Electronic Supplementary Material (ESI) for Molecular BioSystems.

Spot No.	swiss-port No.	Gene name	Protein name	pI	MW	No. Match. Peptides	Cov. (%)	Score	Subcellular location	Functional ontology	matched peptides	MCF7-Rhein / MCF7	T test	MDAMB231-Rhein / MDAMB231	T test
261	P29692	EEF1D	Elongation factor 1-delta	4.9	31217	4/11	20%	70/56	Cytoplasm	Translation regulation	SIQLDGLVWGASK / LVPVGYGIR	-1.035	0.015	-1.32727	0.059
760	P18669	PGAM1	Phosphoglycerate mutase 1	6.8	28900	6/19	35%	108/56	Cytoplasm	Glycolysis	HYGGLTGLNK / VLIAAHGNSLR	-1.07	0.66	-1.6524	0.016
827	Q9UC36	HSPB1	Heat shock protein beta-1	6.0	22826	4/14	19%	68/56	Cytoplasm	Protein folding	LATQSNEITIPVTFESR / DWYPHSR	-1.25	0.18	-1.3334	0.036
1048	P32119	PRDX2	Peroxiredoxin-2	5.7	22049	8/14	36%	129/56	Cytoplasm	Redox regulation	IGKPAPDFK / ATAVVDGAFK	13.041	0.0028	6.7686	0.037
734	P17931	LGALS3	Galectin-3	8.6	26193	10/37	32%	110/56	Secreted	Immuno response	LDNNWGREER / GNDVAFHFNPR	1.24	0.76	1.5748	0.018
834	P60174	TPI1	Triosephosphate isomerase	5.7	31057	13/47	46%	134/56	Cytoplasm	Glycolysis	KFFVGGNWK / FFVGGNWK	1.25	0.67	1.42	0.0094
987	Q06830	PRDX1	Peroxiredoxin-1	8.3	22324	10/29	44%	136/56	Cytoplasm	Redox regulation	TIAQDYGVLK / QITVNDLPVGR	-1.678	0.12	-1.06711	0.42
1251	Q9UC61	ppiA	Peptidyl-prolyl cis-trans isomerase A	7.7	18229	6/37	30%	68/56	Cytoplasm	Protein folding	VSFELFADK/ FEDENFILK	1.56	0.0019	1.978571	0.00053
1232	P23528	CFL1	Cofilin-1	8.2	18719	7/37	32%	60/56	Cytoplasm	Cytoskeleton regulation	SSTPEEVKK / YALYDATYETK	2.0193	0.031	1.0918	0.031

Supplementary Table 2. Differential cysteine labeled proteins identified by ICy 2D-DIGE and MS. Proteins displaying rhein-induced differential labeling of cysteines and lysines using ICy dyes and NHS-Cy2 dyes, respectively, were identified by MALDI-TOF peptide mass mapping. Proteins displaying an average fold-difference of ≥1.3-fold where $p<0.05$ and spots matched in all images are shaded grey. [a]To accurately calculate rhein-induced differential labeling of cysteines in consideration of protein level alteration, the cysteine-labeling ratio was normalized using the lysine-labeling ratio. For cysteine-labeling ratio, average fold-differences of triplicate samples run on different gels from DeCyder analysis show cysteine-labeling ratios for rhein-treated *versus* untreated MCF-7 and MDA-MB-231 cells. Here, the ICy5 signal was used to monitor cysteine-labeling alterations against ICy3 signals used as an internal standard. For lysine-labeling ratio, average fold-differences of triplicate samples run on different gels from DeCyder analysis show lysine-labeling ratios for rhein-treated *versus* untreated MCF-7 and MDA-MB-231 cells. Here, the NHS-Cy2 signal was used to monitor lysine-labeling alterations against ICy3 signals used as an internal standard.