Type 1A

	B1A	B2	B3	B4	B5	B6	B1B	Length (nt)	Pull-down	IC_{50} Ca^{++}-Assay [nM]
169-B1trc	AGCGUG	CCCGGA	*GUG*	GCA	GGGGGACGCGACC	**UGCAAUAAUG**	CACGCU	47	>> E10trc	8
169-F3trc	AGCGUG	CCCGGA	*GUG*	GCA	GGGGGACGCGACC	**UGCAAUUG**	CACGCU	45	>> E10trc	10
169-C1trc	AGCGUG	CCCGGA	*GUG*	GCA	GGGGGACGCGACC	**UGUAAUAAUG**	CACGCU	47	>> E10trc	
169-A3trc	AGCGUG	CCCGGU	*GUG*	GCA	GGGGGACGCGACC	**UGCAAUAAUG**	CGCGCU	47	>> E10trc	
169-B2trc	AGCGUG	CCCGGA	*GUA*	GCA	GGGGGGCGCGACC	**UGCAAUAAUG**	CACGCU	47	>> E10trc	
176-B12trc	AGCGUG	CCCGGU	*GUG*	GUA	GGGGGGCGCGAUC	**UACAAUUG**	CACGCU	45	>> E10trc	
176-D9trc	AGCGUG	CCCGGU	*GUG*	ACA	GGGGGGCGCGACC	**UGCAUUUG**	CACGCU	45	>> E10trc	
176-B10trc	AGCGUG	CCCGGU	*GUG*	GCA	GGGGGGCGCGACC	**UGUAUUUG**	CACGCU	45	> E10trc	
169-F2trc	AGCGUG	CCCGGA	*GUG*	GCA	GGGGGGCGCGACC	**UGCAAUAAUG**	CACGCU	47	> E10trc	14
176-B9trc	AGCGUG	CCCGGU	*GUG*	GCA	GGGGGGCGCGACC	**UGCAAUUG**	CACGCU	45	> E10trc	
176-H9trc	AGCAUG	CCCGGU	*GUG*	GCA	GGGGGGCGCGACC	**UGCAUUUG**	CAUGCU	45	> E10trc	
176-E10trc	AGCGUG	CCCGGU	*GUG*	GUA	GGGGGGCGCGACC	**UACAUUUG**	CACGCU	45	5 nM	4-5

> E10trc, weaker binding than 176-E10trc as determined in competition assay
>> E10trc, much weaker binding than 176-E10trc as determined in competition assay

Fig. 1

Type 1B

								Length (nt)	Pull-down	IC_{50} Ca^{++}-Assay [nM]
176-G9trc	AGUGUG	CCAGCU	*GUG*	AUG	GGGGGGCGCGACC	**CAUUUUA**	CACACU	44	> C9trc	
176-F9trc	AGUGUG	CCAGC	*GUG*	AUG	GGGGGGCGCGACC	**CAUUUUA**	CACACU	43	> C9trc	6
176-C11trc	AGUGUG	CGAGC	*GUG*	AUG	GGGGGGCGCGACC	**CAUUUUA**	CAUACU	43	> C9trc	
176-E11trc	AGUGUG	CCAGC	*GUG*	AUG	GGGGGGCGCGACC	**CAUUUUA**	CAUACU	43	> C9trc	
176-D10trc	AGUAUG	CCAGC	*GUG*	AUG	GGGGGGCGCGACC	**CAUUUA**	CAUACU	42	> C9trc	30
176-H10trc	AGUGUG	CCAG U	*GUG*	AUG	GGGGGGCGCGACC	**CAUUUUA**	CACACU	43	= C9trc	6
176-C9trc	AGCGUG	CCAG U	*GUG*	AUG	GGGGGGCGCGACC	**CAUUUUA**	CACGCU	43	5 nM	4-5
Boxes	B1A	B2	*B3*	B4	B5	**B6**	B1B			

= C9trc, similar binding as 176-C9trc as determined in competition assay
> C9trc, weaker binding than 176-C9trc as determined in competition assay

Fig. 2

Type 2

				Length (nt)	Pull-down	IC_{50} Ca^{++}-Assay	IC_{50} Chemotaxis
180-B1-001	ACGCA	CGUCCCUCACCGGUGCAAGUGAAGCCGCGGCUC	UGCGU	43	> D1-002		
180-A4-002	ACGCA	CCUCCCUCACCGGUGCAAGUGAAGCCGUGGCUC	UGCGC	43	> D1-002		
180-D1-002	ACGCA	CGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUC	UGCGU	43	0.7 nM	5 nM	< 1 nM
Boxes	B1A	B2	B1B				

Derivatives of 180-D1-002

				Length (nt)	Pull-down	IC_{50} Ca^{++}-Assay	IC_{50} Chemotaxis
180-D1-011	GCA	CGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUC	UGCGU	41	= D1-002	5 nM	1.2 nM
180-D1-012	ACGCA	CGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUC	UGC	41	= D1-002	6 nM	2.6 nM
180-D1-018	GCA	CGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUC	UGC	39	> D1-002	<10 nM	2 nM
180-D1-034	CGCA	CGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUC	UGCGU	42	> D1-002		
180-D1-035	CGCA	CGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUC	UGCG	41	= D1-002		
180-D1-036	GCA	CGUCCCUCACCGGUGCAAGUGAAGCCGUGGCUC	UGCG	40	= D1-002	3-4 nM	0.5 nM
Boxes	B1A	B2	B1B				

= D1-002, similar binding as 180-D1-002 as determined in competition assay
> D1-002, weaker binding than 180-D1-002 as determined in competition assay

Fig. 3

Type 3

	B1A	B2A	B3	B2B	B4	B5A	B6		B1B	length (nt)	Pull-down	IC_{50} Chemo-taxis [nM]
178-A8	GUGCUGC	GUAGU	*GGAAG*	ACUAC	CUAAUGA	**CAGC**	CGAAU	**GCUG**	GCAGCAC	49	> 178-D5	
178-F7	GUGCUGC	GUAGU	*GGAAG*	ACUAC	CUAAUGA	**CAGC**	CUAAU	**GCUG**	GCAGCAC	49	> 178-D5	
178-G7	GUGCUGC	GUAGU	*GGAAG*	ACUAC	CUUAUGA	**CAGC**	CGAAU	**GCUG**	GCAGCAC	49	> 178-D5	
178-C6	GUGCUGC	GUAGU	*GAAAA*	ACUAC	UGCCAGUG	**GGU**	CAGA	**GCUA**	GCAGCAC	48	> 178-D5	
178-E7	GUGCUGC	GGAGU	*UAAAA*	ACUCC	CUAAGACA	**GGC**	CAGA	**GCCG**	GCAGCAC	48	> 178-D5	
178-G6	GUGCUGC	GGAGU	*UGAAA*	ACUCC	CUAAGACA	**GGC**	CAGA	**GCCG**	GCAGCAC	48	> 178-D5	
178-A7	GUGCUGC	GUAGU	*GGAAG*	ACUAC	CUAUGA	**CAGC**	CUAAU	**GCUG**	GCAGCAC	48	> 178-D5	
178-C7	GUGCUGC	GGAGU	*UAAAA*	ACUCC	CUAAGACA	**GGC**	UAGA	**GCCG**	GCAGCAC	48	> 178-D5	
178-E5	GUGCUGC	GGCGU	*GAAAA*	ACGCC	CUGCGA	**CUGC**	CCUUUAU	**GCAG**	GCAGCAC	48	4	
181-F1	GUGCUGC	GUAGU	*GAAAA*	ACUAC	CAACGACU	**GGC**	UAGA	**GCCG**	GCAGCAC	48	= 178-D5	
181-B2	GUGCUGC	GUAGU	*GAAAG*	ACUAC	CUGUGA	**CAGC**	CGAAU	**GCUG**	GCAGCAC	48	= 178-D5	
181-C2	GUACUGC	GUAGU	*UAAAA*	ACUAC	CAACGACU	**GGC**	UAGA	**GCCG**	GCAGCAC	48	= 178-D5	
178-A6	GUGCUGC	GUAGU	*UAAAA*	ACUAC	CAACGACU	**GGC**	UAGA	**GCCG**	GCAGCAC	48	= 178-D5	0.5
178-D6	GUGCUGC	GUAGU	*UAAAA*	ACUAC	CAGCGACA	**GGC**	UAGA	**GCCG**	GCAGCAC	48	0.5 nM	
178-D5	GUGCUGC	GUAGU	*UAAAA*	ACUAC	CAGCGACU	**GGC**	UAGA	**G**	:AGCAC	48	0.5 nM	0.5
181-A2	GUGCUGC	GUAGU	*GAGAA*	ACUAC	CAACGACU	**GGC**	UAGA	**G**	:AGCAC	48	0.1 nM	0.5

Boxes

= 178-D5, similar binding as 178-D5 as determined in com on assay
> 178-D5, weaker binding than 178-D5 as determined in cor ion assay

Fig. 4

Derivatives of 178-D5 and 181-A2

										length (nt)	Pull-down	Biacore
178-D5-020	GGCUGC	GUAGU	*UAAAA*	ACUAC	CAGCGACU	**GGC**	UAGA	**GCCG**	GCAGCC	46	1.5 nM	
178-D5-027	GGCGC	GUAGU	*UAAAA*	ACUAC	CAGCGACU	**GGC**	UAGA	**GCCG**	GCGCC	44	27 nM	
178-D5-030	GUGCGC	GUAGU	*UAAAA*	ACUAC	CAGCGACU	**GGC**	UAGA	**GCCG**	GCGCAC	46	= 178-D5	
181-A2	GUGCUGC	GUAGU	*GAGAA*	ACUAC	CAACGACU	**GGC**	UAGA	**GCCG**	GCAGCAC	48		0.37 nM
181-A2-002	GUGCGC	GUAGU	*GAGAA*	ACUAC	CAACGACU	**GGC**	UAGA	**GCCG**	GCGCAC	46		= 181-A2
181-A2-004	GUGCC	GUAGU	*GAGAA*	ACUAC	CAACGACU	**GGC**	UAGA	**GCCG**	GGCAC	44		= 181-A2
181-A2-005	GUGGC	GUAGU	*GAGAA*	ACUAC	CAACGACU	**GGC**	UAGA	**GCCG**	GCCAC	44		= 181-A2
181-A2-006	GUCGC	GUAGU	*GAGAA*	ACUAC	CAACGACU	**GGC**	UAGA	**GCCG**	GCGAC	44		= 181-A2
181-A2-007	UGCGC	GUAGU	*GAGAA*	ACUAC	CAACGACU	**GGC**	UAGA	**GCCG**	GCGCA	44		= 181-A2
181-A2-008	UGCGC	GUAGU	*GAGAA*	ACUAC	CAACGACU	**GGC**	UAGA	**GCCG**	GCAGC	44		> 181-A2
181-A2-011	GCUGC	GUAGU	*GAGAA*	ACUAC	CAACGACU	**GGC**	UAGA	**GCCG**	GCAGC	44		> 181-A2
181-A2-012	GGUGC	GUAGU	*GAGAA*	ACUAC	CAACGACU	**GGC**	UAGA	**GCCG**	GCACC	44		> 181-A2
181-A2-015	UGGC	GUAGU	*GAGAA*	ACUAC	CAACGACU	**GGC**	UAGA	**GCCG**	GCCA	42		> 181-A2
181-A2-016	GCGC	GUAGU	*GAGAA*	ACUAC	CAACGACU	**GGC**	UAGA	**GCCG**	GCGC	42		> 181-A2
181-A2-017	GUGC	GUAGU	*GAGAA*	ACUAC	CAACGACU	**GGC**	UAGA	**GCCG**	GCAC	42		= 181-A2
181-A2-018	GGGC	GUAGU	*GAGAA*	ACUAC	CAACGACU	**GGC**	UAGA	**GCCG**	GCCC	42		= 181-A2
181-A2-019	GAGC	GUAGU	*GAGAA*	ACUAC	CAACGACU	**GGC**	UAGA	**GCCG**	GCUC	42		= 181-A2
181-A2-020	CGGC	GUAGU	*GAGAA*	ACUAC	CAACGACU	**GGC**	UAGA	**GCCG**	GCCG	42		= 181-A2
181-A2-021	CCGC	GUAGU	*GAGAA*	ACUAC	CAACGACU	**GGC**	UAGA	**GCCG**	GCGG	42		= 181-A2
181-A2-022	CAGC	GUAGU	*GAGAA*	ACUAC	CAACGACU	**GGC**	UAGA	**GCCG**	GCUG	42		> 181-A2
181-A2-023	CUGC	GUAGU	*GAGAA*	ACUAC	CAACGACU	**GGC**	UAGA	**GCCG**	GCAG	42		= 181-A2
Boxes	B1A	B2A	*B3*	B2B	B4	**B5A**	B6	**B5B**	B1B			

= 178-D5, similar binding as 178-D5 as determined in competition assay
= 181-A2, similar binding as 181-A2 in Biacore measurement
> 181-A2, weaker binding than 181-A2 in Biacore measurement

Fig. 5

Type 4

				length (nt)	Pull-down [nM]	IC_{50} Ca^{++}-Assay [nM]	IC_{50} Chemo-taxis [nM]
184-B8trc	AGCGUGUU	AGUGAAGUGGGUGGCAGGUAAAG	GACACGCU	39	48		
184-C6trc	AGCGUGGU	AGCGGUGUGGGUGGUAGGUAAAG	GCCACGCU	39	56		
184-H5trc	AGCGUGAU	AGAAGAGCGGGUGGUAGGUAAAG	GUCAGGCU	39	69		
184-A7trc	AGCGUGUU	AGGUAGGGUGGUAGUAAGUAAAG	GACACGCU	39	29		
174-D4-004	CCGCUU	AGGU-GGGUGGUAGUAAGUAAAG	GGGCGG	34	2-4	2-5	2
166-A4-002	GCGCGAG	CAGGU-GGGUGGUAGAAUGUAAAGA	CUCGCGUC	39		3-5	
187-A5trc	AGCGUGUU	AGGU-GGGUGGUAGUAAGUAAAG	GACACGCU	38	20		
187-A5-001	CGUGUU	AGGU-GGGUGGUAGUAAGUAAAG	GACACG	34	23		
187-A5-002	GUGUU	AGGU-GGGUGGUAGUAAGUAAAG	GACAC	32	26		
187-H5trc	AGCGUGUU	AGGU-GGGUGGUAGUAAGUAAAG	GGCACGCU	38	16		
187-H5-002	CGUGUU	AGGU-GGGUGGUAGUAAGUAAAG	GGCACG	34	15		
187-H5-003	GUGUU	AGGU-GGGUGGUAGUAAGUAAAG	GGCAC	32	17		
187-H5-004	UGUU	AGGU-GGGUGGUAGUAAGUAAAG	GGCA	30	40		
Boxes	B1A	B2	B1B				

Fig. 6

Other sequences

		length (nt)	Pull-down	Biacore	IC_{50} Ca^{++}-Assay	IC_{50} Chemotaxis
177-B3	GGACGAGAGUGACAAAUGAUAUAACCUCCUGACUAACGCUGCGGGCGACAGG	52	12 nM	> 178-D5		
177-C1	GGACCUAUCGCUAAGACAACGCGCAGUCUACGGGACAUUCUCCGCGGACAGG	52	> 178-D5			
177-C2	GGACAAUUGUUACCCCCGAGAGAGACAAAUGAGACAACCUCCUGAAGACAGG	52	9	> 178-D5		
177-E3	GGACGAAAGUGAGAAAUGAUACAACCUCCUGUUGCUGCGAAUCCGGACAGG	51	> 178-D5			
177-D1	GGACGUAAAAGACGCUACCCGAAAGAAUGUCAGGAGGGUAGACCGACAGG	50	> 178-D5			
177-E1	GGACUAGAAACUACAAUAGCGGCCAGUUGCACCGCGUUAUCAACGACAGG	50	> 178-D5			
177-A1	GGACUAGUCAGCCAGUGUGUAUAUCGGACGCGGGUUUAUUUACUGACAGG	50	> 178-D5			
177-G3	GGACUGUCCGGAGUGUGAAACUCCCCGAGACCGCCAGAAGCGGGGACAGG	50	5 nM	> 178-D5		
177-C3	GGACUUCUAUCCAGGUGGGUGGUAGUAUGUAAAGAGAUAGAAGUGACAGG	50	5 nM	> 178-D5		
177-A2	GGACGAGAGCGAACAAUGAUAUAACCUCCUGACGGAAAGAGAUCGACAGG	50	13 nM	> 178-D5		
170-E4trc	CCUGUGCUACACGCAGUAAGAAGUGAACGUUCAGUAUGUGUGCACAGG	48			20 nM	
166-D2trc	CGUGAGCCAGGCACCGAGGGCGUUAACUGGCUGAUUGGACACGACACG	48			+	
174-A2trc	CGUGAACAUGCAAGCUAAGCGGGGCUGUUGGUUGCUUGGCCCGCCACG	48			+	
174-E2trc	CGUGCAGAGAGAGACCAACCACGUAAAAUCAACCUAAUGGGCCGCACG	48			+	
183-G3trc	CGUGCAGAGAGAGACCAACCACGUAAAAUCAACCUAAUGGGCCGCACG	48	2-5 nM		2-3 nM	+
183-B2trc	CGUGAACAUUCAAGCUAAGCGGGGCUGUUGGUUGCUUGGCCCGCCACG	48	5-10 nM		2-6 nM	+
166-B2trc	CGUGCCGAGGCGGCGACCAGCGUUACUUAGAGAGGCUUUGGCACCACG	48	25 nM		2-15 nM	
166-G3trc	CGUGAUAACAGCCGUCGGUCAAGAAAACAAAGUUCGGGCGGCGCACG	47			+	
166-D1trc	CGUGGGUGGCGCACCGAGGGCGAAAAGCCACCAGUAAAGAUAGACCG	47			+	
183-H2trc	CGUGUGAUCUCCUUUGGGGUGAUUAGCUUAGAGACUUCCCACACG	45	2-5 nM		10 nM	+
167-A7trc	GCACCUUCGCCUAAUACACGUGCCGGCUAGCUAAUACUCGUCCGC	45		180 nM	150 nM	
167-C7trc	GCACGACUUGGGCGACCAGUGAUACUUAGAGAGCAAGUCGUCGGC	45		5 nM	+	
167-B5trc	GCGCGCGCUCAGUAAGAAAUUGAAAGUUCAGAAUGUCGUCGCGC	44			+	
184-D7trc	AGUGUGUGGCAGGCUAAGGAGAUAUUCCGAGACCACGCU	39	800 nM			
184-D6trc	AGUGUGUGGCAGACUAUGGAUAGACUCCGAGACCACGCU	39	650 nM			
184-E5trc	AGCGUGAGGCGACCAGCGGAUUACUUAGAGAGUCACGCU	39	100 nM			
184-G6trc	AGCGUGAAGGGGACCAGCGUUACUUACAGAGUUCACGCU	39	160 nM			
184-B7trc	AGCGUGUGAUGUAUGUAGCACCGUAUCAGAGGACACGCU	39	27 nM			
184-B6trc	AGCGUGAGGCGACCCGUGUUUCGUAGAGAGUCACGCU	37	60 nM			

+, substance active in assay; no IC_{50} determined

> 178-D5, weaker binding than 178-D5 as determined in competition assay

Fig. 7

Murine-Specific Spiegelmers

188-A3-001 and Derivatives

		Length (nt)	Pull-down	IC_{50} Ca^{++}-Assay[nM]	IC_{50} Chemo-taxis[nM]
188-A3-001	GAGAUGGCGACAUUGGUUGGGCAUGAGGCGAGGCCCUUUGAUGAAUCCGCGGCCAUUC	58	< 1 nM		
188-A3-004	GAUGGCGACAUUGGUUGGGCAUGAGGCGAGGCCCUUUGAUGAAUCCGCGGCCAUUC	56	< 1 nM		
188-A3-005	GGCGACAUUGGUUGGGCAUGAGGCGAGGCCCUUUGAUGAAUCCGCGGCCAUUC	53	< 1 nM		
188-A3-006	GGCGACAUUGGUUGGGCAUGAGGCGAGGCCCUUUGAUGAAUCCGCGGCCAUU	52	< 1 nM	12	4
188-A3-007 = mNOX-E36	GGCGACAUUGGUUGGGCAUGAGGCGAGGCCCUUUGAUGAAUCCGCGGCCA	50	~0.2 nM	12	7

189-G7-001 and Derivatives

		Length (nt)	Pull-down	IC_{50} Ca^{++}-Assay[nM]	IC_{50} Chemo-taxis[nM]
189-G7-001	GCUGGUUACCGAGGGGGCGUCGUUGGAGUUUGGUUGGUUGUCACCAGC	48	< 1 nM	20-30	
189-G7-002	CUGGUUACCGAGGGGGCGUCGUUGGAGUUUGGUUGGUUGUCACCAG	46	< 1 nM	40-50	6.5
189-G7-003	UGGUUACCGAGGGGGCGUCGUUGGAGUUUGGUUGGUUGUCACCA	44	< 1 nM		
189-G7-007	GCCGGUUACCGAGGGGGCGUCGUUGGAGUUUGGUUGGUUGUCACCGGC	48		20	
189-G7-008	GCCGGCUACCGAGGGGGCGUCGUUGGAGUUUGGUUGGUUGUCGCCGGC	48	~ 1 nM	12	5
189-G7-010	GCGCGUACCGAGGGGGCGUCGUUGGAGUUUGGUUGGUUGUCCGCGC	46		40	
189-G7-012	GGGCCUACCGAGGGGGCGUCGUUGGAGUUUGGUUGGUUGUCGGCCC	46		> 50	

Fig. 8

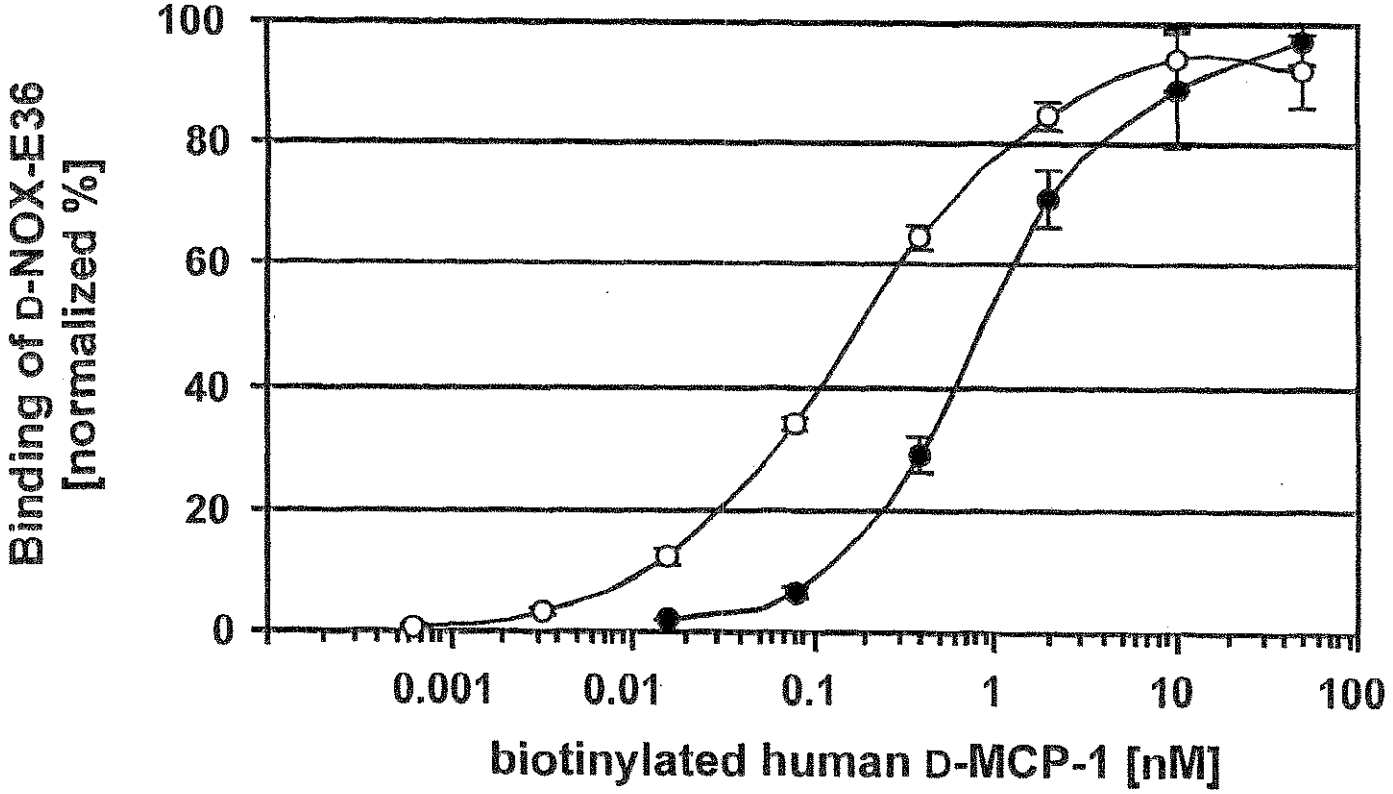


Fig. 9

full circles, KD at 37°C 890 ± 65 pM
hollow circles, KD at room temperature, 146 ± 13 pM

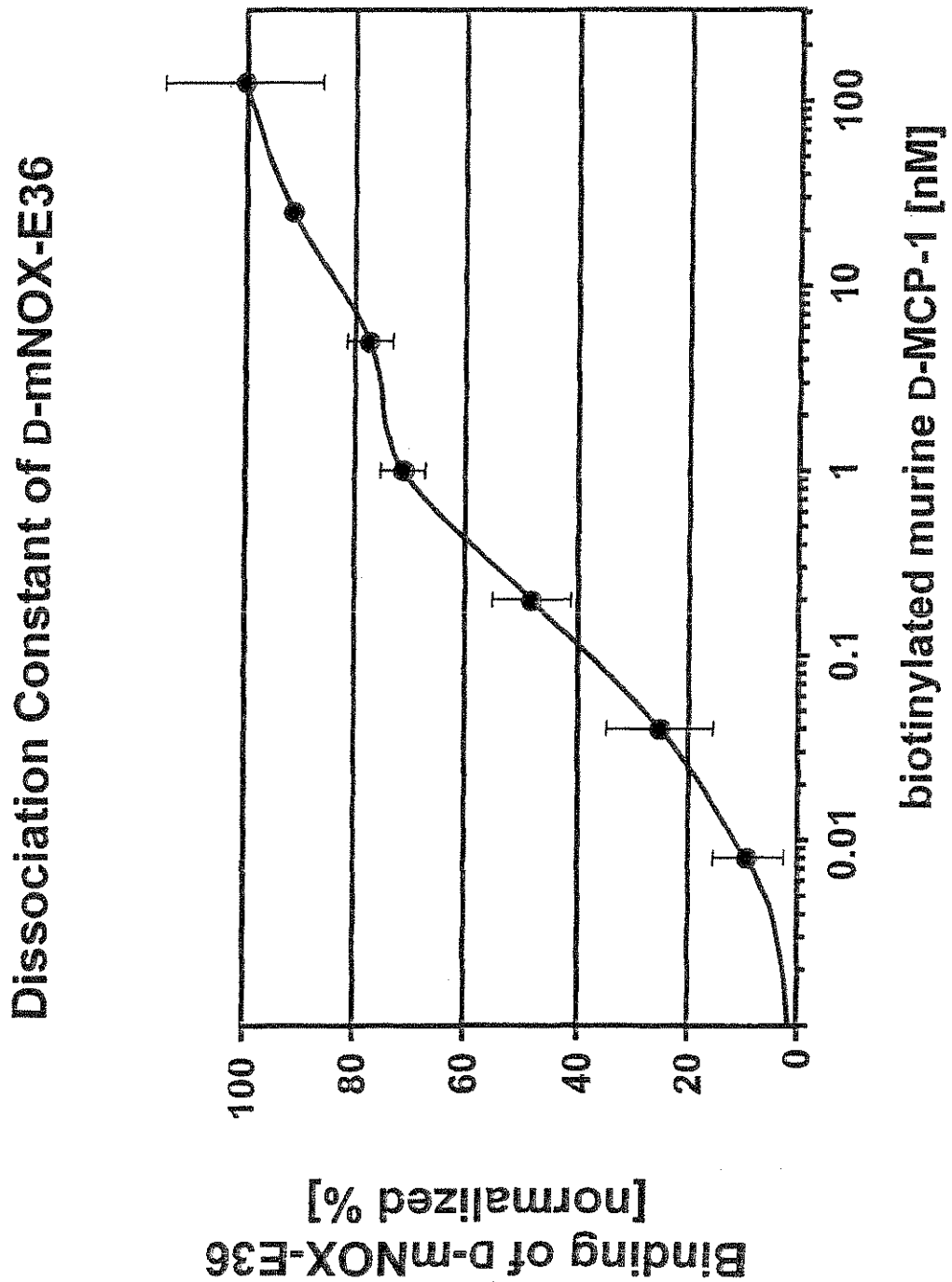

Dissociation Constant of D-mNOX-E36
Binding of D-mNOX-E36 [normalized %]
100
80
60
40
20
0
0.01
0.1
1
10
100
biotinylated murine D-MCP-1 [nM]

Fig. 10

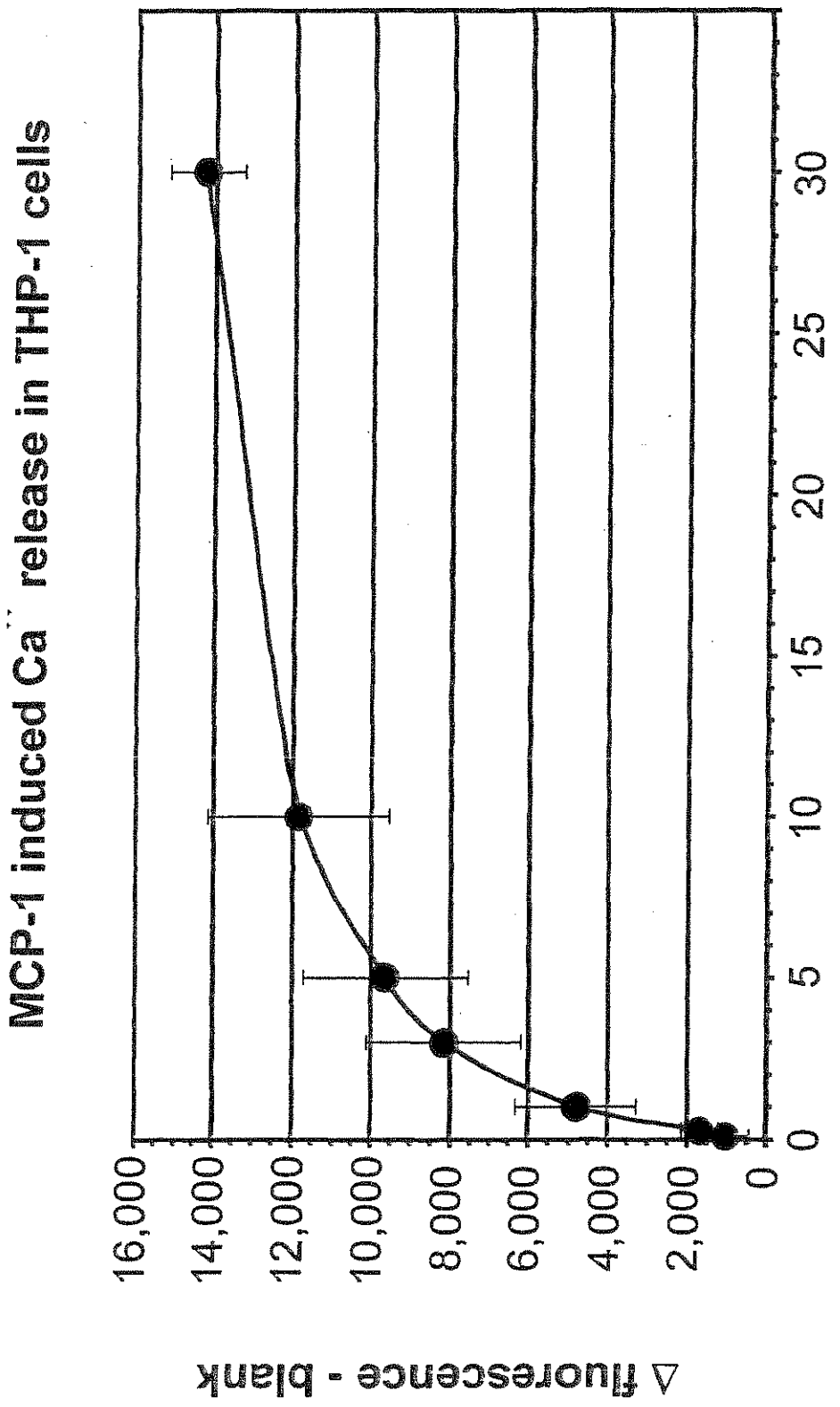

MCP-1 induced Ca++ release in THP-1 cells
Δ fluorescence - blank
16,000
14,000
12,000
10,000
8,000
6,000
4,000
2,000
0
0
5
10
15
20
25
30
huMCP-1 [nM]

Fig. 11

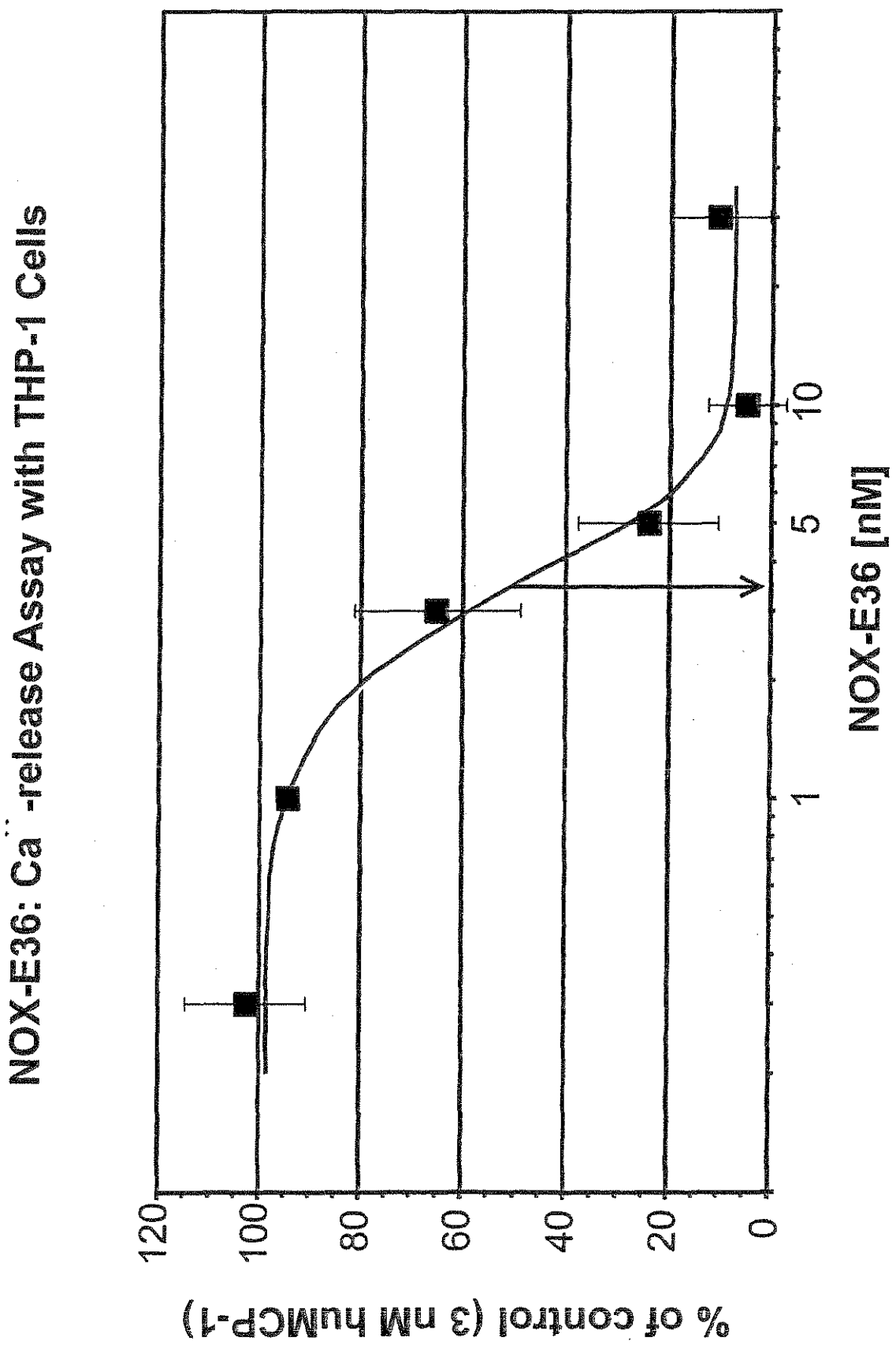

NOX-E36: Ca++-release Assay with THP-1 Cells
% of control (3 nM huMCP-1)
120
100
80
60
40
20
0
1
5
10
NOX-E36 [nM]

Fig. 12

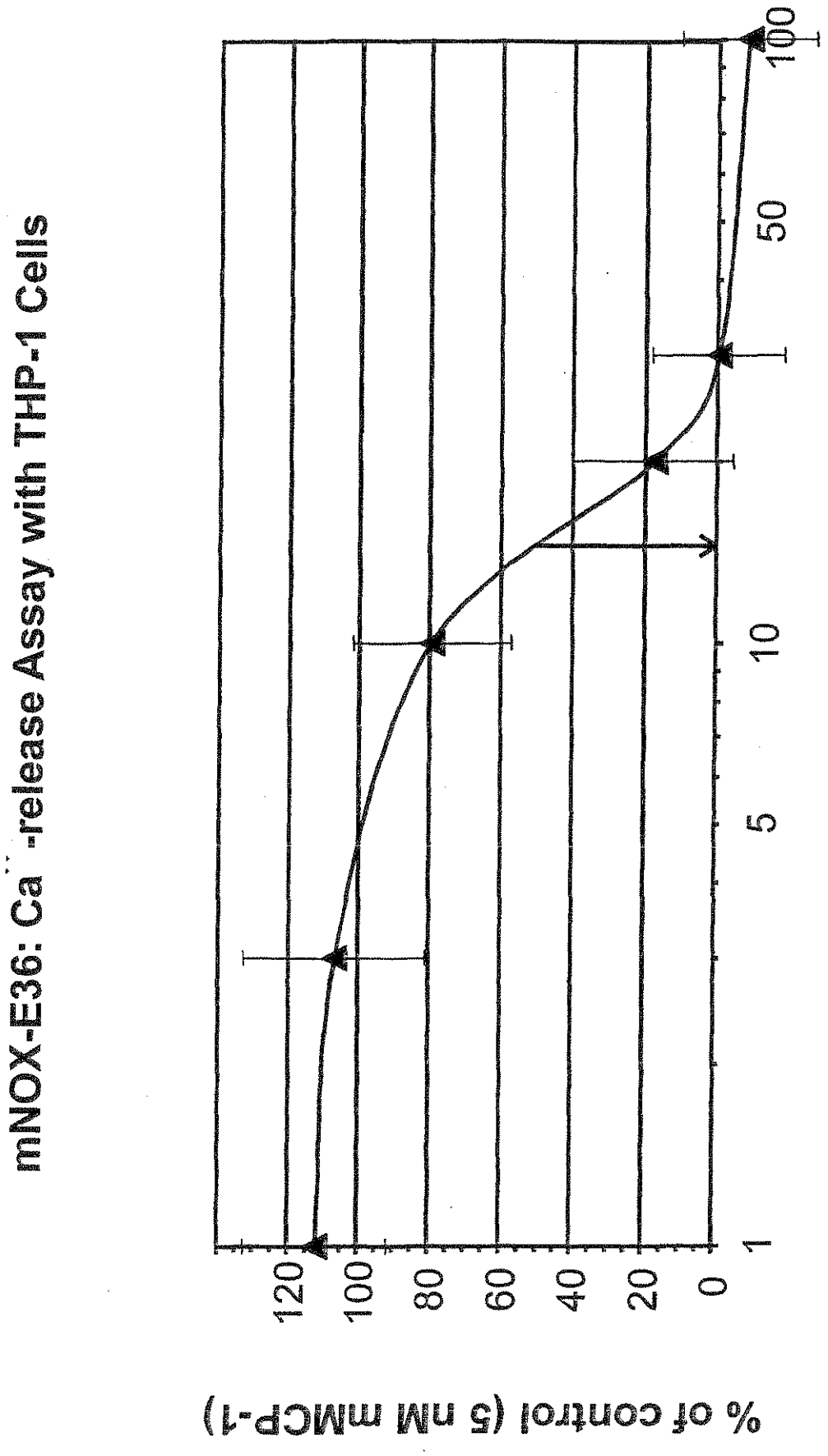

mNOX-E36: Ca++-release Assay with THP-1 Cells
% of control (5 nM mMCP-1)
120
100
80
60
40
20
0
1
5
10
50
100
mNOX-E36 [nM]

Fig. 13

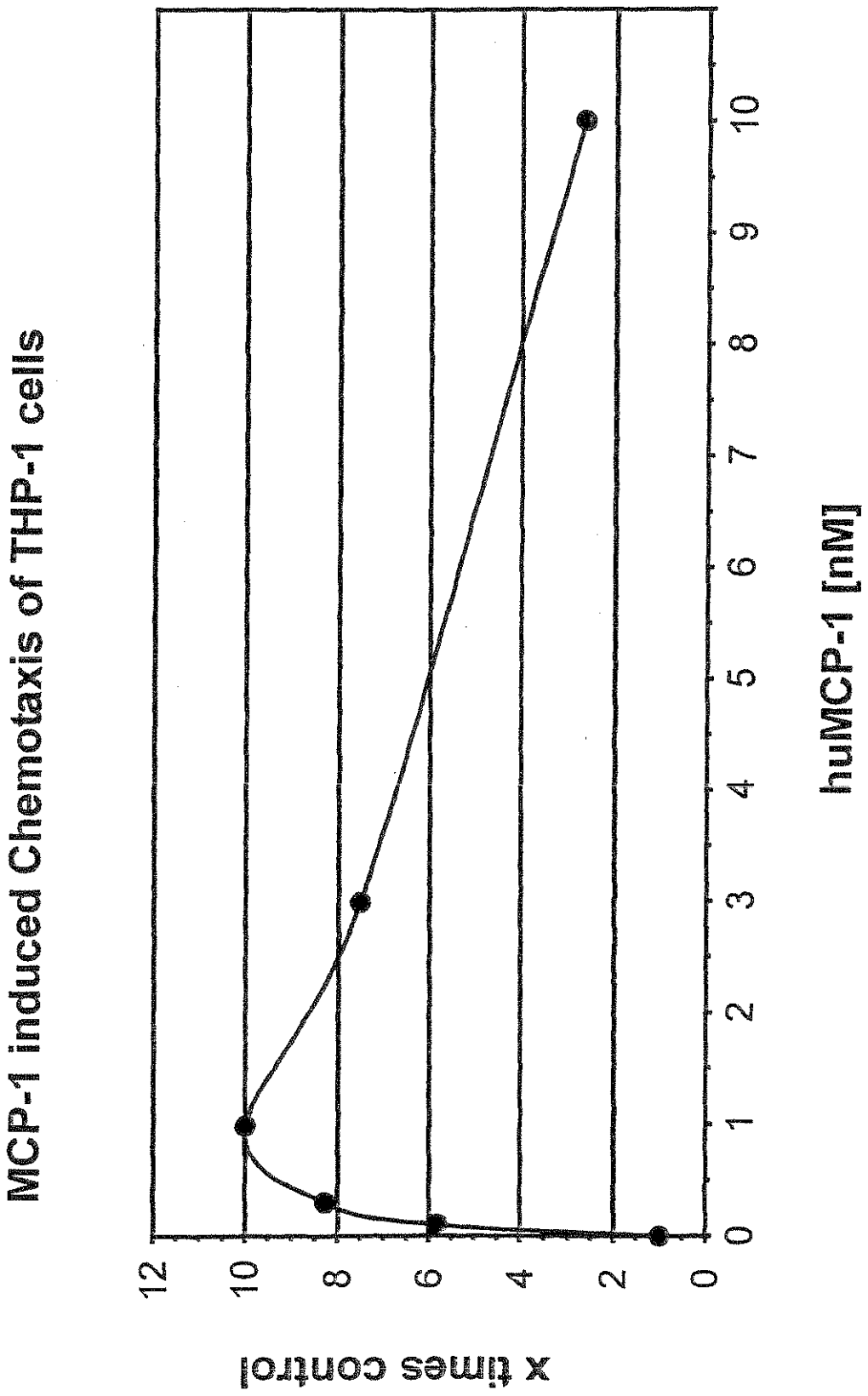

MCP-1 induced Chemotaxis of THP-1 cells
x times control
huMCP-1 [nM]
0
2
4
6
8
10
12
0
1
2
3
4
5
6
7
8
9
10

Fig. 14

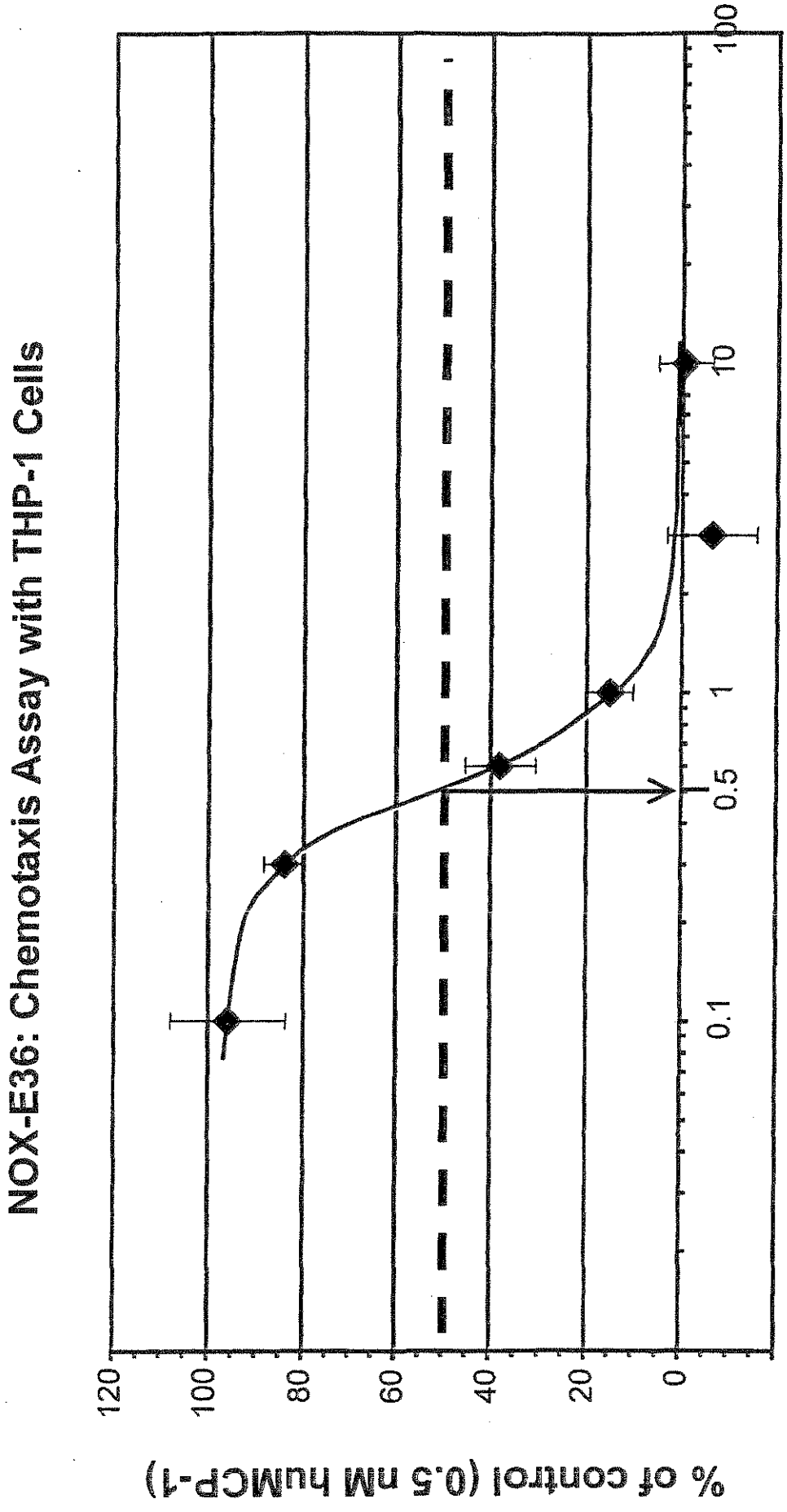

NOX-E36: Chemotaxis Assay with THP-1 Cells
% of control (0.5 nM huMCP-1)
120
100
80
60
40
20
0
0.1
0.5
1
10
100
NOX-E36 [nM]

Fig. 15

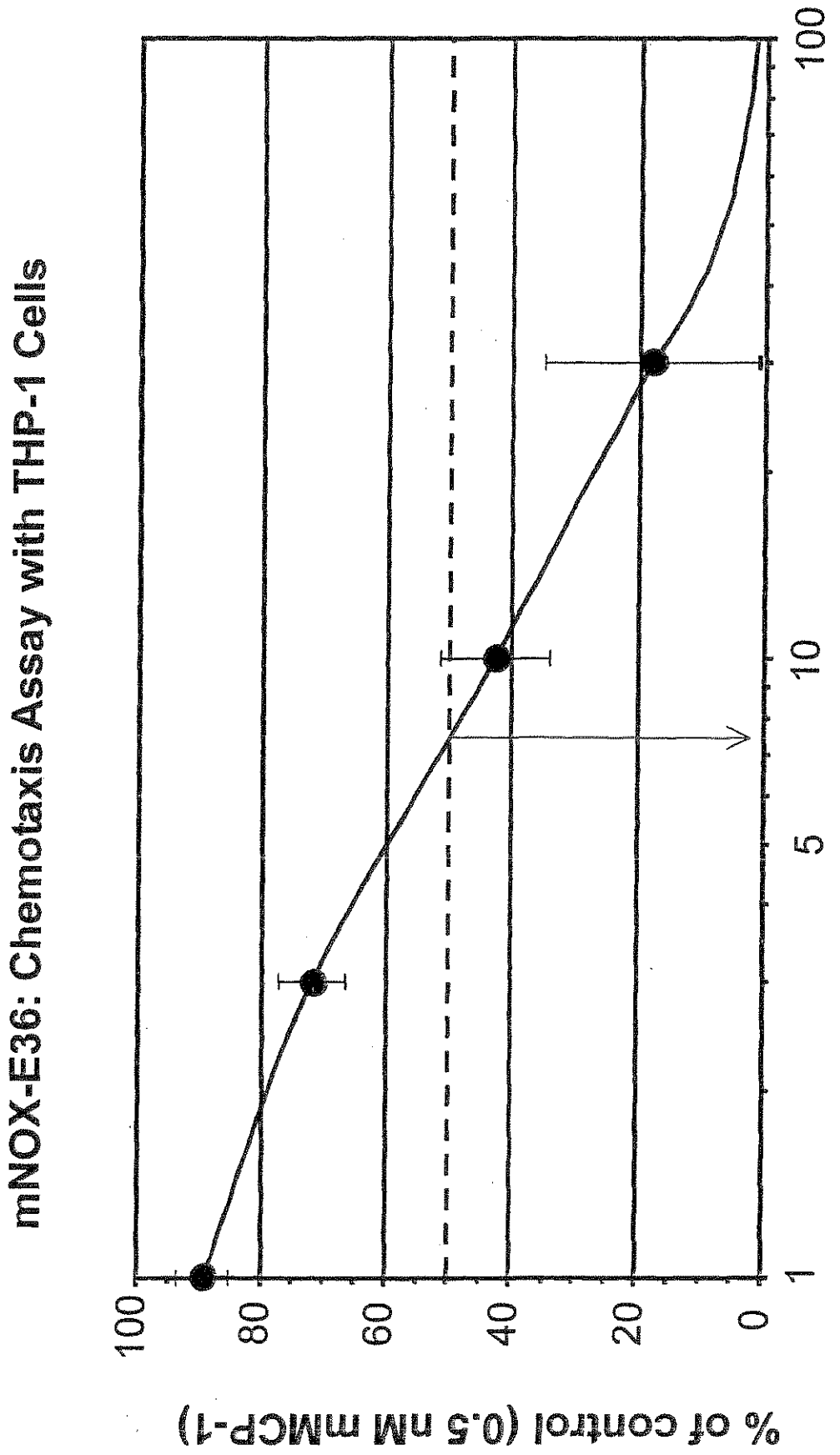

mNOX-E36: Chemotaxis Assay with THP-1 Cells
% of control (0.5 nM mMCP-1)
100
80
60
40
20
0
1
5
10
100
mNOX-E36 [nM]

Fig. 16

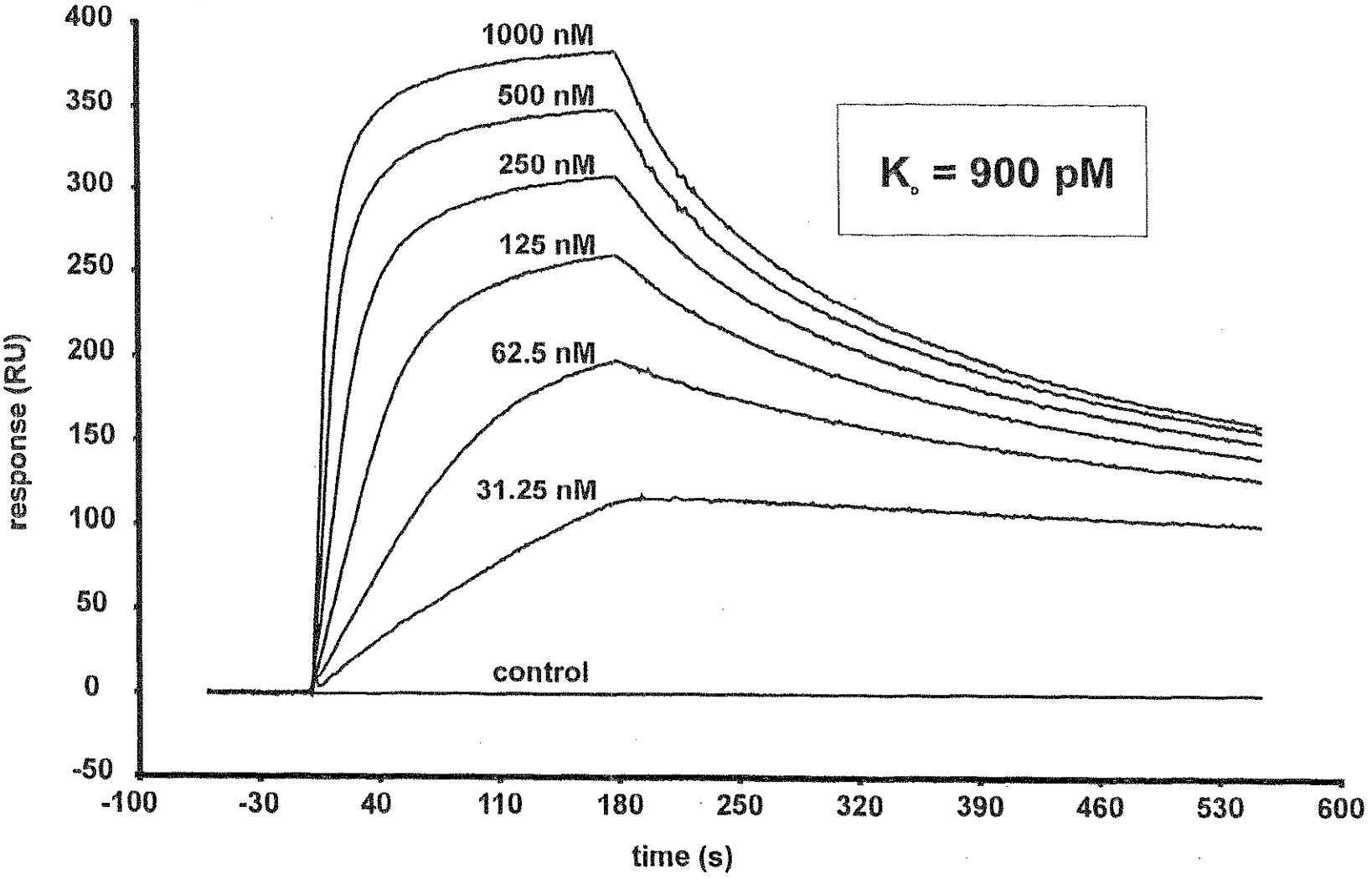


Fig. 17 Kinetics of SpiegelmerNOX-E36 binding to human MCP-1

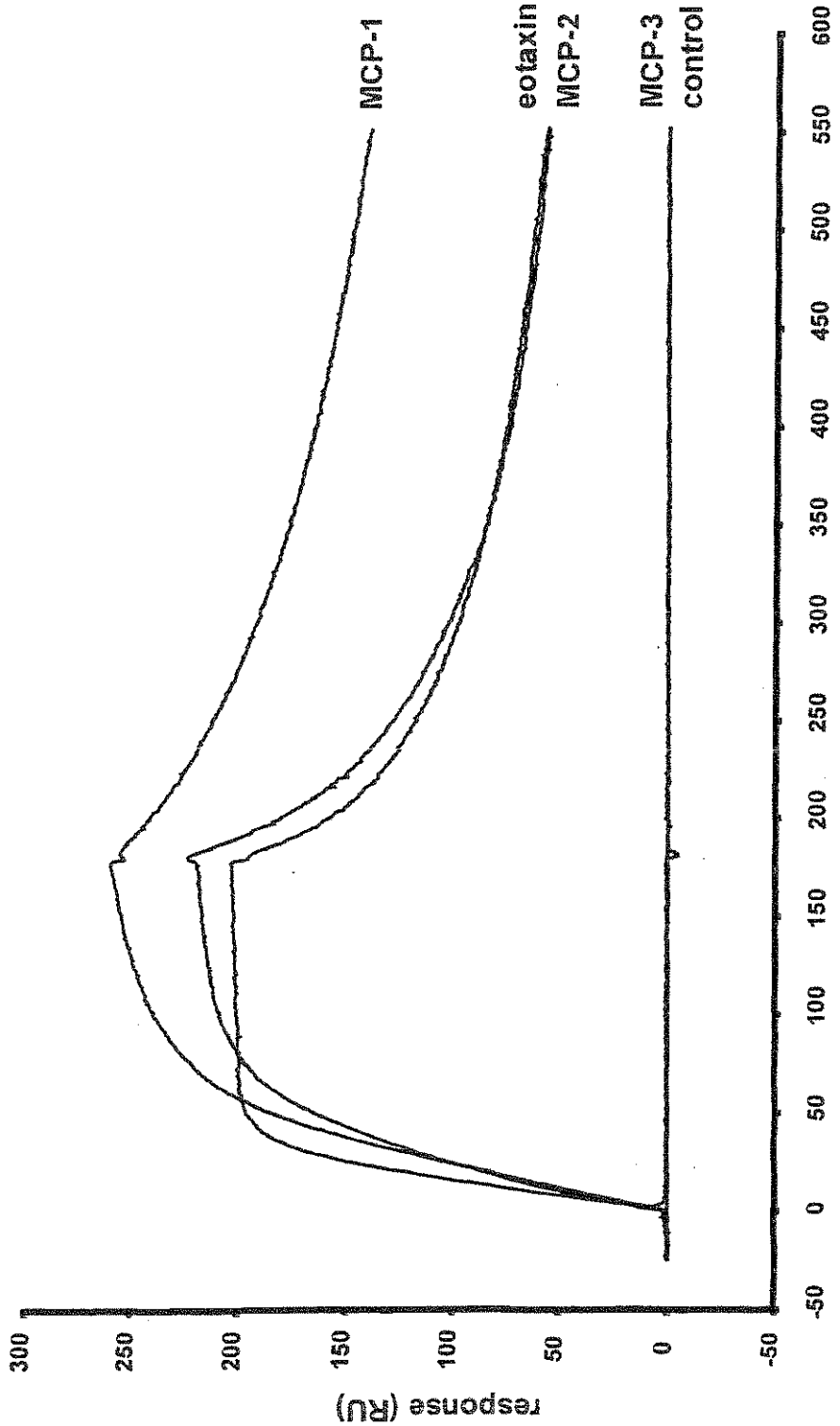


Fig. 18 Spiegelmer NOX-E36 binding to human MCP- family proteins and eotaxin

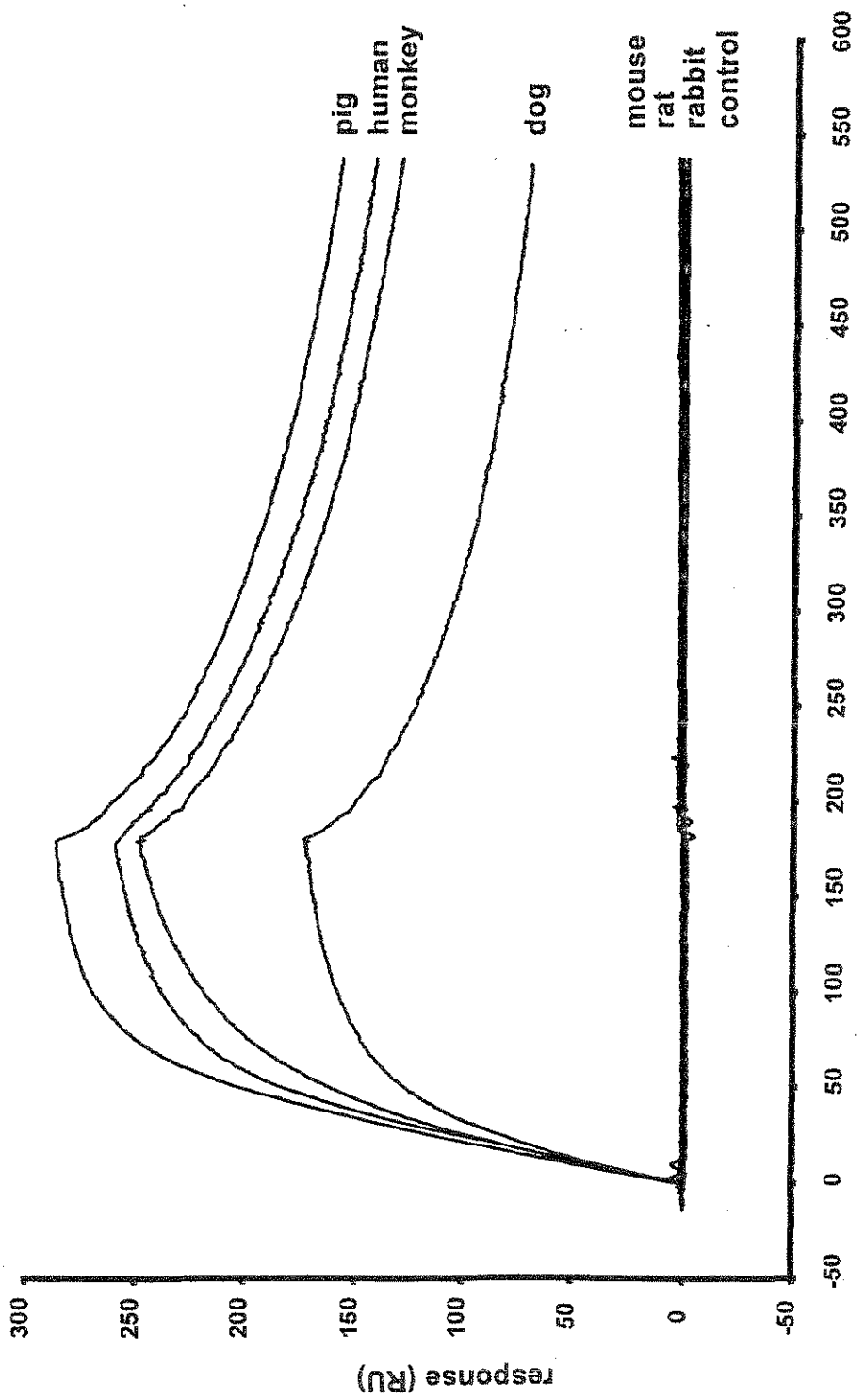


Fig. 19 Spiegelmer NOX-E36 binding to MCP-1 from different species

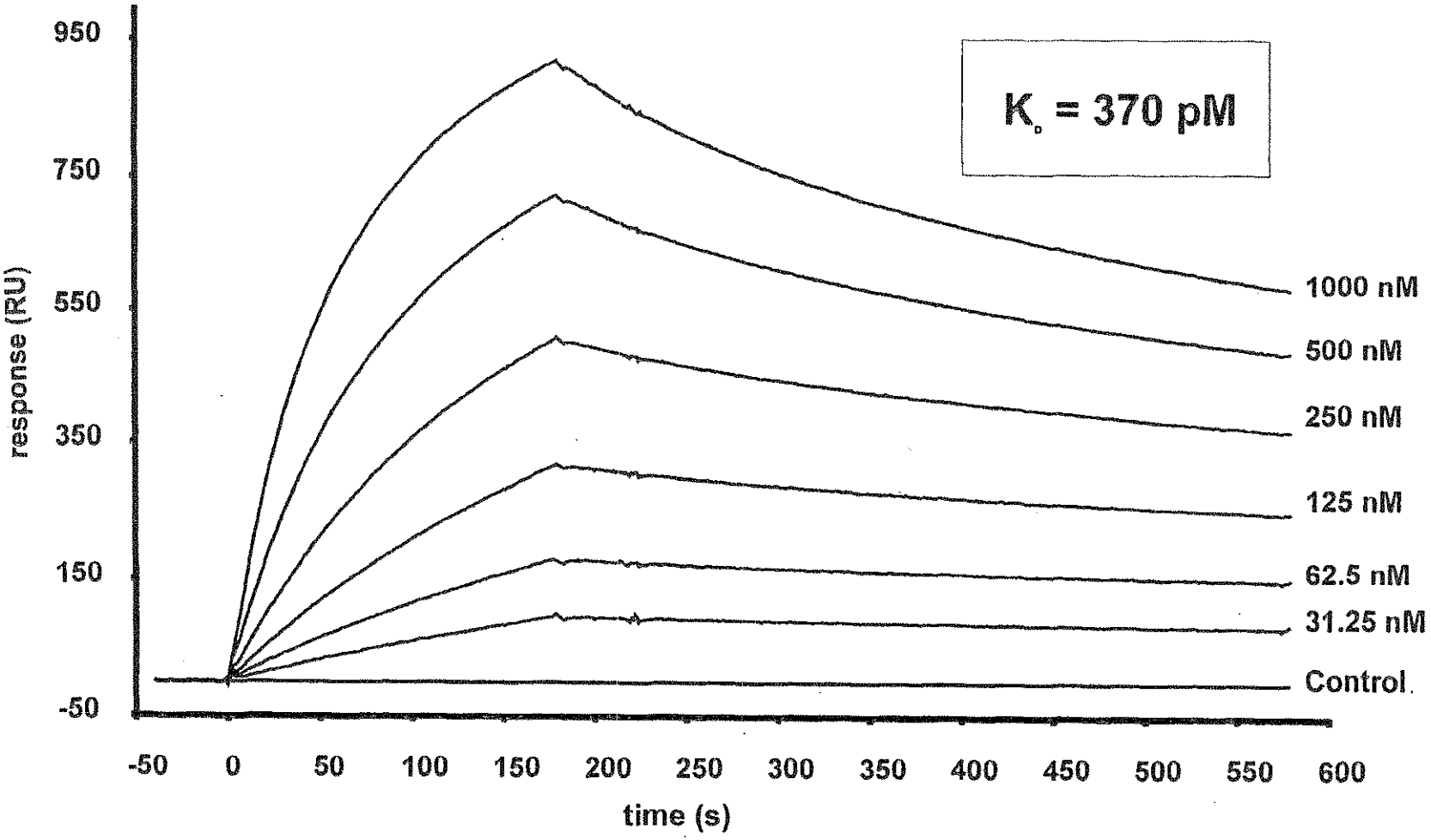


Fig. 20

Kinetics of Spiegelmer 181-A2-018 binding human MCP-1

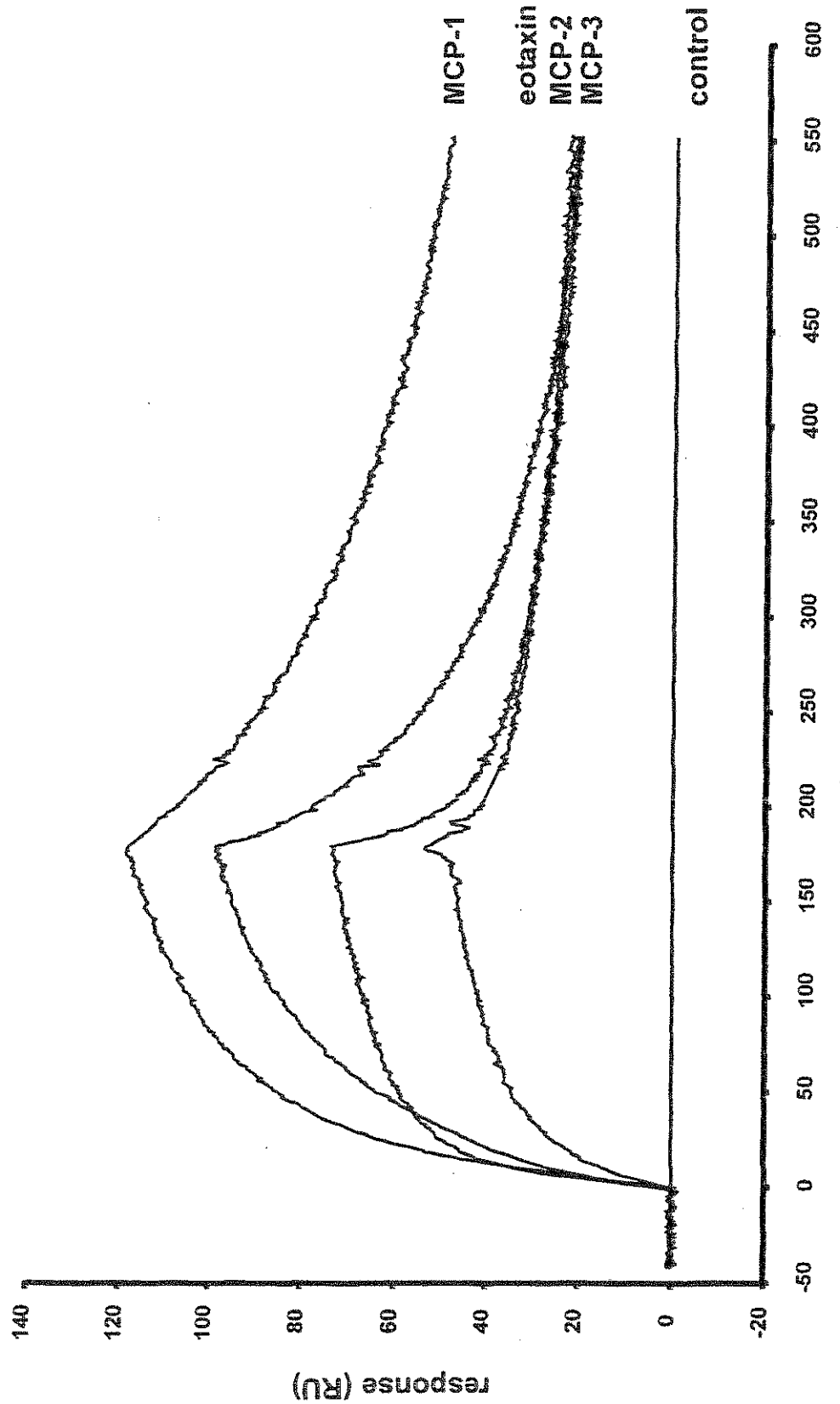


Fig. 21

Spiegelmer 181-A2-018 binding to human MCP- family proteins and eotaxin

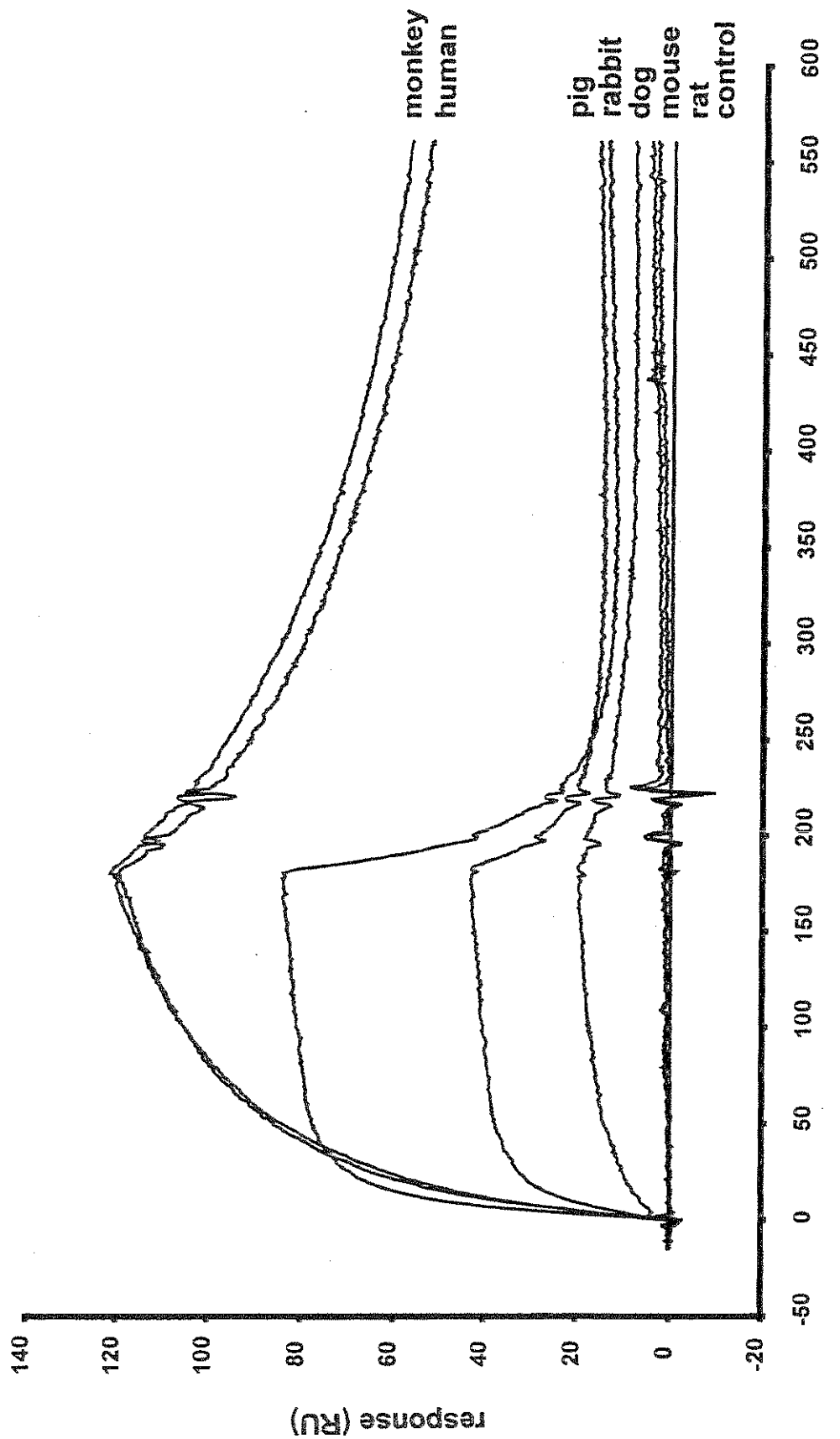


Fig. 22

Spiegelmer 181-A2-018 binding to MCP-1 from different species

1	**QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWVQDSMDHLDKQTQTPKT**
2	QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWVQDSMDHLDKQIQTPKP
3	QPDAINSPVTCCYTLTSKKISMQRLMSYRRVTSSKCPKEAVIFKTIAGKEICAEPKQKWVQDSISHLDKKNQTPKP
4	QPDAINSPVTCCYTFTGKKISSQRLGSYKRVTSSKCPKEAVIFKTILAKEICADPEQKWVQDAVKQLDKKAQTPKP
5	QPDAIISPVTCCYTLTNKKISIQRLASYKRVTSSKCPKEAVIFKTVLNKEICADPKQKWVQDSMAHLDKKSQTQTA
6	QPDAVNSPVTCCYTFTNKTISVKRLMSYRRINSTKCPKEAVIFMTKLAKGICADPKQKWVQDAIANLDKKMQTPKT
7	QPDAINSQVACCYTFNSKKISMQRLMNYRRVTSSKCPKEAVIFKTILGKELCADPKQKWVQDSINYLNKKNQTPKP
8	QPVGINTSTTCCYRFINKKIPKQRLESYRRTTSSHCPREAVIFKTKLDKEICADPTQKWVQDFMKHLDKKTQTPKL
9	GP--ASVPTTCCFNLANRKIPLQRLESYRRITSGKCPQKAVIFKTKLAKDICADPKKKWVQDSMKYLDQKSPTPKP
10	QPDSVSIPITCCFNVINRKIPIQRLESYTRITNIQCPKEAVIFKTKRGKEVCADPKERWVRDSMKHLDQIFQNLKP
11	QPDAVNAPLTCCYSFTSKMIPMSRLESYKRITSSRCPKEAVVFVTKLKREVCADPKKEWVQTYIKNLDRNQMRSEP
12	QPDAVNAPLTCCYSFTGKMIPMSRLENYKRITSSRCPKEAVVFVTKLKREICADPNKEWVQKYIRKLDQNQVRSET

	Protein	% identity with human MCP-1
1	*Homo sapiens* MCP-1	100%
2	*Macaca mulatta* (Rhesus monkey) MCP-1	97%
3	*Sus scrofa* (Pig) MCP-1	79%
4	*Equus caballus* (Horse)	78%
5	*Canis familiaris* (Dog) MCP-1	76%
6	*Oryctolagus cuniculus* (Rabbit) MCP-1	75%
7	*Bos Taurus* (Bovine)	72%
8	*Homo sapiens* MCP-3	71%
9	*Homo sapiens* Eotaxin	64%
10	*Homo sapiens* MCP-2	62%
11	*Mus musculus* (Mouse) MCP-1	55%
12	*Rattus norvegicus* (Rat) MCP-1	55%

Fig. 23

Specificity of NOX-E36 and 181-A2-018

	NOX-E-036 K_D [nM]	181-A2-018 K_D [nM]
hMCP-1	0.89	0.37-0.6
hMCP-2	5-10	10
hMCP-3	-	10
eotaxin	5-10	10-20
monkey MCP-1	0.90	0.6
porcine MCP-1	0.82	> 1000
canine MCP-1	1.2	> 1000
rabbit MCP-1	-	> 1000
rat MCP-1	-	-
mouse MCP-1	-	-

-, not binding

Fig. 24A

Chemokine/synonym	binding
CCL1/I-309	-
CCL2/MCP-1	+
CCL3/MIP-1α	+
CCL4/MIP-1β	-
CCL5/RANTES	-*
CCL7/MCP-3	-
CCL8/MCP-2	+
CCL11/eotaxin	+
CCL13/MCP-4	(+)
CCL14/HCC-1	-
CXCL1/GROα	-
CXCL2/GROβ	-
CXCL3/GROγ	-
CXCL4/PF4	-**
CXCL5/ENA-78	-
CXCL6/GCP-2	-**
CXCL7/NAP-2	+
CXCL8/IL-8	-
CXCL9/MIG	-*
CXCL10/IP-10	-
CXCL11/I-TAC	-**
CXCL12α/SDF-1α	-
CXCL12β/SDF-1β	-
CX_3CL1/Fractalkine	-
XCL1/Lymphotactin	-

Binding was classified as follows:

+, specific binding < 10 nM;

(+), NOX-E36 specific binding > 1 μM;

-, no interaction measurable;

-*, unspecific polyanion (PoC or dextran matrix) binding > 250 nM;

-**, unspecific polyanion (PoC or dextran matrix) binding > 10 μM.

Fig. 24 B

	Association rate constant k_a [$M^{-1}s^{-1}$]	Dissociation rate constant k_d [s^{-1}]	Dissociation constant K_D [nM]
CCL2/MCP-1	$1.8 \pm 0.4 \times 10^5$	$1.9 \pm 0.1 \times 10^{-4}$	1.1 ± 0.2
CCL3/MIP-1α	$1.6 \pm 0.3 \times 10^5$	$6.4 \pm 1.1 \times 10^{-4}$	4.1 ± 1.3
CCL7/MCP-3	–	–	–
CCL8/MCP-2	$2.0 \pm 0.7 \times 10^5$	$6.7 \pm 2.0 \times 10^{-4}$	4.2 ± 2.5
CCL11/Eotaxin	$1.6 \pm 0.4 \times 10^5$	$1.1 \pm 0.6 \times 10^{-3}$	7.7 ± 5.2
CCL13/MCP-4	–	–	> 1,000
CXCL7/NAP-2	$1.8 \pm 0.5 \times 10^5$	$4.1 \pm 0.4 \times 10^{-4}$	2.5 ± 0.9

Fig. 24 C

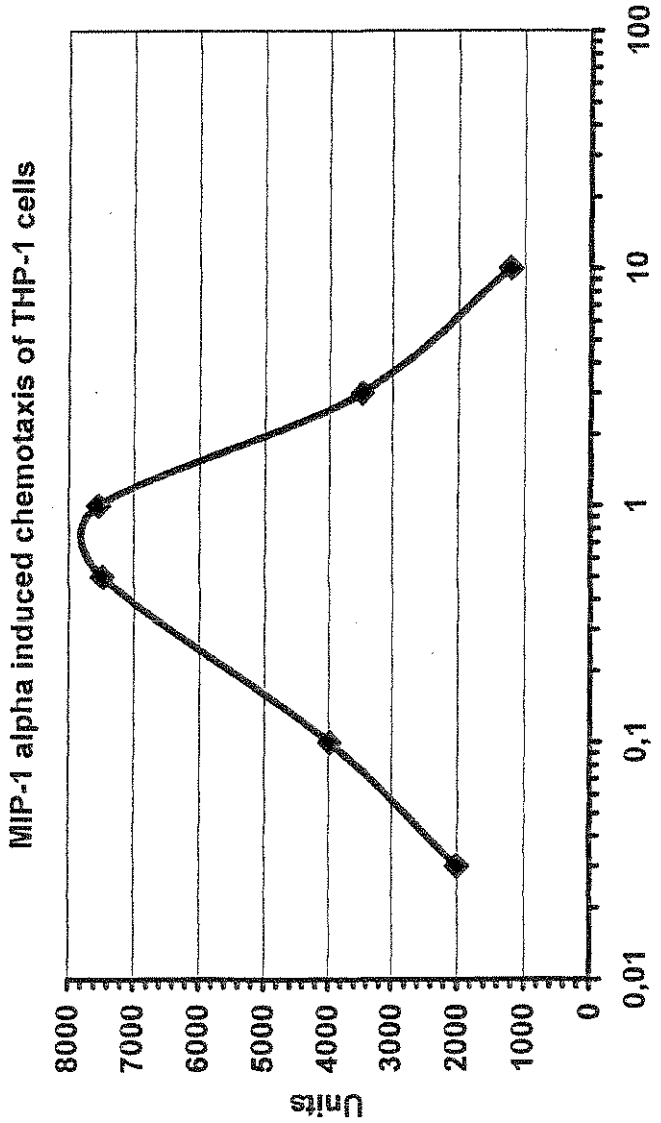

MIP-1 alpha induced chemotaxis of THP-1 cells
Units
8000
7000
6000
5000
4000
3000
2000
1000
0
0,01
0,1
1
10
100
MIP-1 alpha [nM]

Fig. 24 D

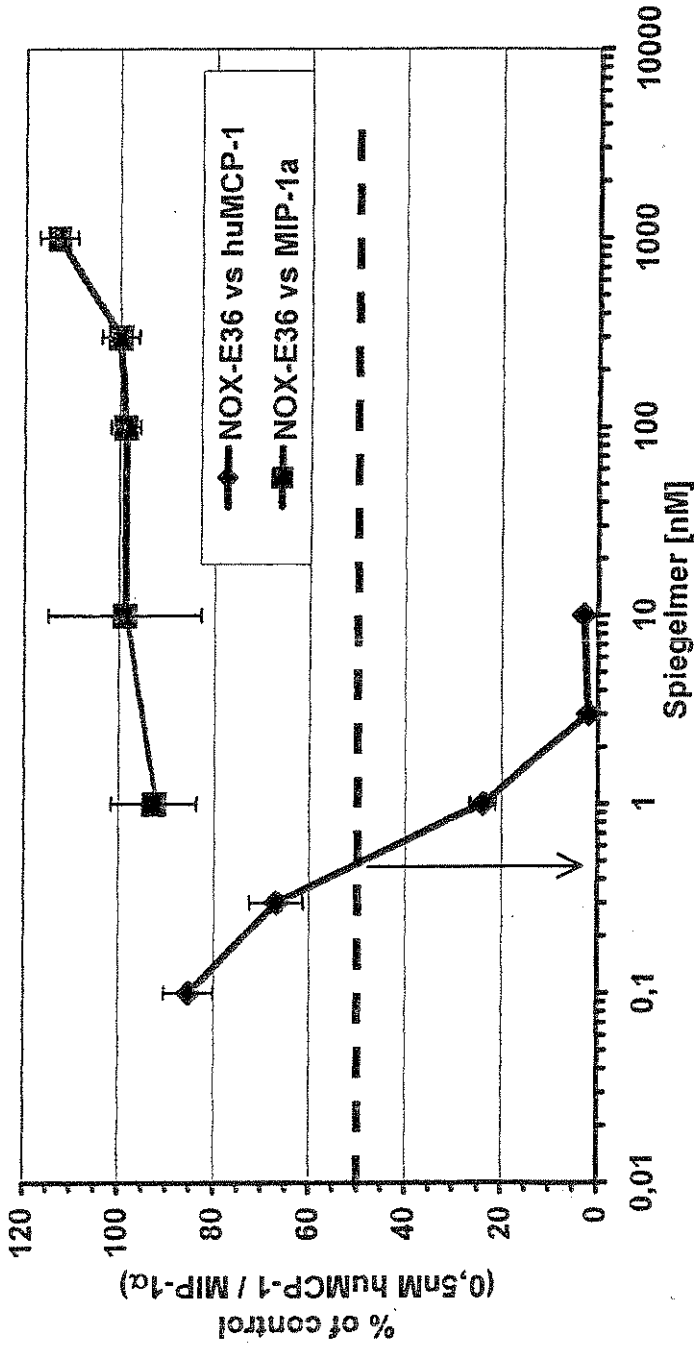

% of control
(0,5nM huMCP-1 / MIP-1α)
120
100
80
60
40
20
0
0,01
0,1
1
10
100
1000
10000
Spiegelmer [nM]
NOX-E36 vs huMCP-1
NOX-E36 vs MIP-1a

Fig. 24 E

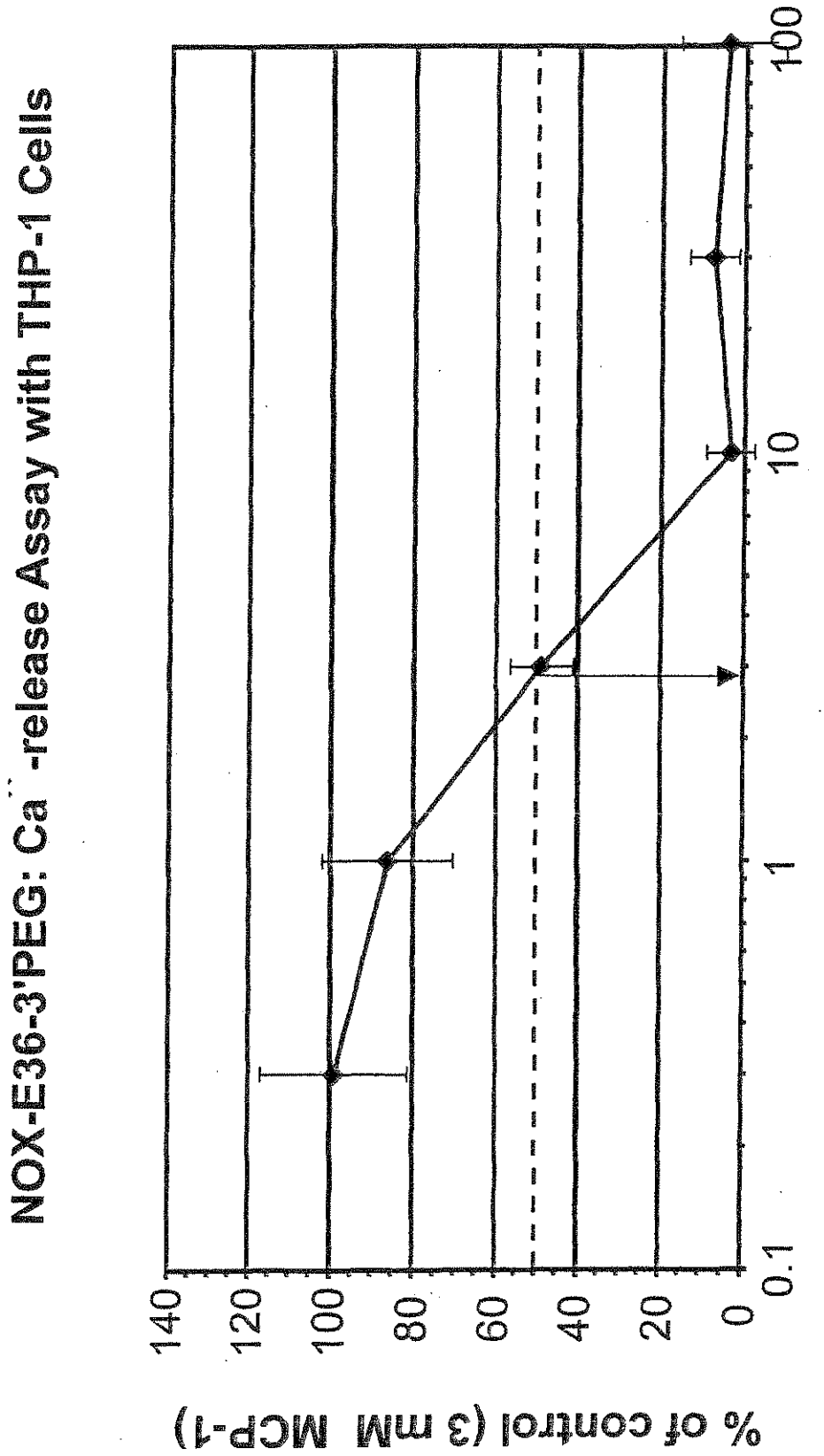

NOX-E36-3'PEG: Ca++-release Assay with THP-1 Cells
% of control (3 nM MCP-1)
140
120
100
80
60
40
20
0
0.1
1
10
100
NOX-E36-3'PEG [nM]

Fig. 25

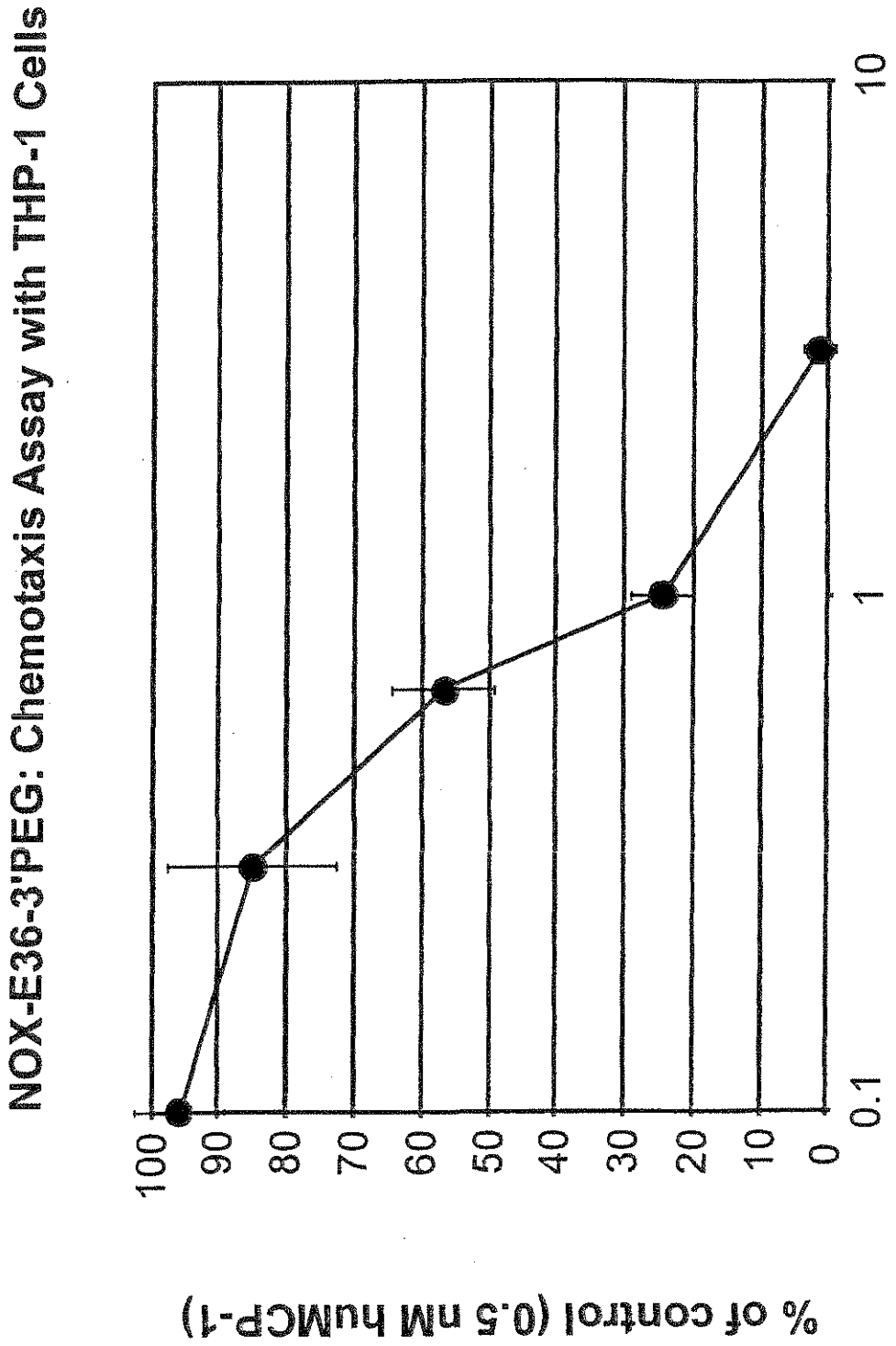

NOX-E36-3'PEG: Chemotaxis Assay with THP-1 Cells
% of control (0.5 nM huMCP-1)
100
90
80
70
60
50
40
30
20
10
0
0.1
1
10
NOX-E36-3'PEG [nM]

Fig. 26

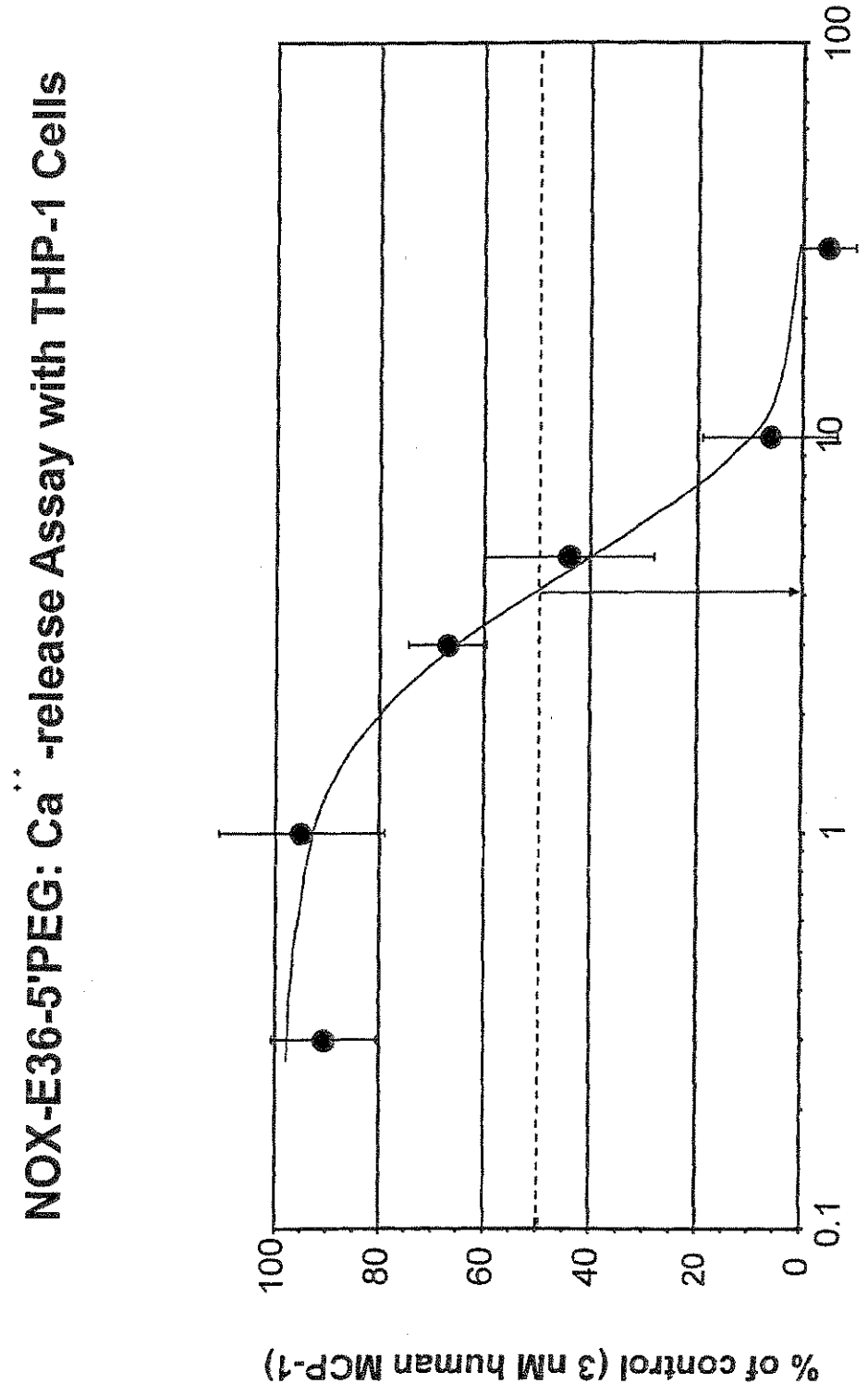

NOX-E36-5'PEG: Ca++-release Assay with THP-1 Cells
% of control (3 nM human MCP-1)
100
80
60
40
20
0
0.1
1
10
100
NOX-E36-5'PEG (nM)

Fig 27A

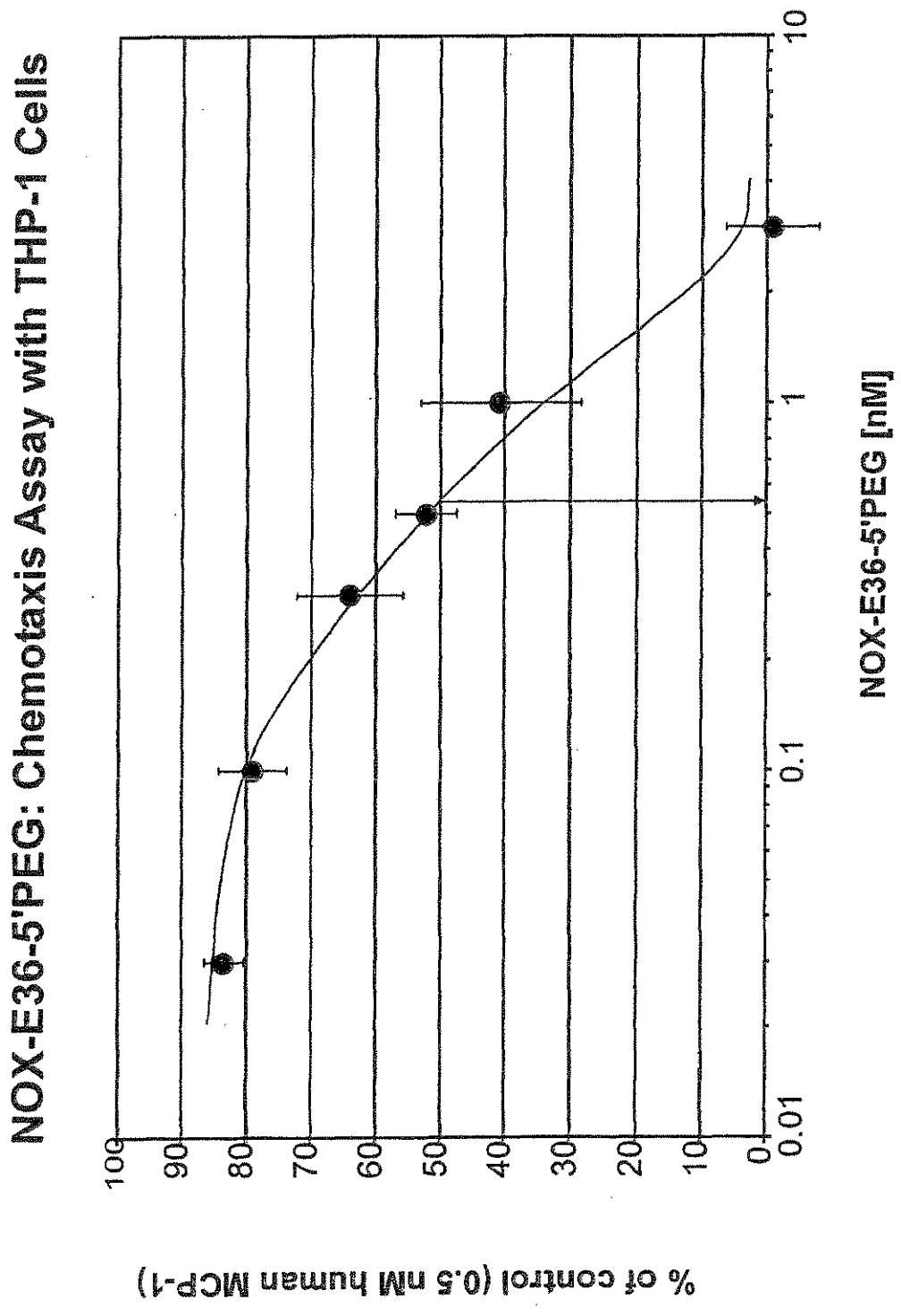

NOX-E36-5'PEG: Chemotaxis Assay with THP-1 Cells
% of control (0.5 nM human MCP-1)
100
90
80
70
60
50
40
30
20
10
0
0.01
0.1
1
10
NOX-E36-5'PEG [nM]

Fig 27B

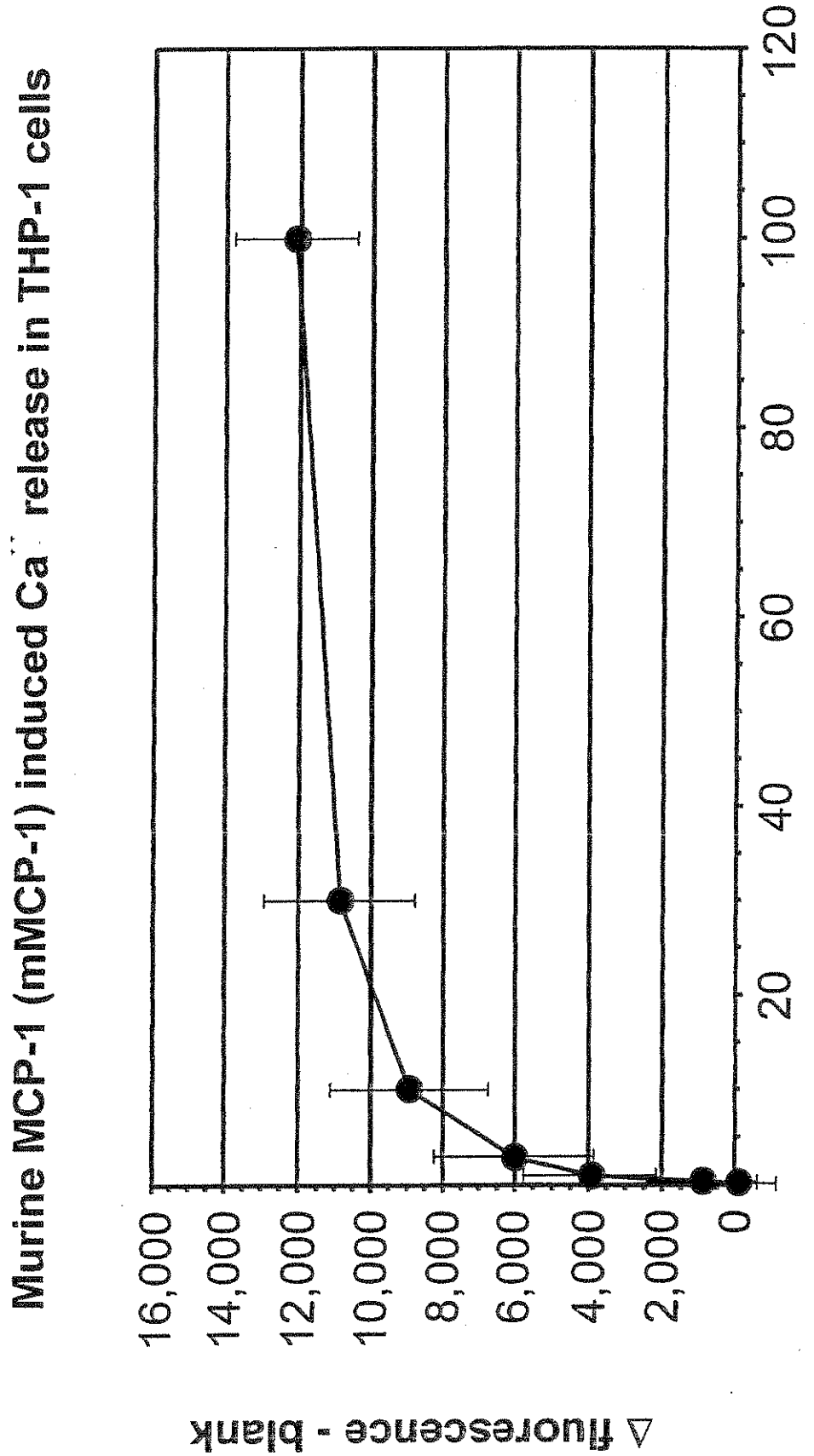

Murine MCP-1 (mMCP-1) induced Ca++ release in THP-1 cells
Δ fluorescence - blank
16,000
14,000
12,000
10,000
8,000
6,000
4,000
2,000
0
0
20
40
60
80
100
120
mMCP-1 [nM]

Fig. 28

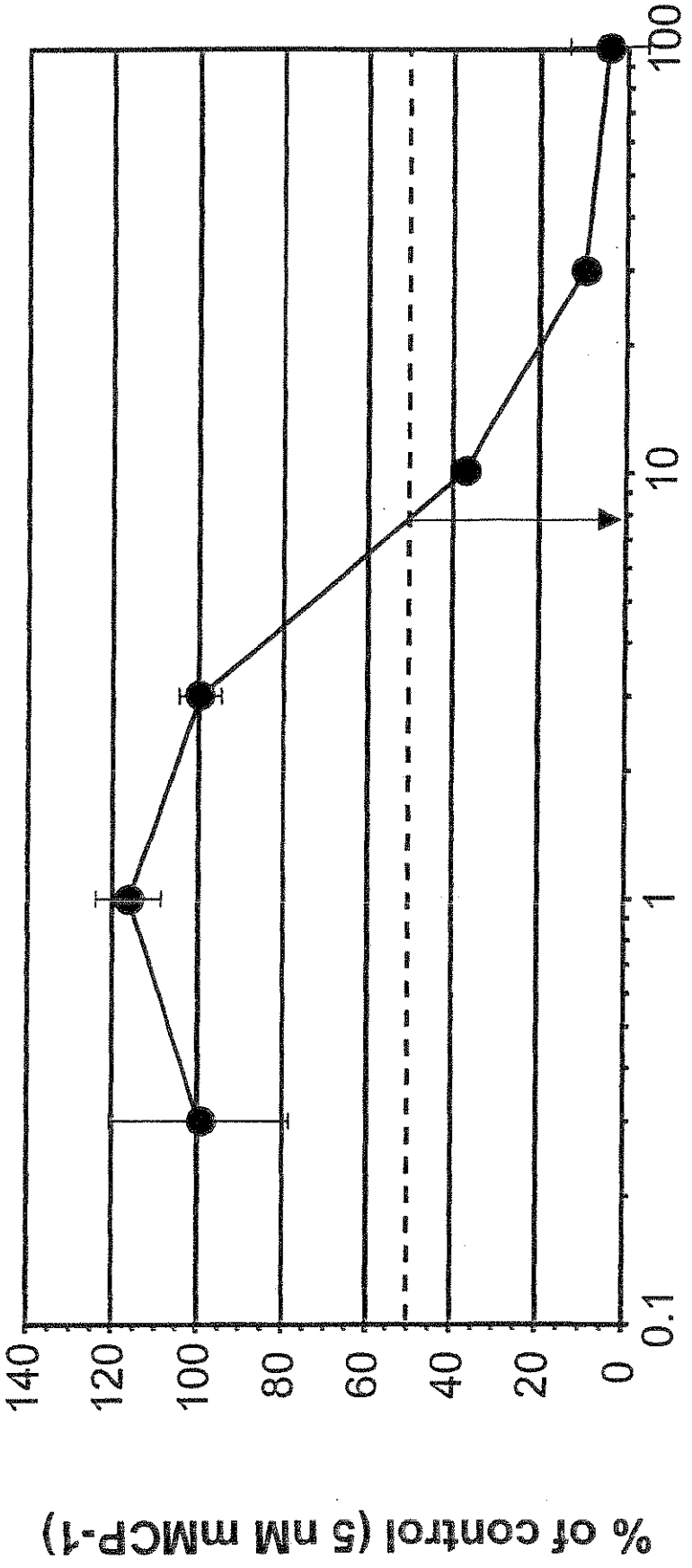

mNOX-E36-3'PEG: Ca++-release Assay with THP-1 Cells
% of control (5 nM mMCP-1)
140
120
100
80
60
40
20
0
0.1
1
10
100
mNOX-E36-3'PEG [nM]

Fig. 29

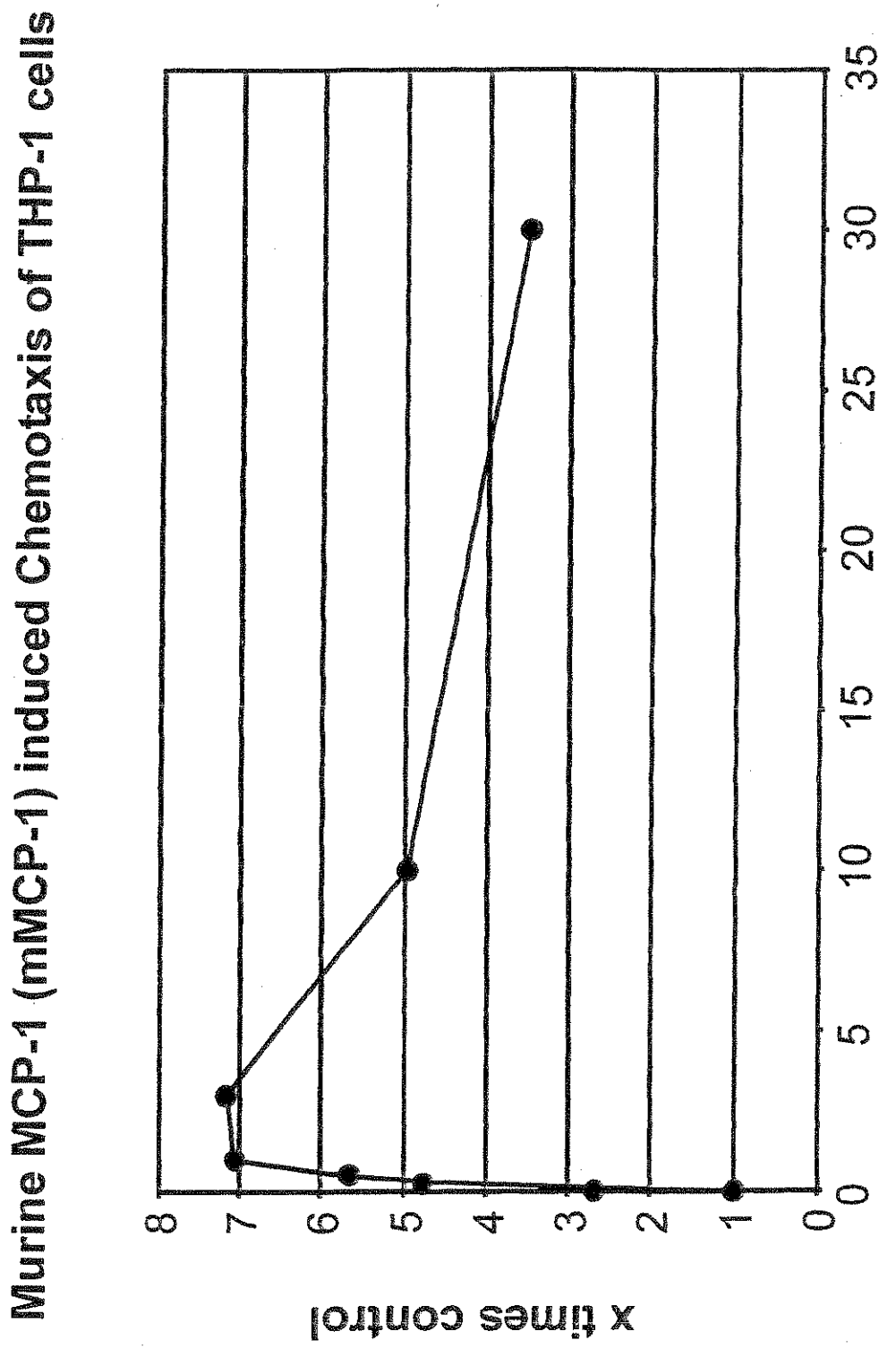

Murine MCP-1 (mMCP-1) induced Chemotaxis of THP-1 cells
x times control
0
1
2
3
4
5
6
7
8
0
5
10
15
20
25
30
35
mMCP-1 [nM]

Fig. 30

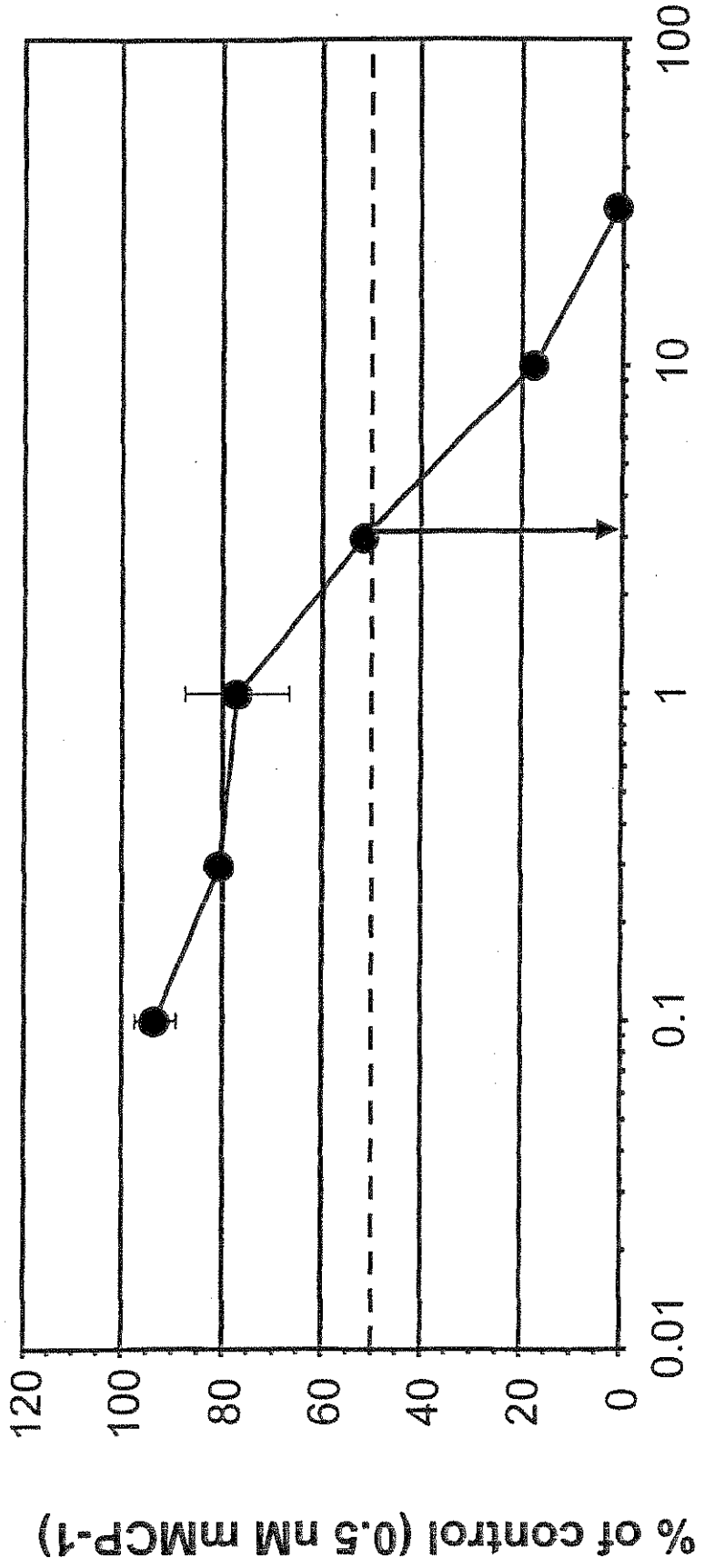

mNOX-E36-3'PEG: Chemotaxis Assay with THP-1 Cells
% of control (0.5 nM mMCP-1)
120
100
80
60
40
20
0
0.01
0.1
1
10
100
mNOX-E36-3'PEG [nM]

Fig. 31

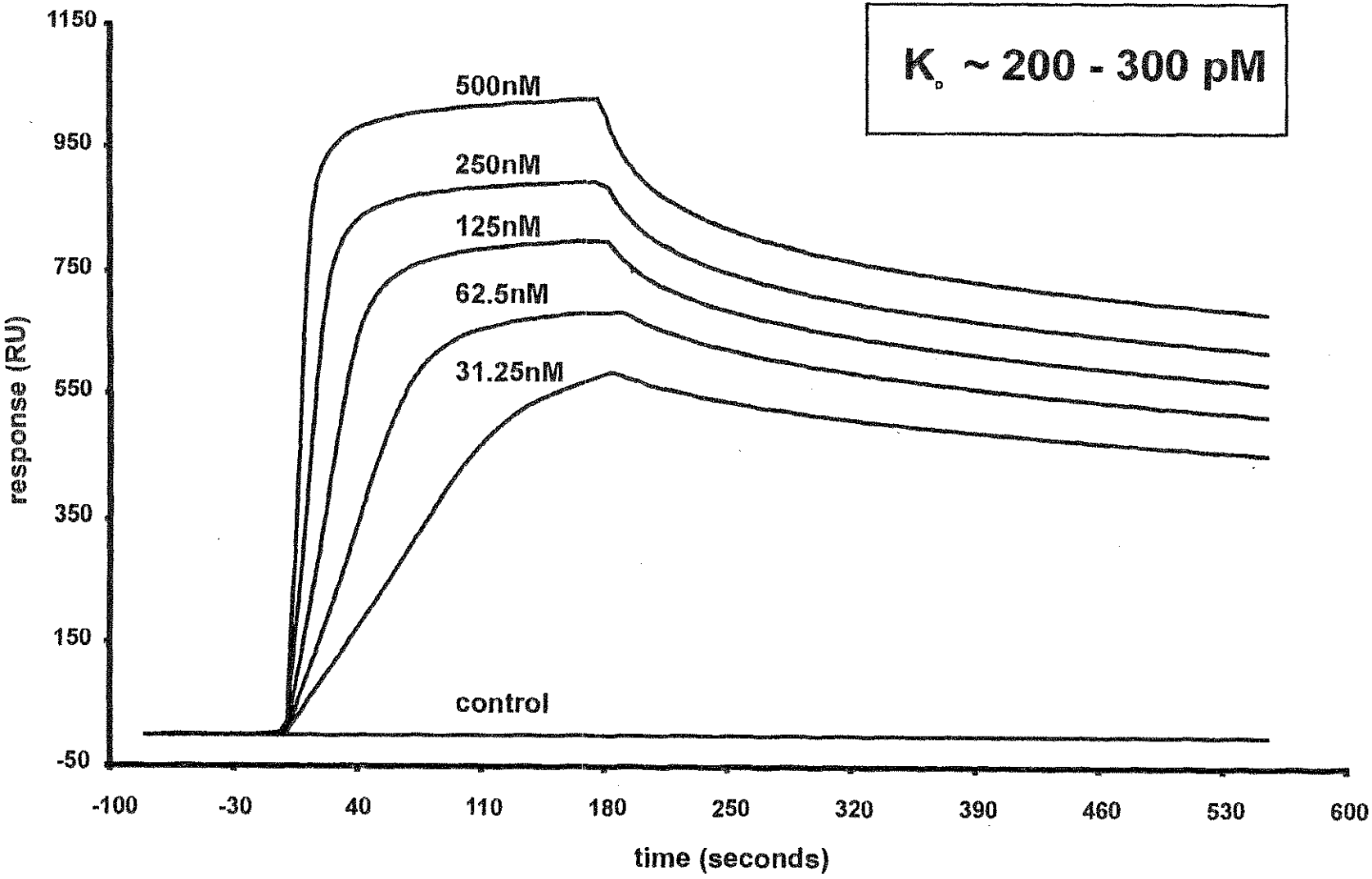


Fig. 32 Kinetics of D-mNOX-E36 binding to murine D-MCP-1

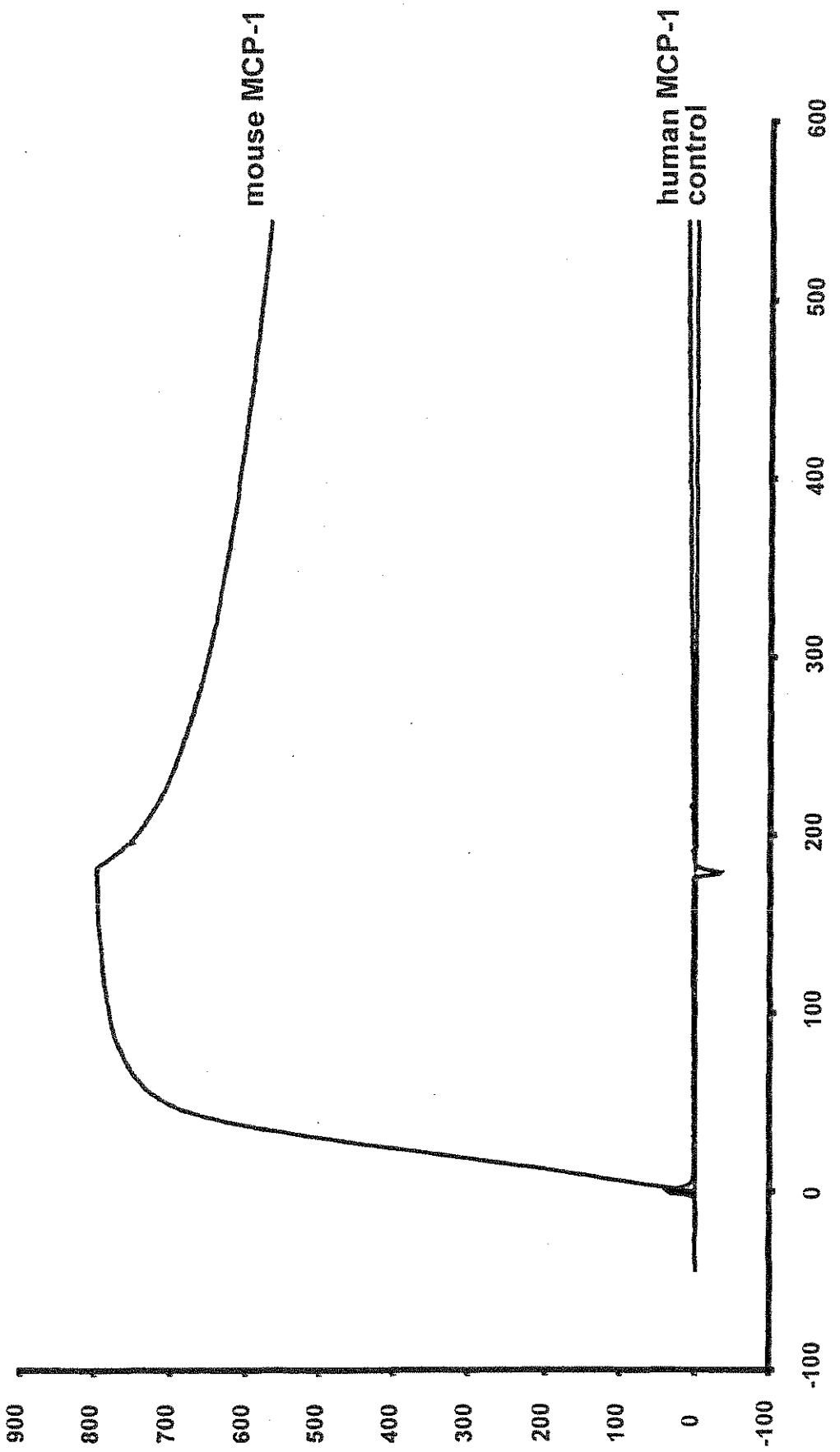


Fig. 33 D-mNOX-E36 binding to murine and human D-MCP-1

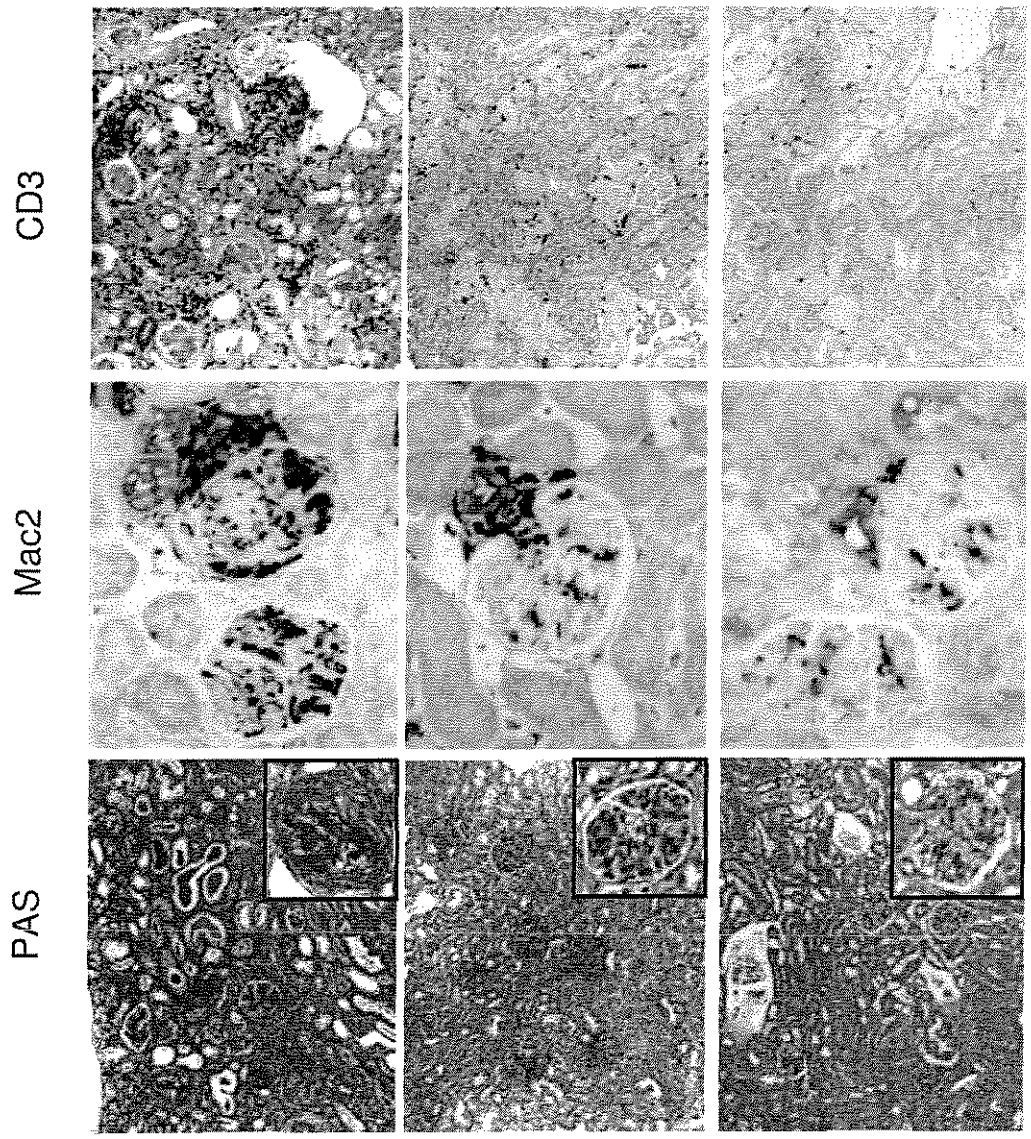


Fig. 34

	Vehicle	PoC	mNOX-E36	PoC-PEG	mNOX-E36-3'PEG
Renal disease					
GFR [µl/min]	179 ± 41	200 ± 49	245 ± 69	157 ± 74	293 ± 72
U albumin/creatinin ratio	15.6 ± 10.1	4.3 ± 1.4	6.8 ± 1.8	3.8 ± 0.5	2.4 ± 0.7
IgG_1 [glom. score]	1.5 ± 0.4	1.6 ± 0.2	1.6 ± 0.5	1.7 ± 0.2	1.7 ± 0.5
IgG_{2a} [glom. score]	0.9 ± 0.3	1.0 ± 0.3	1.0 ± 0.3	1.1 ± 0.3	1.0 ± 0.3
Activity index [score]	17.4 ± 4.9	17.8 ± 4.2	10.3 ± 5.0*	17.4 ± 2.7	9.4 ± 4.2*
Chronicity index [score]	6.0 ± 2.0	7.2 ± 2.6	2.6 ± 2.5	5.4 ± 1.0	1.6 ± 1.8*
Mac-2+ [cells/glom]	13.4 ± 2.0	12.6 ± 0.9	8.5 ± 2.3*	13.6 ± 2.3	8.2 ± 3.5*
Mac-2+ [cells/hpf]	20.3 ± 8.1	20.6 ± 6.7	10.8 ± 5.1	19.3 ± 3.7	7.7 ± 4.0*
CD3+ [cells/hpf]	44.6±14.7	39.4 ± 7.5	23.8±10.2	36.2 ± 3.1	19.0 ± 8.0*
Lung injury [score]	1.6 ± 0.8	1.6 ± 0.4	0.6 ± 0.5*	1.4 ± 0.4	0.4 ± 0.5*
Skin lesions [% of mice]	60	60	28	80	28

U albumin/creatinin ratio = urinary albumin/creatinine ratio in µg/mg, values are means ± SEM; * $p < 0.05$ Spiegelmer vs. respective PoC control.

Fig. 35

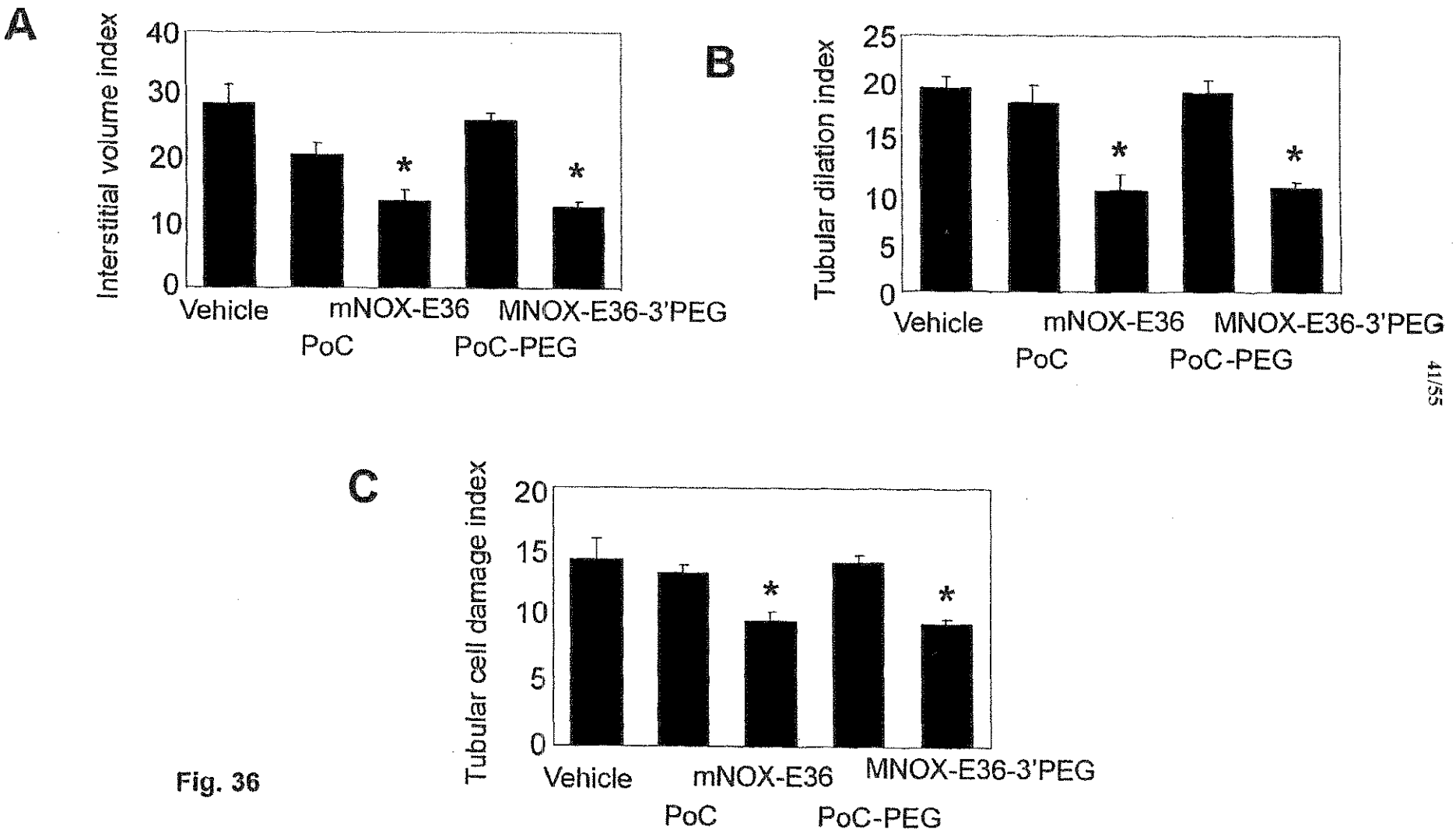

A
Interstitial volume index
40
30
20
10
0
*
*
Vehicle
mNOX-E36
PoC
MNOX-E36-3'PEG
PoC-PEG
B
Tubular dilation index
25
20
15
10
5
0
*
*
Vehicle
mNOX-E36
PoC
MNOX-E36-3'PEG
PoC-PEG
C
Tubular cell damage index
20
15
10
5
0
*
*
Vehicle
mNOX-E36
PoC
MNOX-E36-3'PEG
PoC-PEG

Fig. 36

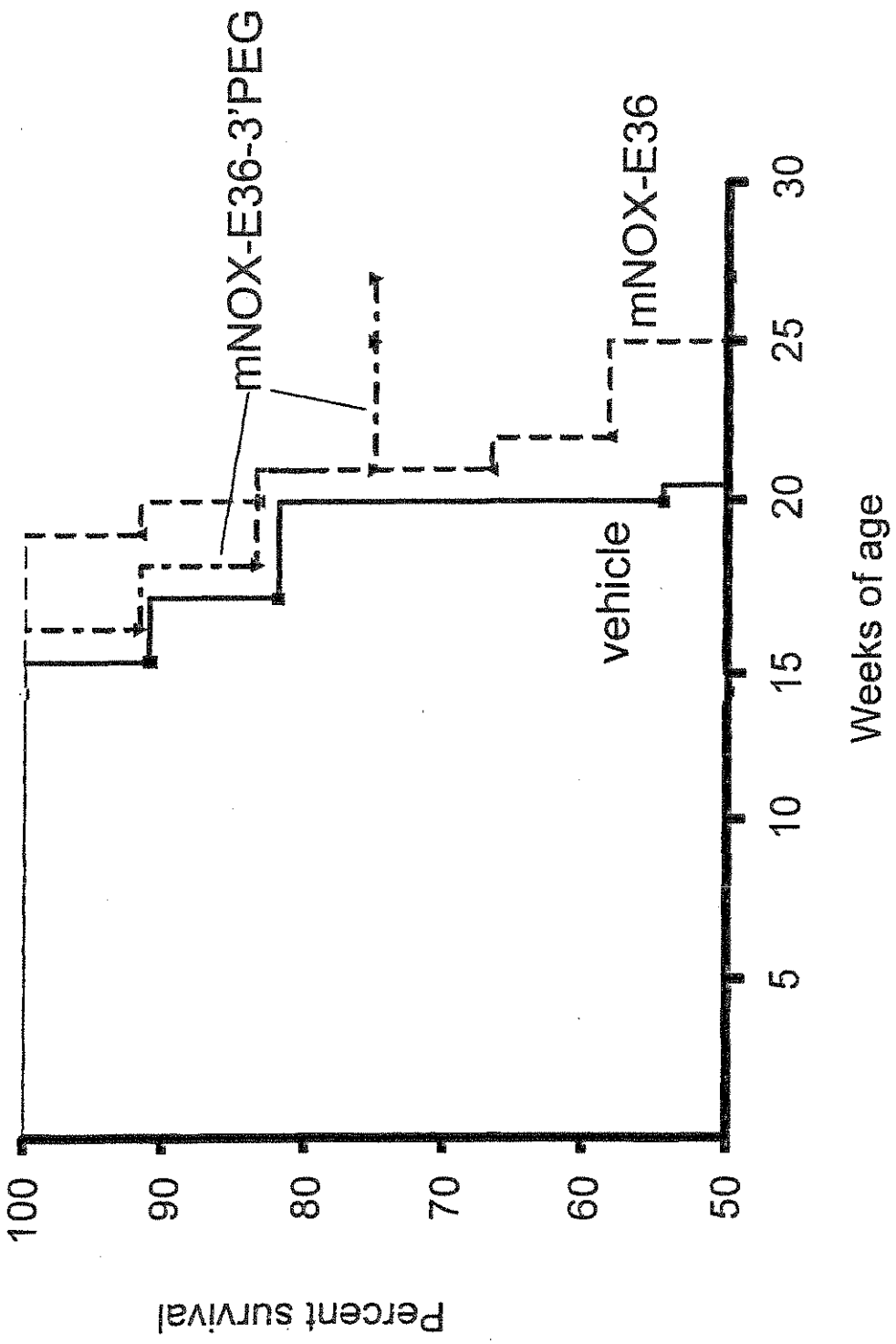

mNOX-E36-3'PEG
mNOX-E36
vehicle
Percent survival
100
90
80
70
60
50
5
10
15
20
25
30
Weeks of age

Fig. 37

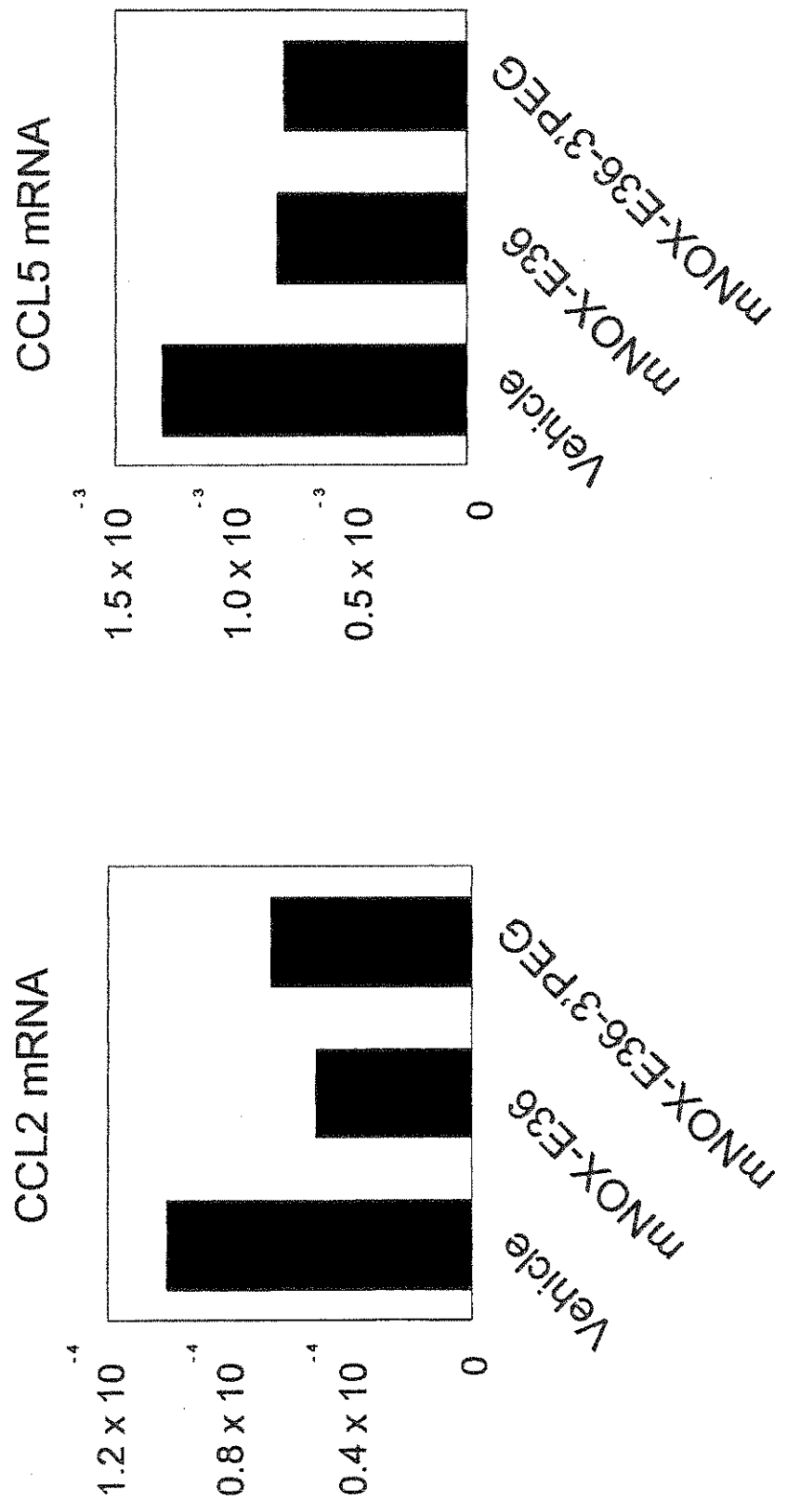

CCL5 mRNA
1.5 x 10 -3
1.0 x 10 -3
0.5 x 10 -3
0
Vehicle
mNOX-E36
mNOX-E36-3'PEG
CCL2 mRNA
1.2 x 10 -4
0.8 x 10 -4
0.4 x 10 -4
0
Vehicle
mNOX-E36
mNOX-E36-3'PEG

Fig. 38

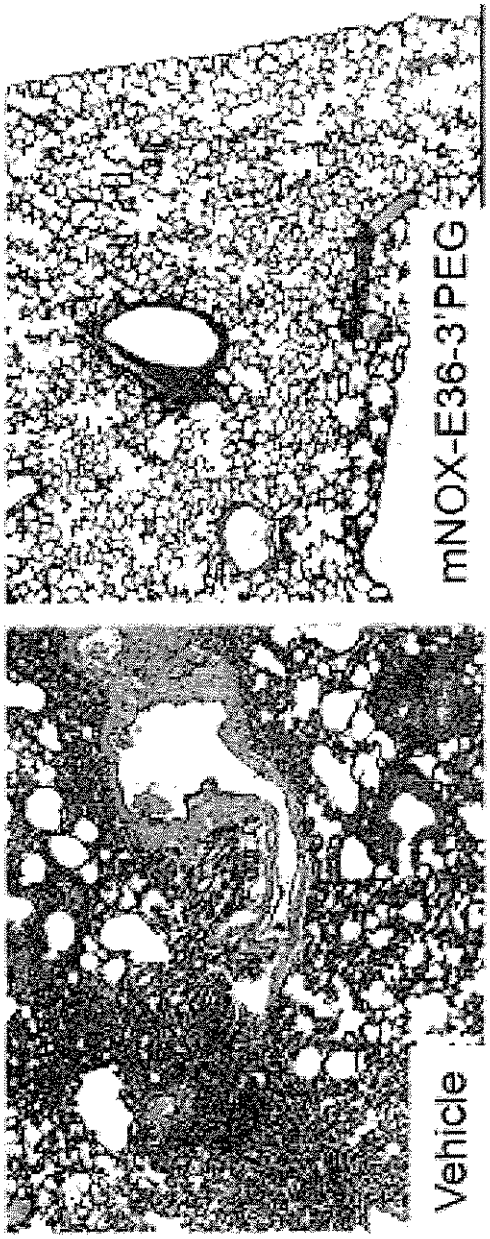


Fig. 39

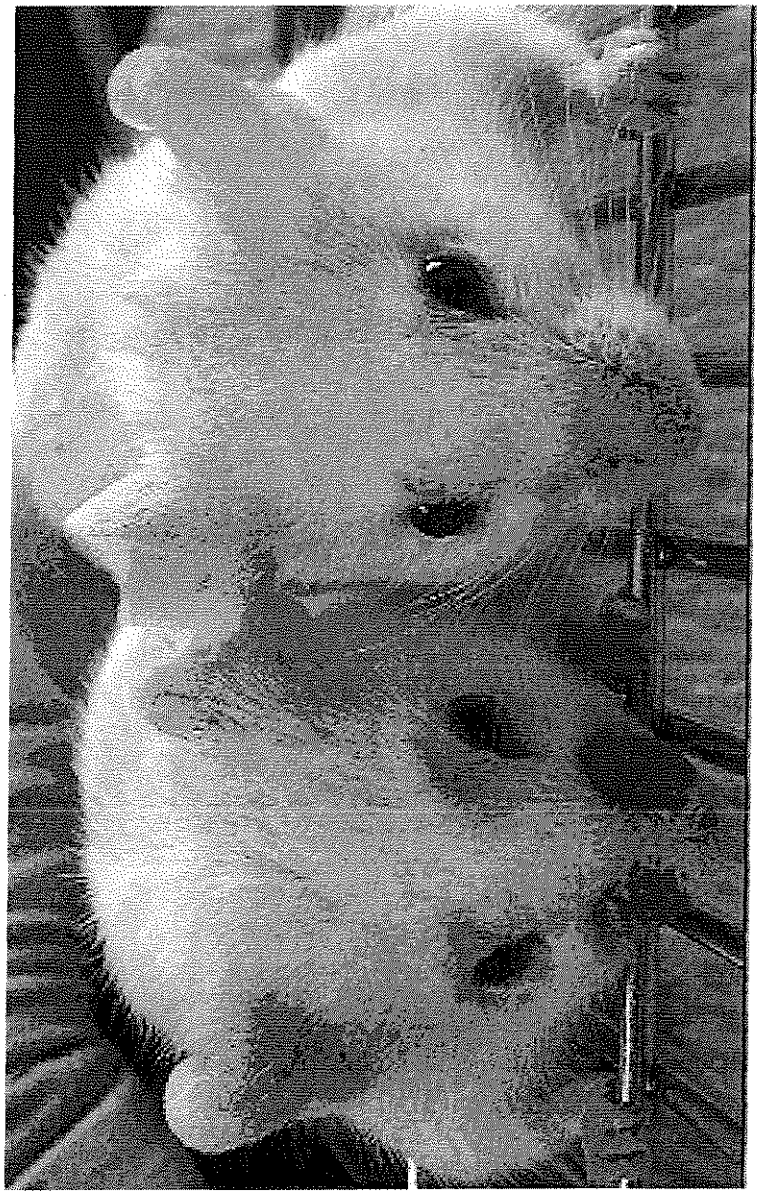


Fig. 40

	Vehicle	PoC	mNOX-E36	PoC-PEG	mNOX-E36-3'PEG
Lymphoproliferation					
Spleen weight [% BW]	1.8 ± 0.4	2.0 ± 0.2	1.6 ± 0.4	1.7 ± 0.1	1.6 ± 0.3
LN weight [% BW]	2.3 ± 0.7	1.8 ± 0.1	1.7 ± 0.3	1.7 ± 0.2	1.7 ± 0.7
Serum anti dsDNA					
IgG_1 [µg/ml]	11.7 ± 3.6	7.5 ± 2.8	11.7 ± 3.4	8.2 ± 1.2	6.6 ± 1.2
IgG_{2a} [µg/ml]	2.0 ± 0.3	1.9 ± 0.3	2.1 ± 0.1	2.0 ± 0.2	1.9 ± 0.2
IgG_{2b} [µg/ml]	17.6 ± 5.6	18.9 ± 5.2	22.6 ± 3.3	28.3 ± 2.5	20.6 ± 3.8

LN = bulk of mesenterial lymph nodes, values are means ± SEM

Fig. 41

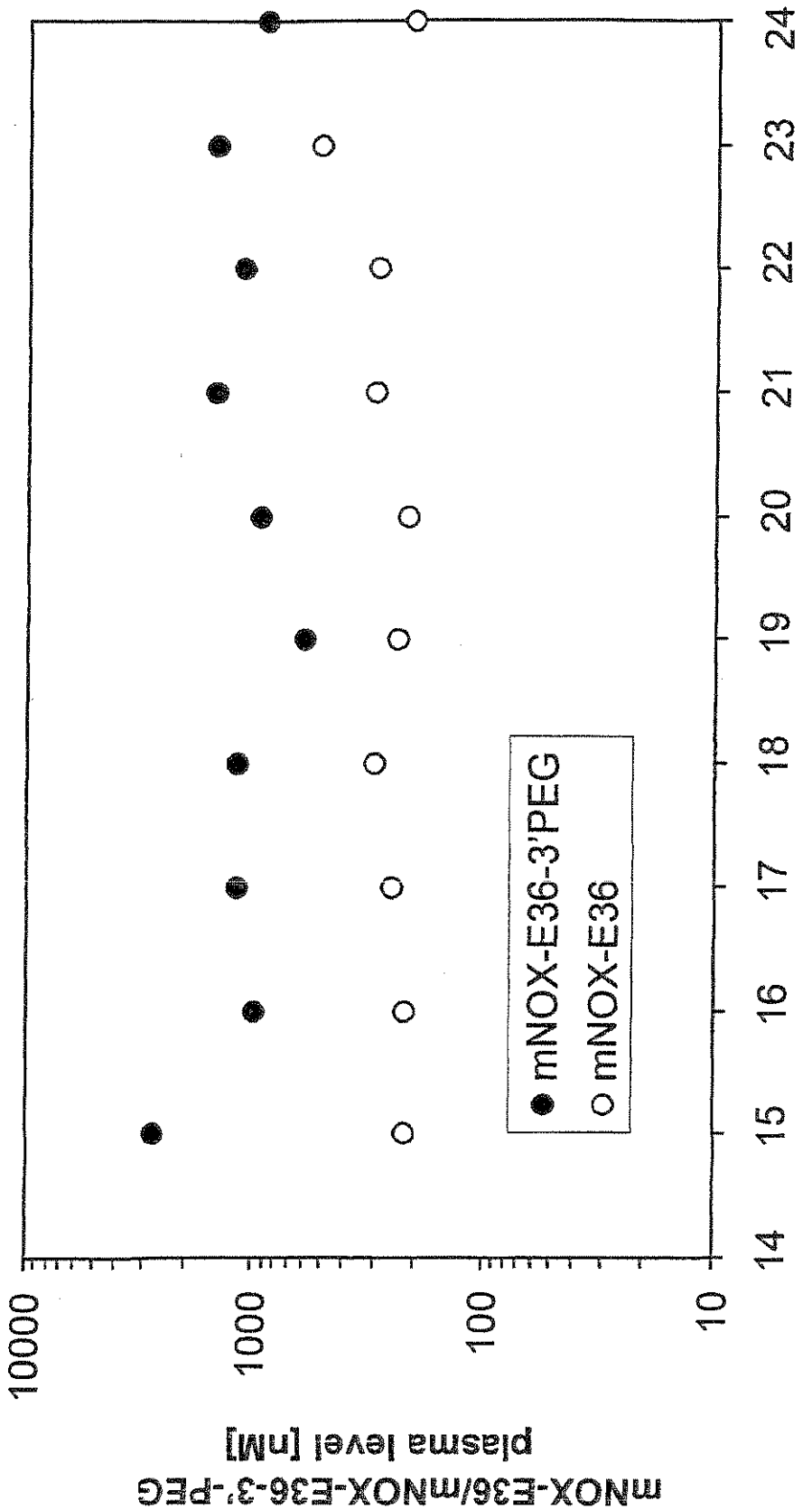

mNOX-E36/mNOX-E36-3'-PEG
plasma level [nM]
10000
1000
100
10
14
15
16
17
18
19
20
21
22
23
24
Week of age
mNOX-E36-3'PEG
mNOX-E36

Fig. 42

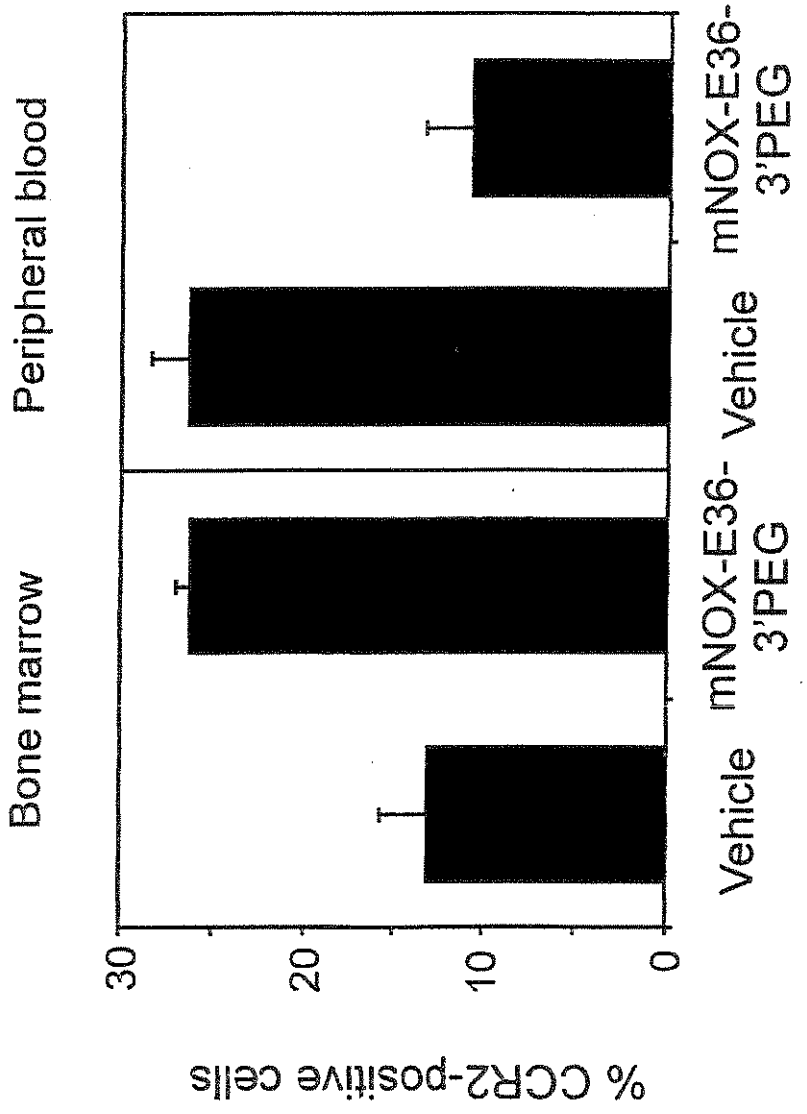

Bone marrow
Peripheral blood
% CCR2-positive cells
30
20
10
0
Vehicle
mNOX-E36-3'PEG
Vehicle
mNOX-E36-3'PEG

Fig. 43

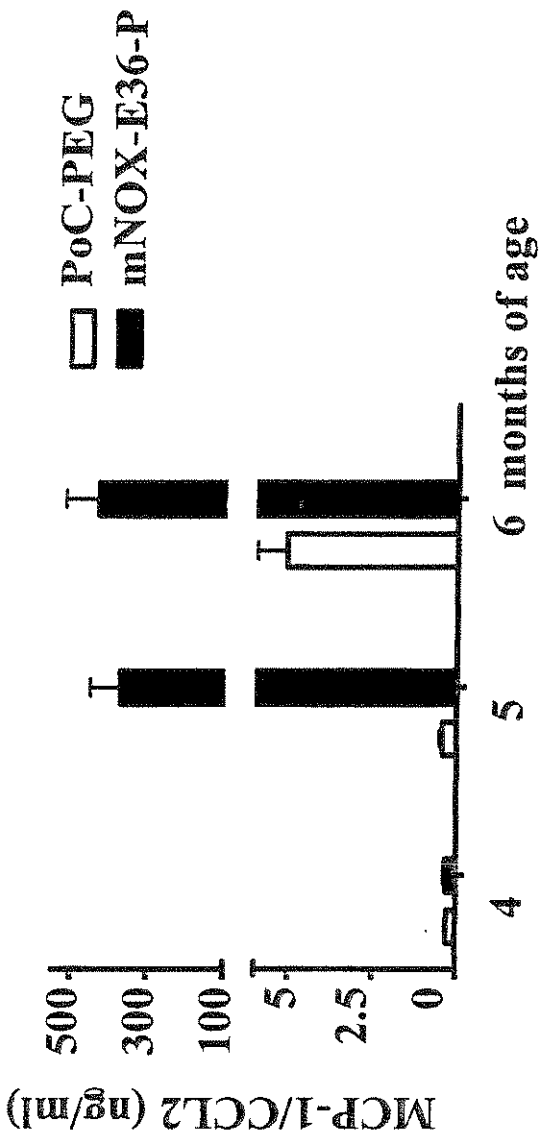

PoC-PEG
mNOX-E36-P
MCP-1/CCL2 (ng/ml)
500
300
100
5
2.5
0
4
5
6 months of age

Fig. 44

		2K		1K		
		Wildtype nil	db/db nil	db/db nil	db/db PoC-PEG	db/db mNOX-E36-3'PEG
Cellular response [cells/glomerulus or hpf]						
Glomerular	Mac-2+ cells	0.3 ± 0.1	1.8 ± 0.2	5.0 ± 0.7*	5.9 ± 0.4	3.5 ± 0.3#
	Ki-67+ cells	0.7 ± 0.1	0.9 ± 0.2	2.4 ± 0.2*	3.1 ± 0.3	1.1 ± 0.2#
Interstitial	Mac-2+ cells	3.2 ± 0.3	8.6 ± 1.0	19.2 ± 2.8*	23.8 ± 3.3	12.3 ± 1.2#

Values are means ± SEM; *, $p < 0.05$ 1K db/db vs 2K db/db; #, $p < 0.05$ mNOX-E36-3'PEG vs. PoC-PEG

Fig. 45

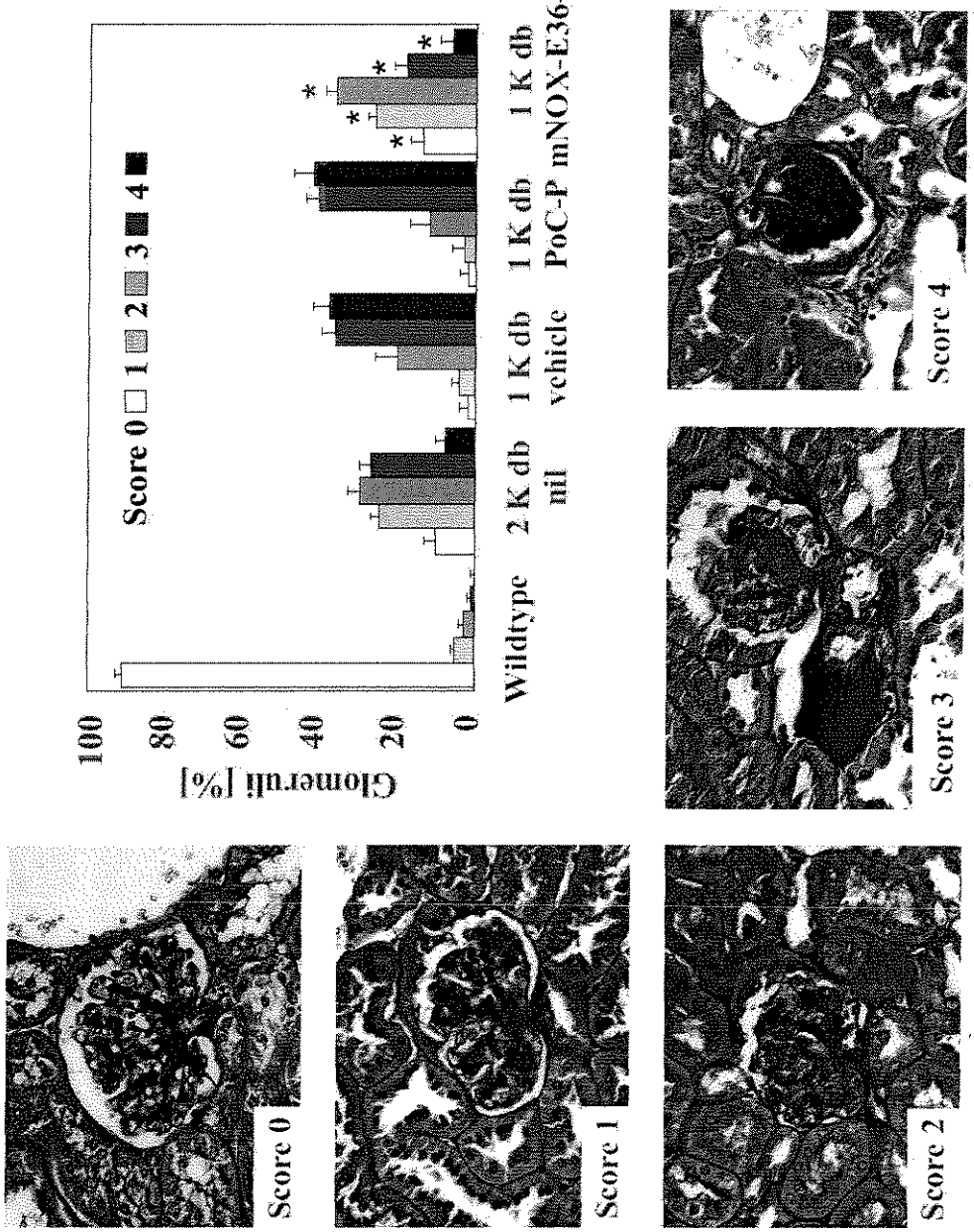

Score 0
Score 1
Score 2
Score 3
Score 4
Score 0 1 2 3 4
Clomeruli [%]
100
80
60
40
20
0
Wildtype
2 K db
nil
1 K db
vehicle
1 K db
PoC-P
1 K db
mNOX-E36-P
*

Fig. 46

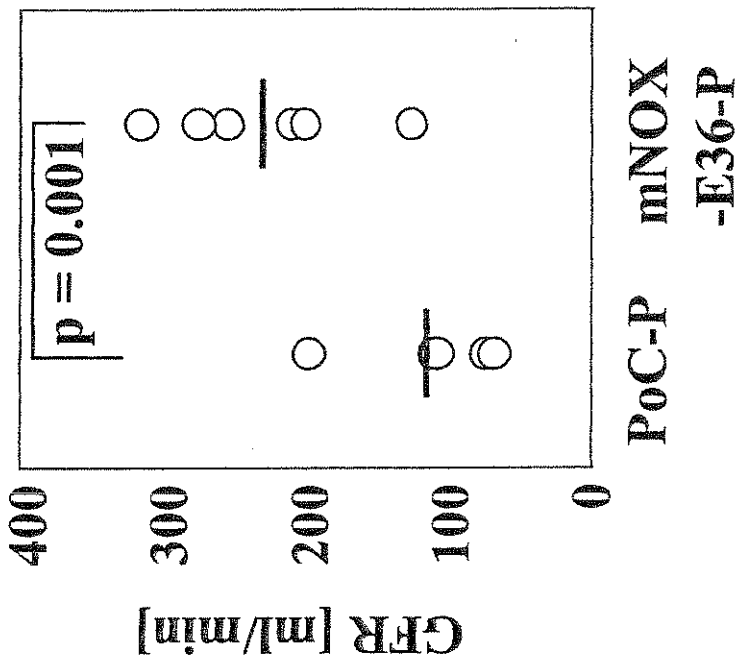


Fig. 47

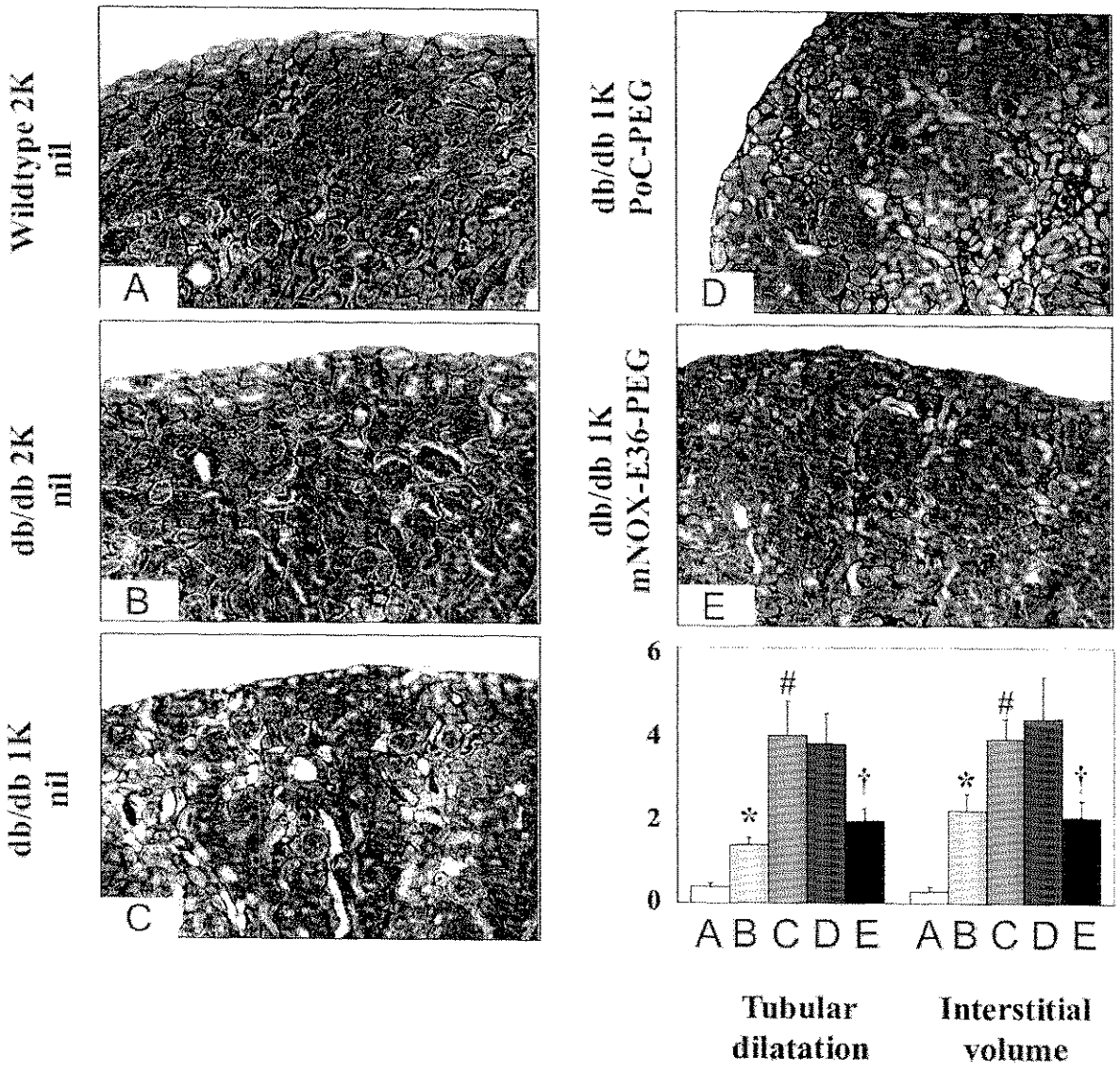

Wildtype 2K
nil
db/db 2K
nil
db/db 1K
nil
db/db 1K
PoC-PEG
db/db 1K
mNOX-E36-PEG
A
B
C
D
E
6
4
2
0
#
*
†
A B C D E A B C D E
Tubular
dilatation
Interstitial
volume

Fig. 48

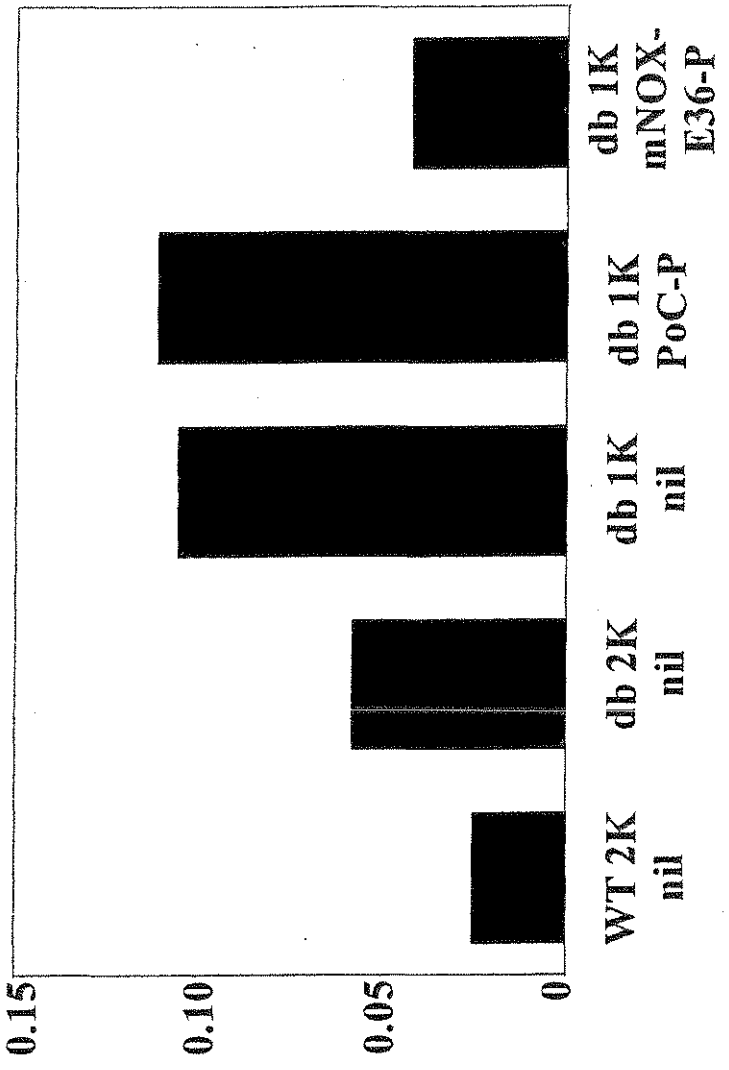

0.15
0.10
0.05
0
WT 2K nil
db 2K nil
db 1K nil
db 1K PoC-P
db 1K mNOX-E36-P

Fig. 49

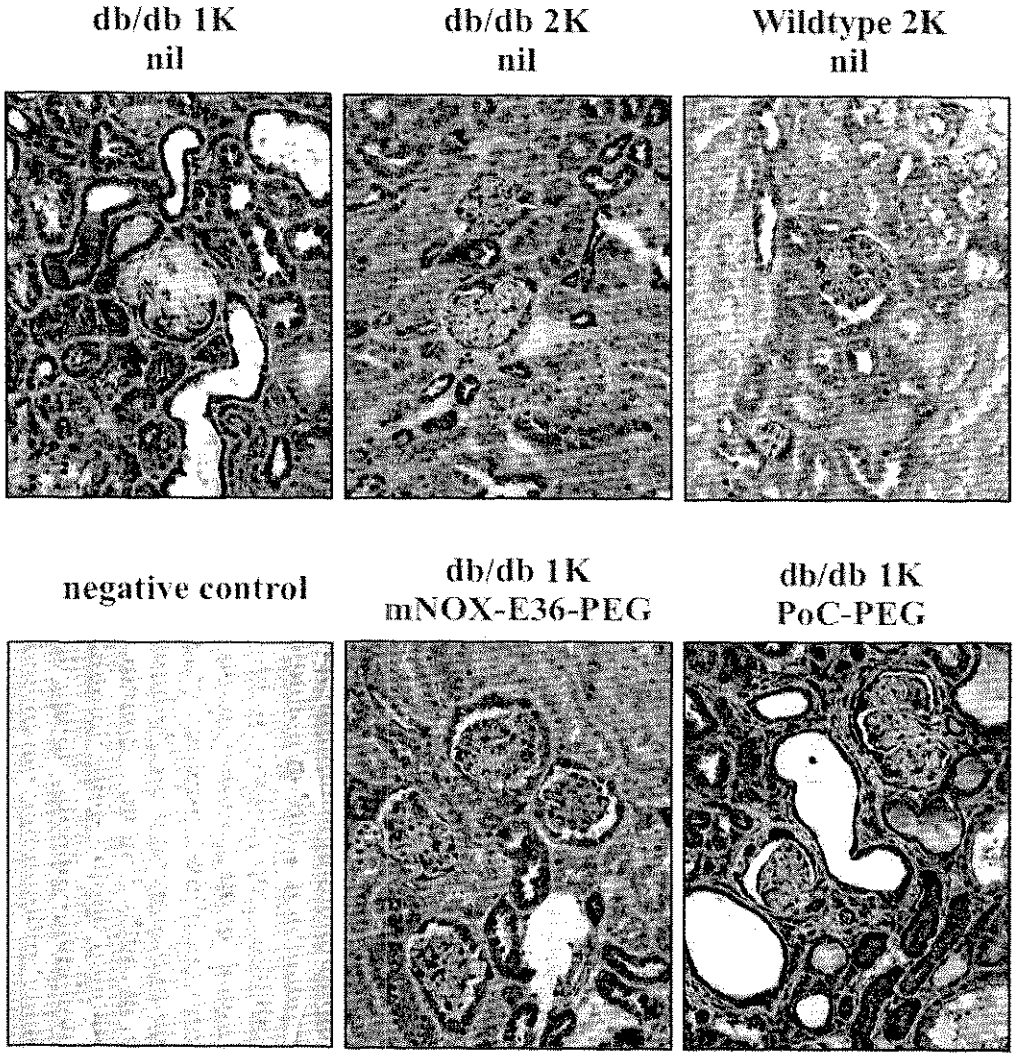

db/db 1K
nil
db/db 2K
nil
Wildtype 2K
nil
negative control
db/db 1K
mNOX-E36-PEG
db/db 1K
PoC-PEG

Fig. 50

SEQUENCE LISTING

<110> NOXXON Pharma AG

<120> MCP-1 binding nucleic acids

<130> SP9585A

<160> 285

<170> PatentIn version 3.1

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<211> 76

<212> PRT

<213> Homo sapiens

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            20                  25                  30

Ser Ser Lys Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Ile Val Ala
        35                  40                  45

Lys Glu Ile Cys Ala Asp Pro Lys Gln Lys Trp Val Gln Asp Ser Met
    50                  55                  60

Asp His Leu Asp Lys Gln Thr Gln Thr Pro Lys Thr
65                  70                  75
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<213> Mus musculus

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20 25 30

Ser Ser Arg Cys Pro Lys Glu Ala Val Val Phe Val Thr Lys Leu Lys
35 40 45

Arg Glu Val Cys Ala Asp Pro Lys Lys Glu Trp Val Gln Thr Tyr Ile
50 55 60

Lys Asn Leu Asp Arg Asn Gln Met Arg Ser Glu Pro Thr Thr Leu Phe
65 70 75 80

Lys Thr Ala Ser Ala Leu Arg Ser Ser Ala Pro Leu Asn Val Lys Leu
85 90 95

Thr Arg Lys Ser Glu Ala Asn Ala Ser Thr Thr Phe Ser Thr Thr Thr
100 105 110

Ser Ser Thr Ser Val Gly Val Thr Ser Val Thr Val Asn
115 120 125

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<211> 76

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<213> Maca mulatta

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20 25 30

Ser Ser Lys Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Ile Val Ala
35 40 45

Lys Glu Ile Cys Ala Asp Pro Lys Gln Lys Trp Val Gln Asp Ser Met

50 55 60

Asp His Leu Asp Lys Gln Ile Gln Thr Pro Lys Pro
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<213> Sus scrofa

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20 25 30

Ser Ser Lys Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Ile Ala Gly
35 40 45

Lys Glu Ile Cys Ala Glu Pro Lys Gln Lys Trp Val Gln Asp Ser Ile
50 55 60

Ser His Leu Asp Lys Lys Asn Gln Thr Pro Lys Pro
65 70 75

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20 25 30

Ser Ser Lys Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Val Leu Asn
35 40 45

Lys Glu Ile Cys Ala Asp Pro Lys Gln Lys Trp Val Gln Asp Ser Met
50 55 60

Ala His Leu Asp Lys Lys Ser Gln Thr Gln Thr Ala
65 70 75

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20 25 30

Ser Thr Lys Cys Pro Lys Glu Ala Val Ile Phe Met Thr Lys Leu Ala
35 40 45

Lys Gly Ile Cys Ala Asp Pro Lys Gln Lys Trp Val Gln Asp Ala Ile
50 55 60

Ala Asn Leu Asp Lys Lys Met Gln Thr Pro Lys Thr Leu Thr Ser Tyr
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Ser Thr Thr Gln Glu His Thr Thr Asn Leu Ser Ser Thr Arg Thr Pro
85 90 95

Ser Thr Thr Thr Ser Leu
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<211> 76

<212> PRT

<213> Homo sapiens

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Asn Lys Lys Ile Pro Lys Gln Arg Leu Glu Ser Tyr Arg Arg Thr Thr
            20                  25                  30

Ser Ser His Cys Pro Arg Glu Ala Val Ile Phe Lys Thr Lys Leu Asp
        35                  40                  45

Lys Glu Ile Cys Ala Asp Pro Thr Gln Lys Trp Val Gln Asp Phe Met
    50                  55                  60

Lys His Leu Asp Lys Lys Thr Gln Thr Pro Lys Leu
65                  70                  75
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<213> Homo sapiens

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            20                  25                  30

Lys Cys Pro Gln Lys Ala Val Ile Phe Lys Thr Lys Leu Ala Lys Asp
        35                  40                  45

Ile Cys Ala Asp Pro Lys Lys Lys Trp Val Gln Asp Ser Met Lys Tyr
    50                  55                  60

Leu Asp Gln Lys Ser Pro Thr Pro Lys Pro
65                  70
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<210> 9

<211> 76

<212> PRT

<213> Homo sapiens

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20 25 30

Asn Ile Gln Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Lys Arg Gly
35 40 45

Lys Glu Val Cys Ala Asp Pro Lys Glu Arg Trp Val Arg Asp Ser Met
50 55 60

Lys His Leu Asp Gln Ile Phe Gln Asn Leu Lys Pro
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<210> 35

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<210> 54

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<212> RNA

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35 40 45

Lys Glu Ile Cys Ala Asp Pro Lys Gln Lys Trp Val Gln Asp Ser Met
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Arg Glu Val Cys Ala Asp Pro Lys Lys Glu Trp Val Gln Thr Tyr Ile
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<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(50)

<223> synthetic

<400> 215
ggacuaguca gccagugugu auaucggacg cgggguuuauu uacugacagg 50

<210> 216

<211> 50

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(50)

<223> synthetic

<400> 216
ggacuguccg gagugugaaa cucccccgaga ccgccagaag cggggacagg 50

<210> 217

<211> 50

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(50)

<223> synthetic

<400> 217
ggacuucuau ccaggugggu gguaguaugu aaagagauag aagugacagg 50

<210> 218

<211> 50

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(50)

<223> synthetic

<400> 218
ggacgagagc gaacaaugau auaaccuccu gacggaaaga gaucgacagg 50

<210> 219

<211> 48

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(48)

<223> synthetic

<400> 219
ccugugcuac acgcaguaag aagugaacgu ucaguaugug ugcacagg 48

<210> 220

<211> 48

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(48)

<223> synthetic

<400> 220
cgugagccag gcaccgaggg cguuaacugg cugauuggac acgacacg 48

<210> 221

<211> 48

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(48)

<223> synthetic

<400> 221
cgugaacaug caagcuaagc ggggcuguug guugcuuggc ccgccacg 48

<210> 222

<211> 48

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(48)

<223> synthetic

<400> 222
cgugcagaga gagaccaacc acguaaaauc aaccuaaugg gccgcacg 48

<210> 223

<211> 48

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

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<221> D-RNA

<222> (1)..(48)

<223> synthetic

<400> 223
cgugcagaga gagaccaacc acguaaaauc aaccuaaugg gccgcacg 48

<210> 224

<211> 48

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(48)

<223> synthetic

<400> 224
cgugaacauu caagcuaagc ggggcuguug guugcuuggc ccgccacg 48

<210> 225

<211> 48

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(48)

<223> synthetic

<400> 225
cgugccgagg cggcgaccag cguuacuuag agaggcuuug gcaccacg 48

<210> 226

<211> 47

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(47)

<223> synthetic

<400> 226
cgugauaaca gccgucgguc aagaaaacaa aguucgggcg gcgcacg 47

<210> 227

<211> 47

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(47)

<223> synthetic

<400> 227
cguggguggc gcaccgaggg cgaaaagcca ccaguaaaga uagaccg 47

<210> 228

<211> 45

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(45)

<223> synthetic

<400> 228
cgugugaucu ccuuuggggu gauuagcuua gagacuuccc acacg 45

<210> 229

<211> 45

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(45)

<223> synthetic

<400> 229
gcaccuucgc cuaauacacg ugccggcuag cuaauacucg uccgc 45

<210> 230

<211> 45

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(45)

<223> synthetic

<400> 230
gcacgacuug ggcgaccagu gauacuuaga gagcaagucg ucggc 45

<210> 231

<211> 44

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(44)

<223> synthetic

<400> 231
gcgcgcgcuc aguaagaaau ugaaaguuca gaaugucguc gcgc 44

<210> 232

<211> 39

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(39)

<223> synthetic

<400> 232
agugugguggc aggcuaagga gauauuccga gaccacgcu 39

<210> 233

<211> 39

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(39)

<223> synthetic

<400> 233
agugugguggc agacuaugga uagacuccga gaccacgcu 39

<210> 234

<211> 39

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(39)

<223> synthetic

<400> 234
agcgugaggc gaccagcgga uuacuuagag agucacgcu 39

<210> 235

<211> 39

<212> RNA

<213> artificial sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(39)

<223> synthetic

<400> 235
agcgugaagg ggaccagcgu uacuuacaga guucacgcu 39

<210> 236

<211> 39

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(39)

<223> synthetic

<400> 236
agcgugugau guauguagca ccguaucaga ggacacgcu 39

<210> 237

<211> 37

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(37)

<223> synthetic

<400> 237
agcgugaggc gacccguguu ucguagagag ucacgcu 37

<210> 238

<211> 40

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(40)

<223> synthetic

<220>

<221> D-RNA

<222> (1)..(40)

<223> 5' PEGylation

<400> 238
gcacgucccu caccggugca agugaagccg uggcucugcg 40

<210> 239

<211> 40

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(40)

<223> synthetic

<220>

<221> D-RNA

<222> (1)..(40)

<223> 3'-PEGylation

<400> 239
gcacgucccu caccggugca agugaagccg uggcucugcg 40

<210> 240

<211> 58

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(58)

<223> synthetic

<400> 240
gagauggcga cauugguugg gcaugaggcg aggcccuuug augaauccgc ggccauuc 58

<210> 241

<211> 56

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(56)

<223> synthetic

<400> 241
gauggcgaca uugguugggc augaggcgag gcccuuugau gaauccgcgg ccauuc 56

<210> 242

<211> 53

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(53)

<223> synthetic

<400> 242
ggcgacauug guugggcaug aggcgaggcc cuuugaugaa uccgcggcca uuc 53

<210> 243

<211> 52

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(52)

<223> synthetic

<400> 243
ggcgacauug guugggcaug aggcgaggcc cuuugaugaa uccgcggcca uu 52

<210> 244

<211> 50

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(50)

<223> synthetic

<400> 244
ggcgacauug guugggcaug aggcgaggcc cuuugaugaa uccgcggcca 50

<210> 245

<211> 48

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(48)

<223> synthetic

<400> 245
gcugguuacc gaggggcgu cguuggaguu ugguugguug ucaccagc 48

<210> 246

<211> 46

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(46)

<223> synthetic

<400> 246
cugguuaccg aggggcguc guuggaguuu gguugguugu caccag 46

<210> 247

<211> 44

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(44)

<223> synthetic

<400> 247
ugguuaccga gggggcgucg uuggaguuug guugguuguc acca 44

<210> 248

<211> 48

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

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<221> D-RNA

<222> (1)..(48)

<223> synthetic

<400> 248
gccgguuacc gagggggcgu cguuggaguu ugguugguug ucaccggc 48

<210> 249

<211> 48

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(48)

<223> synthetic

<400> 249
gccggcuacc gaggggggcgu cguuggaguu ugguuggguug ucgccggc 48

<210> 250

<211> 46

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(46)

<223> synthetic

<400> 250
gcgcguaccg agggggcguc guuggaguuu gguuggguugu ccgcgc 46

<210> 251

<211> 46

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> D-RNA

<222> (1)..(46)

<223> synthetic

<400> 251

gggccuaccg agggggcguc guuggaguuu gguugguugu cggccc 46

<210> 252

<211> 76

<212> PRT

<213> Rattus rattus

<400> 252

Gln Pro Asp Ala Val Asn Ala Pro Leu Thr Cys Cys Tyr Ser Phe Thr
1 5 10 15

Gly Lys Met Ile Pro Met Ser Arg Leu Glu Asn Tyr Lys Arg Ile Thr
20 25 30

Ser Ser Arg Cys Pro Lys Glu Ala Val Val Phe Val Thr Lys Leu Lys
35 40 45

Arg Glu Ile Cys Ala Asp Pro Asn Lys Glu Trp Val Gln Lys Tyr Ile
50 55 60

Arg Lys Leu Asp Gln Asn Gln Val Arg Ser Glu Thr
65 70 75

<210> 253

<211> 50

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> L-RNA

<222> (1)..(50)

<223> synthetic

<220>

<221> L-RNA

<222> (1)..(50)

<223> 5'-PEGylation

<400> 253
ggcgacauug guugggcaug aggcgaggcc cuuugaugaa uccgcggcca 50

<210> 254

<211> 50

<212> RNA

<213> Artificial Sequence

<220>

<223> MCP-1 binder

<220>

<221> L-RNA

<222> (1)..(50)

<223> synthetic

<220>

<221> L-RNA

<222> (1)..(50)

<223> 3'-PEGylation

<400> 254
ggcgacauug guugggcaug aggcgaggcc cuuugaugaa uccgcggcca 50

<210> 255

<211> 11

<212> DNA

<213> Artificial Sequence

<220>

<223> NOX-E36 Capture probe

<220>

<221> L-DNA

<222> (1)..(11)

<223> synthetic

<220>

<221> L-DNA

<222> (1)..(11)

<223> -(spacer18)2-nh4+ at 3' end

<400> 255
gagggacgtg c 11

<210> 256

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> NOX-E36 Detect probe

<220>

<221> L-DNA

<222> (1)..(9)

<223> synthetic

<220>

<221> L-DNA

<222> (1)..(9)

<223> 5'- Biotin-(Spacer18)

<400> 256
cgcagagcc 9

<210> 257

<211> 73

<212> PRT

<213> Artificial Sequence

<220>

<223> CCL1/I-309

<220>

<221> L-Protein

<222> (1)..(73)

<223> synthetic

<400> 257

Lys Ser Met Gln Val Pro Phe Ser Arg Cys Cys Phe Ser Phe Ala Glu
1 5 10 15

Gln Glu Ile Pro Leu Arg Ala Ile Leu Cys Tyr Arg Asn Thr Ser Ser
20 25 30

Ile Cys Ser Asn Glu Gly Leu Ile Phe Lys Leu Lys Arg Gly Lys Glu
35 40 45

Ala Cys Ala Leu Asp Thr Val Gly Trp Val Gln Arg His Arg Lys Met
50 55 60

Leu Arg His Cys Pro Ser Lys Arg Lys
65 70

<210> 258

<211> 69

<212> PRT

<213> Artificial Sequence

<220>

<223> CCL3/MIP-1?

<220>

<221> L-Protein

<222> (1)..(69)

<223> synthetic

<400> 258

Ser Leu Ala Ala Asp Thr Pro Thr Ala Cys Cys Phe Ser Tyr Thr Ser
1 5 10 15

Arg Gln Ile Pro Gln Asn Phe Ile Ala Asp Tyr Phe Glu Thr Ser Ser
20 25 30

Gln Cys Ser Lys Pro Gly Val Ile Phe Leu Thr Lys Arg Ser Arg Gln
35 40 45

Val Cys Ala Asp Pro Ser Glu Glu Trp Val Gln Lys Tyr Val Ser Asp
50 55 60

Leu Glu Leu Ser Ala
65

<210> 259

<211> 69

<212> PRT

<213> Artificial Sequence

<220>

<223> CCL4/MIP-1beta

<220>

<221> L-Protein

<222> (1)..(69)

<223> synthetic

<400> 259

Ala Pro Met Gly Ser Asp Pro Pro Thr Ala Cys Cys Phe Ser Tyr Thr
1 5 10 15

Ala Arg Lys Leu Pro Arg Asn Phe Val Val Asp Tyr Tyr Glu Thr Ser
20 25 30

Ser Leu Cys Ser Gln Pro Ala Val Val Phe Gln Thr Lys Arg Ser Lys
35 40 45

Gln Val Cys Ala Asp Pro Ser Glu Ser Trp Val Gln Glu Tyr Val Tyr
50 55 60

Asp Leu Glu Leu Asn
65

<210> 260

<211> 68

<212> PRT

<213> Artificial Sequence

<220>

<223> CCL5/RANTES

<220>

<221> L-Protein

<222> (1)..(68)

<223> synthetic

<400> 260

Ser Pro Tyr Ser Ser Asp Thr Thr Pro Cys Cys Phe Ala Tyr Ile Ala
1 5 10 15

Arg Pro Leu Pro Arg Ala His Ile Lys Glu Tyr Phe Tyr Thr Ser Gly
20 25 30

Lys Cys Ser Asn Pro Ala Val Val Phe Val Thr Arg Lys Asn Arg Gln
35 40 45

Val Cys Ala Asn Pro Glu Lys Lys Trp Val Arg Glu Tyr Ile Asn Ser
50 55 60

Leu Glu Met Ser
65

<210> 261

<211> 82

<212> PRT

<213> Artificial Sequence

<220>

<223> CCL13/MCP-4

<220>

<221> L-Protein

<222> (1)..(82)

<223> synthetic

<400> 261

Phe Asn Pro Gln Gly Leu Ala Gln Pro Asp Ala Leu Asn Val Pro Ser
1 5 10 15

Thr Cys Cys Phe Thr Phe Ser Ser Lys Lys Ile Ser Leu Gln Arg Leu
20 25 30

Lys Ser Tyr Val Ile Thr Thr Ser Arg Cys Pro Gln Lys Ala Val Ile
35 40 45

Phe Arg Thr Lys Leu Gly Lys Glu Ile Cys Ala Asp Pro Lys Glu Lys
50 55 60

Trp Val Gln Asn Tyr Met Lys His Leu Gly Arg Lys Ala His Thr Leu
65 70 75 80

Lys Thr

<210> 262

<211> 74

<212> PRT

<213> Artificial Sequence

<220>

<223> CCL14/HCC-1

<220>

<221> L-Protein

<222> (1)..(74)

<223> synthetic

<400> 262

Thr Lys Thr Glu Ser Ser Ser Arg Gly Pro Tyr His Pro Ser Glu Cys
1 5 10 15

Cys Phe Thr Tyr Thr Thr Tyr Lys Ile Pro Arg Gln Arg Ile Met Asp
20 25 30

Tyr Tyr Glu Thr Asn Ser Gln Cys Ser Lys Pro Gly Ile Val Phe Ile
35 40 45

Thr Lys Arg Gly His Ser Val Cys Thr Asn Pro Ser Asp Lys Trp Val
50 55 60

Gln Asp Tyr Ile Lys Asp Met Lys Glu Asn
65 70

<210> 263

<211> 73

<212> PRT

<213> Artificial Sequence

<220>

<223> CXCL1/GROalpha

<220>

<221> L-Protein

<222> (1)..(73)

<223> synthetic

<400> 263

Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr Leu Gln
1 5 10 15

Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser Pro Gly
20 25 30

Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn Gly Arg
35 40 45

Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys Lys Ile Ile Glu
50 55 60

Lys Met Leu Asn Ser Asp Lys Ser Asn
65 70

<210> 264

<211> 73

<212> PRT

<213> Artificial Sequence

<220>

<223> CXCL2/GRObeta

<220>

<221> L-Protein

<222> (1)..(73)

<223> synthetic

<400> 264

Ala Pro Leu Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr Leu Gln
1 5 10 15

Gly Ile His Leu Lys Asn Ile Gln Ser Val Lys Val Lys Ser Pro Gly
20 25 30

Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn Gly Gln
35 40 45

Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Lys Lys Ile Ile Glu
50 55 60

Lys Met Leu Lys Asn Gly Lys Ser Asn
65 70

<210> 265

<211> 73

<212> PRT

<213> Artificial Sequence

<220>

<223> CXCL3/GROgama

<220>

<221> L-Protein

<222> (1)..(73)

<223> synthetic

<400> 265

Ala Ser Val Val Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr Leu Gln
1 5 10 15

Gly Ile His Leu Lys Asn Ile Gln Ser Val Asn Val Arg Ser Pro Gly
20 25 30

Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn Gly Lys
35 40 45

Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Gln Lys Ile Ile Glu
50 55 60

Lys Ile Leu Asn Lys Gly Ser Thr Asn
65 70

<210> 266

<211> 70

<212> PRT

<213> Artificial Sequence

<220>

<223> CXCL4/PF4

<220>

<221> L-Protein

<222> (1)..(70)

<223> synthetic

<400> 266

Glu Ala Glu Glu Asp Gly Asp Leu Gln Cys Leu Cys Val Lys Thr Thr
1 5 10 15

Ser Gln Val Arg Pro Arg His Ile Thr Ser Leu Glu Val Ile Lys Ala
20 25 30

Gly Pro His Cys Pro Thr Ala Gln Leu Ile Ala Thr Leu Lys Asn Gly
35 40 45

Arg Lys Ile Cys Leu Asp Leu Gln Ala Pro Leu Tyr Lys Lys Ile Ile
50 55 60

Lys Lys Leu Leu Glu Ser
65 70

<210> 267

<211> 77

<212> PRT

<213> artificial sequence

<220>

<223> CXCL5/ENA-78

<220>

<221> L-Protein

<222> (1)..(77)

<223> synthetic

<400> 267

Gly Pro Ala Ala Ala Val Leu Arg Glu Leu Arg Cys Val Cys Leu Gln
1 5 10 15

Thr Thr Gln Gly Val His Pro Lys Met Ile Ser Asn Leu Gln Val Phe
20 25 30

Ala Ile Gly Pro Gln Cys Ser Lys Val Glu Val Val Ala Ser Leu Lys
35 40 45

Asn Gly Lys Glu Ile Cys Leu Asp Pro Glu Ala Pro Phe Leu Lys Lys
50 55 60

Val Ile Gln Lys Ile Leu Asp Gly Gly Asn Lys Glu Asn
65 70 75

<210> 268

<211> 77

<212> PRT

<213> Artificial Sequence

<220>

<223> CXCL6/GCP-2

<220>

<221> L-Protein

<222> (1)..(77)

<223> synthetic

<400> 268

Gly Pro Val Ser Ala Val Leu Thr Glu Leu Arg Cys Thr Cys Leu Arg
1 5 10 15

Val Thr Leu Arg Val Asn Pro Lys Thr Ile Gly Lys Leu Gln Val Phe
20 25 30

Pro Ala Gly Pro Gln Cys Ser Lys Val Glu Val Val Ala Ser Leu Lys

35 40 45

Asn Gly Lys Gln Val Cys Leu Asp Pro Glu Ala Pro Phe Leu Lys Lys
50 55 60

Val Ile Gln Lys Ile Leu Asp Ser Gly Asn Lys Lys Asn
65 70 75

<210> 269

<211> 94

<212> PRT

<213> Artificial Sequence

<220>

<223> CXCL7/NAP-2

<220>

<221> L-Protein

<222> (1)..(94)

<223> synthetic

<400> 269

Ser Ser Thr Lys Gly Gln Thr Lys Arg Asn Leu Ala Lys Gly Lys Glu
1 5 10 15

Glu Ser Leu Asp Ser Asp Leu Tyr Ala Glu Leu Arg Cys Met Cys Ile
20 25 30

Lys Thr Thr Ser Gly Ile His Pro Lys Asn Ile Gln Ser Leu Glu Val
35 40 45

Ile Gly Lys Gly Thr His Cys Asn Gln Val Glu Val Ile Ala Thr Leu
50 55 60

Lys Asp Gly Arg Lys Ile Cys Leu Asp Pro Asp Ala Pro Arg Ile Lys
65 70 75 80

Lys Ile Val Gln Lys Lys Leu Ala Gly Asp Glu Ser Ala Asp
85 90

<210> 270

<211> 79

<212> PRT

<213> artificial sequence

<220>

<223> CXCL8/IL-8

<220>

<221> L-Protein

<222> (1)..(79)

<223> synthetic

<400> 270

Glu Gly Ala Val Leu Pro Arg Ser Ala Lys Glu Leu Arg Cys Gln Cys
1 5 10 15

Ile Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe Ile Lys Glu Leu
20 25 30

Arg Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr Glu Ile Ile Val
35 40 45

Lys Leu Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro Lys Glu Asn Trp
50 55 60

Val Gln Arg Val Val Glu Lys Phe Leu Lys Arg Ala Glu Asn Ser
65 70 75

<210> 271

<211> 103

<212> PRT

<213> artificial sequence

<220>

<223> CXCL9/MIG

<220>

<221> L-Protein

<222> (1)..(103)

<223> synthetic

<400> 271

Thr Pro Val Val Arg Lys Gly Arg Cys Ser Cys Ile Ser Thr Asn Gln
1 5 10 15

Gly Thr Ile His Leu Gln Ser Leu Lys Asp Leu Lys Gln Phe Ala Pro
20 25 30

Ser Pro Ser Cys Glu Lys Ile Glu Ile Ile Ala Thr Leu Lys Asn Gly
35 40 45

Val Gln Thr Cys Leu Asn Pro Asp Ser Ala Asp Val Lys Glu Leu Ile
50 55 60

Lys Lys Trp Glu Lys Gln Val Ser Gln Lys Lys Lys Gln Lys Asn Gly
65 70 75 80

Lys Lys His Gln Lys Lys Lys Val Leu Lys Val Arg Lys Ser Gln Arg
85 90 95

Ser Arg Gln Lys Lys Thr Thr
100

<210> 272

<211> 77

<212> PRT

<213> artificial sequence

<220>

<223> CXCL10/IP-10

<220>

<221> L-Protein

<222> (1)..(77)

<223> synthetic

<400> 272

Val Pro Leu Ser Arg Thr Val Arg Cys Thr Cys Ile Ser Ile Ser Asn
1 5 10 15

Gln Pro Val Asn Pro Arg Ser Leu Glu Lys Leu Glu Ile Ile Pro Ala
20 25 30

Ser Gln Phe Cys Pro Arg Val Glu Ile Ile Ala Thr Met Lys Lys Lys
35 40 45

Gly Glu Lys Arg Cys Leu Asn Pro Glu Ser Lys Ala Ile Lys Asn Leu
50 55 60

Leu Lys Ala Val Ser Lys Glu Arg Ser Lys Arg Ser Pro
65 70 75

<210> 273

<211> 73

<212> PRT

<213> artificial sequence

<220>

<223> CXCL11/I-TAC

<220>

<221> L-Protein

<222> (1)..(73)

<223> synthetic

<400> 273

Phe Pro Met Phe Lys Arg Gly Arg Cys Leu Cys Ile Gly Pro Gly Val
1 5 10 15

Lys Ala Val Lys Val Ala Asp Ile Glu Lys Ala Ser Ile Met Tyr Pro
20 25 30

Ser Asn Asn Cys Asp Lys Ile Glu Val Ile Ile Thr Leu Lys Glu Asn
35 40 45

Lys Gly Gln Arg Cys Leu Asn Pro Lys Ser Lys Gln Ala Arg Leu Ile
50 55 60

Ile Lys Lys Val Glu Arg Lys Asn Phe
65 70

<210> 274

<211> 72

<212> PRT

<213> artificial sequence

<220>

<223> CXCL12alpha/SDF-1alpha

<220>

<221> L-Protein

<222> (1)..(72)

<223> synthetic

<400> 274

Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser
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 Met
65 70

<210> 275

<211> 72

<212> PRT

<213> Artificial Sequence

<220>

<223> CXCL12beta/SDF-1beta

<220>

<221> L-Protein

<222> (1)..(72)

<223> synthetic

<400> 275

Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser
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 Met
65 70

<210> 276

<211> 76

<212> PRT

<213> Artificial Sequence

<220>

<223> CX3CL1/Fractalkine

<220>

<221> L-Protein

<222> (1)..(76)

<223> synthetic

<400> 276

Gln His His Gly Val Thr Lys Cys Asn Ile Thr Cys Ser Lys Met Thr
1 5 10 15

Ser Lys Ile Pro Val Ala Leu Leu Ile His Tyr Gln Gln Asn Gln Ala
20 25 30

Ser Cys Gly Lys Arg Ala Ile Ile Leu Glu Thr Arg Gln His Arg Leu
35 40 45

Phe Cys Ala Asp Pro Lys Glu Gln Trp Val Lys Asp Ala Met Gln His
50 55 60

Leu Asp Arg Gln Ala Ala Ala Leu Thr Arg Asn Gly
65 70 75

<210> 277

<211> 93

<212> PRT

<213> Artificial Sequence

<220>

<223> XCL1/Lymphotactin

<220>

<221> L-Protein

<222> (1)..(93)

<223> artificial

<400> 277

Val Gly Ser Glu Val Ser Asp Lys Arg Thr Cys Val Ser Leu Thr Thr
1 5 10 15

Gln Arg Leu Pro Val Ser Arg Ile Lys Thr Tyr Thr Ile Thr Glu Gly
20 25 30

Ser Leu Arg Ala Val Ile Phe Ile Thr Lys Arg Gly Leu Lys Val Cys
35 40 45

Ala Asp Pro Gln Ala Thr Trp Val Arg Asp Val Val Arg Ser Met Asp
50 55 60

Arg Lys Ser Asn Thr Arg Asn Asn Met Ile Gln Thr Lys Pro Thr Gly
65 70 75 80

Thr Gln Gln Ser Thr Asn Thr Ala Val Thr Leu Thr Gly
85 90

<210> 278

<211> 40

<212> RNA

<213> Artificial Sequence

<220>

<223> biotinylated NOX-E36

<220>

<221> L-RNA

<222> (1)..(40)

<223> synthetic

<220>

<221> L-RNA

<222> (1)..(40)

<223> 5' BIotin

<400> 278
gcacgucccu caccggugca agugaagccg uggcucugcg 40

<210> 279

<211> 40

<212> RNA

<213> Artificial Sequence

<220>

<223> POC

<220>

<221> L-RNA

<222> (1)..(40)

<223> synthetic

<400> 279
uaaggaaacu cggucugaug cgguagcgcu gugcagagcu 40

<210> 280

<211> 40

<212> RNA

<213> Artificial Sequence

<220>

<223> POC-PEG

<220>

<221> L-RNA

<222> (1)..(40)

<223> synthetic

<220>

<221> L-RNA

<222> (1)..(40)

<223> 5' PEGylation

<400> 280
uaaggaaacu cggucugaug cgguagcgcu gugcagagcu 40

<210> 281

<211> 11

<212> DNA

<213> Artificial Sequence

<220>

<223> mNOX-E36 Capture probe

<220>

<221> L-DNA

<222> (1)..(11)

<223> synthetic

<220>

<221> L-DNA

<222> (1)..(11)

<223> 3' -(spacer18)2-NH4+

<400> 281
ccaatgtcgc c 11

<210> 282

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> mNOX-E36 Detect probe

<220>

<221> L-DNA

<222> (1)..(9)

<223> synthetic

<220>

<221> L-DNA

<222> (1)..(9)

<223> 5'- biotin-(spacer18)2-

<400> 282
cgcagagcc 9

<210> 283

<211> 76

<212> PRT

<213> Equus caballus

<400> 283

Gln Pro Asp Ala Ile Asn Ser Pro Val Thr Cys Cys Tyr Thr Phe Thr
1 5 10 15

Gly Lys Lys Ile Ser Ser Gln Arg Leu Gly Ser Tyr Lys Arg Val Thr
20 25 30

Ser Ser Lys Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Ile Leu Ala
35 40 45

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

Lys Gln Leu Asp Lys Lys Ala Gln Thr Pro Lys Pro
65 70 75

<210> 284

<211> 76

<212> PRT

<213> Bos Taurus

<400> 284

Gln Pro Asp Ala Ile Asn Ser Gln Val Ala Cys Cys Tyr Thr Phe Asn
1 5 10 15

Ser Lys Lys Ile Ser Met Gln Arg Leu Met Asn Tyr Arg Arg Val Thr
20 25 30

Ser Ser Lys Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Ile Leu Gly
35 40 45

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

Asn Tyr Leu Asn Lys Lys Asn Gln Thr Pro Lys Pro
65 70 75

<210> 285

<211> 125

<212> PRT

<213> Rattus norvegicus

<400> 285

Gln Pro Asp Ala Val Asn Ala Pro Leu Thr Cys Cys Tyr Ser Phe Thr
1 5 10 15

Gly Lys Met Ile Pro Met Ser Arg Leu Glu Asn Tyr Lys Arg Ile Thr
20 25 30

Ser Ser Arg Cys Pro Lys Glu Ala Val Val Phe Val Thr Lys Leu Lys
35 40 45

Arg Glu Ile Cys Ala Asp Pro Asn Lys Glu Trp Val Gln Lys Tyr Ile
50 55 60

Arg Lys Leu Asp Gln Asn Gln Val Arg Ser Glu Thr Thr Val Phe Tyr
65 70 75 80

Lys Ile Ala Ser Thr Leu Arg Thr Ser Ala Pro Leu Asn Val Asn Leu
85 90 95

Thr His Lys Ser Glu Ala Asn Ala Ser Thr Leu Phe Ser Thr Thr Thr
100 105 110

Ser Ser Thr Ser Val Glu Val Thr Ser Met Thr Glu Asn
115 120 125