RNA structure is intimately connected to RNA function. Because RNA structure is highly sensitive to the physico-chemical environment, including temperature, crowding, pH, and Mg^{2+} concentration, the structure of the same RNA molecule can differ radically in vitro vs. in vivo. We recently developed a method, Structure-seq, which combines chemical probing of RNA structure with high throughput sequencing to allow characterization of RNA secondary structure genome-wide and in vivo (1-3). In Structure-seq, in vivo treatment with dimethyl sulfate (DMS) covalently modifies As and Cs at their Watson-Crick face when those nucleobases are not base-paired or protected. Such modifications can be read out genome-wide as stops in reverse transcription. Our initial application of Structure-seq to Arabidopsis revealed significant correlations between DMS reactivity and alternative polyadenylation, alternative splicing, and gene function (1). Our recent application of Structure-seq to rice provides structural information on more than 14,000 mRNAs and unveils hidden connections between temperature-induced RNA structure changes and gene expression.