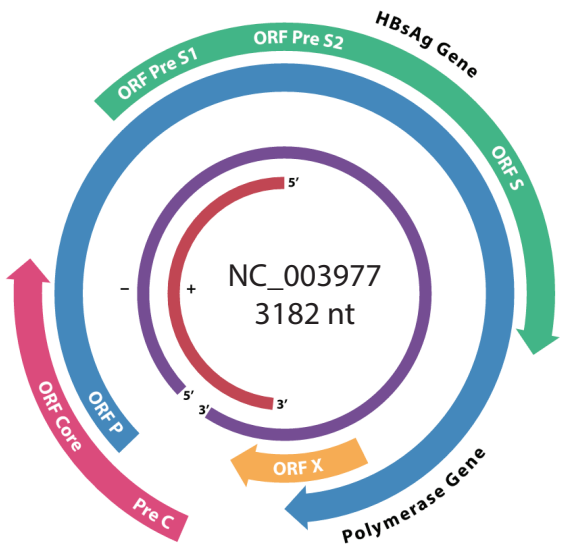


Overview of annotation pipeline for Hepatitis B Virus

INPUT:

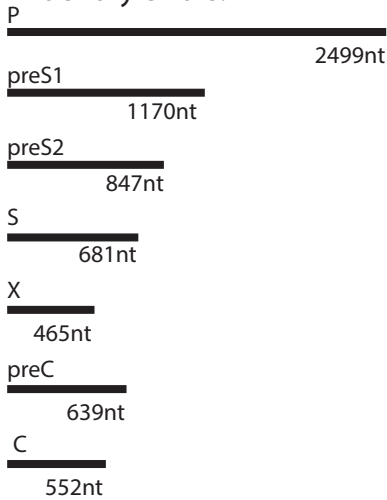
1. RefSeq annotation



2. Target sequence(s) to annotate:



Combine models into 'features', translate, find stop codons, and identify errors:



OUTPUT:

1. Tabular annotations of all features:
KJ410493:P:-909-1623
KJ410493:preS1:-335-835
KJ410493:preS2:-11-835
KJ410493:S:155-835
KJ410493:X:1374-1838
KJ410493:preC:1814-2446
KJ410493:C:1901-2446
2. List of all 'error codes':
EU628610:Rep:trc
3. Nucleotide and protein multiple alignments (optional)

