KN-1

Human Protein Complexes Involved in Neurodevelopment. Joel L. Sussman[a,b], Israel Silman[c,b]. [a]*Dept of Structural Biology,* [b]*The Israel Structural Proteomics Center (ISPC).* [c]*Neurobiology Dept, Weizmann Institute of Science, Rehovot, Israel.*
E-mail: Joel.Sussman@weizmann.ac.il

The study of human protein complexes has proven to be particularly difficult, in part due to the fact that many individual eukaryotic proteins, when examined in isolation, are seen to have large continuous regions that are intrinsically disordered. An interesting example of this can be seen in a family of neural cell adhesion proteins, which are single-pass transmembrane proteins, and bear substantial sequence similarity to cholinesterases (ChEs). The regions of sequence similarity correspond to only parts of their complete sequences, thus establishing the ChE domain as a modular domain incorporated into a group of protein*s that* we have called 'cholinesterase-like adhesion molecules' (CLAMs). CLAMs are devoid of catalytic activity, since they lack residues crucial for catalysis. They play, however, a key role in the earliest stages of the development of the central nervous system (CNS) and mutations in the ChE domain of one of them, neuroligin, are associated with autism and mental retardation. The cytoplasmic domains of CLAMs bear no sequence homology to any known protein. *In silico* studies on the analysis of the structure of CLAMS, via FoldIndex© [1] (http://bioportal.weizmann.ac.il/fldbin/findex), has predicted which regions are likely to be unfolded. These results are compared to physicochemical studies, which demonstrate experimentally that the cytoplasmic domains of the CLAMS are, in fact, Intrinsically Disordered Proteins (IDP) [2],[3],[4]. FoldIndex© is also being used routinely, at the Israel Structural Proteomics Center (http://www.weizmann.ac.il/ISPC), to aid in crystallization of proteins by first predicting which regions of a protein sequence is likely to be intrinsically disordered, and subsequently eliminating these stretches from the construct that is cloned.

[1] Prilusky, J., Felder, C. E., Zeev-Ben-Mordehai, T., Rydberg, E., Man, O., Beckmann, J. S., Silman, I. & Sussman, J. L., *Bioinformatics*, **2005**, 21, 3435. [2] Zeev-Ben-Mordehai, T., Rydberg, E.H., Solomon, A., Toker, L., Botti, S., Auld, V.J., Silman, I. & Sussman, J.L., *Proteins*, **2003**, 53, 758. [3] Paz, A., Zeev-Ben-Mordehai, T., Lundqvist, M., Sherman, E., Mylonas, E., Weiner, L., Haran, G., Svergun, D.I., Mulder, F.A.A., Sussman, J.L. & Silman, I., *Biophys. J*, **2008**, 95, 1928. [4] Dunker, A.K, Silman, I., Uversky, V.N. & Sussman, J.L. *Curr Opin Struct Biol*, **2008**, 18, 756.

Keywords: SAXS; crystallographic and NMR; structural disorder

KN-2

Prenucleation Clusters and Crystallization Control by Additives. Helmut Cölfen. *Max-Planck-Institute of Colloids and Interfaces, Colloid Chemistry, Research Campus Golm, Am Mühlenberg, D-14424 Potsdam, Germany.*
E-mail: Coelfen@mpikg.mpg.de

In recent years, increasing evidence was reported that crystallization from solution does not exclusively follow the classical pathway of atom / ion / molecule mediated layer wise growth of a critical crystal nucleus. This was triggered by the discovery of amorphous or even liquid precursors to single crystals in Biomineralization and additive controlled crystallization events. Particle mediated crystallization pathways were found to be important besides the classical crystallization path. As all these reaction channels can lead to a single crystal end product, it is often difficult to reveal how this single crystal has formed.
In this presentation, examples will be given for stable subcritical $CaCO_3$ clusters, which can already be found prior to nucleation [1]. Nucleation of the subsequent amorphous phase seems to be triggered by cluster aggregation. Finally, crystals are formed. Crystallization control in classical and nonclassical (particle mediated) crystallization can therefore be controlled at various reaction levels by polymer additives. These additives can already have an influence on the crystallization reaction before nucleation has taken place. The reaction path diversifies into classical and nonclassical crystallization after nucleation and consequently the possibilities to modify crystal growth by additives. The role of amorphous and liquid precursor particles and oriented aggregation and mesocrystal formation will be discussed highlighting the importance of such reaction channels in Biomineralization but also for crystallization as such.

[1] Gebauer D., Völkel A., Cölfen H. *Science* **2008**, 322, 1819.

Keywords: prenucleation clusters; non classical crystallisation; crystallization control

KN-3

Modern Developments in Inelastic X-ray Scattering Under Extreme Conditions of Temperature and Pressure. Esen Ercan Alp. *Advanced Photon Source, Argonne National Laboratory, Argonne, Illinois 60439.*
E-Mail: eea@aps.anl.gov

The recent advances made in inelastic X-ray scattering methods with meV resolution will be reviewed. Measurement of phonon density of states, Debye sound velocity, phonon dispersion relations, bulk and shear modulus, dynamic viscosity, stiffness, and resilience of variety of materials, under extreme conditions will be discussed with specific applications in proteins, and minerals under high pressure, or nano-particles and surfaces. This work is supported by US DOE-BES Materials Science under contract number W-31-109-ENG-38. Most of this work is done in close collaboration with Drs. W. Sturhahn, T. Toellner, J. Zhao, A. Alatas, H. Yavas, B. Leu and L. Gao, all of Argonne National Laboratory, and their collaborators around the world.

Keywords: X-ray scattering; materials science; extreme conditions