

# Getting the best from your structural data: beyond black boxes

## Program

### Wednesday 5 October

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8.25 - 8.30	Welcome and Introduction	<b>J. Cavarelli</b>
8.30 - 9.20	Quality indicators in crystallography	<b>Kay Diederichs</b>
9.20 - 10.10	Principles of EM single particle analysis	<b>Helen Saibil</b>
<i>10.10- 10.30</i>	<i>Coffee break</i>	
10.30- 11.20	Looking forward to the fully automated and optimal data collection using synchrotron radiation	<b>Alexander Popov</b>
11.20- 12.10	The battle of Signal vs Noise	<b>James Holton</b>
12.10-13:00	Will I solve my structure: SAD phasing and automated structure determination	<b>Thomas Terwilliger</b>
<i>13.00 - 14.20</i>	<i>Lunch</i>	
14.30 - 18.30	Practicals sessions : 3 sessions in parallel	

### Thursday 6 October

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8.15 - 9.05	Principles of XDS data processing	<b>Kay Diederichs</b>
9.05 - 9.55	MOSFLM	<b>Harry Powell</b>
<i>9.55 - 10.15</i>	<i>Coffee Break</i>	
10.15- 11.05	HKL3000	<b>Wladek Minor</b>
11.05- 11.55	EMFit	<b>Michael Rossmann</b>
11.55-12:45	Principles of Cryo-electron tomography and subtomogram averaging	<b>Florian Schur</b>
<i>12.45 - 14.20</i>	<i>Lunch</i>	
14.30 - 18.30	Practicals sessions : 3 sessions in parallel	

## Friday 7 October

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8.30 - 9.20	Model-building using cryo-EM and crystallographic maps	<b>Thomas Terwilliger</b>
9.20 - 10.10	Ligand validation	<b>Bernhard Rupp</b>
<i>10.10- 10.30</i>	<i>Coffee break</i>	
10.30- 11.20	3 D classification	<b>Marin Van Heel</b>
11.20- 12.10	Getting the most out of Structural Biology Facilities at SOLEIL: present and future, and potential complementarity	<b>Andrew Thompson</b>
12.10-13:00	Structure analysis of macromolecular solutions with small-angle X-ray scattering	<b>Dmitri Svergun</b>
<i>13.00 - 14.20</i>	<i>Lunch</i>	
14.30 - 18.30	Practicals sessions : 3 sessions in parallel	

## Saturday 8 October

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9.00 - 9.50	Serial and In-situ crystallography, large complexes, and low-energy phasing on EMBL@PETRAIII beamlines	<b>Gleb Bourenkov</b>
9.50 - 10.40	Evolving Data Collection Strategies for Experimental Phasing: from single crystal to serial crystallography	<b>Vincent Olieric</b>
<i>10.40 - 11.00</i>	<i>Coffee break</i>	
11.00 - 11.50	Integration of cryo-EM with X-ray diffraction	<b>Bruno Klaholz</b>
11.50 - 12.00	Conclusions	<b>J. Cavarelli</b> <b>A. Urzhumtsev</b>