





	24 h			48 h		
	2E-5	2E-4	2E-3	2E-5	2E-4	2E-3
Bad	-1,06	-1,02	-1,06	1,04	1,07	1,04
Bax	1,31	-1,23	-1,05	2,39*	-1,02	-1,05
Bcl-2	-1,03	1,09	-1,04	1,12	1,21*	1,13
Bcl-x	-1,50*	-1,16	-1,72*	1,07	1,04	-1,08
Pro-Caspase-3	-1,16	1,10	1,00	1,12	1,56	1,72
Cleaved Caspase-3	-1,15	1,12	-1,05	1,31*	1,38*	1,04
Catalase	2,07*	2,93*	2,70*	1,14	1,20	1,16
cIAP-1	-1,18	1,07	-1,06	1,02	1,17*	1,07
cIAP-2	-1,12	1,14	1,08	1,03	1,07	1,01
Claspin	-1,22	-1,04	-1,09	-1,02	1,10	-1,01
Clusterin	-1,18	1,03	1,03	-1,01	1,17	1,03
Cytochrome c	-1,27	1,04	-1,08	-1,02	1,26	1,08
TRAIL R1/DR4	1,29	1,15	-1,03	1,23	1,09*	1,11
TRAIL R2/DR5	1,05	1,03	1,03	1,13	1,19*	1,16*
FADD	-1,23	-1,16	-1,23	1,07	1,23	1,13
Fas/TNFRSF6/CD95	-1,19	1,00	-1,18	1,11	1,32*	1,31*
HIF-1 α	-1,14	-1,10	-1,22	1,03	1,13	1,13
HO-1/HMOX1/HSP32	-1,15	-1,03	-1,14	1,07	1,17	1,03
HO-2/HMOX2	-1,32	-1,11	-1,20	-1,35	1,16	1,04
HSP27	-1,01	1,13	1,08	-1,02	1,10	1,05
HSP60	-1,11	1,02	-1,12	1,02	1,07	1,11*
HSP70	-1,11	1,04	-1,16	1,06	1,09	-1,10*
HTRA2/Omi	-1,25	1,00	-1,09	1,09	1,22*	1,09
Livin	-1,08	1,02	-1,03	1,11*	1,17*	1,03
PON2	1,06	1,03	1,13	1,07	1,08	-1,02
p21/CIP1/CDKN1A	1,10	1,17*	1,25*	1,01	1,41*	1,13*
p27/Kip1	1,16	1,02	1,06	1,12	1,13*	1,03
Phospho-p53 (S15)	-1,39*	-1,14	-1,18	-1,05	1,08	1,03
Phospho-p53 (S46)	-1,18	-1,05	-1,15	1,08	1,10*	1,08
Phospho-p53 (S392)	-1,23	-1,05	-1,19	-1,01	1,16	1,07
Phospho-Rad17 (S635)	-1,19	-1,06	-1,08	-1,45*	1,15	1,01
SMAC/Diablo	-1,35	-1,16	-1,18	-1,15	1,09	-1,03
Survivin	-1,27	-1,19	-1,25*	1,10	1,23*	1,11
TNF RI/TNFRSF1A	-1,43*	-1,25	-1,33*	1,12	1,15*	-1,03
XIAP	-1,09	-1,02	1,02	1,15	1,32*	1,14

Supplementary Table S1. Expression levels of 35 proteins related to or involved in apoptosis were analyzed using the Proteome Profiler™ Human Apoptosis Array Kit. Numbers in bold with asterix are significant from the control. Results represent average quantification related to controls, $n=3$. * $P \leq 0.05$ indicates significant difference from control-treated cells obtained with nonparametric Mann-Whitney test.

	Fold change > 1.5
	Fold change 1.3 to 1.5
	Fold change -1.3 to -1.5
	Fold change > -1.5