

# Abstract

Synthetic biology relies upon working with two main types of biological macromolecules - nucleic acids and proteins. Natural proteins represent only a small percentage of the whole amino-acid sequence space. Most of it may conceal an enormous potential (unexplored by nature as well as scientific endeavor), which has started to be carefully explored only in the recent decades. Characterization of non-native proteins includes several key aspects: structure and its stability, function, patterns of interaction with other molecules (of different chemical nature) and *in vivo* tolerance. This work focuses on the functional testing of *de novo* polypeptide molecules, either appearing as novelties of genome non-coding regions or as products of artificial bioengineering design.

**Key words:** *de novo* proteins, function screening, protein libraries, protein design, sequence space