NPTEL Syllabus

NOC: Mass spectrometry based proteomics - Video course

COURSE OUTLINE

Mass spectrometry is an advanced analytical technique for accurate mass measurement. It does so by producing charged molecular species in vacuum followed by its separation in the magnetic and electric fields on the basis of their mass to charge (m/z) ratio. MALDI and ESI coupled with mass analyzers are commonly used mass spectrometer configuration in proteomics. The human proteome draft was decoded by using high-resolution liquid chromatography coupled with mass spectrometry.

In this module, we will discuss the basics of mass spectrometry, sample preparations, liquid chromatography, hybrid mass spectrometers and quantitative proteomics techniques such as iTRAQ, SILAC and TMT using mass spectrometry. The course will also provide the basic knowledge about sample preparation, mass spectrometry workflow, different chromatography technologies and quantitative proteomics.

COURSE DETAIL

<table>
<thead>
<tr>
<th>Week No.</th>
<th>Topics</th>
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| 1.       | Proteomics introduction and sample preparation  
Lec 1: Introduction to proteomics  
Lec 2: Why proteomics and sample preparation  
Lec 3: Protein extraction  
Lec 4: In-gel & in-solution digestion  
Lec 5: Fundamentals of mass spectrometry |
| 2.       | Basics of mass spectrometry  
Lec 6: Chromatography technologies  
Lec 7: Liquid chromatography  
Lec 8: Mass spectrometry: Ionization sources  
Lec 9: Mass spectrometry: Mass analyzers  
Lec 10: MALDI sample preparation and analysis |
| 3. | **Quantitative proteomics**  
Lec 11: Introduction to quantitative proteomics  
Lec 12: Hybrid mass spectrometry configurations  
Lec 13: SILAC: In vivo labeling  
Lec 14: iTRAQ: In vitro labeling  
Lec 15: TMT: In vitro labeling |
| 4. | **Proteomics and systems biology**  
Lec 16: Quantitative proteomics data analysis  
Lec 17: Proteomics and systems biology-I  
Lec 18: Proteomics and systems biology-II  
Lec 19: Proteomics applications  
Lec 20: Challenges in proteomics |