- **RNA virus cycles**

Including viruses with:

single-stranded (+)RNA genomes,

Single stranded (-)RNA genomes (segmented and i non-segmented),

dsRNA genomes

Viruses with reverse transcriptase in the cycle will be discussed separately.

(-) RNA – viruses:

• all are enveloped with helical nucleocapsids

Order *Mononegavirales* (non-segmented genome)

Paramyxoviridae (mumps, measles, RSV)

Rhabdoviridae (rabies virus, VSV)

Filoviridae (Ebola, Marburg, etc.)

Bornaviridae (Borna – fatal neurological disease of mammals)

Other viral families:

Arenaviridae (2 segments, vertebrate hosts – LCMV, Lassa virus, all ambisense)

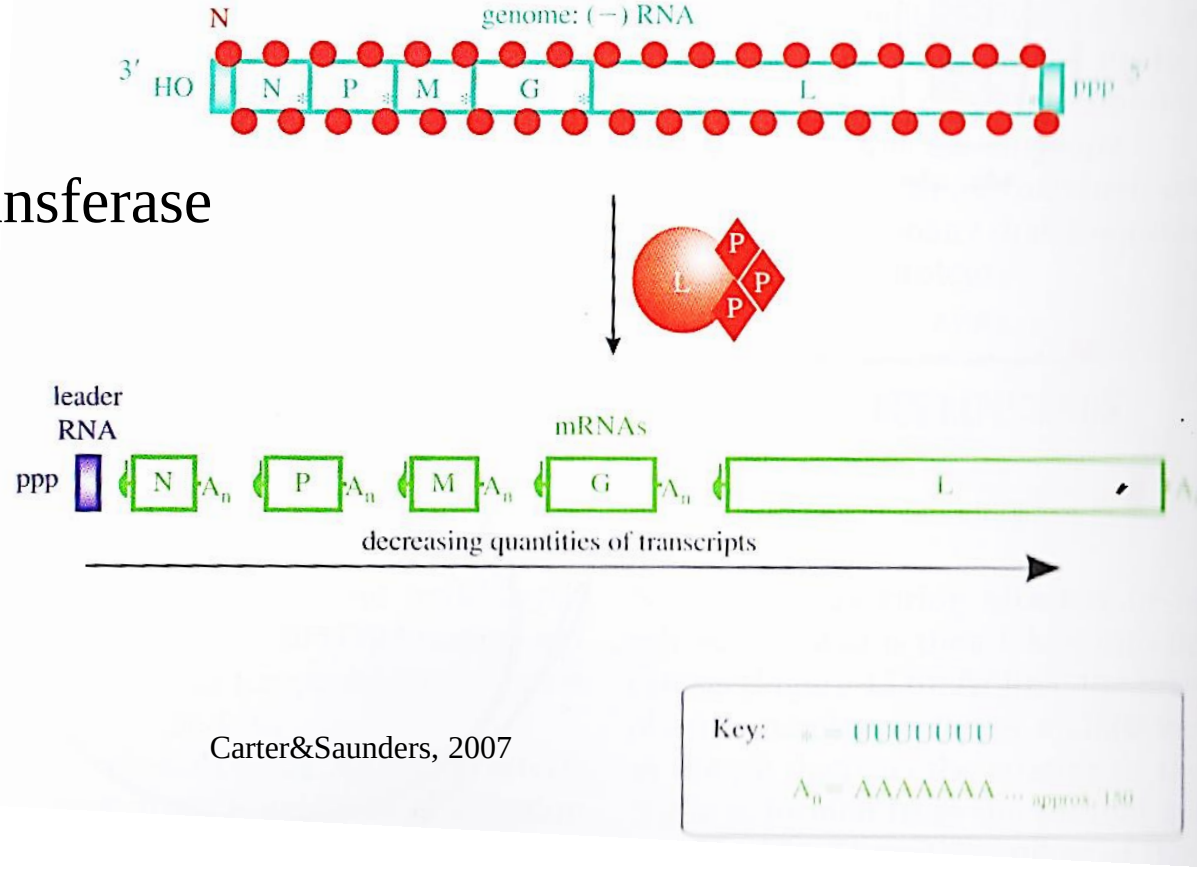
Bunyviridae (3 segments, hantaviruses, animal, plant viruses, some ambisense)

Orthomyxoviridae (influenza A, B – 8 segments, C, D – 7 segments)

Rhabdoviridae – wide host range (mammals, fish, insects, plants)

Many replicate in the cytoplasm, plant and insect viruses in the nucleus.
Vesicular stomatitis virus – VSV, important animal pathogen
Rabies virus –RV, unique transcription control

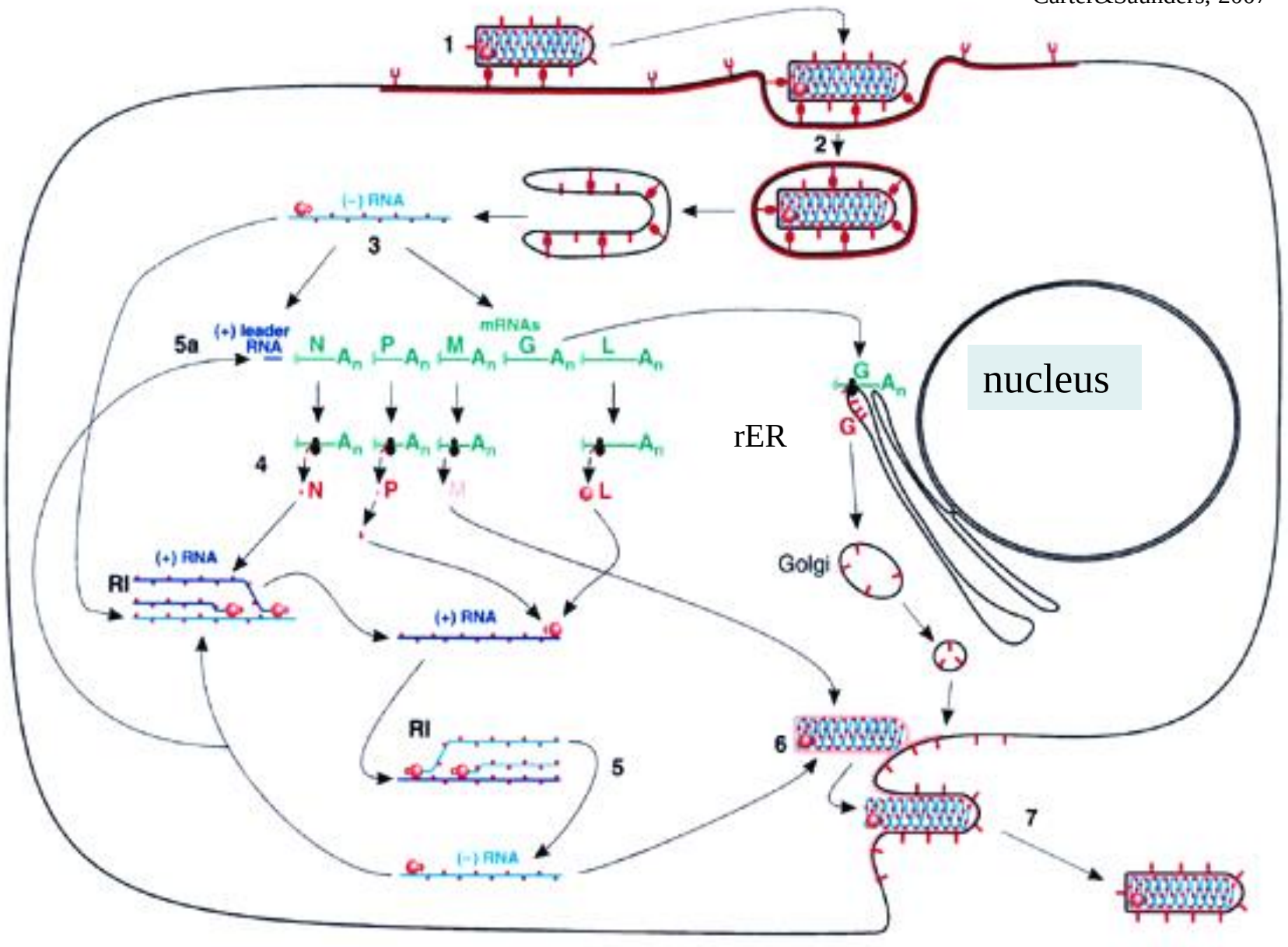
Protein L functions:
RdRp
polyribonukleotidyl-transferase
methyl-transferase
poliA-polymerase
kinase



Carter&Saunders, 2007

Rhabdovirus replication cycle

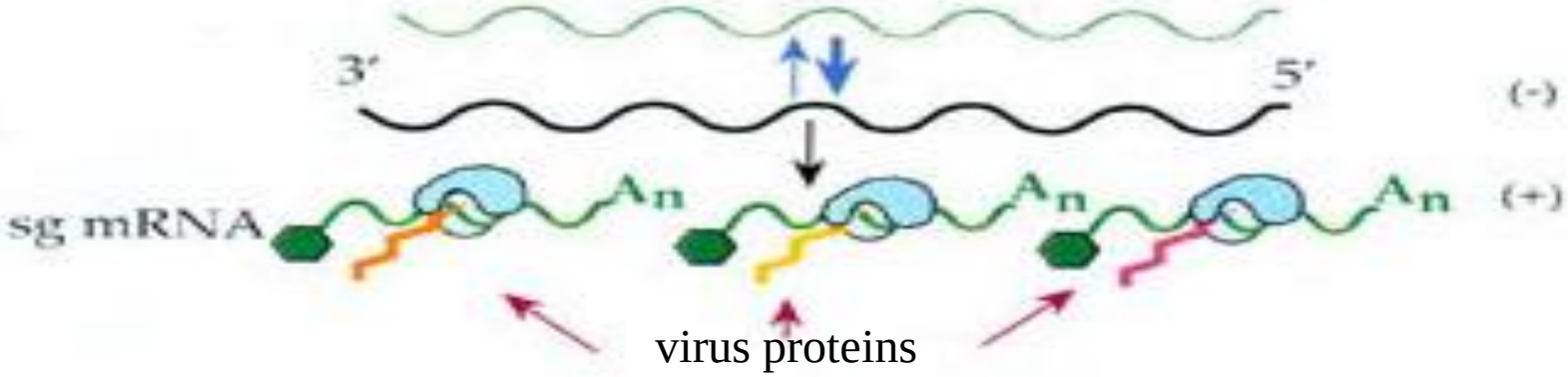
Carter&Saunders, 2007



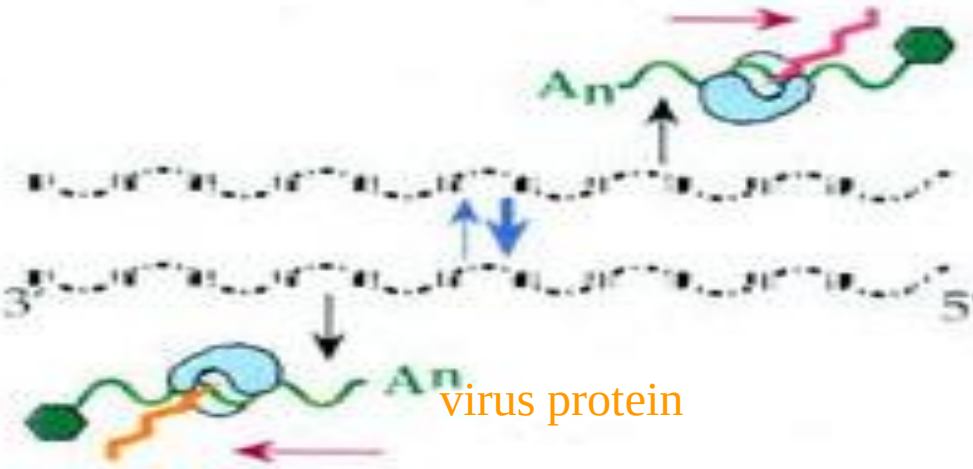
Ambisense genomes

(-)RNA virus transcription and translation strategies

Adapted from Strauss&Strauss, 2002



virus protein



"ambisense" -genome

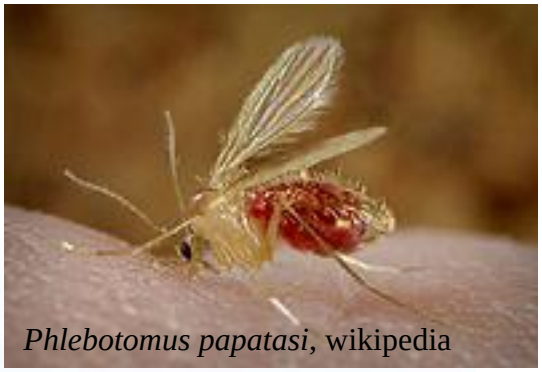
ribosome

replication

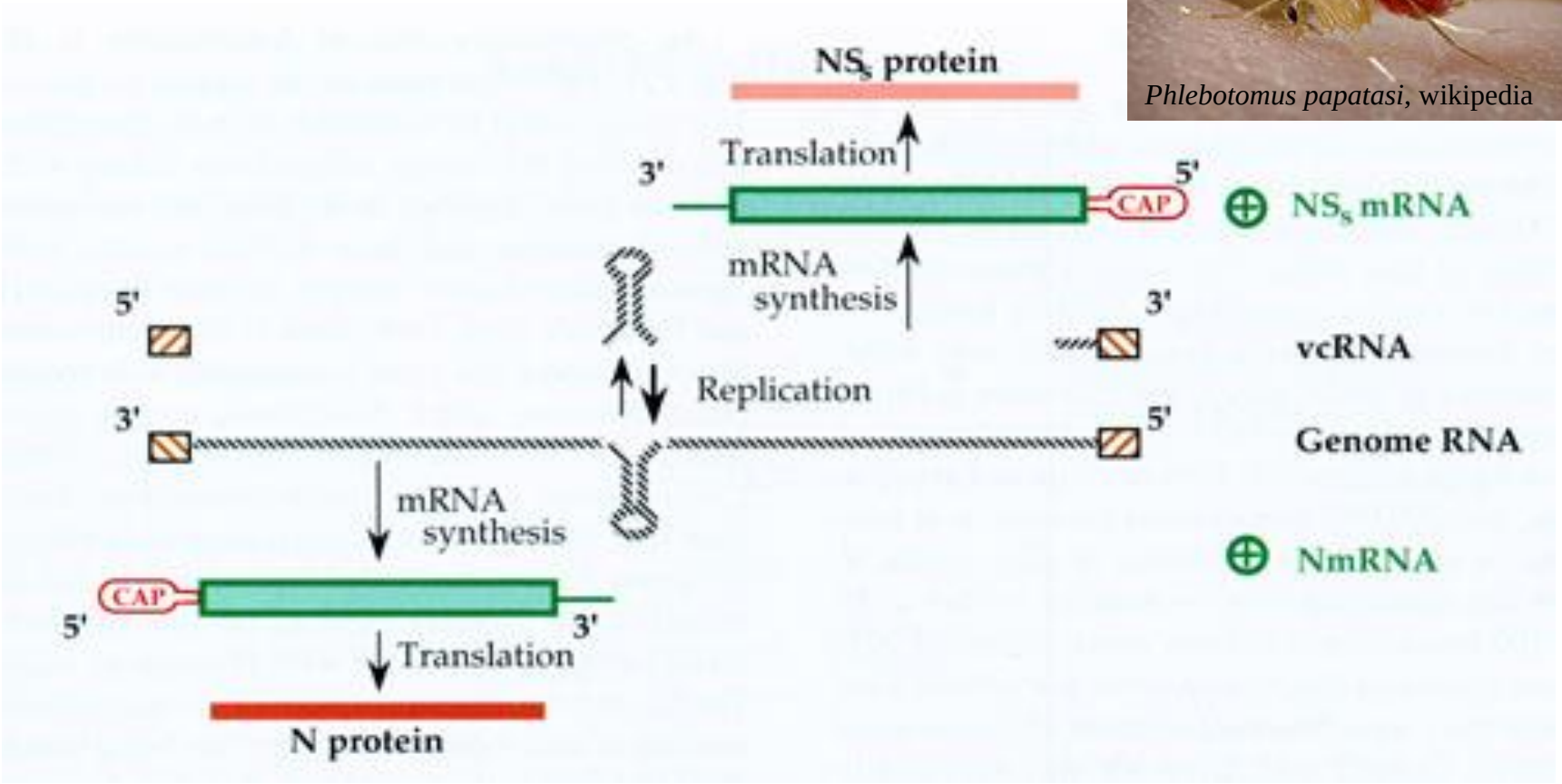
subgenomic mRNA synthesis

cap or VPg

Flebovirus (Rift Valley fever, pappatachi fever) *Bunyaviridae*



Phlebotomus papatasi, wikipedia



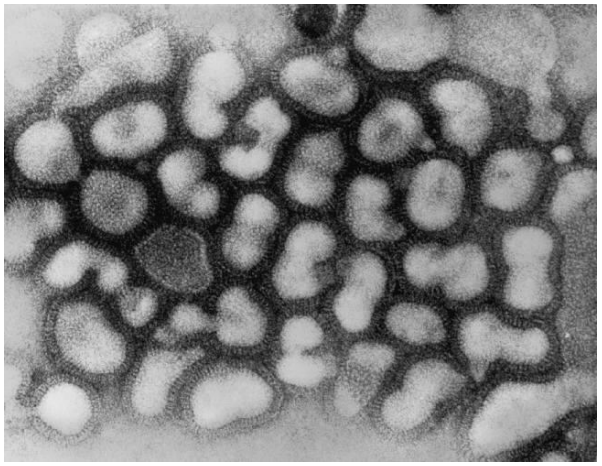
self complementary ends

Adapted from Strauss&Strauss, 2002

Avian Flu


AHH-CHOO!
Gary Varvel
THE INDIANAPOLIS STAR
©2005 CREATORS SYND.
—APOLOGIES TO WARNER BROS.

Flu virus (influenza, *Orthomyxoviridae*)



Four types of influenza:

A – IAV, pandemics, dangerous pathogen of humans, horses, pigs, poultry (“chicken plague”), isolated in 1933.

B – IBV, occasional epidemics, milder pathogen of humans, very young or very old patients are endangered, isolated in 1940.

C – ICV, mild disease, not epidemic, most of us infected as children, separate genus, isolated in 1947, pathogen of humans and pigs, genome with 7 segments.

D – IDV, isolated from pigs in 2011, bovine reservoir host, transmission to humans, small ruminants, no human diseases documented, 7 segments in the genome.

Su *et al.* 2017, Virulence 8(8): 1580–1591. doi: 10.1080/21505594.2017.1365216

IAV - genome segments (in size order) and functions of their transcripts:

PB2, PB1, PA

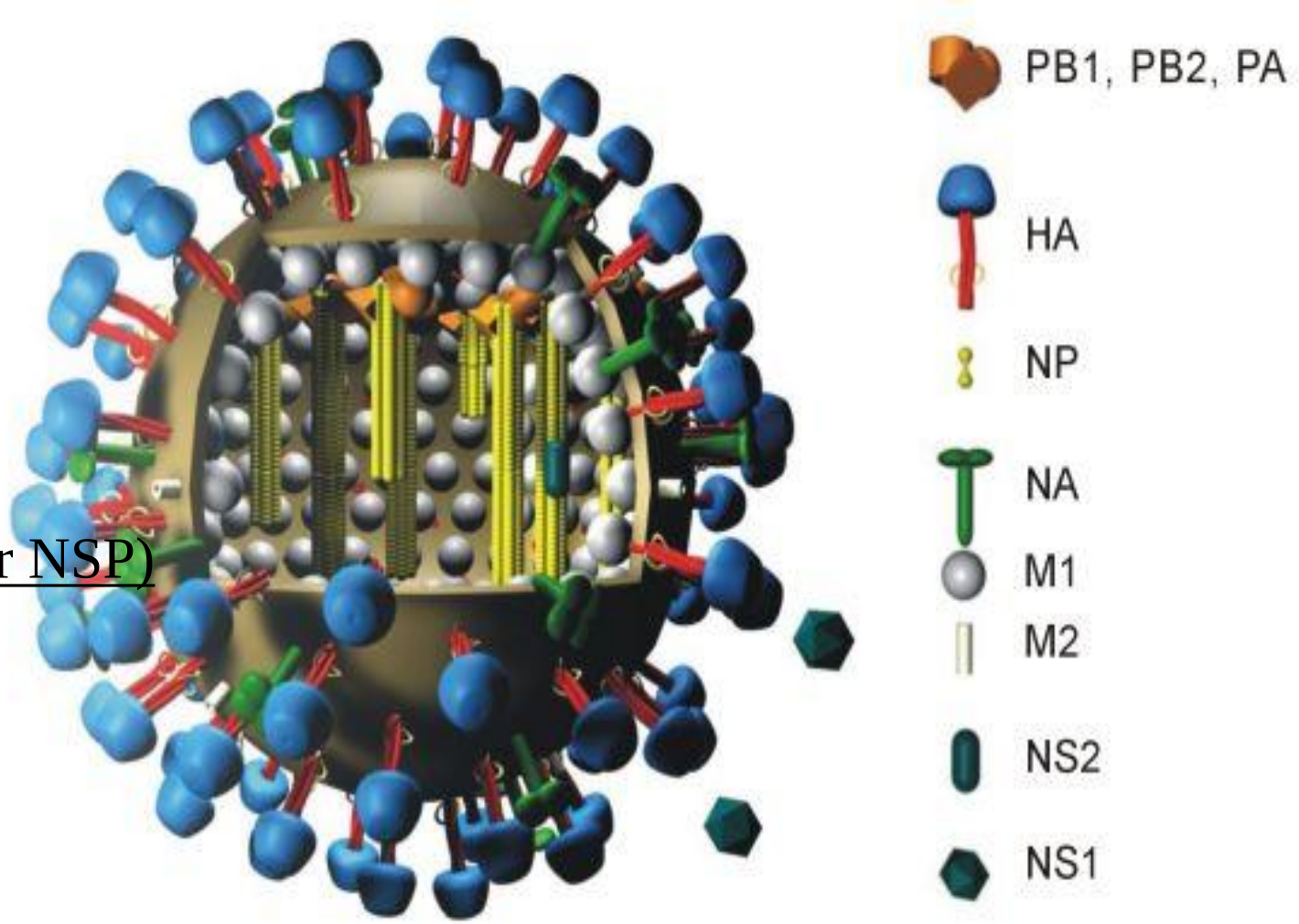
HA (trimer)

NP

NA (tetramer)

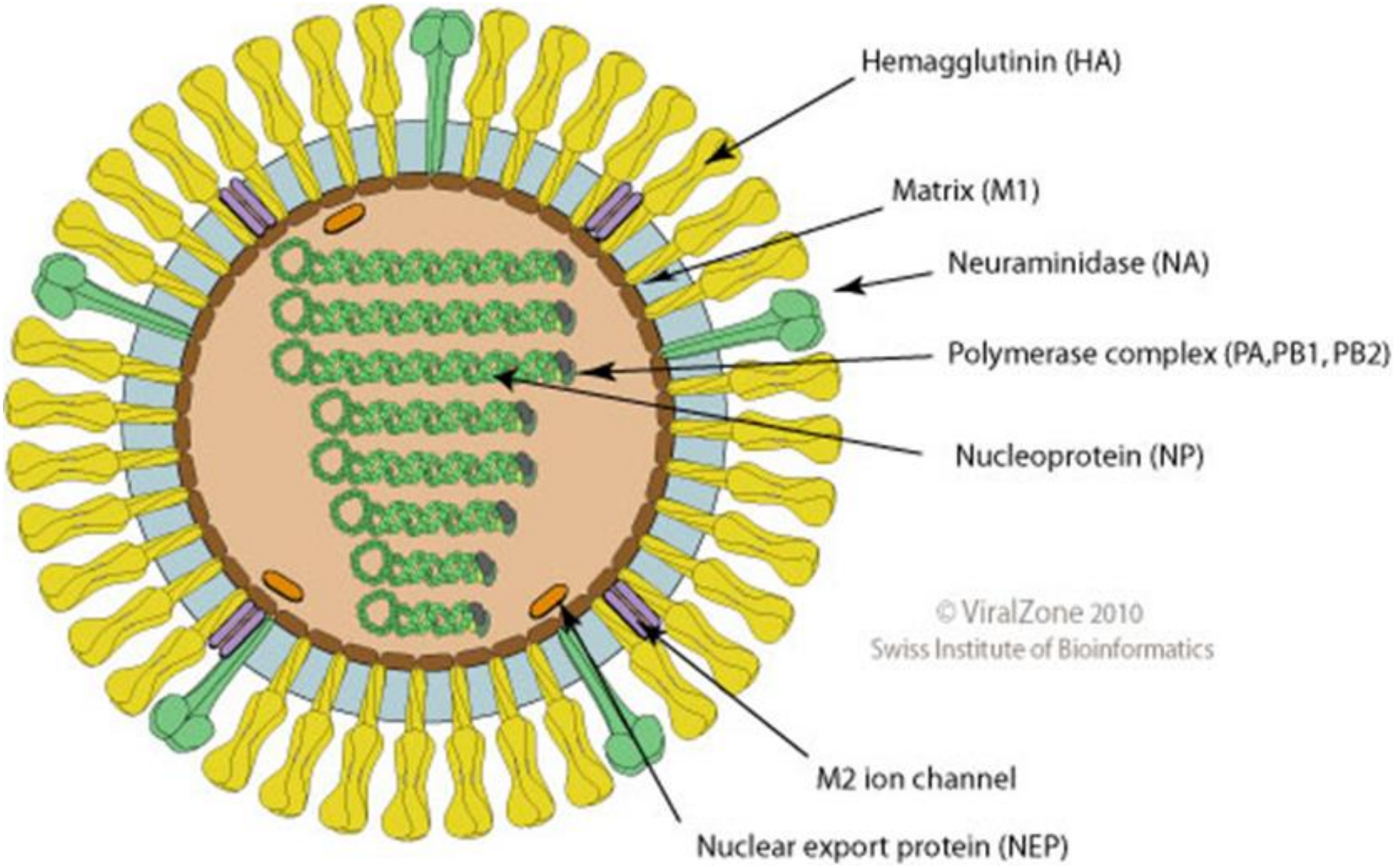
M (M1, M2),

NS (NS1, NS2 or NSP)



3D Modell Influenzavirus * Quelle: Eigene Herstellung * Zeichner: M. Eickmann (wikipedia)

IAV - genome segments and functions of their transcripts:

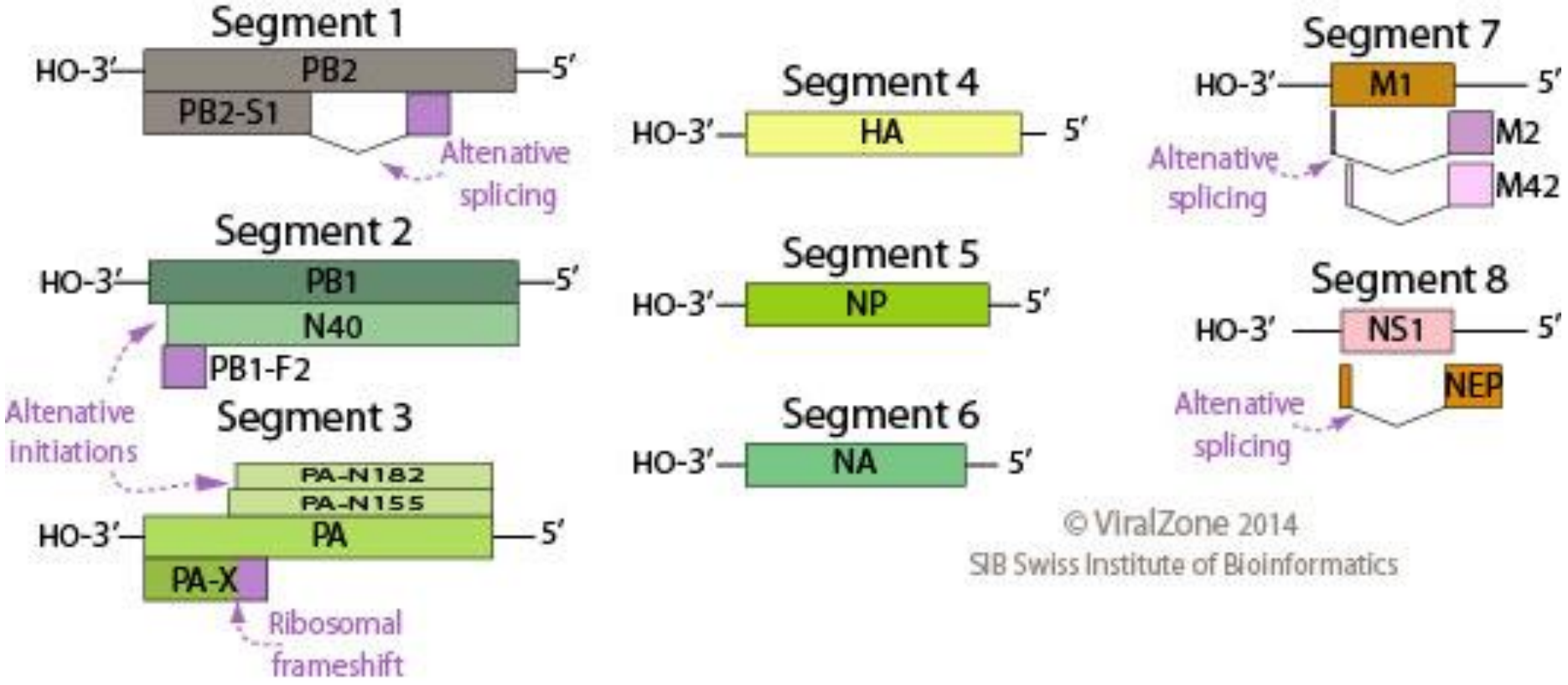


IAV genome segments translation and functions:

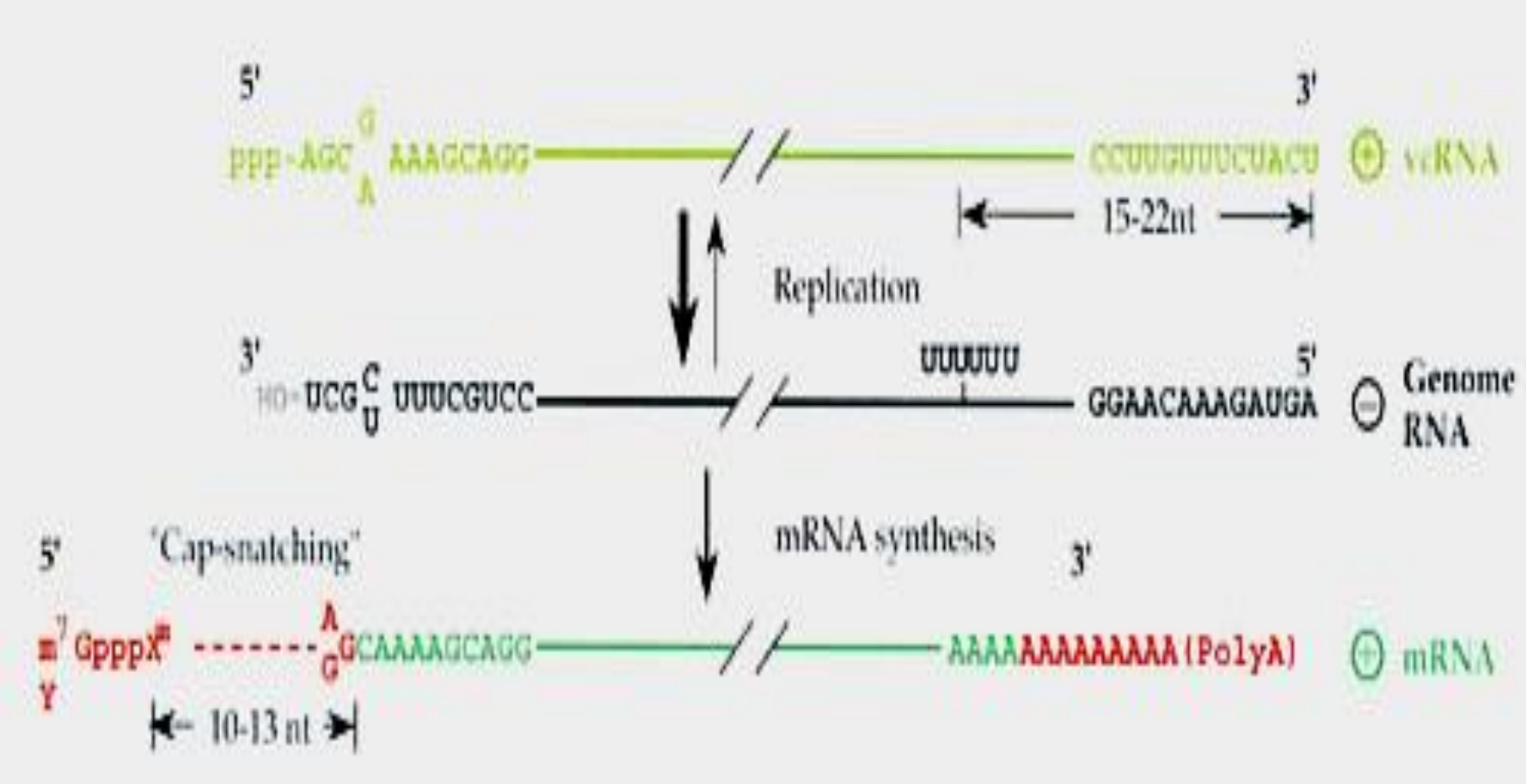
PB2 („cuts and pastes” the cap, pol), PB1 (PB1-N40, PB1-F2, pol), PA - polymerase

HA (trimer, hemaglutinine), NP (nucleoprotein), NA (tetramer, neuraminidase)

M (membrane proteins: M1- matrix, M2- ion channel), NS (nonstructural protein NS1, recognizes cellular mRNA caps, inhibits prosessing and mRNA export, interferon response, NS2=NEP nuclear export protein)

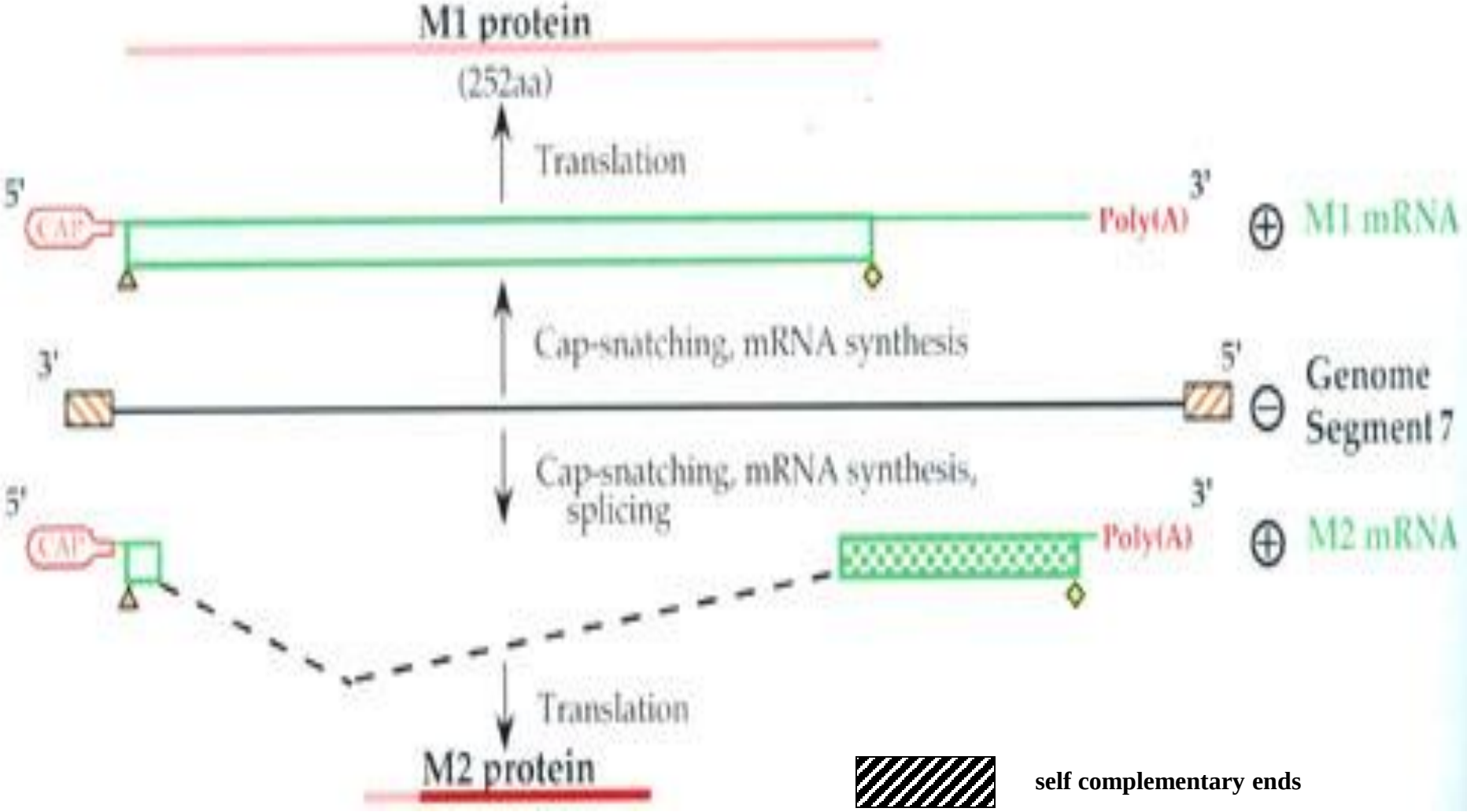


Influenzavirus – cap snatching and mRNA synthesis

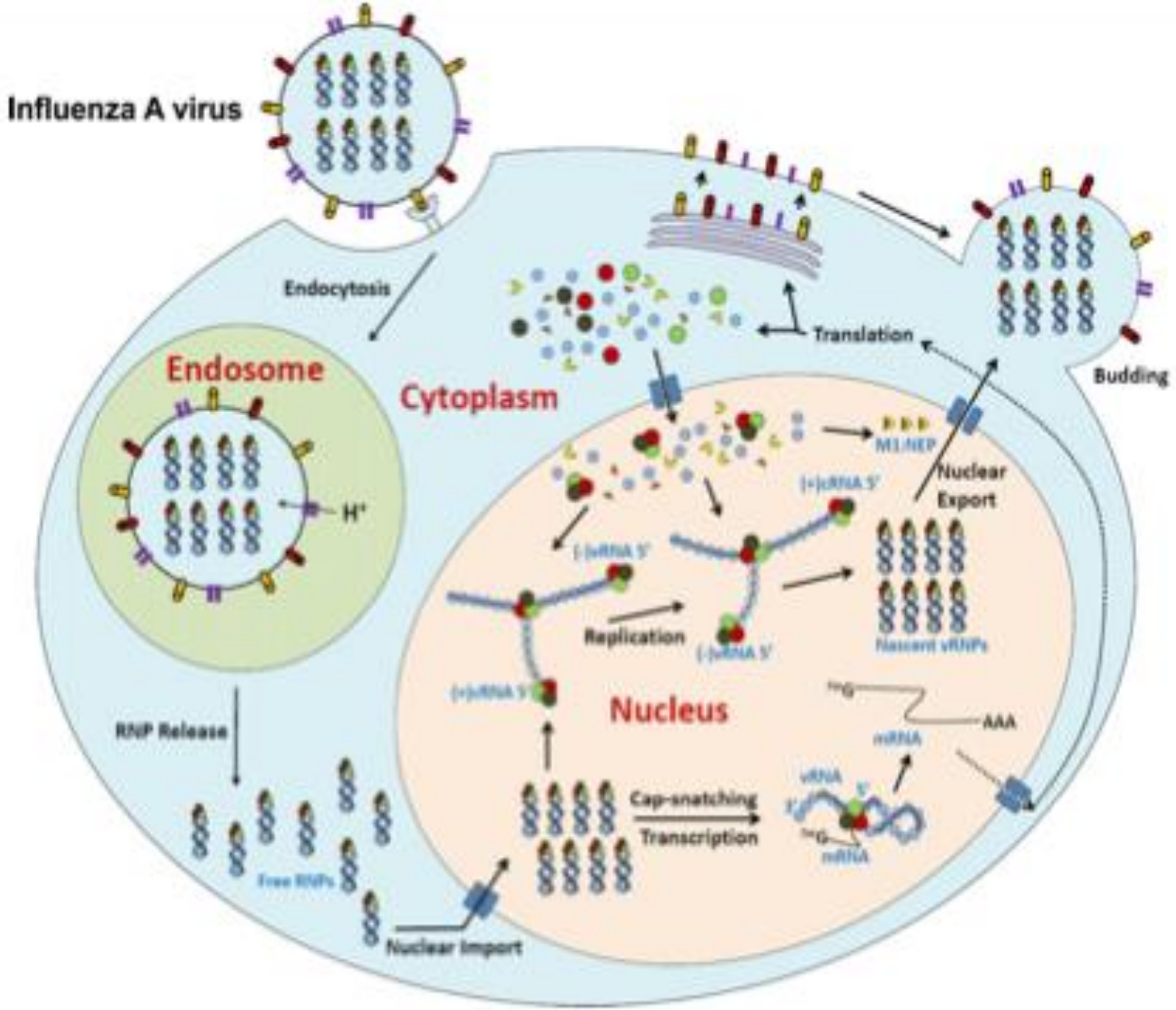


Strauss&Strauss, 2002

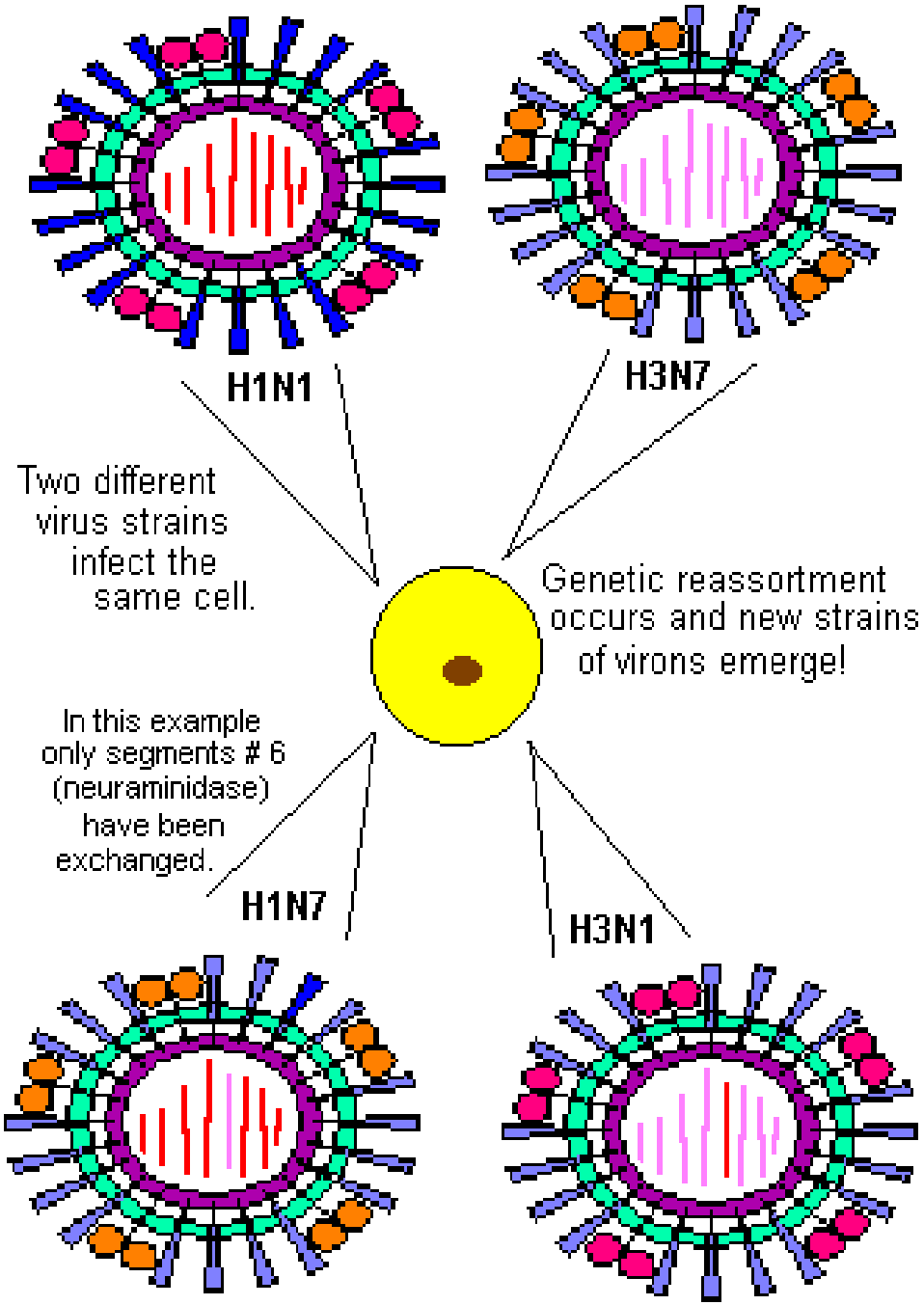
Post-transcriptional modification (*splicing*) of some IAV proteins



Adapted from Strauss&Strauss, 2002



W. Zheng, Y.J. Tao / FEBS Letters 587 (2013) 1206–1214



HA:NA= 4-5:1, about 500 spikes, main virulence determinants (the ability to cause a disease).

Influenzavirus A - 18 types of HA and 11 types of NA.

All but bat's H17N10 and H18N11 found in aquatic birds (e.g. ducks).