



SARS CoV2 / COVID19

Properties of Coronaviruses: a large family of viruses

- **Genome:** SS RNA, Linear, non-segmented, positive sense, 27-32 kb
- **Virion:** Spherical, 80-130 nm in diameter, Helical nucleocapsid
- **Envelope:** Contains large, widely spaced, club or petal shaped spikes
- **Replication:** Cytoplasm; particles mature by budding into Endoplasmic Reticulum and Golgi
- **Cause:** Colds and SARS

Classification criteria

Nucleic acid

Symmetry of capsid

Naked or enveloped

Genome architecture

Baltimore class

Icosahedral

Naked

- ds 10–18 segments
- ds 2 segments
- (+) ss
- (+) ss

Enveloped

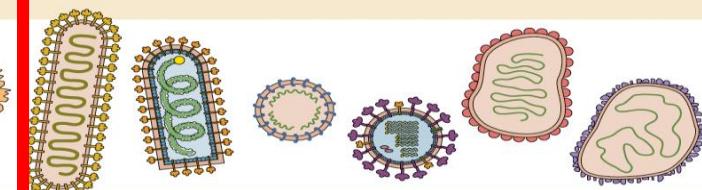
- (+) ss
- (+) ss
- (+) ss 2 copies

RNA

Helical

Enveloped

- (+) ss
- (-) ss
- (-) ss 3 segments
- (-) ss 8 segments
- (-) ss 2 segments



Family name

Reo	Birna	Calici	Picorna	Flavi	Toga	Retro	Corona	Filo	Rhabdo	Bunya	Orthomyxo	Paramyxo	Arena
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DNA

Classification criteria

Nucleic acid

Symmetry of capsid

Naked or enveloped

Genome architecture

Baltimore class

Icosahedral

Complex

Naked

- ss linear (+) or (-)
- ss circular
- ds circular
- ds circular
- ds linear

Enveloped

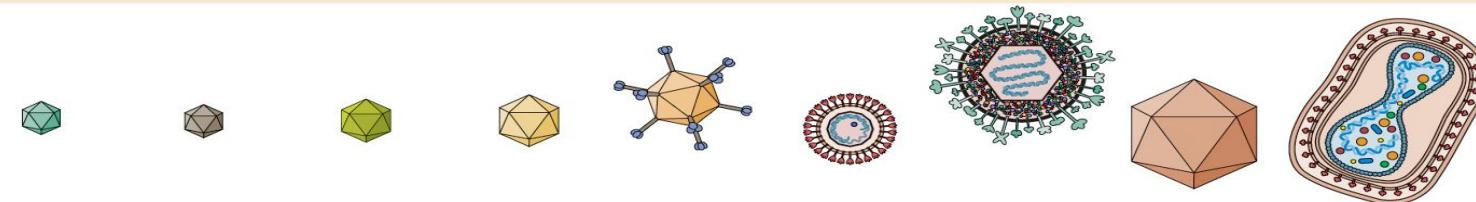
- ds circle gapped
- ds linear

Naked/ enveloped (cytoplasmic)

- ds linear

Enveloped (cytoplasmic)

- ds covalently joined ends

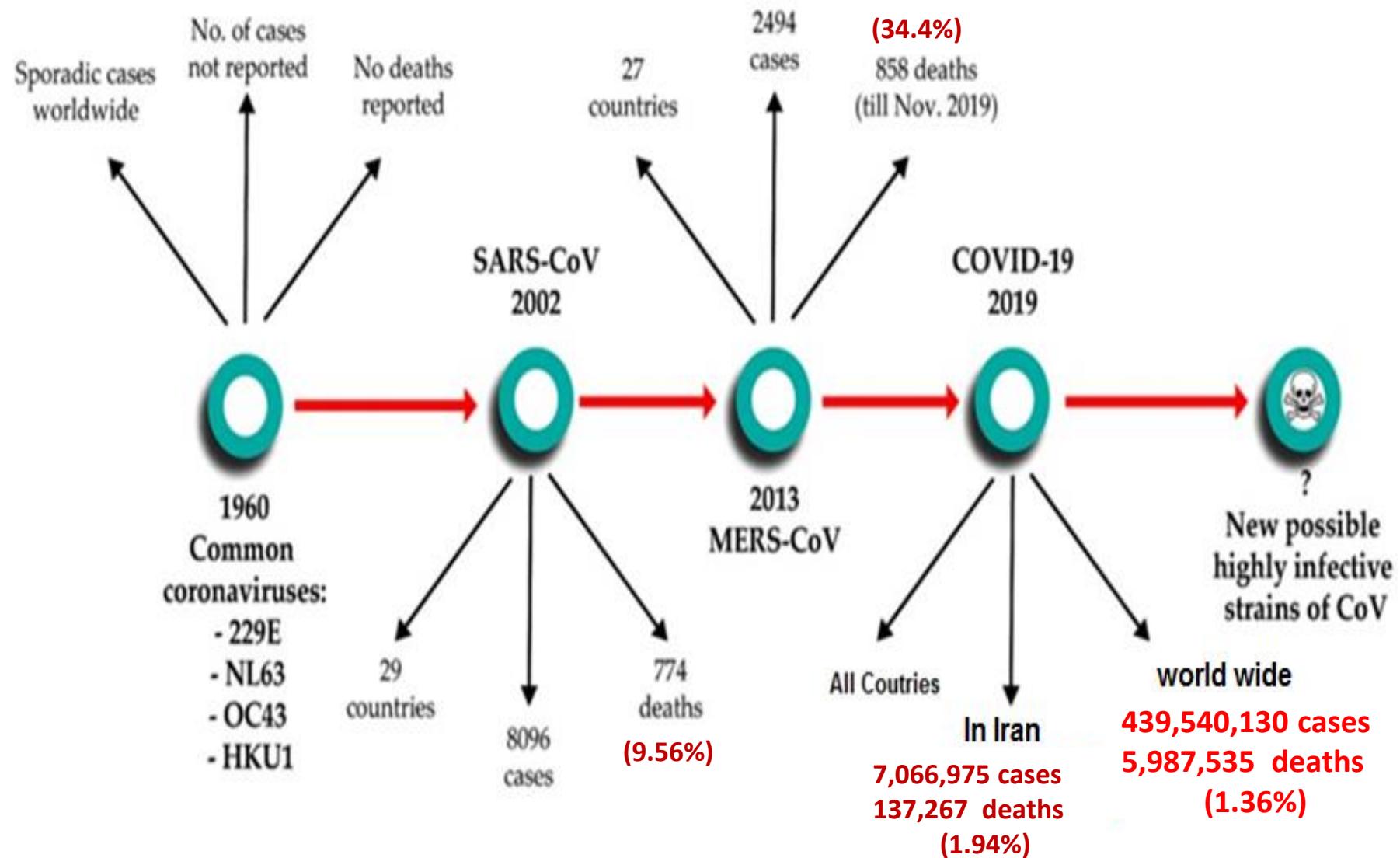


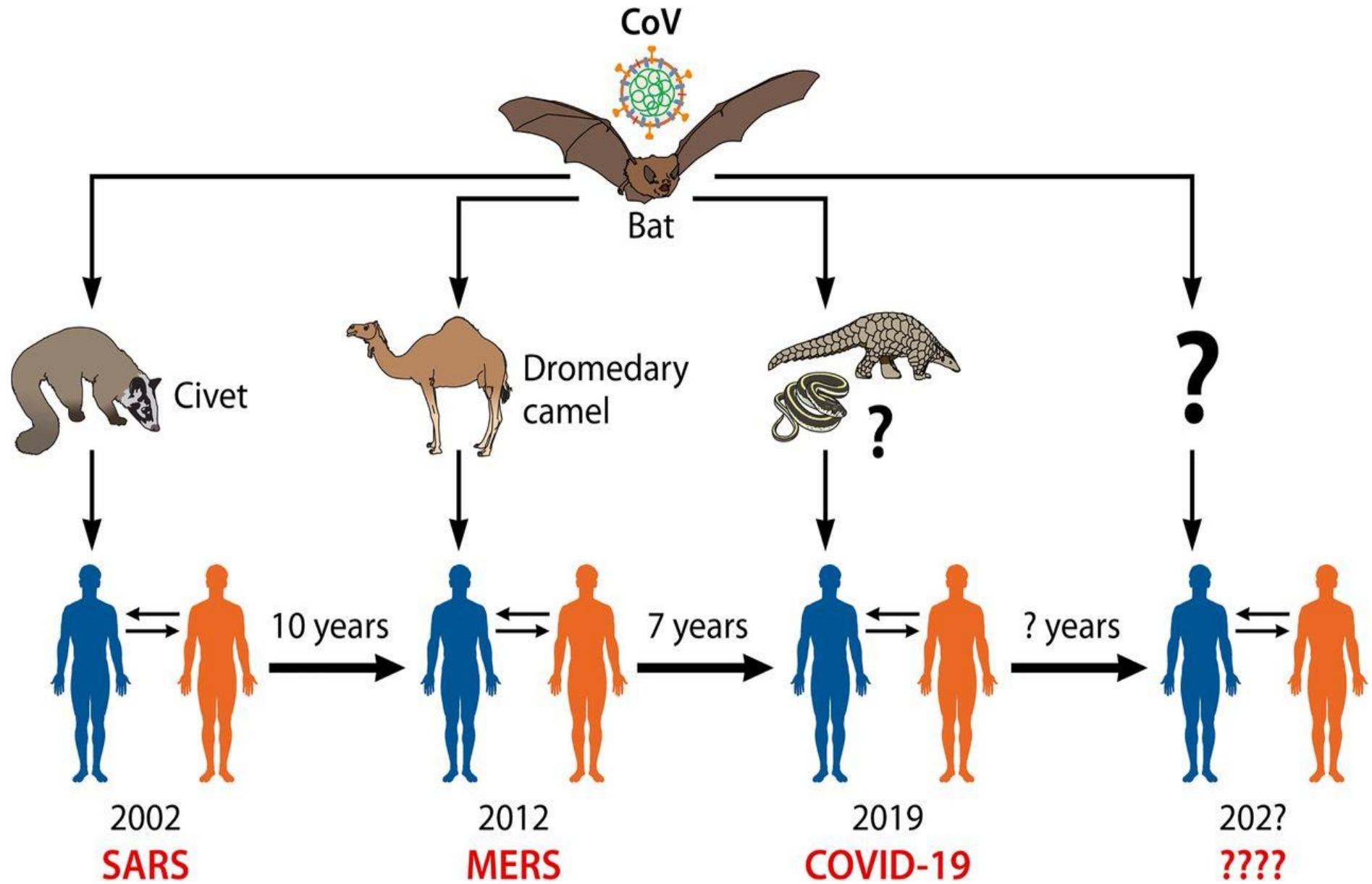
Family name

Parvo	Circo	Polyoma	Papilloma	Adeno	Hepadna	Herpes	Irido	Pox
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Family	Sub-Family	Genus	species
Corneavidae	Corneavirinae	Alpha Coronavirus	Bat coronavirus CDPHE15 Bat coronavirus HKU10 Human Bat coronavirus 229E Human Bat coronavirus NL63 Miniopterus bat Human Bat coronavirus1 Miniopterus bat Human Bat coronavirus HKU8 Mink coronavirus1 Porcine epidemic diarrhea virus Rhinolophus bat coronavirus HKU2 Scotophilus but corona Beta coronavirus virus 512
		Beta Coronavirus	Beta coronavirus 1 Hedgehog coronavirus 1 Human coronavirus HKU 1 Human Coronavirus OC43 Murine coronavirus Pipistrelles bat coronavirus HKU 5 Roulettes bat coronavirus HKU 9 SARS-CoV (Sever Acute Respiratory Syndrom Coronavirus) Tylonycteris bat coronavirus HKU 4 MERS-CoV (Middle East respiratory syndrome-related coronavirus) SARS-CoV2 or COVID19
		Delta Coronavirus	Bulbul coronavirus HKU 11 Common moorhen coronavirus HKU 21 Coronavirus HKU 15 Munia coronavirus HKU 13 Night heron coronavirus HKU 19 Thrush coronavirus HKU 12 White-eye coronavirus HKU 16 Wig eon coronavirus HKU 20
		Gamma Coronavius	Avian coronavirus Beluga Whale coronavirus SW1

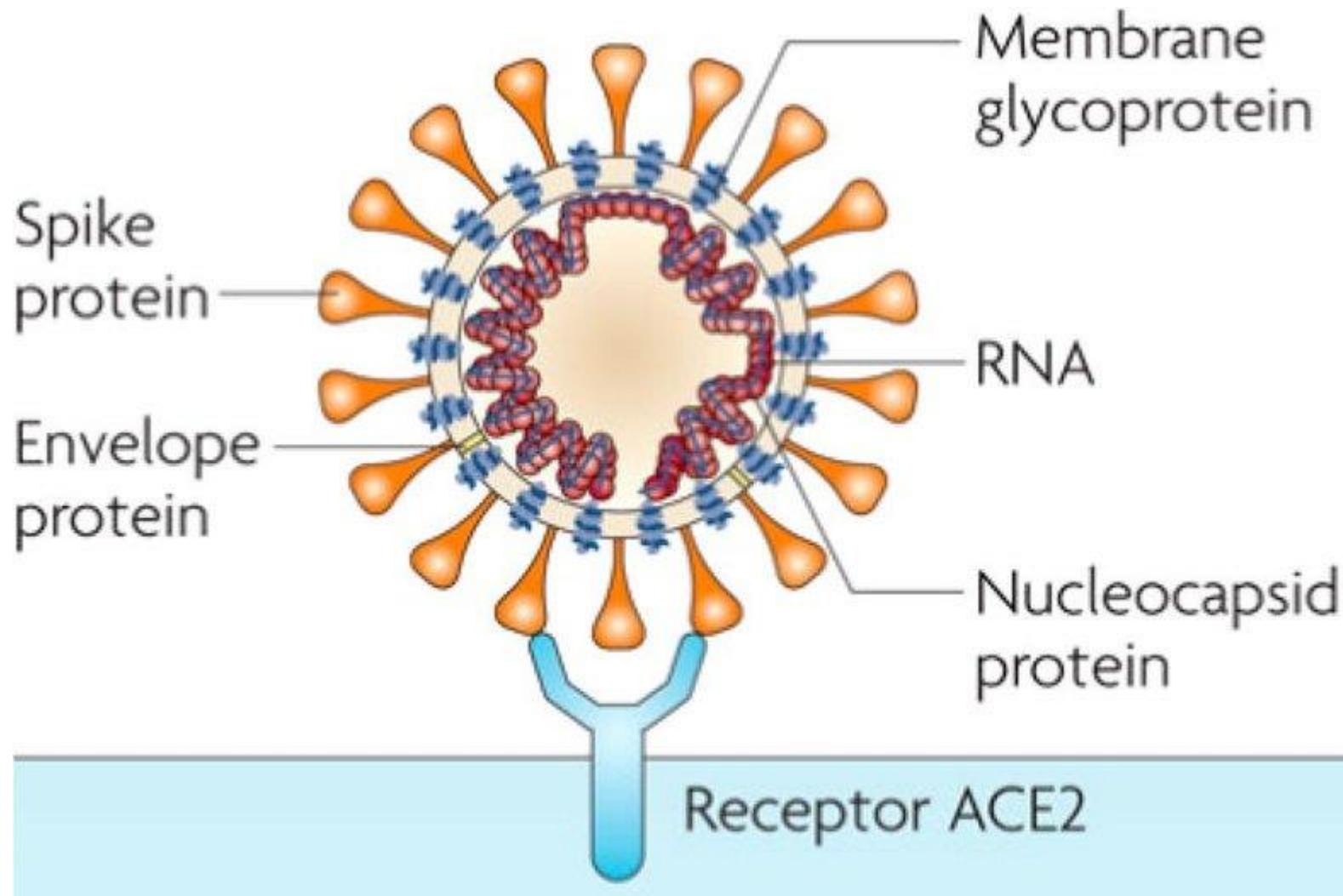
میزان ابتلا و مرگ و میر در دنیا و ایران بر اثر کووید ۱۹ تا ۱۴۰۰/۱۲/۱۱

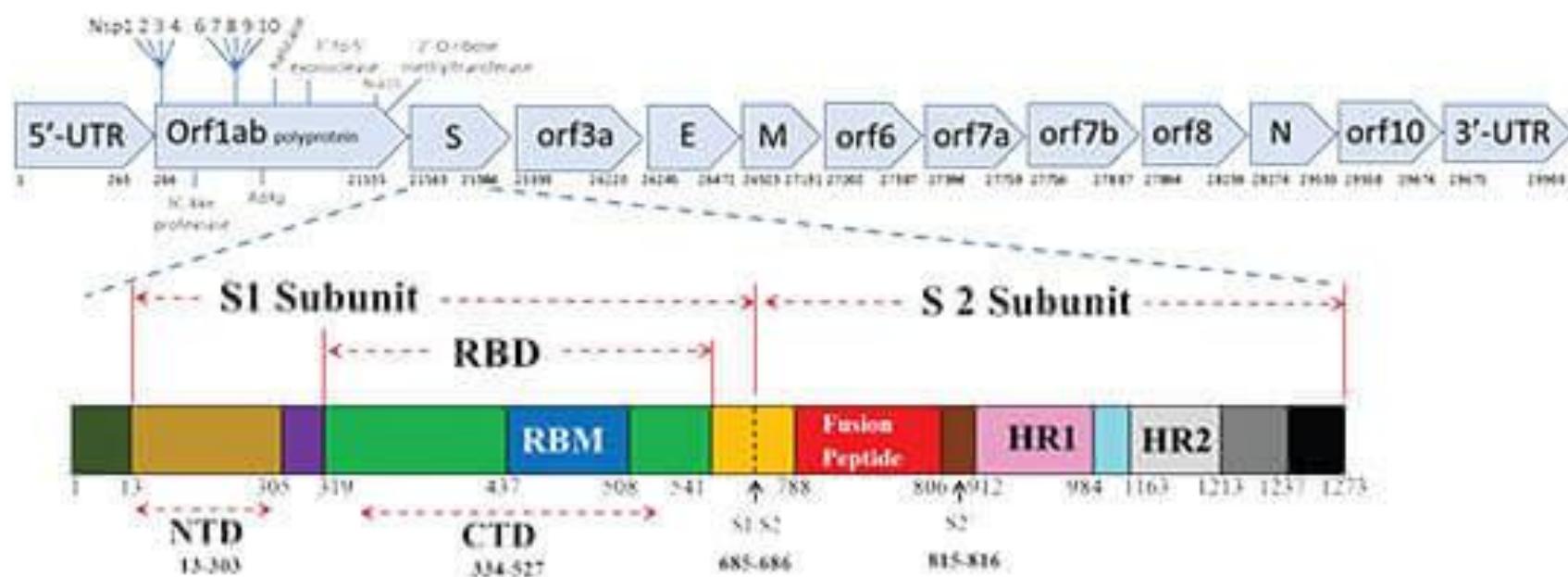
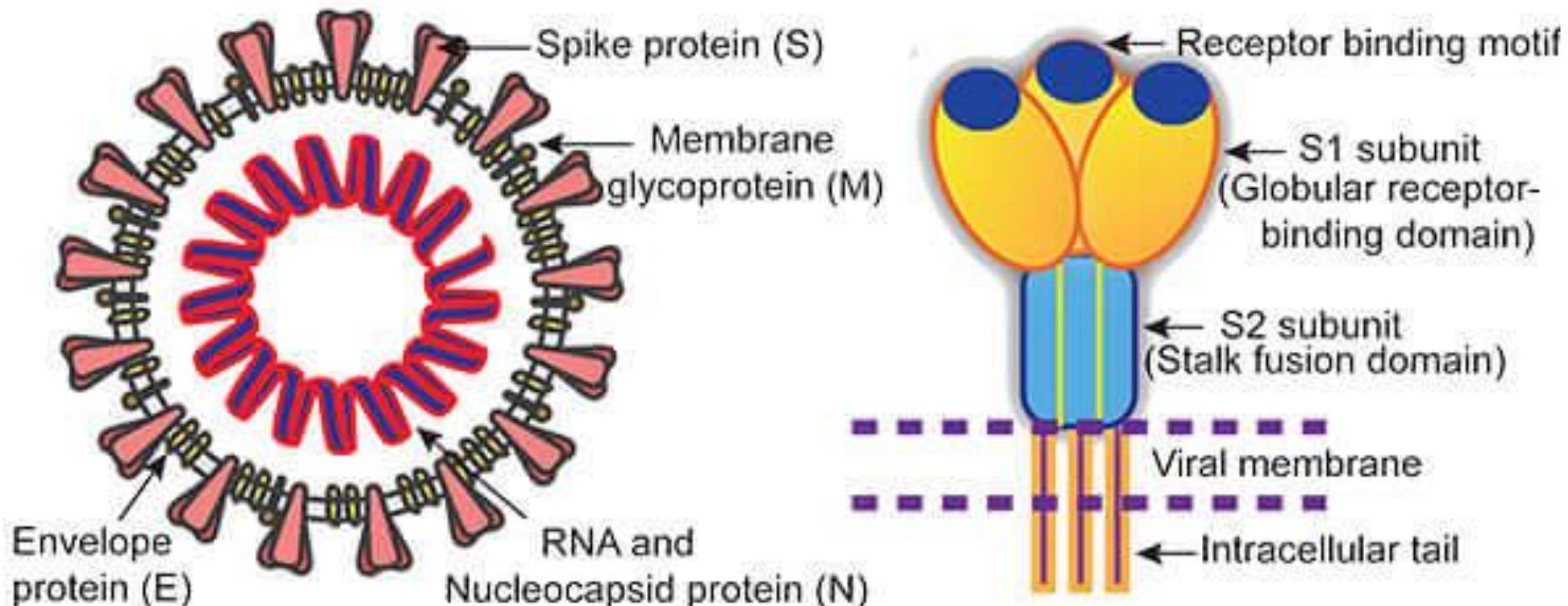




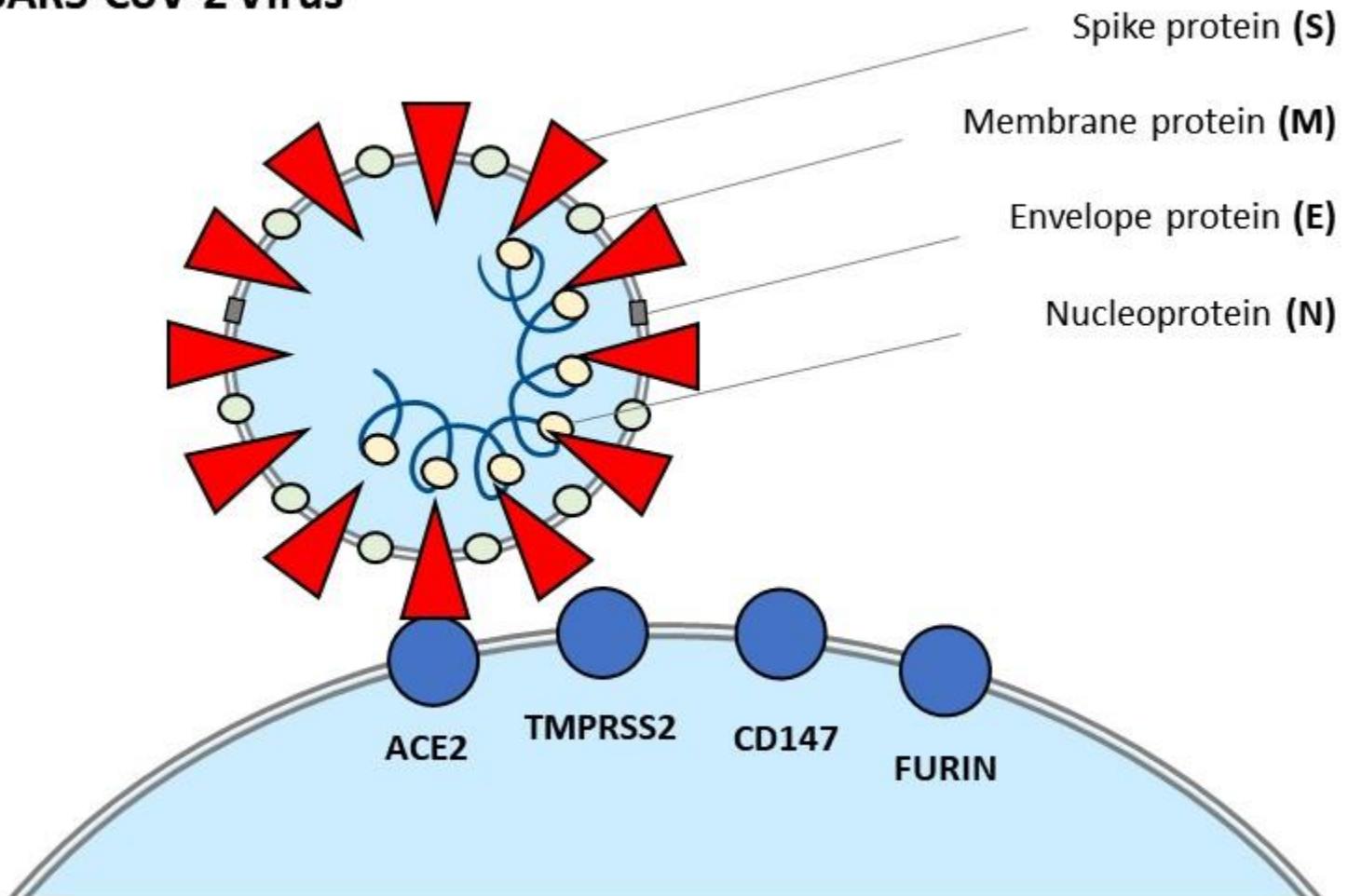
How Does Coronaviruses Spread?



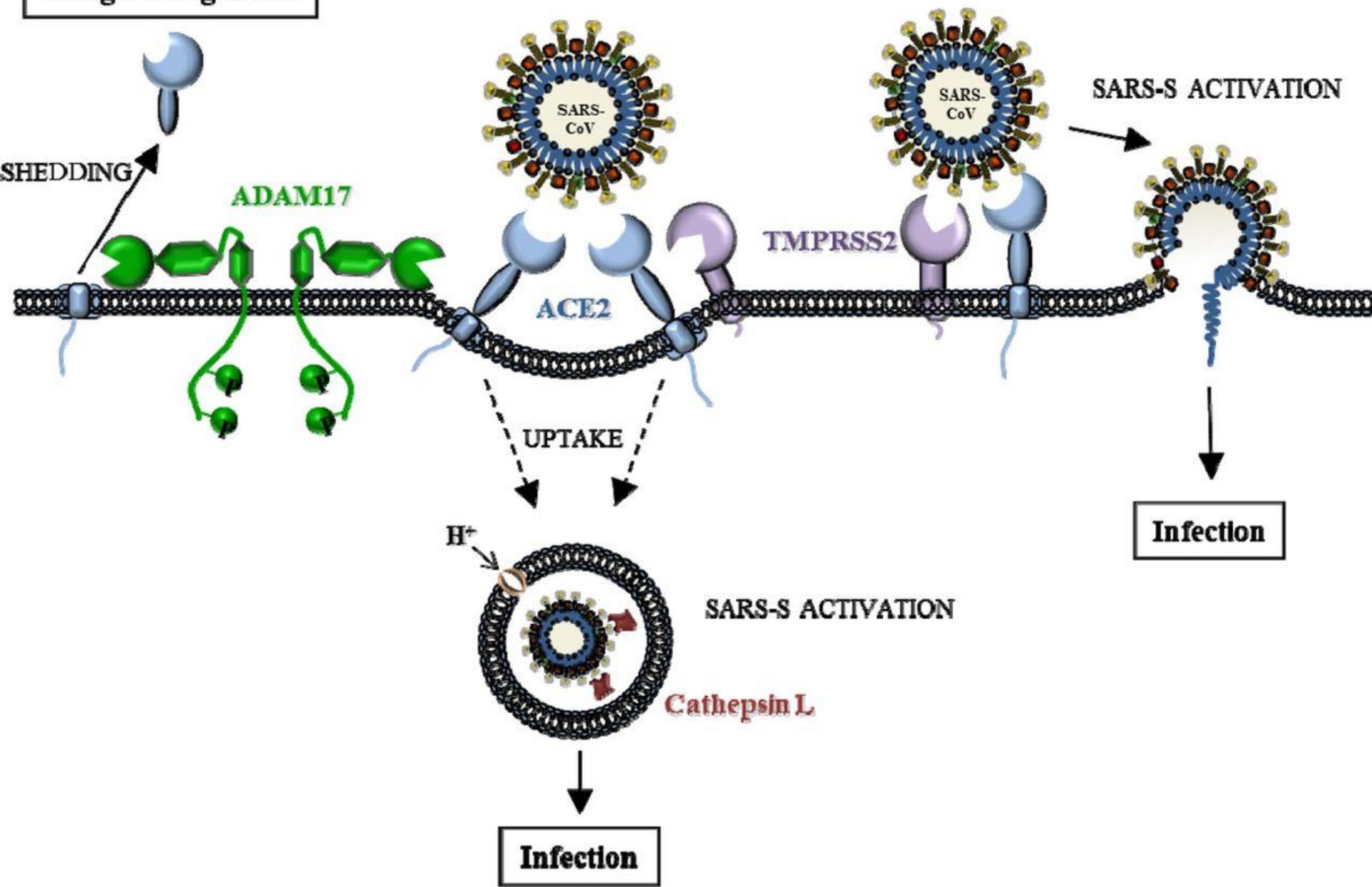




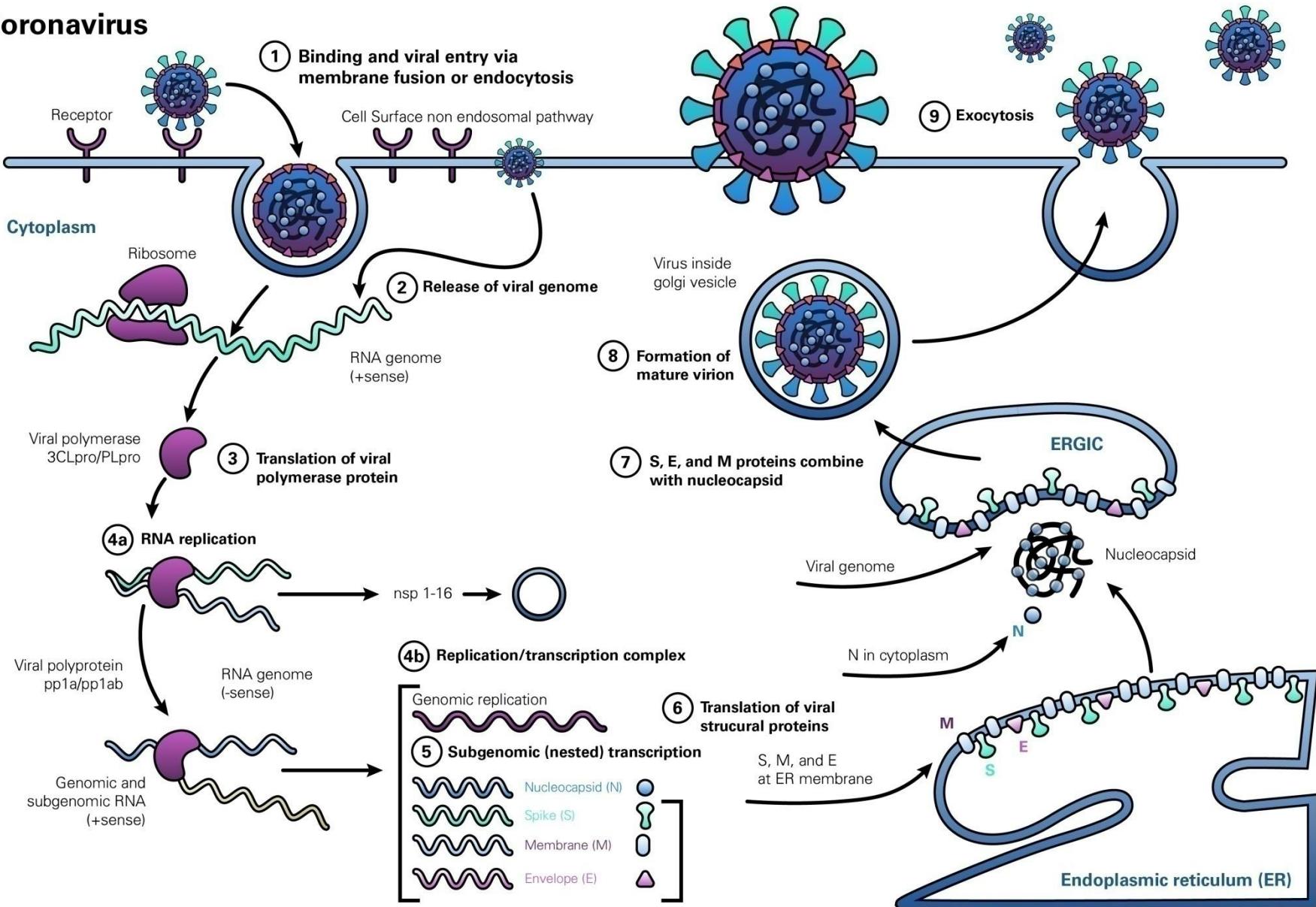
The SARS-CoV-2 Virus



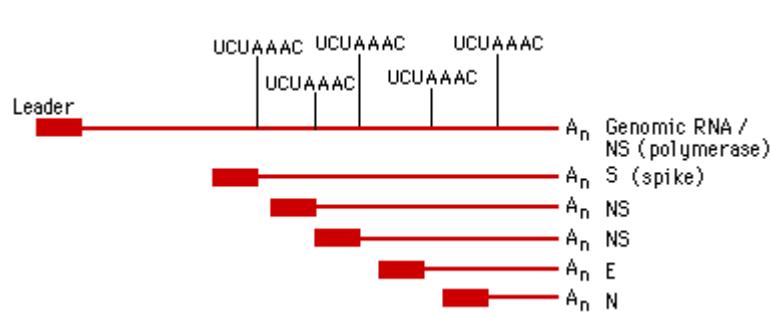
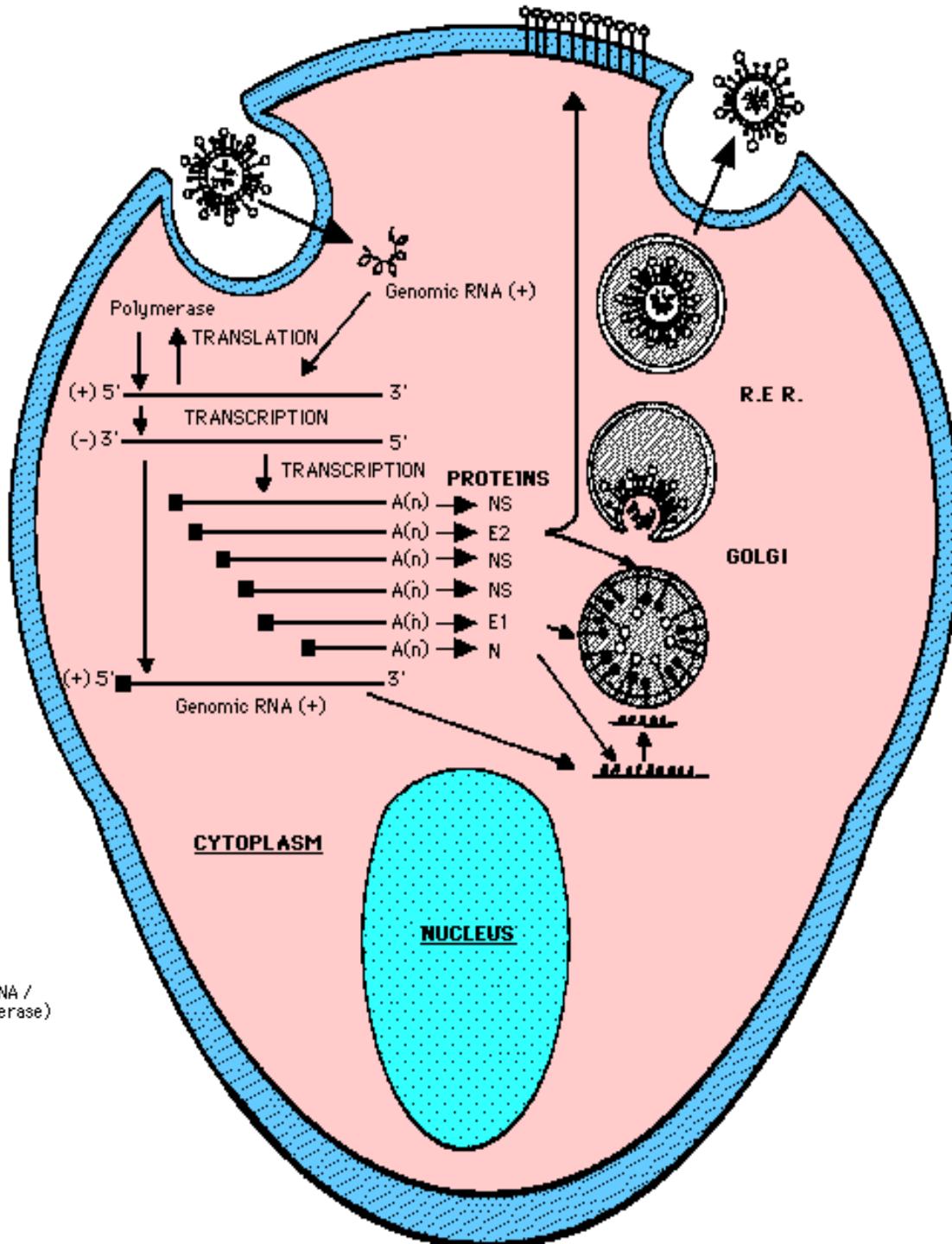
Lung Pathogenesis



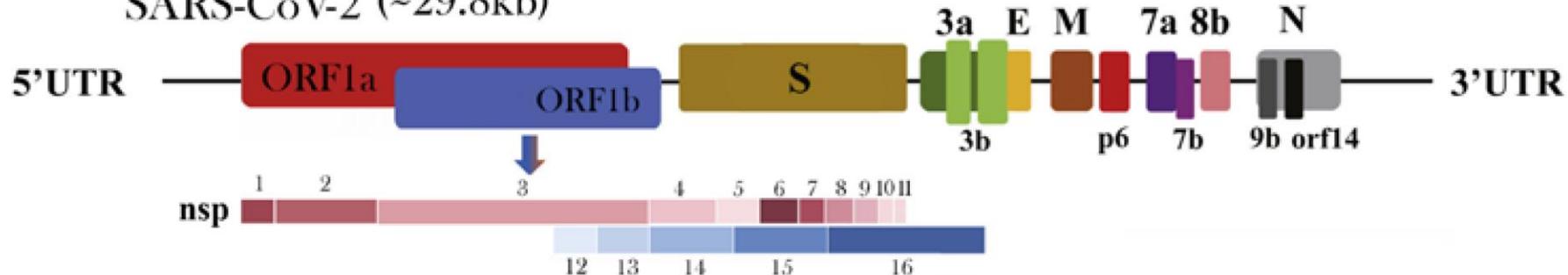
Coronavirus



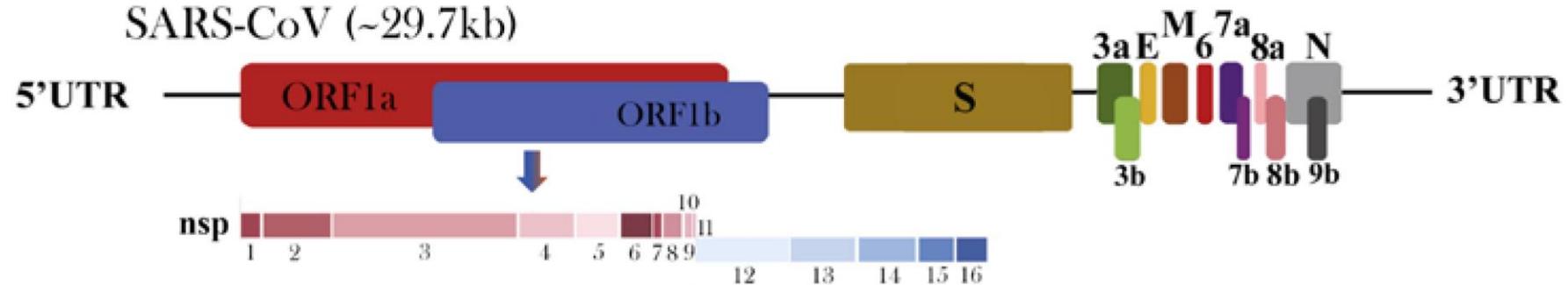
• *Viral replication*



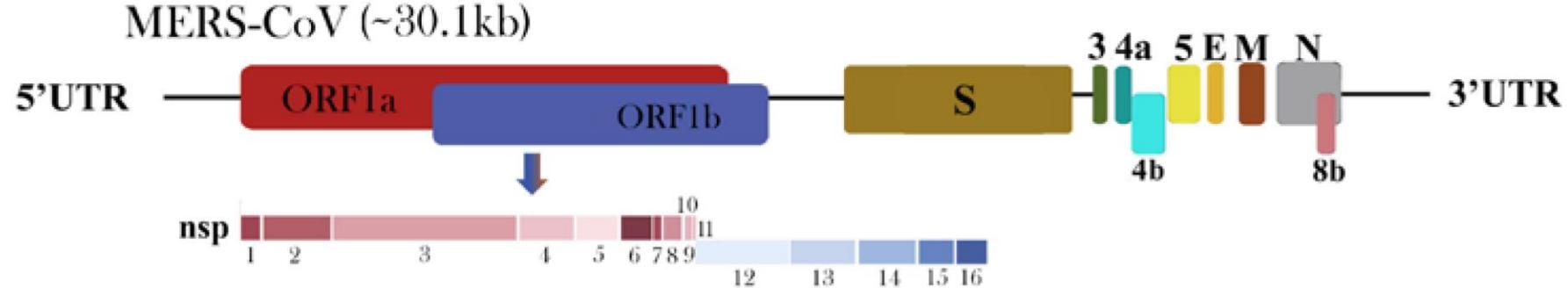
SARS-CoV-2 (~29.8kb)

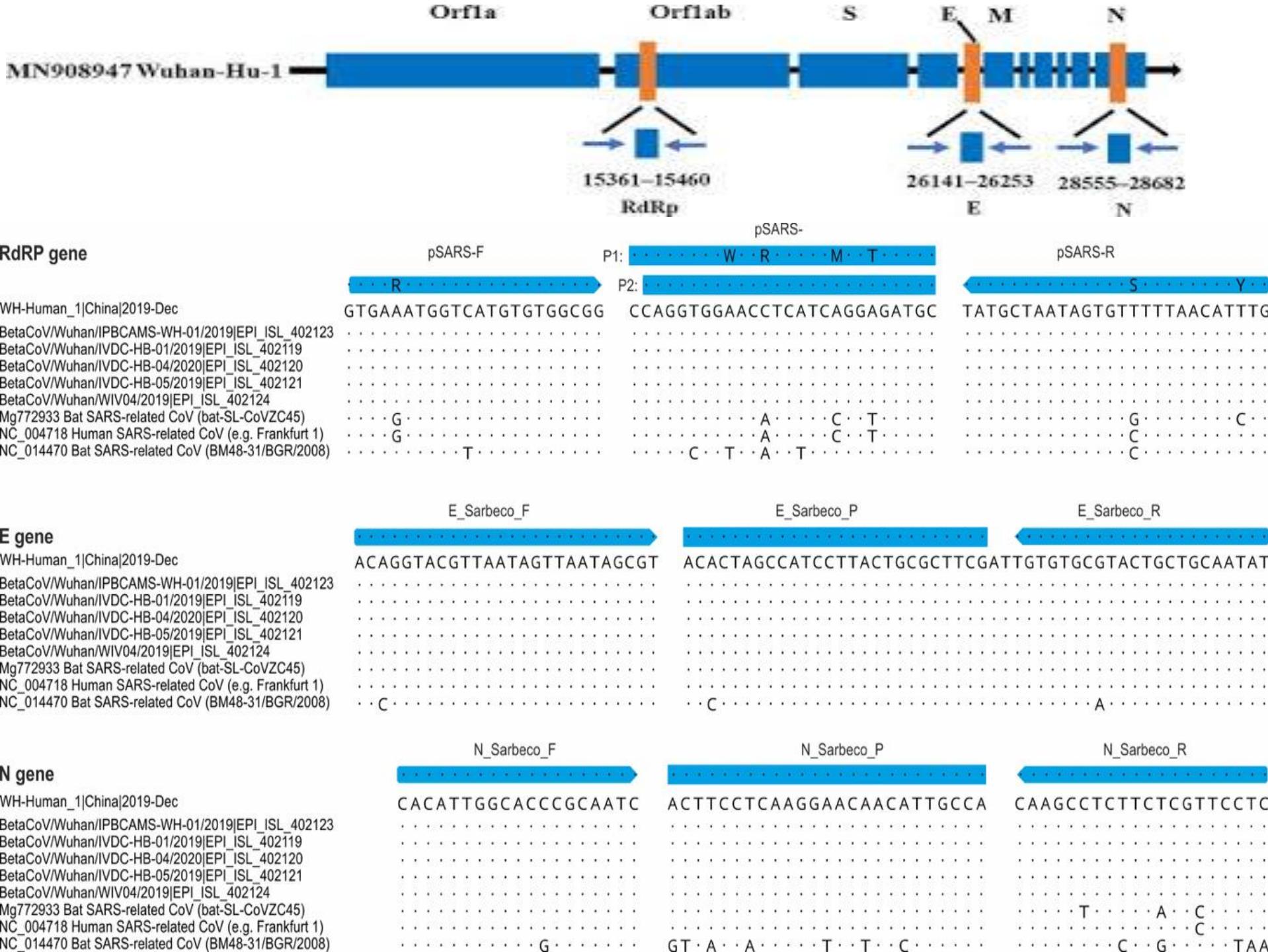


SARS-CoV (~29.7kb)



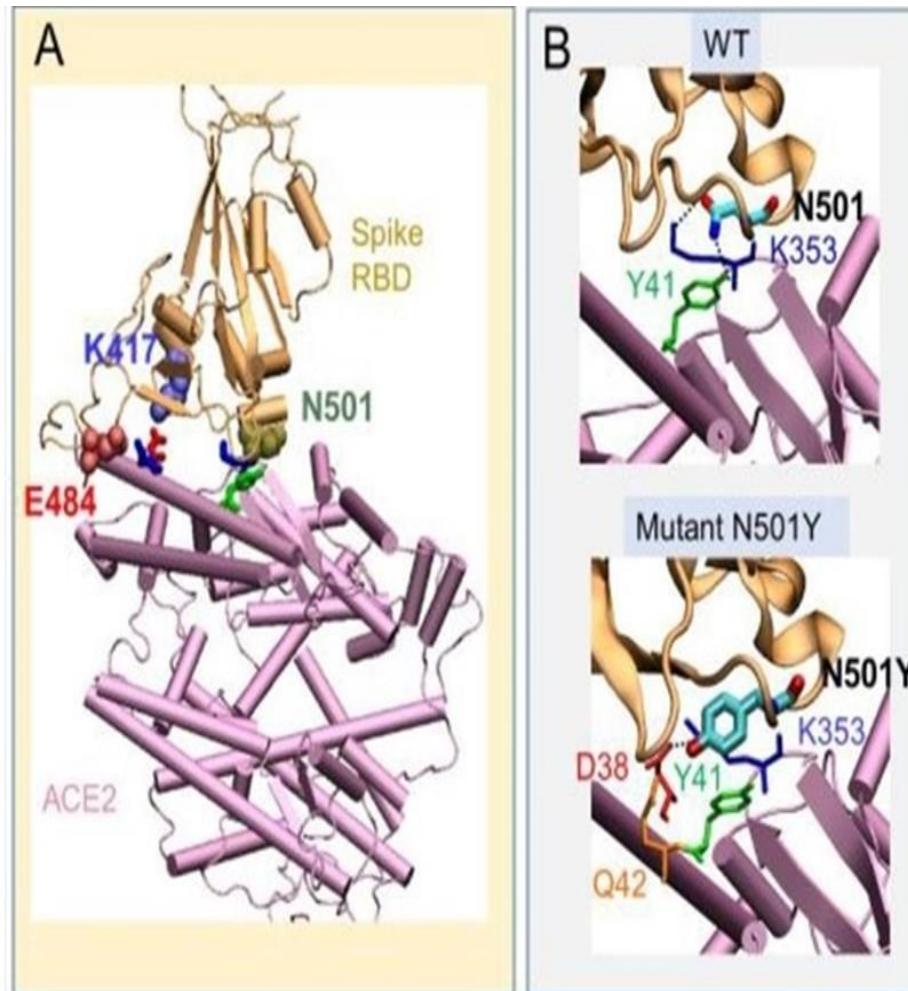
MERS-CoV (~30.1kb)





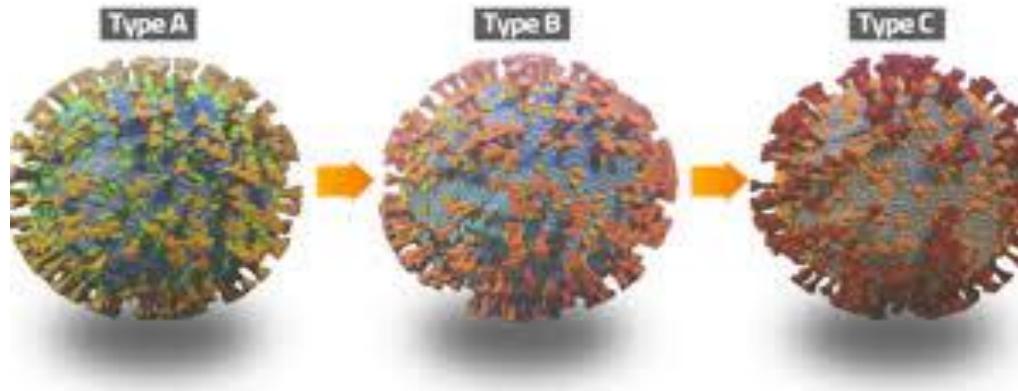


The most important mutations and variants of SARS-CoV-2



Mutation

COVID-19 Will Mutate

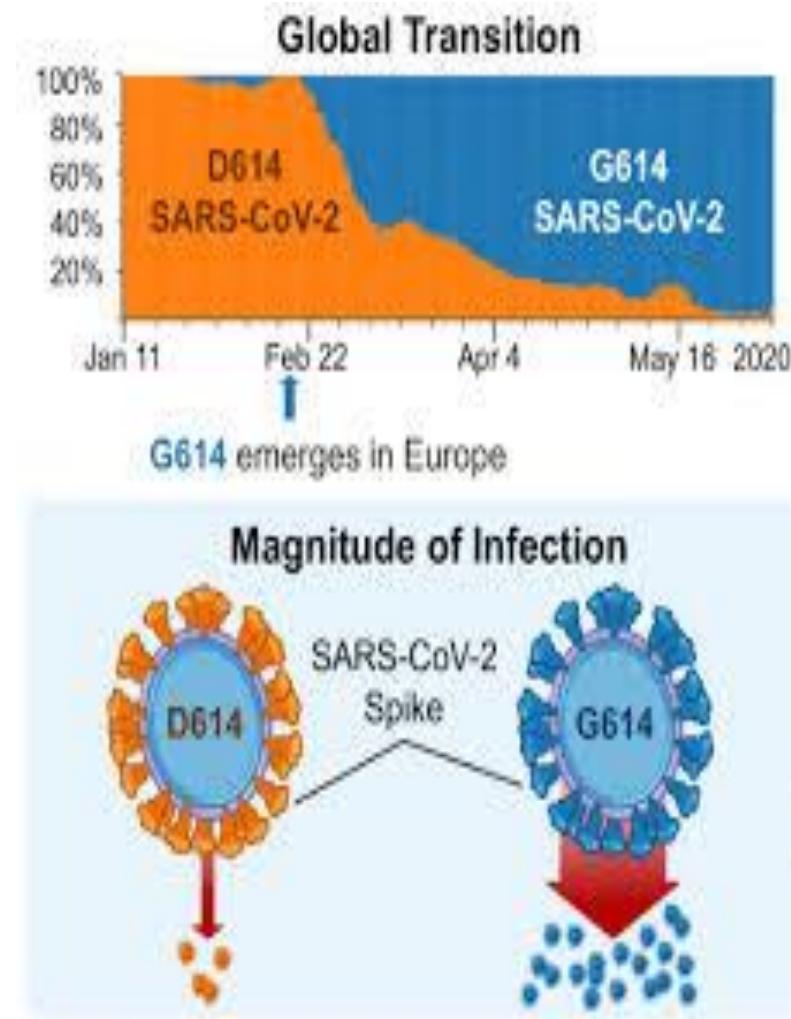


- A mutation is an **alteration in the nucleotide sequence** of the genome of an organism or virus.

The higher per-site mutation rates of RNA viruses can be explained in part by the RNA-dependent RNA polymerases (RdRp) that replicate their genomes. Unlike many DNA polymerases, RdRp do not have proofreading function and are thus unable to correct mistakes during replication.

D614G SARS-CoV-2 mutation

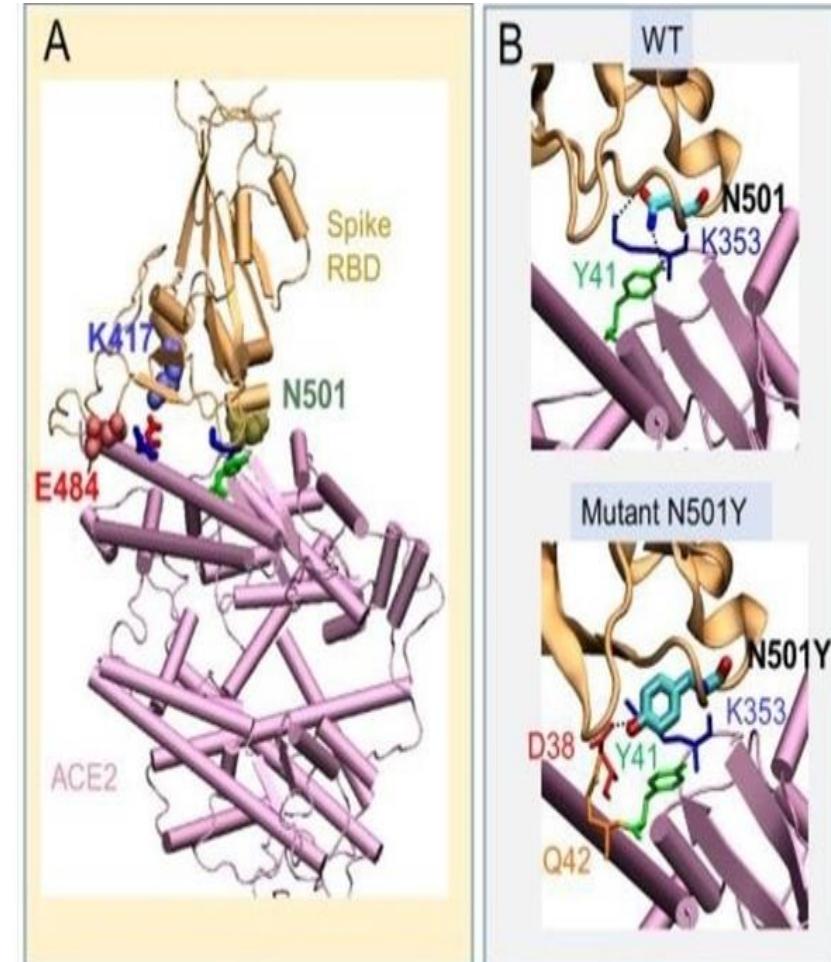
- February 2020, China.
- D614G (Spike protein).
(D)Aspartic acid \Rightarrow (G)Glycine
- D614G are better adapted to enter the human host cell.
- D614G variant appears to have evolved for greater transmissibility in humans rather than for greater pathogenicity.



Alpha variant (B.1.1.7)

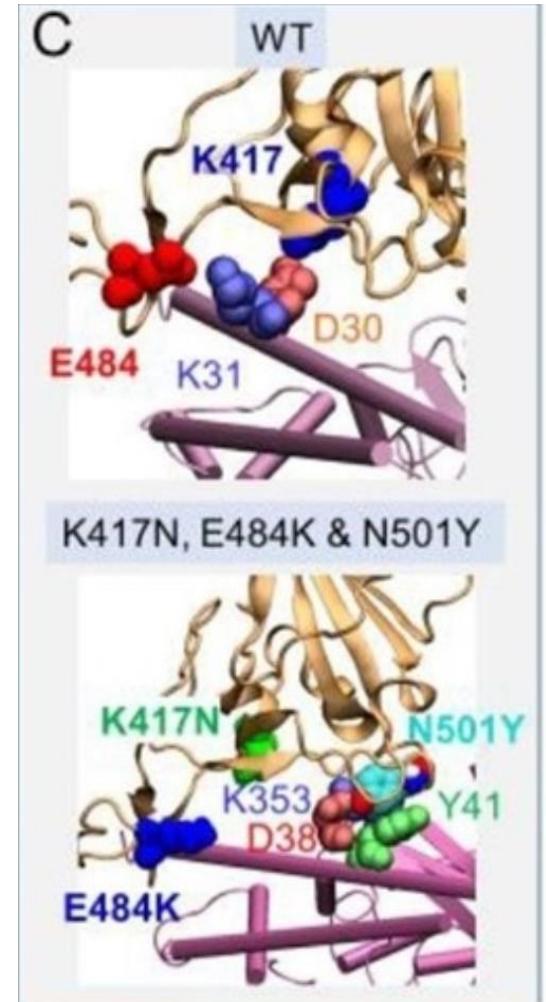
SARS-CoV-2 VOC 202012/01 or 501Y.V1

- Identified in September 2020 , UK
- 30 Dec. 2020, 46 other countries (**a lot of cases in Iran**).
- Increased transmissibility (50% more than the original form).
- 23 mutations compared with the original Wuhan strain, with eight of those in the virus's spike protein
- **N501Y** increase the strength of binding of SARS-CoV-2 to the ACE-2 and more infectious.
- But there is no evidence to suggest that the variant has any impact on the severity of disease.
 - N501Y, (Asparagin ➔ Tyrosine)
 - D614G, (Aspartic acid ➔ Glycine)
 - P681H, (Proline ➔ Histidine)



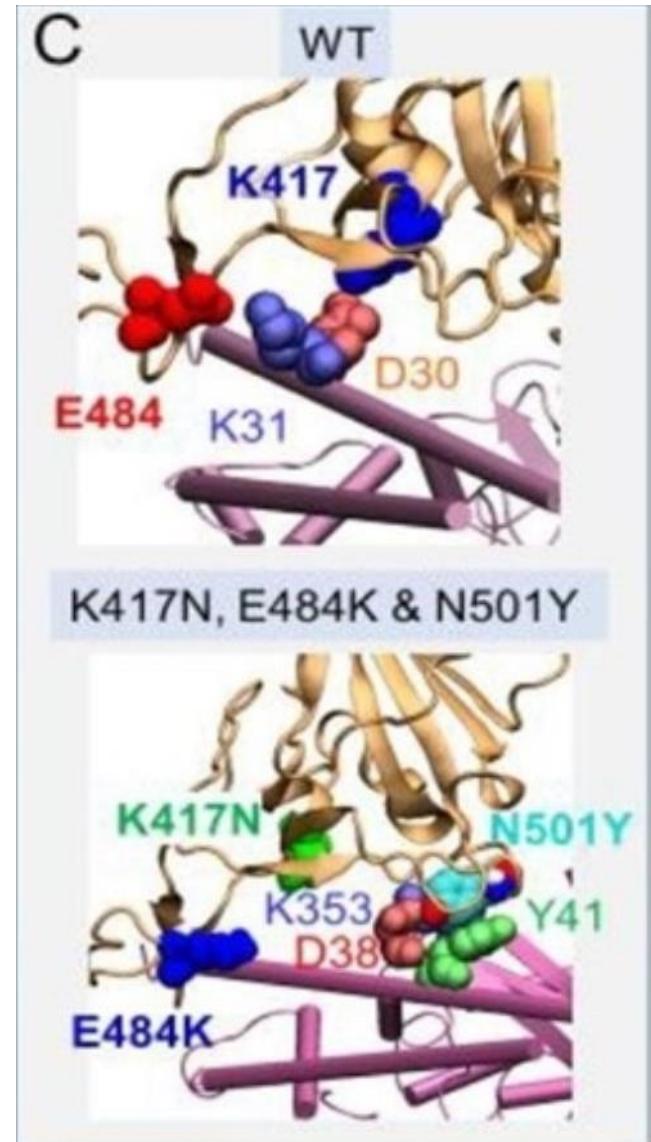
Beta variant (B.1.351) or 20H/501Y.V2

- October, 2020, South Africa
- 30 December, 2020, 19 other countries
- Higher viral load.
- Increased transmissibility.
- No associated with more severe disease or worse outcomes.
- 501.V2 variant could lead to some **escape from vaccine and immune protection**
- **K417N** is expected to effect on polyclonal and monoclonal antibodies and likely contribute to immune evasion.
- This tiny alteration (**E484K**) is reported to be an "escape mutation" may possibly make the vaccine less effective against it. (N5 loop in NTD)
- K417N, (Lysie → Asparagine)
- E484K, (Glutamic acid → Lysine)
- N501Y, (Asparagin → Tyrosine)
- D614G, (Aspartic acid → Glycine)
- A701V, (Alanine → Valine)



Gamma variant (P.1) or 501Y.V3

- First was identified in four travelers from Brazil with 17 mutations in November 2020.
- This variant contain N501Y (More transmission) and E484K (Escape of antibody) and K417T.
- These mutation are **effective on the production of previous infection antibody, vaccination or virus neutralization.**
- K417T, (Lysine → Threonine)
- E484K, (Glutamic acid → Lysine)
- N501Y, (Asparagin → Tyrosine)
- D614G, (Aspartic acid → Glycine)
- H655Y, (Histidine → Tyrosine)



Variant of SARS-CoV-2

- **Delta variant (B.1.617.2)** identified in India in October 2020
 - The delta variant has several important mutations in the spike protein,
 - Allow the variant to attach more firmly to ACE2 receptors
 - most transmissible version of the novel coronavirus to date — potentially up to 60% more transmissible than the alpha variant
- L452R, (Leucine → Arginine)
- T478K, (Threonine → Lysine)
- D614G, (Aspartic acid → Glycine)
- P681R, (Proline → Arginine)

Variants of Concern

WHO Label	Lineage + additional mutation	Country first detection	Spike mutation of interest	Year/Month of first detection
Alpha	B.1.1.7	UK	آسپارژین به تیروزین, N501Y, D614G, پرولین به هیستیدین P681H	Sep. 2020
Beta	B.1.351	South Africa	لیزین به آسپاراژین, K417N, E484K, گلوتامیک اسید به لیزین N501Y, آسپارژین به تیروزین, D614G, آسپارتیک اسید به گلایسین A701V, آلانین به والین	Sep. 2020
Gama	P.1	Brazil	لیزین به تیروزین, K417T, E484K, گلوتامیک اسید به لیزین N501Y, آسپارژین به تیروزین, D614G, آسپارتیک اسید به گلایسین H655Y, هیستیدین به تیروزین	Nov. 2020
Delta	B.1.617.2	India	لوسین به آرژینین, L452R, ترئونین به لیزین T478K, آسپارتیک اسید به گلایسین, D614G, پرولین به آرژینین, P681R,	Oct. 2020
Eta	B.1.525	Nigeria	گلوتامیک اسید به لیزین, E484K, آسپارتیک اسید به گلایسین, D614G, گلوتامین به هیستیدین, Q677H,	Dec.2020
Theta	P.3	Philippines	گلوتامیک اسید به لیزین, E484K, آسپارژین به تیروزین, N501Y, آسپارتیک اسید به گلایسین, D614G, پرولین به آرژینین, P681R,	Jan. 2021
Kappa	B.1.617.1	India	لوسین به آرژینین, L452R, گلوتامیک اسید به گلوتامین, E484Q, آسپارتیک اسید به گلایسین, D614G, پرولین به آرژینین, P681R,	Dec.2020
Lambda	C.37	Peru	لوسین به آرژینین, L452R, فنیل آلانین به سرین, F490S, آسپارتیک اسید به گلایسین, D614G,	Dec.2020

Variant of SARS-CoV-2

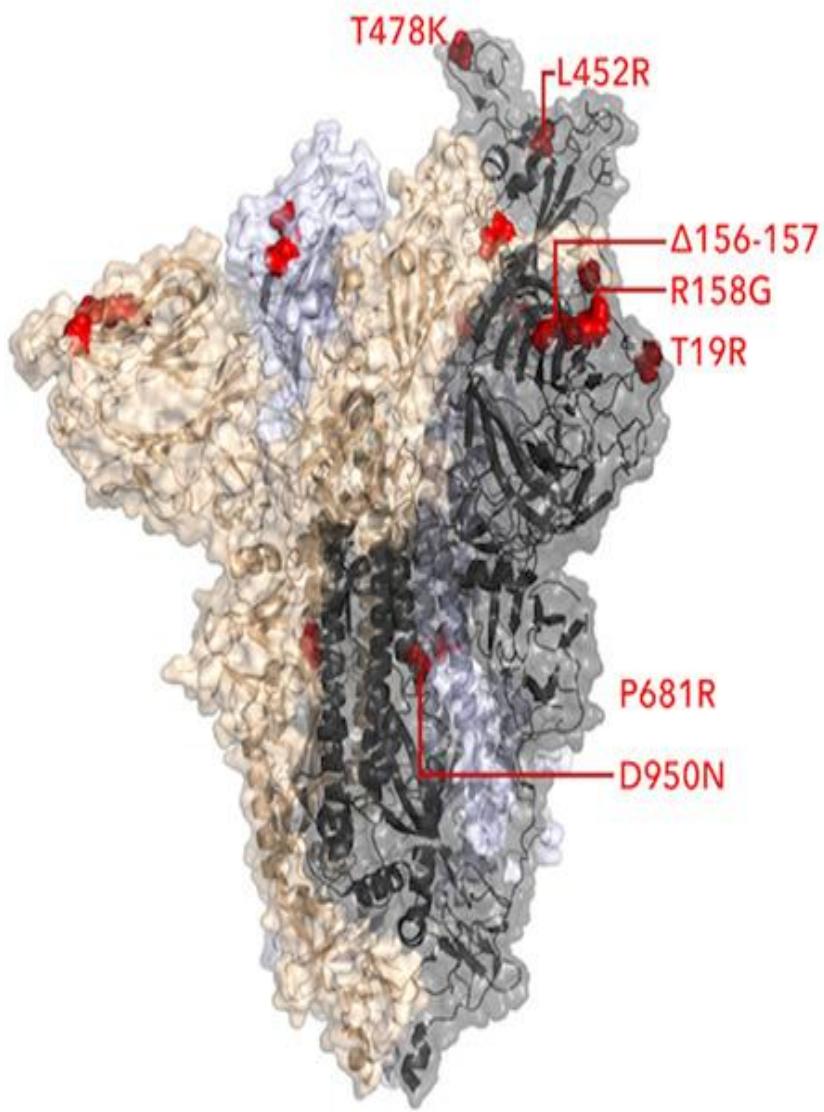
- **Omicron variant (B.1.1.529)** first identified in South Africa in Nov 2021
 - More than 30 mutations in the genes that code for its spike protein, with 10 of those genes coding for parts of the “**Receptor Binding Domain,**”
 - Omicron's other mutations have also shown up in past variants and may lead to higher transmissibility or may help the virus evade the immune system
 - Omicron has the N501Y (**Asparagine to Tyrosine**) mutation, which is also found in the Alpha variant, and is thought to make the virus more contagious

Spike protein mutation in Delta and Omicron variant compared to wild-type (Wuhan-Hu-1)

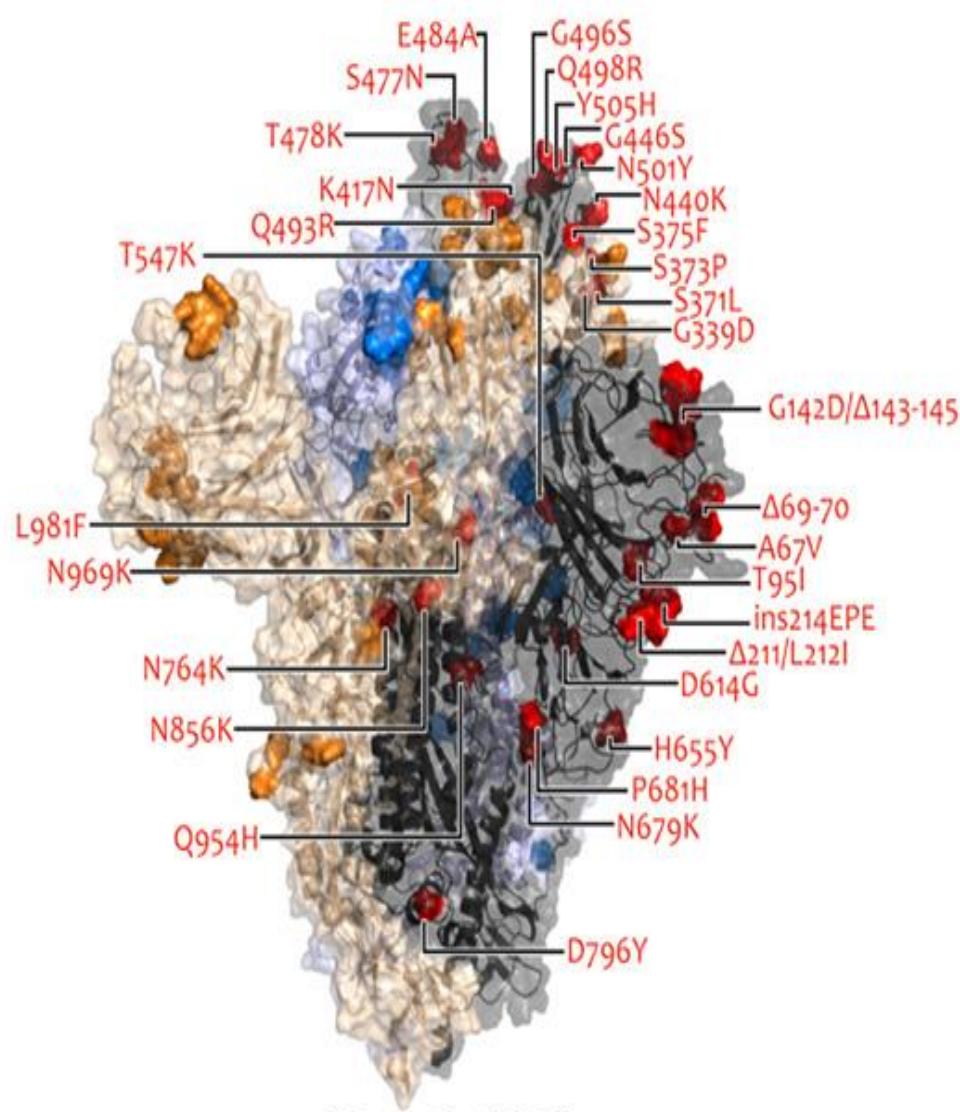
Variant	Sequence ID	Mutation
Wuhan-Hu-1 (wild-type)	NCBI ID:P0DTG2	-
Delta Variant (B.1.617.2)	NCBI: QWK65230.1	T19R, G142D, Δ156-157, R158G, Δ213-214, L452R, T478K, D614G, P681R, D950N
Omicron (B.1.1.529)	GSAID ID: R40B60_BHP_3321001247/2021	A67V, Δ69-70, T95I, G142D, Δ143-145, N211I, L212V, ins213-214RE, V215P, R216E, G339D, S371L, S373P, S375F, K417N, N440K, G446S, S477N, T478K, E484A, Q493R, G496S, Q498R, N501Y, Y505H, T547K, D614G, H655Y, N679K, P681H, N764K, D796Y, N856K, Q954H, N969K, L981F

Note: Receptor-binding domain (**residues 319–541**) are marked as bold in both Delta and Omicron variants. Δ Represents deletion, ins represent insertion.

(A) Delta



(B) Omicron



(B.1.617.2)

(B.1.1.529)

Omicron variants

- **Omicron sublineage (BA.1)**
 - predominant sublineage
 - 95% of samples from North America and 87% of samples from South America
- **Omicron sublineage (BA.2)**
 - identified mainly in Africa
 - BA.2 differs from original omicron variant in its genetic sequence, including some amino acid differences in the spike protein and other proteins
 - BA.1 and BA.2 share 32 mutations, but differ by 28
 - lacks the characteristic S-gene target failure (SGTF)-causing deletion ($\Delta 69-70$)
 - Reinfection with BA.2 following infection with BA.1 has been documented
- **Omicron sublineage (BA.3)**
 - BA.3, is very rare
 - land 71.0%, South_Africa 12.0%, United Kingdom 4.0%, Germany 3.0%, France 2.0%

Omicron variants:

- No evidence of any change has been found in terms of transmissibility, clinical presentation, severity, or evasion of the immune response for these sublineages

A photograph of a forest path in autumn. The ground is covered with fallen orange and yellow leaves. Bare trees stand tall on both sides, their trunks light-colored. Some trees still have a few autumn leaves clinging to their branches. The overall atmosphere is quiet and peaceful.

با تشکر از توجه شما