

## **Massive non natural proteins structure prediction using grid technologies.**

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### **Abstract**

The number of natural proteins represents a small fraction of all the possible protein sequences and there is an enormous number of proteins never sampled by nature, the so called “never born proteins” (NBPs). A fundamental question in this regard is if the ensemble of natural proteins possesses peculiar chemical and physical properties or if it is just the product of contingency coupled to functional selection. A key feature of natural proteins is their ability to form a well defined three-dimensional structure. Thus, the structural study of NBPs can help to understand if natural protein sequences were selected for their peculiar properties or if they are just one of the possible stable and functional ensembles. In this paper we report the study of the structural properties of a large dataset of NBPs in order to identify peculiar features that distinguish NBP from natural proteins.