**Supplementary Figure 1**

Standard curve for quantification of Cys using DTNB. Based on a comparison of changes in Cys concentration between control and beads sample the binding capacity of the beads was calculated to be 2.2 µmol Cys ml⁻¹ gel. The same values were obtained after 30 or 60 min incubations.
Supplementary Figure 2
Base peak ion chromatograms for fractions from Hg-beads analysed by 1-D nanoLC data dependent tandem mass spectrometry (QStar).
Supplementary Figure 3

In silico tryptic digestion of all yeast proteins. The graph shows the numbers of proteins that contain peptides (m/z 350 to 3500) per protein with Cys (-♦-) in their sequence or the total number of peptides (m/z 350 to 3500) per protein (-■-). A uniform distribution was calculated for all tryptic peptides and ~68 % of proteins have < 6 Cys-containing peptides/protein.
Supplementary Figure 4

Distribution of yeast proteins identified based on the number of unique significant peptides (Mowse > 36) required for Mascot identifications from QStar data.

A. Analysis of tryptic peptides from yeast lysates shows the majority (~70%) of proteins were identified with 2 or more peptides. B. Analysis of the peptides after Hg-beads shows the majority of proteins (~60%) were identified from a single peptide. (■) 2 peptides (■) 3 peptides (■) 4 peptides (■) 5 peptides (■) or ≥ 6 peptides (□).

Different functional classes of proteins were identified from yeast lyastes before (C) and after (D) Hg-beads from QStar data. Fewer high abundant ribosomal and heat shock proteins were identified after enrichment of Cys-containing peptides. Analysis of the peptides shows the majority of proteins are identified from a enzymes (■) ribosomal (■) heat shock (■) hypothetical (■) nuclear (■) elongation factors (■) or miscellaneous (□) classes.
Supplementary Figure 5a

Yeast protein abundances have been determined and the number of molecules per cell estimated from Ghaemmaghami et al (■) (Nature 425, (2003) 737). Yeast proteins identified after elution of Hg-beads and online 2-D LC and LTQ-Ft Ultra (□) have been compared to these proteins. A similar distribution of proteins is observed and compares well with total yeast proteins identified in previous studies (Genome Biol (2006) 7, R50).
Supplementary Figure 5b
Comparison of the percentage of proteins identified at each concentration bin. Estimated molecules per cell from Ghaemmaghami et al (□) (Nature 425, (2003) 737) total identifications from 2DLC/FT MS (■) identifications from 2-D LC FT MS with Cys in sequence (■) identifications from 2DLC/FT MS derived only from peptides without Cys in sequence (■). A bias towards higher abundance proteins was observed for identified proteins that do not contain Cys in their amino acid sequence. Indicating a predilection for identify higher abundance proteins from these peptides because of the high sensitivity and rapid collection of fragmentation spectra using the LTQ-FT Ultra.