

# Phage-Centric Central Dogma Reminders

Refer to the [Introduction to Bioinformatics in the Phage Discovery Guide](#) for background information of Phage-Centric Central Dogma.

Key Concepts to Know:

- Phages are inert when not in a cell
- Phages replicate when in a prokaryotic cell. (no nucleus and follow the Bacterial Code Table)
- Viral genome is a single chromosome, can be RNA or DNA; can be double stranded or single stranded DNA (all actinobacteriophages to date have been dsDNA)
- DNA is made up of polymers of nucleotides – adenine (A), thymine (T), cytosine (C), and guanine (G). They pair A-T and C-G.
- The two strands of DNA in a double helix are antiparallel, with 5' to 3' orientation in opposite directions.
- Central Dogma:

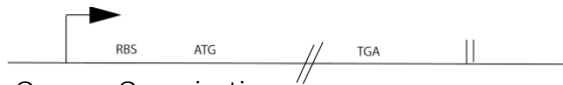


- End product of transcription is an RNA transcript
- Translation occurs in the ribosome and results in the production of a protein from the RNA transcript
- A gene is a unit of DNA that codes for a protein or RNA (like a tRNA).
- Promoters are DNA sequences that signal the start of transcription
- Terminators are DNA sequences that signal the stop of transcription
- Only one of the two strands of DNA for a particular gene is transcribed.
- Codons that start translation are START codons (ATG, GTG and TTG)
- Codons that stop translation are STOP codons (TAA, TAG and TGA)
- An Open Reading Frame (ORF) is the space between a start and a stop. A gene resides inside an ORF.
- Translation occurs in the ribosome as the RNA transcript is bound to the ribosome.
- The DNA sequence that binds to the ribosome is the Shine-Dalgarno sequence, AGGAGGA. It is 7-10 bases upstream of start.
- A DNA sequence that codes for amino acids can be interpreted in 3 separate ways in the forward direction and 3 in the reverse, comprising 6 frame translation.
- It would be inefficient if every gene used the machinery to start the transcription and translation processes. So many genes are part of operons – a group of genes that share a common promoter and terminator.
- Virus genomes do not include much intergenic space; in fact, genes in an operon often overlap by a few nucleotides.
- Genome **annotation** is the prediction of the genes and other features coded within a phage genome and their potential functions.

To recap: Write a caption to this figure.

☐ A graphic help to phage gene architecture:

Prokaryotic Gene Organization



Operon Organization



More realistic phage operon organization

