



Friday, March 23, Session IV

L14

PIPELINE FOR PROTEIN STRUCTURE DETERMINATION BY CRYOEM

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Following recent leaps in technical performance of both hardware and software related to Cryogenic Electron Microscopy (CryoEM), it has become possible to determine the structure of biological macromolecules at atomic resolution. This revolution in achievable cryoEM resolution has provided another powerful technique for structure determination of macromolecular complexes and thus opened new possibilities for many biological systems that have been proven difficult or impossible to solve by methods of X-ray diffraction or NMR. Many high-profile research institutions have therefore adopted high-end cryoEM methodology and number of specialized cryoEM facilities have

been funded to respond to the increasing demand for structure determination by cryoEM. Additionally, large pharmaceutical companies scope and test cryoEM for their portfolio of analytical methods, as cryoEM can be also applied to smaller molecular complexes (~100 kDa). However, it also produces some hurdles related to the approach to these new techniques, both from sample preparation, data acquisition and image processing perspectives. This lecture will present the current pipeline for protein structure determination by cryoEM and demonstrate the advantages and latest advances of cryoEM on specific examples.

L15 - Pall ForteBio Europe: BLI technology as a tool for biomolecular interactions (see p. 56)

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NANOTEMPER TECHNOLOGIES – WHEN PROTEIN QUALITY MATTERS. NEW ARISING STAR- TYCHO NT.6

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pare the relative quality and stability of a protein sample during any step of a purification or characterization workflow. Results are generated in three minutes using Tycho NT.6 and that means better and faster decisions can be made on the next experimental steps. The influences of buffer formulation and/or storage conditions on relative stability and similarity of either freshly prepared or batch-to-batch preparations are swiftly determined. Tycho NT.6 automatically generates thermal unfolding profiles, identifies inflection temperatures (T_i), analyzes interactions effects on relative stability and monitors fluorescence sample brightness providing keen insight on sample quality and possible functionality.



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