



# Genome-wide study of mRNA degradation and transcript elongation in *Escherichia coli*

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# Background

Coordination of RNA synthesis and degradation is an essential part of gene expression.

The spatial localization of RNA in bacterial cells has been studied in detail by microscopy (Llopis et al, 2010; Nevo-Dinur et al, 2011).

The kinetics of RNA synthesis have been measured directly in *E. coli* using fluorescently tagged RNA molecules (Golding & Cox, 2004)..

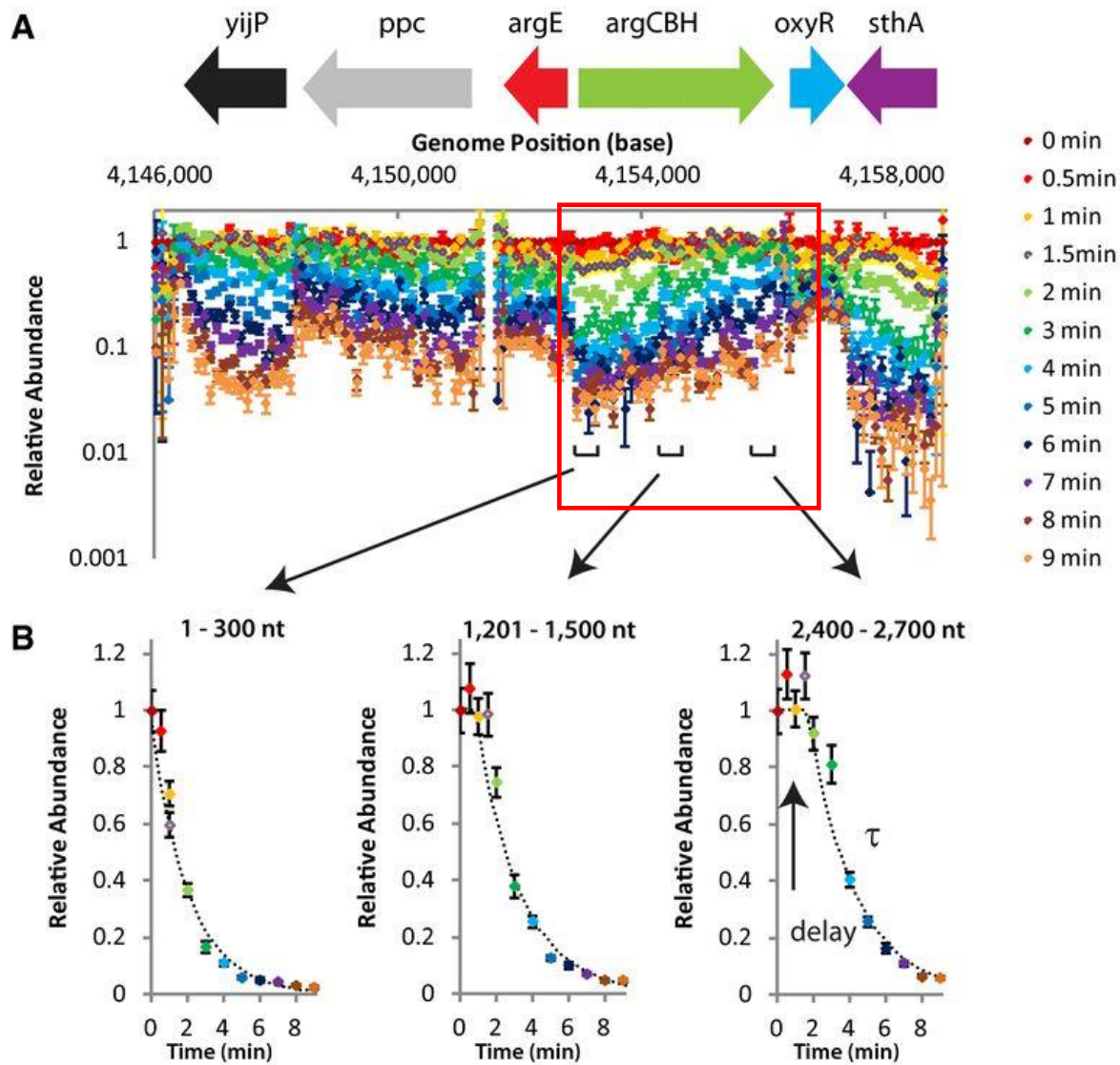
only one or few RNAs



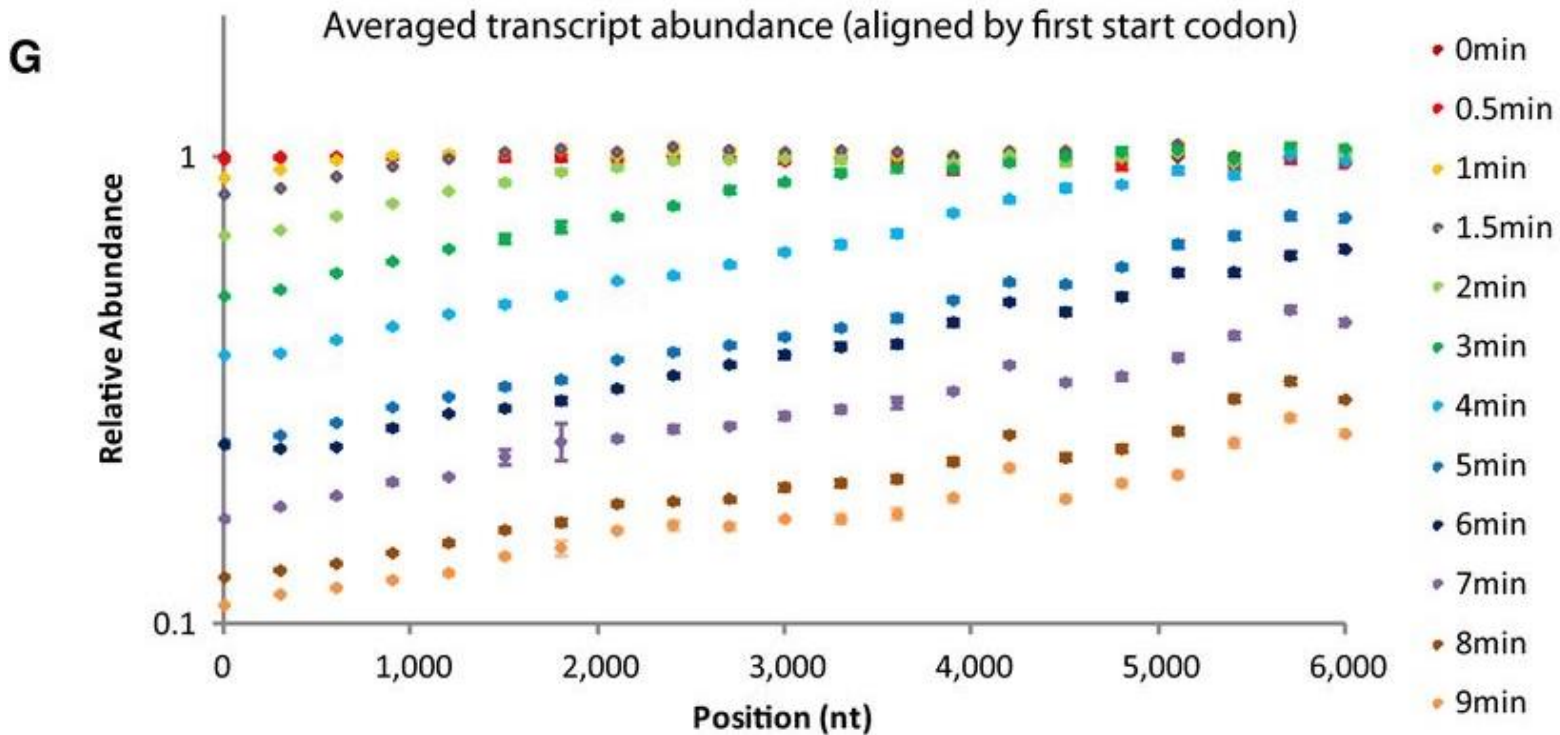
## Prevalence of high-throughput techniques

- increase the amount of information through genome-wide measurements
- allows researchers to study nucleic acids with even higher base resolution.
- RNA-seq has been successfully used in genome-wide studies .

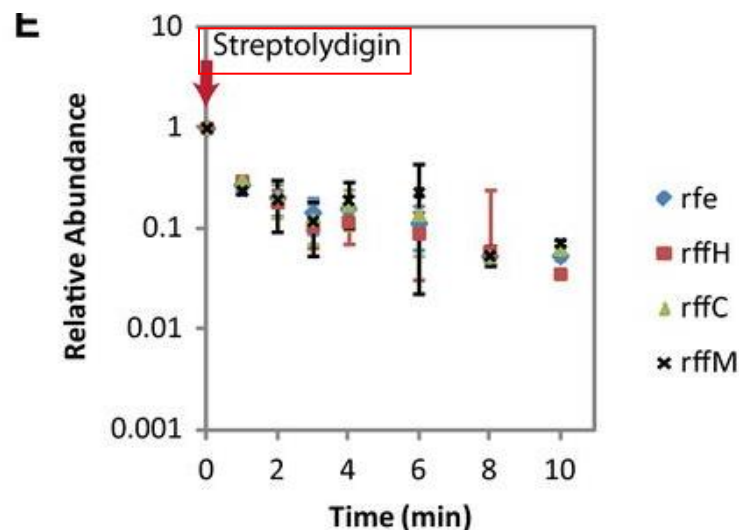
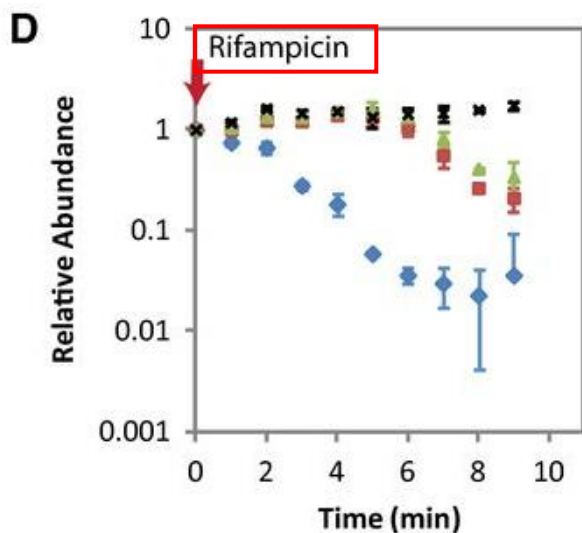
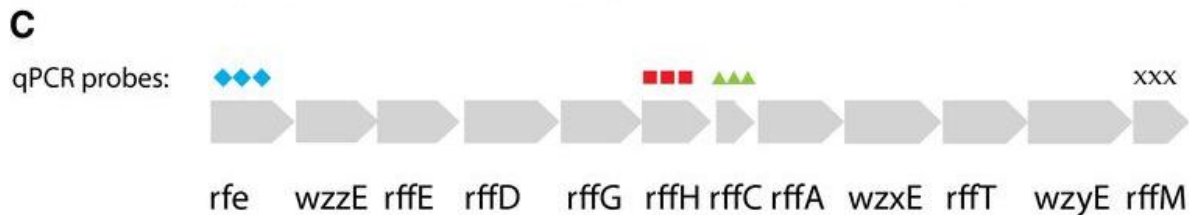
**Rifampicin** , the RNAP **initiation** inhibitor



The differences in 5' and 3' abundances are due to a **delay** in the appearance of **degradation**.

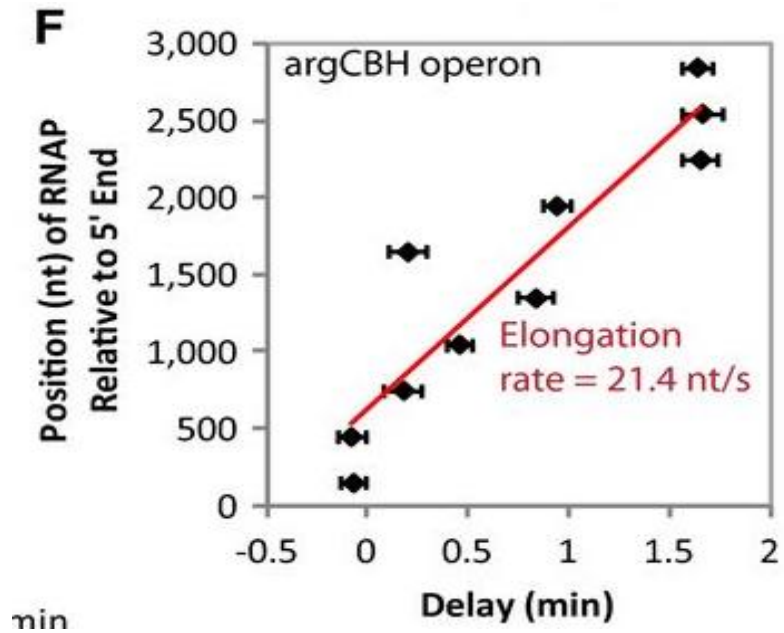
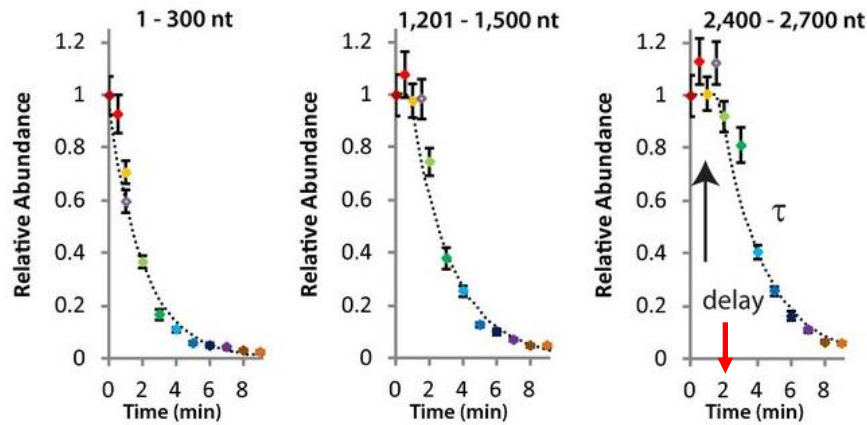


RNA degradation generally happens in a **5' to 3' direction**



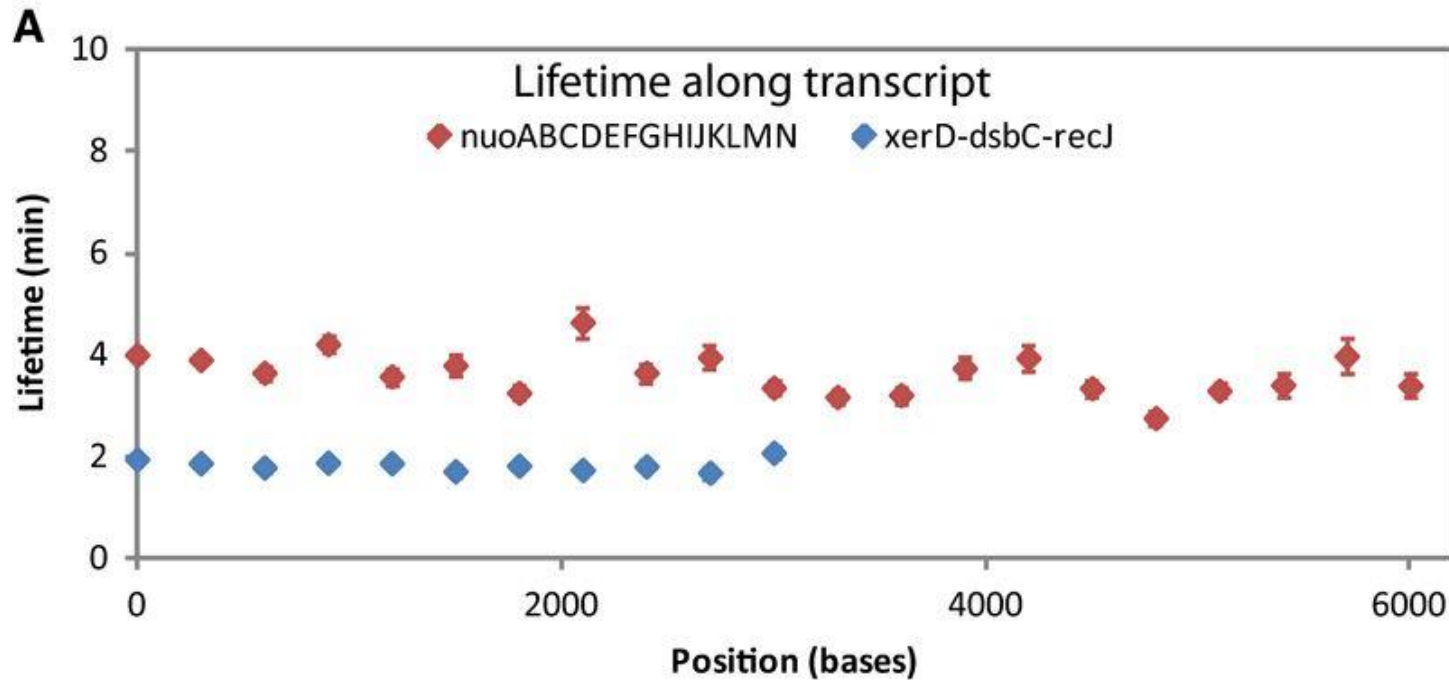
**Rifampicin** RNAP initiation inhibitor  
**Streptolydigin** RNAP elongation inhibitor

Elongating RNAPs are primarily responsible for this degradation delay



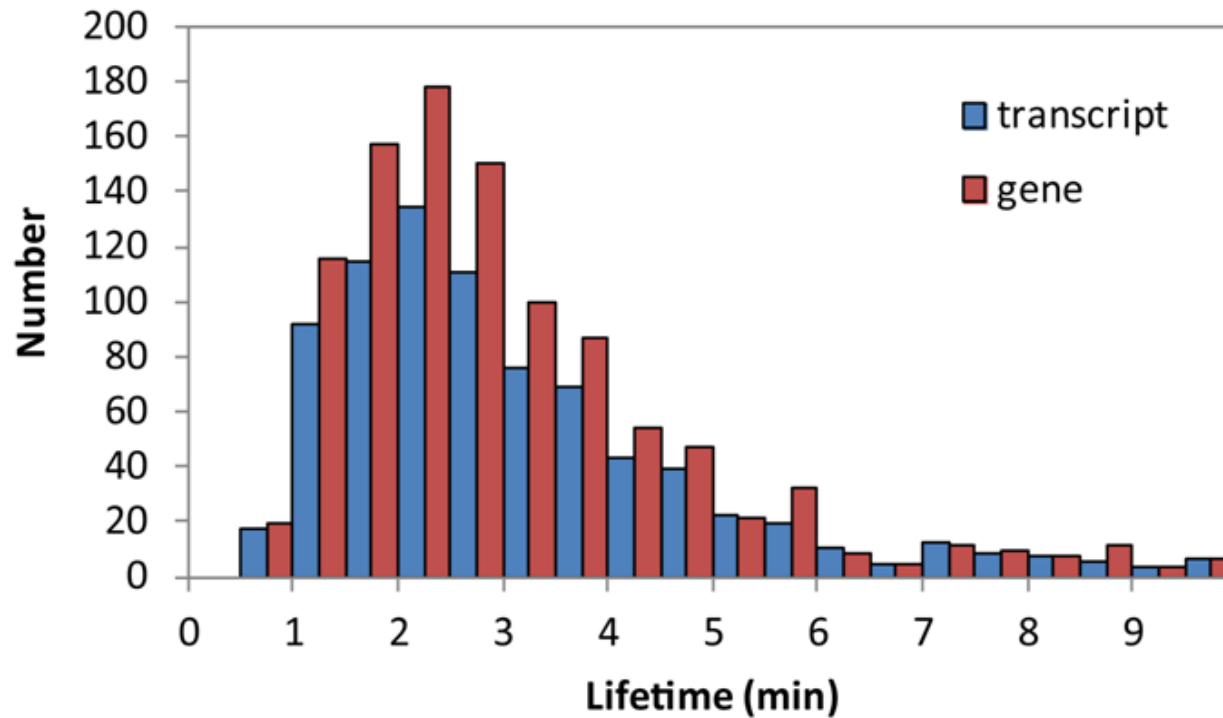
Delay time across the length of the RNA was performed to extract the elongation rate .





All positions along an RNA generally have a lifetime similar to other segments on the same transcript

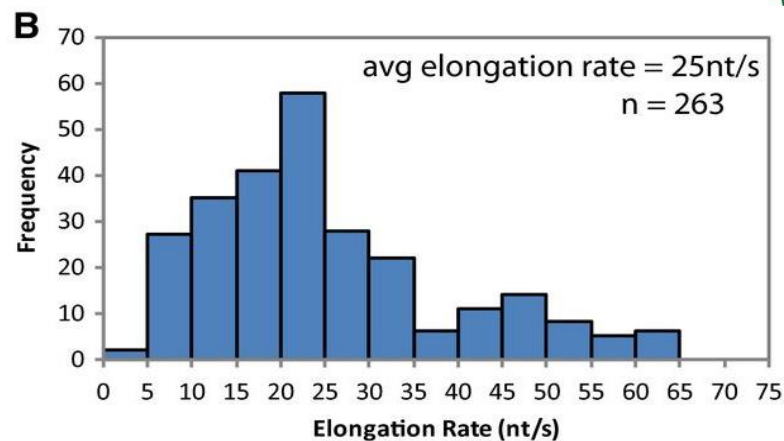
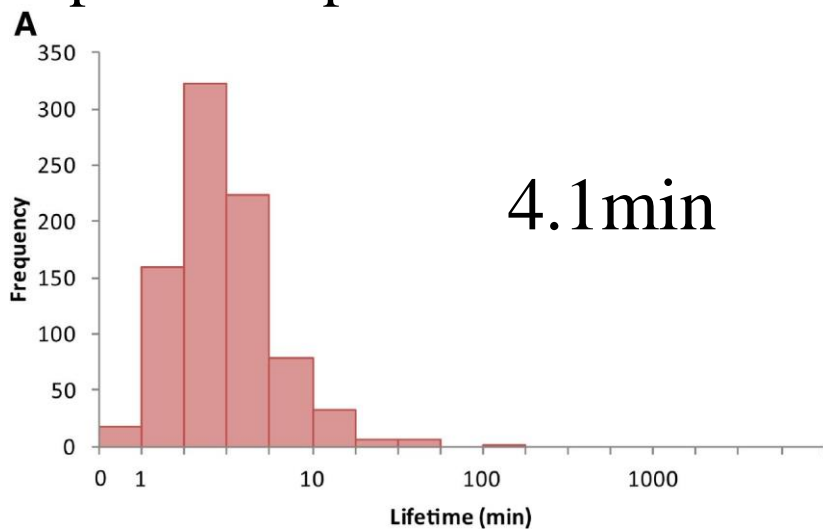




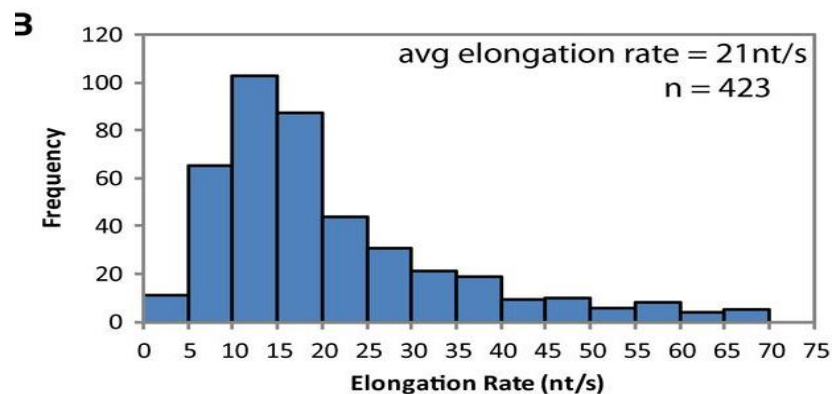
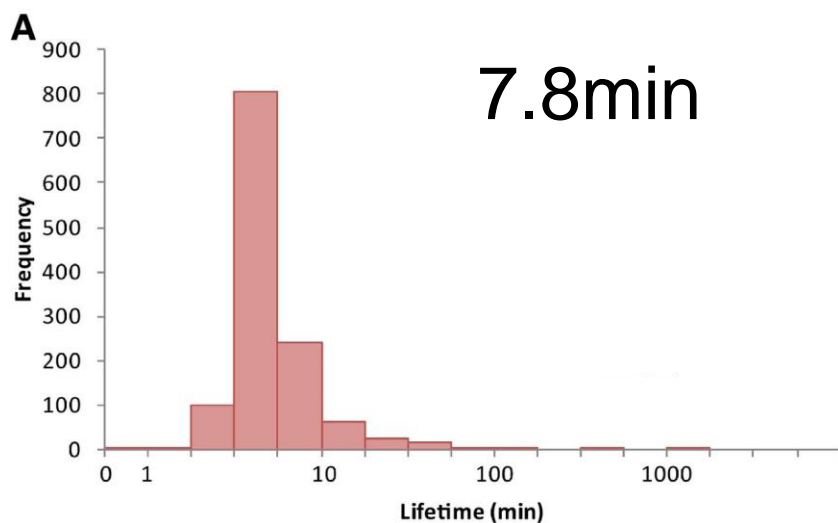
The distribution of lifetimes of operons and genes is similar

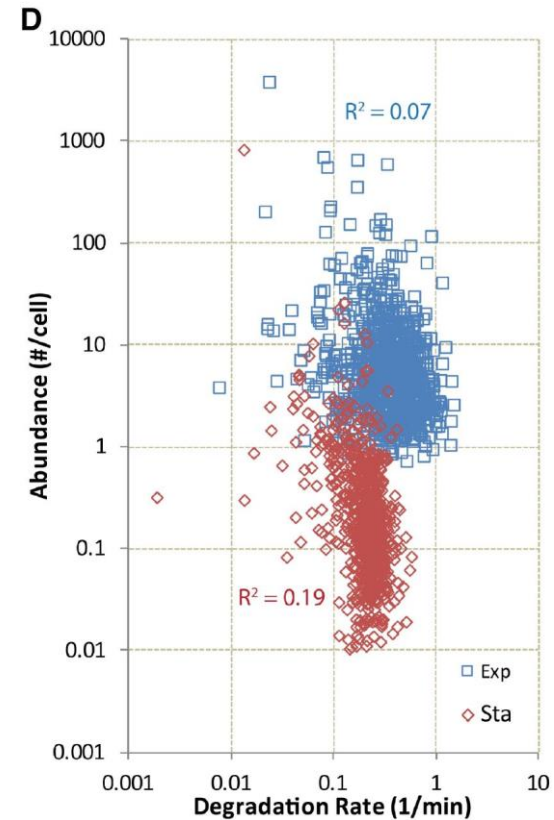
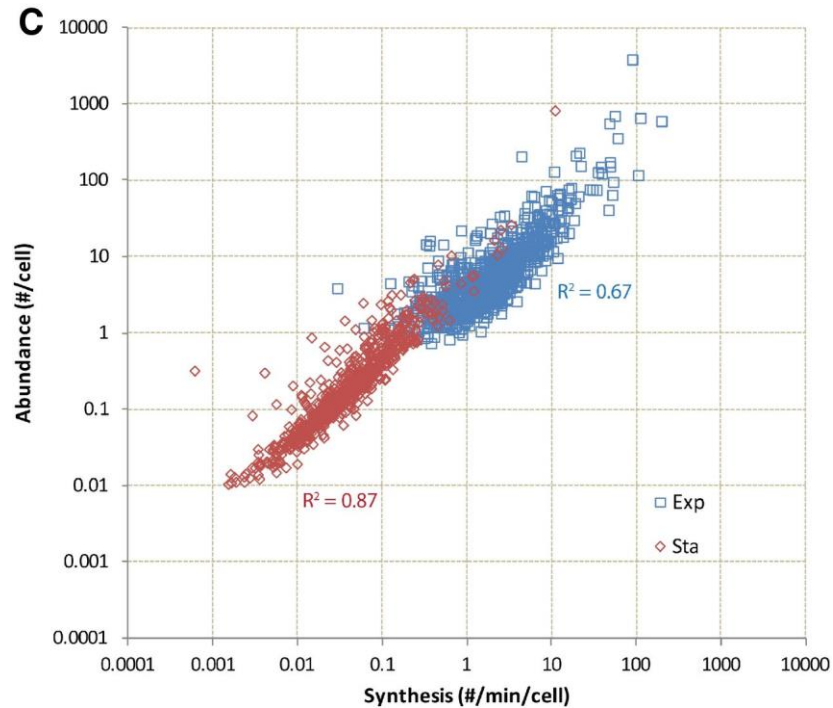


# Exponential phase

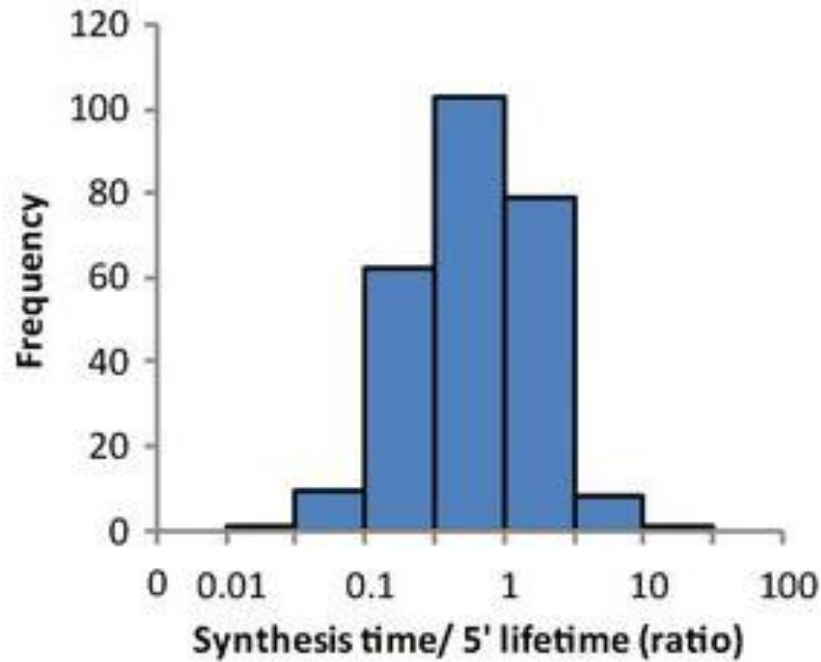


# Stationary phase





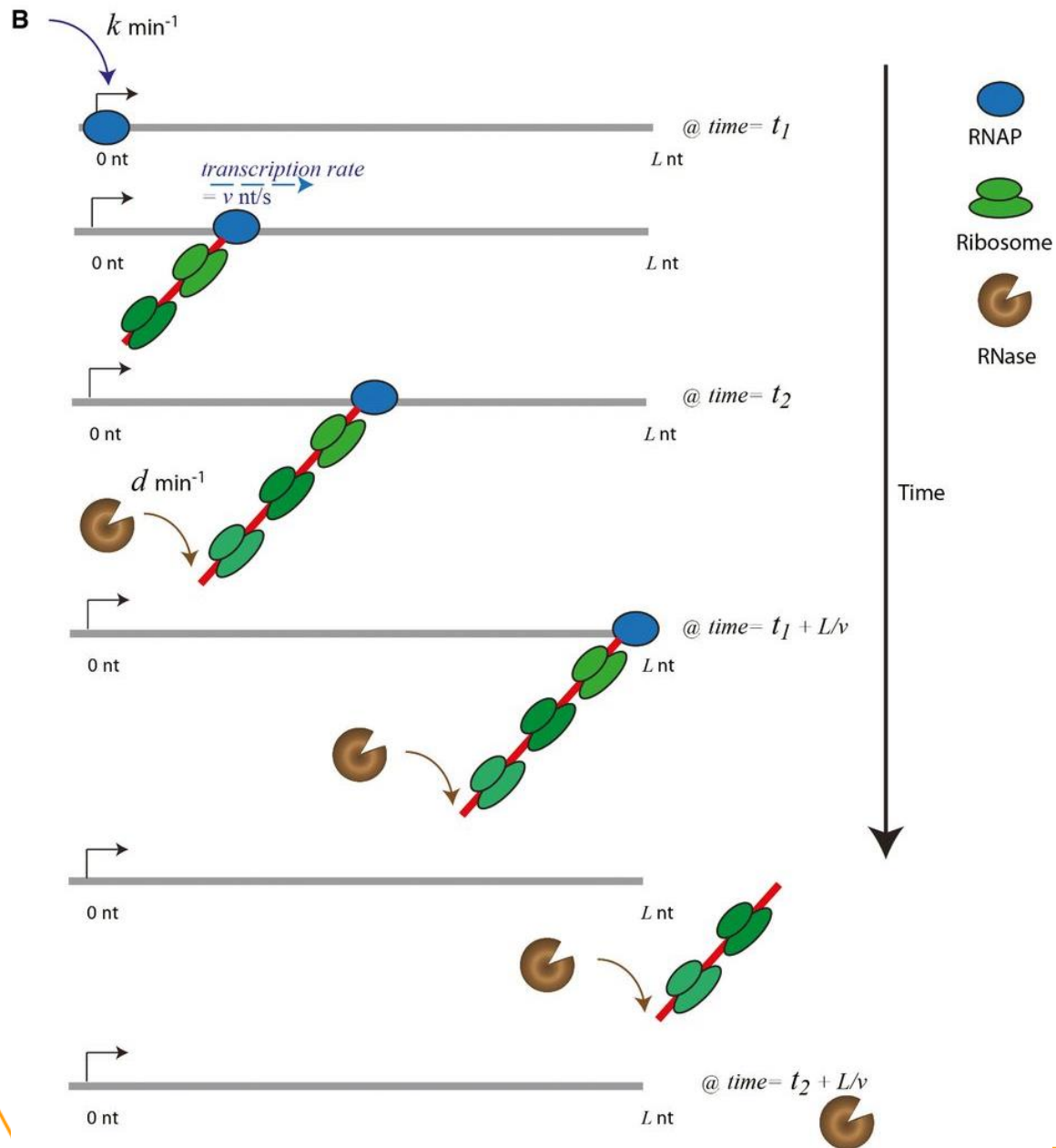
RNA abundance was better explained by changes in synthesis rates than in degradation rate



263 transcripts

Co-transcriptional degradation is potentially common.

# The co-transcriptional degradation model





## Conclusion

In E.coli, there exists co-transcriptional degradation in a 5' to 3' direction.

## Inspiration

- RNA-seq is a useful method. It can not only be used in transcriptome analysis, but also can be used in other scientific research.
- Studying RNA degradation can find neat solution to medical issue. For example, design a drug that can degradate abnormal mRNA in cell, which action results in little production of functional protein.

## Deficiency

It provides limits to the models of RNA degradation on a genome-wide scale. In addition to this shortcoming, this paper provide a elaborately designing experiment and it is worth reference to apply to other study



Thanks for you attention!