Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Summary of pGpp, ppGpp and pppGpp binding targets. Fractions of different radiolabel binding under different conditions are listed. Z-score is calculated by the formula that Z-score = $(\text{logit}(x)-\text{logit}(\text{median}))/\text{SD}(\text{logit}(x))$, where $\text{logit}(x) = \log_{10}(x/1-x)$, "$x$" is the fraction of radiolabel binding, "median" is the median of "x" on one plate, "SD($\text{logit}(x)$)" is the standard deviation of "$\text{logit}(x)$" on one plate. Calculation of Z-scores ignores "x" that is below or equals zero.* The differences in the fraction of pppGpp binding of some proteins in different libraries might be due to the differential expression levels from His-tagged and HisMBP-tagged vectors. Different solubility of His-tagged and HisMBP-tagged proteins (MBP tends to increase the solubility of tagged protein) may also contributes to this difference. NT: not tested; NA: not available due to 0% radiolabel binding.

File Name: Supplementary Data 2

Description: Normalized ion counts of metabolites measured by LC-MS (Raw data of Figure 4a).