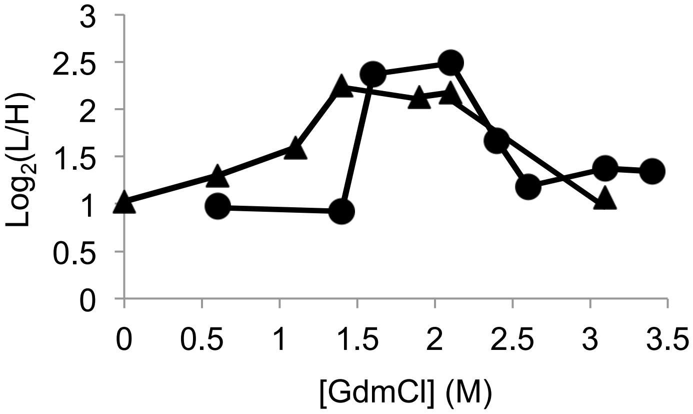
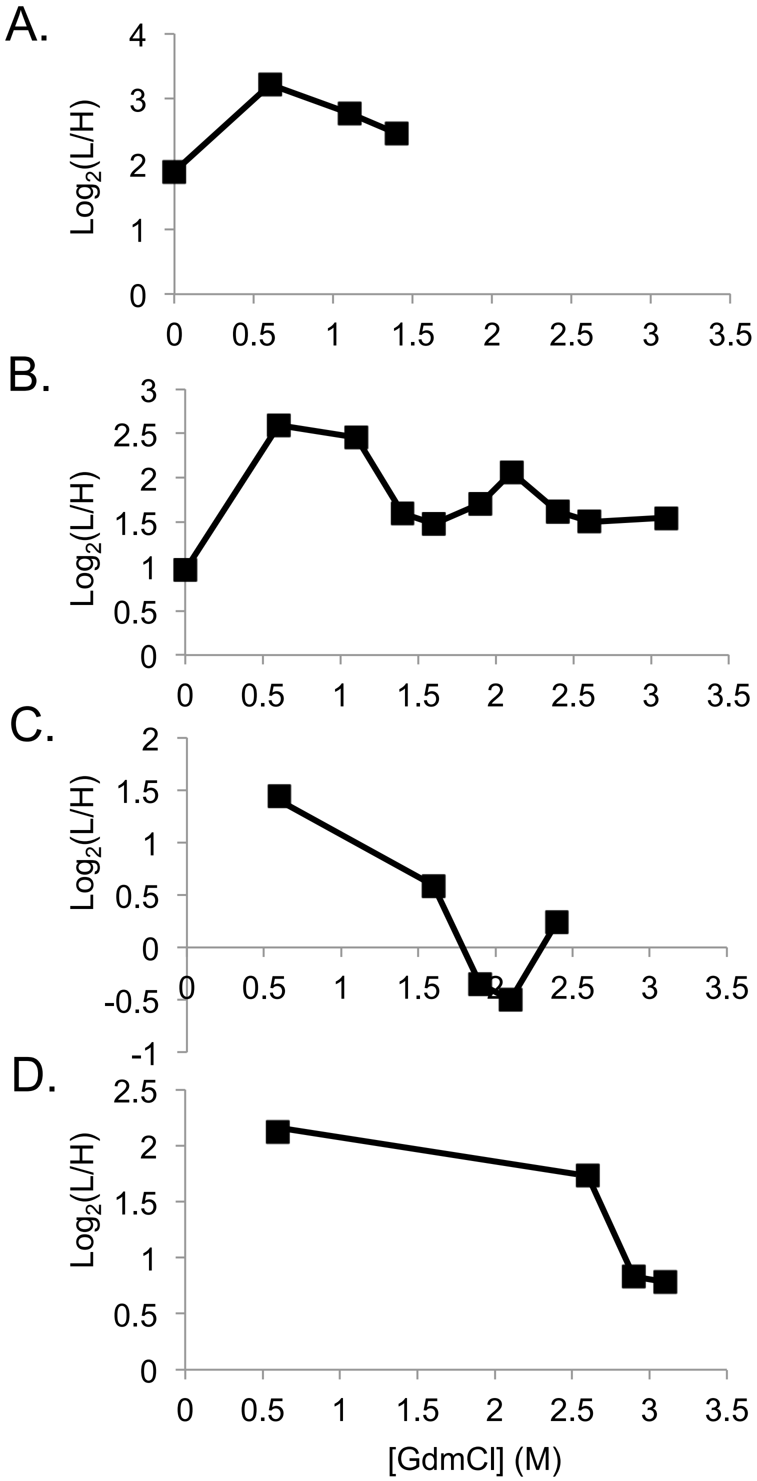
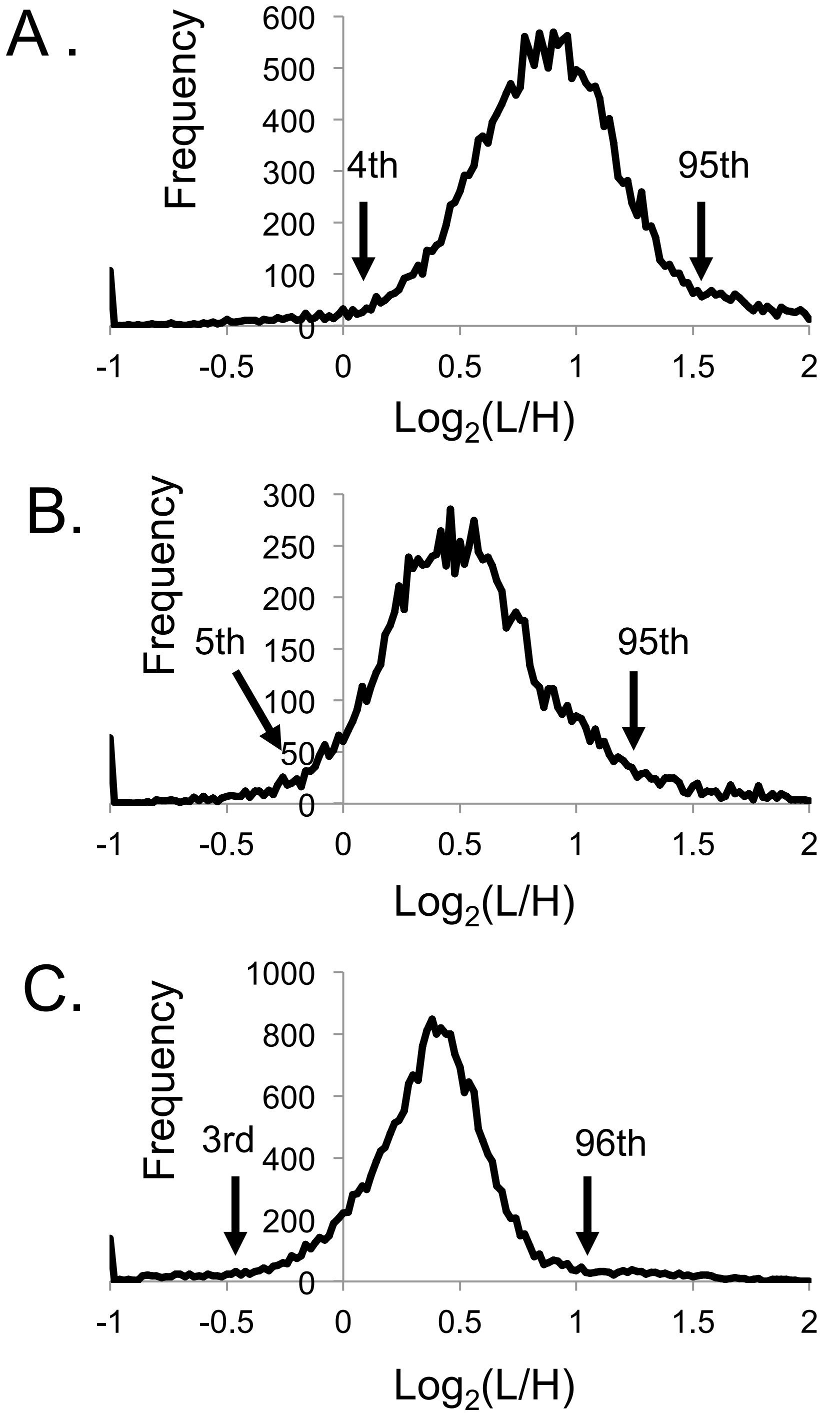


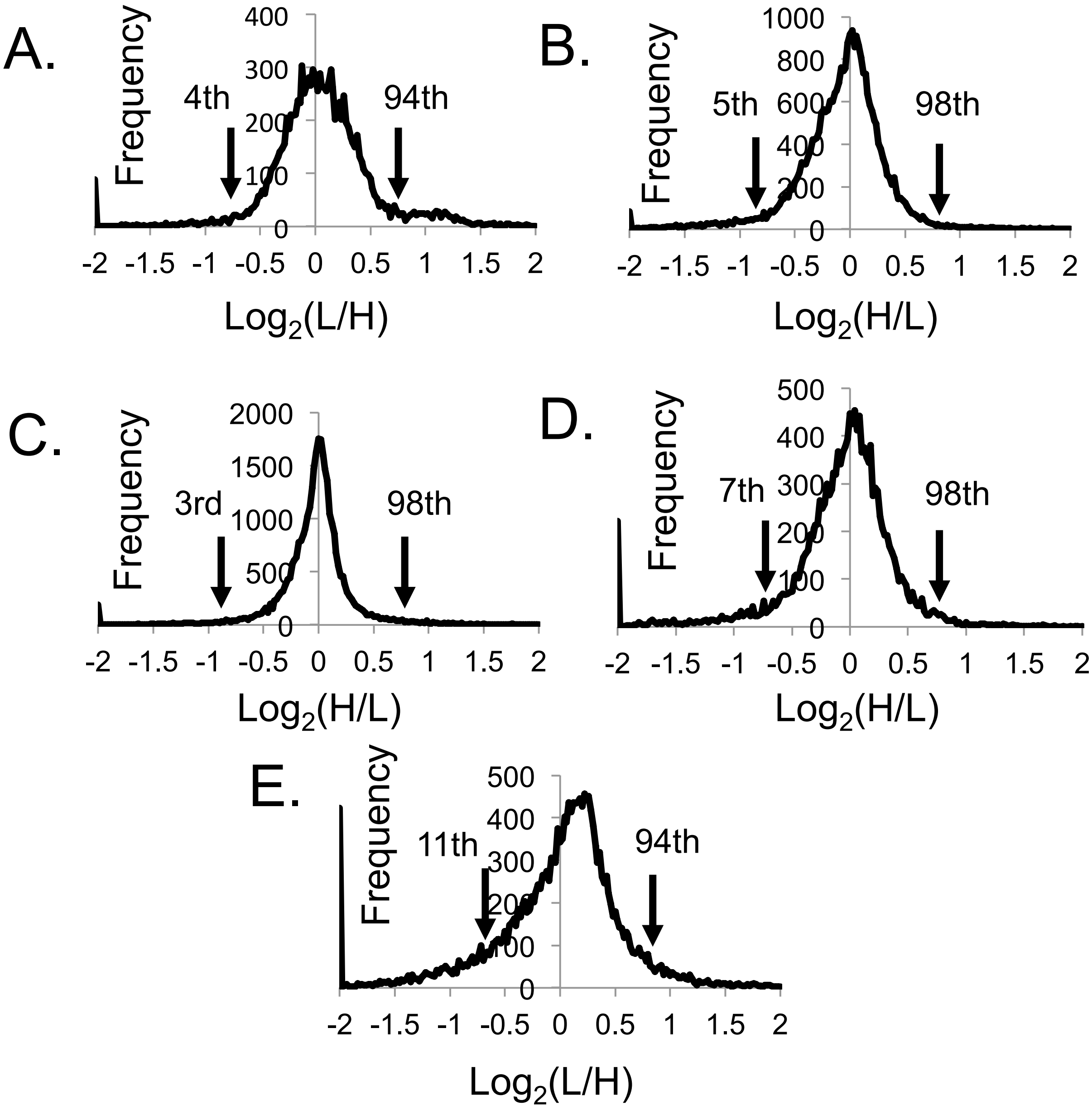
Supplemental Figure S1. SILAC-SPROX data obtained on suspected false positive in CsA-Binding Experiment 1. Shown are the data obtained on two elongation factor 1α peptides, FVPSKPMCVEAFSEYPPLGR (triangles) and SVEM(ox)HHEQLEQGVPGDNVGFNVK (circles), that are likely false positives (see text).



Supplemental Figure S2. SILAC-SPROX data obtained on the four peptide hits identified in the Control Experiment. Shown in (**A**), (**B**), (**C**), and (**D**) are the data obtained on VINDAFGIEEGLMTTVHSMTATQK from glyceraldehyde-3-phosphate dehydrogenase-1, NFTPEQISSMVLGK from heat shock protein SSA1, TITPm(ox)GGFVHYGEIK from the 60S ribosomal protein L3, and LLQTPIDm(ox)SLKPNDAESEKEVIDTILALVK 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 $\mathrm{Log_2(L/H)}$ values that are 1.7-fold away from the median. Noted above each arrow is the percentile associated with the indicated $\mathrm{Log_2(L/H)}$ 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 $\text{Log}_2(\text{L/H})$ or $\text{Log}_2(\text{H/L})$ values that are 1.7-fold away from the median. Noted above each arrow is the percentile associated with the indicated $\text{Log}_2(\text{L/H})$ or $\text{Log}_2(\text{H/L})$ value.