

Monday 29th April:

Biological Cryo-imaging User Meeting: eBIC & B24

13:00 - 18:00	Registration open
14:00	Martin Walsh (Biological cryo-imaging group leader) Welcome
14:05	Katie Cunnea & Alun Ashton (eBIC) eBIC User Program: Update and
	future plans
14:45	Ilias Kounatidis (B24 research associate) B24 update and future plans
15:30	Coffee
	User talks
16:00	Alister Burt Cryo-ET of Bacterial Chemotaxis Machinery in E. coli Minicells
16:20	Kyle Morris AP-1 trimerisation and conformation switching: allosteric control by
	HIV-1 Nef in the context of tetherin downregulation
16:40	Daniel Mann CryoEM structure of the lipid transporter MLA
17:00	Nita Shah CryoEM reveals how plants turn off carbon fixation in the dark
17:20	Kamal Nahas Correlative microscopy: HSV biology
17:40	Maud Dumoux Correlative microscopy: Chlamydia biology
	User meeting discussion
18:00	Chaired by Sean Connell Diamond User Committee (DUC) representative
19:00	Pizza & Beer mixer







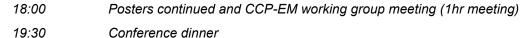
Tuesday 30th April:



CCP-EM Spring Symposium

8:30	Registration	
9:30	Welcome & what's new in CCP-EM (Colin Palmer, 35mins),	
	eBIC (Andy Howe, 20mins) & EMDB (Gerard Kleywegt, 35mins)	
11:00	Coffee	
Session 1 - So	ftware Tools	
11:30	John Rubinstein CryoEM for scarce and unstable membrane protein complexes	
12:15	Kevin Cowtan Extending model building and refinement tools for Cryo-EM	
	applications	
12:45	Shaun Rawson Rapid evaluation of EM datasets	
13:15	Lunch	
Session 2 - Ap	plications / model building	
14:30	Doryen Bubeck CryoEM of the membrane attack complex reveals how proteins	
	cross lipid bilayers	
15:00	Grzegorz Chojnowski De novo construction of atomic models into	
	electron-microscopy maps with ARP/wARP 8.0	
15:15	Tristan Croll Interactive model building in ISOLDE	
15:30	Pamela Williams Expanding the industrial structural biologist's toolkit with cryoEM	
16:00	Coffee and poster session	
Session 3 - Microscopy		
17:00	Felix Weis How to get the maximum out of your cryo-EM data collection session	

David Bhella | The Scottish Centre for Macromolecular Imaging - early adopters of



17:30

18:00



the JEOL CryoARM300



Wednesday 1st May:



CCP-EM Spring Symposium

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Session	4 -	Samble	preparation

9:00	Giulia Weissenberger (CryoSol) VitroJet: Bridging the Gap in Sample Prep
9:15	Michele Darrow (TTP Labtech) Chameleon: Next Generation Sample Preparation
	for CryoEM based on Spotiton
9:30	Thomas Braun Microfluidic Sample Preparation for EM: Protein Isolation,
	High-Resolution cryo-EM, and 'Differential Visual Proteomics'
10:00	Stephen Muench New approaches to grid preparation in cryo Electron Microscopy
10:30	Coffee and poster session

Session 5 - Miscellaneous

11:30	Louise Fairall Architecture of the MiDAC histone deacetylase complex
11:45	Thorsten Wagner Automated particle picking and preprocessing in SPHIRE
12:15	Lunch

Session 6 - Tomography

13:30	Sonja Welsch News on Thermo Fisher Scientific's 2019 developments for
	cryoTEM
14:00	Stefan Pfeffer Structural insights into the co-translational machinery for protein
	folding and maturation
14:30	Wanda Kukulski Cellular membrane architectures studied by correlative
	microscopy and electron cryo-tomography
15:00	Coffee

Session 7 - Software tools

15:30	Maximilian Beckers Thresholding of cryo-EM density maps by false discovery
	rate control
15:45	Jose Miguel de la Rosa Trevin Development of basic building blocks and
	distributed computing for automatic data processing
16:00	Sjors Scheres Developments in RELION-3
16:45	Closing remarks



