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New trends in protein nanocystallography by a combination of cell free expression, APA microarrays, LB nanotemplate and Monte Carlo simulation

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One of the newest approaches to structural proteomics is protein nanocrystallography at the intersection between nanotechnology and proteomics. This now consolidated field results from the combination of advanced nanotechnologies – particularly Atomic Force Microscopy (AFM), thin-film nanotemplate technology, nanogravimetry, Raman Spectrometry– and of advances in synchrotron radiation, namely micro-nanofocused diffraction and micro-nano GISAXS. Recently has provided unique opportunity for the design and development of new protein biocrystals and drugs utilizing bacterial hell's gate globin, octopus rodhopsins, bovine cytochromes, human kinases and laccases. Newest examples of significant potential applications for medicine emerged at the interface of Langmuir-Blodgett engineering, organic chemistry, molecular dynamics and label-free protein arrays. These advancements on structural proteomics is due to third generation synchrotron radiation sources emitting synchrotron X-ray beams that are trillion times more brilliant than those produced by X-ray tubes, requiring quite smaller crystals for the 3D-structure determination. However, one cannot indefinitely compensate for small crystal size with increased beam intensity since at some stage so much X-ray energy is being deposited in a small volume that the protein structure and crystalline order will be destroyed by primary radiation damage very quickly Radiation damage to crystalline proteins using X-rays is a problem, which limits the structural information that can be extracted from the sample and only the significant radiation stability induced in the crystal formed by our LB nanotemplate method open new avenues in structural proteomics obtaining protein crystals for the most important proteins like membrane proteins with required quality, quantity (easy and speed of production) and reduced radiation damage. These requirements remain the major open problems in protein crystallography overcome by the summarized emerging trends up to the Monte Carlo simulation for the structure-function determination of numerous proteins still unsolved. The utilization of Monte Carlo simulation is essential in high energy physics, but could become useful to correctly evaluate the dose delivered to a crystal sample during a planned experiment of nanocrystallography before the usage of synchrotron radiation on protein crystals.

Biography

Claudio Nicolini received the Doctoral degree in Physics from the University of Padua & moved to Brown University, MIT and BNL, then to Temple University School of Medicine as Professor of Pathology and in 1976 Chairman of Biophysics, later at Stanford and Arizona State University. In 1985, he was called as "Eminent Scientist" to the Chair of Biophysics of the University of Genoa, in Italy until 2012, where he was Director Biophysics Institute, Distbimo and Cirsnnob. From 1993 he is Life President of the Fondazione ELBA Nicolini and of Nanoworld Institute. In 2008 he was elected Foreign Member of the Russian Academy of Sciences and on 2010 honoris causa Professor of Biophysics and Nanobiotechnology at Moscow State University. His main scientific activities concerned cancer research, biophysics and nanotechnology, pioneering world-wide chromatin structure-function, bioelectronics and nanobiotechnology.