Chemoproteomics analysis of LPS-stimulated macrophages (Figure 3, Figures S4-S7)

We used SAMPEI to map protein modifications induced during the response of mouse RAW264.7 macrophage cells to lipopolysaccharide (LPS), a potent inducer of macrophage activation and differentiation that involves extensive protein and metabolic signaling. Cell proteomes were extracted, proteolyzed using trypsin, and fractionated using SCX chromatography prior to LC/MS analysis. Raw files were analyzed using X!tandem for conventional database search and generation of target spectra, followed by SAMPEI analysis for unbiased identification of modifications

Raw MS data are publicly available via the PRIDE repository with dataset identifiers PXD019853.

Files

The dataset contains the following files:

- RAW264p7_LPS_tryp_SCX_all.txt: X!tandem output from MS raw data
- RAW264p7_LPS_tryp_SCX_SAMPEI_input.txt: target spectra submitted to SAMPEI.
- RAW264p7_LPS_tryp_SCX_SAMPEI_output.txt: SAMPEI output, containing the identified modified peptides.