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#Example of transcription and translation using zikaVirus
#Biostrings package has already been loaded for this
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> # Unlist the set and select the first 21 letters as dna_seq, then print it
> dna_seq <- subseq(unlist(zikaVirus), end = 21)
> dna_seq
 21-letter "DNAString" instance
seq: AGTTGTTGATCTGTGTGAGTC
>
> # 1.1 Transcribe dna_seq as rna_seq, then print it
> rna_seq <- RNAString(dna_seq)
> rna_seq
 21-letter "RNAString" instance
seq: AGUUGUUGAUCUGUGUGAGUC
>
> # 1.2 Translate rna_seq as aa_seq, then print it
> aa_seq <- translate(rna_seq)
> aa_seq
 7-letter "AAString" instance
seq: SC*SV*V
>
> # 2.1 Translate dna_seq as aa_seq_2, then print it
> aa_seq_2 <- translate(dna_seq)
> aa_seq_2
 7-letter "AAString" instance
seq: SC*SV*V
```