

Post-translational modification (PTM) identification

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Identify and analyze PTMs in large-scale, 12 hour minimum (\$564 internal, \$720 external) per project.

1. List of modified and unmodified peptides with mass-shifts

Identify modified peptides along with the unmodified counterparts.

- **Deliverables:**
 - reports generated by MODa (mass-shifts and peptide-spectral matches)
- **Tools Used:**
 - **MODa:** (<http://prix.hanyang.ac.kr/download/moda.jsp>) used to identify mass-shifts on given peptides

2. Mapping mass-shifts to post-translational modifications and substitutions

Mapping the mass-shifts identified in step 1. to actual post-translational modifications and/or substitutions

- **Deliverables:**
 - Mass-shift to PTM mapping
- **Tools Used:**
 - **ABRF delta mass:** (<https://www.abrf.org/index.cfm/dm.home?AvgMass=all>) used to identify PTMs mapping to mass-shifts identified above (i.e., 80 Dalton mass-shift on Serine indicates phosphorylation)

3. Comprehensive list of all modified peptides

List of all peptides mapped to proteins along with the site of modification (i.e., Serine phosphorylation)

- **Deliverables:**
 - Excel file that has list of all modified peptide-spectral matches