39th Rhine-Knee Regiomeeting

Integrative Structural Biology — AI, biophysics and structural methods
Hotel Neu-Schönstatt, Quarten (SG), Switzerland · 7–9 October 2026

PSI

Wednesday 7 October 2026

15:00–16:30	Registration	
16:30–17:30	**Welcome apéro**	
17:30–17:45	Opening remarks — Organizing committee	
17:45–18:30	**Keynote I** · **Cornelius Gati** (University of Southern California, Los Angeles) *Understanding Ligand Efficacy at the μ-Opioid Receptor by Cryo-EM*	
18:30–20:15	**Dinner**	
20:15–21:45	**Session 1: Next-Gen Cryo-Electron Microscopy** — 6 talks · 15 min each (12 + 3 Q&A)	
20:15–20:30	**Juan Estévez-Gallego** — PSI, Villigen *Structural basis of microtubule destabilization by GTP hydrolysis*	T01
20:30–20:45	**Alberto Caregnato** — University of Geneva *Molecular Glue at the Cell Surface: How CIF Peptides Assemble and Activate Plant Receptor Complexes*	T02
20:45–21:00	**Hugo R. Vaca** — IGBMC, Strasbourg *Unlocking the Ubiquitin Code: Structural Snapshots of UBE3A Activation in Neurodevelopment and Cancer*	T03
21:00–21:15	**Maria Jose Marcaida** — EPFL, Lausanne *Cryo-EM structures of the porin MspA in detergent and polymer nanodiscs*	T04
21:15–21:30	**Anh-Phu Nguyen** — AFMB, CNRS – Aix-Marseille University *Structural and functional characterization of GacS, the membrane-bound histidine kinase controlling infection modes in Pseudomonas aeruginosa, and development of novel inhibitory nanobodies*	T05
21:30–21:45	**Rakhshana Bala Krishnan** — IGBMC, Strasbourg *Reconstitution of the human elongation complex to study its structure by cryo-EM*	T06
21:45–24:00	**Networking & social exchange**	

Thursday 8 October 2026

07:00–08:30	**Breakfast**	
08:30–09:15	**Keynote II** · **Matthew J. Rodrigues** (Diamond Light Source, Didcot) *XFEL Snapshots Reveal the Activation Mechanism of Rhodopsin, the Mammalian Dim-Light Visual Receptor*	
09:15–10:30	**Session 2: Advanced Structural Methods – serial and time-resolved crystallography** — 5 talks · 15 min each (12 + 3 Q&A)	
09:15–09:30	**Michal W. Kepa** — PSI, Villigen *Cristallina-MX: Serial and time-resolved protein crystallography at SwissFEL*	T07
09:30–09:45	**Thomas Mason** — PSI, Villigen *Drop-on-Chip Rapid-Mixing for Time-Resolved Serial Crystallography at SwissFEL*	T08
09:45–10:00	**René Rasche** — PSI, Villigen *Initial Photochemistry of Vision by TR-SFX: Towards Femtosecond-Resolved Snapshots of Retinal Isomerization in Rhodopsin*	T09
10:00–10:15	**Sofia M. Kapetanaki** — MAX IV Laboratory, Lund *Insights in the signal transduction pathway of a photoactivated adenylate cyclase*	T10
10:15–10:30	**Yanyan Chen** — Serial X AB, Gothenburg *Serial X – Simple Solutions for Serial Synchrotron Crystallography*	T11
10:30–11:00	**Znüni break & group picture**	
11:00–12:00	**Session 3: Advanced Biophysical Methods – integrative characterization of interactions and dynamics** — 4 talks · 15 min each (12 + 3 Q&A)	
11:00–11:15	**Théo D'Andrea** — IBMC, CNRS, Strasbourg *Overcoming the bacterial antibiotic resistances using a macrolide–antimicrobial peptide chimera*	T12
11:15–11:30	**Andreas Zoumpoulakis** — Sorbonne University, Paris *Deciphering the Role of Modulators in Human Kir2.1 Potassium Channel Gating through Integrative Approaches*	T13
11:30–11:45	**Matthias Zeug** — University of Basel *Structural Basis for RasGAP Activity Regulation*	T14
11:45–12:00	**Pedro Jiménez-Sandoval** — University of Lausanne *Sensing danger in sugar: structural basis of DAMP recognition by IGP1*	T15
12:00–13:15	**Lunch**	
13:30–18:00	**Excursion**	
18:45–20:30	**Conference dinner**	
20:30–21:15	**Keynote III** · **Sandra Markovic-Müller** (leadXpro AG, Villigen) *Unlocking Challenging Membrane Proteins for Drug Discovery at leadXpro*	
21:15–22:00	**Session 4: Cryo-Electron Microscopy II** — 3 talks · 15 min each (12 + 3 Q&A)	
21:15–21:30	**Hugo Muñoz-Hernández** — ETH Zürich *A cryo-EM processing pipeline for microtubules using CryoSPARC (MiCSPARC)*	T16
21:30–21:45	**Günter Fritz** — University of Hohenheim, Stuttgart *Maturation of the respiratory NQR complex from bacterial pathogens*	T17
21:45–22:00	**Anna Higgins** — Thermo Fisher Scientific *Innovation Inside and Out: The Power of 200 kV, Introducing Glacios 3*	T18
22:00–24:00	**POSTER SESSION** — Dedicated poster session with drinks	

Friday 9 October 2026

07:00–08:30	**Breakfast**	
08:30–09:15	**Keynote IV** · **Alisia Fadini** (Columbia University, New York) *OpenFold as a Prior: Guiding Structure Prediction through Experiments with ROCKET*	
09:15–12:00	**Session 5: Artificial Intelligence, Automation and Computational Methods** — 7 talks · 15 min each (12 + 3 Q&A)	
09:15–09:30	**Jiaxin Duan & David Perl** — PSI, Villigen *Automation at the SLS 2.0 Macromolecular Crystallography (MX) Beamlines*	T19
09:30–09:45	**Ryan O'Dea** — PSI, Villigen *PROBIXI – Self-Calibrating Probabilistic Peak Detection for Serial X-Ray Crystallographic Data*	T20
09:45–10:00	**Alexandre G. Urzhumtsev** — IGBMC, Strasbourg *FT-free calculation of Variable Resolution Maps in CCTBX and Phenix*	T21
10:00–10:15	**Filipa Engrola** — PSI, Villigen *Warming Up Fragment Screening: Cryo2RT Data and AI Structure Prediction in the EP System*	T22
10:15–10:30	**Jakob Teetz** — ETH Zürich *Integrating Molecular Dynamics Simulations and NMR Relaxometry through Explicit Models of Protein Side-Chain Dynamics*	T23
10:30–11:00	**Znüni break**	
11:00–11:15	**Vernon Smith** — Bruker *Structure-Based Drug Discovery in the Home-Lab*	
11:15–11:30	**Mila Schmidlin** — University of Basel *High affinity de novo binders enable structural studies of the bacterial lipid transporter AsmA*	T24
11:30–12:00	**Martin Pacesa** — University of Zurich *BindCraft2: open and universal design of protein binders for any target*	T25
12:00–12:15	Concluding remarks & handover to the 2027 organizers	
12:15–14:00	**Farewell lunch & departure**	

Book of abstracts
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https://indico.psi.ch/event/18148/page/3643-book-of-abstracts