

CSSB Networking Symposium

Date: 9 December 2021

Location: https://desy.zoom.us/j/82370657728; Meeting ID: 823 7065 7728; Passcode: 640171

Welcome		
9:00	Welcome & CSSB Overview Chris Meier, Scientific Director CSSB	

Session 1: Molecular approaches to malaria Session Chairs: Michael Filarsky / Tim Gilberger	
9:20	Introduction: Walter and Eliza Hall Institute of Medical Research (WEHI), Australia
9:25	Malaria parasite invasion, versatile structural scaffolds and alternate erythrocyte receptors Wai-Hong Tham (WEHI)
9:50	Discovery of novel antimalarials and their use as chemical tools to discover new biology of the malaria parasite Alan Cowman (WEHI)

10:15	The phospholipase PNPLA2 and its link to the malaria parasite's respiratory chain
	Emma Pietsch, CSSB (Gilberger)

10:25 Coffee Break

	Session 2: Pathogen – Host Interactions
	Session Chairs: Jens B. Bosse / Michael Kolbe
10:35	Introduction: University of Cambridge, United Kingdom
10:40	The many ways of interfering with interferon by vaccinia virus Geoffrey L. Smith (Cambridge)

11:05 Structural and in vivo characterisation of the Type IX Secretion system/gliding motility motor Rory Hennell James, CSSB (Marlovits)

11:15 Coffee Break

	Session 3: TB and structural MS Session Chairs: Thomas Marlovits / Jörg Labahn	
11:25	Introduction: Institut de Pharmacologie et de Biologie Structurale, France	
11:30	Metallobiology at the host-pathogen interface: the case of tuberculosis Olivier Neyrolles (IPBS)	
11:55	Structural Mass Spectrometry of the proteasome Julien Marcoux (IPBS)	

12:20	MS-SPIDOC: Mass spectrometry meets single particle imaging



	Thomas Kierspel, CSSB (Uetrecht)	
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12:30 Lunch

	Session 4: From transporters to SARS-CoV2 Session Chairs: Christian Löw / Thomas Gutsmann	
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13:15	Introduction: University of Aarhus, Centre for Structural Biology, Denmark	
13:20	Structure, function and mechanism of human chloride transporter NKCC1	
	Poul Nissen (AU)	
13:45	Elucidating the mechanism of a NAD-depleting RES-domain toxin	
	Ragnhild Bager Skjerning (AU)	

14:10	Inhibitor screening and structural characterization of virulence factors from SARS-CoV-2
	Spyros D. Chatziefthymiou, CSSB (Kolbe)

14:20 Coffee Break

Session 5: Computational Systems Biology Session Chairs: Maya Topf / Jan Kosinski	
14:30	Introduction: Humboldt-Universität zu Berlin, Germany
14:35	Regulation of ion fluxes between Plasmodium falciparum and infected red blood cells. Edda Klipp (HU-Berlin)
15:00	Purifying and characterizing parasite tubulins as potential drug targets Simone Reber (HU-Berlin)

15:25	AI-based modeling reveals nuclear pore complexity
	Marc Siggel, CSSB (Kosinski)

15:35 Coffee Break

	Session 6: Macromolecular complexes Session Chairs: Kay Grünewald / Holger Sondermann
15:45	Introduction: Utrecht University, The Netherlands
15:50	A clearer picture of the ER translocon complex Friedrich Förster (UU)
16:15	Elucidating the molecular mechanisms of protein aggregation in C. elegans as a living model system Tessa Sinnige (UU)

16:40	Opening new opportunities for Kd determination and screening of MHC peptide complexes
	Janine-Denise Kopicki, CSSB (Uetrecht)

Networking Session Chairs: Rainer Kaufmann / Charlotte Uetrecht / Martin Hällberg	
16:50	Closing Remarks
16:55	Networking

