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## PRESS RELEASE

### **International collaboration between IMBB-FORTH and the Ludwig Maximilian University of Munich (Germany), with the contribution of researchers from the Universities of Groningen (The Netherlands) and Leuven (Belgium) shed light on the role of Structural Dynamics in protein evolvability**

*How does nature utilize the same repertoire of folds in proteins to diversify specificity and ultimately their function?* Research carried out in the group for Dynamic Structural Biology (IMBB-FORTH) headed by Dr. Gouridis and their collaborators focused on such a long-standing fundamental question in molecular biology. The results of this work are published today in the prominent international journal in Proceedings of the National Academy of Sciences (PNAS).

#### **The IMBB team**

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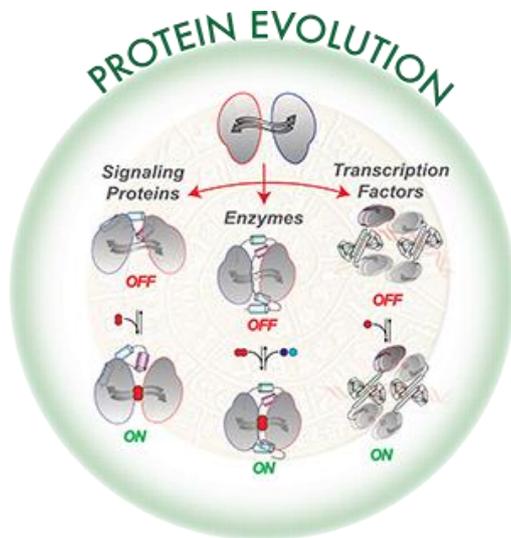


Proteins are responsible nearly for all processes occurring within cells. Thus, protein malfunction represents the molecular etiology of diseases and death. The activity of such biomolecules relies on their capacity to vary their shape or structure over time. Such variations are finely-regulated through their interaction with small molecules and/or other biopolymers, and termed Structural Dynamics. Here we show that Structural Dynamics have been essential to adapt proteins to the continuously fluctuating chemical environment over the last 3.5 billion of years on earth.

For this, we performed a structural and evolutionary analysis on ~600 extant proteins with a conserved and ancestral structural core encountered throughout the tree of life. We complemented this analysis with detailed biophysical characterization of selected examples residing in critical nodes of the evolutionary tree.



We show that modifications of the structural core, largely at its termini, enabled distinct structural dynamics. Such diversified the structural core to evolve, giving rise to protein acting as transcription factors, enzymes, signaling or conferring transport-related functions. These finding are likely to be applicable to a large number of protein architectures.



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**Relevant links:**

[www.pnas.org](http://www.pnas.org)  
<https://www.imbb.forth.gr/en/research-en/item/5040-giorgos-gouridis>