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	Nota di contenuto	Introduction -- Comparative Analysis of the Higher-order Structure of RNA -- Graph Applications to RNA Structure and Function -- Prediction and Coarse-Grained Modeling of RNA Structures -- RNA Folding Using Site-Directed Spin Labeling -- The RNA Recognition Motif and Messenger RNA -- Memory Effects in RNA folding dynamics revealed by single molecule fluorescence -- An integrated picture of HDV ribozyme catalysis -- Combining biochemical and structural information to model RNA-protein complex assembly -- Following RNA Folding From Local and Global Perspectives -- The Roles of Chaperones in RNA Folding.
	Sommario/riassunto	Structured RNAs are everywhere, functioning throughout gene expression with key roles ranging from catalysis to regulation. New functional RNAs are being discovered all the time; in fact, it is now clear that a much greater fraction of eukaryotic genomes is devoted to coding for RNA than protein. Many of these RNAs must traverse complex energy landscapes to find their functional three-dimensional structures. Along the way, they may encounter native and non-native folding intermediates, chaperone proteins, and assemble with partner proteins. This volume, written by experts in the field, discusses the current understanding of the biophysical principles that govern RNA folding, with featured RNAs including the ribosomal RNAs, viral RNAs, and self-splicing introns. In addition to the fundamental features of

RNA folding, the central experimental and computational approaches in the field are presented with an emphasis on their individual strengths and limitations, and how they can be combined to be more powerful than any method alone; these approaches include NMR, single molecule fluorescence, site-directed spin labeling, structure mapping, comparative sequence analysis, graph theory, course-grained 3D modeling, and more. This volume will be of interest to professional researchers and advanced students entering the field of RNA folding.