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Sommario/riassunto	<p>Proteins represent one of the most abundant classes of biological macromolecules and play crucial roles in a vast array of physiological and pathological processes. The knowledge of the 3D structure of a protein, as well as the possible conformational transitions occurring upon interaction with diverse ligands, are essential to fully comprehend its biological function. In addition to globular, well-folded proteins, over the past few years, intrinsically disordered proteins (IDPs) have received a lot of attention. IDPs are usually aggregation-prone and may form toxic amyloid fibers and oligomers associated with several human pathologies. Peptides are smaller in size than proteins but similarly represent key elements of cells. A few peptides are able to work as tumor markers and find applications in the diagnostic and therapeutic fields. The conformational analysis of bioactive peptides is important to design novel potential drugs acting as selective modulators of specific receptors or enzymes. Nevertheless, synthetic peptides reproducing different protein fragments have frequently been implemented as model systems in folding studies relying on structural investigations in water and/or other environments. This book contains contributions (seven original research articles and five reviews published in the journal Molecules) on the above-described topics and, in detail, it includes structural studies on globular folded proteins, IDPs and bioactive peptides. These works were conducted using different</p>

experimental methods.
