

Universal Molecular Characteristics: Transcription

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Bio590S
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Overview

- 3⁰⁵ – 3²⁰: Review Key Topics
 - Transcription Mechanisms
 - Transcription Regulation
 - Elongation First Hypothesis
 - Other RNA polymerases
- 3²⁰ – 3⁴⁵: Journal Club of Smollett Paper
- 3⁴⁵ – 4¹⁵: Research discussion questions
- 4¹⁵ – 4³⁰: Discuss Findings
- 4³⁰ – 5¹⁰: “Elevator-Pitch R21” Activity

Core of Transcription

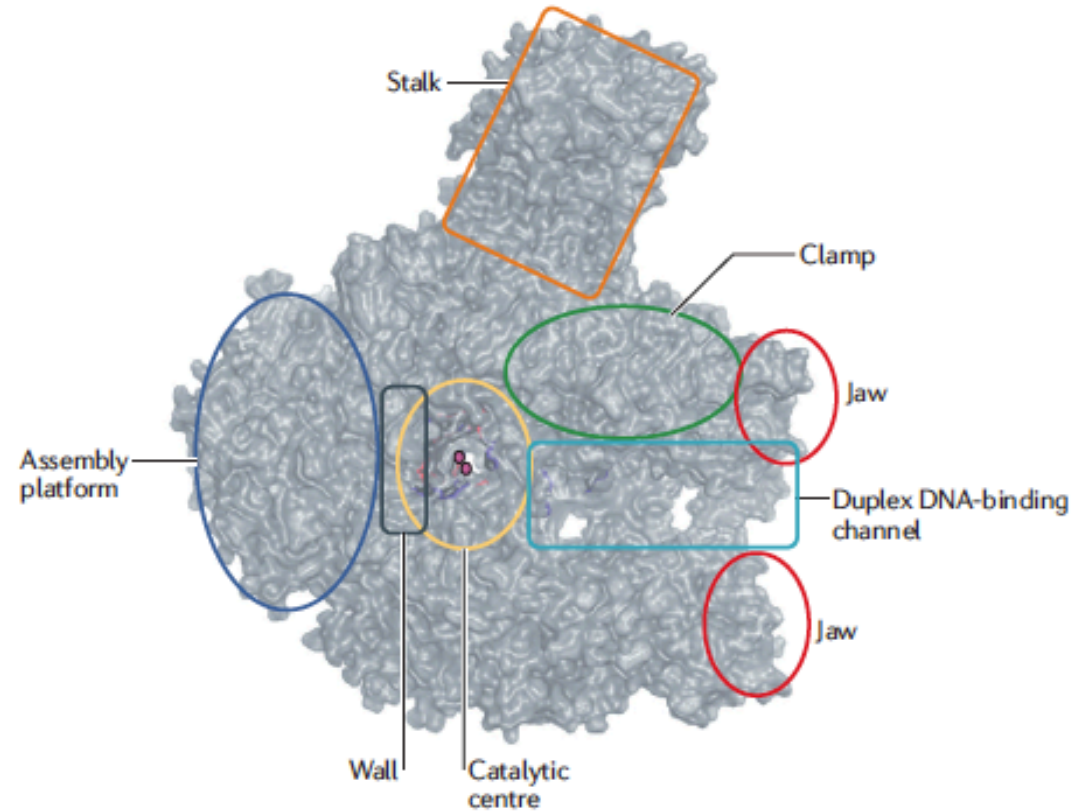
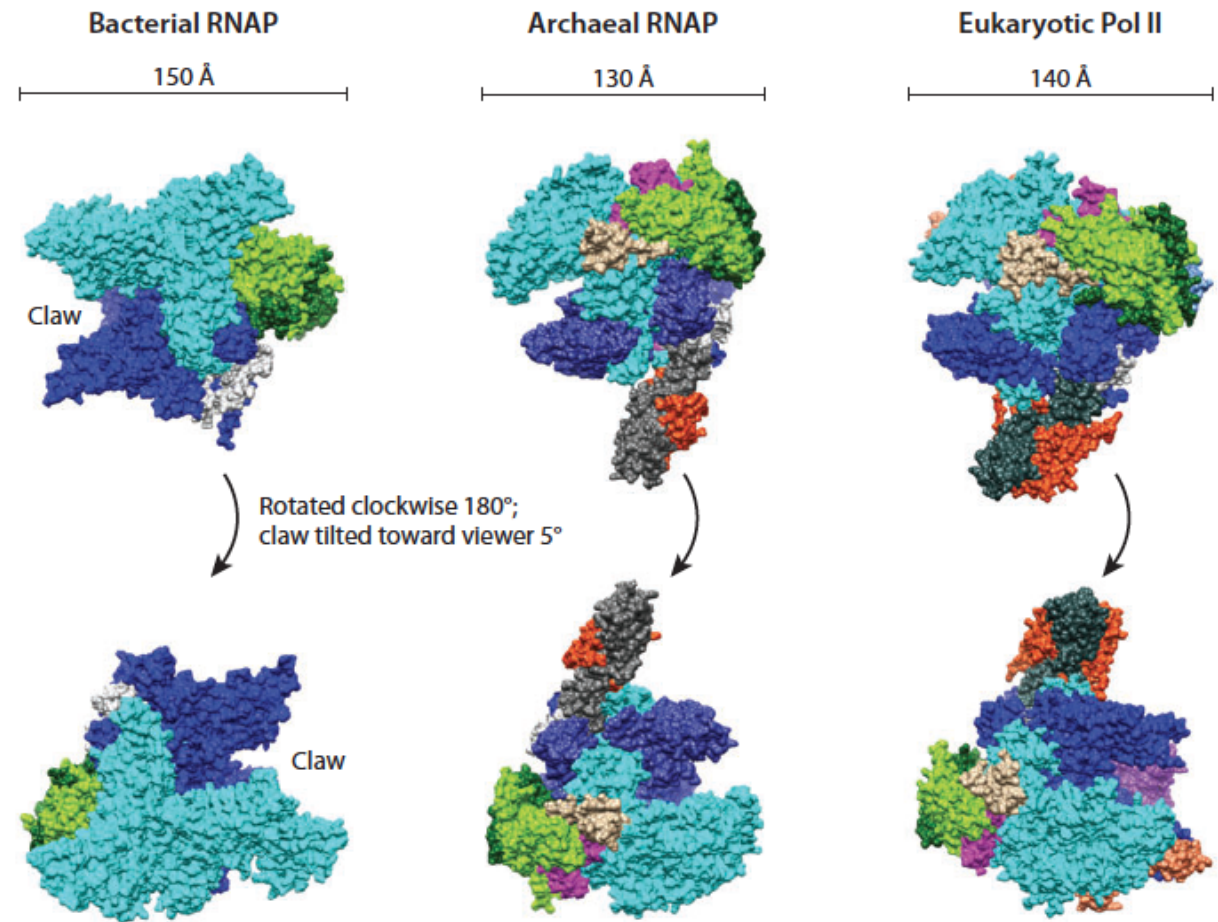


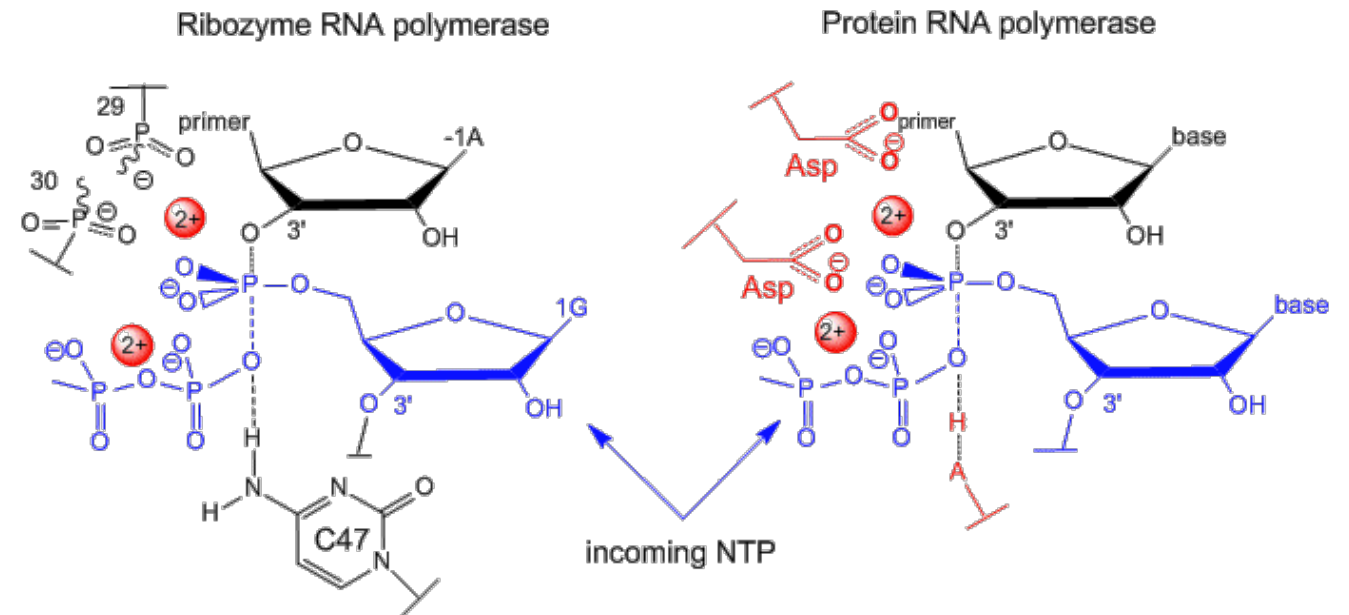
Figure 2 | **Overall architecture of RNA polymerase.** This simplified diagram of RNA polymerase shows important structural and functional features discussed in the main text, including the assembly platform, the active site, the DNA-binding channel, the jaws and the wall, clamp and stalk domains. The two active-site Mg^{2+} ions are indicated as magenta spheres. The structural information was obtained from eukaryotic RNAPII Protein Data Bank entry [1Y1W](#).

Core of Transcription

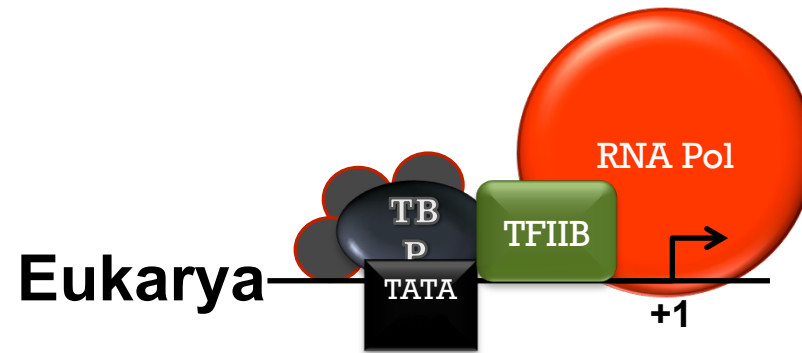
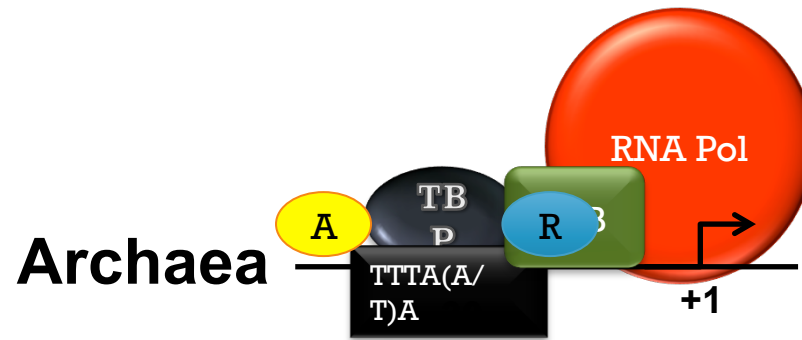
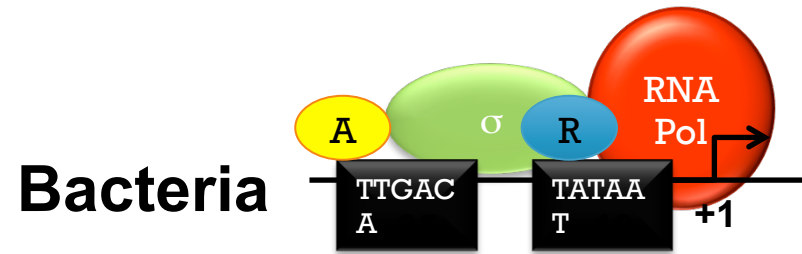


Hinton (2013) Annual Rev Microbiol 67:113-39

Conserved Mechanism



Key Differences

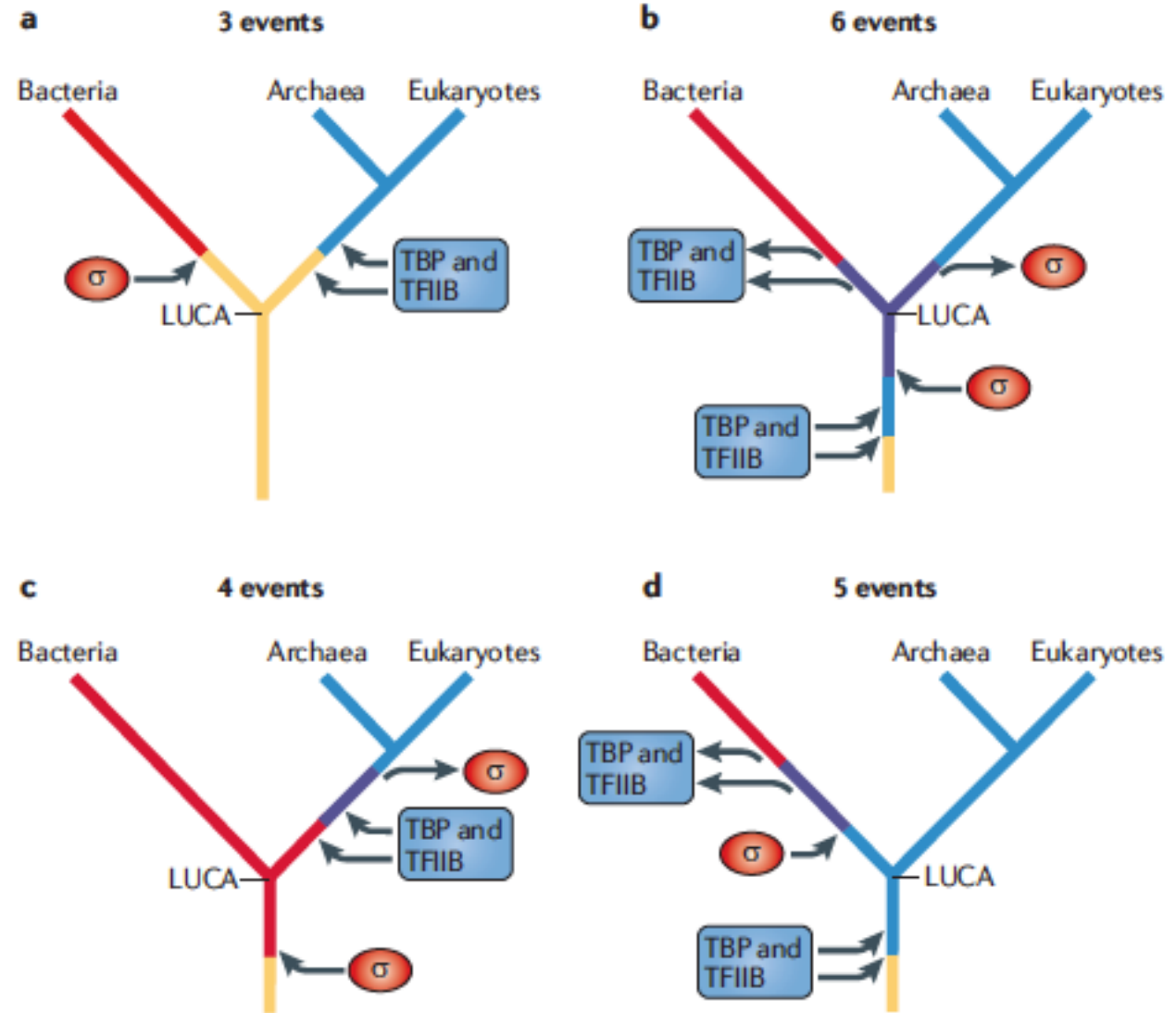


Hinton (2013) Annual Rev Microbiol 67:113-39

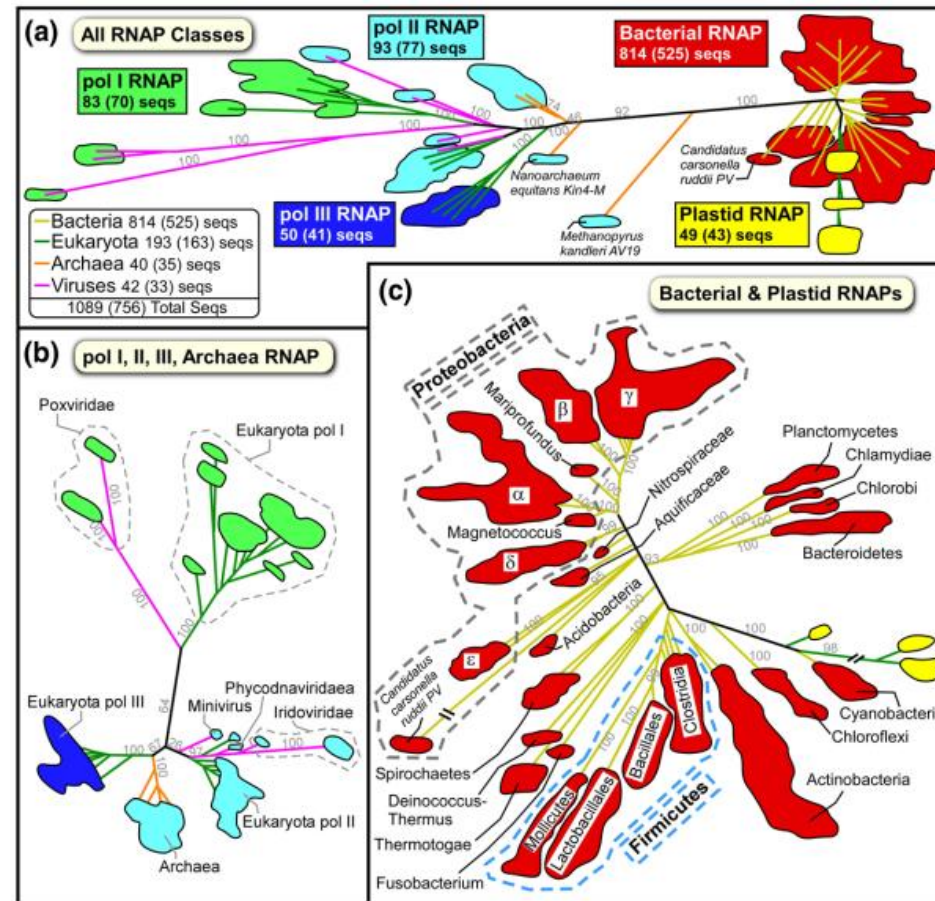
What's there? What isn't?

- Conserved transcription factors
 - Spt5-SPT5-NusG Family
- Absence of homologues
 - Sigma factors
 - TBP/TFIIB
- Number of evolutionary events
- Significance of Elongation

Elongation First Hypothesis

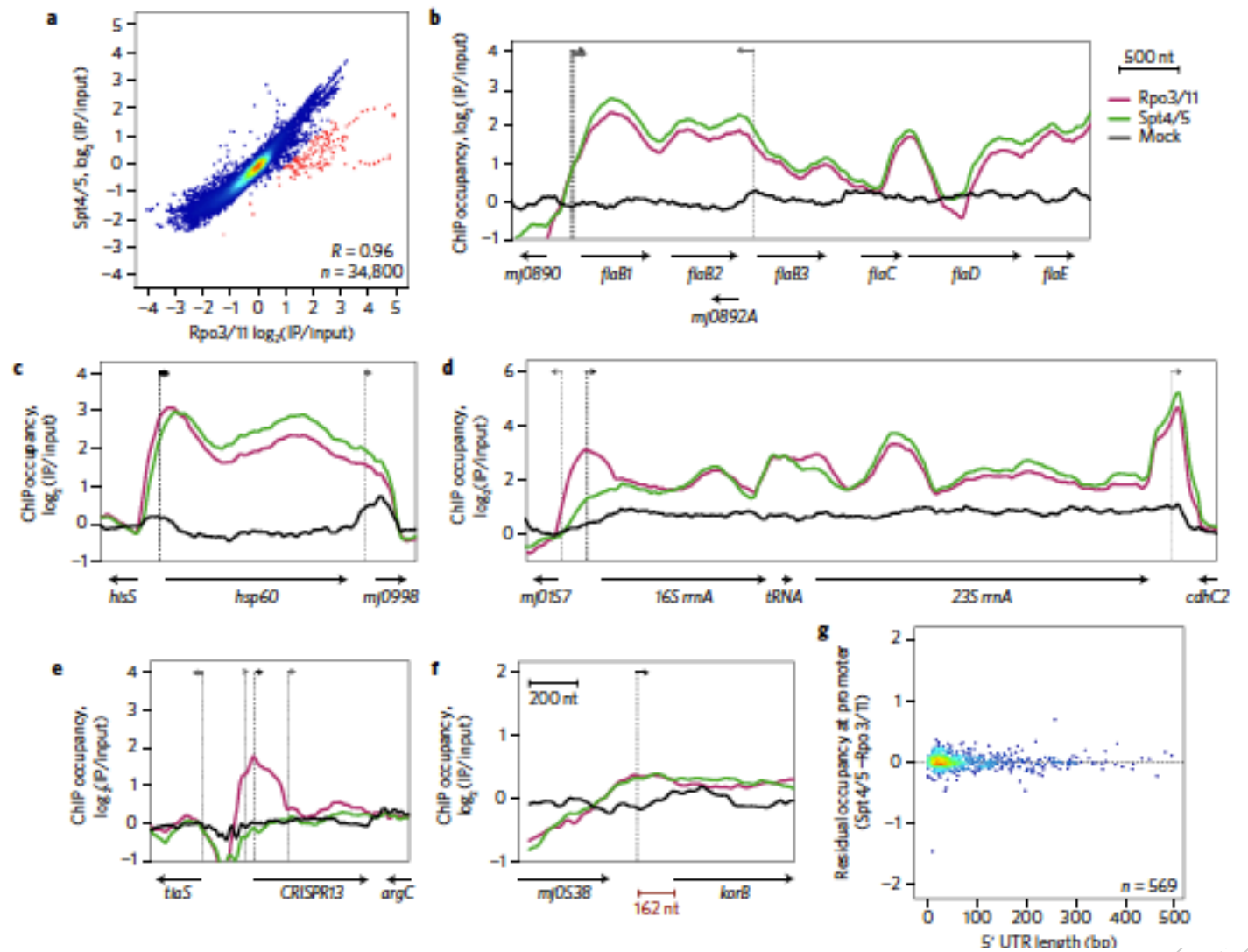


Other RNAPs



- “Right handed” RNA polymerases
 - RNA-dependent RNA polymerases
 - Viral DNA-dependent DNA polymerases

Smollett's Work



Evaluating Smollett's Methods


- What is it? How does it work? What does it tell us?
 - What are the strengths of or advantages to using the technique?
 - What are the weaknesses or disadvantages to using the technique?
 - Evaluate the use of it in Smollett (2017)
-
- ChIP Seq
 - Alignment Motifs
 - Pairwise Genome-wide Correlation

Discussion Questions

- What does the current data (since 2011) say about the validity of the elongation-first hypothesis? Does it corroborate or challenge it?
- What is known about “simple” eukaryotes, such as protists, regarding their transcription machinery? How do these mechanisms fit in with what we know about other transcription mechanism, and what could it tell us about the machinery of LUCA?
- What influence, if any, does analysis of transcription machinery data exert on the three versus two domain tree argument?
- What is known about non-canonical RNAPs and how does that data fit in to the evolutionary history of transcription?

The background features a series of concentric circles in light gray, some solid and some dashed, creating a ripple effect. In the center, there is a large red speech bubble with a white outline. The text "The Elevator Pitch R21" is written in white inside the bubble.

The Elevator Pitch R21

The background of the slide features a series of thin, curved, concentric lines in a light gray color, creating a sense of depth and movement. These lines are more prominent on the left side and fade towards the right.

Critical Anatomy of an R21

- **Specific Aims**
- **Research Strategy**
 - **Significance**
 - **Innovation**
 - **Approach**

Your challenge!

- From your discussion question, identify a gap in the current literature
 - What do we not know?
- Formulate a research question and hypothesis
- Select one aim
 - What's one piece of the puzzle you can solve with an experiment/analysis?
- Describe your methods and rationale
 - What do we think? What do we know? What can we prove?