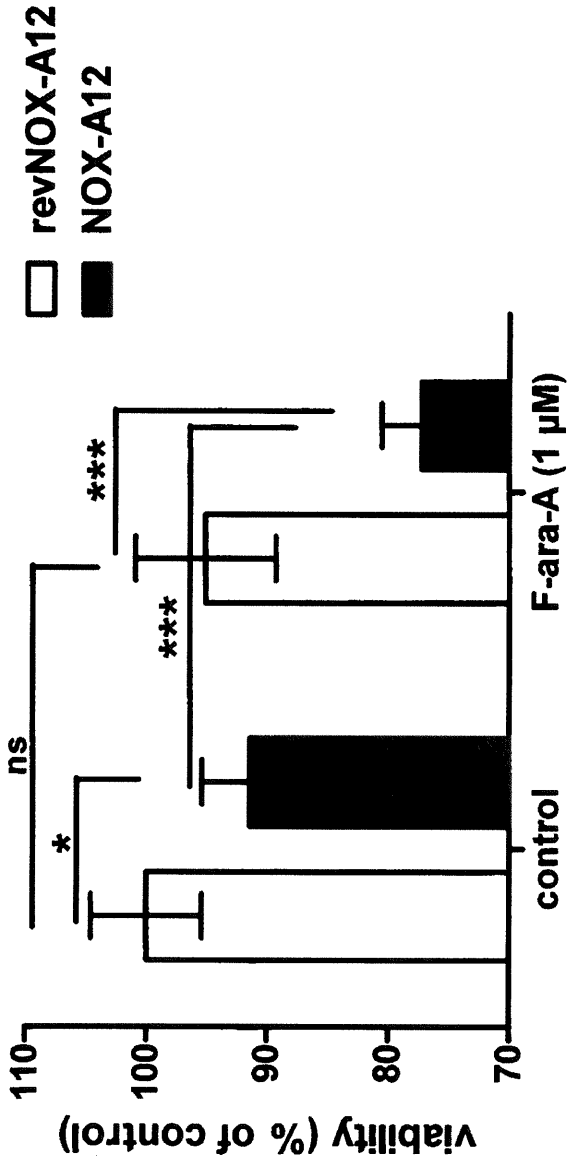

revNOX-A12
NOX-A12
viability (% of control)
110
100
90
80
70
ns
*
***
***
control
F-ara-A (1 µM)

Fig. 16

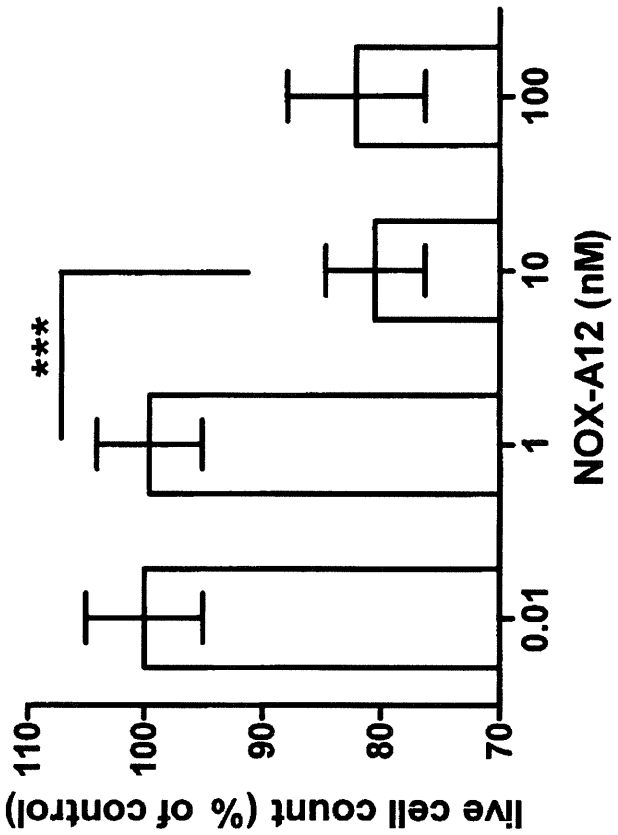

live cell count (% of control)
110
100
90
80
70
***
0.01
1
10
100
NOX-A12 (nM)

Fig. 17

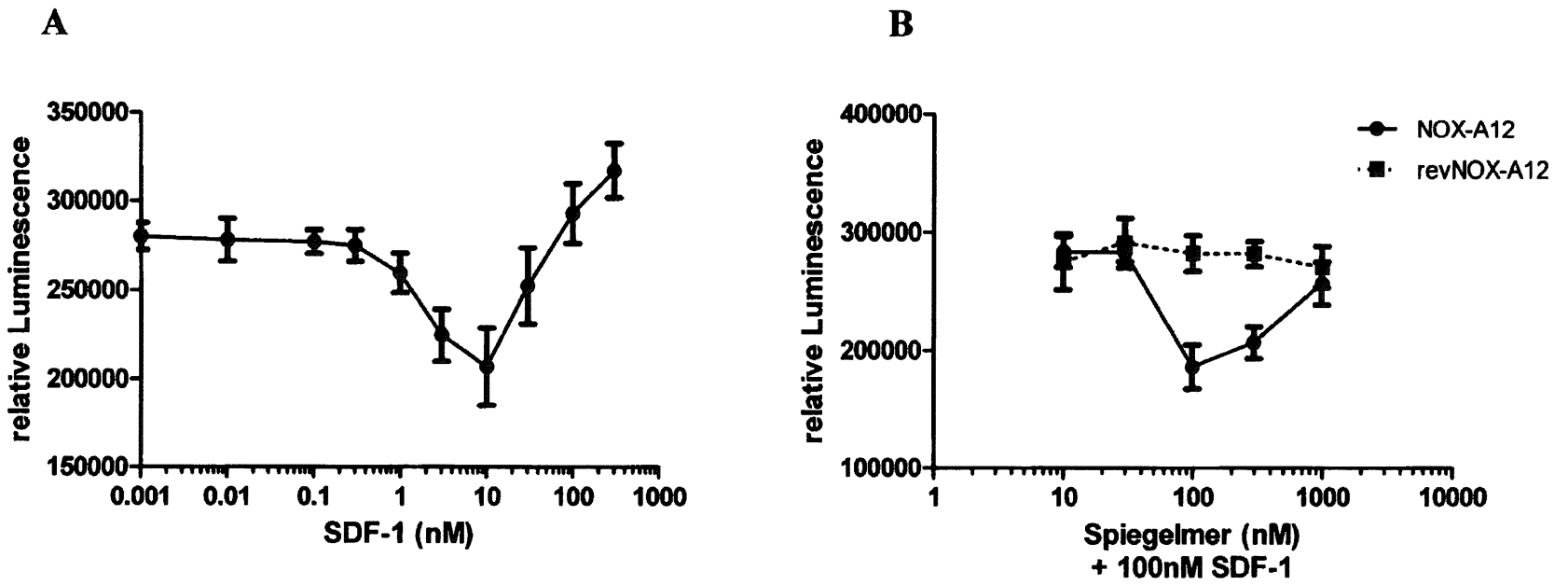

A
350000
300000
250000
200000
150000
relative Luminescence
0.001
0.01
0.1
1
10
100
1000
SDF-1 (nM)
B
400000
300000
200000
100000
relative Luminescence
1
10
100
1000
10000
Spiegelmer (nM)
+ 100nM SDF-1
NOX-A12
revNOX-A12

Fig. 18

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<130> SG3704A

<150> EP 10 009 397.0
<151> 2010-09-09

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Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Asn Arg Gln
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Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys
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Ala Leu Asn Lys
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His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn Thr Pro
20 25 30

Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Asn Arg Gln
35 40 45

Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys
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Ala Leu Asn Lys Arg Phe Lys Met
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1 5 10 15

His Ile Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn Thr Pro
20 25 30

Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Asn Arg Gln
35 40 45

Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys
50 55 60

Ala Leu Asn Lys
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1 5 10 15

His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn Thr Pro
20 25 30

Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Asn Arg Gln
35 40 45

Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys
50 55 60

Ala Leu Asn Lys Arg Phe Lys
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