

## Computational modeling and design of RNA 3D structure and protein-RNA complexes

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**Motivation:** Protein-RNA interactions play fundamental roles in many biological processes, such as regulation of gene expression, RNA splicing, and protein synthesis. The understanding of these processes improves as new structures of protein-RNA complexes are solved and the molecular details of interactions analyzed. However, experimental determination of protein-RNA complex structures by high-resolution methods is tedious and difficult. Therefore, studies on protein-RNA recognition and complex formation present major technical challenges for macromolecular structural biology. Alternatively, protein-RNA interactions can be predicted by computational methods. Although less accurate than experimental measurements, theoretical models of macromolecular structures can be sufficiently accurate to guide experimental analyses and aid in the interpretation of their results.

**Methods:** I will present an overview of strategies and methods for computational modeling of RNA structure and RNA-protein complexes developed in our laboratory (available at <http://genesilico.pl>), and I will illustrate it with practical examples of structural predictions.

### Results - references:

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