

Integrative biology in protein structure determination

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Hybrid methods, which combine and integrate several biochemical and biophysical techniques, have rapidly caught up in the last twenty years to provide a way to obtain a fuller description of proteins and molecular complexes with sizes and complexity otherwise not easily affordable. In my lecture, I will review the use of a robust hybrid methodology based on a mixture of NMR, SAXS, site directed mutagenesis and molecular docking which we have developed to determine the structure of weakly interacting molecular complexes and describe intrinsically unstructured proteins. We applied this approach to gain insights into the structure of different proteins and protein complexes. Our results were validated both by X-ray structures and by other groups who adopted the same approach. I will discuss the advantages and the limitations of our methodology and propose new avenues, which could improve it.