

Supplementary Information For: High Throughput Determination of RNA Structures

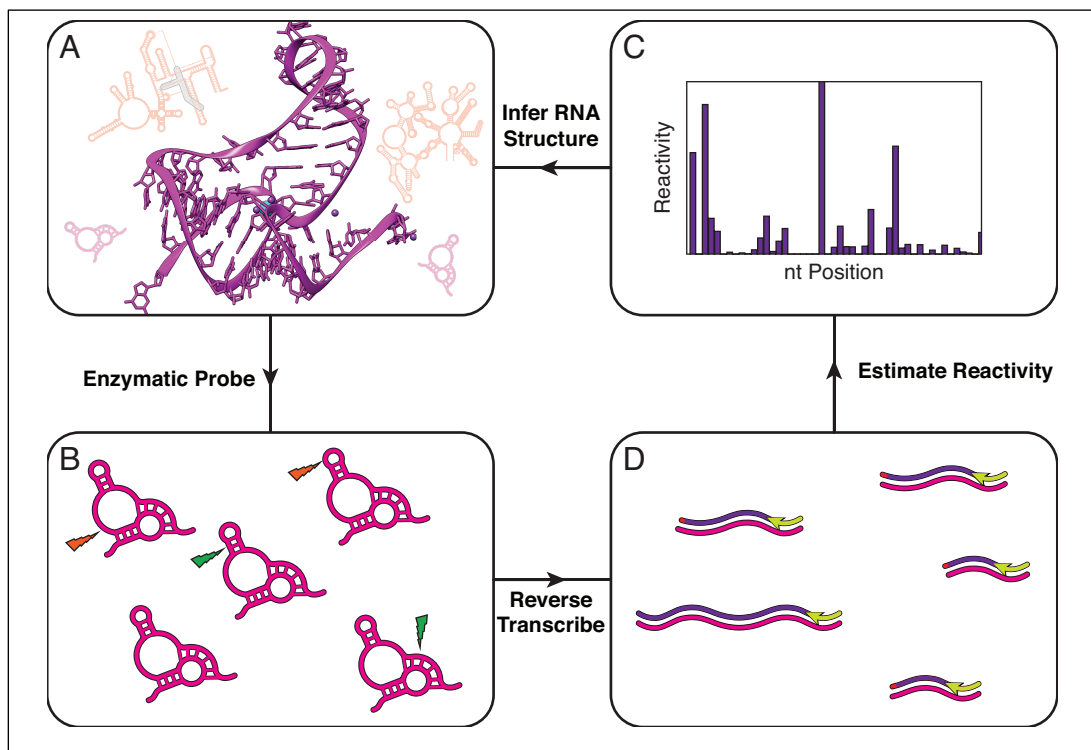
Eric J. Strobel^{1*}, Angela M Yu^{2*} and Julius B. Lucks¹

1 - Department of Chemical and Biological Engineering, Northwestern University, 2145 Sheridan Rd., Evanston, IL 60201

2 - Tri-Institutional Program in Computational Biology and Medicine, Cornell University, Ithaca, New York, Weill Cornell Medical College, New York, New York, Memorial Sloan-Kettering Cancer Center, New York, New York, USA

Correspondence to J. B. L.

e-mail: jblucks@northwestern.edu



Supplementary Figure 1 | **Determining RNA structures with high throughput sequencing.** A version of Figure 2 illustrating how nuclease digests can be coupled with reverse transcription and high throughput sequencing to map RNA structures¹⁻⁵.

Supplementary Table 1 | **RNA structure modeling approaches that have been used with high throughput RNA structure probing methods.** Specific approaches are listed for each technique included in Table 1.

Method	Demonstrated Structure Modelling
Enzymatic Probes	
PARS ^{1,2} and PARTE ⁶	Vienna RNA Package ⁷ SeqFold ⁸
FragSeq ³	Direct analysis of cutting scores, aggregate analysis of cutting scores over transcriptome
dsRNA-seq and ssRNA-seq ^{4,5}	Structure score calculation by comparing dsRNA-seq and ssRNA-seq
Small Molecule Probes	
SHAPE-Seq ⁹⁻¹³	Structural modelling with RNAstructure Package ¹⁴⁻¹⁶
DMS-seq ¹⁷	Direct analysis of reactivities, aggregate analysis over transcriptome
Mod-seq ¹⁸	Direct analysis of reactivities
CIRS-seq ¹⁹	Aggregate analysis of reactivities over transcriptome, RNAstructure Package ^{14,15} , RNA Structure Framework for transcriptome-wide structural modelling ²⁰
Structure-Seq ^{21,22,40,41}	Aggregate analysis of reactivities over transcriptome, RNA structure modelling with RNAstructure Package ^{14,15} , StructureFold for transcriptome-wide structural modelling ²³
ChemModSeq ^{24,25}	EM ^{24,25} or BUM-HMM ²⁶ approach, to classify nucleotides into reactivity bins, analysis of classified data
MAP-Seq ²⁷⁻²⁹	Direct analysis of reactivities, Reconstruction of RNA secondary structures from mutate-and-map datasets using REEFIT ²⁹
SHAPE-MaP ³⁰	Differential SHAPE analysis between conditions to identify RNA-ligand/protein interactions ³¹ ; Structure modelling with RNAstructure Package ¹⁴⁻¹⁶ , and comparative sequence alignment ^{32,33} , Visualization of suboptimal conformations ³⁴
RING-MaP ³⁵	RING analysis to identify tertiary interactions ³⁵ and direct base pair interactions ³⁶ , clustering analysis on sequencing reads to identify sub-populations
icSHAPE ³⁷	Direct analysis of reactivities, aggregate analysis over transcriptome, VTD analysis to uncover differences with in vitro folding
MOHCA-Seq ³⁸	COHCOA framework for identify 2D proximity maps, three dimensional modelling with Rosetta
SHAPES ³⁹	Direct analysis of reactivities
DMS-MaP-Seq ⁴²	Aggregate analysis of reactivities over transcriptome, RNA structure modelling with RNAfold Package ⁴³
Ligation-Based Methods	
RNA Proximity Ligation ⁴⁴	Direct analysis of ligation junctions with respect to secondary structure models
LIQR-Seq ⁴⁵	Detection of ligation junctions and secondary structure models from known models and <i>in silico</i> prediction on ligated products
PARIS ⁴⁶	Detection of ligated junctions and their consensus structure prediction from RNAalifold
SPLASH ⁴⁷	Detection of ligated junctions, comparison to known crystal and secondary structures, and compared found ligation products to a snoRNA prediction program (PLEXY)

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