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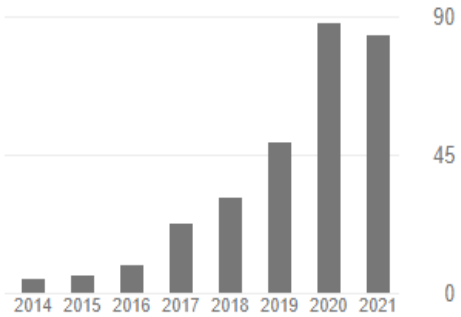

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Short Communication

Effect of Ammonium Chloride in addition to standard of care in outpatients and hospitalized COVID-19 patients: A randomized clinical trial

Zeinab Siami[a], Sepehr Aghajanian[b], Somayeh Mansouri[b], Zakiye Mokhames[c], Reza Pakzad[d,e], Kourosh Kabir[f], Mehdi Norouzi[g,h], Alireza Soleimani[a], Mojtaba Hedayat Yaghoobi[a], Shahrzad Shadabi[b], Ramin Tajbakhsh[i], Ali Kargar Kheirabad[g,**], Sayed-Hamidreza Mozhgani[j,k,*]

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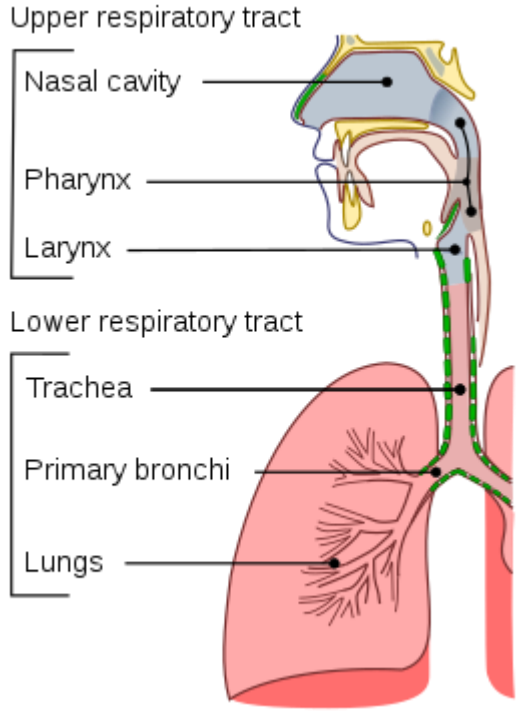
Introduction

Respiratory tract infections (RTIs) are infectious diseases involving the respiratory tract. An infection of this type usually is further classified as an upper respiratory tract infection (URI or URTI) or a lower respiratory tract infection (LRI or LRTI).

Lower respiratory tract infections are generally more severe than upper respiratory infections. LRIs are the leading cause of death among all infectious diseases.



Introduction

Of the viruses that cause respiratory infections in humans, most have seasonal variation in prevalence.

- Influenza, Human orthopneumovirus (RSV) and human coronaviruses are more prevalent in the winter.
- Adenovirus, Human bocavirus and Human metapneumovirus occur year-round.
- Rhinoviruses (which cause the common cold) occur mostly in the spring and fall.
- Human parainfluenza viruses have variable peaks depending on the specific strain.
- Enteroviruses, with the exception of rhinoviruses, tend to peak in the summer.

Coronaviridae

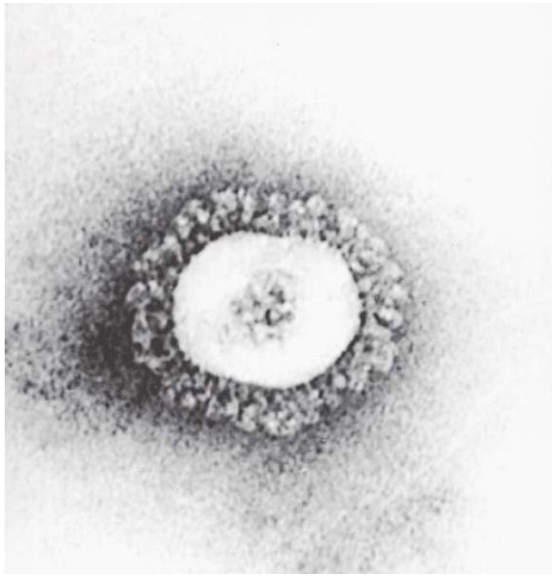
Coronaviruses

Coronaviruses are large, enveloped RNA viruses.

The human coronaviruses cause common colds, may cause lower respiratory tract infections.

Novel coronaviruses have been identified as the cause of:

- Severe acute respiratory syndrome (SARS 1 & 2)
- Middle East respiratory syndrome (MERS)



Coronaviridae

Classification

There are two subfamilies:

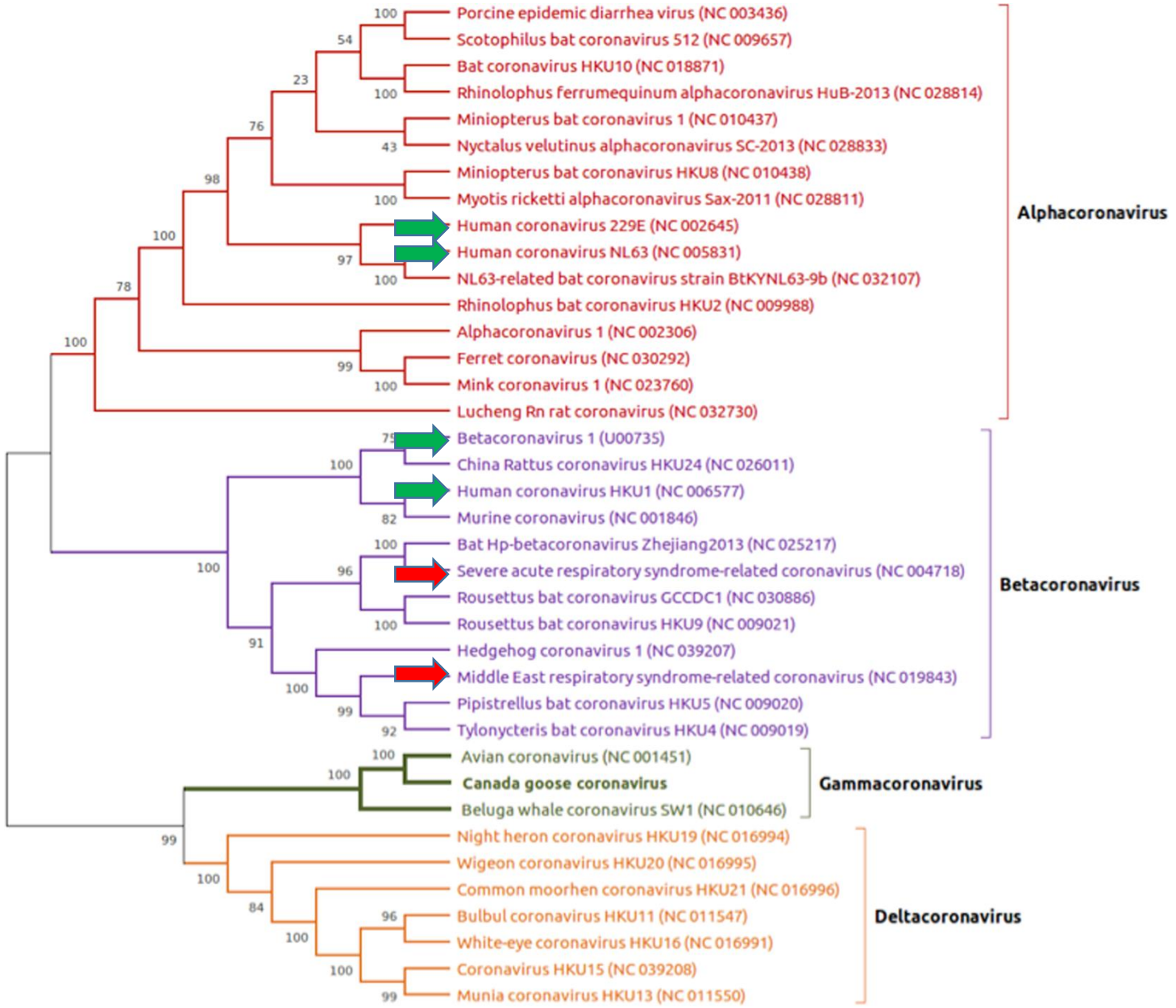
- Coronavirinae
- Torovirinae

six genera:

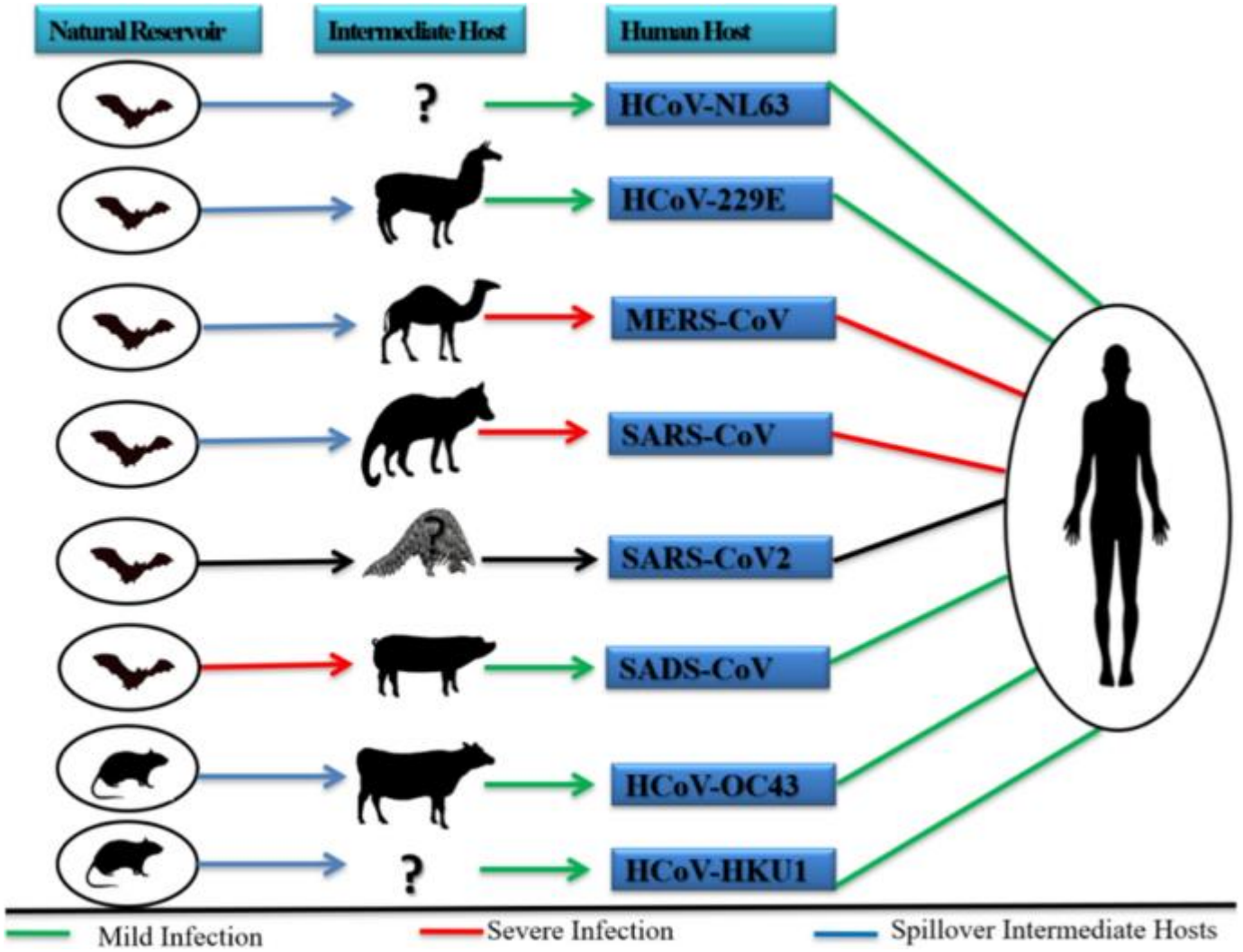
- Alphacoronavirus
- Betacoronavirus
- Gammacoronavirus
- Deltacoronavirus
- Bafinivirus
- Torovirus

The first two and the last genera contain viruses able to infect humans.

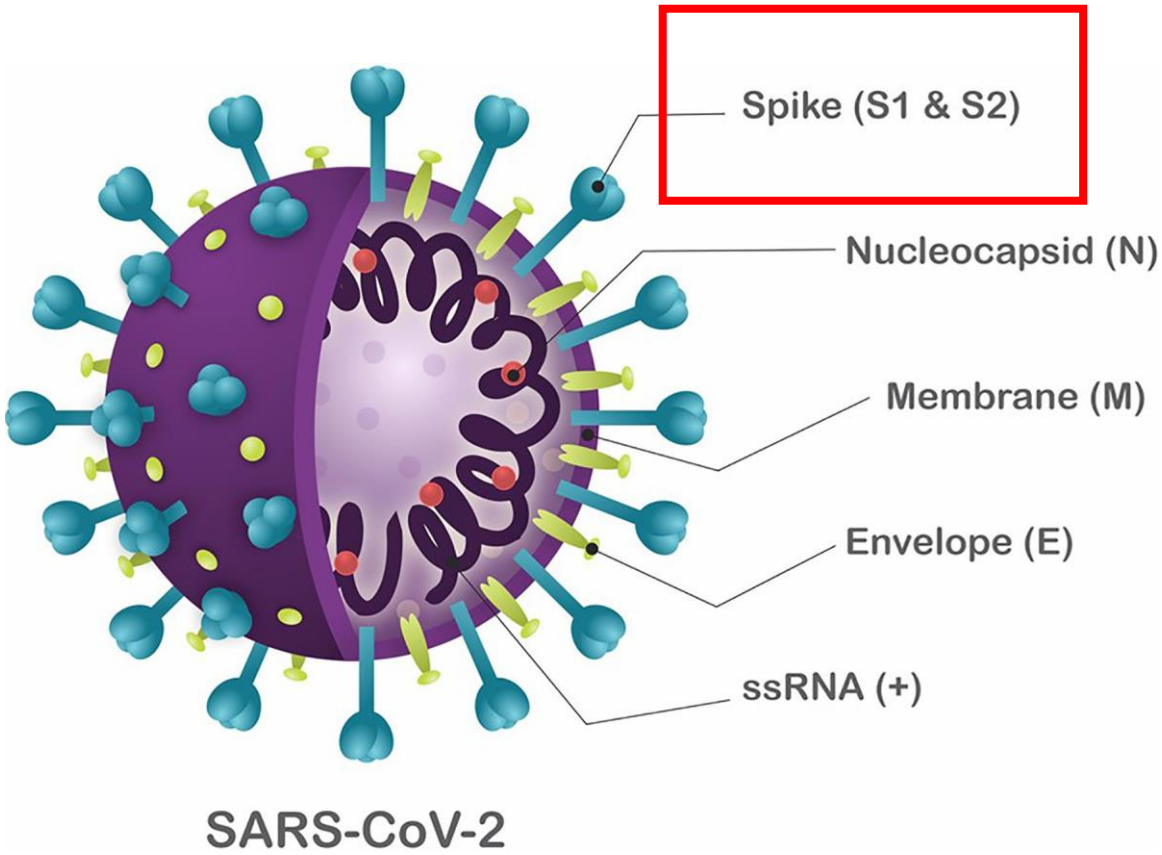
The Toroviruses are associated with diarrheal disease.

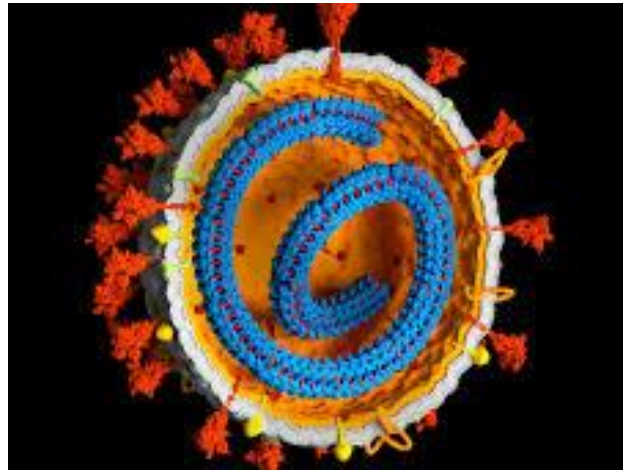


Origin of SARS-CoV-2

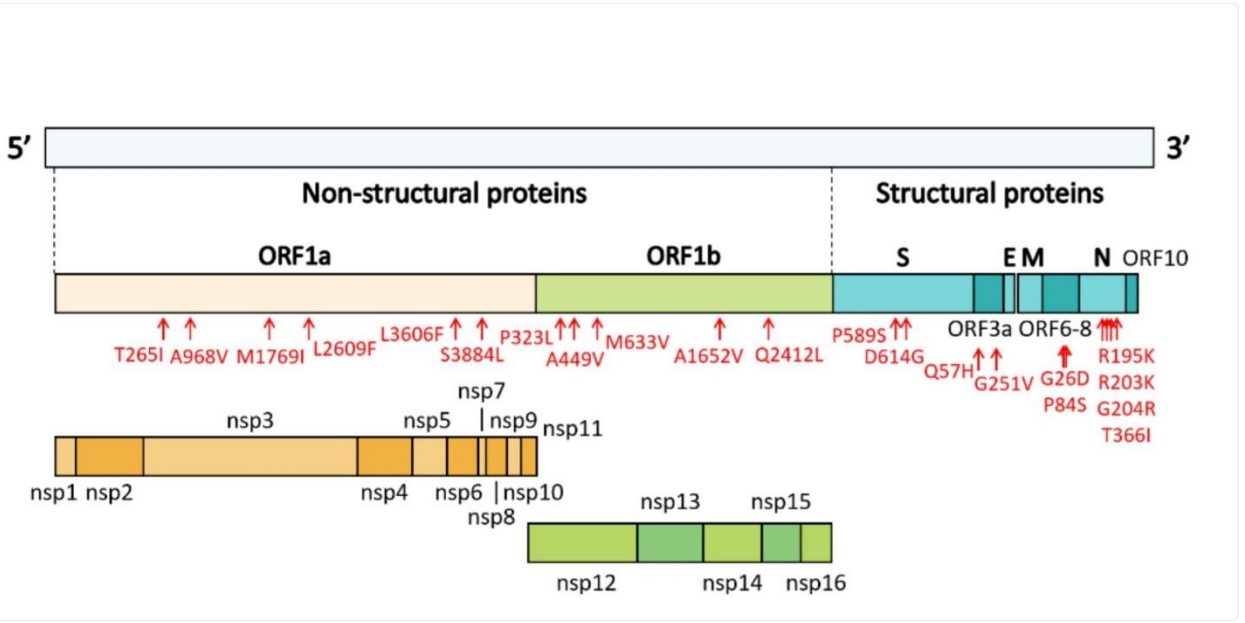


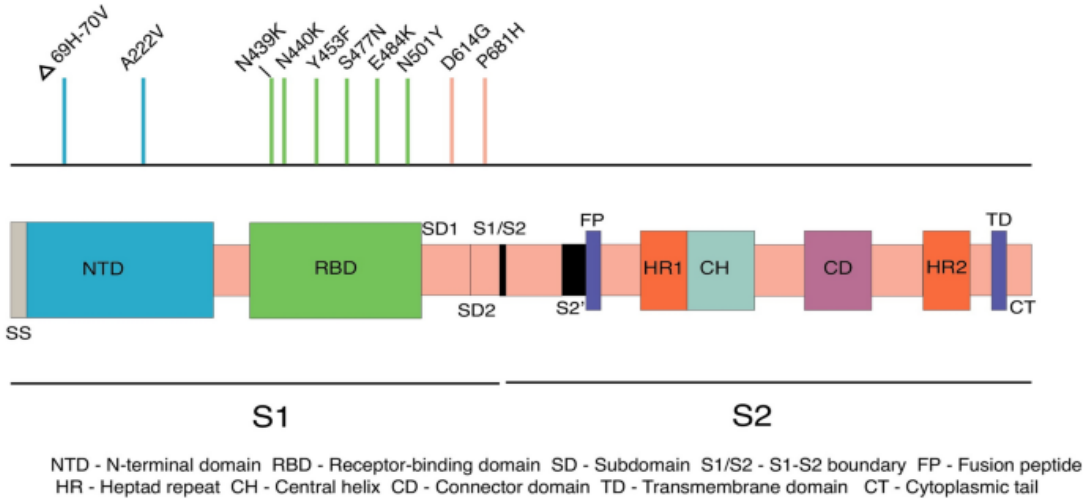
Viral Structure



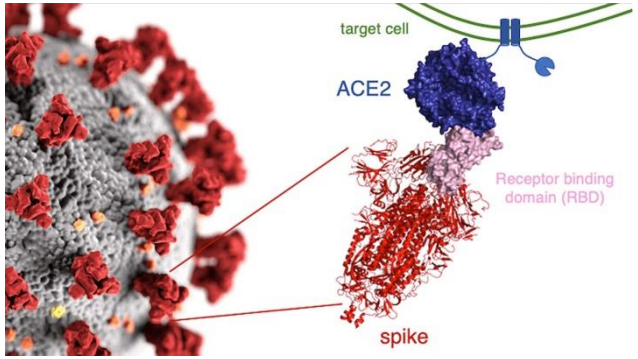


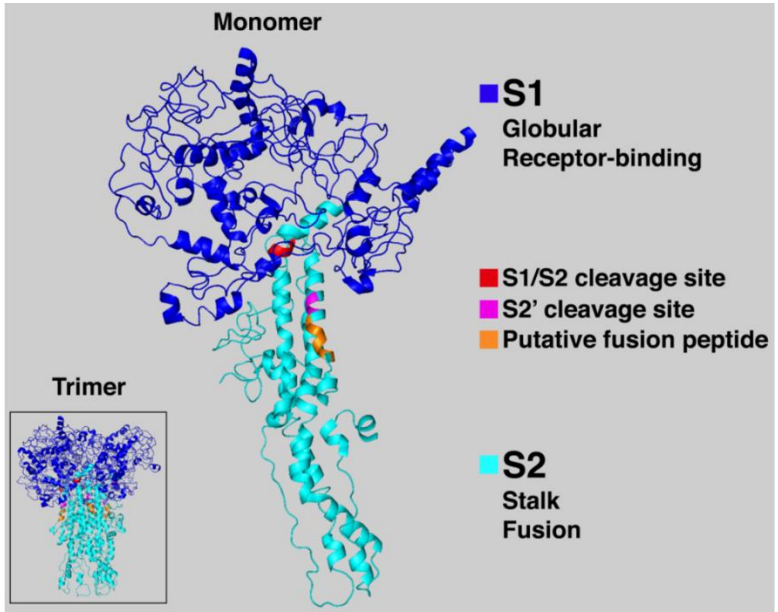
Genomic Structure

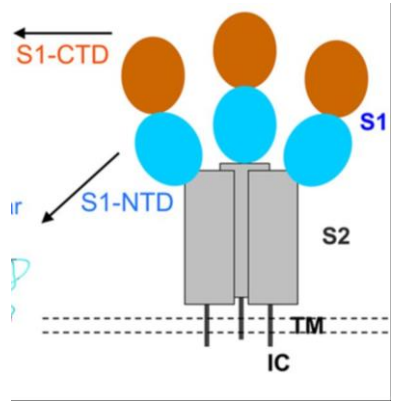




NTD - N-terminal domain RBD - Receptor-binding domain SD - Subdomain S1/S2 - S1-S2 boundary FP - Fusion peptide
HR - Heptad repeat CH - Central helix CD - Connector domain TD - Transmembrane domain CT - Cytoplasmic tail







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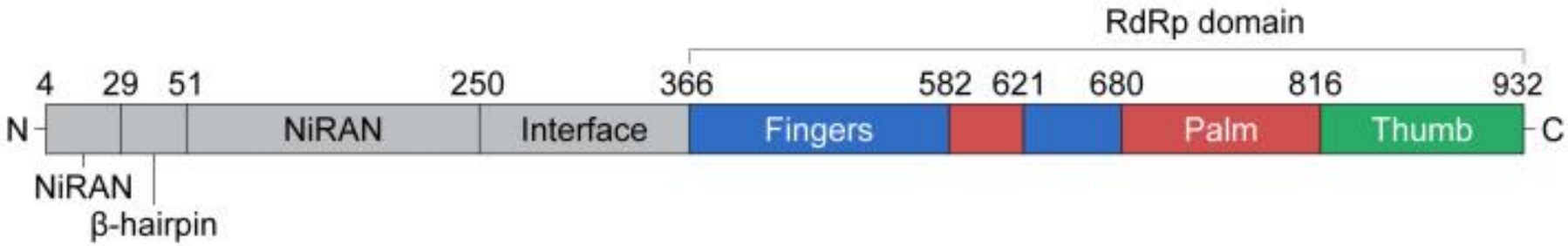

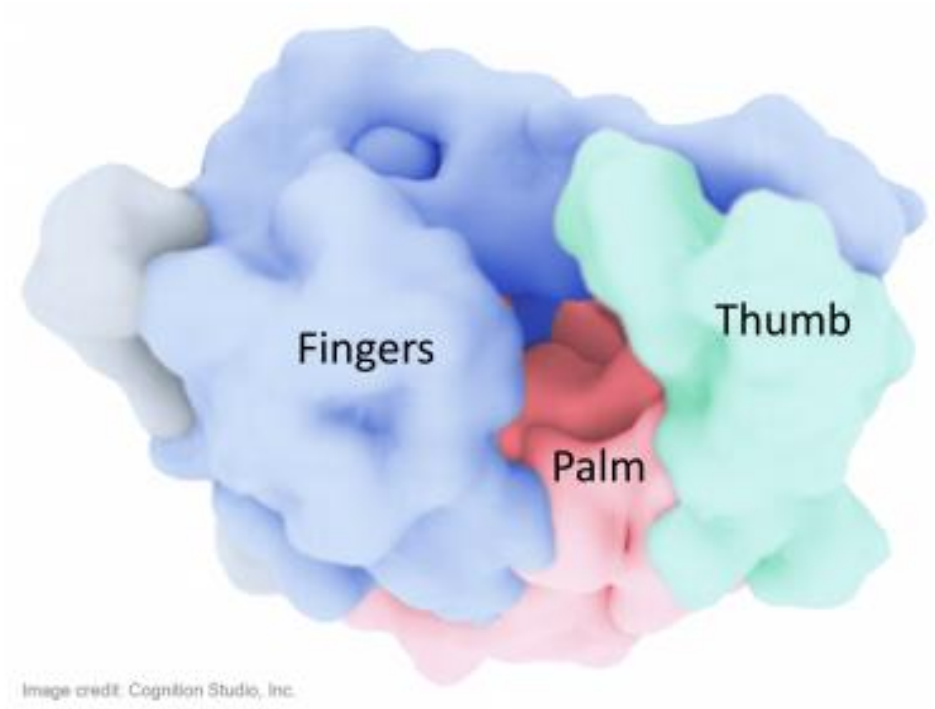

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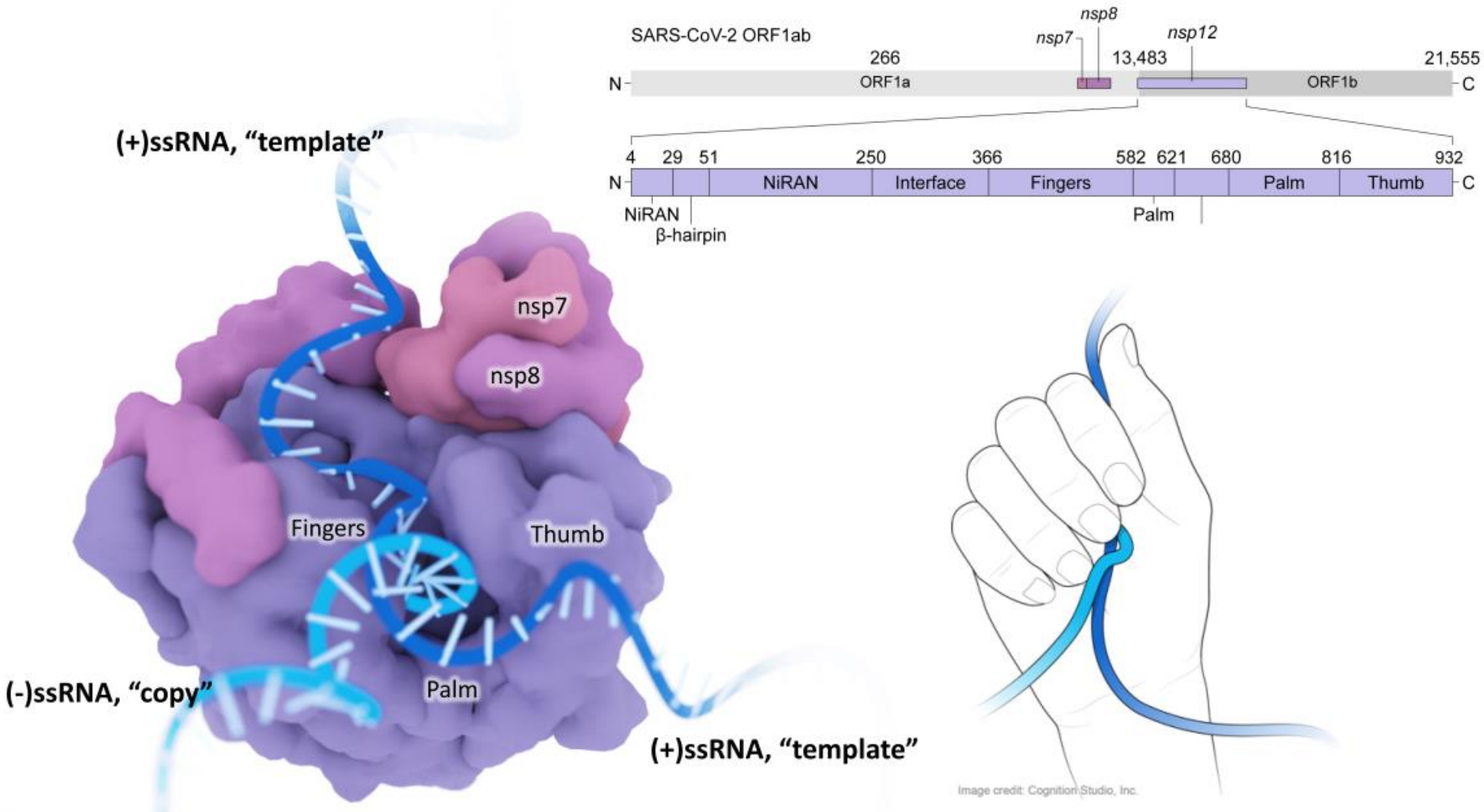
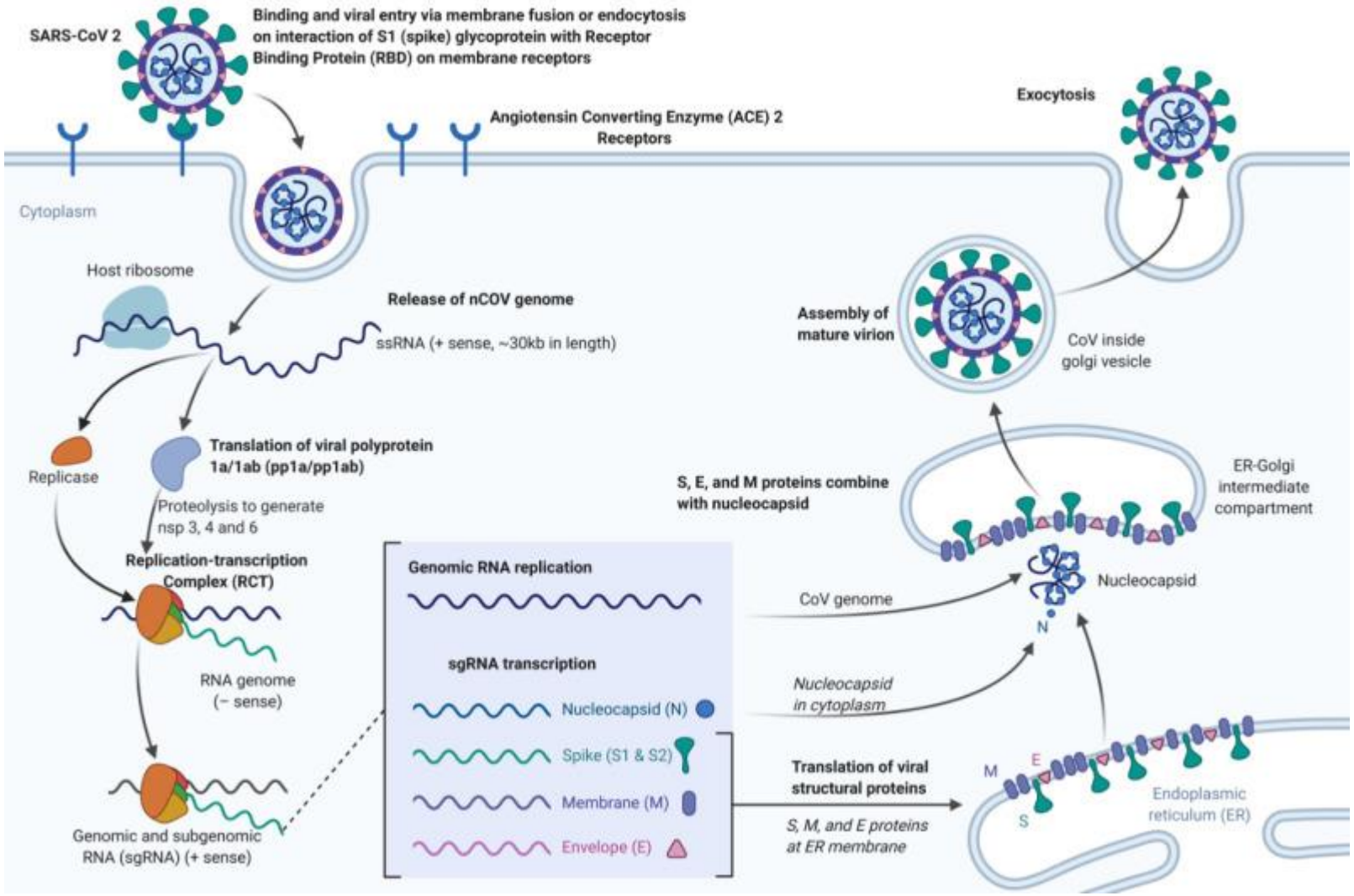


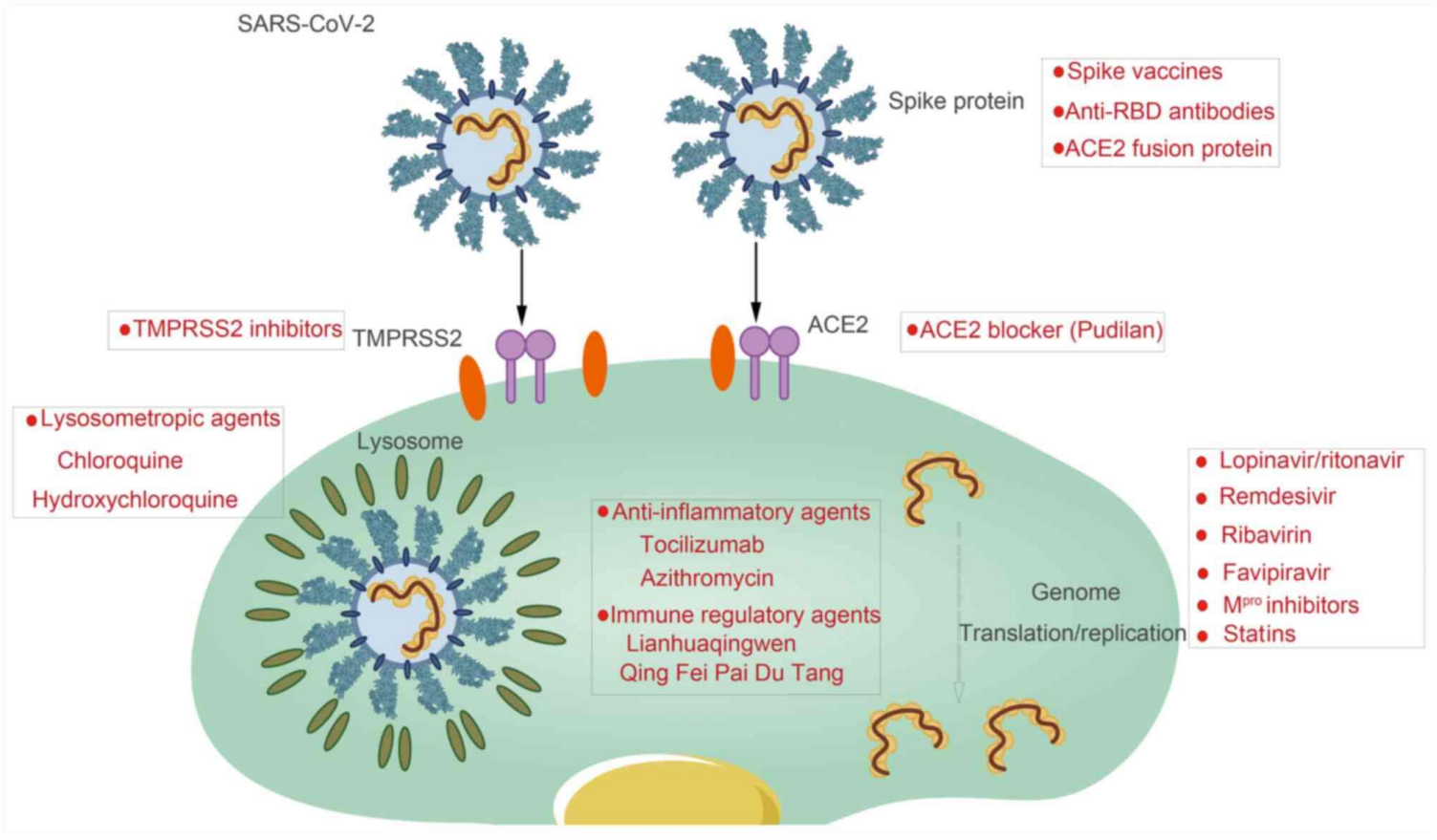
Replication Cycle



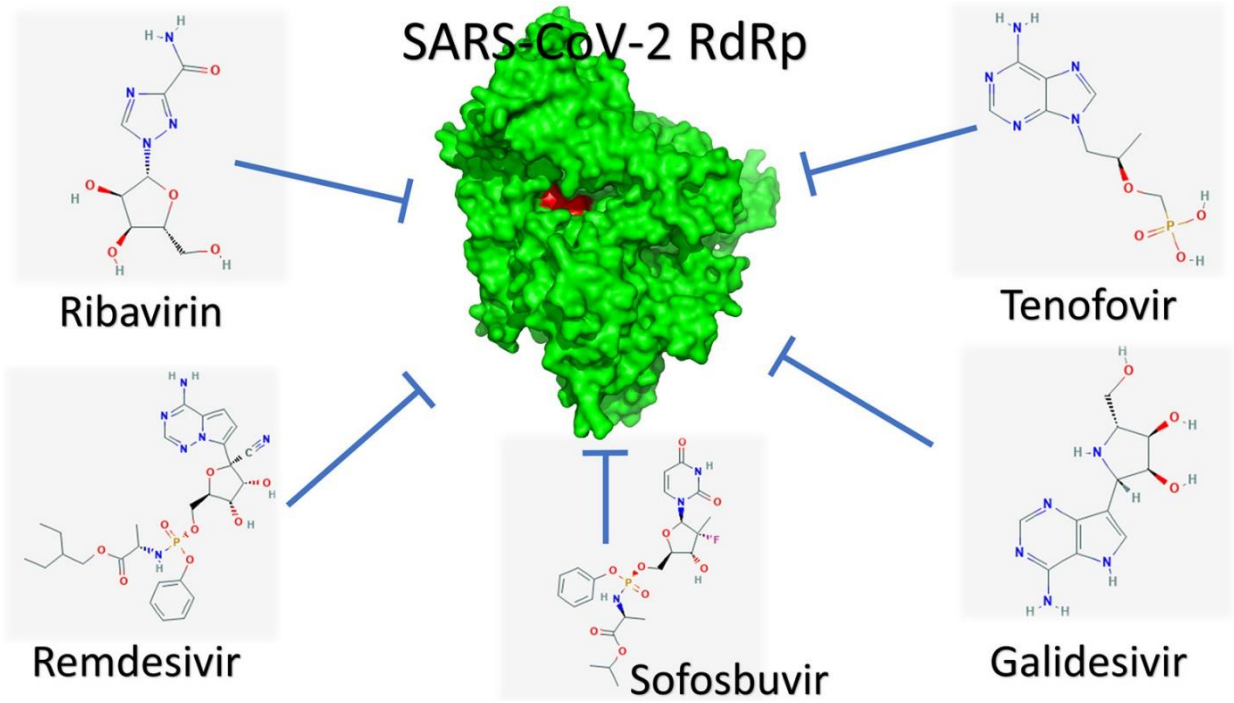
Antiviral Agents

SARS-CoV-2 employs the serine protease TMPRSS2 for S protein priming.

TMPRSS2; transmembrane protease serine



Antiviral Agents



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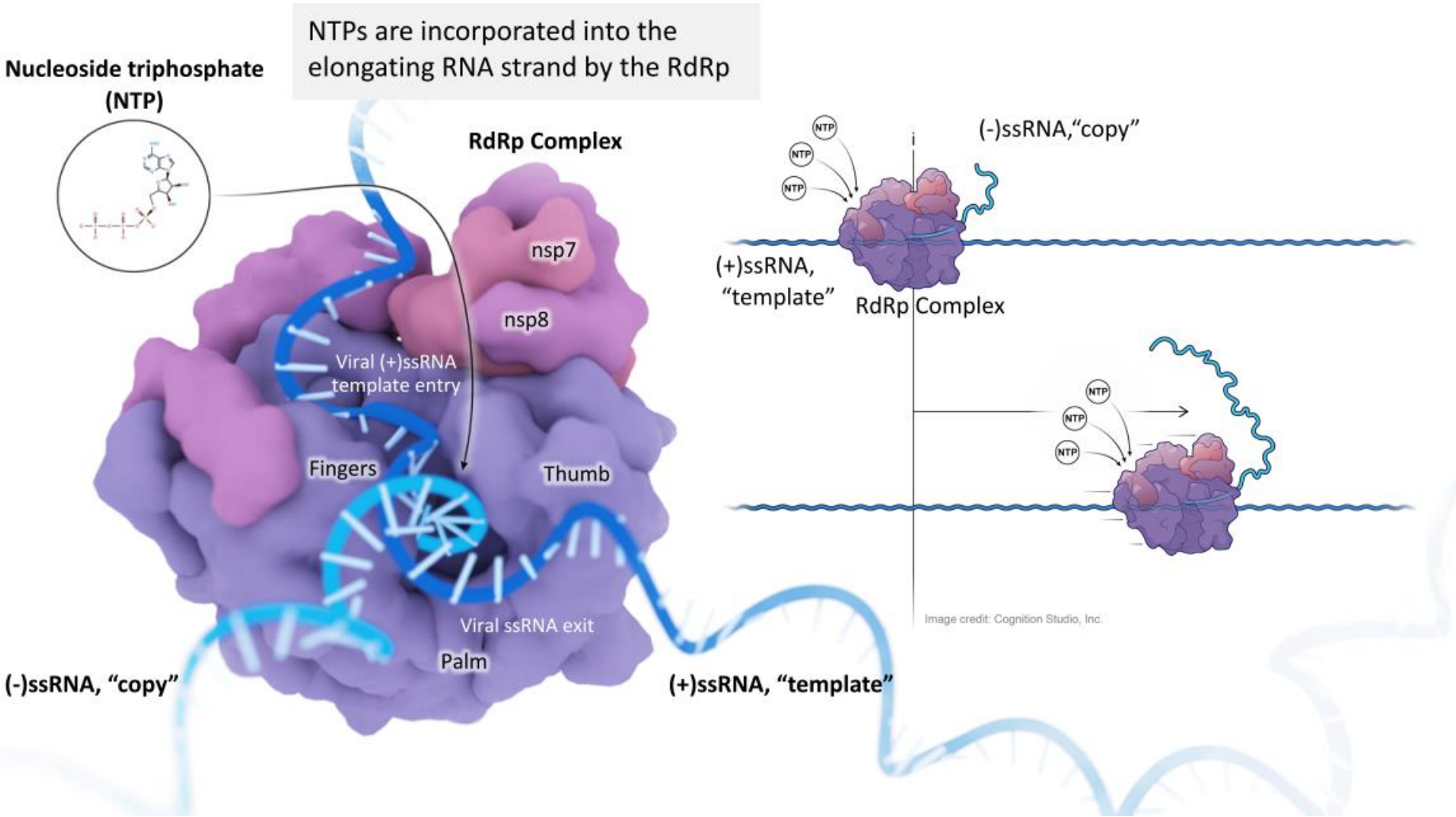

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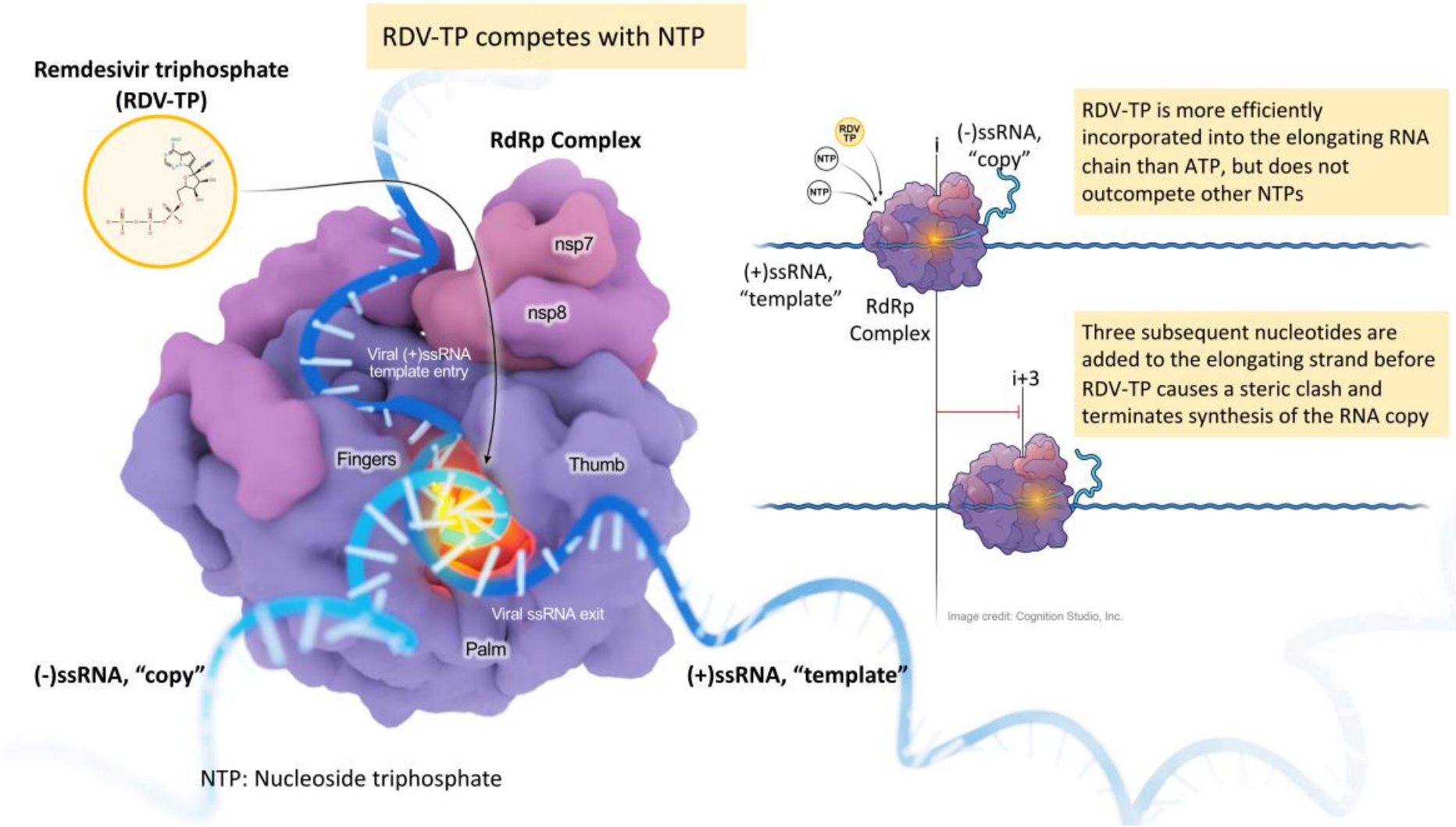

Antiviral Agents

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SARS-CoV-2 variants

Amino Acid	3 letter	1 letter
Alanine	Ala	A
Arginine	Arg	R
Asparagine	Asn	N
Aspartic acid	Asp	D
Cysteine	Cys	C
Glutamic acid	Glu	E
Glutamine	Gln	Q
Glycine	Gly	G
Histidine	His	H
Isoleucine	Ile	I
Leucine	Leu	L
Lysine	Lys	K
Methionine	Met	M
Phenylalanine	Phe	F
Proline	Pro	P
Serine	Ser	S
Threonine	Thr	T
Tryptophan	Trp	W
Tyrosine	Tyr	Y
Valine	Val	V

SARS-CoV-2 variants

Variants of Concern (VOC)

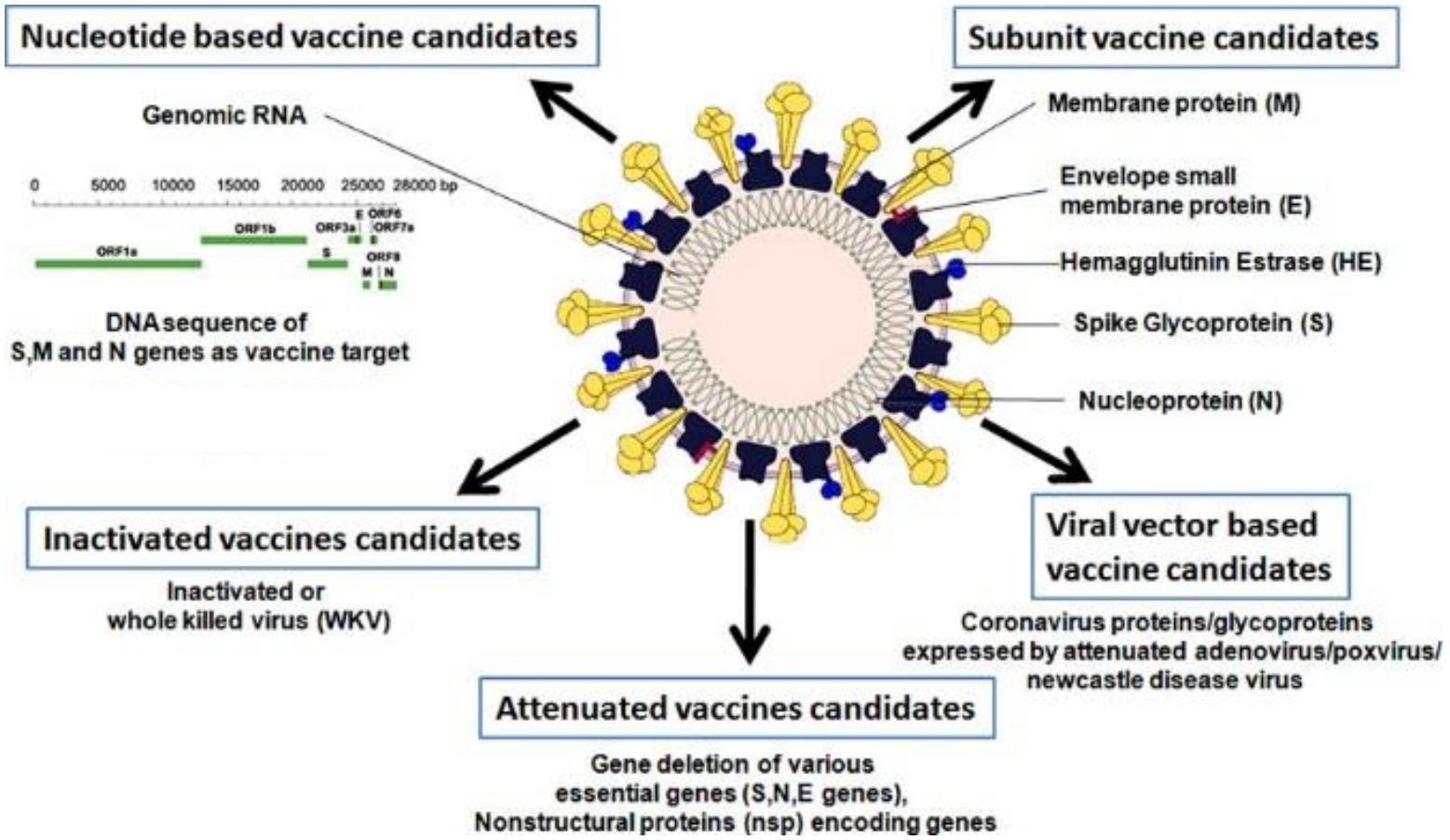
WHO label	Lineage + additional mutations	Country first detected (community)	Spike mutations of interest	Year and month first detected	Evidence for impact on transmissibility	Evidence for impact on immunity	Evidence for impact on severity	Transmission in EU/EEA
Alpha	B.1.1.7	United Kingdom	N501Y, D614G, P681H	September 2020	Yes (v) (1)	No	Yes (v) (2, 3)	Community
	B.1.1.7+E484K	United Kingdom	E484K, N501Y, D614G, P681H	December 2020	Yes (v) (1)	Yes (v) (4, 5)	Yes (v) (2)	Outbreaks
Beta	B.1.351	South Africa	K417N, E484K, N501Y, D614G, A701V	September 2020	Yes (v) (6)	Yes (v) (7, 8)	Yes (v) (3, 9)	Community
Gamma	P.1	Brazil	K417T, E484K, N501Y, D614G, H655Y	December 2020	Yes (v) (10)	Yes (v) (11)	Yes (v) (3)	Community
Delta	B.1.617.2	India	L452R, T478K, D614G, P681R	December 2020	Yes (v) (12)	Yes (v) (13-15)	Yes (v) (14, 16)	Dominant

SARS-CoV-2 variants

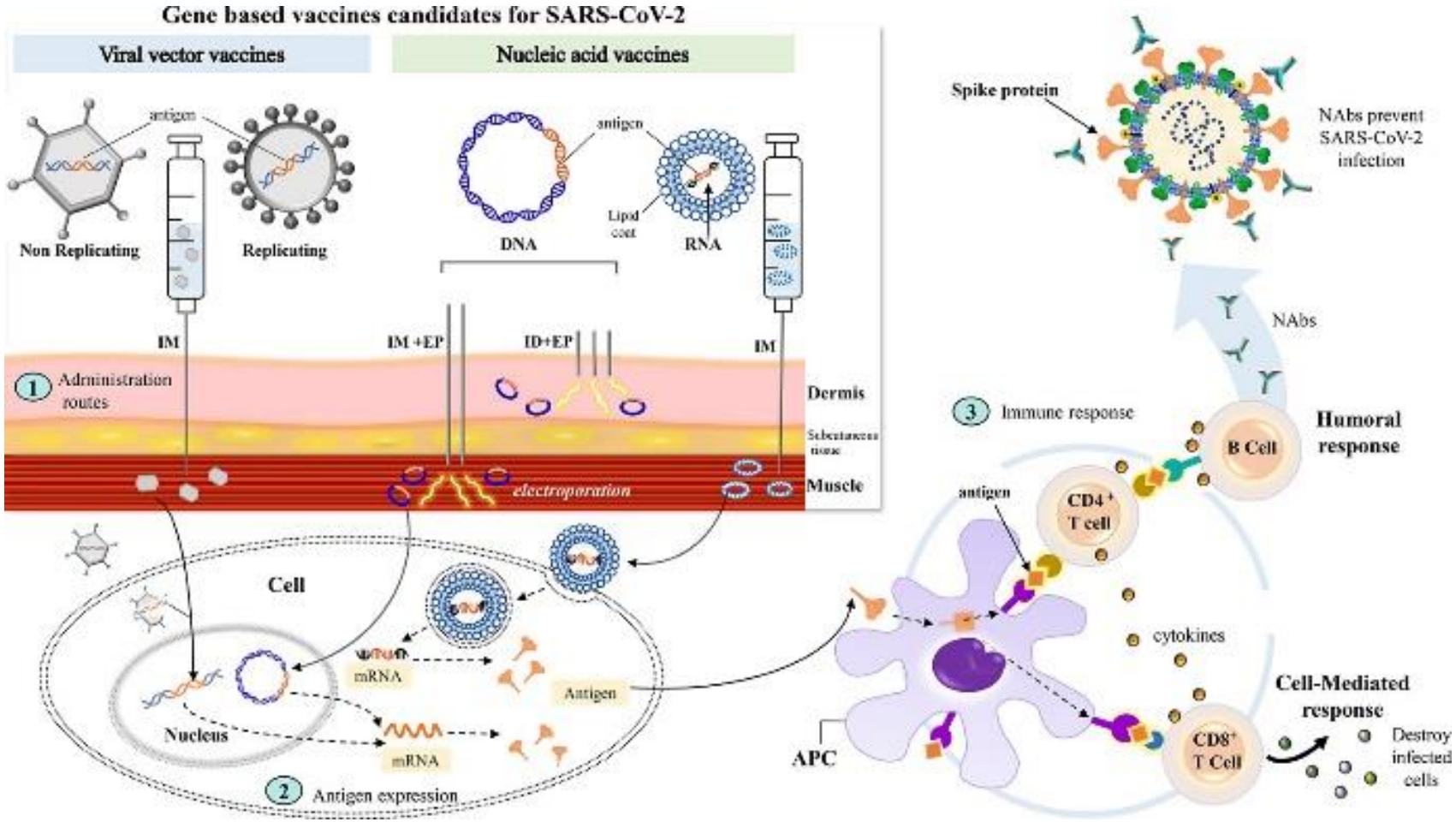
Variants of Interest (VOI)

WHO label	Lineage + additional mutations	Country first detected (community)	Spike mutations of interest	Year and month first detected	Evidence for impact on transmissibility	Evidence for impact on immunity	Evidence for impact on severity	Transmission in EU/EEA
Eta	B.1.525	Nigeria	E484K, D614G, Q677H	December 2020		Yes (m) (4)		Community
Theta	P.3	The Philippines	E484K, N501Y, D614G, P681H	January 2021	Yes (m) (1)	Yes (m) (4)		Sporadic/Travel
Kappa	B.1.617.1	India	L452R, E484Q, D614G, P681R	December 2020	Yes (v) (17)	Yes (v) (18-21)		Outbreaks
	B.1.620	Unclear (b)	S477N, E484K, D614G, P681H	February 2021		Yes (m) (4, 22)		Outbreaks
	B.1.621	Colombia	R346K, E484K, N501Y, D614G, P681H	January 2021	Yes (m) (1)	Yes (m) (4)		Sporadic/Travel
Lambda	C.37	Peru	L452Q, F490S, D614G	December 2020		Yes (23, 24)		Detected (a)

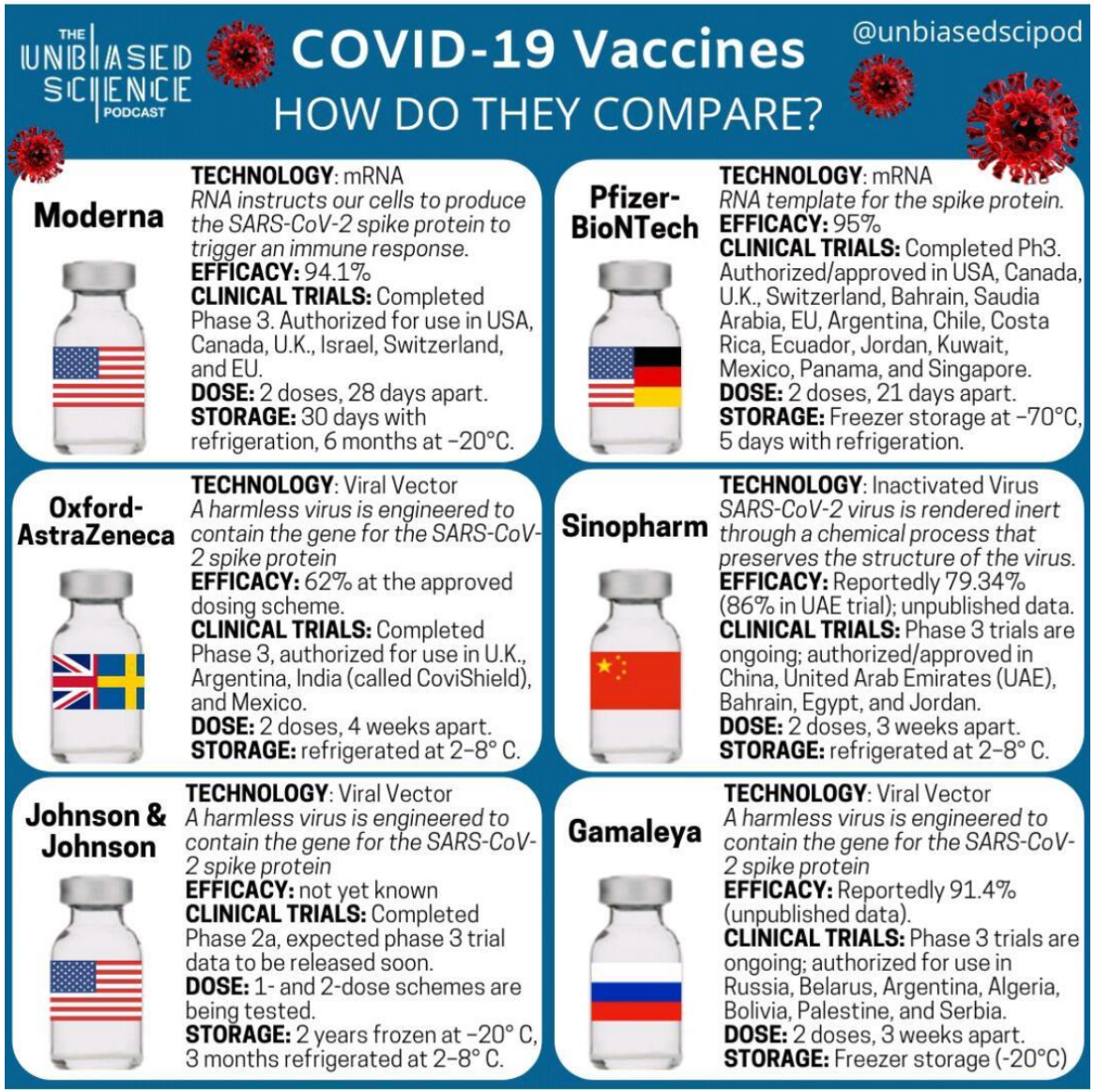
Vaccination strategies



Vaccination strategies



Vaccination strategies



Immunity

As with other respiratory viruses, immunity develops but is not absolute.

Laboratory Diagnosis

Prevention, and Control

Control measures that were effective in stopping the spread of SARS-2 included isolation of patients, quarantine of those who had been exposed, and travel restrictions, as well as the use of gloves, gowns, goggles, and respirators by health care workers.

Thank you