

HUPO Proteomics Informatics Course
Monday September 09 – Friday 13, 2019
Adelaide, Australia



The ISB **Trans-Proteomic Pipeline** (TPP) course that will focus on the use of our open-source software tools for the analysis, validation, storage and interpretation of data obtained from large-scale quantitative proteomics experiments and methods, and tandem mass spectrometry in DDA and DIA modes.

Through daily lectures and hands-on tutorials, course participants become proficient in the use of TPP tools including **PeptideProphet**, **iProphet**, **ProteinProphet**, **ASAPRatio**, **DISCO**, and other components of the TPP. We will demonstrate Amazon Web Services cloud computing to expand your computing capacity via the TPP. There will also be instruction on using SPC resources such as **SRMAtlas**, **PeptideAtlas**, **SWATHAtlas** and other software packages. In addition, we will have sample preparation tutorials with our collaborators (John Wilson, Cold Spring Harbor Laboratories and Magnus Palmblad, Leiden University) for the latest sample prep tips and downstream workflows using Jupyter and R.

5-day course at the new UniSA Health Innovation Building, 500 meters away from the Convention Centre in Adelaide, Australia. Sept 09–13 (1 week prior to HUPO 2019)

Cost is A\$415 student, A\$515 HUPO member, A\$765 HUPO non-member
Registration at: <http://www.hupo2019.org>

For more info contact Theresa Davis at +1.206.732.1484 or infoproteome@systemsbiology.org