

Theme: MS data analysis, statistical & bioinformatics analysis

For discovery proteomics, global PTMs & protein complex study

4-day workshop

3rd floor Conference room Building #1



- Section I: Basic Mass Spectrometry, proteomics case study and Hand-on LC-MS Analysis Day 1
- Section II: MS database searching by MaxQuant and Mascot Day 2
- Section III: Statistical analysis and Bioinformatics analysis, PTM, Day 3
- Section IV: Thermal Proteome Profiling, untargeted metabolomics/lipidomics Day 4

For more information about this workshop, *please contact Dr. Meng at* 15010054101

March 26, 2019

Day 1:

8:00 - 8:30 am:	Registration room 108
8:30 - 9:00 am	Opening ceremony and Introduction to Workshop and workshop agenda overview Center leader: Sheng Zhang, Director, Cornell Proteomics and Metabolomics Facility
9:10 - 10:00 am	Experiment 1: Protein denaturing, reduction and alkylation of <i>E coli</i> Lysate samples for shotgun proteomics analysis: Attendees divided into 3 groups. 2-3 people in sub-group for one sample Instructors: Drs. Zhang, Meng, Feng Dan; Mrs Xia Bin room 118, 120
10:10 - 11:00 am	Lecture 1: Experimental design and sample preparation prior to MS analysis Instructors: Dr. Zhang for design and Dr. Meng for sample preparation
11:10 - 12:00 am	Lecture 2: Basics of mass spectrometry (MS) & LCMS proteomics workflows Instructor: Dr. Zhang Third Floor Conference Room
12:00am - 12:10pm	Experiment 2: In solution trypsin digestion room 118,120
12:10 - 1:00 pm	Lunch
1:00 to 1:50 pm	Lecture 3: Global quantitative proteomics and quantitative PTMs Sheng Zhang, Director, Proteomics and Metabolomics Facility Third Floor Conference Room
2:10- 3:10 pm	Experiment 3: Lab tour and LC-MS instrument demo: Attendees divided into 3 groups (20 min/tour rotation). NanoLC-MS/MS for Ecoli lysate by DDA in 6600 TripleTOF: by Dr. Meng TMT10plex or TMT11plex labeled sample analysis : by Dr. Zhang First dimensional High pH RPLC-based fractionation: by Ms. Xia Bin <i>Third Floor Conference Room</i>
3:20 to 4:20 pm	Lecture 4: Protein Complex study by IP-pull down and cross linking MS Sheng Zhang, Director, Proteomics and Metabolomics Facility Third Floor Conference Room
4:30- 5:10 pm:	Experiment 4: Stop trypsin digestion & set up nanoLC-MS/MS analysis Overnight run for in-solution digested <i>E coli</i> samples (with 90-min gradient for each run) 7 samples on 6600, by <i>Dr. Meng</i> (attendees #1- #7) 7 samples on Orbitrap Fusion, by Dr. Zhang (attendees #8 - #13) <i>room 118,120</i>

March 27, 2019

Day 2	2:
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- 8:30 9:15 Pending(Thermo)
- 9:15 -10:00 Pending(Sciex)

 10:00 - 10:20 am:
 Laptop computer setup

 Each attendee needs to bring his/her own laptop, distribute individual MGF, PKL to each attendee by

 Instructor:

 Third Floor Conference Room

- 10:20 10:50 am
 Lecture 5: Introduction to Mascot-based MS database searching & data interpretation

 Dr. Qingshi Meng
- 10:50 12:00 am
 Experiment 5: Database searching practice for E coli samples by Mascot 2.6

 use the distributed MGF, PKL files using Mascot public search engine or local server

 For both raw data files generated from 6600 QTOF and Orbitrap Fusion

 Instructors: Drs. Meng, Zhang, Xia Bing
- 12:00 1:00 pm Lunch
- 1:30 pm 2:00pm Lecture 6: Introduction to MaxQuant-based MS database searching Dr. Zhang, Cornell Proteomics and Metabolomics Facility Third Floor Conference Room
- 2:00pm 3:30pm Experiment 6: MaxQuant searching practice for protein IDs and LFQ of E coli samples For raw data files generated from Orbitrap Fusion, exporting results into Excel Distribute individual raw files to each attendee
- **3:30 to 4:00 pm Experiment 7: MaxQuant Database search practice: for SILAC and iTRAQ/TMT samples** Distribute individual raw files from Orbitrap Fusion to each attendee

4:00 to 4:50 pm Experiment 8: MaxQuant Database search practice: LFQ for IP pulldown samples and quantitative PTMs Instructors: Sheng Zhang, Dr. Meng and Xia Bing Distribute individual raw files from Orbitrap Fusion to each attendee

- 4:50- 5:10 pm Lecture 7: How to understand global search report from MaxQuant & Mascot results Instructors: Dr. Zhang 4 Supplementary documents for understanding MaxQuant, Mascot, PD 2.2.
- 5:10 5:40 pm Experiment 9: Summary of the full workshop group results for Ecoli shotgun analysis Distribute individual excel files (result for individually prepared *Ecoli* sample) to each attendee Instructors: *Sheng Zhang and Dr. Meng*

March 28, 2018

Day 3:

8:30 - 9:00 am:	Lecture 8: Statistical analysis of global proteomics: how to determine DEPs 1) By Excel;
	2) Perseus software;
	3) EasyFit Program
	Instructor: Sheng Zhang
9:00 - 9:45 am	Experiment 10: Perseus statistical practice: MQ-TMT data with 2-sample t-test Instructor: Sheng Zhang, Dr. Meng
9:40 - 10:30 am	Experiment 11: Perseus statistical practice: MQ-SILAC data with ANOVA test Instructor: Sheng Zhang, Dr. Meng
10:30 - 11:15 am	Experiment 12: Perseus statistical practice: MQ-Label-free data with 2-sample test Instructor: Sheng Zhang, Dr. Meng
11:15 - 12:00 am	Experiment 13: Perseus statistical practice: TMT6plex data with 1-sample t-test Instructor: Sheng Zhang, Dr. Meng
12:00 - 1:00 pm	Lunch Biotech Bldg., room 130
1:30 – 2:00 pm	Lecture 9: Bioinformatics analysis (GO/KEGG enrichment) of global proteomics data sets using Clusterprofiler in R language and DAVID 6.8, Protein-protein interaction network by String 10.0 Instructor: <i>Dr. Meng</i>
2:00 - 3:15 pm	Experiment 14: Bioinformatics analysis practice Instructors: Drs. Meng and Zhang
3:15 - 3:35 pm	Lecture 10: Web-based bioinformatics tools to make plots/figures for scientific presentations Instructor: Dr. Zhang
3:35 - 4:00 pm	Experiment 15: Practice for making plots using online tools Instructors: Drs. Meng and Zhang
4:00 - 5:30 pm	Lecture 11: PTM (1) phosphorylation, acylation, uniquitination, glutathionylation, nitrification,

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Day 4:

8:30 - 9:15 am	Lecture 11: PTM (2) Glycosylation
9:15- 10:00 am:	Lecture 11: Thermal Proteome Profiling (TPP) for protein-ligand & protein-protein interactions Instructor: Sheng Zhang
10:10- 10:50 am:	Lecture 12: Experimental Design and Workflow for Untargeted metabolomics Instructor: Sheng Zhang
11:00 - 11:30 am	Lecture 13: Untargeted lipidomics Instructor: Sheng Zhang
11:30 - 12:00 pm	Summary of workshop and issue of certificate

12:00 - 1:00 pm Lunch