Supporting Information

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Table S1. Experiment 1: Sequest ion scores for peptides assigned to peroxiredoxin-2; mass 21,765

MS/MS spectra	Observed	M_r (expt)	Mass accuracy, ppm	Miss	XCorr	DeltaCn	Peptide
Peptide 1	606.3415	1,210.6684	+1.0	0	2.26	0.52	(R)QITVNDLPVGR(S)
Peptide 2	798.9002	1,595.7859	+1.6	0	3.22	0.54	(K)SAPDFTATAVVDGAFK(E)

MS/MS spectra, tandem mass spectrum matched to indicated peptide; Observed, observed mass in spectrum (mass/charge value), e.g., if doubly charged (+2) ion observed, observed mass is half actual peptide mass; M_r (expt), average mass of peptide; Mass accuracy, value indicating difference between observed peptide mass and expected value calculated from actual peptide sequence. ppm, parts per million; Miss, indication of number of missed tryptic cleavage sites in peptide; XCorr (SEQUEST data only), cross correlation score given to peptide match: value that indicates how close spectrum fits to ideal spectrum for matched peptide (ideally Xcorr should be greater than 2.0, though size of peptide will influence this (larger peptides tend to give higher values); Delta Cn (SEQUEST data only), the delta correlation score. Indicates how different first hit is from second hit in search results (ideally delta Cn should be greater than 0.1); Peptide, sequence matched by search algorithm (SEQUEST or MASCOT) to indicated MS/MS spectrum.

Table S2. Experiment 2: MASCOT ion scores for peptides assigned to peroxiredoxin-2; mass 21,765

MS/MS spectra	Observed	M_r (expt)	Mass accuracy, ppm	Miss	Score	Expect	Peptide
Peptide 1	438.763	875.5114	−0.29	0	43	0.00045	(R)GLFIIDAK(G)
Peptide 2	554.804	1,107.5935	0.98	0	40	0.0019	(K)SLSQNYGVLK(N)
Peptide 3	597.8278	1,193.6411	0.53	0	40	0.002	(R)QITVNDLPVGR(S)
Peptide 4	798.8988	1,595.783	−0.07	0	80	3.70E-07	(K)SAPDFTATAVVDGAFK(E)
Peptide 5	853.9881	1,705.9616	0.13	0	65	2.80E-06	(K)EGGLGPLNIPLLADVTK(S)
Peptide 6	612.3601	1,834.0583	1.06	1	32	0.0025	(R)KEGGLGPLNIPLLADVTK(S)
Peptide 7	676.3432	2,026.0078	−2.05	1	28	0.075	(K)SLSQNYGVLKNDEGIAYR(G)

MS/MS spectra, tandem mass spectrum matched to indicated peptide; Observed, observed mass in spectrum (mass/charge value), e.g., if doubly charged (+2) ion observed, observed mass is half actual peptide mass; M_r (expt), average mass of peptide; Mass accuracy, value indicating difference between observed peptide mass and expected value calculated from actual peptide sequence. ppm, parts per million; Miss, indication of number of missed tryptic cleavage sites in peptide; Score (MASCOT only), value derived by calculation of probability (P) that the observed match between the experimental data and sequence present in database searched is a random event (value is given as -10Log(P); Expect (MASCOT only), indicates number of matches with equal or better scores that could occur by chance (lower the expect value the more significant the score indicated); Peptide, sequence matched by search algorithm (SEQUEST or MASCOT) to indicated MS/MS spectrum.