

Figure S1. HPLC and LCMS analysis of oxidized *Ov*-GRN-1 fragments. HPLC traces are shown on the left and the masses of the main peaks (highlighted with an asterisk (*)) are shown on the right. The initial peak for GRN-L3 is from PBS

Table S1. Chemical shifts for the *Ov*-GRN-1 fragments

GRN-L1				GRN-L2				GRN-L3						
3	4.709	0.002	HA	1	3	4.431	0.001	HA	1	3	4.143	0.000	HA	1
5	3.598	0.000	HB2	1	5	3.368	0.000	HB2	1	4	1.524	0.000	QB	1
6	2.963	0.000	HB3	1	6	3.220	0.000	HB3	1	11	8.874	0.000	H	2
14	4.406	0.003	HA	2	12	8.676	0.000	H	2	13	4.760	0.000	HA	2
16	2.369	0.001	HB2	2	14	4.762	0.000	HA	2	15	3.207	0.000	HB2	2
17	1.992	0.007	HB3	2	16	1.805	0.000	HB2	2	16	3.009	0.000	HB3	2
22	2.079	0.002	QG	2	17	1.945	0.000	HB3	2	22	8.834	0.001	H	3
23	3.790	0.002	HD2	2	22	1.733	0.000	QG	2	24	4.330	0.000	HA	3
24	3.750	0.002	HD3	2	26	3.311	0.000	QD	2	26	1.842	0.000	HB2	3
28	7.924	0.000	H	3	28	7.303	0.002	HE	2	27	1.728	0.000	HB3	3
30	5.173	0.001	HA	3	41	4.440	0.001	HA	3	32	1.593	0.000	QG	3
32	3.090	0.000	HB2	3	43	2.439	0.000	HB2	3	36	3.174	0.000	QD	3
33	2.797	0.000	HB3	3	44	2.001	0.001	HB3	3	38	7.202	0.000	HE	3
42	4.429	0.001	HA	4	47	2.256	0.001	HG2	3	49	8.399	0.000	H	4
44	2.278	0.001	HB2	4	48	2.131	0.002	HG3	3	53	3.955	0.000	QA	4
45	1.973	0.002	HB3	4	50	4.019	0.002	HD2	3	56	8.227	0.001	H	5
50	2.027	0.001	QG	4	51	3.708	0.001	HD3	3	58	4.230	0.000	HA	5
53	3.812	0.002	QD	4	52	3.712	0.000	QD	3	60	1.511	0.000	HB2	5
56	7.408	0.000	H	5	55	8.956	0.000	H	4	61	1.392	0.000	HB3	5
58	3.932	0.000	HA	5	57	4.338	0.000	HA2	4	75	0.834	0.000	QQD	5
60	1.865	0.000	HB	5	58	3.807	0.000	HA3	4	78	8.653	0.000	H	6
61	0.686	0.000	QG1	5	62	7.991	0.001	H	5	80	4.714	0.000	HA	6
62	0.600	0.000	QG2	5	64	4.719	0.000	HA	5	82	3.137	0.000	HB2	6
74	7.805	0.000	H	6	66	2.312	0.000	HB2	5	83	3.323	0.000	HB3	6
76	4.853	0.000	HA	6	67	2.133	0.000	HB3	5	91	7.301	0.000	HD2	6
78	3.284	0.000	HB2	6	72	2.398	0.000	QG	5	92	8.629	0.000	HE1	6
79	2.844	0.000	HB3	6	76	7.670	0.000	HE21	5	95	8.259	0.000	H	7
81	7.130	0.000	QD	6	77	6.938	0.000	HE22	5	97	3.752	0.000	HA2	7
82	6.819	0.000	QE	6	81	8.684	0.001	H	6	98	4.075	0.000	HA3	7
98	8.138	0.001	H	7	83	4.526	0.000	HA	6	102	8.242	0.001	H	8
100	4.348	0.000	HA	7	85	4.253	0.000	HB	6	104	4.585	0.001	HA	8
102	4.322	0.000	HB	7	86	1.342	0.000	QG2	6	106	3.042	0.001	HB2	8
103	1.246	0.000	QG2	7	95	8.780	0.000	H	7	107	2.962	0.001	HB3	8
112	8.572	0.001	H	8	97	4.846	0.000	HA	7	109	7.105	0.001	QD	8
114	4.830	0.000	HA	8	99	3.558	0.000	HB2	7	110	6.836	0.000	QE	8
118	3.273	0.000	QB	8	100	3.192	0.000	HB3	7	126	8.453	0.001	H	9
										128	3.953	0.000	HA2	9
										129	3.825	0.000	HA3	9
										133	8.120	0.000	H	10
										135	4.391	0.002	HA	10
										136	1.360	0.001	QB	10
										143	8.224	0.000	H	11
										145	4.478	0.000	HA	11
										147	3.258	0.000	HB2	11
										148	3.051	0.000	HB3	11

Table S2. Structural statistics for the GRN loop ensembles

Experimental restraints	GRN-L1	GRN-L2	GRN-L3
Interproton distance restraints	26	24	30
<i>Intraresidue</i>	16	19	17
<i>Sequential</i>	10	5	13
<i>Medium range (i-j < 5)</i>	0	0	0
<i>Long range (i-j ≥ 5)</i>	0	0	0
Dihedral angle restraints	2	3	3
R.m.s. deviations from mean coordinate structure (Å)			
Backbone atoms	1.52 ± 0.50	1.48 ± 0.50	2.88 ± 0.67
All heavy atoms	2.81 ± 0.91	2.96 ± 1.08	4.38 ± 0.86
Ramachandran Statistics			
% in most favoured region	61.2	48.3	36.7
% in additionally allowed region	38.8	48.3	63.3
% in generously allowed region		1.7	
% in disallowed region		1.7	

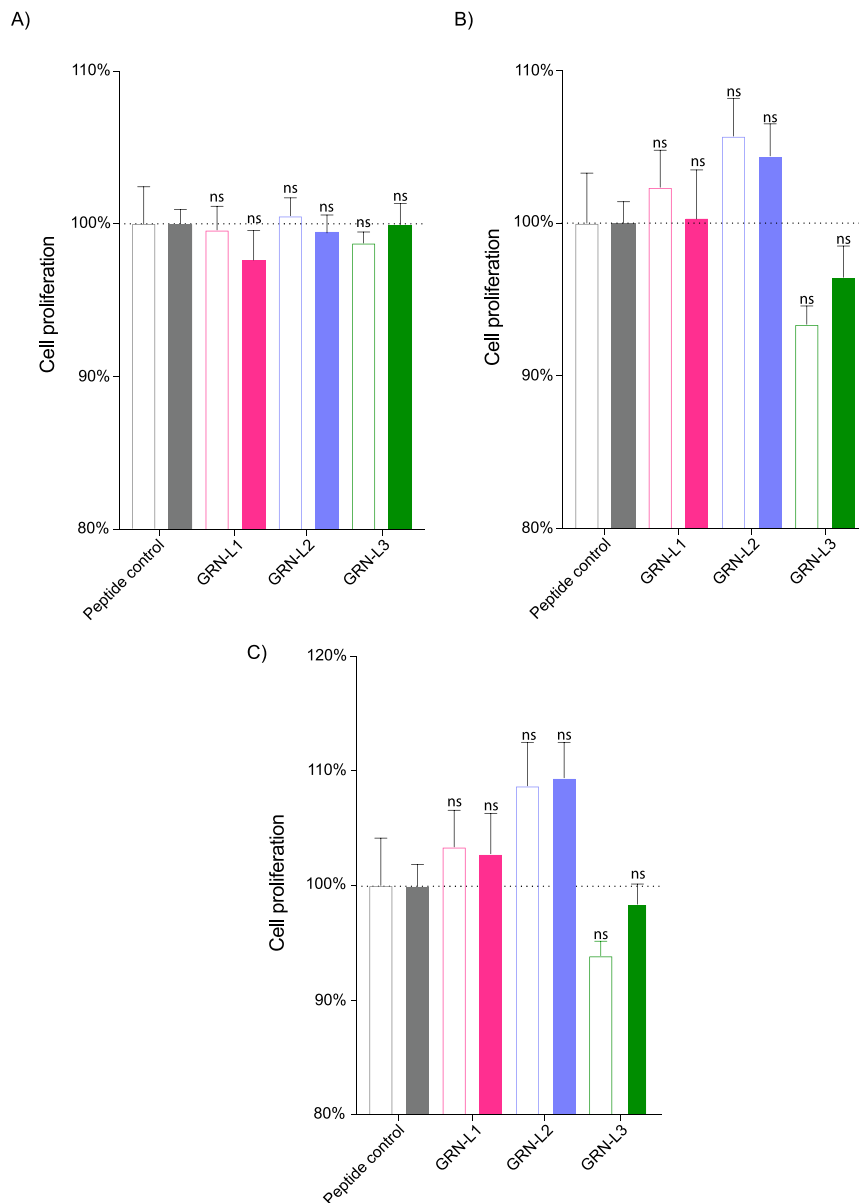


Figure S2. Cell proliferation of the *Ov*-GRN-1 fragments. Cell proliferation measured at A. Day 1, B. Day 2 and C. Day3. Empty columns and solid columns represent concentrations of 200 nmol/L and 1 μmol/L, respectively. The proliferation rates relative to peptide control are plotted as mean ± SEM bars. Data were analysed by one-way ANOVA against peptide control (Not significant = ns).

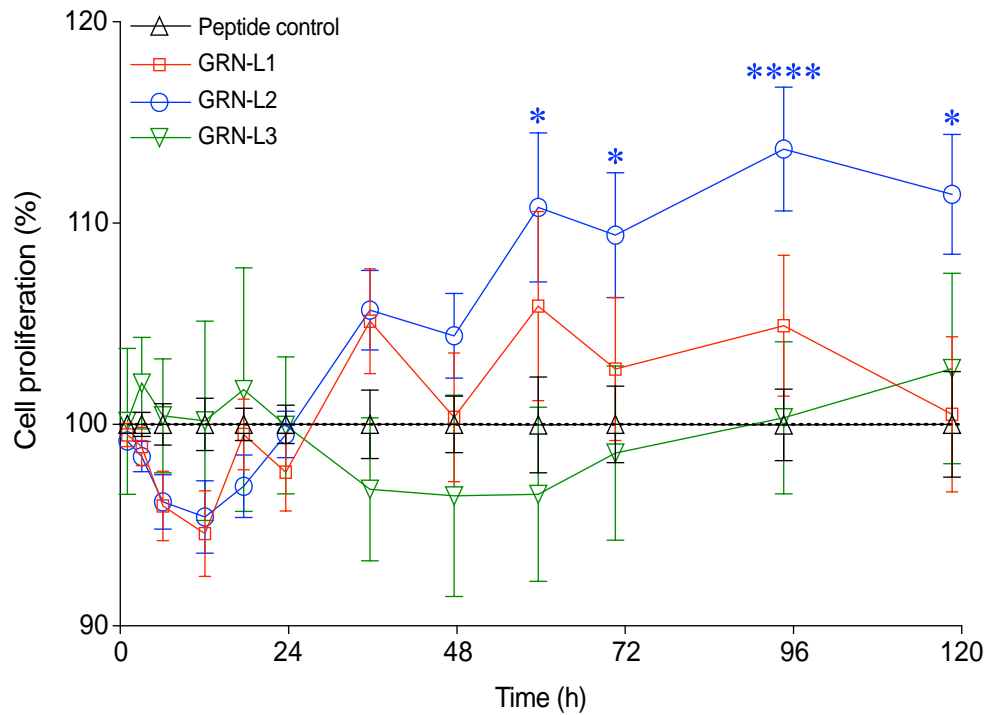


Figure S3. Real-time cell proliferation analysis of the *Ov*-GRN-1 fragments using xCELLigence. Fibroblast cells were treated with the three *Ov*-GRN-1 fragment peptides at concentrations of 200 nmol/L and 1 μ mol/L. For clarity only 1 μ mol/L is shown. Cell index was measured 4 days after treatment. The proliferation rates relative to peptide control are plotted as mean \pm SEM bars. The statistical analysis was performed using two-way ANOVA for multiple comparisons against peptide control (**** = $P < 0.0001$, * = $P < 0.05$).