Structure prediction of cyclic peptides via molecular dynamics and machine learning

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A major obstacle to cyclic peptide development is that little structural information is available for these molecules, making it difficult to perform structure-based design or understand why different cyclic peptide sequences display different binding affinity, membrane permeability, and other properties. The lack of structural information is due to the fact that most cyclic peptides adopt multiple conformations in solution, existing as structural ensembles, which are very difficult to characterize using experimental techniques such as solution NMR spectroscopy. In this talk, I will describe how by combining molecular dynamics simulation and machine learning, we can now provide simulation-quality cyclic peptide structure predictions in seconds. We expect such a capability to rapidly predict cyclic peptide structures to enable researchers to understand the structural basis for the diverse properties of different cyclic peptides and greatly accelerate the development of this unique class of molecules.