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Looking back at 2023

As 2023 comes to an end, we take this opportunity to look back through the pages of *Nature Structural & Molecular Biology* and consider some of the year's highlights.

2023 has been a memorable year at *Nature Structural & Molecular Biology*: we are happy to have published some great science and insightful Reviews & Analysis, and our editorial team featured some fresh faces! Here, we overview a few of the most important advances that we have published in this past year.

In 2023, we reaffirmed our commitment to publish mechanistically insightful and conceptually novel research on a range of biological processes. Starting in the nucleus, studies by García-Nieto et al., Taschner & Gruber, Psakhye et al. and Richeldi et al. provided insights into the diverse roles of the main SMC complexes (cohesin and Smc5/6) in organizing and maintaining chromatin structure, and how the complexes are differentially regulated to carry out their essential functions. Regulation of gene expression, and how replication, chromatin and epigenetic states affect this, remain central questions in molecular biology, and some important efforts in these areas by Stoy et al., Brouwer et al., Forte et al., Li et al., Chen et al., Abdulhay et al., Zhao et al., Bernardini et al., Fréchard et al. and Park et al. were featured in the pages of our journal this year. Notable insights on genome stability and responses to DNA damage were also provided by Liang & Blundell, McGinty & Sunyaev, Bujarrabal-Dueso et al., Hertz et al., Liu et al., Myler et al. and Swift et al..

On the way out of the nucleus, we were excited to read work by Yelland et al., Hayne et al., Sekulovski et al. and Mao et al. on RNA processing and translation, with this latter study shedding light on an unexpected frameshifting mechanism to generate translational 'noise' in response to nutrient starvation, while the Jaskolowski et al. visualised the TRAP complex bound to the translating ribosome and Sec61 translocon inserting proteins into the endoplasmic reticulum, and Wu et al. provided mechanistic insight on how the EMC inserts the C-terminal transmembrane domains of membrane proteins post-translationally. At the opposite end of the proteostasis cycle, Haselbach & Brown presented a time-resolved cryo-EM analysis of how a ubiquitin ligase builds a proteasomal degradation signal.

In a year in which artificial intelligence (AI) systems were everywhere, we were happy to publish two community assessments on the potentials of AlphaFold2 to predict protein structure, and the protein interactome, as well as an insightful accompanying News & Views piece by Bouatta & AlQuraish. On the other hand, An et al. reported on how deep-learning methods can be applied to design closed repeat proteins with central binding pockets, and Akdel et al. designed novel αβ folds that do not exist in nature. We were also delighted to publish studies shedding light on essential cellular process such as work by Nakamura et al. on ferroptosis, studies from Lacey et al. and Chen et al. on transport in cilia and structure of sperm axonemes, respectively, and work by Hvorecny et al. and Adamoski et al. on enzyme filamentation.

As always, things are eventful at the membrane. Insights into the role of TRIM E3 ligases in membrane repair were provided in a study by Park et al., and work by Moss et al., Azad et al. and Lopez-Robles et al. provided mechanistic insights into the dynamics of membrane remodelling. Membrane proteins, particularly receptors and transporters, continue to garner interest. Work by Suo et al., Parker et al. and Dou et al. shed light onto organic cation and anion transporters, while papers from Zhu et al. and Nayak et al. provided insights into the structure, transport cycle and uptake inhibition of the GABA transporter GAT1.

From studies of HIV capsid assembly, to understanding fundamental steps of early embryonic development, we were delighted with the diversity of studies we published in 2023 and could not be more excited about the science we will get to read in 2024!

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