

FIOCRUZ
Instituto Oswaldo Cruz
Programa de Pós-Graduação em Biologia Celular e Molecular

Programa

II Workshop Tópicos avançados em Proteômica

Dr. Gabriel Padrón

División de Química Física, Centro de Ingeniería Genética y Biotecnología, Habana, Cuba

Organização:

Dra. Patricia Cuervo, Laboratório de Pesquisa em Leishmaniose, IOC, FIOCRUZ, RJ

Dra. Ana Gisele da Costa Neves Ferreira, Laboratório de Toxinologia, IOC, FIOCRUZ, RJ

Dr. Leonardo Saboia Vahia, Laboratório de Pesquisa em Leishmaniose, IOC, FIOCRUZ, RJ

Dr. Marcos Catanho, Laboratório de Genômica Funcional e Bioinformática, IOC, FIOCRUZ,
RJ

PROGRAMA DO WORKSHOP
Primeira parte – Preparação de amostras
08-12 de junho de 2015

Segunda-feira: 08/06/2015	Terça-feira: 09/06/2015	Quarta-feira: 10/06/2015	Quinta-feira: 11/06/2015	Sexta-feira: 12/06/2015
Filter aided sample preparation (FASP) methods	Quantitative proteome analysis: Total Protein Approach, Proteomic Ruler	Phosphoproteomic Methods	Phosphoproteomic Methods	Data analysis and summary
9:00h – 9:30h Opening remarks – Dr. Gabriel Padron 9:35h – 10:30h Lecture: Introduction to FASP methods. Dr. Jasek Wisniewsky (Max Planck)	9:00h – 11:00h Lab work: Isolation and quantitation of peptides. Dr. Jasek Wisniewsky	9:00h – 10:00h Summary: Total Protein Approach, Proteomic Ruler. Dr. Jacek Wisniewsky	9:00 h – 12:30h Lab work: Phosphopeptide isolation. Dr. Giuseppe Palmisano	9:00 h – 10:00h– Summary of Phosphoproteomic Methods. Dr. Giuseppe Palmisano
10:30 h - 10:50 – Café	11:00h-11:20h -Café	10:00h-10:20h - Café		10:00h – 10:20 Café
10:50-13:00 Lab work: Sample lysis and quantitation: Dr. Jasek Wisniewsky	11:20 h – 12:10h Summary: Dr. Jasek Wisniewsky	10:20h – 11:20h Lecture: Introduction to Phosphoproteomic Methods. Dr. Giuseppe Palmisano 11:20 h – 13:30h Lab work: Sample lysis and quantitation. Dr. Giuseppe Palmisano		10:45h – 12:00h Data analysis of MS results of proteins identified by FASP procedure. Dr. Jacek Wisniewsky
13:00h – 14:00h ALMOÇO	12:10h – 13:20h ALMOÇO	13:30h – 14:30h ALMOÇO	12:30h – 13:30h ALMOÇO	12:00h – 13:00h ALMOÇO
14:00-17:30 h – Lab work: Protein processing and protein digestion (overnight). Dr. Jasek Wisniewsky	13:20h -14:30h – Lecture: Introduction to Total Protein Approach, Proteomic Ruler – Dr. Jasek Wisniewsky	14:30 h – 17:30 Lab work: Protein processing and protein digestion (overnight). Dr. Giuseppe Palmisano	13:30 h – 17:30h Lab work: Phosphopeptide isolation. Dr. Giuseppe Palmisano	13:00 h – 15:00 Data analysis of MS results of phosphopeptides and phosphosites identification. Dr. Giuseppe Palmisano
	14:30-15:00 -Café			15:00-15:20 Café
	15:20 – 16:20 – Data analysis: Dr. Jasek Wisniewsky.			15:30 h-16:20h – Closing remarks. Gabriel Padron, Jacek Wisniewsky and Giuseppe Palmisano

PROGRAMA DO WORKSHOP
Segunda parte – Bioinformática em proteômica
31 agosto a 04 setembro de 2015

Segunda-feira: 31/08/2015	Terça-feira: 01/09/2015	Quarta-feira: 02/09/2015	Quinta-feira: 03/09/2015	Sexta-feira: 04/09/2015
SKYLINE	SKYLINE	SKYLINE	Bioinformatic analysis of proteomic data: finding the biological sense of protein identifications	Bioinformatic analysis of proteomic data: finding the biological sense of protein identifications
9:00h – 9:10h Opening remarks – Dr. Gabriel Padron and Dr. Brendan MacLean 9:15h – 10:10h Lecture: Moving from discovery to targeted proteomics – focus on SRM - Ariel Bensimon	9:00h – 10:00h Lecture: Protein quantification - Ariel Bensimon .	9:00h – 10:00h Lecture: Data independent acquisition (DIA) – Dr. Jarrett Egertson	9:00 h – 10:00h Lecture: Use of Cytoscape versions 2.8 and 3.2. Dr. Arielis Rodríguez	9:00 h – 10:00h– Data analysis: Dr. Arielis Rodríguez
10:10 h - 10:30 – Café	10:00h-10:30h -Café	10:00h-10:30h - Café	10:00h-10:30h - Café	10:00h – 10:30 Café
10:30-11:15h Lecture: Introduction to Skyline – Dr. Brendan MacLean 11:15-12:30 Tutorial: Targeted method editing in Skyline – Dr. Brendan MacLean	10:30 – 11:30h Lecture: Statistical considerations for experimental design and data analysis – Dr. Brendan MacLean 11:30-12:30 Tutorial: Group comparison statistics and reports in Skyline – Dr. Brendan MacLean	10:30 – 12:00h Tutorial: Data independent acquisition (DIA) data analysis – Dr. Jarrett Egertson 12:00 – 12:30h Lecture: DIA Chorus cloud chromatogram extraction – Dr. Brendan MacLean	10:30 h – 12:30h Lecture: Use of CellDesigner and drugDisrupNet. Dr. Arielis Rodríguez	10:30h – 12:30h - Data analysis: Dr. Arielis Rodríguez
12:30 – 13:30h ALMOÇO	12:30 – 13:30h ALMOÇO	12:30 – 13:30h ALMOÇO	12:30h – 13:30h ALMOÇO	12:30h – 13:30h ALMOÇO
13:30-15:00 h – Tutorial: Targeted method refinement in Skyline – Dr. Brendan MacLean	13:30 -14:00h Lecture: Overview and keys to success in processing DDA data with Skyline Dr. Brendan MacLean 14:00-15:30 Tutorial: Label-free quantitative analysis of DDA data with Skyline – Dr. Brendan MacLean	13:30 h – 14:30 Lecture: Panorama web repository for Skyline documents – Dr. Brendan MacLean	13:30 – 15:30h - Data analysis: Dr. Arielis Rodríguez	13:30 – 15:30 h - Data analysis: Dr. Arielis Rodríguez
15:00-15:30 -Café	15:30-16:00 -Café	14:30-15:00 -Café	15:30-16:00 Café	15:30-16:00 Café
15:30 – 16:15 Lecture: Determination of optimal SRM assay parameters - Ariel Bensimon 16:15 – 18:00 – Data analysis in SKYLINE: Dr. Brendan MacLean .	16:00 – 17:30h Tutorial: Parallel reaction monitoring (PRM) with Skyline – Dr. Jarrett Egertson	15:00-16:30 h Jeopardy Quiz 16:30-17:30 h Summary: – Dr. Brendan MacLean	16:00 – 17:30h Data analysis: Dr. Arielis Rodríguez	16:00 -17:30h – Data analysis: Dr. Arielis Rodríguez 17:30 – 18:00 h - Closing remarks.