

Supplementary Table S1

Spot No.	Protein ID	Alternative names	Mascot Score	Best peptide CI %	% Sequence coverage
1 ↓	eIF5A1	eIF-4D	250	100.0	31.1
7 ↓	Hsp27	HspB-1, Hsp28	400	100.0	34.2
9 ↓	NM23	NDKA, NME1, NDPKA, NM23-H1A	407	99.9	40.8
10 ↓	DJ-1	PARK7	229	99.7	30.7
6 ↑	PRDX2	NKEFB, TDPX1	429	99.8	36.9
11 ↑	TrpRS	IFI53, IFP53, WRS, WARS	211	99.9	26.1

Table S1. Identification of drug-dependent spots

Spots from stained gels were diced and washed with 30% acetonitrile in 50 mM ammonium bicarbonate prior to DTT reduction and iodoacetamide alkylation (21). After trypsin digestion overnight at 37°C, proteins were analyzed by MALDI-TOF-TOF MS essentially as described previously (21) and identified by searching the combined MS and MS/MS spectra against the human NCBI database using a local MASCOT search engine (V. 1.9) on a GPS (V. 3.5, ABI) server. Mascot scores reflect the probability (P) that the observed match between the experimental data and the database sequence is a random event. Proteins containing at least one peptide with Confidence Interval (CI) value $\geq 95\%$ were considered confidently identified. Arrows denote that the protein increased (↑) or decreased (↓) in response to both CPX and DEF.