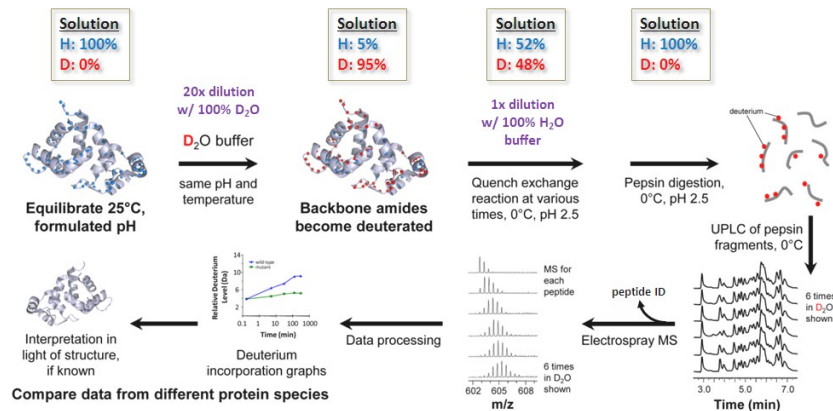


## 蛋白质氘交换质谱分析

- 检测蛋白质在溶液条件下的折叠状态, 聚合状态和构象变化。Detect the protein folding state, unfolding and unfolding movements, oligomerization states and protein conformational changes in protein level.
- 检测蛋白质与其他分子间的相互作用强弱与结合位点。相互作用检测用于检测蛋白质与蛋白质, 蛋白质与多肽, 蛋白质与药物小分子, 蛋白质与核酸, 蛋白质与细胞膜等之间的作用位点和作用强弱。Detect protein binding states and provide information about the interactions between proteins and ligands(protein-protein, protein-peptides, protein-drug molecules, proteinDNA, protein-membrane, etc.). H/D exchange Mass Spectrometry can detect both the binding strength and binding positions in both protein and peptide level.

样品要求: 蛋白-配体和蛋白样品, 样品浓度~1ug/ul, 需要 10-20ul, 最好没有去垢剂。平台提供蛋白质氘交换需要用到的 H<sub>2</sub>O buffer 和 D<sub>2</sub>O bufferr。

### Continuous labeling – the most common experiment



Marcisin & Engen (2010). *Anal Bioanal Chem.* 397, 967.  
Houde et al. (2011). *J. Pharm. Sci.* 100(6), 2071.