Macromolecular Crystallography School
MCS2020 13 - 18 April 2020

Instituto de Química-Física "Rocasolano, CSIC, Madrid (Spain), 13-18 April 2020

	Mon. 13th	***Tue. 14th***	***Wed. 15th***	***Thu. 16th***	***Fri. 17th***	***Sat. 18th***
08:30-09:00	Production of protein samples for crystallization and other biophysical techniques ***Dr M. Solá***	Data collection. Considerations and compromises. Data quality. Noise, errors, and mistakes ***Dr K. Diederichs***	New phasing approaches from the *Bari Factory* ***Dr C. Giacovazzo***	*PHENIX.* General introduction to structure refinement and *phenix.refine* ***Dr P. Afonine***	*REFMAC* and tools for low resolution refinement ***Dr R. Nicholls***	*Micro ED* ***Dr C. Millán***
09:00-09:30						
09:30-10:00						Fundamentals on *cryo-EM* ***Dr C. San Martín***
10:00-10:30						
10:30-11:00	Coffee break	Coffee break	Coffee break	Coffee break	Coffee break	Coffee break
11:00-11:30	Automated pipelines for protein crystallography and fragment screening ***Dr J. Márquez***	Principles of data processing with *XDS.* Serial Crystallography at Synchrotron ***Dr K. Diederichs***	*PHENIX:* General introduction and general overview of automated structure solution ***Dr P. Adams***	*PHENIX:* Ensemble, ligand and low-resolution refinement. Validation and map calculation ***Dr P. Afonine***	Workshop on *REFMAC* ***Dr R. Nicholls***	Sample preparation, initial screening and optimization for *cryo-EM* ***Dr R. Fernández-Leiro***
11:30-12:00						
12:00-12:30						
12:30-13:00	Free-time for lunch	Free-time for lunch	Free-time for lunch	Free-time for lunch	Free-time for lunch	Free-time for lunch
13:00-13:30						
13:30-14:00	*AUTO-RICKSHAW*: New automated procedures for processing / phasing ***Dr. S. Panjikar***	Workshop on *XDS* ***Dr K. Diederichs***	Density modification in *PHENIX* ***Dr P. Adams***	Workshop on refinement and validation in *PHENIX* ***Dr P. Adams*** ***Dr P. Afonine***	Refinement and manual model building using *COOT* ***Dr P. Emsley***	From micrographs to atomic model: Data processing overview in *cryo-EM* ***Dr R. Fernández-Leiro***
14:00-14:30						
14:30-15:00						
15:00-15:30						
15:30-16:00	Break	Break	Break	Break	Break	*FAREWELL*
16:00-16:30	Multidata sets ***Dr S. Panjikar***	General overview about *SHELX, PHASER* and *ARCIMBOLDO* ***Dr I. Usón***	Workshop on *MR* and phasing in *PHENIX* ***Dr P. Adams*** ***Dr P. Afonine***	*CCP4*: General introduction ***Dr E. Krissinel***	Workshop on *COOT* ***Dr P. Emsley***	
16:30-17:00						
17:00-17:30						
17:30-18:00	Biophysical methods in solution ***Dr. B. Monterroso***	Student's presentations (*)	Student's presentations (*)	***FIESTA !***		
18,00-18:30		Discussions, questions and time for student's projects (*)	Discussions, questions and time for student's projects (*)			
18.30-19:00						
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At the end of each day, discussion sections will be moderated by Drs. J.A. Hermoso, A. Albert, I. Usón and M. Solá, with the participation of remaining teachers.

(*) Students will be requested to prepare a short introductory presentation (max. 3 PowerPoint slights in pdf format) on their group, current stage of their project, personal motivation and/or their crystallographic problems. At the same time, they should feel free to bring their own data to discuss with the teachers and the rest of students.