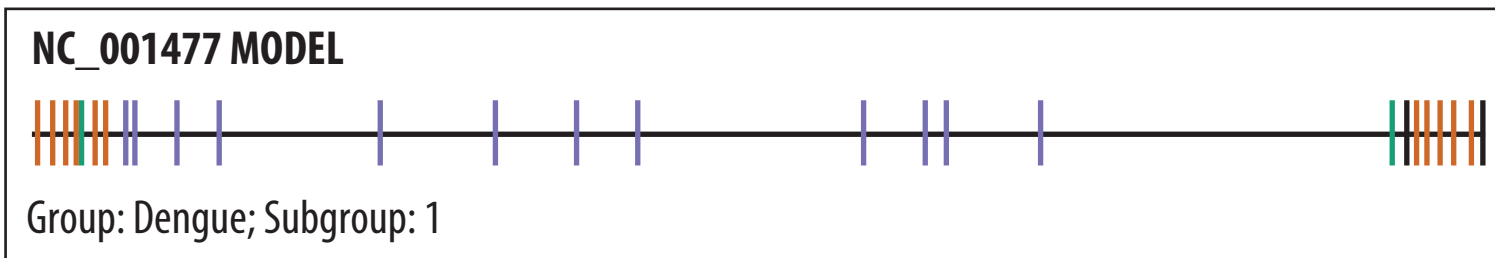# Stage 3: Alignment and feature mapping

Align each sequence to its best-matching model (Infernal's cmalign)

input sequences that match best to NC_001477:

NC_001477 MODEL

Group: Dengue; Subgroup: 1

gap or low confidence at feature boundary
(indf5gap, indf3gap, indf5loc, indf3loc alert)

NC_001477

S5

NC_001477

S6

early stop codon in CDS
(cdsstopn alert)