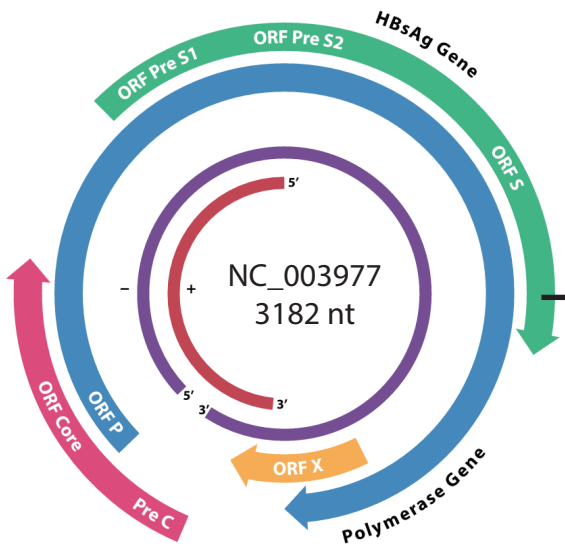


# Overview of annotation pipeline for Hepatitis B Virus

## INPUT:

### 1. RefSeq annotation



### 2. Target sequence(s) to annotate:



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

