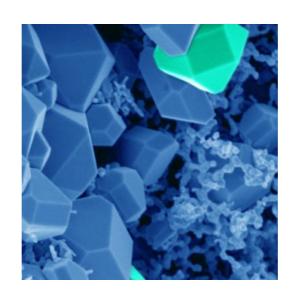


### **Pasteur course**

# 3<sup>rd</sup> INTEGRATIVE STRUCTURAL BIOLOGY



**PROGRAM 2017 - 2018** 

### Pasteur course

# 3<sup>rd</sup> INTEGRATIVE STRUCTURAL BIOLOGY

2017 - 2018 (16 - 20 July, 2018)

**Course Organizers** 

Claudine Mayer
Michael Nilges
Nicolas Wolff
Institut Pasteur

The Course will take place at

The Institut Pasteur
28, rue du Docteur Roux
75724 PARIS Cedex 15
François Jacob - Building 26-28
Education Center (Building 06, Room 4)

#### **Description of the course**

Problems in structural biology today can very often not be solved by one technique alone, but need to be solved by a combination of methods, including NMR, X-ray crystallography, electron microscopy, structural mass spectrometry, and SAXS. The heterogeneous data coming from these methods need to be combined with advanced molecular modeling techniques. The Institut Pasteur is one of the few institutions that unites expertise in all major structural biology techniques and in molecular modeling on one site. The goal of the course is to provide young scientists that have more specialized knowledge in one of the techniques an overview over the broad range of modern structural methods available. Special emphasis will be given to computational approaches to integrate data (such as IMP, ARIA, ...).

The course is principally aimed at the mature graduate student / postdoctoral level, but applications from scientists at all levels are encouraged. The course will consist of lectures, which will give introductions into the principles and limitations of the different techniques, and practical work on data analysis with the major structure refinement / modeling programs.

## Pasteur course – 3<sup>rd</sup> Integrative Structural Biology

Sunday, July 1	15	Arrival of participants		
20:00	Inforn	mal get together / Dinner		
Monday, July	16	Protein production	Chair: Bruno Miroux	
Amphitheatre	Franço	ois Jacob		
9:00 -10:00	Welcome to the participants and Administrative information			
10:00 - 10:30	General presentation of the course Michael Nilges (Paris)			
10:30 - 11:00	1 slide presentation of the participants			
11:00 - 11:45	Heter	rologous production of complex samples	Imre Berger (Bristol)	
Bioinformatics room 4 (building 6)				
12:00 - 12:45	Gene	e design and codon metrics	Gregory Boel (Paris)	
12:45 - 14:00	Lunch			
14:00 - 14:45	Microbial expression systems for membrane proteins Bruno Miroux (Paris)			
14:45 - 15:30	Amphipols nanodisc and SMA for membrane protein stabilization and purification  Manuela Zoonen (Paris)			
15:30 - 16:15	Membrane Protein Reconstitution Martin Picard (Paris)		Martin Picard (Paris)	
16:15 - 16:45	Coffee break			
16:45 - 17:30 (Paris)	Qualit	ty control and characterization of purified proteins-1	Bertrand Raynal	
17:30 - 18:15	Qualit	ty control and characterization of purified proteins-2	Sébastien Brulé (Paris)	
18:30 - 20:30	Dinne	er (Buffet) / Poster session		
Tuesday, July	17	X-ray diffraction	Chair: Isabelle Broutin	
Amphitheatre François Jacob				
9:00 - 9:30	No st	ructure without crystal, the long road to get it	Isabelle Broutin (Paris)	
9:30 - 10:30	How	the crystal got its spots	Pierre Legrand (Saclay)	
10:30 - 10:45	Coffe	e break		

10:45 - 11:45	From diffraction data to initial phases and from phases to model building and validation  Marc Delarue (Paris)					
11:45 - 12:15	How bacterial RND transporters efflux	Isabelle Broutin (Paris)				
12:15 – 12:45	antibiotics out of the cell Integrated structural biology for ribosome bioge understanding	enesis Magali Blaud (Paris)				
13:00 - 14:30	Lunch					
Bioinformatics room 4 (building 6)						
14:30 - 18:00	Practical session From data processing to structure refinement	Marco Bellinzoni (Paris)				
Wednesday, J	uly 18 Liquid/solid NMR	Chair: Sophie Zinn-Justin				
Amphitheatre François Jacob						
9:00 - 10:00	Principles of NMR Soph structure determination et dynamics by liquid s	nie Zinn-Justin (Gif-sur-Yvette) tate NMR				
10:00 - 10:45	Biomolecular interactions by liquid state NMR	Nadia Izadi-Pruneyre (Paris)				
10:45 - 11:15	Coffee break					
11:15 - 12:15	Cutting-edge solid-state NMR to elucidate insoluble protein structures  Birgit Habenstein (Bordeau:					
12:30 - 13:45	Lunch					
13:45 -14:45	From NMR data to structures: principles and contributions to integrative studies of large assemblies  Benjamin Bardiaux (Pa					
Bioinformatics room 4 (building 6)						
15:00 - 18:00	HADDOCK Introduction and Practical session	Alexandre Bonvin (Utrecht)				
18:30 - 20:30	Dinner (Buffet) / Poster session					
Thursday, July	y 19 Electron microscopy	Chair: Dorit Hanein				
9:00 - 10:00	An overview of cryo-EM	Dorit Hanein (San Diego)				
10:00 - 11:00	Image processing basics Niels Volkmann (San Dieg					
11:00 - 11:30	Coffee break					

11:30 - 12:00	Visualizing macromolecular machines	Christo Gatsogiannis (Dortmund)			
12:00 - 12:30	Protein Structures and Dynamics from Cryo-EM	Chiara Rapisarda (Bordeaux)			
12:30 - 14:00	Lunch				
Bioinformatics	room 4 (building 6)				
14:00 - 18:00	Practical session	Christo Gatsogiannis (Dortmund)			
	High resolution single particle cryoEM using SPHIRE	Toshi Moriya (Dortmund)			
18:30 - 19:30	Dinner (Buffet) / Poster session (Modules	1, 2 and 3, building 6)			
Friday, July 20	SAXS – Biophysics	Chair: Patrice Vachette			
Amphitheatre François Jacob					
9:00 - 10:30	Solution X-ray Scattering from Biological macromolecules (1)	Javier Perez (Orsay)			
10:30 - 11:00	Coffee break				
11:00 - 12:30	Tutorials – SAXS data analysis And modeling	Aurelien Thureaux (Orsay) Patrice Vachette (Orsay)			
12:30 - 14:00	Lunch				
Bioinformatics	room 4 (building 6)				
14:00 - 15:30	Integrative strucrural biology	Michael Nilges (Paris)			
15:30 - 16:30	Data deposition and validation at the Worldwide Protein Data Bank (wwPDE	Aleksandras Gutmanas (Hinxton) 3)			
16:30 - 18:00	PDB Practical session	Aleksandras Gutmanas (Hinxton)			
Saturday, July	21 Mass spectrometry	Chair: Julia Chamot-Rooke			
Amphitheatre François Jacob					
9:00 - 9:30	Mass Spectrometry in Structural Biology: an Introduction	Julia Chamot-Rooke (Paris)			
9:30 - 10:30	Structural probing of protein complexes by protein cross-linking and mass spectrome				
10:30 - 11:00	Coffee break				

11:00 - 12:00	,	Thomas Jorgensen (Southern Denmark) ckbone amide hydrogen/deuterium hass spectrometry		
12:00 - 13:00	Higher-order protein struct by native MS and ion mol			
13:00 - 14:00	Lunch (Buffet)			
Bioinformatics room 4 (building 6)  14:00 - 16:00 Practical session: IMP Tutorial Ricardo Pellarin (Paris				
16:30 - 16:45	Coffee break			
16:45 - 17:45	Round table			
17:45 - 18:00	Conclusion of the course	Michael Nilges (Paris)		
Sunday, July 2	3 Departure			

Coffee every afternoon around 16:00 during practical sessions