

# RNA Secondary Structure References

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## Classics

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### **Nussinov et al.: Algorithms for Loop Matchings** **nussinov1978**

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Ruth Nussinov et al. “Algorithms for Loop Matchings”. In: *SIAM Journal on Applied Mathematics* 35 (1978), pp. 68–82.

Annotations: Here the algorithm to find the maximum number of base-pairs is presented for the first time. The previous papers of Tinoco and Uhlenbeck did not aim at solving the dynamic programming problem but were only interested in computing a free-energy based score assuming that single base-pair energies could be additive.

File: `../nussinov1978.pdf`.

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### **Tinoco et al.: Estimation of Secondary Structure in Ribonucleic Acids** **tinoco1971**

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I. Tinoco, O. C. Uhlenbeck, and M. D. Levine. “Estimation of Secondary Structure in Ribonucleic Acids”. In: *Nature* 230 (1971), pp. 362–367.

Annotations: In this seminal paper Tinoco and Uhlenbeck propose that the free energy of hybridization of RNA single strands is base-pair additive.

File: `../tinoco1971.pdf`.

**Tinoco et al.: Improved Estimation of Secondary Structure in Ribonucleic Acids** **tinoco1973**

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I. Tinoco et al. “Improved Estimation of Secondary Structure in Ribonucleic Acids”. In: *Nature New Biology* 246 (1973), pp. 40–41.

File: ../tinoco1973.pdf.

## Reviews

**Eddy: How do RNA Folding Algorithms Work?** **eddy2004**

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Sean R. Eddy. “How do RNA Folding Algorithms Work?” In: *Nature Biotechnology* 22 (2004), pp. 1457–1458. DOI: 10.1038/nbt1104-1457.

File: ../eddy2004.pdf.

## Software

**Harmanci et al.: Efficient pairwise RNA structure prediction using probabilistic alignment constraints in Dynalign** **harmanci2007**

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Arif Ozgun Harmanci, Gaurav Sharma, and David H. Mathews. “Efficient pairwise RNA structure prediction using probabilistic alignment constraints in Dynalign”. In: *BMC Bioinformatics* 8 (2007), p. 130. DOI: 10.1186/1471-2105-8-130. URL: <http://dx.doi.org/10.1186/1471-2105-8-130>.

File: ../harmanci2007.pdf.

## Inverse Folding

**Avihoo et al.: RNAexinv: An Extended Inverse RNA Folding from Shape and Physical Attributes to Sequences** **avihoo2011**

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Assaf Avihoo, Alexander Churkin, and Danny Barash. “RNAexinv: An Extended Inverse RNA Folding from Shape and Physical Attributes to Sequences”. In: *BMC Bioinformatics* 12 (2011), p. 319. DOI: 10.1186/1471-2105-12-319. URL: <http://dx.doi.org/10.1186/1471-2105-12-319>.

File: ../avihoo2011.pdf.

## lncRNA

**Baker: Long Noncoding RNA's: The Search for Function**

**baker2011**

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Monya Baker. “Long Noncoding RNA's: The Search for Function”. In: *Nature Methods* 8 (2011), pp. 379–383.

File: ../baker2011\_lncRNA.pdf.