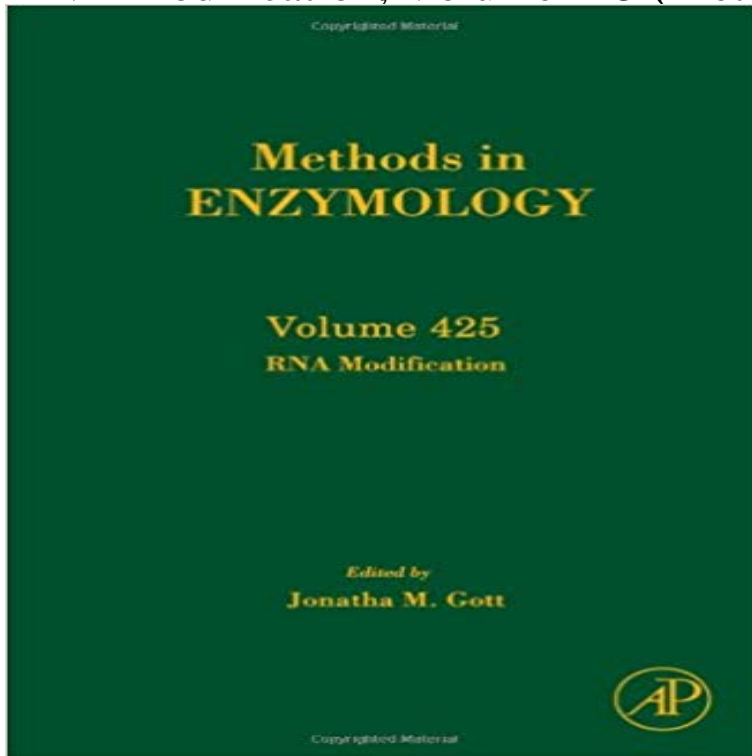


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The presence of modified nucleotides in cellular RNAs has been known for decades and over 100 distinct RNA modifications have been characterized to date. While the exact role of many of these modifications is still unclear, many are highly conserved across evolution and most contribute to the overall fitness of the organism. In recent years, new methods and bioinformatics approaches have been developed for the dissection of modification pathways and functions. These methods intersect a number of related fields, ranging from RNA processing to comparative genomics and systems biology. In addition, many of the techniques described in this volume have broad applicability, particularly in regards to the isolation, characterization, and reconstitution of ribonucleoprotein complexes, expanding the experimental repertoire available to all RNA researchers.

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