

# Taking inspiration from Biopolymers : Foldamers as Protein Mimics

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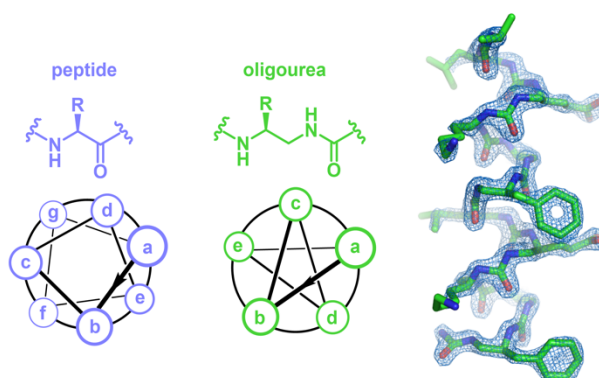
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The discovery that synthetic sequence-specific oligomers can adopt well-defined folded structures – foldamers<sup>1</sup> – has profoundly changed our view of biopolymer mimicry, raising prospects for exploring new chemical spaces and creating novel synthetic architectures with defined functions.<sup>2-</sup>

<sup>4</sup> In this presentation, we will discuss some of our efforts towards this goal, showing how de novo design, careful structural investigation and subsequent sequence engineering of non-peptide helical foldamers may be used to generate effective peptide and protein mimics.

Besides aliphatic and aromatic oligoamide foldamers ( $\beta$ -peptides, peptoids, sulfono- $\gamma$ -AApeptides, quinoline-based oligoamides,...) which have received much of the attention in the field, a few other backbones that do not contain an amide linkage but similarly show a high folding propensity (e.g. aliphatic urea-based oligomers studied in our group) have emerged. Oligourea foldamers which form well-defined and stable helical secondary structures (Fig. 1) reminiscent of the  $\alpha$ -helix combine a number of characteristics – synthetic accessibility, sequence modularity, folding fidelity, and stability to proteolysis – that bode well for their use in various applications.<sup>5</sup>



**Figure 1.** Helical-wheel representations of  $\alpha$ -peptide and oligourea backbones and x-ray structure of a helically-folded oligourea foldamer

Applications developed in our group with a focus on molecular recognition include the design of (i) bioactive peptide mimics with a reduced peptide character and improved pharmacological properties (i.e. modulators of protein-protein interactions and receptor ligands), (ii) foldamer-based organocatalysts as well as more sophisticated architectures like (iii) composite proteins and (iv) foldamer-based nanostructures.

## References

1. S. H. Gellman, *Acc. Chem. Res.* **1998**, *31*, 173-180.
2. G. Guichard, I. Huc, *Chem. Commun.* **2011**, *47*, 5933-5941
3. W. S. Horne, T. N. Grossmann, *Nat. Chem.* **2020**, *12*, 331-337
4. M. Pasco, C. Dolain, G. Guichard, in *Supramolecular Chemistry in Water* (Ed.: S. Kubik), Wiley - VCH Verlag GmbH & Co. KGaA Weinheim, Germany, **2019**, pp. 337-374.
5. S. H. Yoo, B. Li, C. Dolain, M. Pasco, G. Guichard, in *Methods Enzymol.*, Vol. 656 (Ed.: E. J. Petersson), Academic Press, **2021**, pp. 59-92.