BEYOND GENOMES: ASSESSING PROTEIN FUNCTION USING SOLUTION NUCLEAR MAGNETIC RESSONANCE

Marcius da Silva Almeida

The Scripps Research Institute, California, USA. Instituto de Bioquímica Médica, Centro Nacional de Ressonância Magnética Nuclear Jiri Jonas, Universidade Federal do Rio de Janeiro, Rio de Jeneiro, Brazil.

More than 600 genomes have been completely sequenced to date. Noticeably, there is only a minor fraction of genes of which the molecular function and consequently biological process is known (for instance, approximately only one-fifth of annotated human proteins have been experimentally characterized). It is a fact that the knowledge of the 3D structure of a protein can provide a crucial insight into its mode of action and is necessary to describe its molecular function in detail. Because of that a number of consortia have evolved in a genomics-based effort to solve the structure of a massive amount of unique protein targets. Solution NMR is a well established method that fits perfectly well in the post genomics era. It can obviously be used to determine the structure of proteins in solution, but can also be used in a number of ways that corroborate to assess protein molecular function, including: to identify protein fold state, which is important as a target selection criteria and to monitor protein solution conditioning; to assess protein dynamics, which is important to characterize motion within active site's perspective; to identify details in the intermolecular association; for the screening of ligands, and to follow reactions that can lead to unknown products. Within this notion, it is presented the work on structural genomics targets that had been characterized by using mainly solution NMR. This work includes proteins selected from the human Cancer Genome Anatomy Project (CGAP) that had been poorly or not been characterized at all. These targets are called neglected Cancer Related Proteins (CRP) since, as assed by the Serial Analysis of Gene Expression (SAGE), the expression pattern of their genes points to their participation in neoplasic processes.

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