Supplemental Figure S1. SILAC-SPROX data obtained on suspected false positive in CsA-Binding Experiment 1. Shown are the data obtained on two elongation factor 1α peptides, $FVPSKPMCVEAFSEYPPLGR$ (triangles) and $SVEM(ox)HHEQLEQVPGDNVGFNVK$ (circles), that are likely false positives (see text).
Supplemental Figure S2. SILAC-S PROX data obtained on the four peptide hits identified in the Control Experiment. Shown in (A), (B), (C), and (D) are the data obtained on VINDAFGIEEGLMTT VHSMATQK from glyceraldehyde-3-phosphate dehydrogenase-1, NFTPEQISSMV LGK from heat shock protein SSA1, TITPm(ox)GGFV HYEIK from the 60S ribosomal protein L3, and LLQTPIDm(ox)SLKP NDAESEKEVIDTILALVK from pyruvate decarboxylase isozyme-1, (respectively).
Supplementary Figure S3. Global analysis of the L/H ratios observed in the Control and CsA-Binding experiments. Shown are the data for all the identified peptides that were successfully quantified in the Control Experiment (A), CsA Binding Experiment 1 (B), and CsA Binding Experiment 2 (C). The arrows indicate the Log$_2$(L/H) values that are 1.7-fold away from the median. Noted above each arrow is the percentile associated with the indicated Log$_2$(L/H) value.
**Supplemental Figure S4.** Global analysis of the L/H ratios observed in the ATP binding experiments. Shown are the data for all the identified peptides that were successfully quantified in Solution Experiment 1A (A), Solution Experiment 1B (B), Solution Experiment 2 (C), Gel Experiment 1 (D), and Gel Experiment 2 (E). The arrows indicate the Log$_2$(L/H) or Log$_2$(H/L) values that are 1.7-fold away from the median. Noted above each arrow is the percentile associated with the indicated Log$_2$(L/H) or Log$_2$(H/L) value.