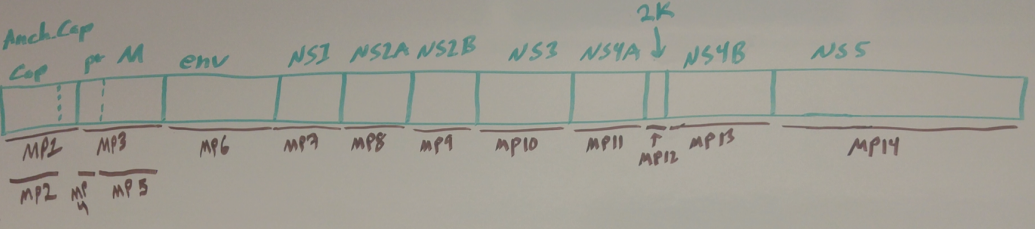


# Overview of annotation pipeline for Dengue Virus

## INPUT:

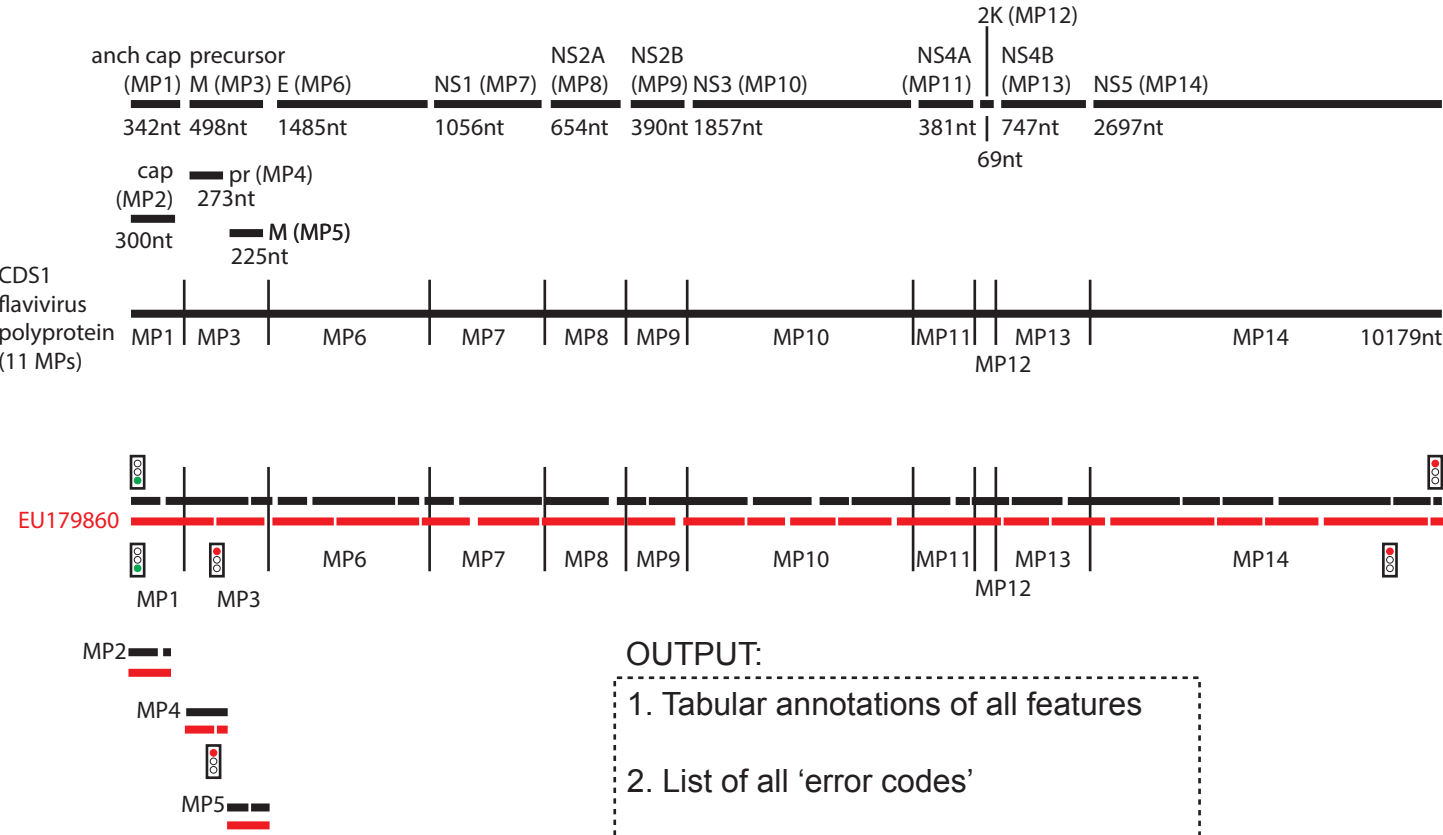
1. RefSeq annotation (NC\_001477)



2. Target sequence(s) to annotate:



Combine models into 'features' (14 MPs and 1 CDS), translate, find stop codons, and identify errors:



## OUTPUT:

- 1. Tabular annotations of all features
- 2. List of all 'error codes'
- 3. Nucleotide and protein multiple alignments (optional)