

Fig. S1 – MS/MS and MS3 spectra of a phosphorylated tryptic peptides from *E. coli* ribosomal proteins. CID MS/MS and MS3 spectra for phosphorylated peptides indicating either a neutral loss of 98 Da from the phosphorylated peptide or addition of 80 Da to the unphosphorylated peptide shown by ^ and #, respectively. (*) indicates the methionine oxidation. Mass spectrometry data was searched against the *E. coli* protein sequences in SwissProt database using Bioworks 3.2.

Fig. S2 – The primary sequence alignments of *E. coli* ribosomal proteins in several bacterial species and the human mitochondrial sequence. Abbreviations for bacterial species: ECOLI; *E. coli*, HAEIN; *Haemophilus Influenzae*, MYCTU; *Mycobacterium tuberculosis*, BACSU; *Bacillus subtilis*; and THET8; *Thermus thermophilus*. Alignments were processed with the CLUSTALW program in Biology Workbench and the results are displayed in BOXSHADE. Asterisks indicate possible phosphorylated residues as detected in the LC-MS/MS analysis of the phosphorylated tryptic peptide.