



“Cryo-EM Validation in the Age of SARS-CoV-2: Methods, Tools and Applications” 18, 19 & 20 November 2020
bit.ly/valid-sars

Day 1 – Wednesday 18 November 2020

Analysis and validation of SARS-CoV-2 EM structures

Session 1 – Chair: Peter Rosenthal

14:00 – Peter Rosenthal – *Opening, welcome and logistics*

14:10 – Ardan Patwardhan – *SARS-CoV-2 structures in EMDB and EMPIAR*

14:30 – Patrick Cramer – *Structural studies of SARS-CoV-2 polymerase and mechanism of remdesivir inhibition*

14:50 – Christiane Schafitzel – *A free fatty acid binding pocket in the locked structure of SARS-CoV-2 spike protein*

15:10 – Beata Turoňová – *In situ structural analysis of SARS-CoV-2 spike reveals flexibility mediated by three hinges*

15:30 – Break

Session 2 – Chair: Garib Murshudov

15:45 – Donald Benton – *Structural Basis of SARS-CoV-2 Receptor Binding*

16:05 – Andrea Thorn – *Findings from the Coronavirus Structural Task Force*

16:25 – Tristan Croll – *Rebuilding SARS-CoV-2 Cryo-EM structures with ISOLDE*

16:45 – Agnel Praveen Joseph – *Reprocessing & validation of structures from SARS-CoV-2, and a web-service for mapping genome mutations*

17:00 – Break

17:30 – Panel discussion (Moderator Peter Rosenthal)

18:00 – End of programme



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Day 2 – Thursday 19 November 2020

Single-particle map and tomogram analysis and validation

Session 3 – Chair: Ardan Patwardhan

14:00 – Carsten Sachse – *Significance and confidence of cryo-maps and resolution values*

14:20 – Sjors Scheres – *Single-particle cryo-EM to atomic resolution*

14:40 – Dmitry Lyumkis – *Tools for Analyzing Directional Resolution and Fourier Space Sampling in Cryo-EM*

15:00 – Tim Grant – *Preventing overfitting in cisTEM by local SNR weighting*

15:20 – Break

Session 4 – Chair: Alan Roseman

15:35 – Katerina Naydenova – *Specimen supports for high-resolution cryoEM: application for determining the structure of the SARS-CoV-2 RNA polymerase in presence of favipiravir*

15:55 – Niko Grigorieff – *Locating molecular assemblies by template matching in 2D and 3D: a comparison*

16:15 – Giulia Zanetti – *Common issues in subtomogram averaging: my perspective on current needs and validation*

16:30 – Valeriy Titarenko – *Global and local model fitting and scoring for cryo-EM maps*

16:45 – Lucas Siemons – *Applications of tilt-pair analysis*

17:00 – Break

17:30 – Panel discussion (Moderator Elena Orlova)

18:00 – End of programme



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Day 3 – Friday 20 November 2020

Map/model validation

Session 5 – Chair: Gerard Kleywegt

14:00 – Martyn Winn – *Cryo-EM validation tools in CCP-EM*

14:20 – Keitaro Yamashita – *Refinement of high resolution cryo-EM SPA structures with symmetry*

14:40 – Rangana Warshamanage – *EMDA validation tools as applied to recent SARS-CoV-2 Structures*

14:55 – Andrei Istrate – *Strudel - model-dependent map-feature validation and application to EM SARS-CoV-2 structures*

15:10 – Paul Adams – *Cryo-EM tools in Phenix for validation and beyond*

15:30 – Break

Session 6 – Chair: Martyn Winn

15:45 – Gerard Kleywegt – *Validation at EMDB and wwPDB*

16:05 – Cathy Lawson – *EMDataResource Validation Challenges: Overview and Outcomes*

16:25 – Zhe Wang – *EM Validation Analysis at EMDB*

16:40 – Wah Chiu – *Quantitative Measure of Resolvability of CryoEM Density*

17:00 – Peter Rosenthal – *Concluding remarks*

17:15 – Break

17:30 – Panel discussion (Moderator Maya Topf)

18:00 – End of programme