**This directory contains the processed data corresponding to the publication:**

Hui, Sheng, et al. "Quantitative proteomic analysis reveals a simple strategy of global resource allocation in bacteria." Molecular systems biology 11.2 (2015): 784.

**The raw mass spectrometry files can be freely downloaded under:** http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD001467

* Folder contents "peptide\_and\_protein\_intensity\_files":
  + The processed files were downloaded from the repository listed above.
* Folder contents "sorted\_differential\_analysis\_files":
  + We used the output tables for differential expression analysis (DEA). In DEA, two experimental conditions are compared with each other and regulation of each protein (i.e. does this protein go up or down) is statistically assessed. For this we used the MS-EmpiRe package, which uses peptide intensities and replicate information for statistical assessment. The main result is a p-value (significance of regulation) and a fold change (approximate strength of regulation) for each protein. The DEA result files for each pair of conditions are contained in the folder. The analyses presented in the paper are based on these DEA results files.
* Folder contents "experimental\_design\_tables":
  + "sample\_to\_condition\_map.tsv":
    - For the DEA, we needed to know, which proteomics samples belong together to the same condition. This mapping is given here.
  + "condition\_to\_perturbation\_map.tsv":
    - As described in the paper, several conditions are grouped together to "types of perturbation", for example different growth rates in the chemostat, or stationary phase. The grouping of experimental condition to type of perturbation is given here.
  + "condition\_to\_growthrate\_map.tsv":
    - The growth rate, which is either proportional or inversly proportional to the death rate, was determined by Schmidt et al. We used the mapping shown here.