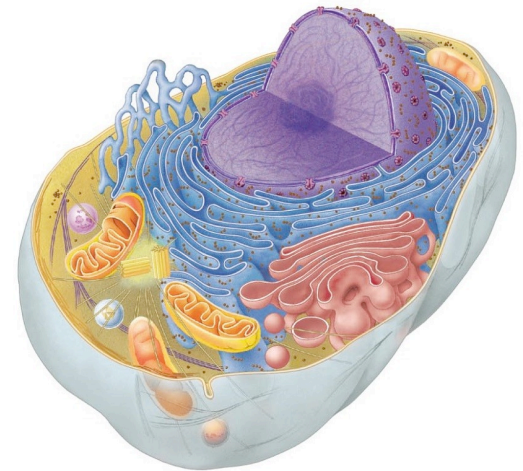


# RIBOSOME STRUCTURE

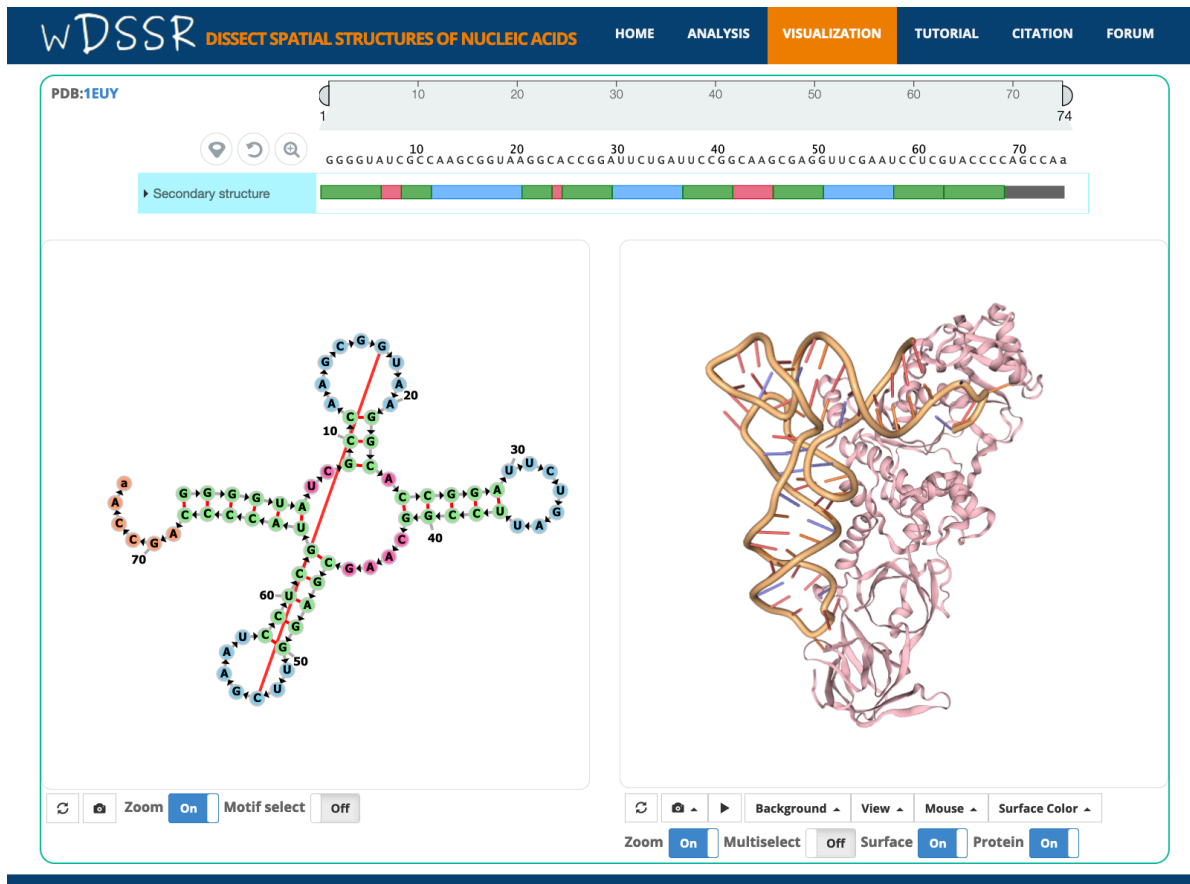
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Caitlin Davis, 2019 DIMACS REU



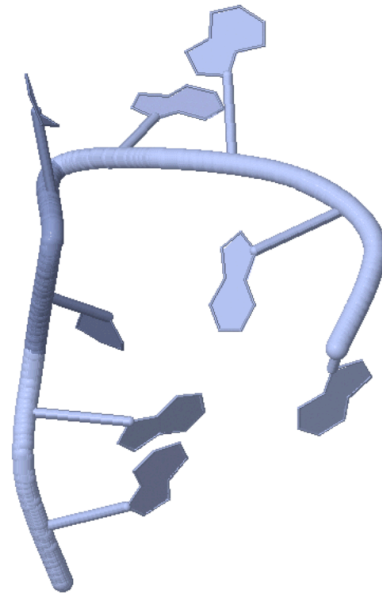
# The Olson group: Biopolymer structure research

- Programs allow analysis and visualization of 1D, 2D, and 3D structures of nucleic acids



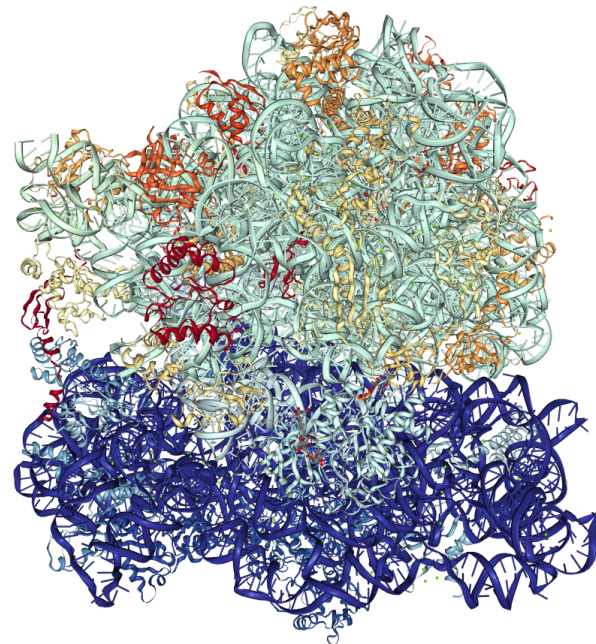
# The Olson group: Biopolymer structure research

- Research aims to understand primary, secondary, and tertiary structures of nucleic acids
  - Relationships between these levels of organization
  - Structural motifs



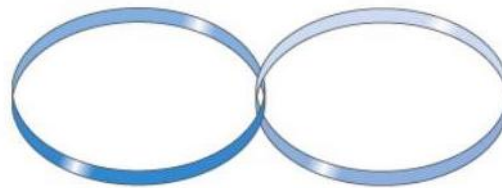
# RNA and ribosomes

- RNA folding parallels that of proteins
- RNA is more flexible than DNA due to the presence of an additional oxygen on each sugar
- RNA is typically single-stranded, but bases have some tendency to pair
- Ribosomes are composed of RNA and proteins
- Despite some differences, ribosomes are relatively similar among organisms

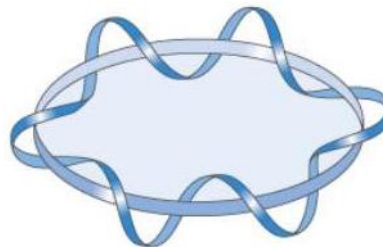


# Topological and geometric properties

- Can be used to study circular DNA and other nucleic acid structures which are constrained at both ends
- Linking number—describes the number of times two strands wrap around each other



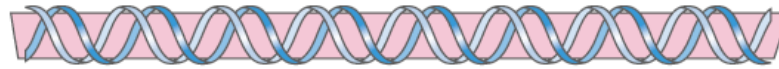
$Lk = 1$   
(a)



$Lk = 6$   
(b)

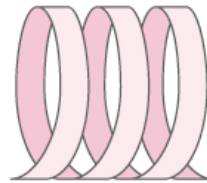
# Topological and geometric properties

- Double stranded structures can be studied as smooth ribbon
- Twist—describes the rate of rotation of the ribbon about its midline
- Writhe—describes the non-planarity of the ribbon's midline



Straight ribbon (relaxed DNA)

(a)



Large writhe, small change in twist

(b)



Zero writhe, large change in twist

(c)

# Acknowledgements

- Thank you to Professor Olson and the Olson group.
- Thank you to the DIMACS REU, and to the NSF which has provided support through grant CCF-1852215.

# References

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- Shuxiang Li, Wilma K Olson, Xiang-Jun Lu, Web 3DNA 2.0 for the analysis, visualization, and modeling of 3D nucleic acid structures, *Nucleic Acids Research*, , gkz394, <https://doi.org/10.1093/nar/gkz394>
- A.S. Rose, A.R. Bradley, Y. Valasatava, J.D. Duarte, A. Prlić, P.W. Rose (2018) NGL viewer: web-based molecular graphics for large complexes. *Bioinformatics* ([doi:10.1093/bioinformatics/bty419](https://doi.org/10.1093/bioinformatics/bty419)).