

# Agenda

## Session 1 (~3 hours)

1. Introduction to cross-linking/mass spectrometry  
XL strategies, reagents
2. **XlinkX** sw in Proteome Discoverer  
Adding XL modification, managing FASTA databases  
XlinkX nodes and parameter settings
3. Hands-on session  
Enolase DSS  
XL visualization of results in **xiView**
4. Hands-on session  
BSA DSSO  
XL visualization in **PyMol**

## Session 2 (~3 hours)

1. Hands-on session  
Protein mix EDC  
Validation of CSMs  
Comparison of results obtained with different search algorithms
2. Hands-on session  
**ChimeraX**  
XL visualization  
combining results from multiple XL experiments
3. Hands-on session  
**Quantitation** of crosslinks  
Thermo Scientific™ Tandem Mass Tag™ (TMT) quantitation  
Label-free quantitation

About the presenters:

[Yi He](#) is responsible for development of XL-MS end-end workflow at Thermo Fisher Scientific and works in San Jose, CA.

[Michaela Scigelova](#) provides customer support to Proteome Discoverer users at Thermo Fisher Scientific in Bremen, Germany.