



"Intrinsically disordered proteins: a new way of looking at protein structure and function."



ntrinsically disordered proteins and complex multidomain proteins are characterized by a dynamic ensemble of conformations that cannot be unequivocally described by traditional static terms of structural biology. These states of proteins are critical in understanding their

function at the atomic level, which will eventually lead to extending the structure-function paradigm to establish "unstructural biology" as a new field (1). The functional importance of structural complexity necessitates new standards and protocols for the description of structural ensembles termed "supertertiary" structure in the case of very large proteins composed of a combination of folded and disordered elements (2). We devised a new database (PED) that holds structural ensembles of proteins (3), which will hopefully enable to have predictive power on the function of IDPs (4), such as allostery in modular multidomain signaling proteins (5).

1) Tompa, P. (2011) Unstructural biology coming of age. Curr. Opin. Struct. Biol. 21: 419.

2) Tompa, P. (2012) On the supertertiary structure of proteins. Nature Chem. Biol. 18, 597.

3) Varadi, M. et al. (2014) pE-DB, a database of protein structural ensembles. *Nucl. Acids. Res.* Nucleic Acids Res. 42: D326.

4) Tompa, P., Varadi, M. (2014) Predicting the Predictive Power of IDP Ensembles. *Structure* 22: 177.

5) Tompa, P. (2014) Multisteric regulation by structural disorder in modular signaling proteins: an extension of the concept of allostery. *Chem. Rev.* (Epub ehaed of print)

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Invité par Eva Jakab Toth

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