**Online Data for “Analysis of SMALP co-extracted phospholipids shows distinct membrane environments for three classes of bacterial membrane protein.”**

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The data files are divided into separate folders according to the target protein or limit of quantification (LoQ) measurement.

**LC-MSMS Data**

Folders:

* FtsA
* PgpB
* ZipA
* LoQ

Folder Content

**FtsA**

3 folders containing .wiff files for the 3 technical replicates of individual biological replicates, labelled “FtsA biological replicate 1” etc. An example fime name is ATO\_FtsA1\_IS100\_5-fold\_C8\_THF-MeOH\_2016Feb13. FtsA1 refers to replicate 1.

Note: “ATO\_FtsA1\_IS100\_5-fold\_C8\_THF-MeOH\_2016Feb13” contains two runs. The appropriate data for analysis is sample 006.

**PgpB**

Contains 2 folders for the DDM and SMALP extraction respectively. Each folder contains data for the 3 technical replicates.

**ZipA**

4 folders.

The 3 folders labelled “ZipA biological replicate 1” etc contain biological replicates 1 to 3. Each folder contains 3 technical replicates as indicated in the file name, e.g. ATO\_ZipA1\_SMALP\_IS\_neat\_replicate1\_C8\_THF-MeOH\_2016May06

The folder labelled “ZipA membrane controls” contains three folders for the induced, uninduced and control data. Each folder contains 3 technical replicates as indicated in the file names.

**LoQ**

Contains the data for the limit of quantification measurements. There are 3 technical replicates for each on column loading. File names indicate the ng on column and replicate number. For example:

“ATO\_LOQ\_0.625ng\_C8\_THF-MeOH\_2016Aug25.wiff” is 0.625 ng on column, technical replicate 1

“ATO\_LOQ\_0.0390625ng\_rep2\_C8\_THF-MeOH\_2016Aug25” is 0.0390625 ng on column, technical replicate 2.

Note: file “ATO\_LOQ\_0.15625ng\_C8\_THF-MeOH\_2016Aug25” contains two runs. The appropriate data for analysis is run index 2.