**Beyond the Structure: how to Deal with Structural Disorder**

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Structural disorder in proteins is probably as precious as a source of information as the structure itself. In fact, disorder implies mobility. If we are able to translate what is observed as disorder, both in X-ray and NMR structures, into dynamics, we are in a better position to understand function. NMR is a powerful tool to analyse mobility in terms of time scales of motions, from seconds down to picoseconds.

Novel approaches on how to deal with disorder by NMR will be shown, with particular reference to metalloproteins. Examples will range from the study of conformational flexibility at the active site of pharmaceutical targets [1] to multiple metal binding stoichiometries [2], from the assessment of relative interdomain motions in multidomain proteins [3] to the elucidation of the structure of a protein-protein complex where one partner is largely unstructured [4].

[1] Bertini I., Calderone V., Fragai M., Lee Y.-M., Luchinat C., Mangani S., Turano, *Proc. Natl. Acad. Sci.*, *in press***.** [2] Calderone V., Dolderer B., Hartmann H.J., Echner H., Luchinat C., Del Bianco C., Mangani S., Weser U., *Proc. Natl. Acad. Sci.*, 2005, **102**, 51. [3] Bertini I., Del Bianco C., Gelis I., Katsaros N., Luchinat C., Parigi G., Peana M., Provenzani A., Zoroddu M.A., *Proc. Natl. Acad. Sci.*, 2004, **101**, 6841. [4] Bertini I., Del Bianco C., Gupta Y., Luchinat C., Parigi G., Peana M., Zoroddu M.A., *in preparation.*

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