

Posters

P01	Jakub Benýšek	Novel inhibitors of the methyltransferase METTL3-METTL14 complex	p. 30
P02	Jan Beránek	Alphafold-driven coarse grained dynamics	p. 30
P03	Lada Biedermannová	Comparative Analysis of DNA and RNA Hydration Patterns: Insights from Crystallographic Data	p. 31
P04	Andrej Bitala	Biophysical and binding characterization of rhesus CMV UL144 as a promising modulator of the T-lymphocyte CD160 pathways	p. 31
P05	Tomáš Brom	Rta - Replication and transcription activator of Epstein-Barr virus: functional and structural implications for novel antiviral strategy	p. 32
P06	Ondřej Bulvas	Revealing the function of the C-terminal part of mycobacterial inosine-5'-monophosphate dehydrogenase	p. 33
P07	Ondřej Cehlár	Insights into the Alzheimer's disease specific pre-aggregation conformation of monomeric tau proteins using DC11 antibody	p. 34
P08	Tatsiana Charnavets	Biophysical techniques at Centre of molecular structure of BIOCEV	p. 34
P09	Josef Cikhart	Computer simulations of the bacterial ribosome using coarse-grained models	p. 35
P10	Radek Crha	Combining of hybrid QM/MM simulations with machine learned potentials	p. 36
P11	Martin Černý	Tale of tails; structural comparison of the RNA polymerase δ -subunits	p. 36
P12	Monika Čížková	Deciphering the role of BscX and BscY subunits in the Bordetella Type 3 Secretion System	p. 37
P13	Vojtěch Duchoslav	Unlocking STING's defenses: fluorinated cyclic dinucleotides resistant to viral poxins revealed by crystallography	p. 38
P14	Mária Gondová	Use of a "helper protein" to improve cryo-EM reconstructions – a case of La Jolla and Motts Mill viruses	p. 38
P15	Tomáš Greňa	Structural characterisation of tau protein filaments	p. 39
P16	Lenka Gryčová	Fluctuations in metabolic content affect the integrity of tau envelopes	p. 39
P17	Zuzana Hlavenková	The structure of bacteriophage phi9224	p. 40
P18	Aneta Hrádková	Structural variability of peptide deformylase	p. 40
P19	Andrea Hušková	Enzymatic Revelations of Abasic Site Interstrand Crosslinks repair facilitated by NEIL3	p. 41
P20	Maša Janošev	Calcium-mediated regulation of the human ubiquitin ligase Nedd4-2	p. 41
P21	Linda Kašiarová	Towards unlocking the potential of staphylokinase for ischemic stroke treatment via a structure-based protein engineering	p. 42
P22	Dalibor Košek	Structural insight into domain architecture and regulation of Nedd4-2 E3 ubiquitin ligase	p. 43
P23	Aneta Kozeleková	How does phosphorylation affect interaction between 14-3-3 ζ and Tau proteins?	p. 43
P24	Irena Kratochvílová	Study of the relationship between embryo quality, speed of development and clinical pregnancy in PGT cycles	p. 44
P25	Kateřina Krejčová	Elucidation of enzymatic mechanisms and structure of Ntaya NS5 enzyme	p. 45
P26	Ivana Křenková	e-INFRA CZ Interactive and FAIR: Beyond Qsub Computing	p. 45

P27	Shilpa Kurupath Bhadavas	Resolving protein dynamics with Stokes and anti-Stokes Raman correlation microscopy	p. 46
P28	Barbora Landová	NEIL3-ssDNA Structure Insights into Repairing Abasic Site Interstrand Crosslinks	p. 47
P29	Stanislav Macháček	Towards the structure of stearyl-acyl carrier protein complex with fatty acyl	p. 47
P30	Lukáš Martínek	Characterization of de novo missense variants in individuals with neurodevelopment disorders and their impact on the structure and function of the protein SHP2	p. 48
P31	Katarína Monková	Structural investigation of the 40S particle	p. 48
P32	Jana Moravcová	Preparation of biological samples for cryo-electron microscopy using the HPF "Waffle" method	p. 49
P33	Lucia Motlová	Structural characterization of selective HDAC6 inhibitor Marbostat-100 with improved stability	p. 50
P34	Liya Mukhamedova	Resolving the early infection stages of the viruses from the order Picornavirales in vivo	p. 50
P35	Hana Nedožrálová	Visualization of tau pathology using in situ cryo-ET	p. 51
P36	Ivana Nemčovičová	Mutational analysis on viral HCMV UL141 protein to specify the binding site of novel antagonist that blocks TRAIL-R2 binding	p. 52
P37	Lucie Nepovímová	Visualising Enterovirus 71 Genome Replication In Situ	p. 52
P38	Zora Nováková	Evolutionary study of histone deacetylase 11	p. 53
P39	Michaela Novotná	Clincelin – our new weapon to combat antibiotic-resistant bacterial pathogens	p. 53
P40	Miguel Padilla Blanco	Mimicking viral evolution by yeast surface display to predict new coronavirus-related pandemics	p. 54
P41	Jiří Pavlíček	Core Facility Devoted to Crystallization of Proteins and Nucleic Acids, Centre of Molecular Structure, IBT CAS	P. 54
P42	Eliška Pirnosová	The comparison of 14-3-3 homo- and heterodimers kinetics	p. 55
P43	Adam Polák	Production of monoclonal antibodies and their co-crystallization with intrinsically disordered protein tau	p. 56
P44	Martin Polák	Pum Pox Virus structure and basis for structural variability of its virus-like particles	p. 57
P45	Eva Pyrihová	Protein Production facility at the Centre of Molecular Structure	p. 58
P46	Karel Skubník	Cryo-EM Reveals RECQ5's Regulatory Role in RNAPII-Mediated Transcription	p. 58
P47	Gabriel Soares Guerra	Unveiling the coupling of transcription and translation in bacteria	p. 59
P48	Anna Štefánik Sobotková	Cryo-EM Reveals the Structure and Infection Mechanism of Phage LUZ19	p. 59
P49	Vojtěch Spiwok	Analysis and acceleration of molecular simulations by time-lagged tSNE	p. 60
P50	Jiří Srogoň	New complexes of the bacterial transcription system	p. 61
P51	Jan Stránský	CF Diffraction Techniques in Centre of Molecular Structure: Employing high-end X-ray technologies for laboratory structural biology	p. 61

P52	Matyáš Suchý	Molecular dynamics simulations of single amino-acid substitution in BRAF:MEK1 complex	p. 62
P53	Marta Šiborová	Structural basis for postfusion-specific binding to Respiratory Syncytial Virus F protein by the antigenic site-I antibody 131-2a	p. 63
P54	Jan Šilhan	Exploring the Structures of the 20S Proteasome and Their Small Molecule Inhibitors Using Cryo-EM	p. 63
P55	Petr Škvára	Structural basis for RNA-cap recognition and methylation by the mpox methyltransferase VP39	p. 64
P56	Hana Šváchová	Cryogenic Electron Microscopy Core Facility at IOCB Prague	p. 64
P57	Guglielmo Tedeschi	Analysis and Sampling of Molecular Simulation with extended Autoencoder architectures	p. 65
P58	Pavla Vaňková	Mass spectrometry as a tool for protein structure analysis	p. 65
P59	Michal Vaško	Insights into Molecular Interactions between nsp14 and nsp10 in SARS-CoV-2 Replication	p. 66
P60	Yevgen Yurenko	Accurate Multi-Scale Computations of Binding Free Energies in Insulin/Insulin Receptor Complex	p. 66
P61	Július Zemaník	QM/MM Reaction Simulations of Alpha-(1,3)-fucosyltransferase of <i>Helicobacter pylori</i>	p. 67