

	Control		2-IB (30ng/ml)	
	Normoxia	Hypoxia	Normoxia	Hypoxia
Bad	88	91	94	38
Bax	96	96	85	40
Bcl-2	90	71	79	52
Bcl-x*	22	12	9	18
Pro-Caspase-3	230	198	247	217
Cleaved Caspase-3	136	124	128	92
Catalase*	5	0	1	0
clAP-1	46	60	61	55
clAP-2	45	53	44	52
Claspain	73	78	64	64
Clusterin	56	63	64	59
Cytochrome C	130	115	129	113
TRAIL R1 / DR4	61	59	55	22
TRAIL R2 / DR5	81	69	90	21
FAAD	97	64	103	63
Fas / TNFRSF6 / CD95	49	35	46	30
HIF1 α	78	54	96	62
H0-1 / HM0X1 / HSP32	53	51	69	48
H0-2 / HM0X2	89	115	111	97
HSP27	121	150	145	128
HSP60	166	151	178	147
HSP70	132	129	141	121
HTRA2 / OM1	93	60	104	64
Surv	48	44	51	48
PON2	79	50	48	28
p21 / CIP1 / CDKN1A	65	49	70	31
p27 / Kip1	55	38	50	26
Phospho-p53 (S15)	75	66	78	57
Phospho-p53 (S46)	56	47	83	56
Phospho-p53 (S392)	28	27	40	32
Phospho-Rad17 (S635)	42	72	48	46
SMAC / Diablo	172	200	198	178
Survivin	194	193	201	156
TNF RI / TNFRSF1A	42	56	42	47
XIAP	66	62	84	65

Supplemental Table 1:

Analysis of proteome profiling of apoptosis-related proteins. Numbers in the table represent the mean densitometric intensities of duplicate sample spots. Proteins that are regulated $\geq 25\%$ by 2-IB after hypoxia (hypoxia vs. hypoxia + 2-IB) are denoted in bold letters. *, proteins with expression levels $\leq 10\%$ of the intensity of the reference spots. Note that several of the proteins are also influenced by 2-IB under normoxic conditions.