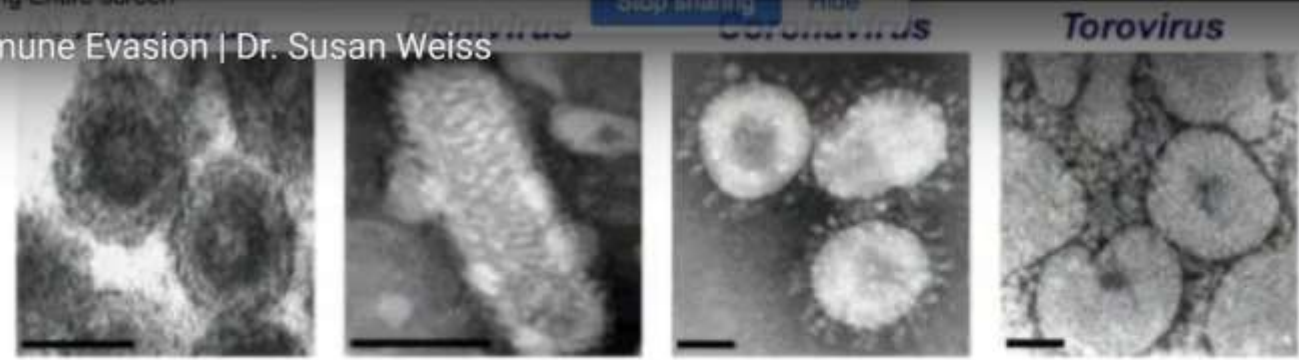
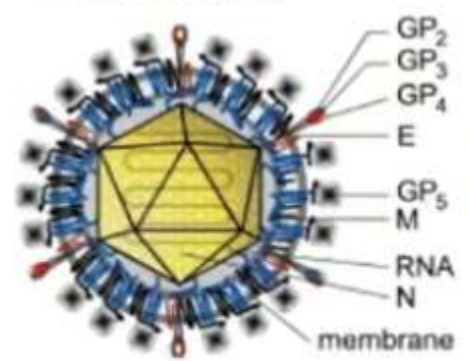


# Nidovirales

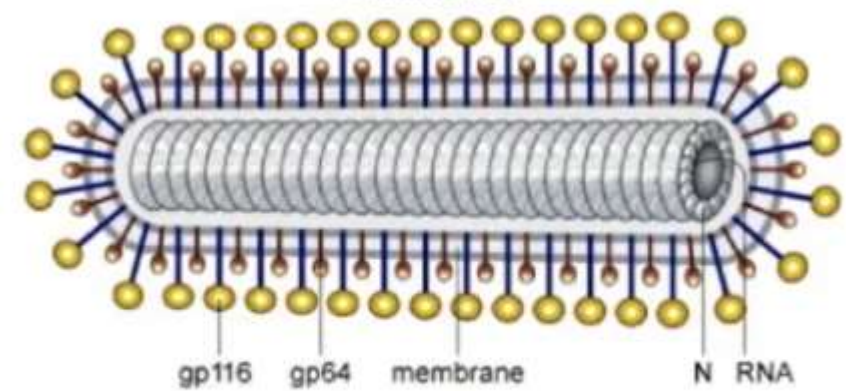
## Coronaviridae



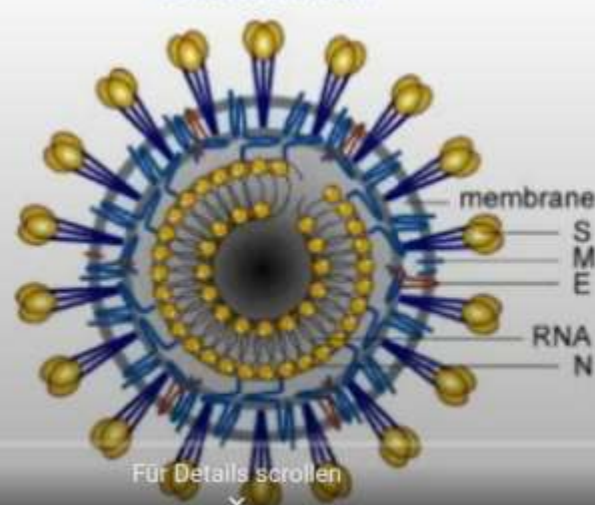
(B) Arterivirus



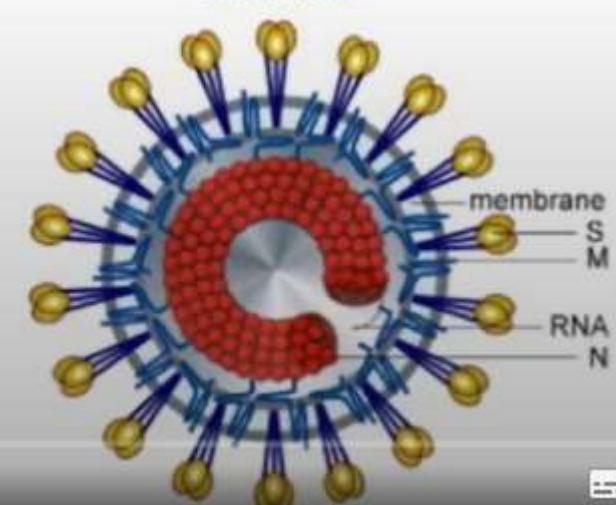
Ronivirus



Coronavirus

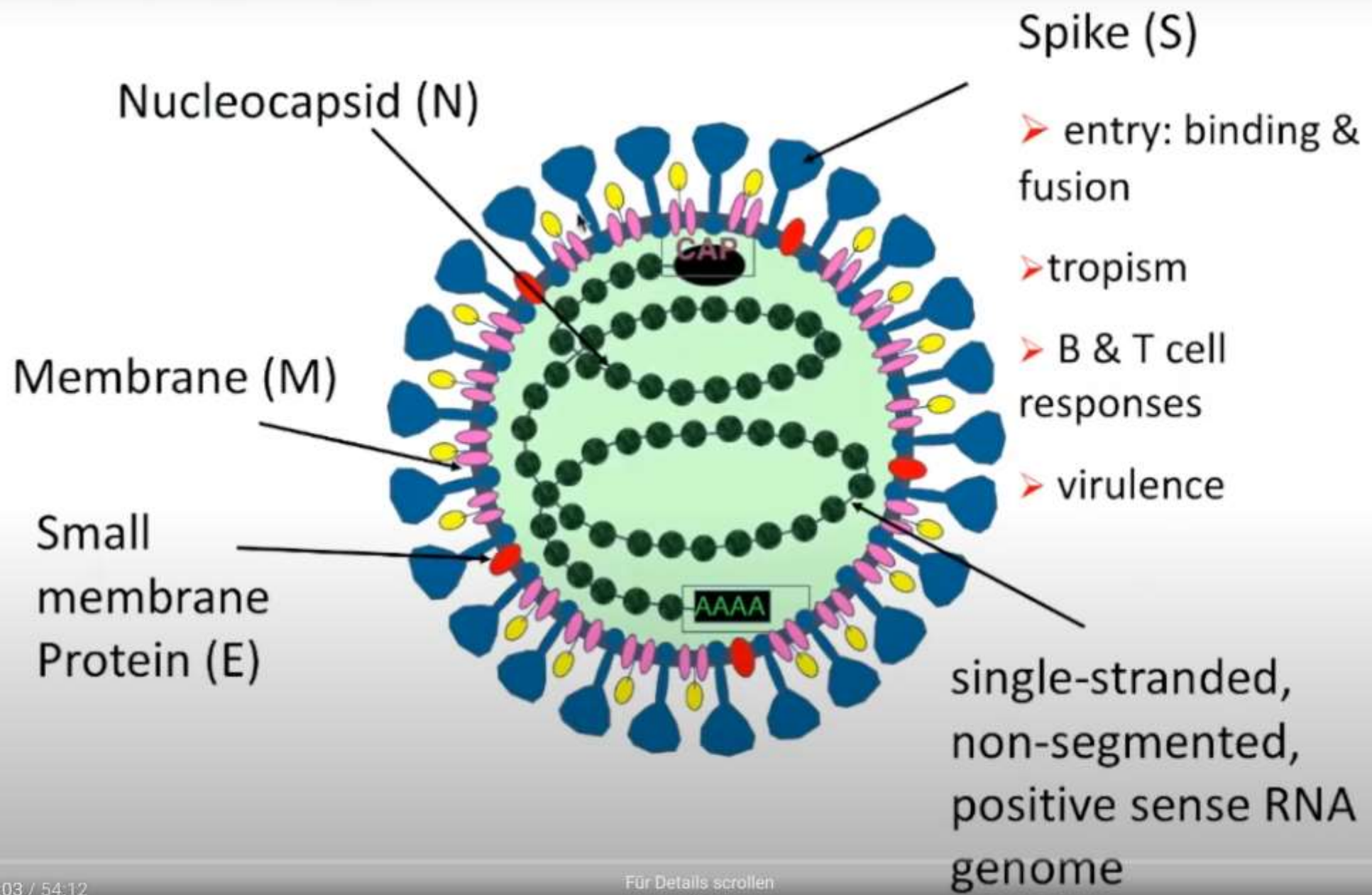


Torovirus

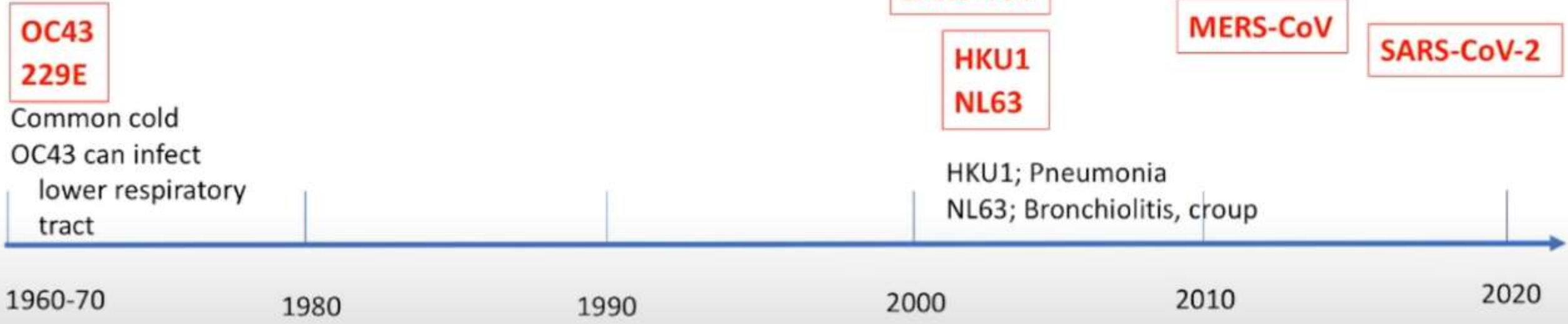


- Nidoviruses are named for the nested subgenomic mRNAs generated during infection
- Enveloped viruses 100-150nm
- Single stranded positive sense RNA genomes

# Coronavirus virion



# Coronavirus Timeline



MHV model  
Animal viruses, vaccines  
Human cold CoVs

Pathogenic human coronaviruses  
SARS-CoV, MERS-CoV, SARS-CoV-2  
Severe respiratory disease  
coronavirus disease-2019 or COVID-19

Press Esc to exit full screen

# SARS-CoV-2 interspecies transmission



Bat



Intermediate species  
Malayan pangolin ???



Human  
↓  
Human to human spread

428,950  
infections

19,152  
deaths



(3.25.20)

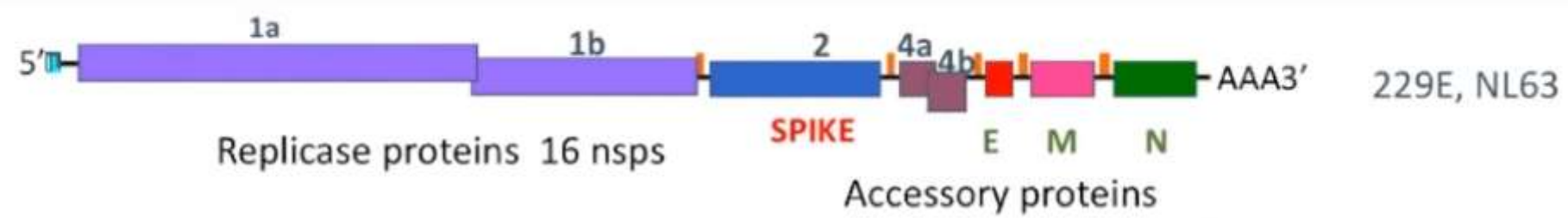
8:48 / 54:12

Für Details scrollen

# Human coronaviruses genome structure

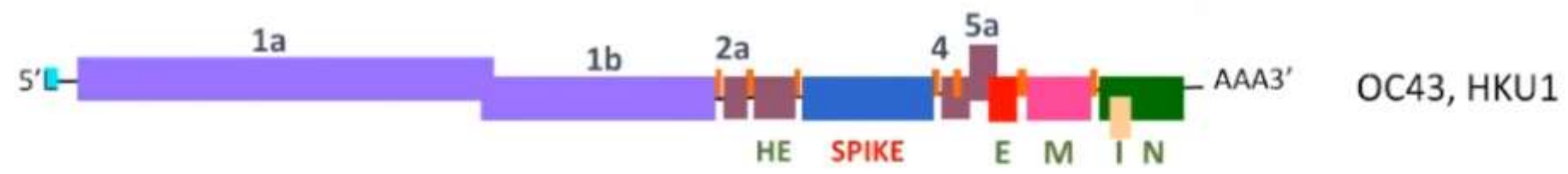
## Alphacoronaviruses

Duvinacovirus  
Setracovirus



## Betacoronaviruses

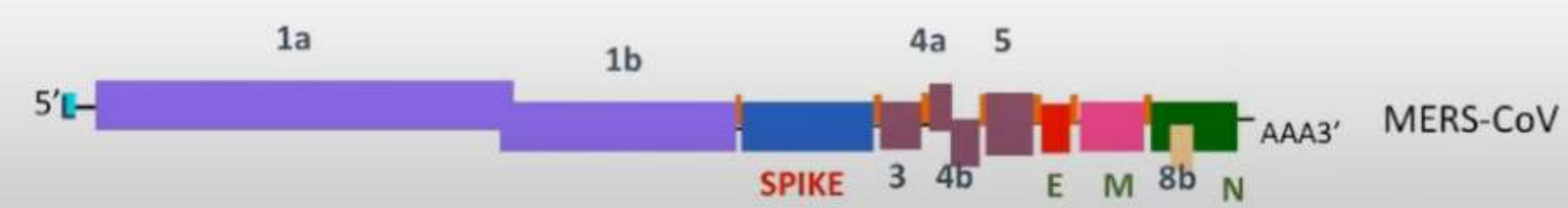
Lineage a,  
Embecovirus



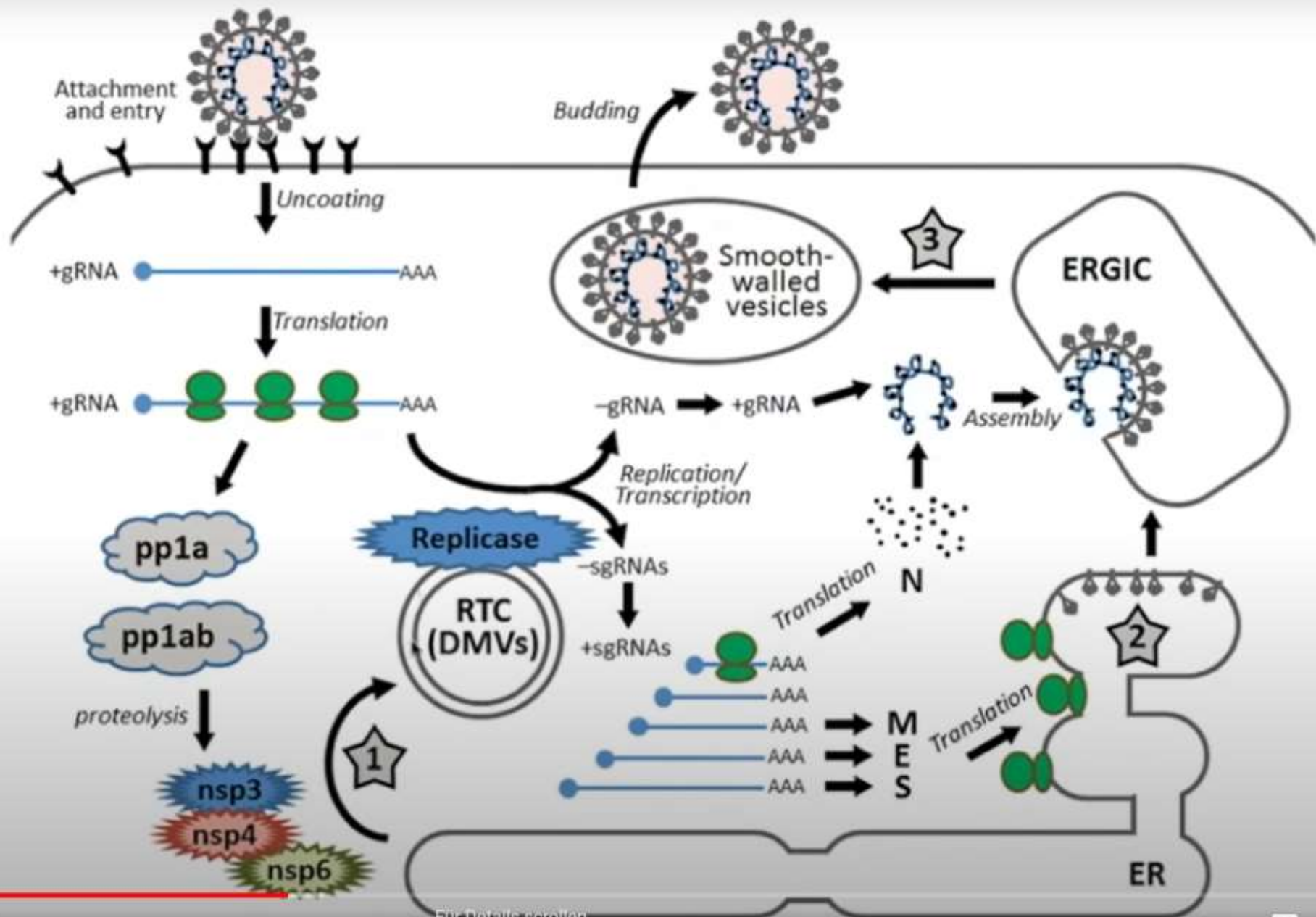
Lineage b,  
Sarbecovirus



Lineage c,  
Embecovirus



# Coronavirus Replication cycle



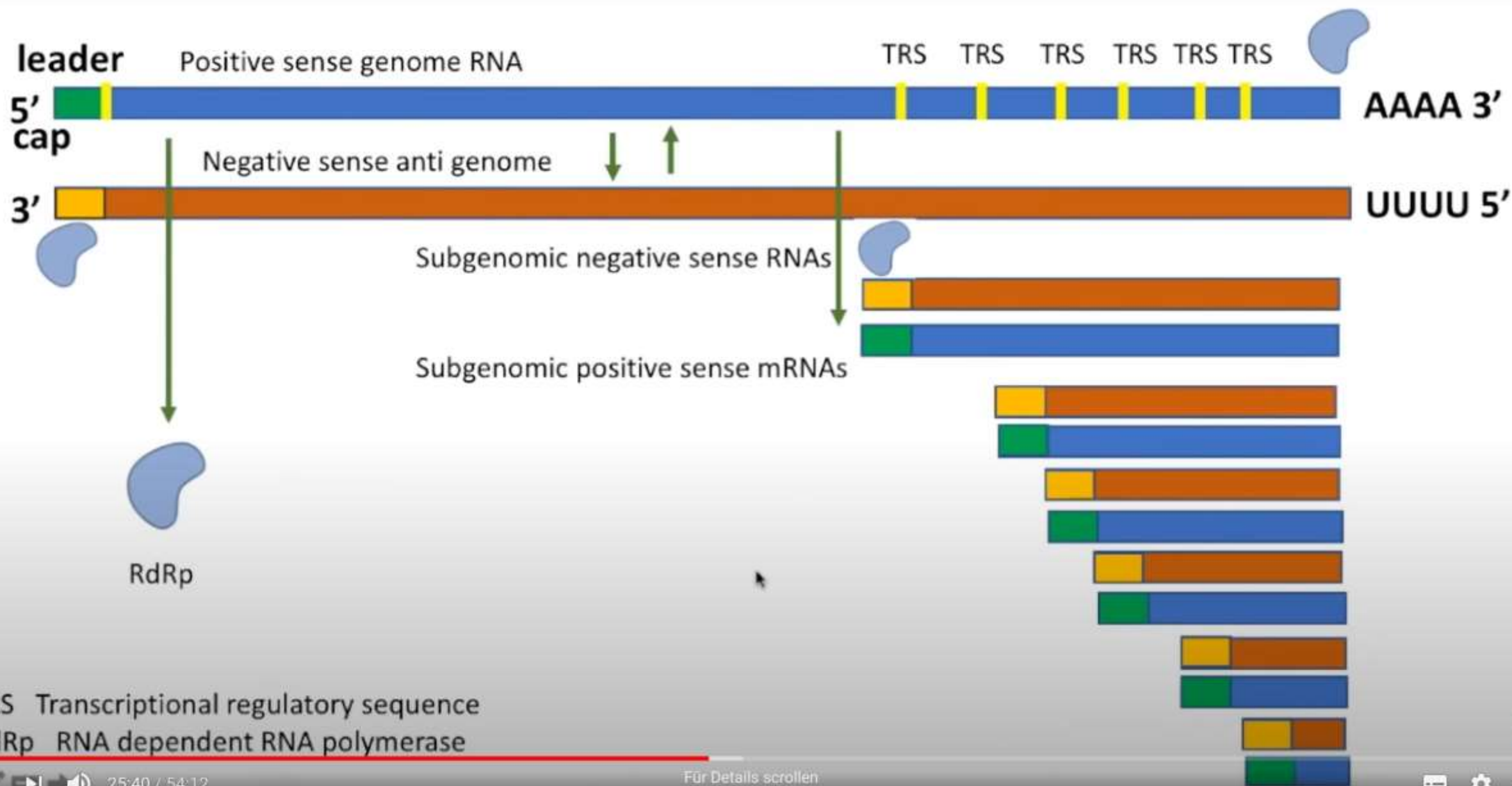
Fung and Liu

Front. Microbiol., 2014

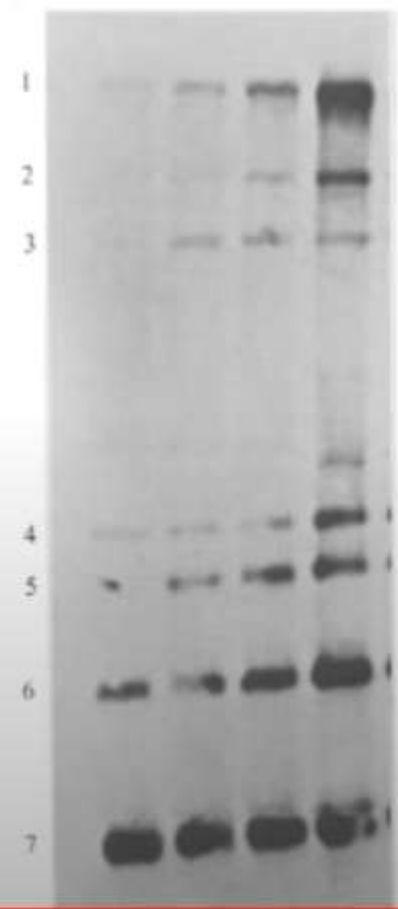
20:25 / 54:12

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# Transcription of coronavirus mRNAs



# RT-qPCR detection of coronavirus RNA

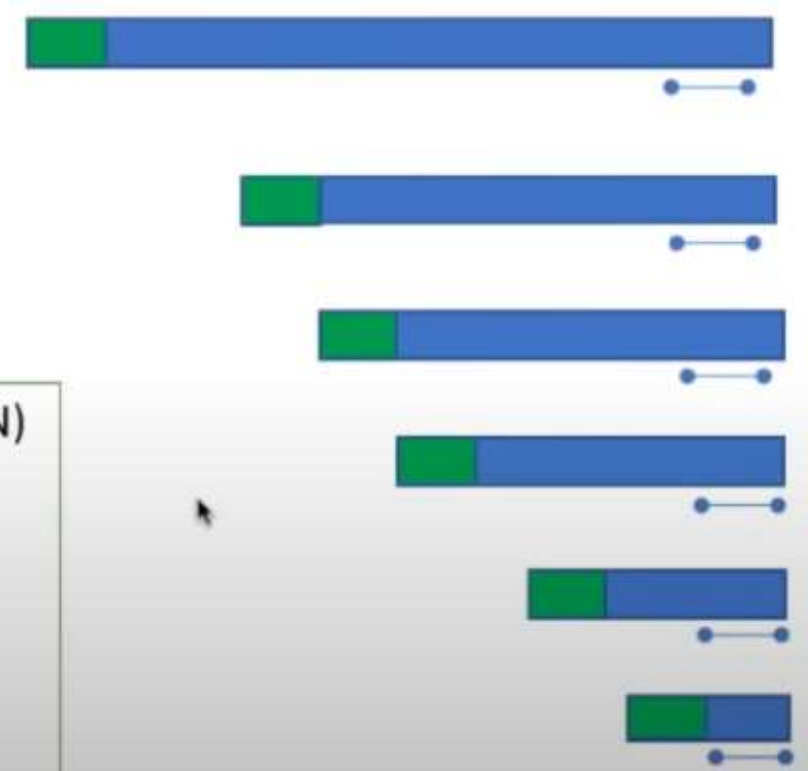


genome

N mRNA

qPCR ORF 1b RdRp primers  
Genome only

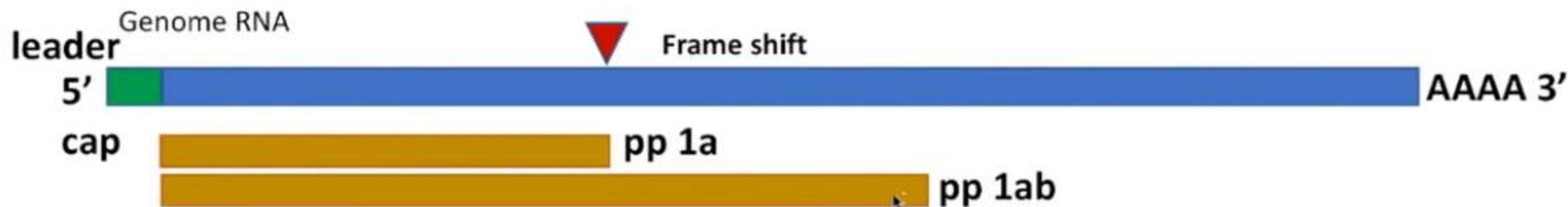
qPCR Nucleocapsid (N) gene primers  
Genome and all mRNAs  
Replicating virus



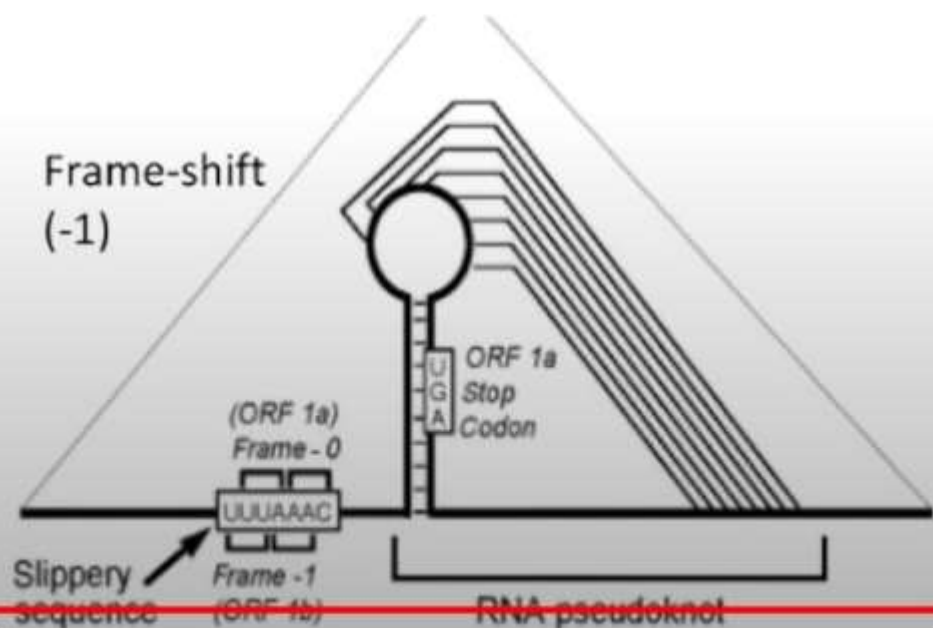
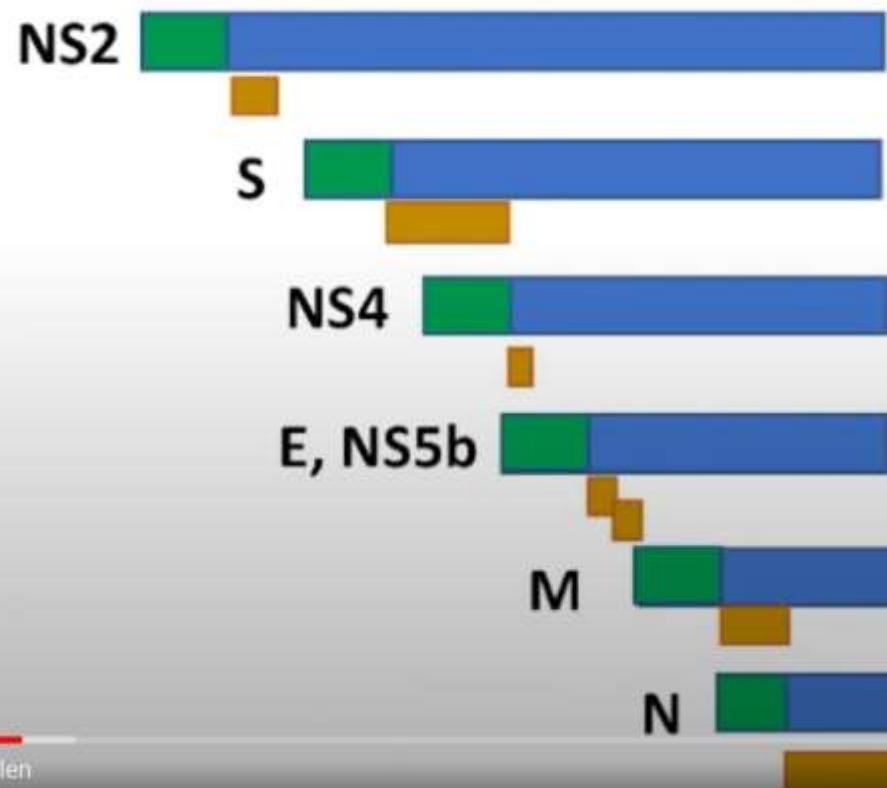
Murine coronavirus



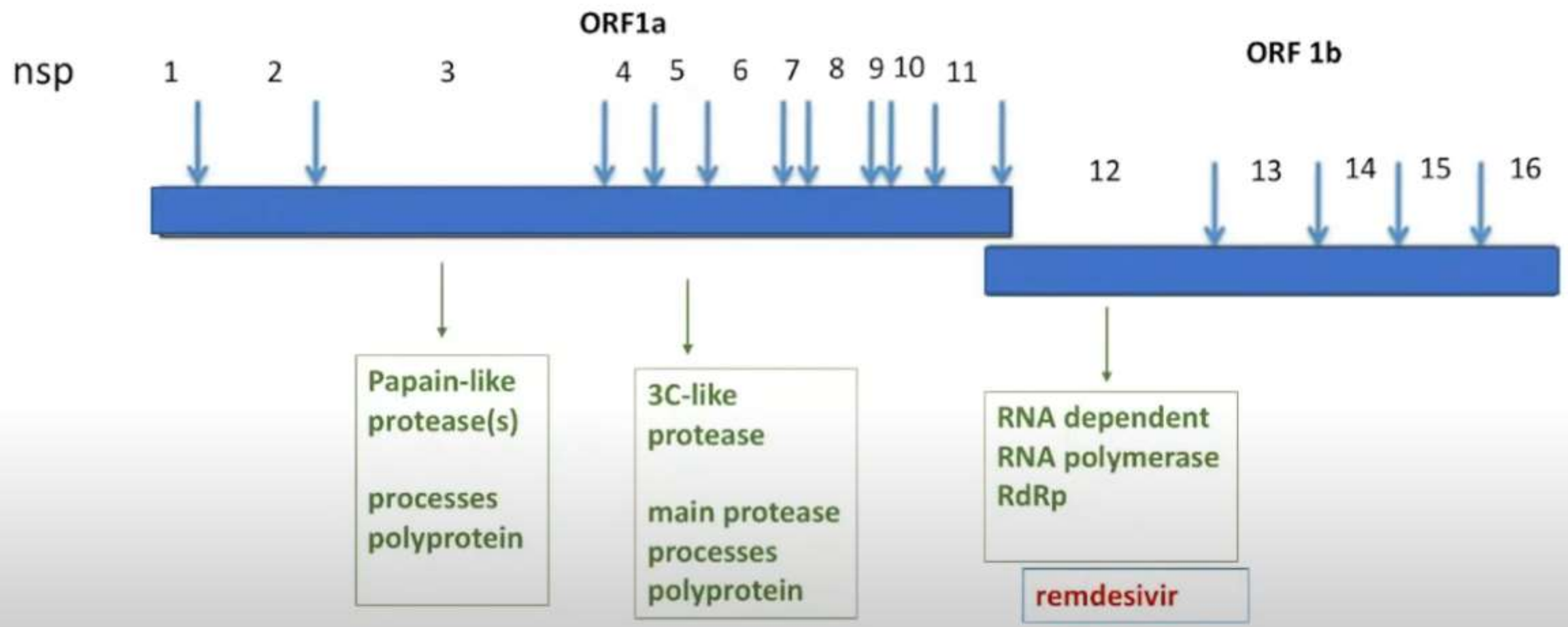
# Translation of coronavirus proteins



## Replicase (16 proteins)

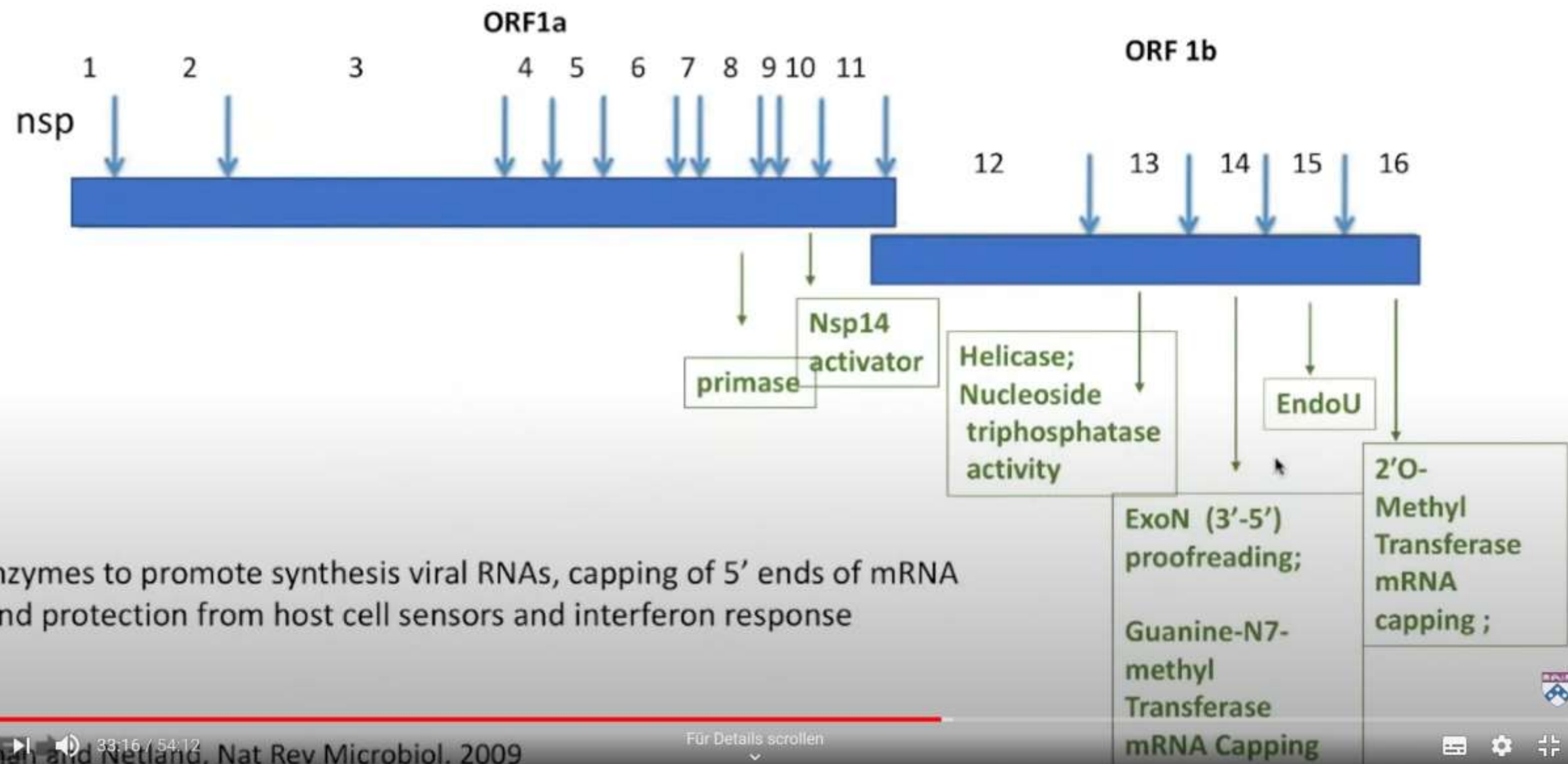


# Coronavirus replicase locus encodes sixteen conserved nonstructural (nsp) proteins



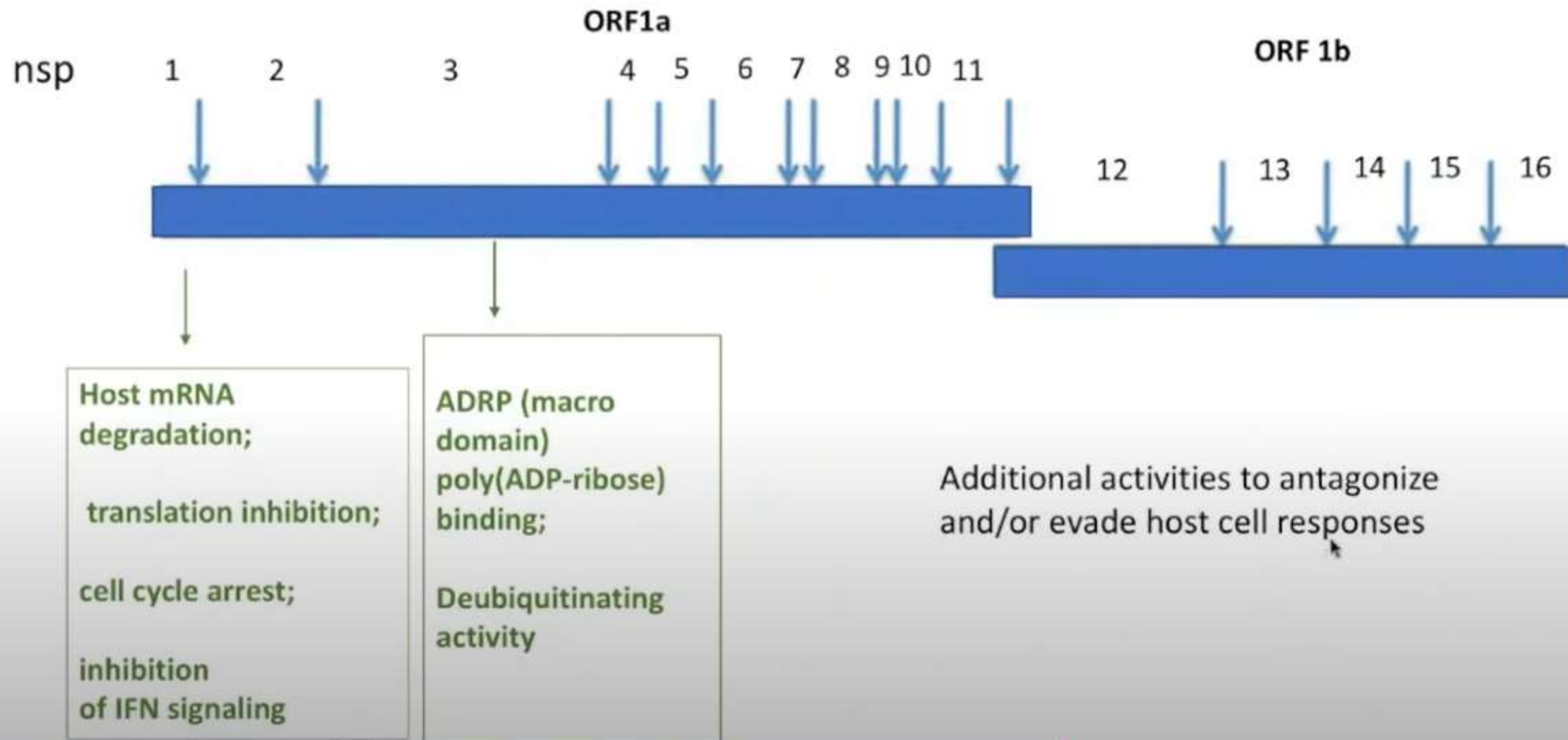
Proteases: Process replicase proteins  
RdRp: Replicate genome and transcribe mRNAs

# Coronavirus replicase locus encodes sixteen conserved nonstructural (nsp) proteins

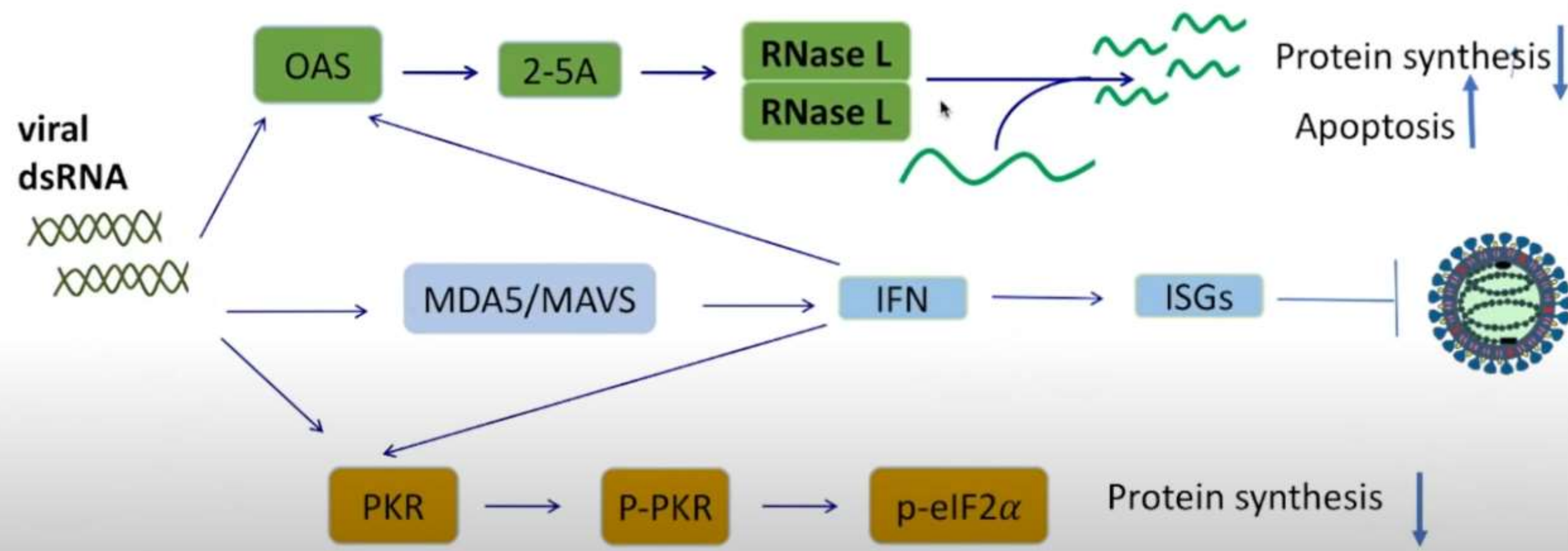


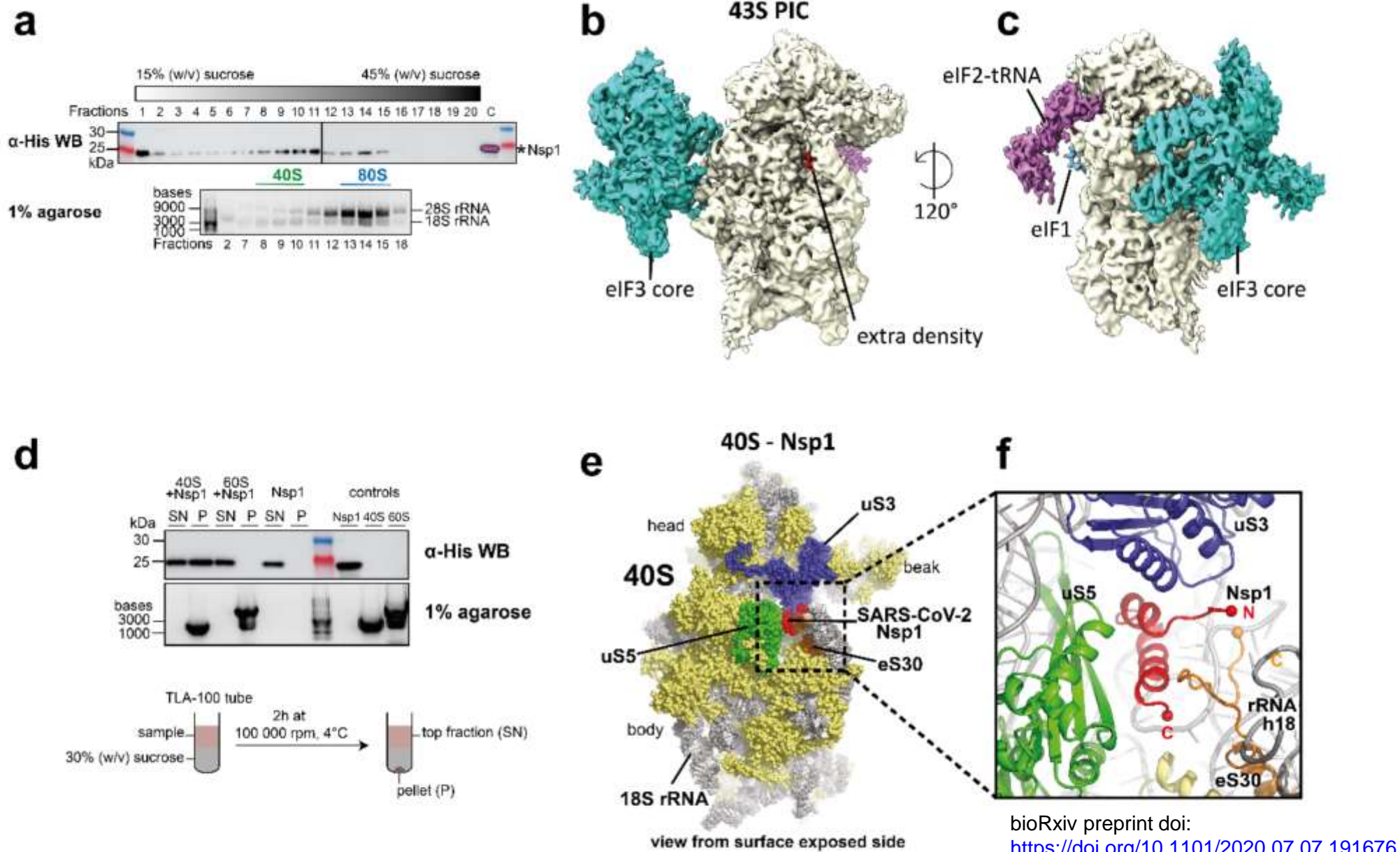
Enzymes to promote synthesis viral RNAs, capping of 5' ends of mRNA and protection from host cell sensors and interferon response

# Coronavirus replicase locus encodes sixteen conserved nonstructural (nsp) proteins

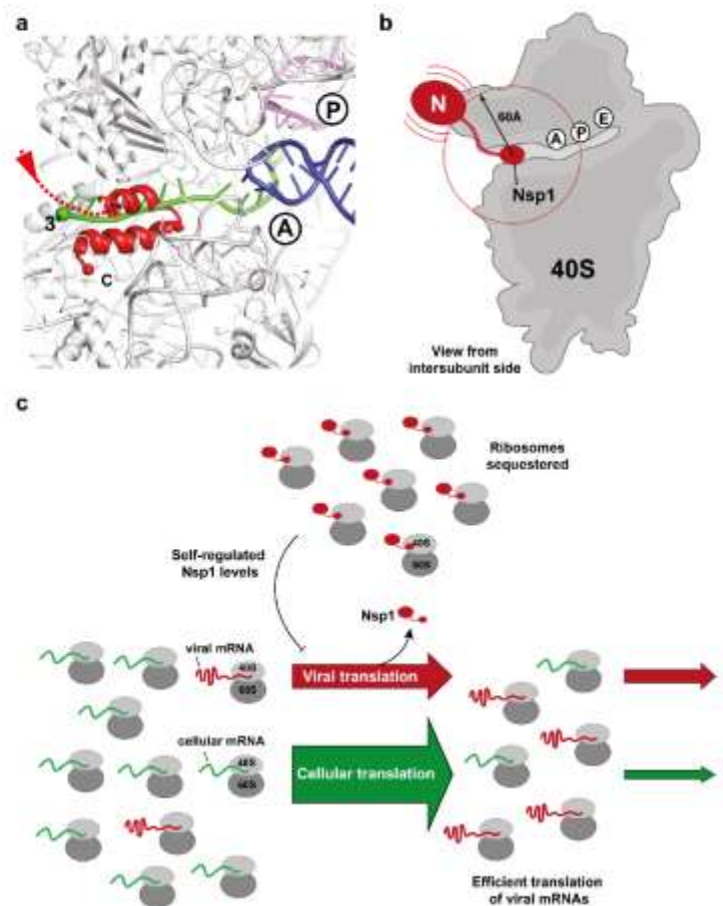


# dsRNA activated antiviral pathways





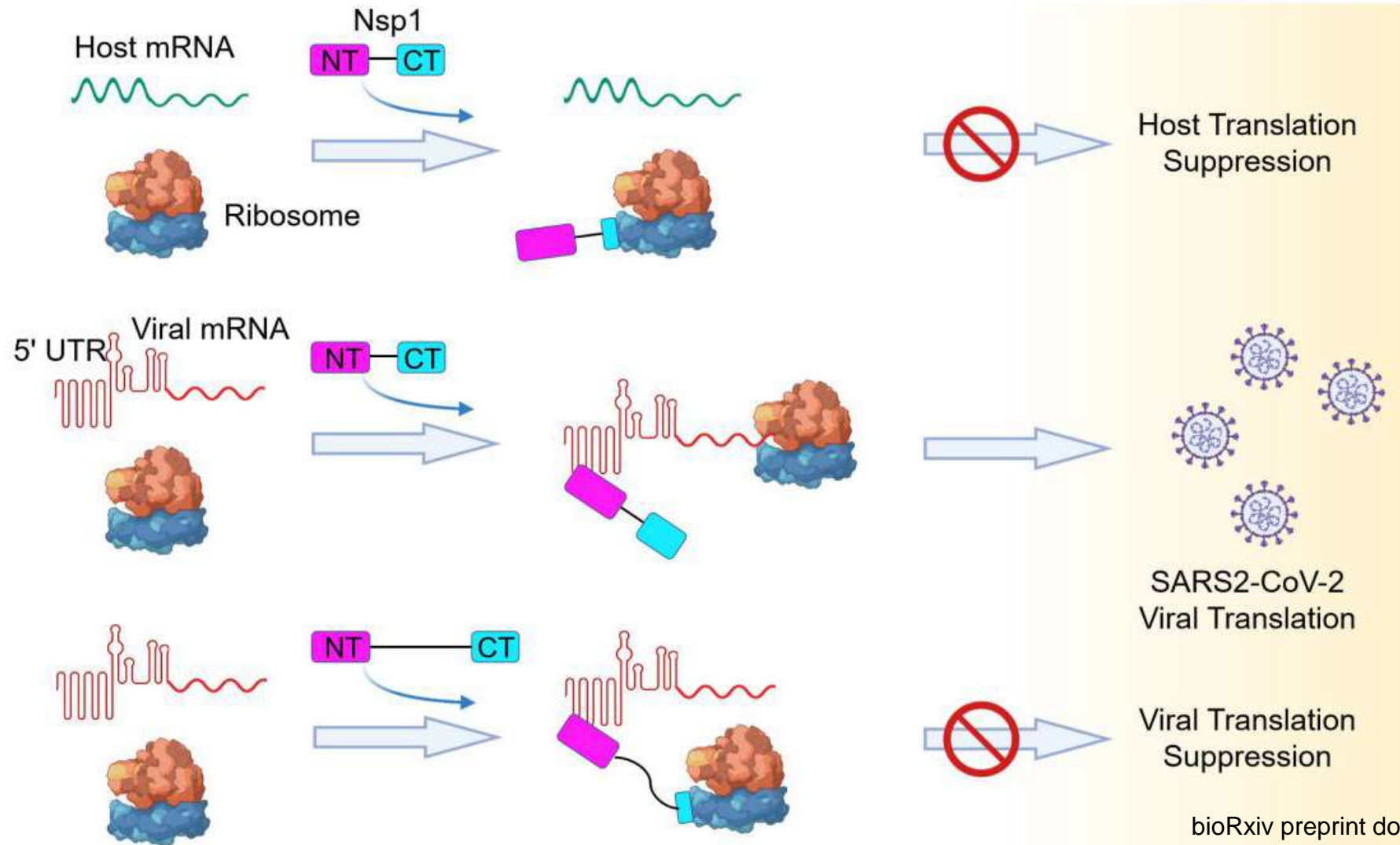
**Figure 1: Structures of ribosomal complexes inhibited by SARS-CoV-2 Nsp1 solved by cryo-EM.**



**Figure 4: Binding of C-terminal domain of SARS-CoV-2 Nsp1 to ribosomal mRNA channel prevents classical mRNA binding by steric hindrance.**

**(a)** Superposition of canonically bound mRNA (green), A- (blue) and P-site (purple) tRNAs (pdb 6HCJ) reveals that Nsp1 (red) prevents classical binding of the mRNA at the entry site due to blockage. **(b)** Nsp1 binds via its C-terminus in proximity of the 40S mRNA entry site. Due to the flexible linker, the N-terminal domain can sample an area of ~60 Å around its attachment point (circle). **(c)** Model for translation inhibition by Nsp1. Upon viral infection and translation of viral genomic mRNA, Nsp1 acts as a translation inhibitor reducing the pool of ribosomes that can engage in translation. Under such ribosome-limiting conditions, viral mRNAs are translated with high efficiency.

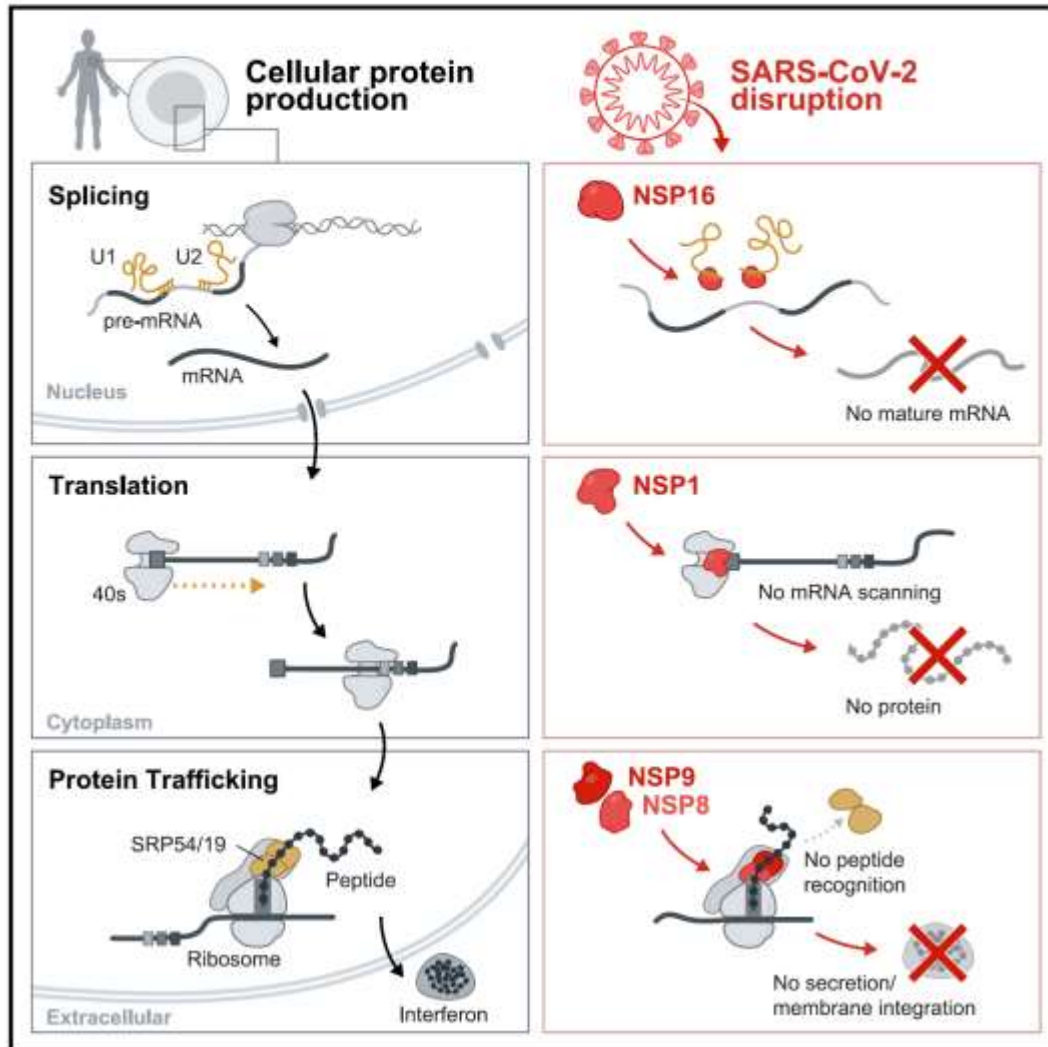
# Model of a Bipartite Mechanism for Nsp1-Mediated Translation Inhibition and Evasion by SARS-CoV-2 5' UTR





# SARS-CoV-2 Disrupts Splicing, Translation, and Protein Trafficking to Suppress Host Defenses

## Graphical Abstract



## Authors

Abhik K. Banerjee, Mario R. Blanco, Emily A. Bruce, ..., Jason W. Botten, Devdoot Majumdar, Mitchell Guttman

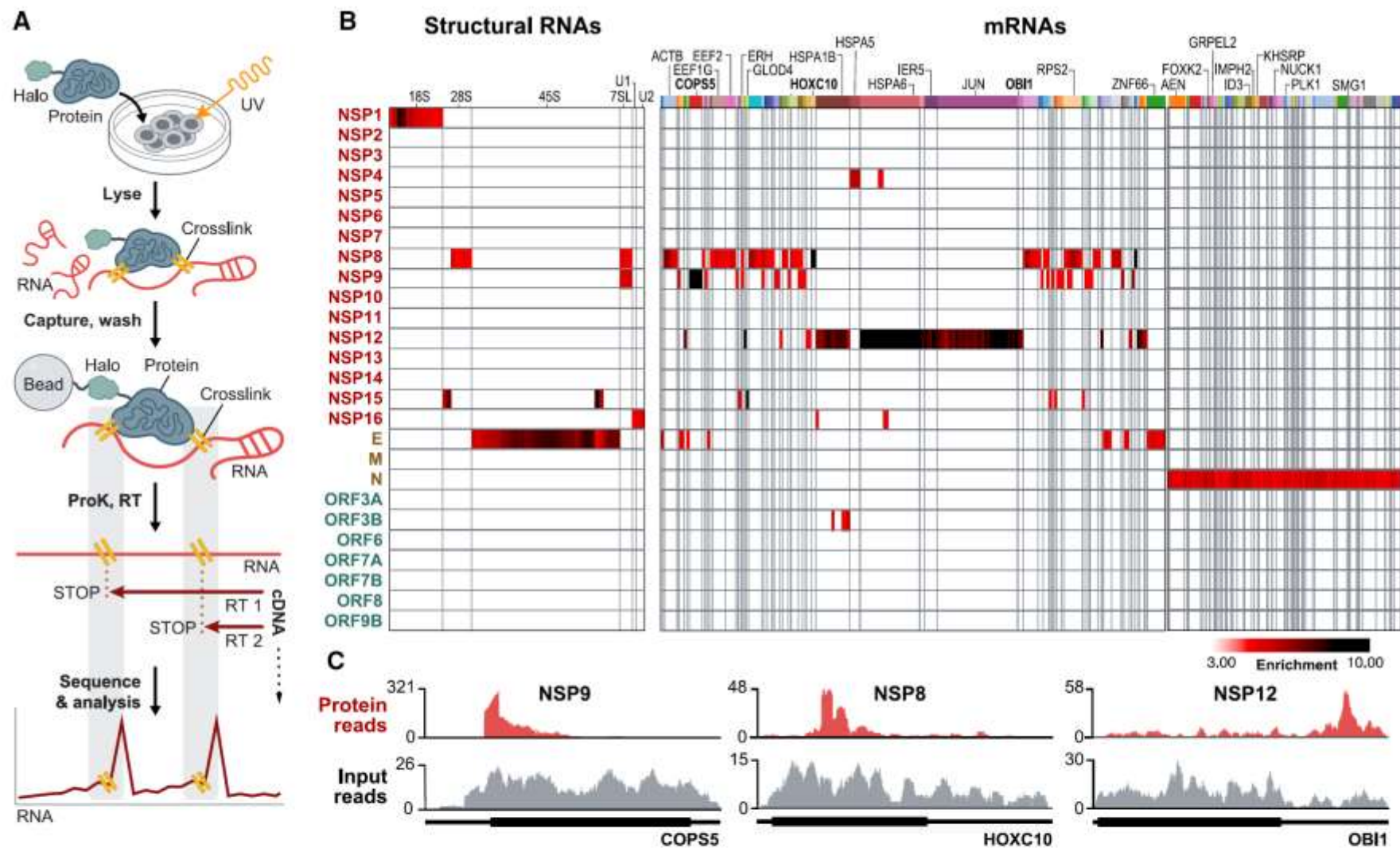
## Correspondence

dev.Majumdar@med.uvm.edu (D.M.),  
mguttman@caltech.edu (M.G.)

## In Brief

SARS-CoV-2 proteins directly engage host RNAs to dysregulate essential steps of protein production and suppress the interferon response.

Banerjee et al., 2020, Cell 183, 1–15  
November 25, 2020 © 2020 Published by Elsevier Inc.  
<https://doi.org/10.1016/j.cell.2020.10.004>



**Figure 1. Global RNA Binding Maps of SARS-CoV-2 Proteins**

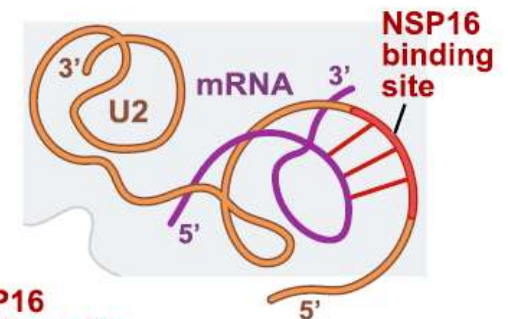
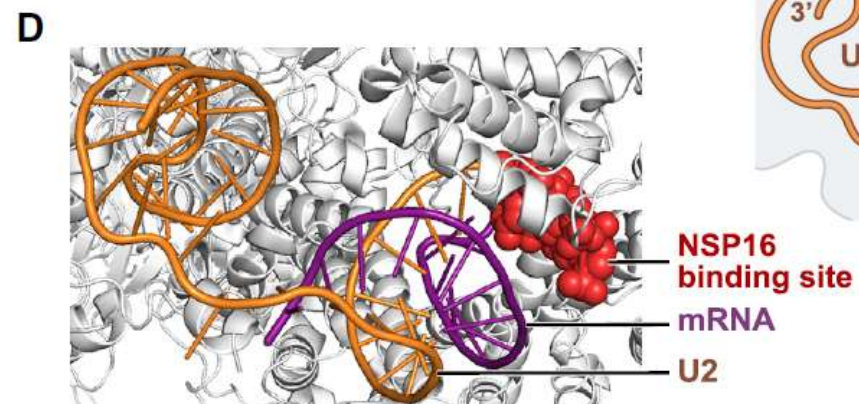
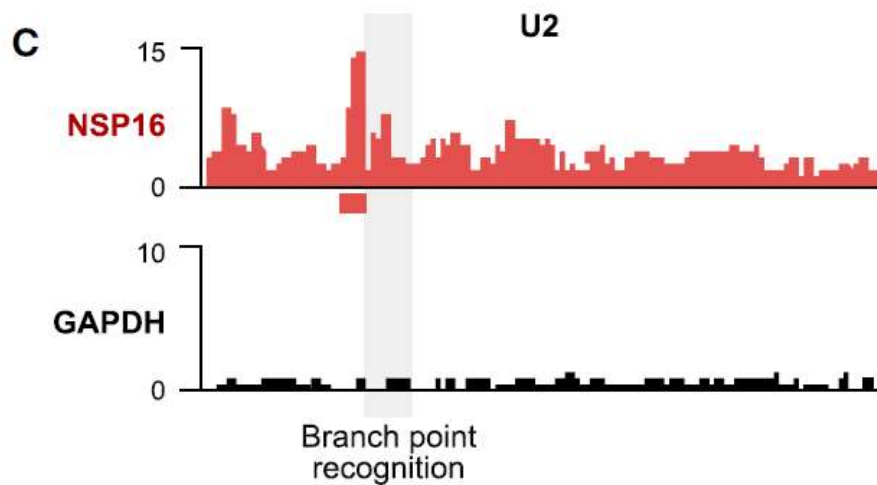
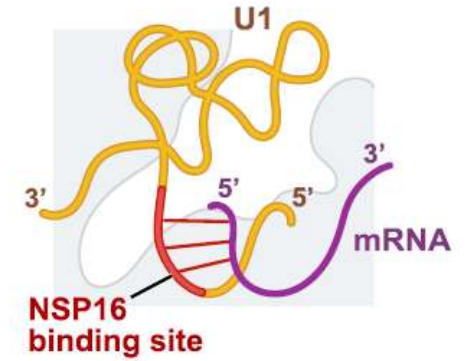
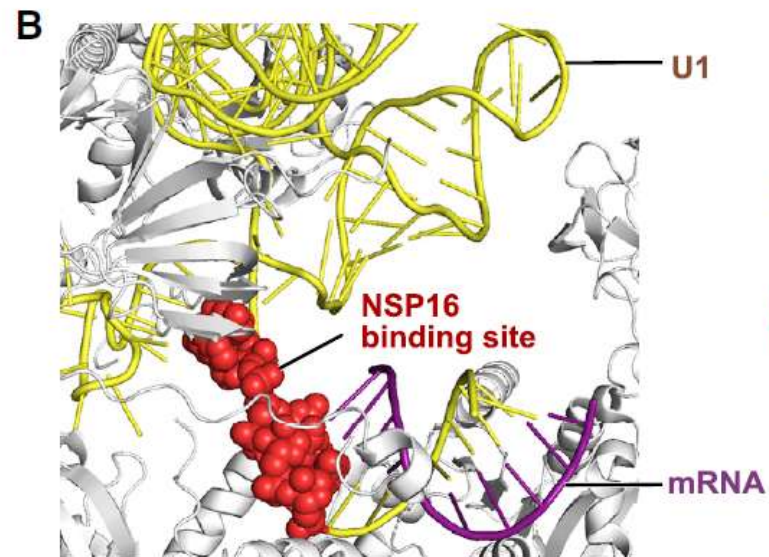
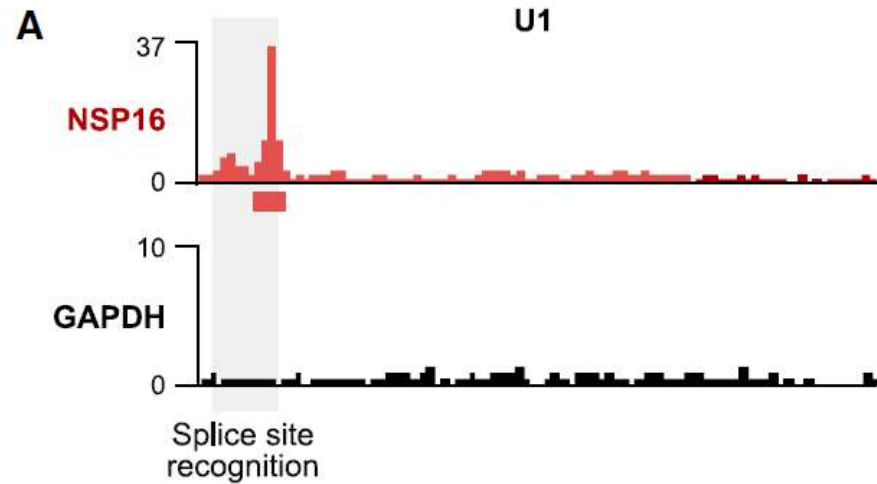
(A) Schematic of our approach.

(B) Enrichment heatmap of each SARS-CoV-2 protein (rows) by significantly enriched 100-nt RNA bins (columns;  $p < 0.001$  and enrichment  $> 3$ -fold; [STAR Methods](#)). Shared colored bars indicate multiple bins within the same mRNA. For spacing reasons, the 82 mRNAs bound by N protein are displayed separately.

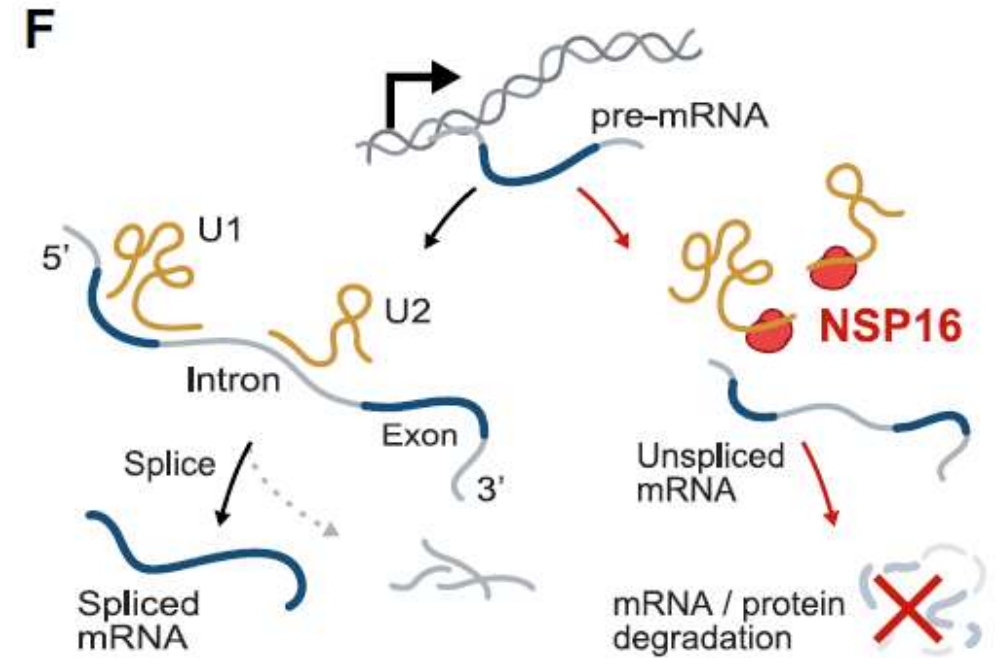
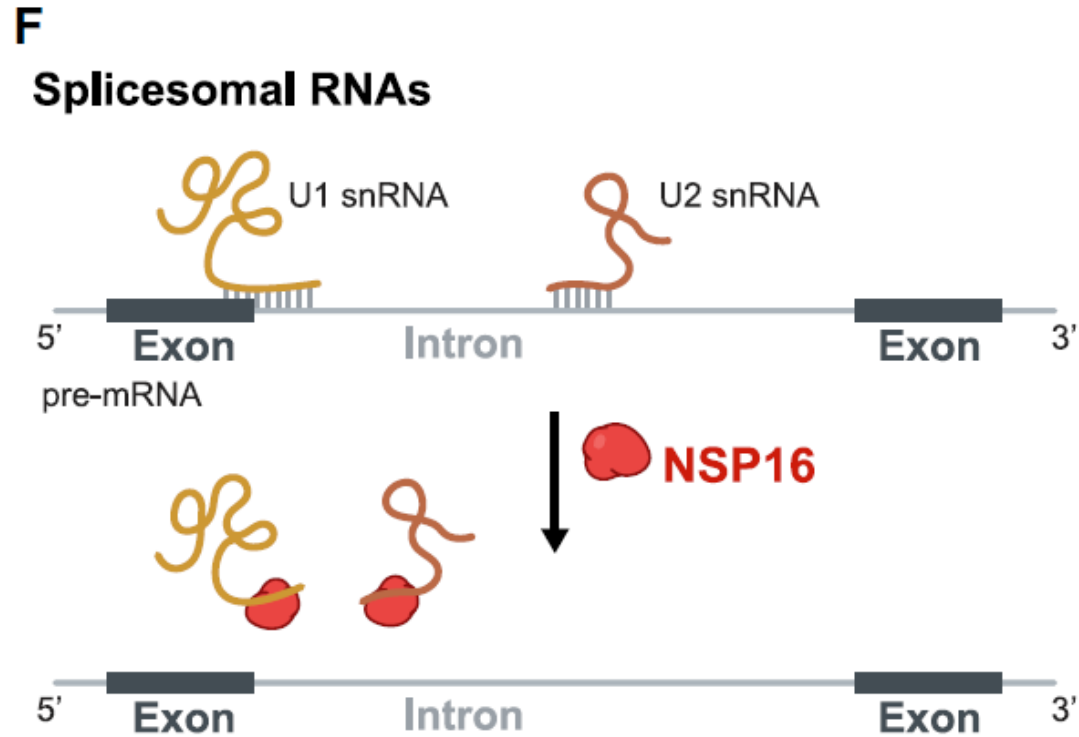
(C) Examples of sequencing reads over specific mRNAs for viral proteins (red) relative to input RNA coverage (gray) are shown. Coding regions (thick lines) and untranslated regions (thin lines) are shown for each mRNA.

See also [Table S1](#).

# NSP 16 binds U1 and U2 snRNA at their pre-mRNA recognition sites



# NSP 16 binds U1 and U2 snRNA at their pre-mRNA recognition sites



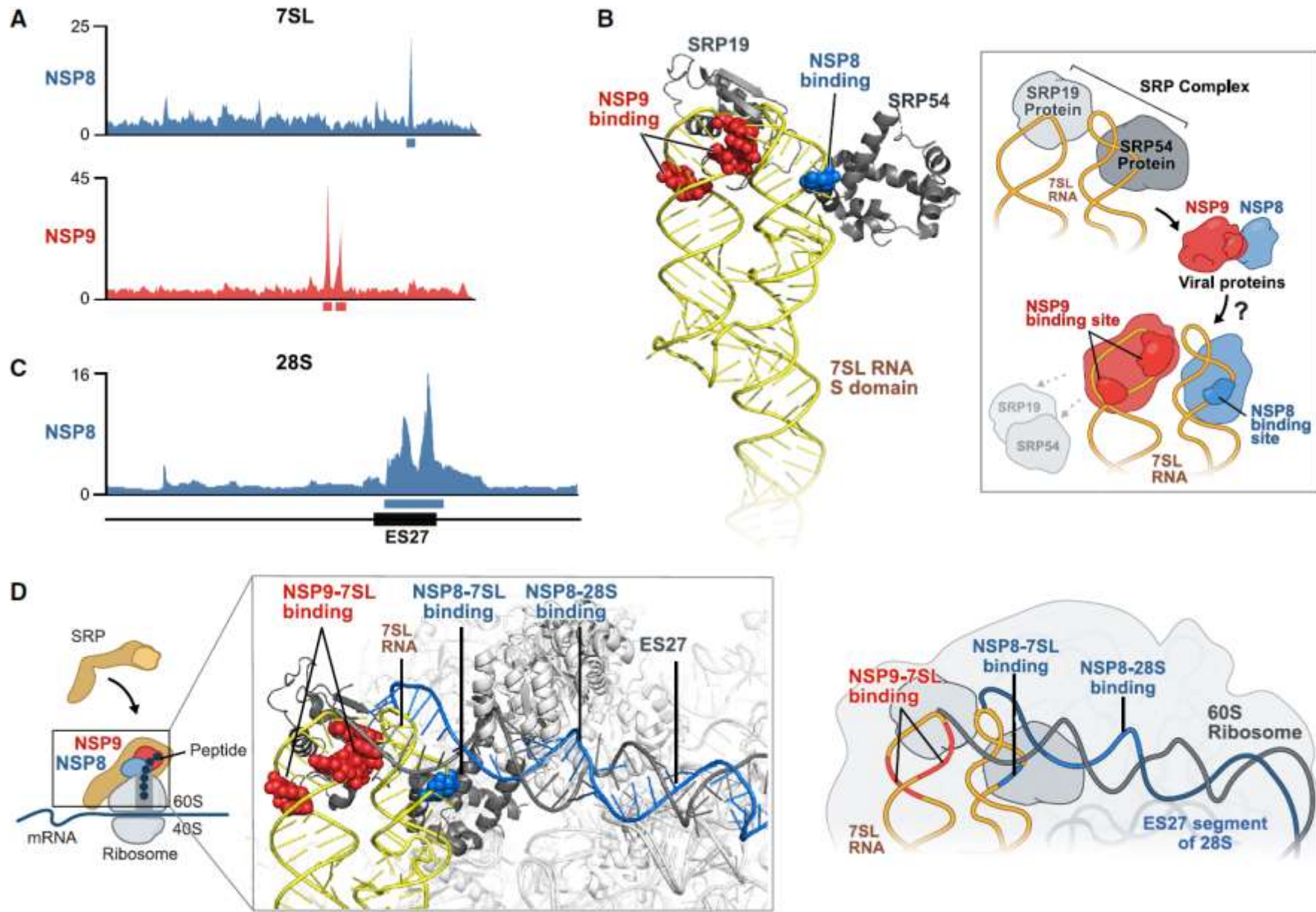


Figure 6. NSP8 and NSP9 Bind to 7SL RNA of the SRP

