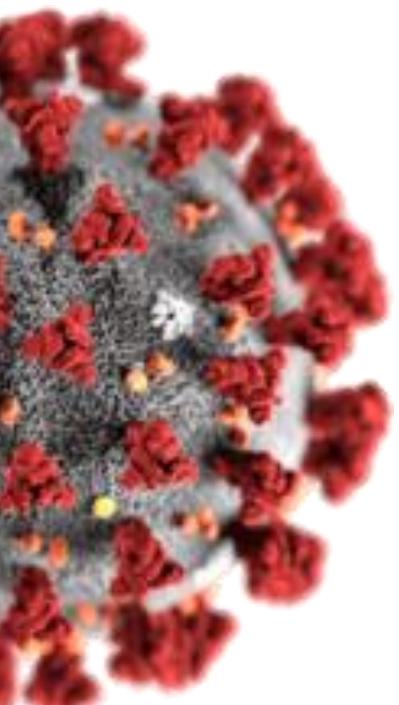


Co jste kdy (ne)chtěli vědět o strukturách SARS-CoV-2

Karel Berka

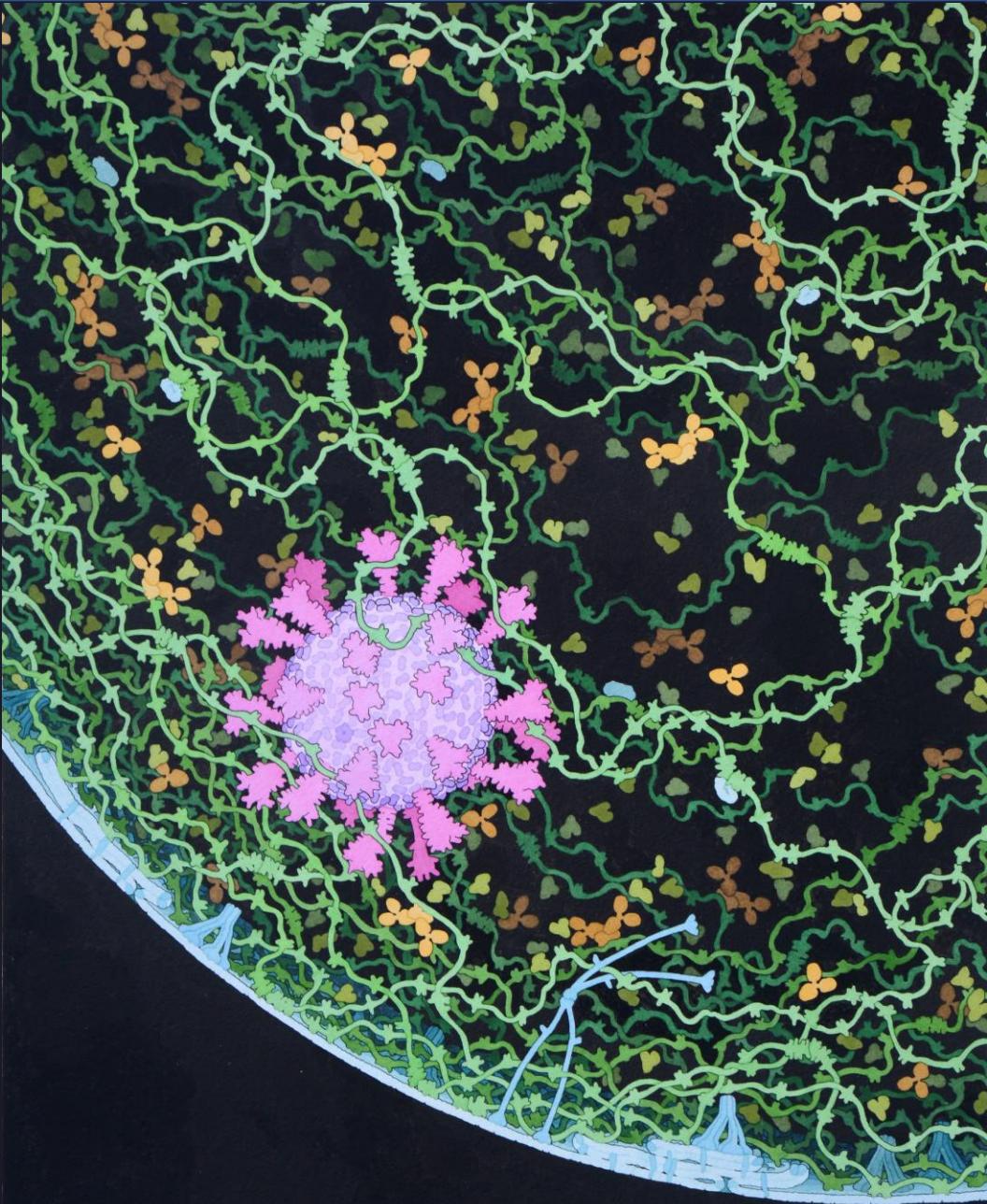
KFC PřF UPOL



Osnova

SARS-CoV-2

- Genom
- Proteiny
 - Viru
 - Hostitele
- Virová kapsle
- Life cycle viru
- Léčba
- Vakcíny



<http://pdb101.rcsb.org/sci-art/goodsell-gallery/respiratory-droplet>

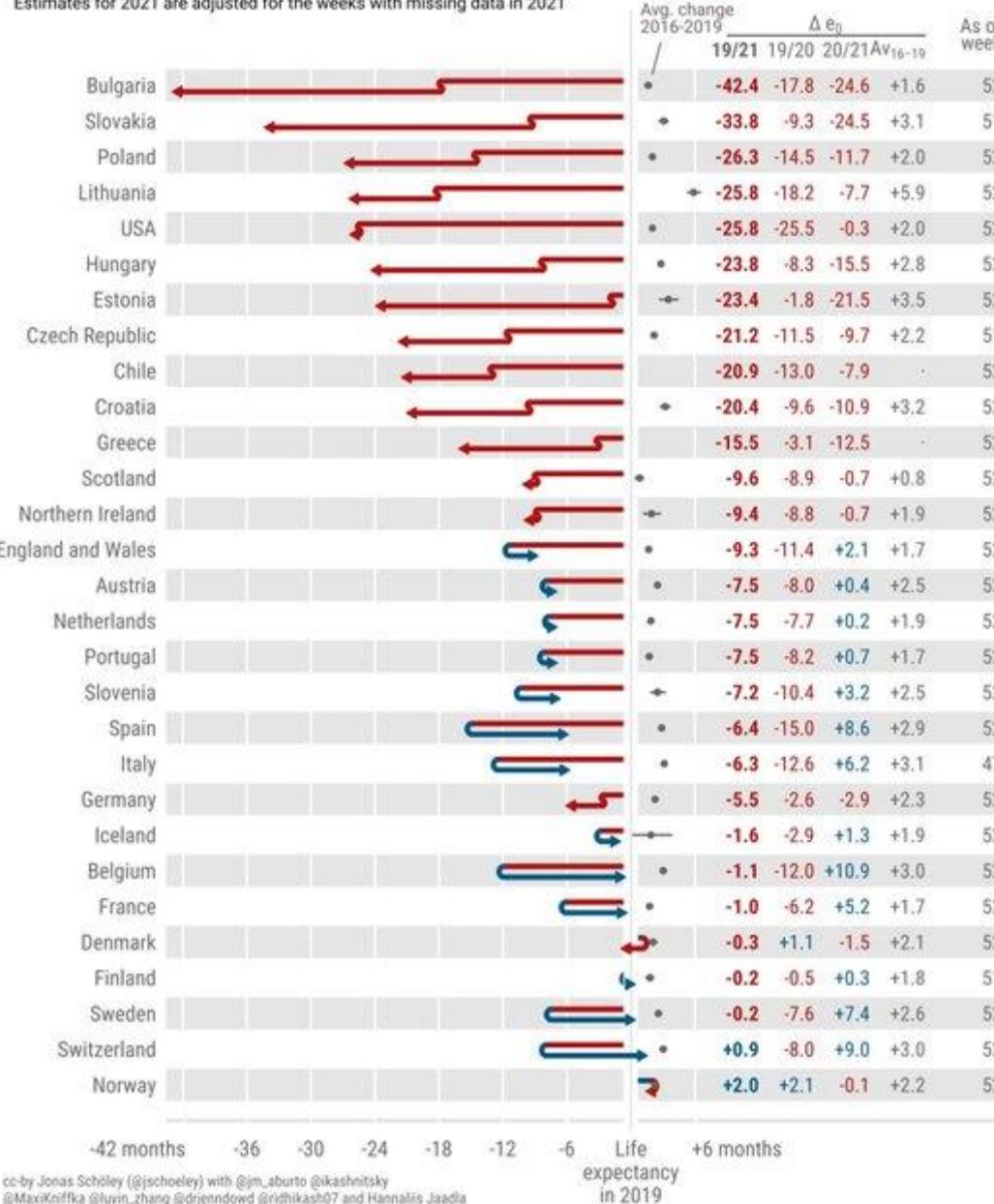
Illustration by David S. Goodsell, RCSB Protein Data Bank; doi: 10.2210/rcsb_pdb/goodsell-gallery-024

Life Cycle

Life expectancy bounce-backs amid continued losses

Life expectancy changes since the start of the COVID-19 pandemic

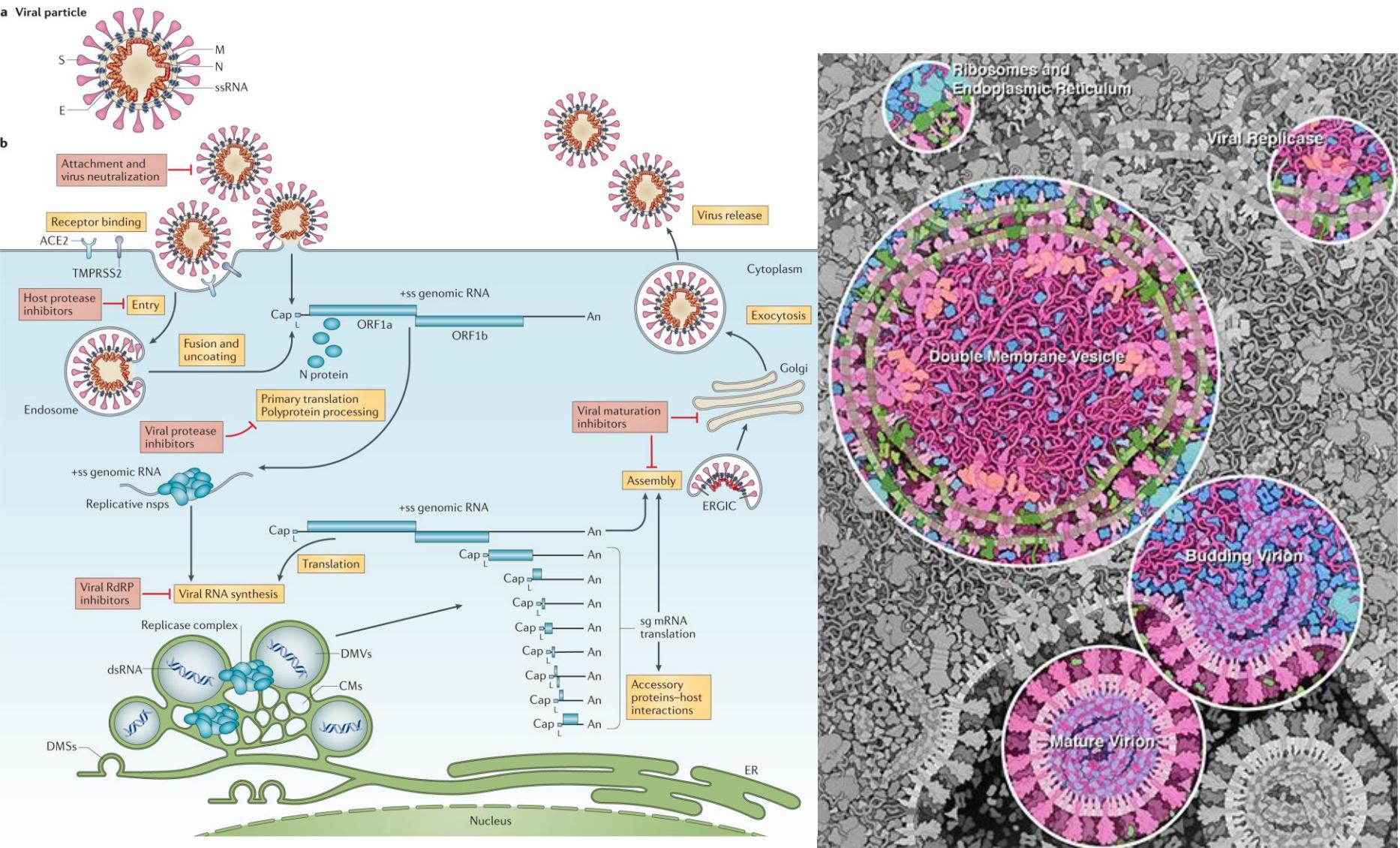
Estimates for 2021 are adjusted for the weeks with missing data in 2021



Life Cycle of SARS-CoV-2

<https://www.youtube.com/watch?v=k2GlafQ9YhY>

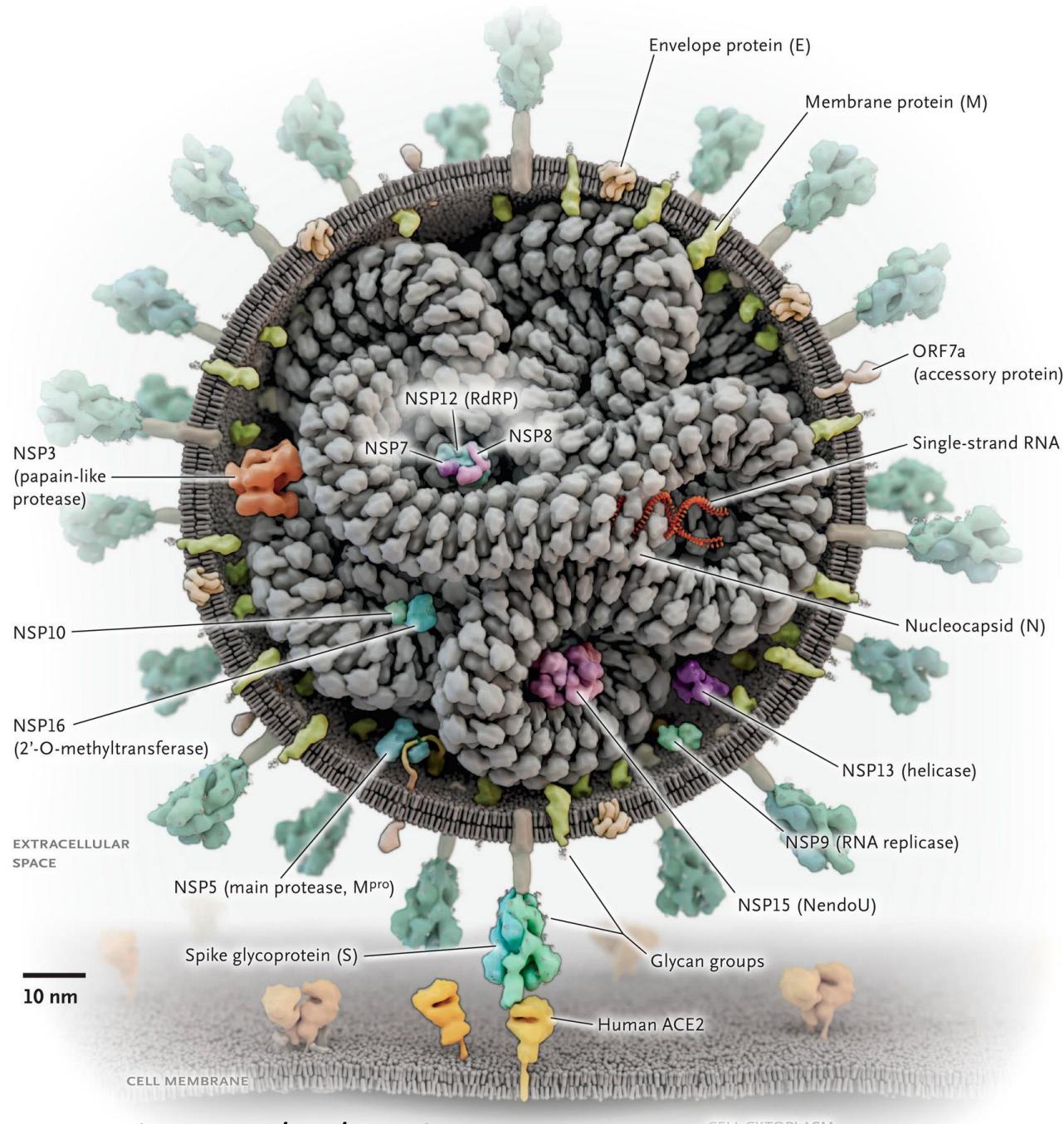
Life Cycle of SARS-CoV-2



<https://www.nature.com/articles/s41579-020-00468-6/figures/1>

<http://pdb101.rcsb.org/sci-art/goodsell-gallery/coronavirus-life-cycle>

Virus Genome/Proteome

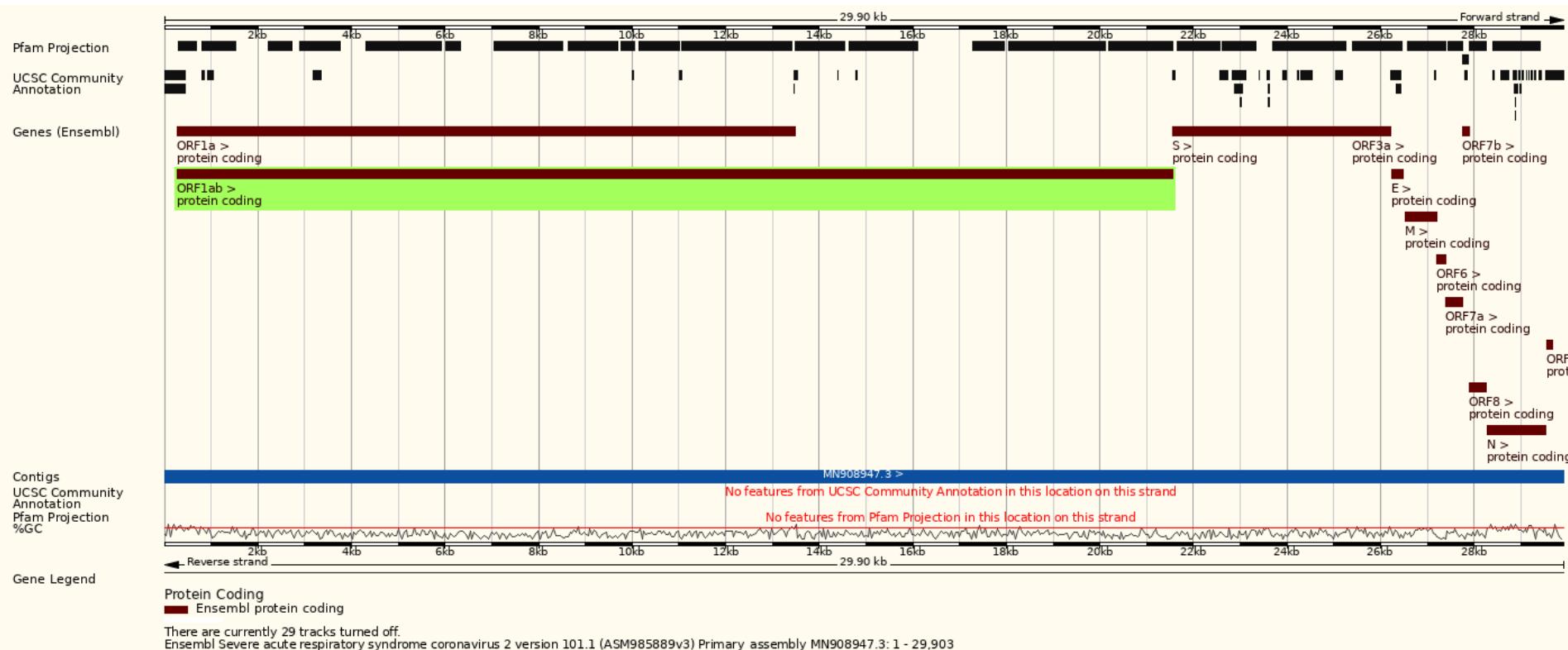


Genom SARS-CoV-2

RNA+ virus

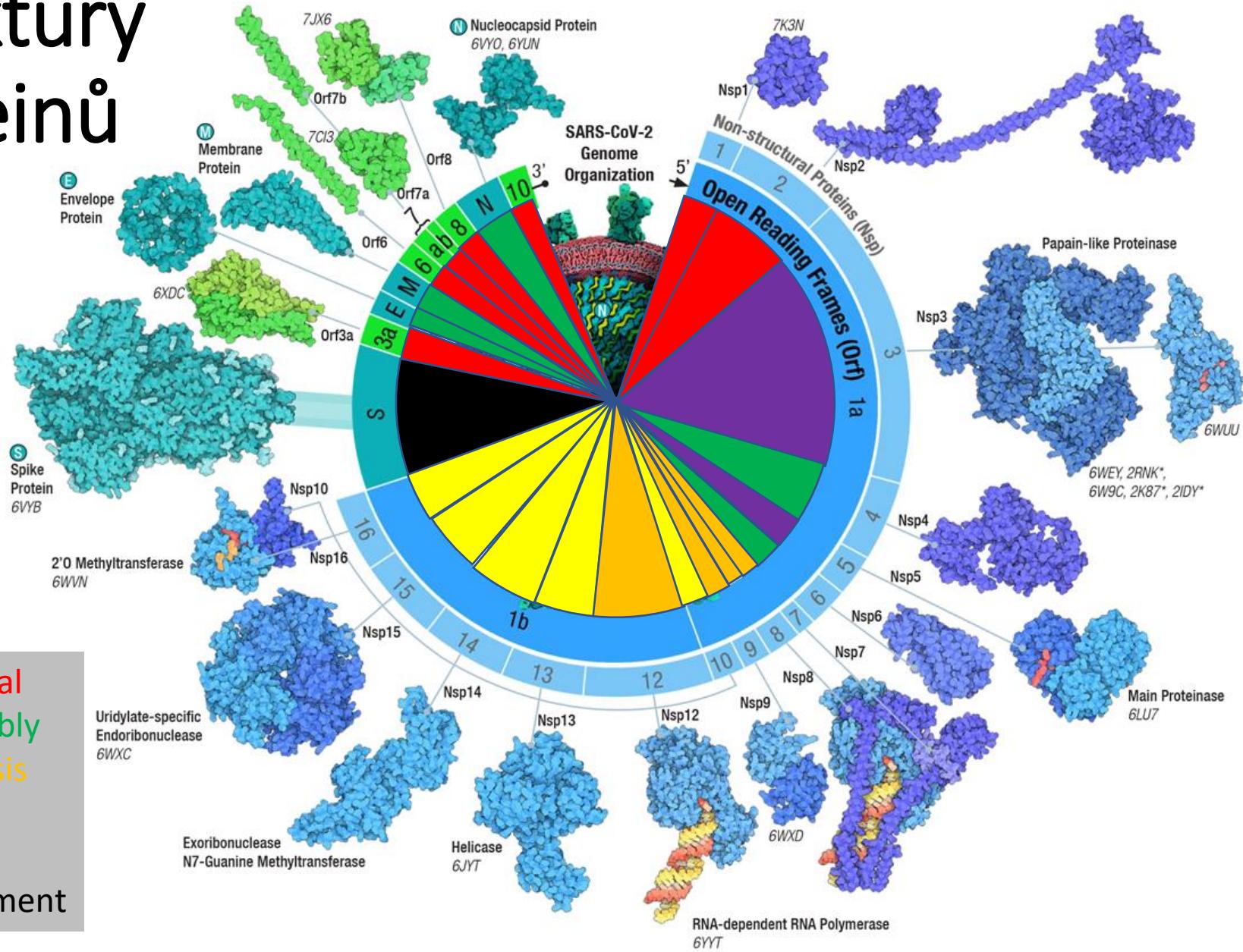
29,903 b

12 coding genes – ORF1ab v sobě obsahuje 16 nsp proteinů



Ensembl Severe acute respiratory syndrome coronavirus 2 version 101.1 (ASM985889v3) Primary_assembly MN908947.3: 1 - 29.903

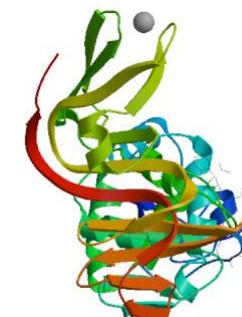
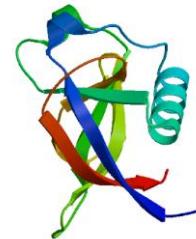
Struktury proteinů



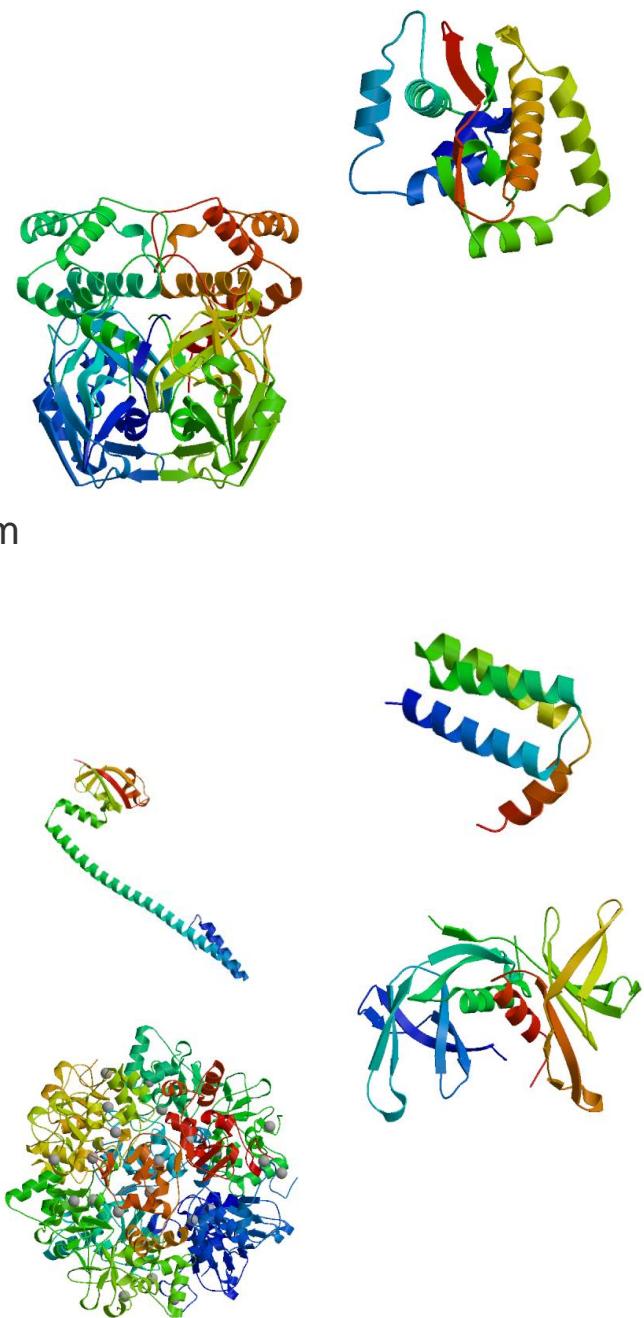
• <https://cdn.rcsb.org/pdb101/learn/resources/flyers/covid-genome/covid-genome-prots.png>

SARS-CoV-2 proteiny

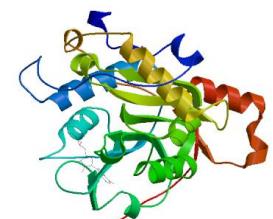
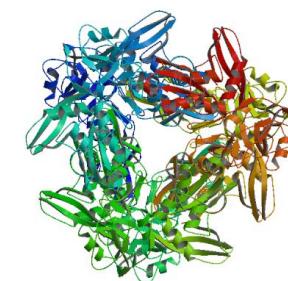
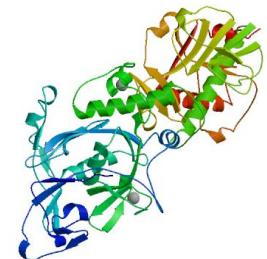
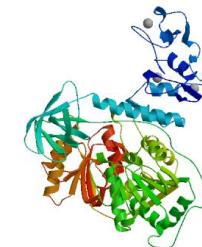
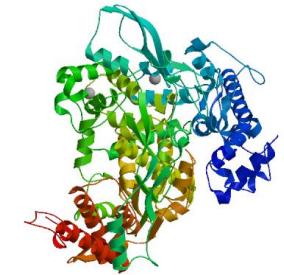
- Replicase polyprotein 1ab
 - **Multifunctional protein involved in the transcription and replication** of viral RNAs. Contains the proteinases responsible for the cleavages of the polyprotein.
- Host translation inhibitor nsp1
 - Inhibits **host translation** by interacting with the 40S ribosomal subunit. The nsp1-40S ribosome complex further induces an endonucleolytic cleavage near the 5'UTR of host mRNAs, targeting them for degradation. Viral mRNAs are not susceptible to nsp1-mediated endonucleolytic RNA cleavage thanks to the presence of a 5'-end leader sequence and are therefore protected from degradation. By suppressing host gene expression, nsp1 facilitates efficient viral gene expression in infected cells and evasion from host immune response.
- Non-structural protein 2 (nsp2)
 - **modulation of host cell survival signaling pathway by interacting with host PHB and PHB2.** Indeed, these two proteins play a role in maintaining the functional integrity of the mitochondria and protecting cells from various stresses
- Non-structural protein 3 (nsp3) - PL-PRO
 - Responsible for the **cleavages of polyprotein**



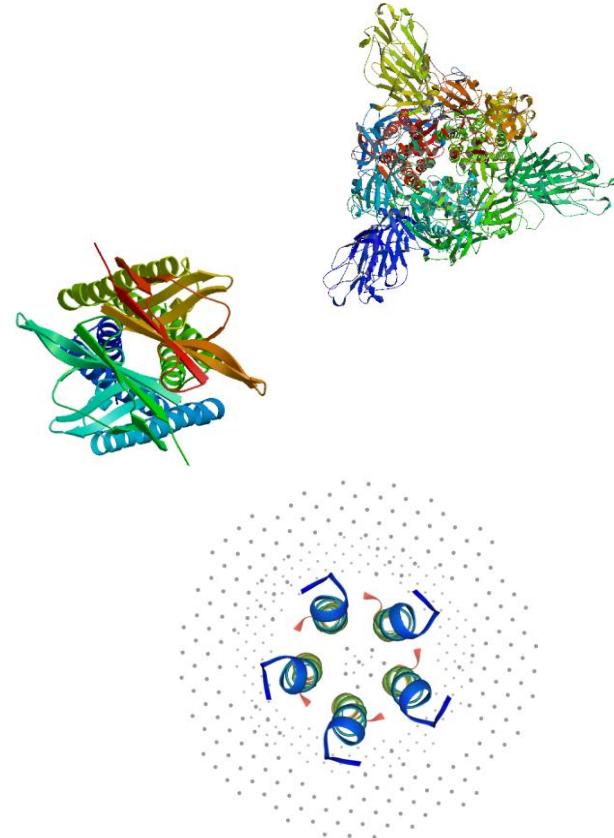
- Non-structural protein 4 (nsp4)
 - assembly of virally-induced cytoplasmic **double-membrane vesicles** necessary for viral replication.
- 3C-like proteinase (3CL-PRO)
 - **Cleaves** the C-terminus of **replicase polyprotein** at 11 sites
- Non-structural protein 6 (nsp6)
 - initial **induction of autophagosomes** from host reticulum endoplasmic. Later, limits the expansion of these phagosomes that are no longer able to deliver viral components to lysosomes
- Non-structural protein 7 (nsp7)
 - **viral RNA synthesis**
- Non-structural protein 8 (nsp8)
 - **viral RNA synthesis**
- Non-structural protein 9 (nsp9)
 - viral replication by acting as a **ssRNA-binding protein**.
- Non-structural protein 10 (nsp10)
 - viral mRNAs **cap methylation**

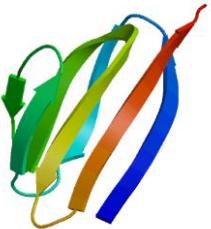


- RNA-directed RNA polymerase (Pol)
 - Responsible for **replication** and **transcription** of the viral RNA genome.
- Helicase (Hel)
 - RNA and DNA **duplex-unwinding** activities with 5' to 3' polarity
- Proofreading exoribonuclease (ExoN)
 - **exoribonuclease** activity acting on both ssRNA and dsRNA in a 3' to 5' direction and a N7-guanine methyltransferase activity.
- Uridylate-specific endoribonuclease
 - Mn(2+)-dependent, uridylate-specific enzyme, which leaves 2'-3'-cyclic phosphates 5' to the **cleaved** bond.
- 2'-O-methyltransferase
 - mRNA **cap 2'-O-ribose** methylation to the **5'-cap structure** of viral mRNAs. - to evade immune system

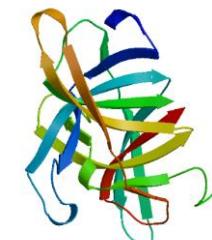
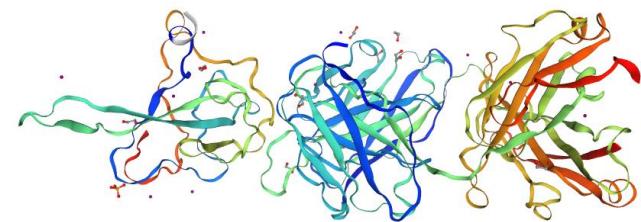
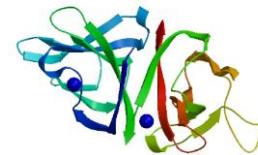


- Spike glycoprotein (S protein)
 - attaches the virion to the cell membrane by binding to human **ACE2 receptor**
- ORF3a protein (ORF3a)
 - potassium sensitive ion channels (**viroporin**) and may modulate virus release. Up-regulates expression of fibrinogen subunits FGA, FGB and FGG in host lung epithelial cells. Induces apoptosis in cell culture
- Envelope small membrane protein (E)
 - central role in **virus morphogenesis and assembly**. Acts as a viroporin and self-assembles in host membranes forming pentameric protein-lipid pores that allow ion transport. Also plays a role in the induction of apoptosis
- Membrane protein (M)
 - viral envelope that plays a central role in **virus morphogenesis and assembly**
 - Regulates the **localization of S protein** at cis-Golgi, the place of virus budding.
- ORF6 protein (ORF6)
 - Disrupts cell nuclear import complex formation by tethering karyopherin alpha 2 and karyopherin beta 1 to the membrane. **blocking the expression of interferon** stimulated genes (ISGs) that display multiple antiviral activities





- ORF7a protein (ORF7a)
 - **antagonist of host tetherin (BST2)**, disrupting its antiviral effect.
May suppress small interfering RNA (siRNA)
- ORF7b protein (ORF7b)
 - No known function – **locates to host Golgi and host endosome**
- ORF8 protein (ORF8)
 - Binds to IL17RA receptor, leading to IL17 pathway activation and an increased secretion of pro-inflammatory factors. **Contributes to cytokine storm during COVID-19 infection..**
- Nucleoprotein (N)
 - **Packages the positive strand viral genome RNA** into a helical ribonucleocapsid (RNP) and plays a fundamental role during viral assembly through its interactions with the viral genome and membrane protein M
- ORF9b protein (ORF9b)
 - **inhibition of host innate immune response** by targeting the mitochondrial-associated adapter MAVS
- ORF9c protein (ORF9c)
 - May play a role in **host-virus interaction.**
- ORF10 protein
 - No known function

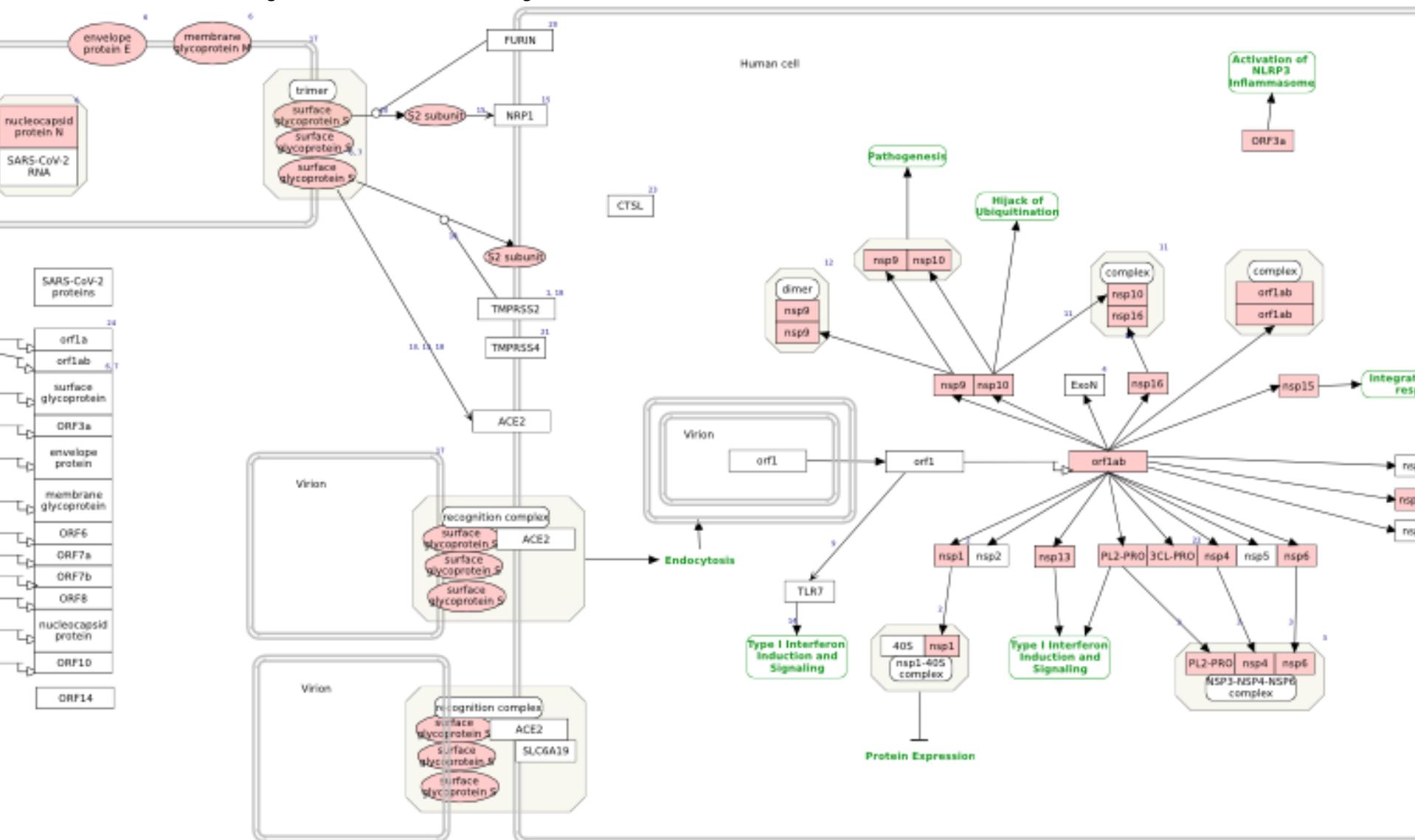


Interactions with Human cells

Reakce organismu na SARS-CoV-2

- Replikace viru - [WP4846](#)
- Viral subversion of host defence:
 - ER stress and unfolded protein response - [WP4861](#)
 - Autophagy and protein degradation - [WP4860](#), [WP4936](#), [WP4863](#)
 - Apoptosis - [WP4864](#)
- Integrative stress response:
 - Renin-angiotensin - [WP4883](#), [WP4965](#)
 - Coagulopathy - [WP4927](#)
- Innate Immune Response:
 - PAMP signalling - [WP4912](#)
 - Induction of interferons and the cytokine storm - [WP4868](#), [WP4880](#), [WP4876](#)
 - Altered host metabolism - [WP4853](#)

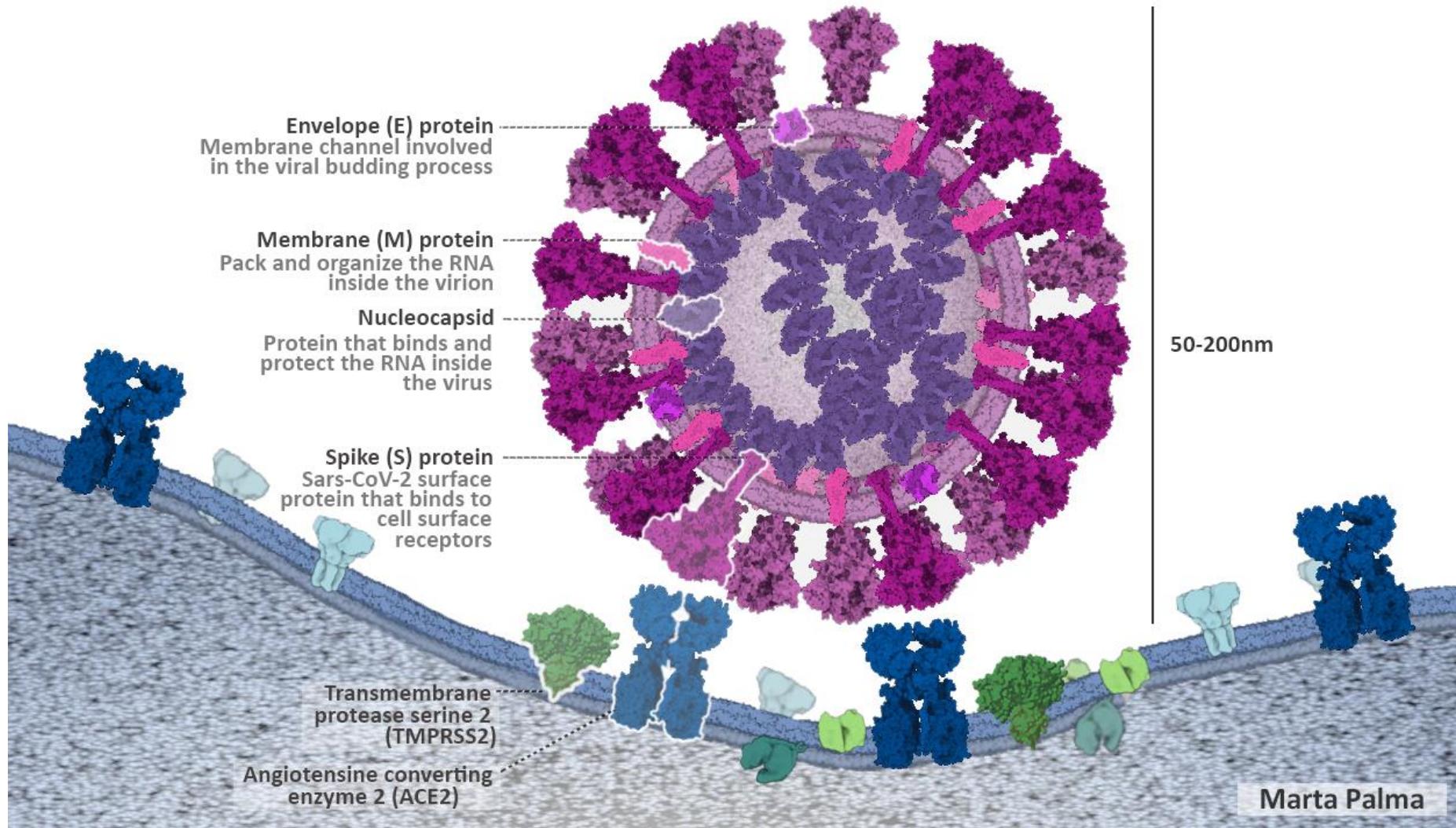
Wikipathways



<https://www.wikipathways.org/index.php/Pathway:WP4846#nogo2>

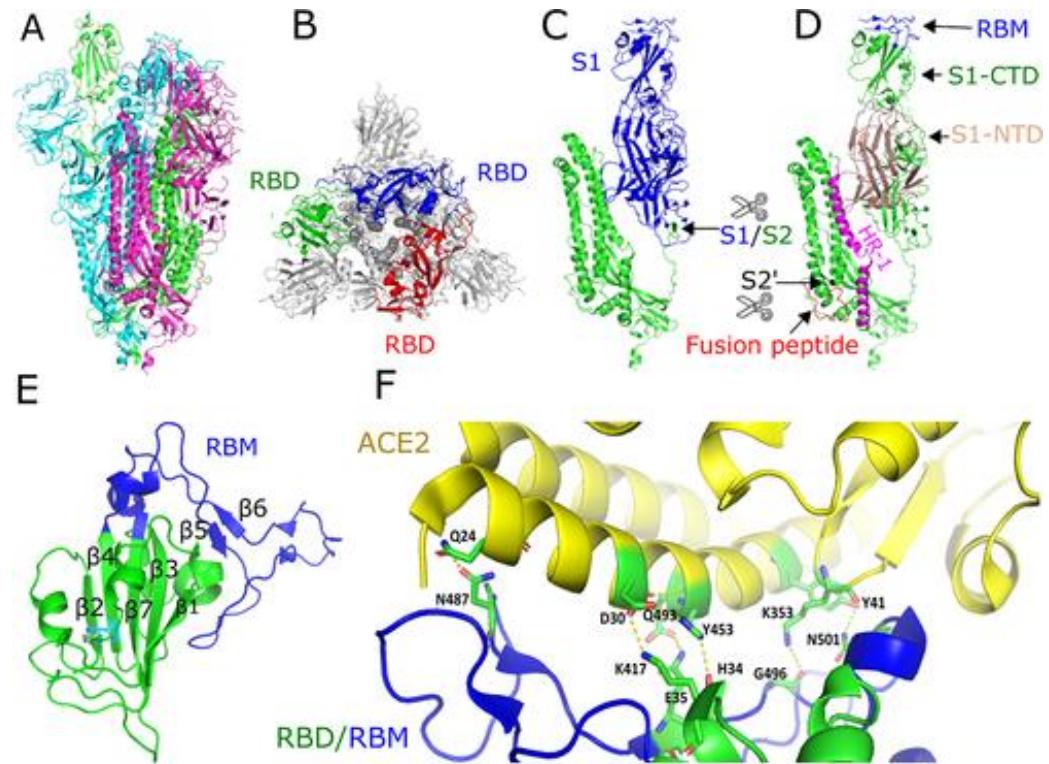
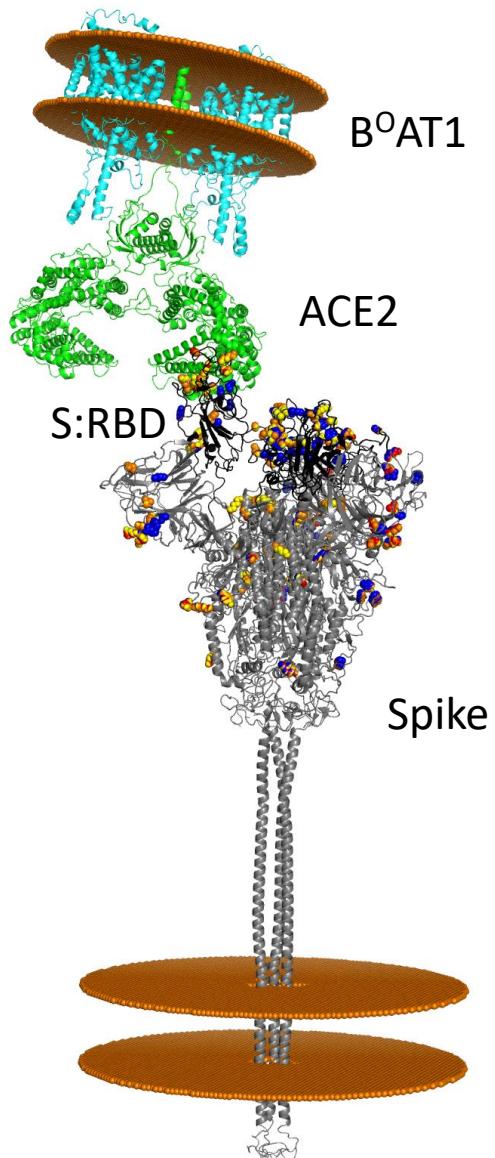
<https://www.embopress.org/doi/full/10.15252/msb.202110387>

Interacting proteins



Marta Palma

SARS-CoV-2 S protein + ACE2

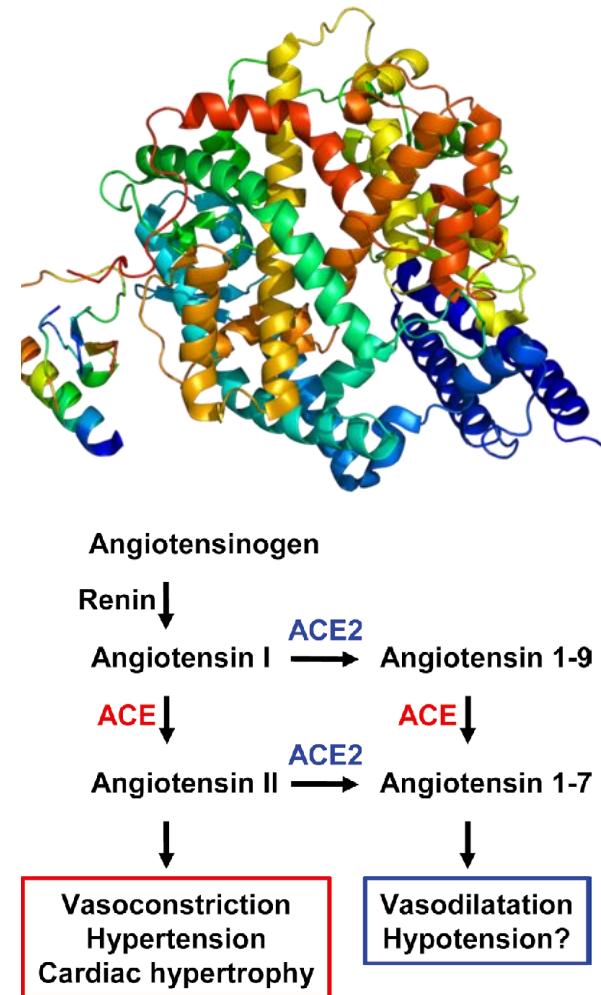
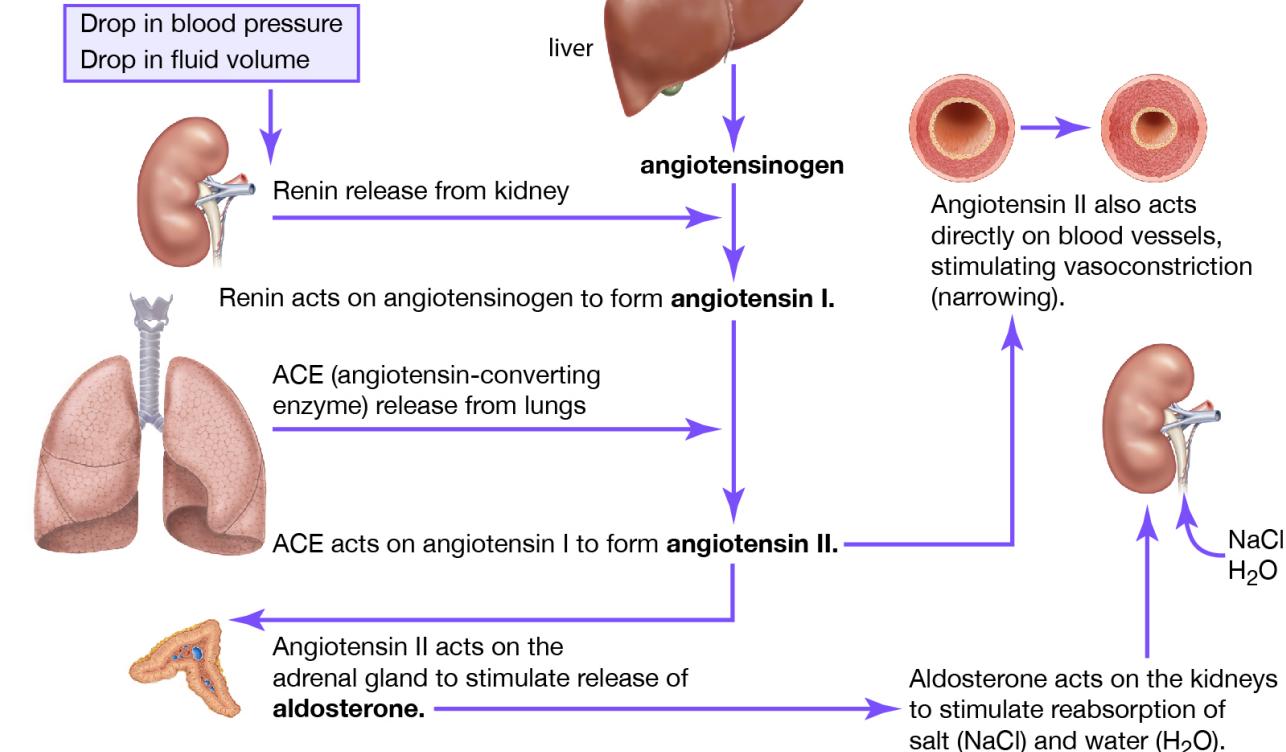


- Hlavní kontakt s buňkami

Mittal A, Manjunath K, Ranjan RK, Kaushik S, Kumar S, et al. (2020) COVID-19 pandemic: Insights into structure, function, and hACE2 receptor recognition by SARS-CoV-2. PLOS Pathogens 16(8): e1008762. <https://doi.org/10.1371/journal.ppat.1008762>
<https://journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1008762>

ACE2 – what is it? Why do we care?

Renin-angiotensin system



Receptor binding domain (RBD) antibodies contribute more to SARS-CoV-2 neutralization when target cells express high levels of ACE2

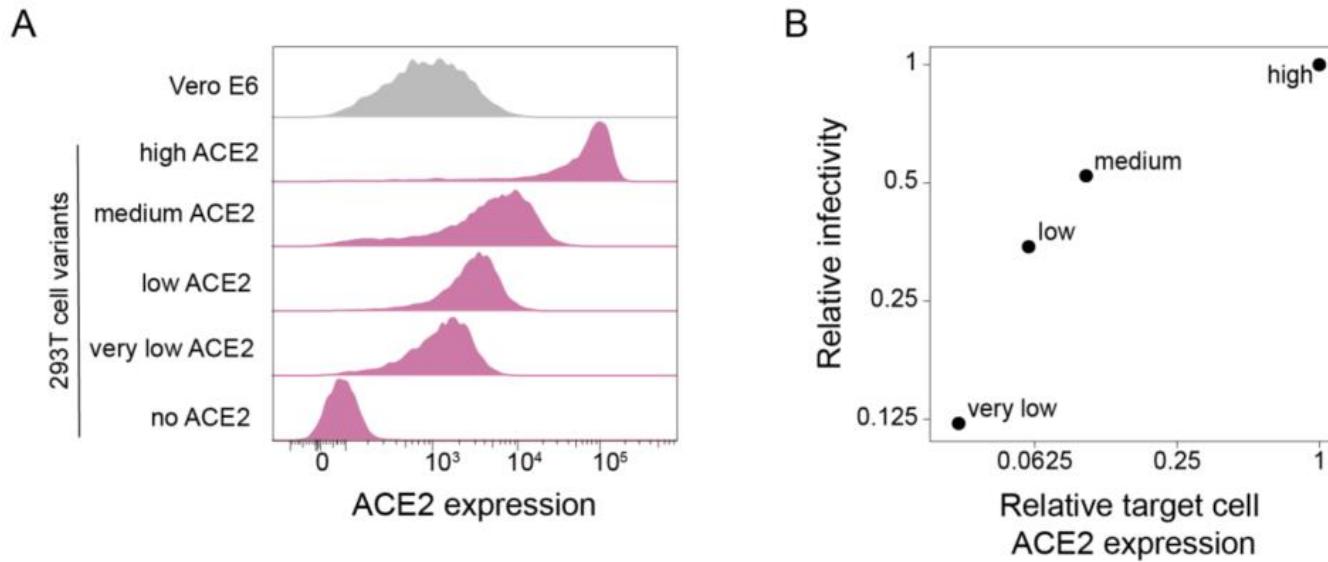
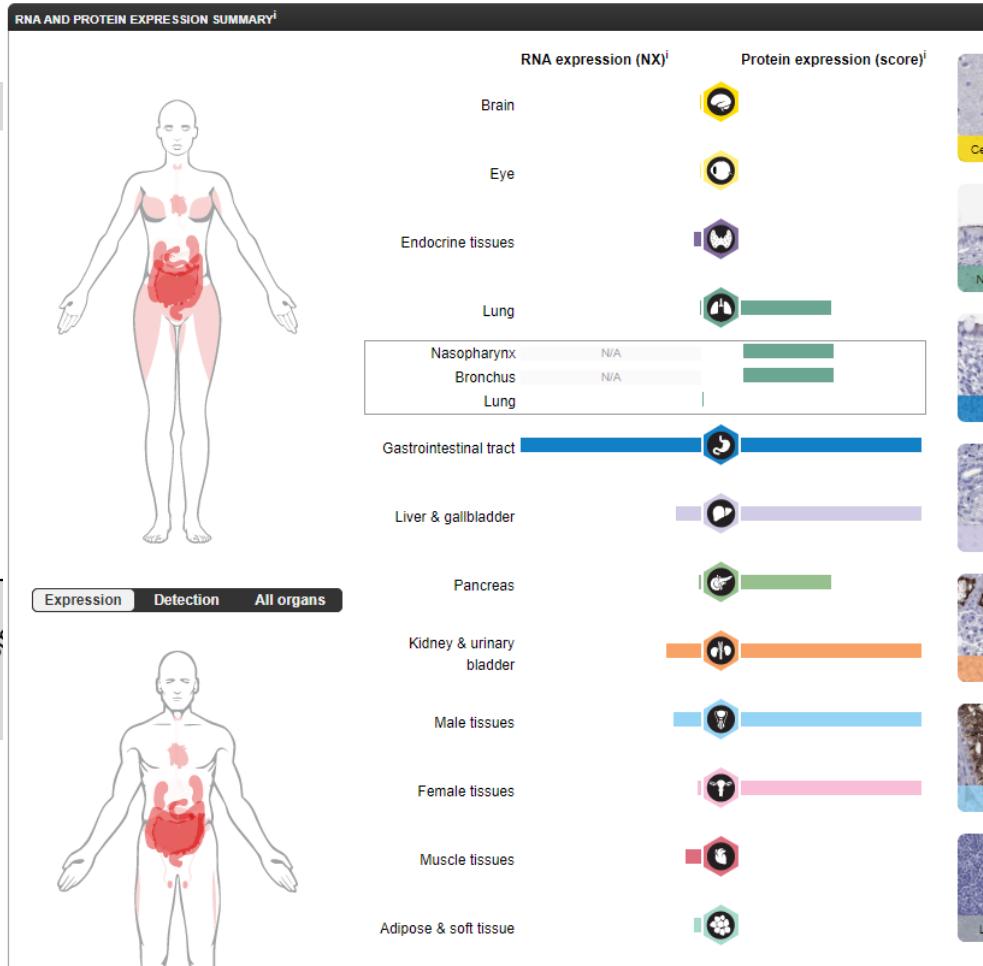
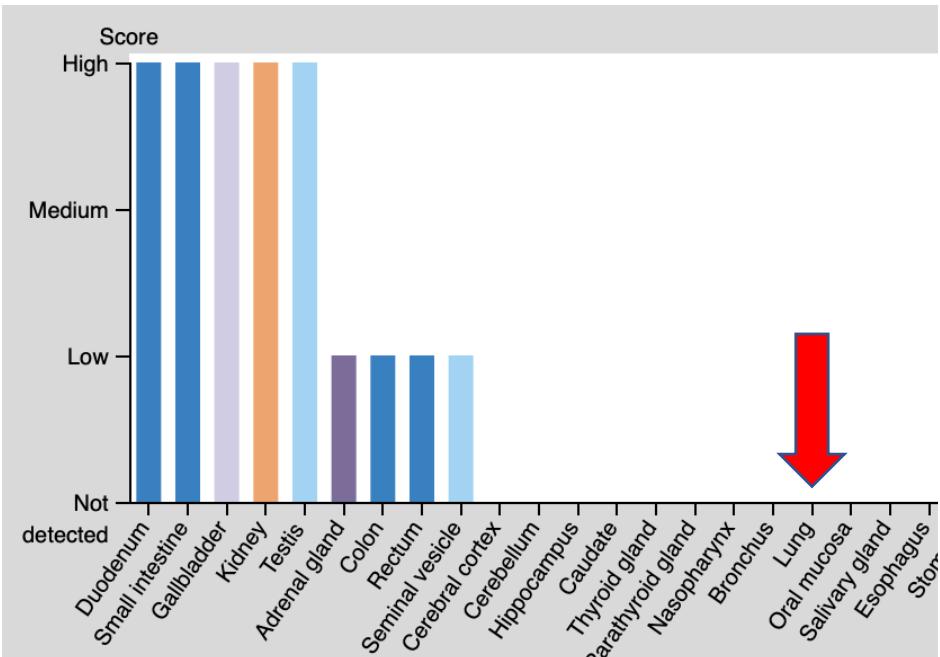
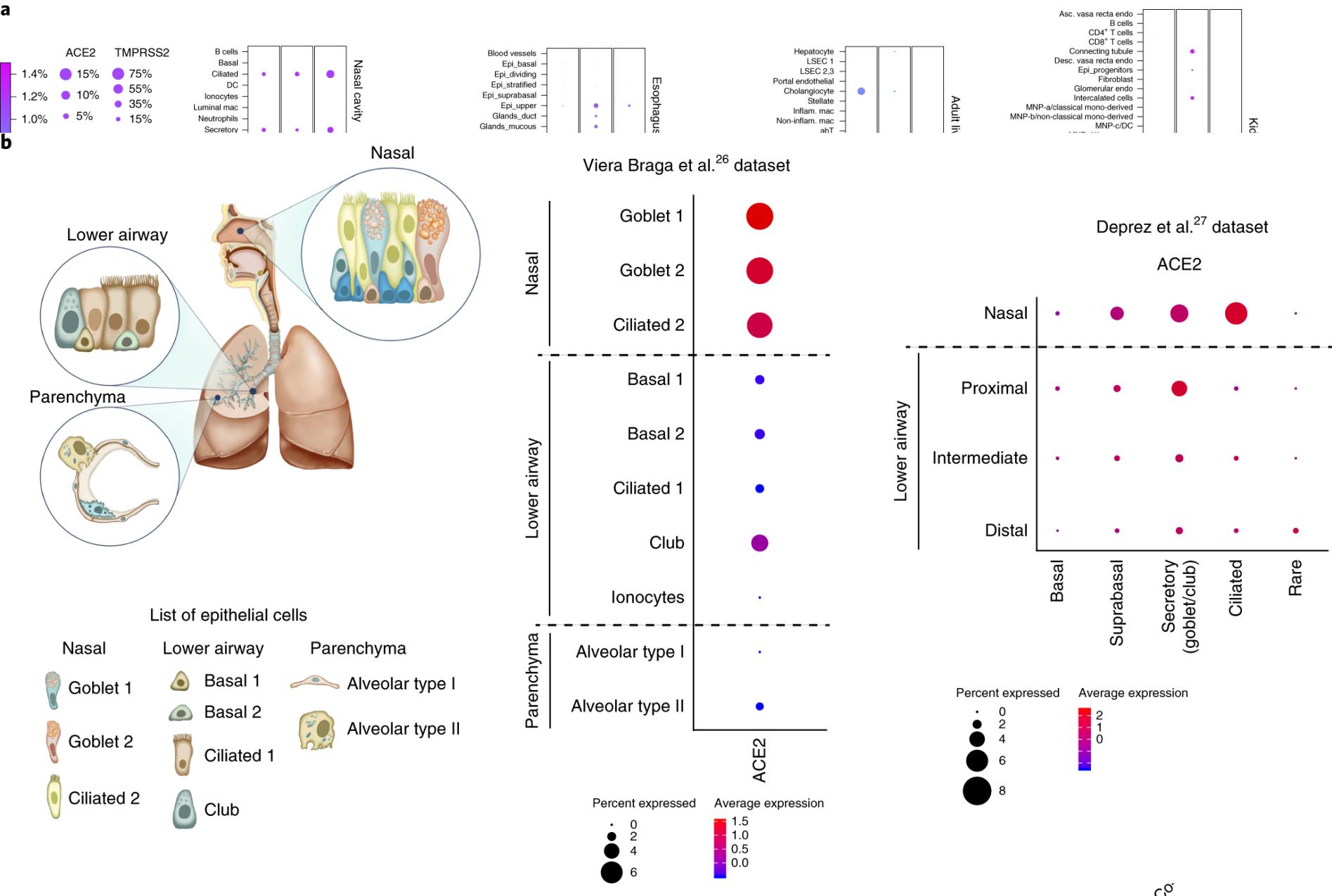


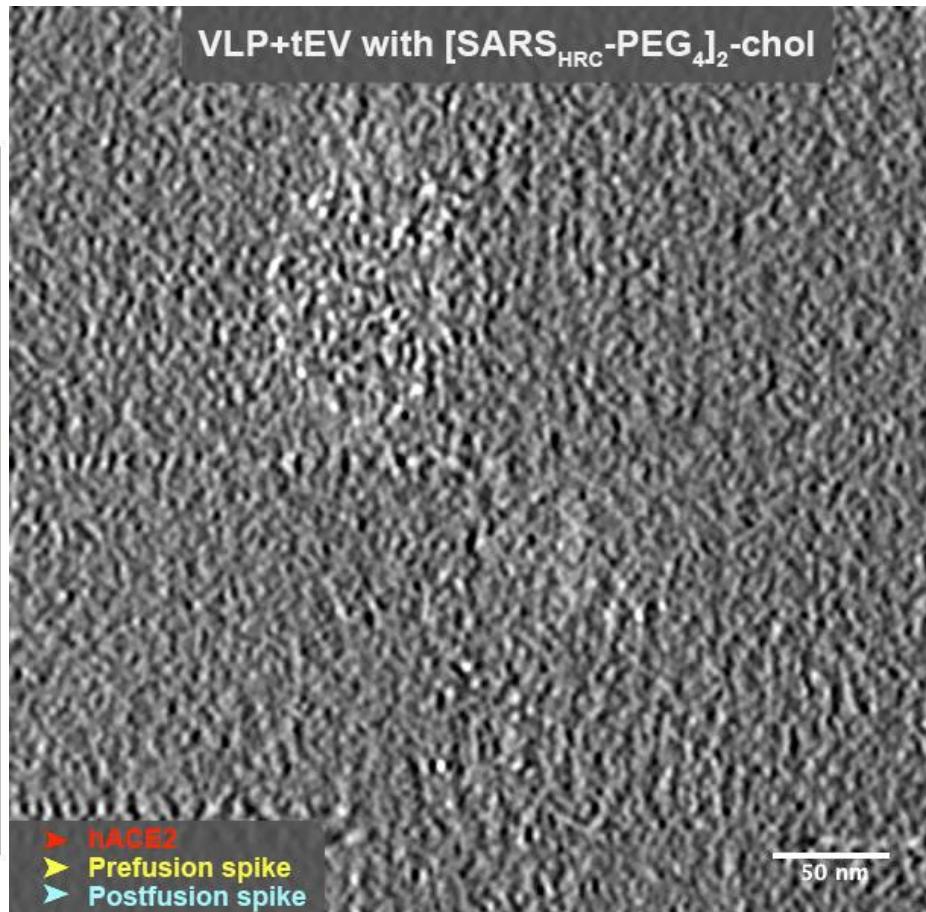
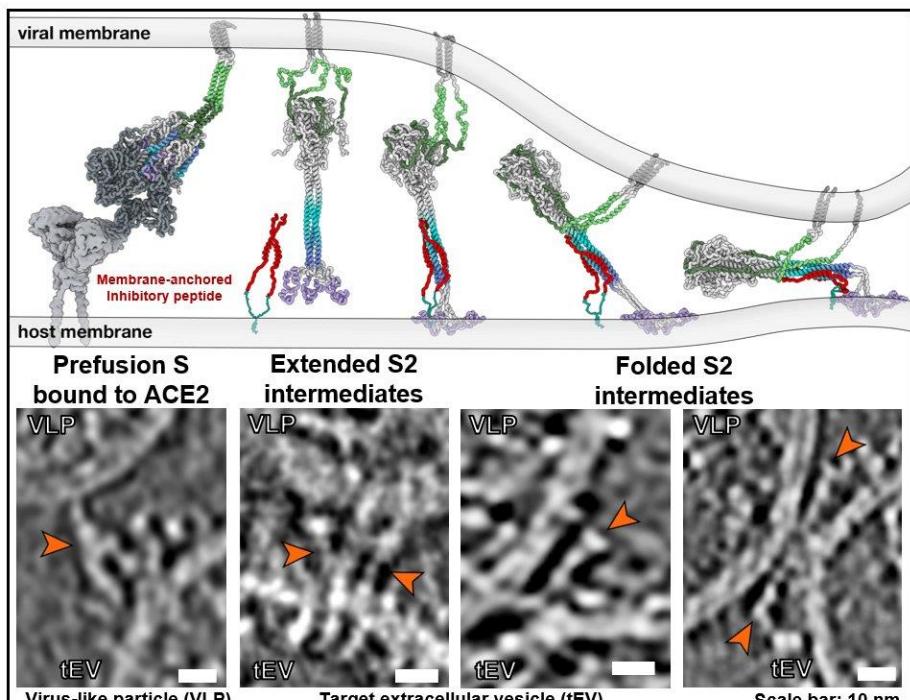
Fig. 1. 293T cell clones expressing ACE2 at different levels. (A) ACE2 expression in 293T cells engineered to express different levels of ACE2. ACE2 surface expression was measured by flow cytometry, and the histograms show the distribution of expression levels over a population of cells. Vero E6 cells are included for comparison. **(B)** Relationship between ACE2 expression in the four 293T target cell clones and infection by lentiviral particles pseudotyped with the SARS-CoV-2 D614G spike.

Expression of ACE2





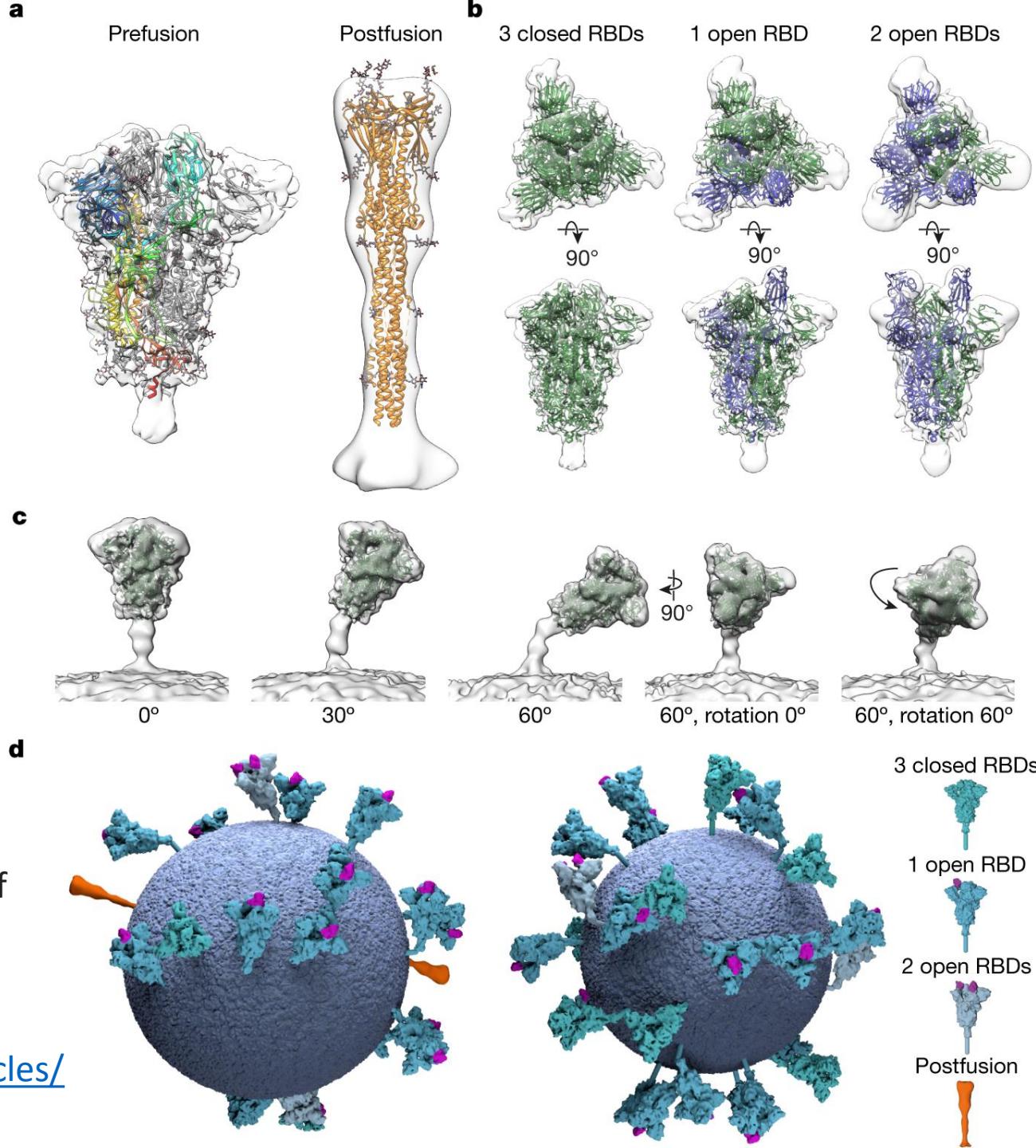
Intermediates in SARS-CoV-2 spike-mediated cell entry



<https://www.science.org/doi/10.1126/sciadv.abo3153>

Spike protein in detail

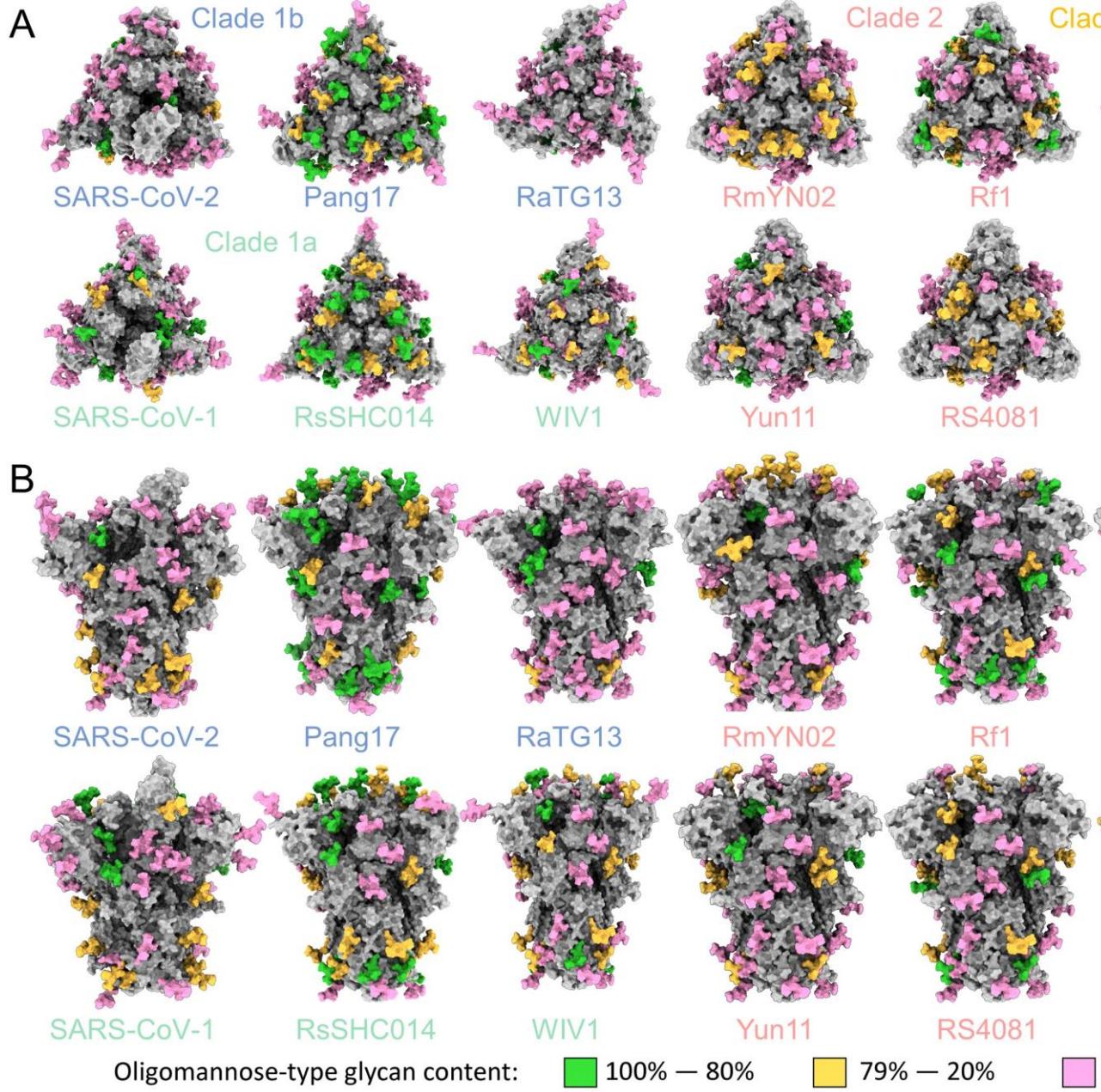
Conformers S proteins



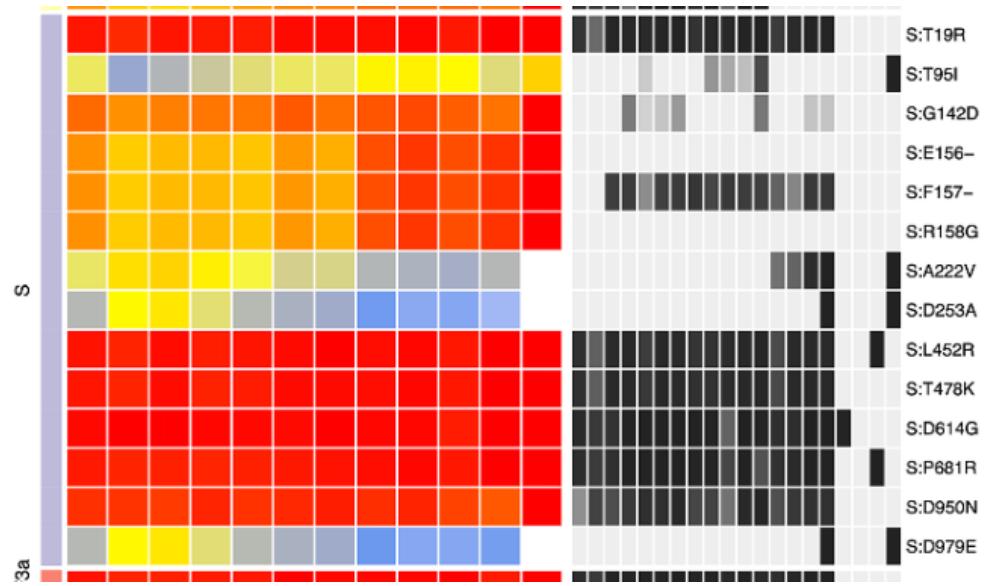
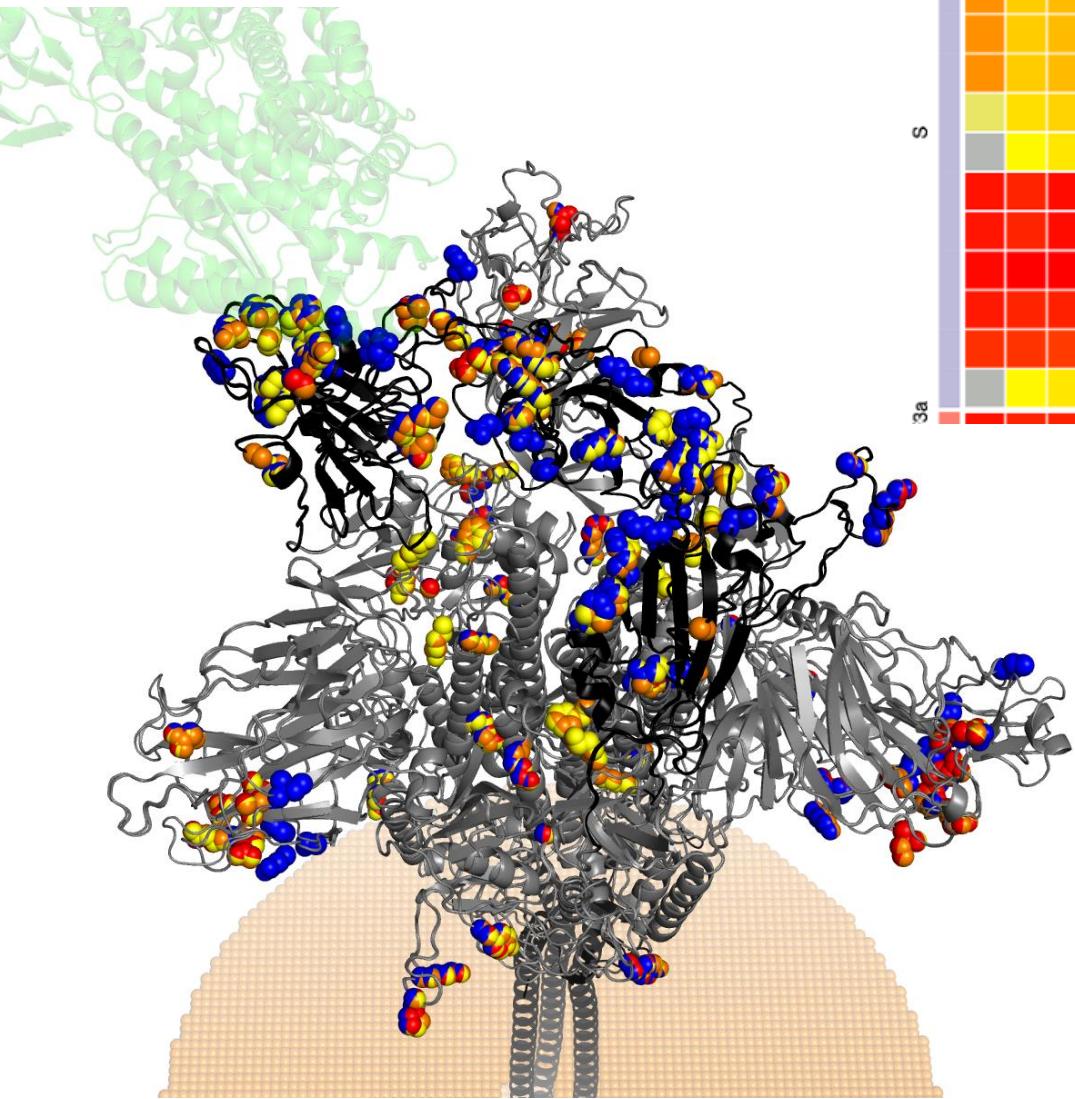
Ke, Z., Oton, J., Qu, K. et al.
Structures and distributions of
SARS-CoV-2 spike proteins on
intact virions.

Nature **588**, 498–502 (2020).
<https://www.nature.com/articles/s41586-020-2665-2/figures/2>

Glycosylation



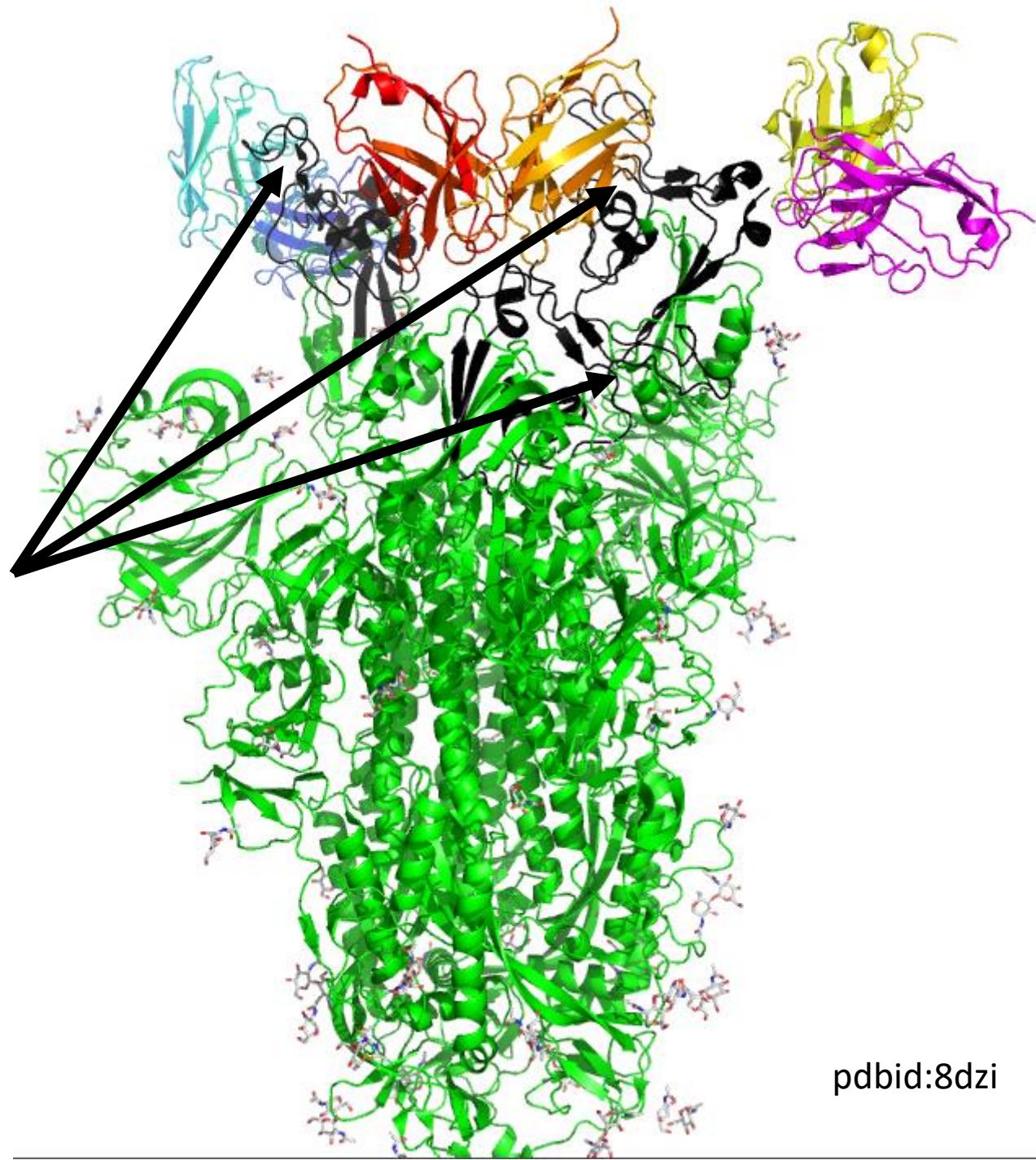
Mutace S proteinu



Antibodies

Interaction with antibodies

- Neutralizing antibodies binds with RBD domain – blocking ACE2 interaction



pdbrid:8dzi

Protilátky



CoV-AbDab

The Coronavirus Antibody Database

B

> Downloads

- Database (CSV)
- ANARCI Numberings (.json)
- PDB Structures (.tar.gz)
- Homology Models (.tar.gz)
- Tracked Datasets (.adix)

D

> Search Database by Attribute

To view all entries, leave all search fields as 'All' and click 'Search'.

| | |
|---------------------------|-----|
| Type: | All |
| Binds to: | All |
| Doesn't bind to: | All |
| Neutralising against: | All |
| Not neutralising against: | All |
| Protein/Epitope: | All |
| Origin: | All |
| Heavy V Gene: | All |
| Heavy J Gene: | All |
| Light V Gene: | All |
| Light J Gene: | All |

Search

C

> Search Database by Sequence

Enter a sequence (either a full-length variant or your query).

Only database entries that are the same length as your query will be returned.

Query sequence:
IQVQLVQSGAEVYQDQGASVVKVSCKASGYTPTI

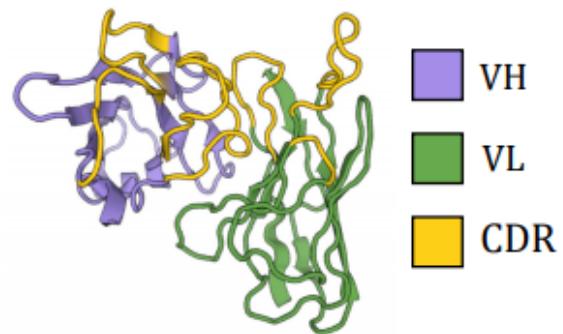
E

| | | Show: 10 | v | entries | | | | | | | | | | | | | |
|-----|---------------------|------------------|--------------------|------------------|-----------|--------------|----------------------------------|--------------|--------------------|------------------|---------------------|------------------|--------------------|------------|----|-------------------|--------------------|
| | | Heavy V Gene | | Heavy J Gene | | Light V Gene | | Light J Gene | | CDR93 | | CDR3 | | Structures | | Ab Homology Model | |
| B38 | IGHV3-53 (Human) | IGHG6 (Human) | IGHV1-9 (Human) | IGHJ2 (Human) | ABEAYHHDV | QQLASHNPPYT | PDB entry 7BZS [PDB] [5kzbdb] | H4 | IGHV1-2 (Human) | IGHG2 (Human) | IGHV2-40 (Human) | IGHJ4 (Human) | ATWFFCSSTSCHRONYFL | HQRIEEFFLT | ND | download or view | Yan Wu et al. 2020 |

F

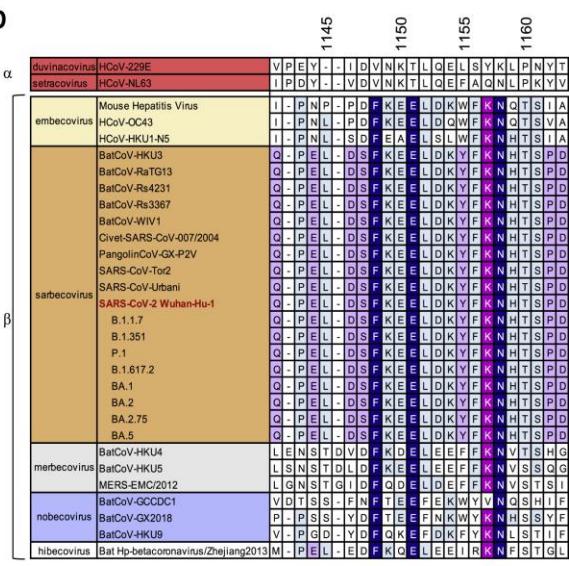
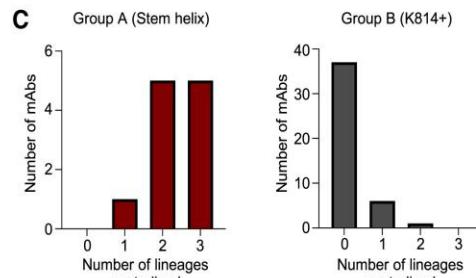
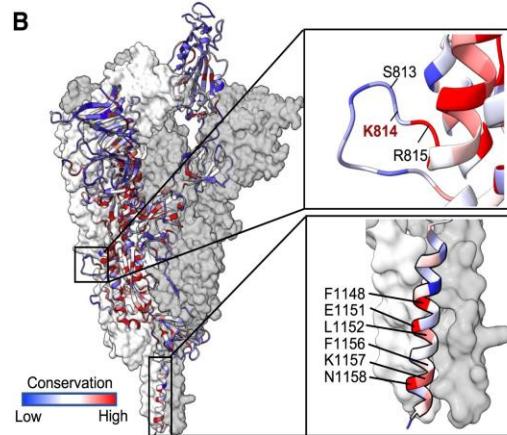
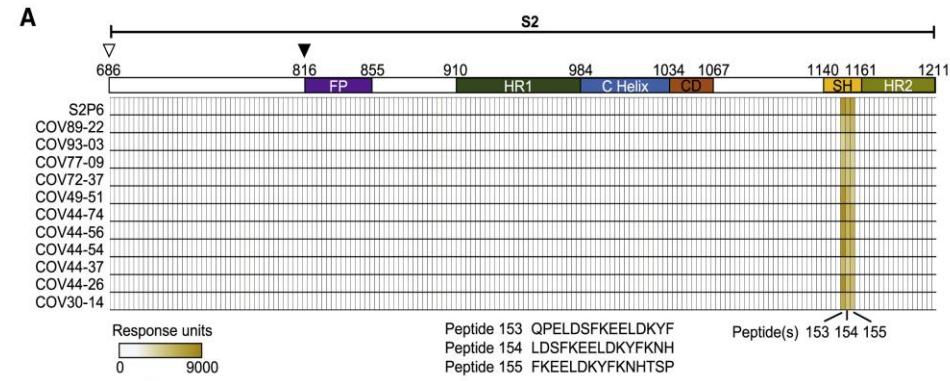
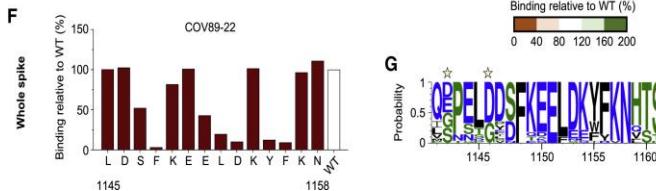
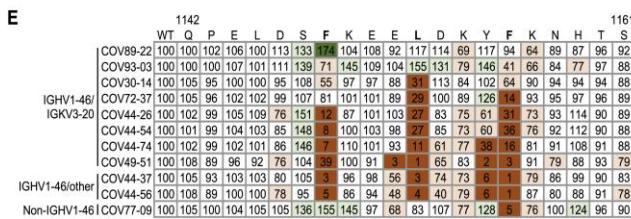
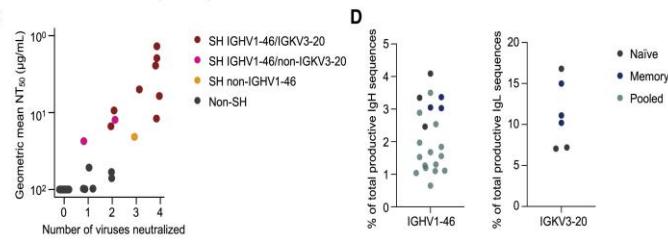
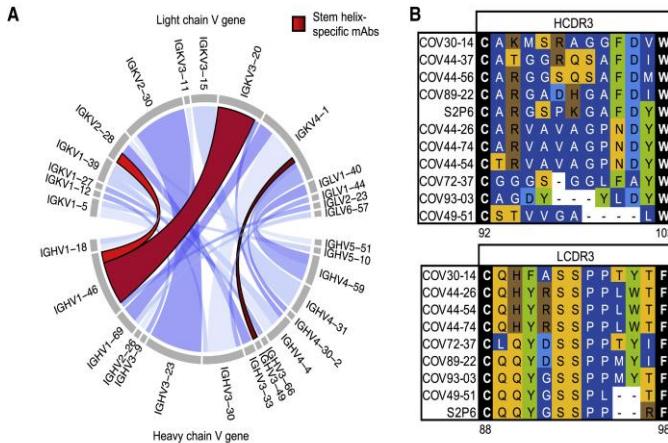
| Database Entry | CDR | Sequence Identity | Ab or Ab | Binds to |
|----------------|-----|-------------------------------------|----------|-----------|
| B38 | H3 | 100.00% | Ab | SARS-CoV2 |
| | | 105 106 107 108 109 114 115 116 117 | | |
| | | A R E A Y G H D V | | |
| | | A R E A Y G H D V | | |
| C148 | H3 | 66.67% | Ab | SARS-CoV2 |
| | | 105 106 107 108 109 114 115 116 117 | | |
| | | A R E I A N Y H D V | | |
| | | A R E I A N Y H D V | | |

G



- VH
- VL
- CDR

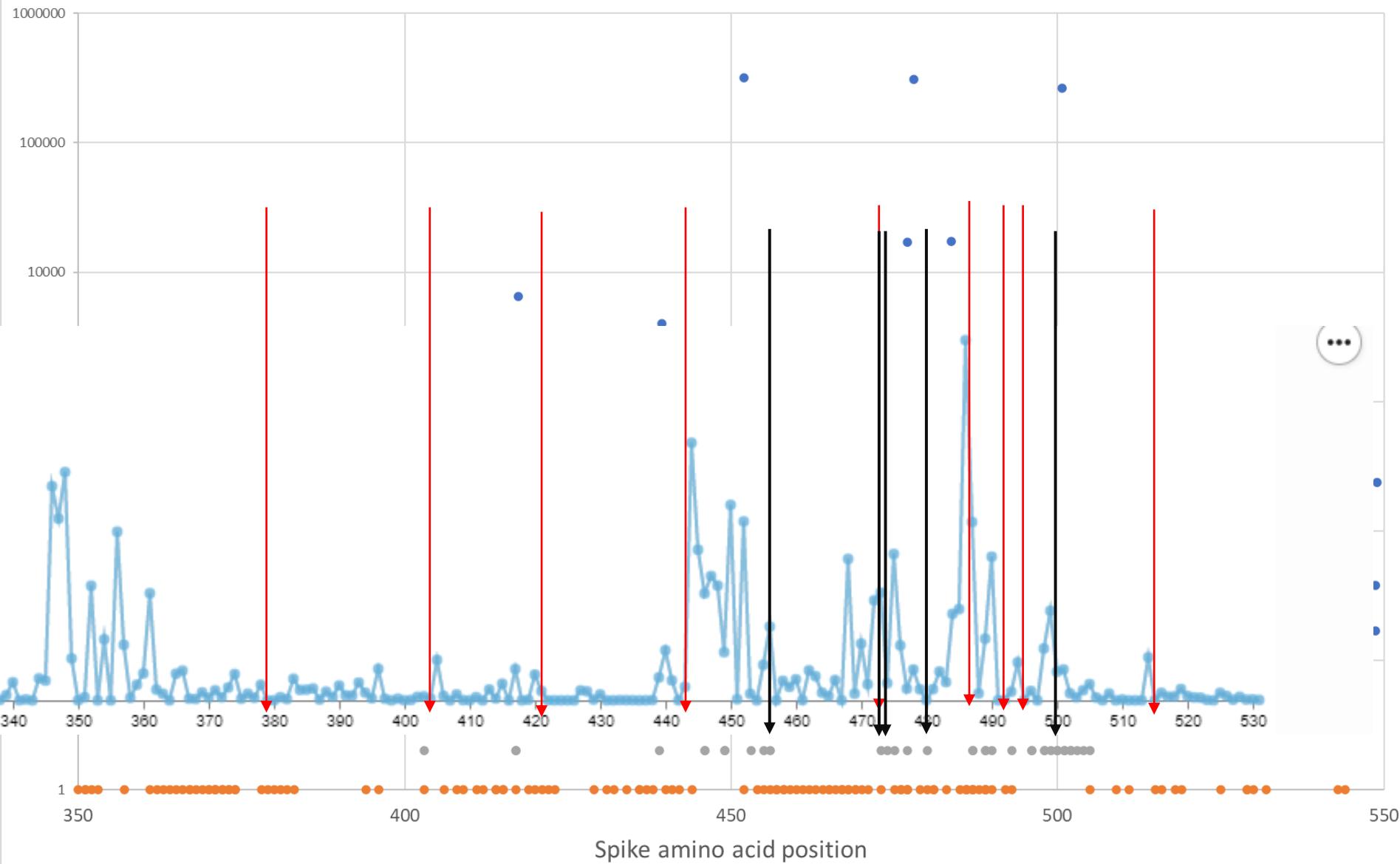
Rare, convergent antibodies targeting the stem helix broadly neutralize diverse betacoronaviruses



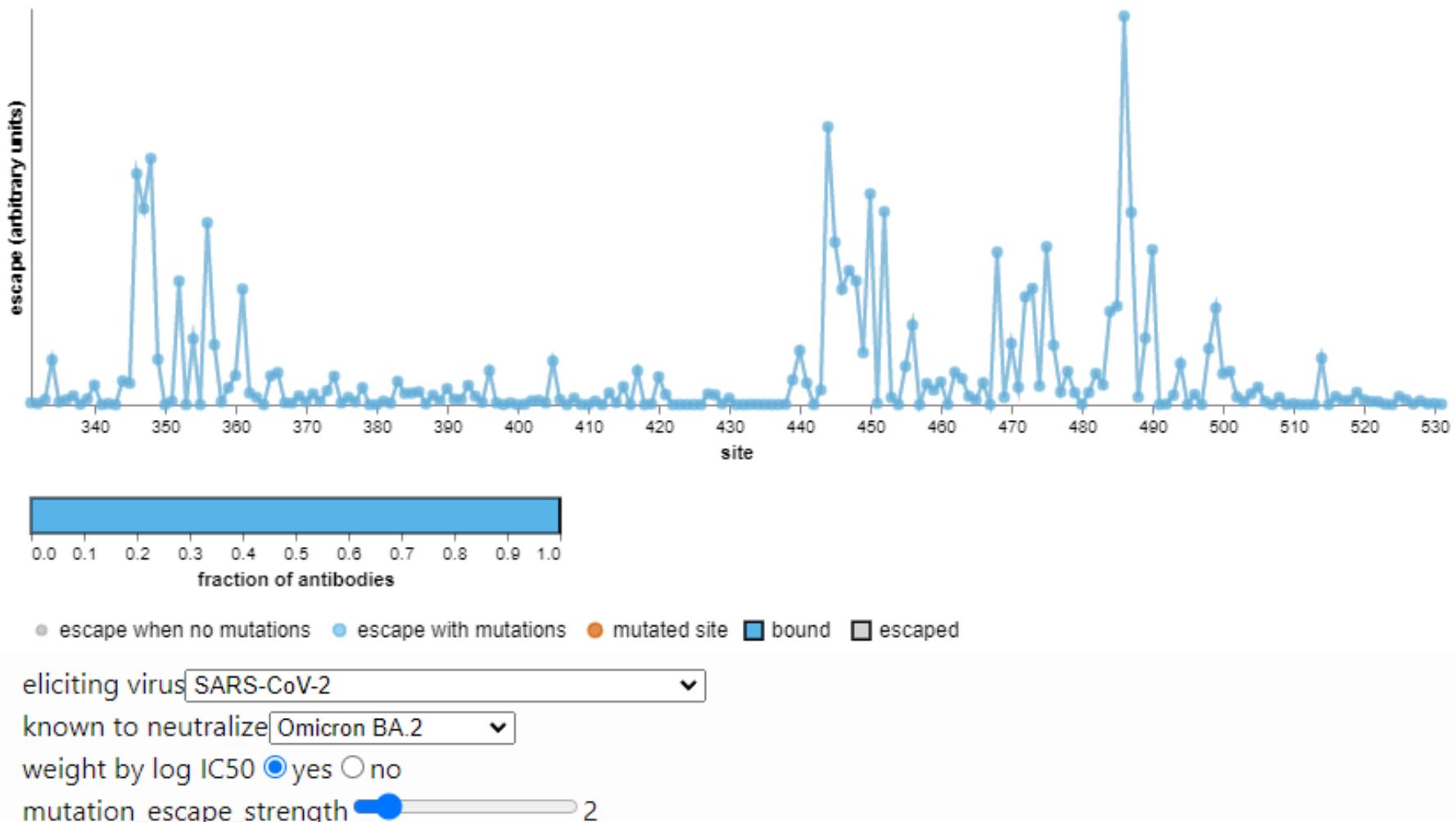
Dacon et al. Rare, convergent antibodies targeting the S1 stem region stably neutralize diverse betacoronaviruses. *Cell Host & Microbe* DOI: 10.1016/j.chom.2022.10.010 Copyright © 2022 [Terms and Conditions](#)

Spike protein interactions with

- glycosylation
- ACE2
- antibodies
- antigens
- mutation counts



Escape calculator for SARS-CoV-2 RBD



https://jbloomlab.github.io/SARS2_RBD_Ab_escape_maps/escape-calc/

<https://academic.oup.com/ve/article/8/1/veac021/6549895>

Genomic surveillance

Varianty - Genomy SARS-CoV-2

Genomic epidemiology of SARS-CoV-2 with subsampling focused globally over the past 6 months

Built with nextstrain/ncov. Maintained by the Nextstrain team. Enabled by data from [GISAID](#).

Showing 2912 of 2912 genomes sampled between Dec 2019 and Aug 2022.

Phylogeny

Clade ▾

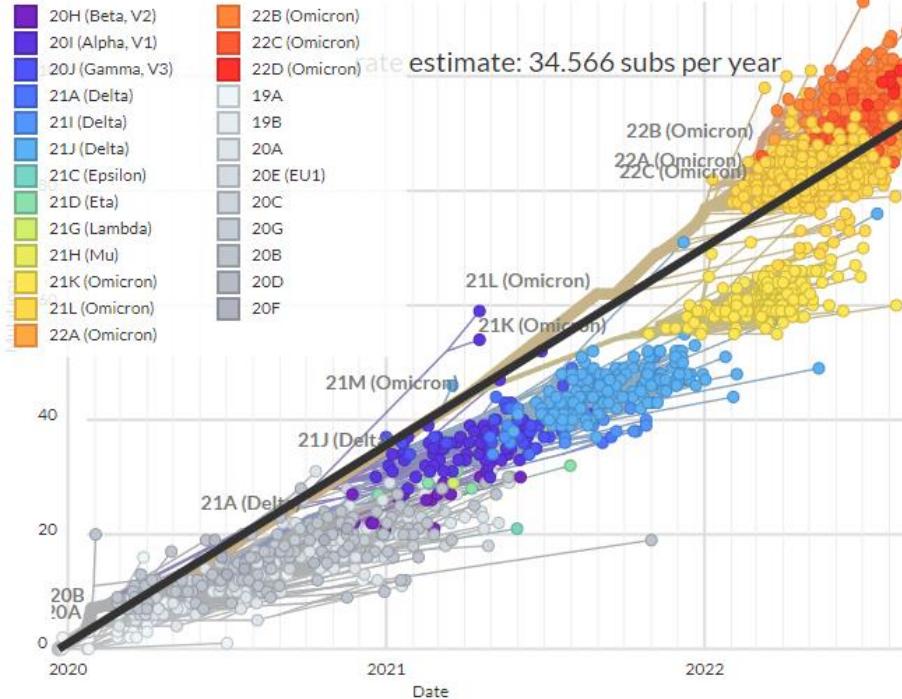
- 20H (Beta, V2)
- 20I (Alpha, V1)
- 20J (Gamma, V3)
- 21A (Delta)
- 21I (Delta)
- 21J (Delta)
- 21C (Epsilon)
- 21D (Eta)
- 21G (Lambda)
- 21H (Mu)
- 21K (Omicron)
- 21L (Omicron)
- 22A (Omicron)



ZOOM TO SELECTED

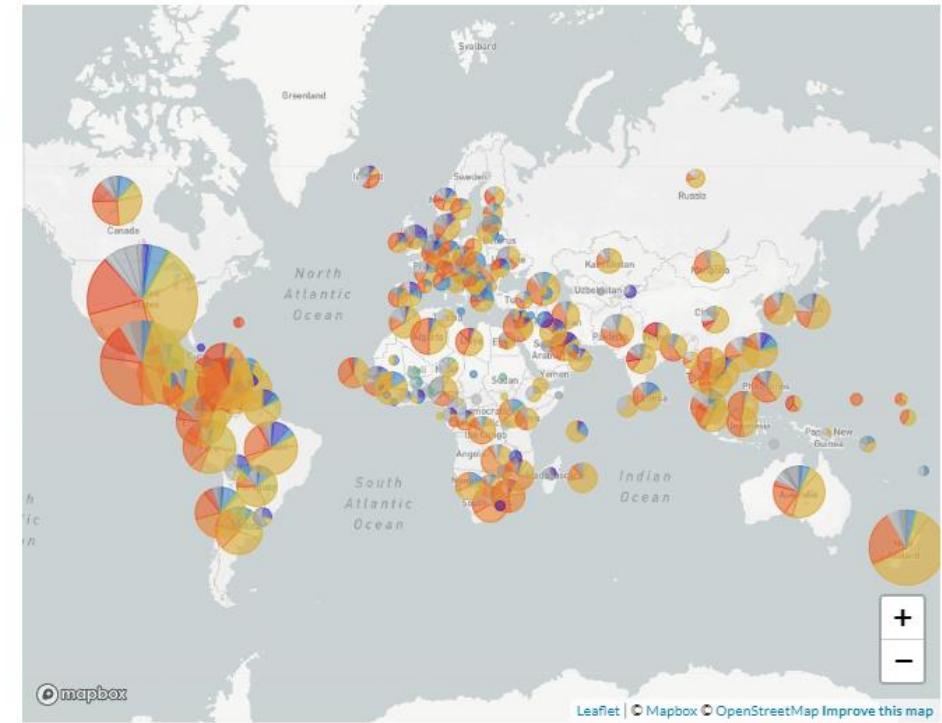
RESET LAYOUT

rate estimate: 34.566 subs per year

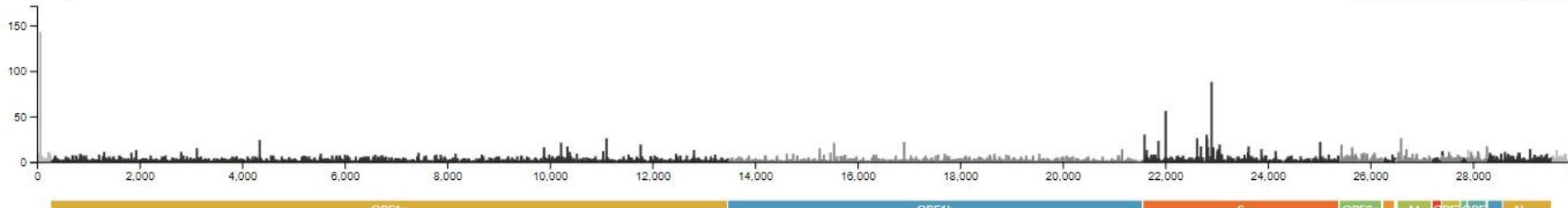


Geography

RESET ZOOM



Diversity



ENTROPY EVENTS

AA NT

Variancy v ČR

Datum odběru (prosím vložte obě hodnoty)

1. 5. 2022

21. 11. 2022

Linie (vyberte jednu nebo více)

Klikni sem

Typ grafu

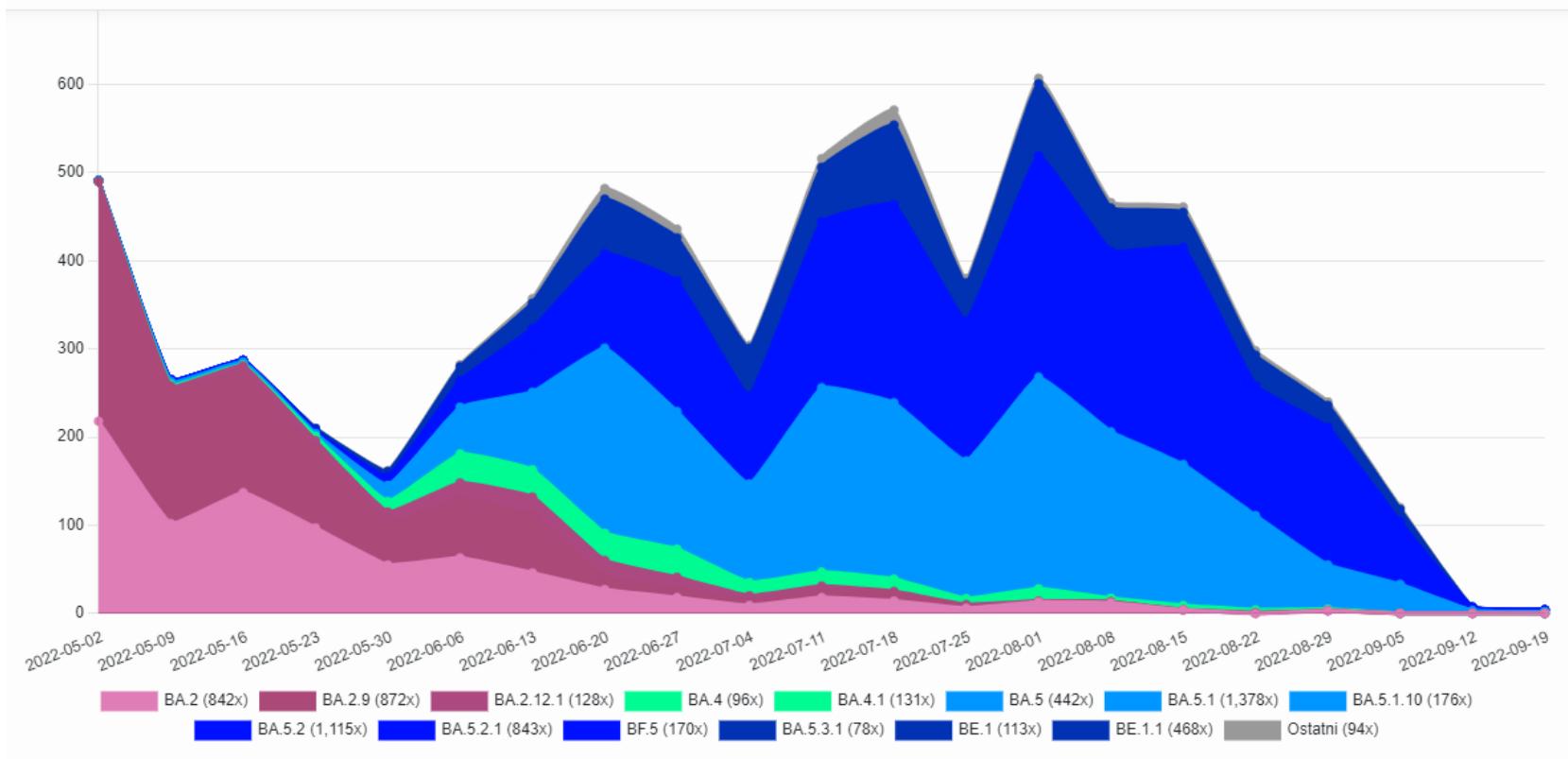
- Absolutní Relativní
 Kumulativní

Zastoupení linii

- Vše Minimálně 1% Minimálně 5%
 Minimálně 10%

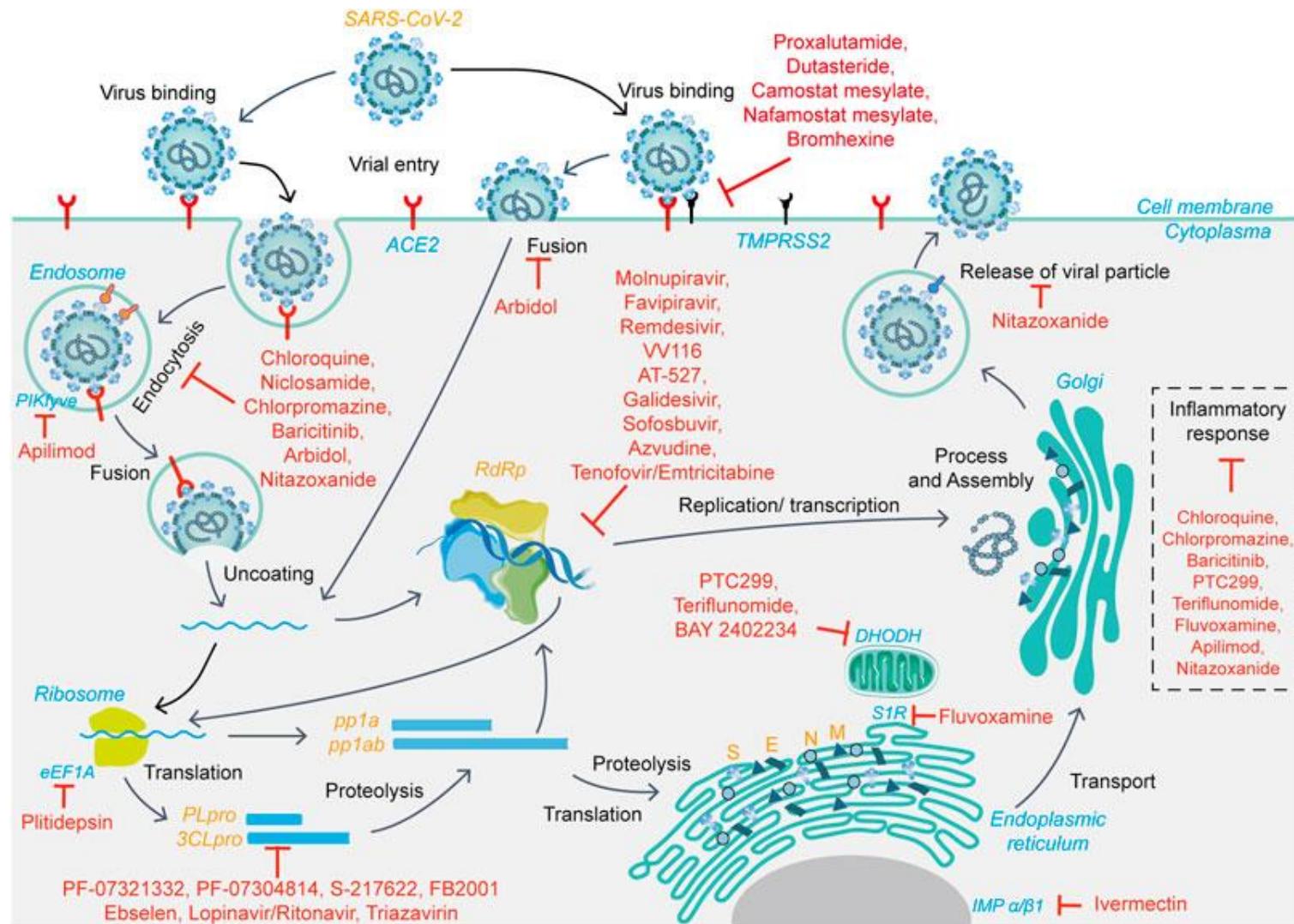
Seskupení v čase

- Týdně Měsíčně



Therapeutics

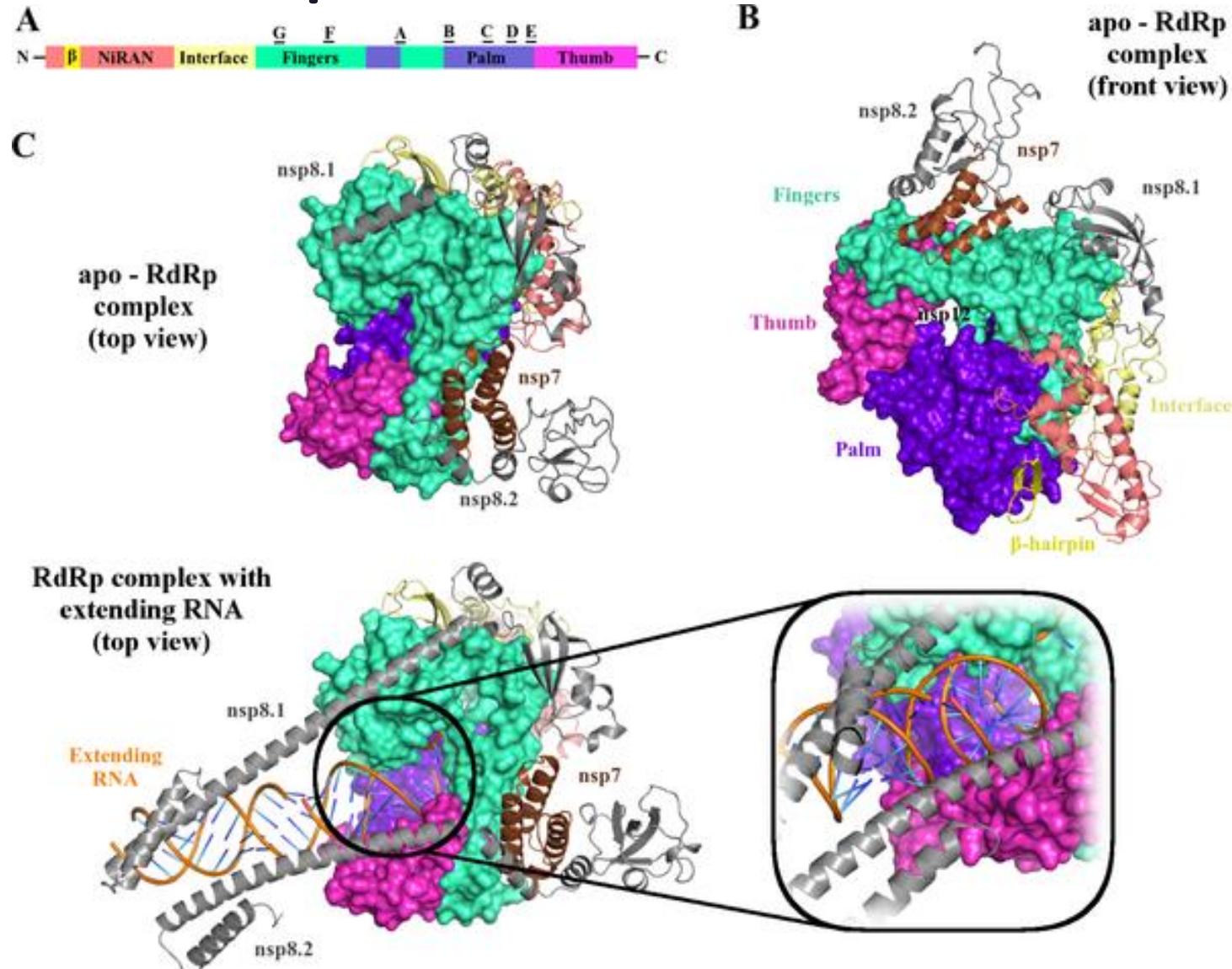
Clinical trials



| Drugs | No. of clinical trials registered ^a | Phase | Molecular target | Development strategy | Approval status (for COVID-19) |
|--------------------------------|--|-------|--|----------------------|--|
| Remdesivir | 77 | 4 | RdRp | Repurposing | Approval by FDA |
| Favipiravir | 46 | 4 | RdRp | Repurposing | EUA in several countries |
| Molnupiravir | 5 | 3 | RdRp | Novel | Approval by MHRA; EUA by FDA |
| AT-527 | 3 | 3 | RdRp | Novel | Non-approved |
| Galidesivir | 1 | 1 | RdRp | Repurposing | Non-approved |
| Sofosbuvir | 8 | 4 | RdRp | Repurposing | Non-approved |
| Azudine | 3 | 3 | RdRp | Repurposing | Non-approved |
| Tenofovir/emtricitabine | 5 | 3 | RdRp | Repurposing | Non-approved |
| PF-07321332 | 8 | 3 | 3CLpro | Novel | EUA by FDA |
| PF-07304814 | 3 | 1 | 3CLpro | Novel | Non-approved |
| s-217622 | — | 2/3 | 3CLpro | Novel | Non-approved |
| FB2001 | 1 | 2/3 | 3CLpro | Novel | Non-approved |
| Ebselen | 2 | 2 | 3CLpro | Repurposing | Non-approved |
| Lopinavir/ritonavir | 24 | 4 | 3CLpro | Repurposing | Non-approved |
| Triazavirin | 2 | 4 | RNA synthesis/3CLpro | Repurposing | Non-approved |
| Chloroquine/hydroxychloroquine | 46/276 | 4 | Endosomal entry | Repurposing | EUA by FDA at earlier outbreak (chloroquine) |
| Umifenovir/arbidol | 3 | 4 | Endosomal entry | Repurposing | Non-approved |
| Niclosamide | 11 | 3 | Endosomal entry | Repurposing | Non-approved |
| Chlorpromazine | 2 | 3 | Endosomal entry | Repurposing | Non-approved |
| Baricitinib | 20 | 4 | Endosomal entry | Repurposing | EUA by FDA |
| Proxalutamide | 5 | 3 | Androgen receptor antagonist | Repurposing | Non-approved |
| Dutasteride | 1 | 2 | 5-alpha-reductase inhibitor | Repurposing | Non-approved |
| Camostat mesylate | 5 | 3 | TMPRSS2 inhibitor | Repurposing | Non-approved |
| Nafamostat mesylate | 2 | 2 | TMPRSS2 inhibitor | Repurposing | Non-approved |
| PTC299 | 1 | 2 | DHODH inhibitor | Repurposing | Non-approved |
| Teriflunomide | 3 | 3 | DHODH inhibitor | Repurposing | Non-approved |
| Nitazoxanide | 23 | 4 | Endosomal entry/Inflammatory response regulation | Repurposing | Non-approved |
| Fluvoxamine | 1 | 3 | Sigma-1 receptors agonist | Repurposing | Non-approved |
| Plitidepsin | 3 | 3 | eEF1A inhibitor | Repurposing | Non-approved |
| Ivermectin | 69 | 4 | IMPA/β1 inhibitor | Repurposing | Non-approved |
| Apilimod | 1 | 2 | PIKFYVE inhibitor | Repurposing | Non-approved |

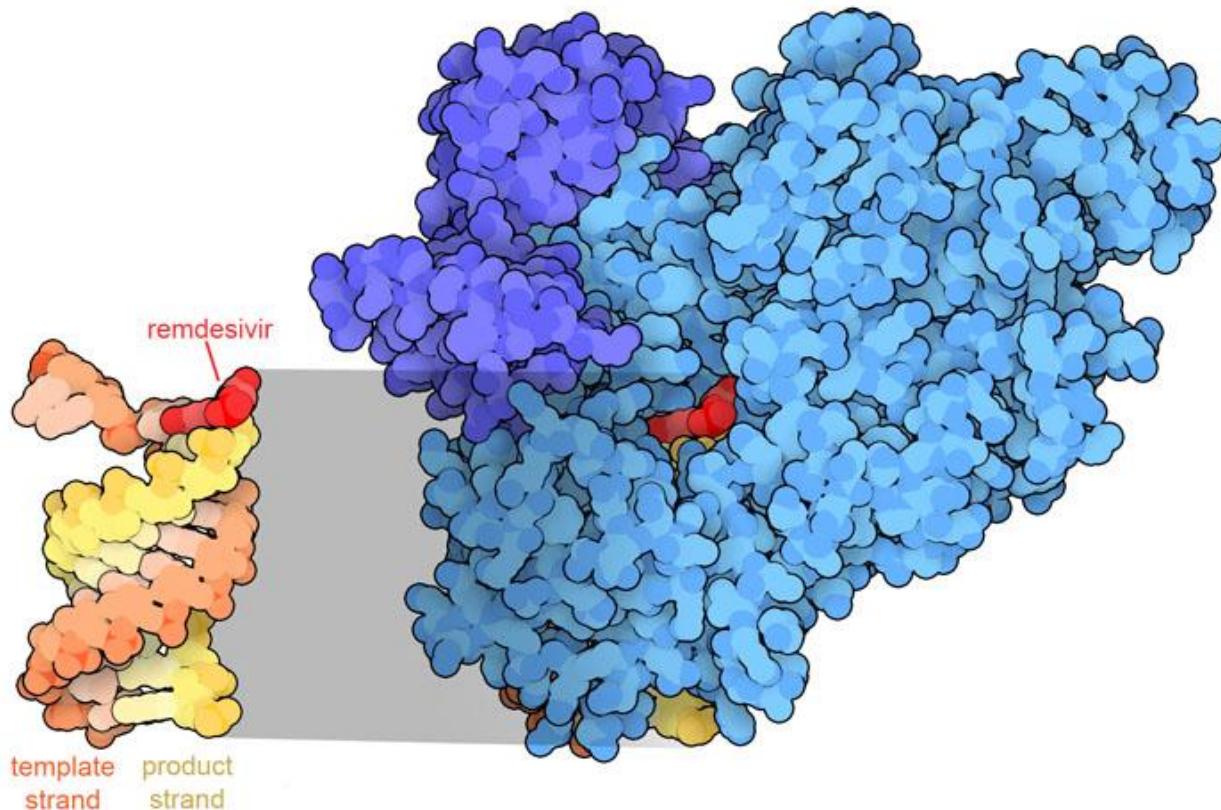
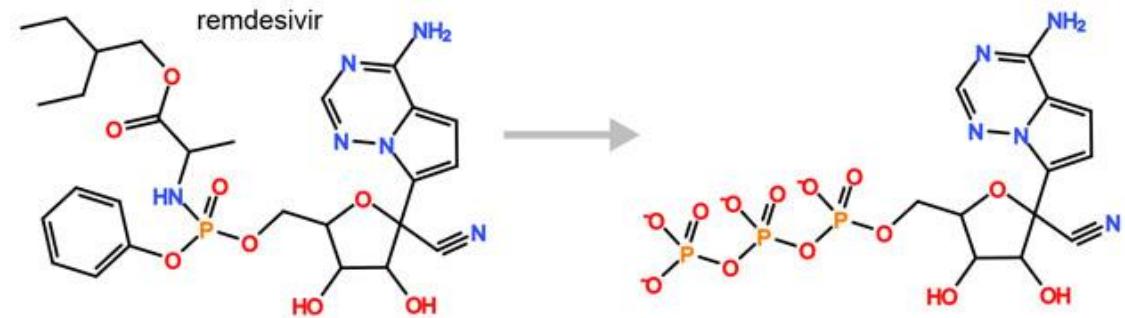
^aRegistered on ClinicalTrials.gov.

Cryo-EM RdRp of SARS-CoV-2.



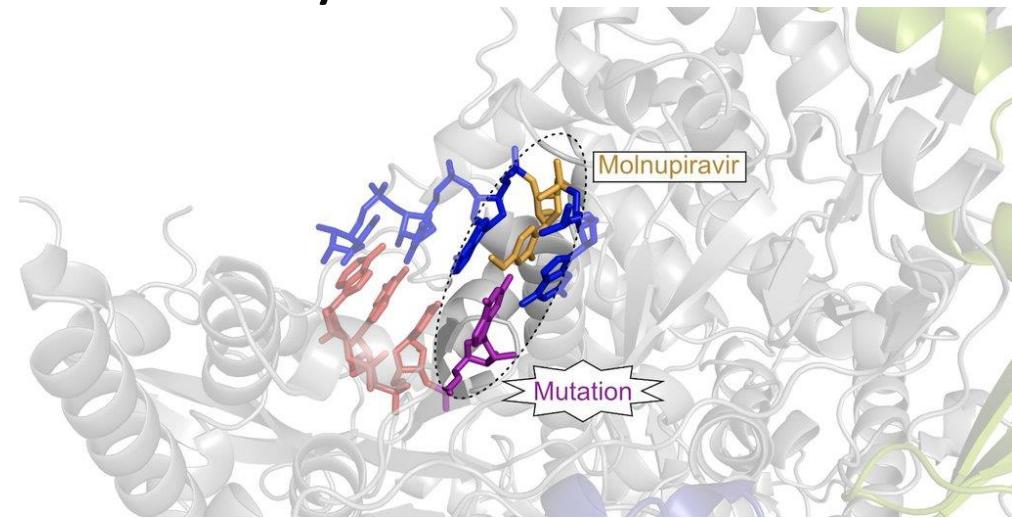
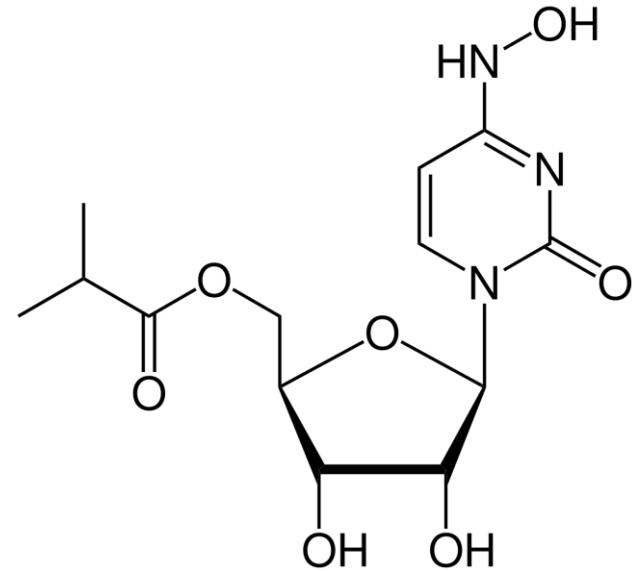
Mittal A, Manjunath K, Ranjan RK, Kaushik S, Kumar S, et al. (2020) COVID-19 pandemic: Insights into structure, function, and hACE2 receptor recognition by SARS-CoV-2. PLOS Pathogens 16(8): e1008762. <https://doi.org/10.1371/journal.ppat.1008762>
<https://journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1008762>

Remdesivir



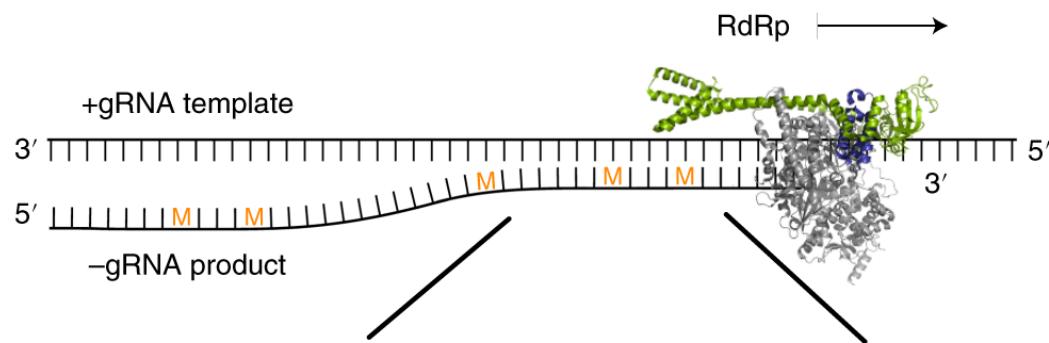
Molnupiravir

- Pilulka
- Blokuje replikaci SARS-CoV-2
- Žádné závažné vedlejší efekty na dobrovolnících
- prevence hospitalizace se závažnými formami a smrtí

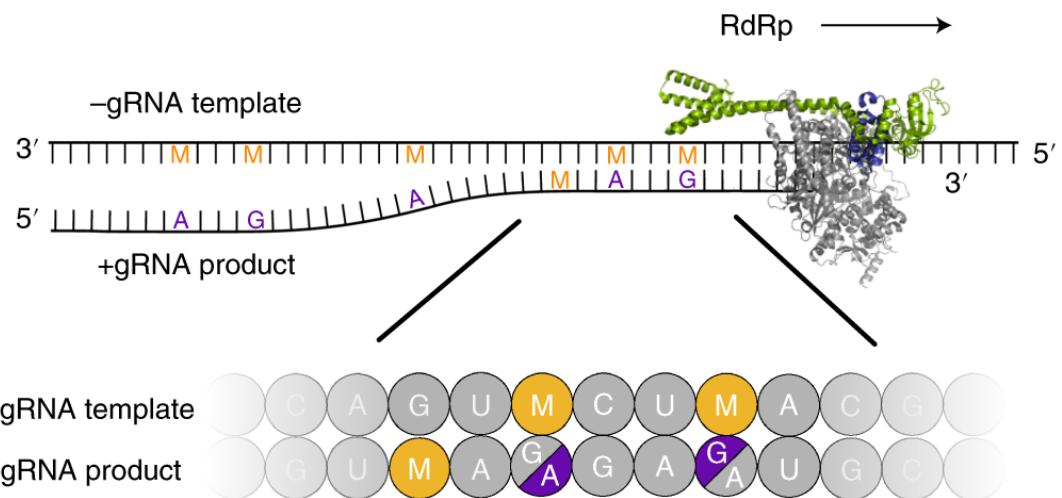


Molnupiravir MoA

Step 1: Incorporation

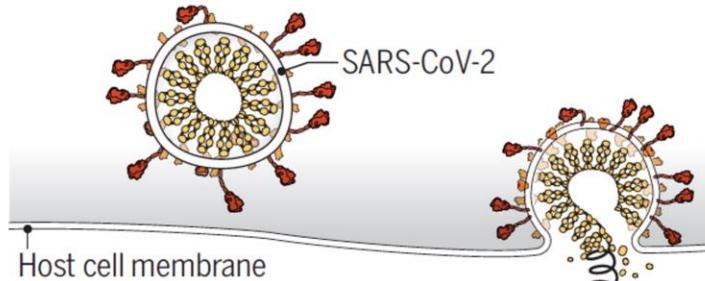


Step 2: Mutagenesis

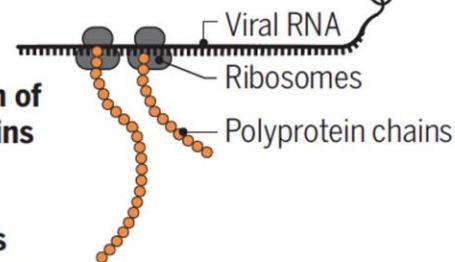


Paxlovid vs Molnupiravir

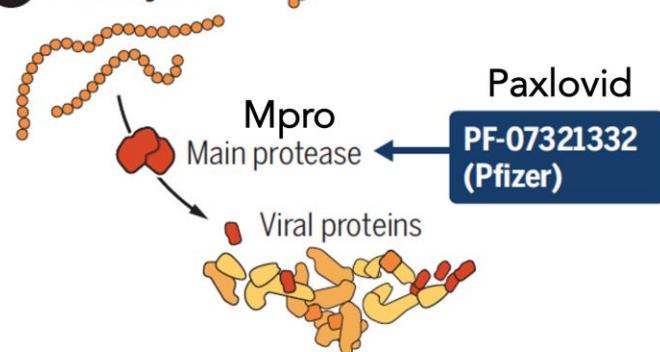
1 Attachment and entry



2 Translation of viral proteins

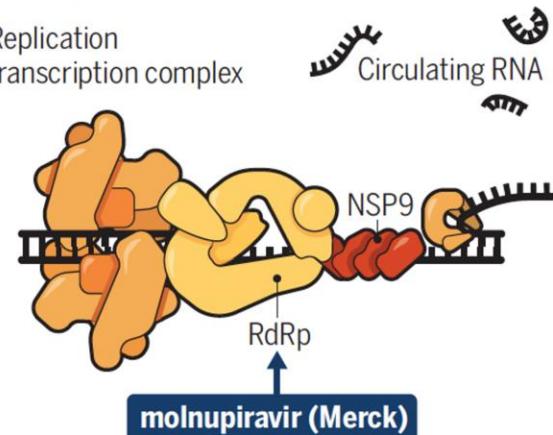


3 Proteolysis



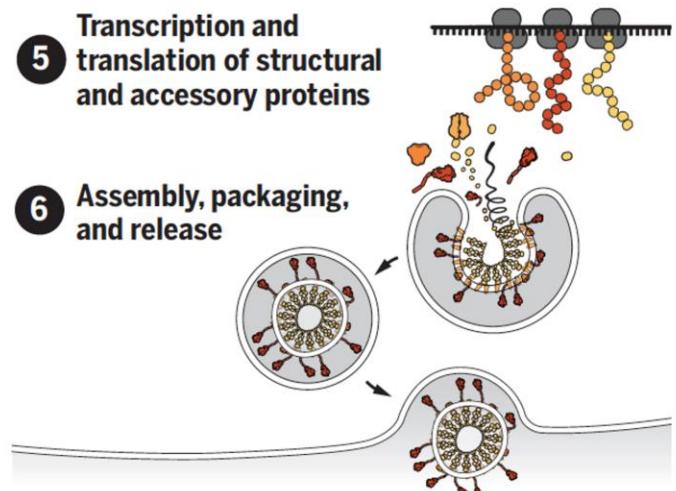
4 RNA replication

Replication transcription complex

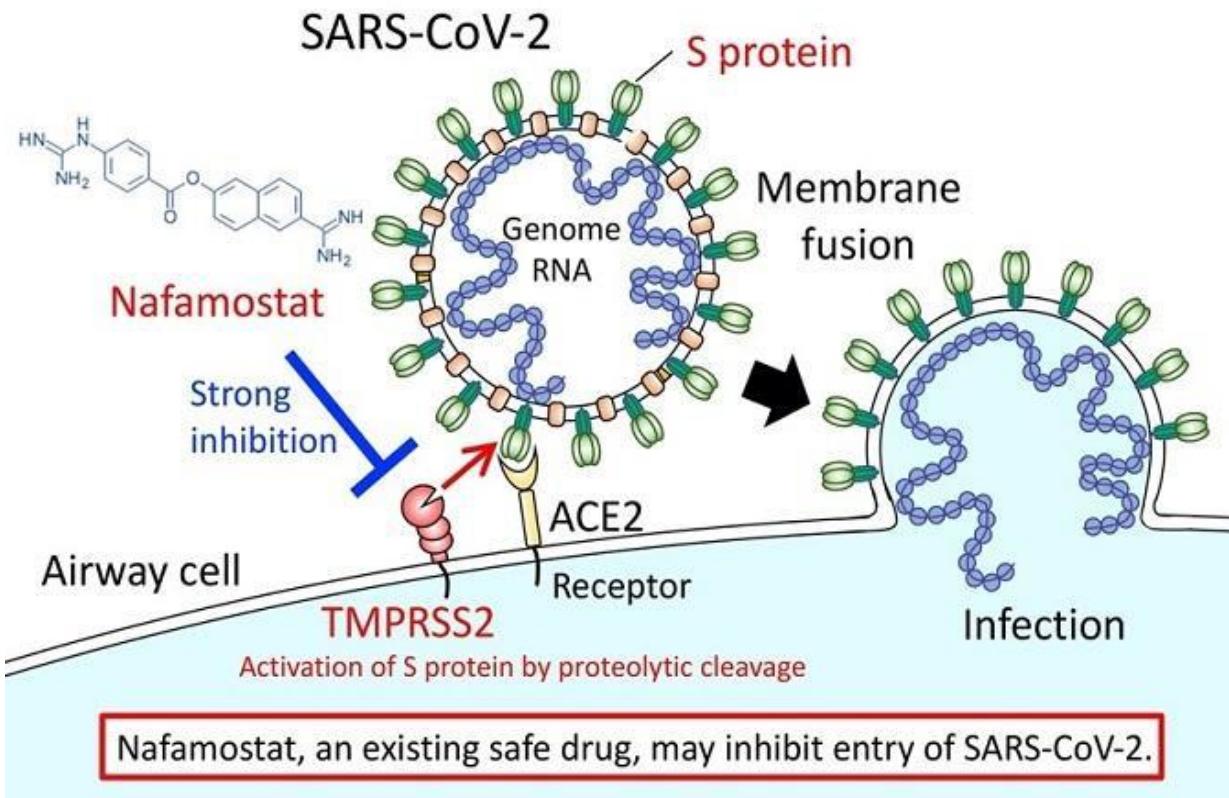


5 Transcription and translation of structural and accessory proteins

6 Assembly, packaging, and release

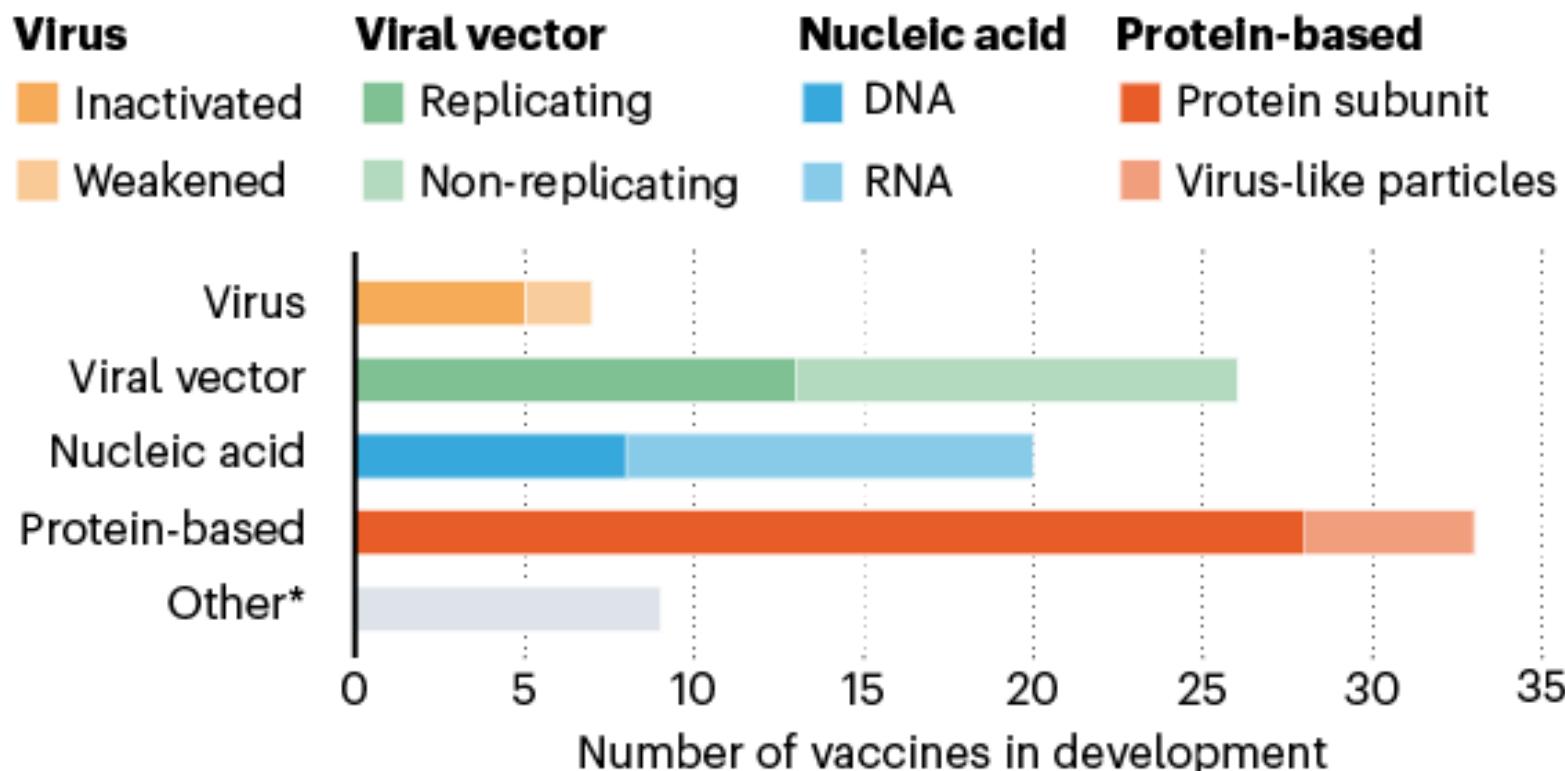


Protease Inhibitors – Spike and Maturation



Vakcíny

AN ARRAY OF VACCINES



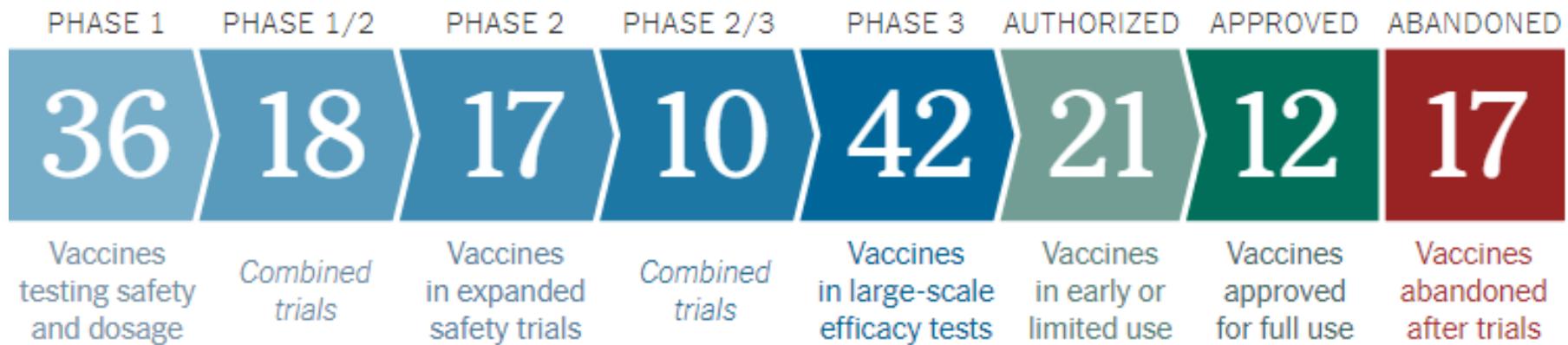
* Other efforts include testing whether existing vaccines against poliovirus or tuberculosis could help to fight SARS-CoV-2 by eliciting a general immune response (rather than specific adaptive immunity), or whether certain immune cells could be genetically modified to target the virus.

©nature

Vakcíny ve vývoji

Coronavirus Vaccine Tracker

By [Carl Zimmer](#), [Jonathan Corum](#), [Sui-Lee Wee](#) and Matthew Kristoffersen Updated Aug. 31, 2022

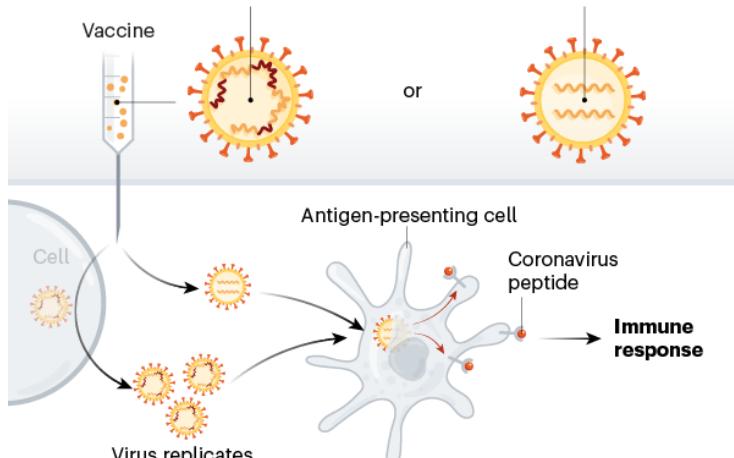


Vakcíny I

VIRUS VACCINES

Weakened virus

A virus is conventionally weakened for a vaccine by being passed through animal or human cells until it picks up mutations that make it less able to cause disease. Codagenix in Farmingdale, New York, is working with the Serum Institute of India, a vaccine manufacturer in Pune, to weaken SARS-CoV-2 by altering its genetic code so that viral proteins are produced less efficiently.



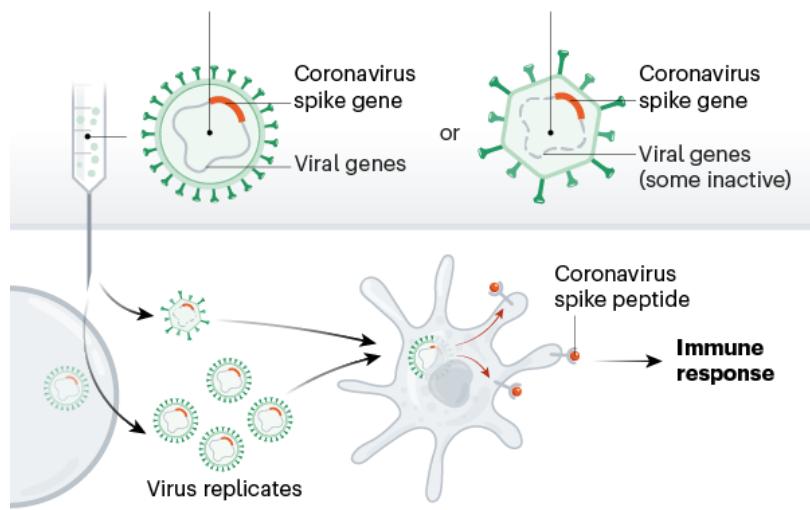
Inactivated virus

In these vaccines, the virus is rendered uninfected using chemicals, such as formaldehyde, or heat. Making them, however, requires starting with large quantities of infectious virus.

VIRAL-VECTOR VACCINES

Replicating viral vector (such as weakened measles)

The newly approved Ebola vaccine is an example of a viral-vector vaccine that replicates within cells. Such vaccines tend to be safe and provoke a strong immune response. Existing immunity to the vector could blunt the vaccine's effectiveness, however.



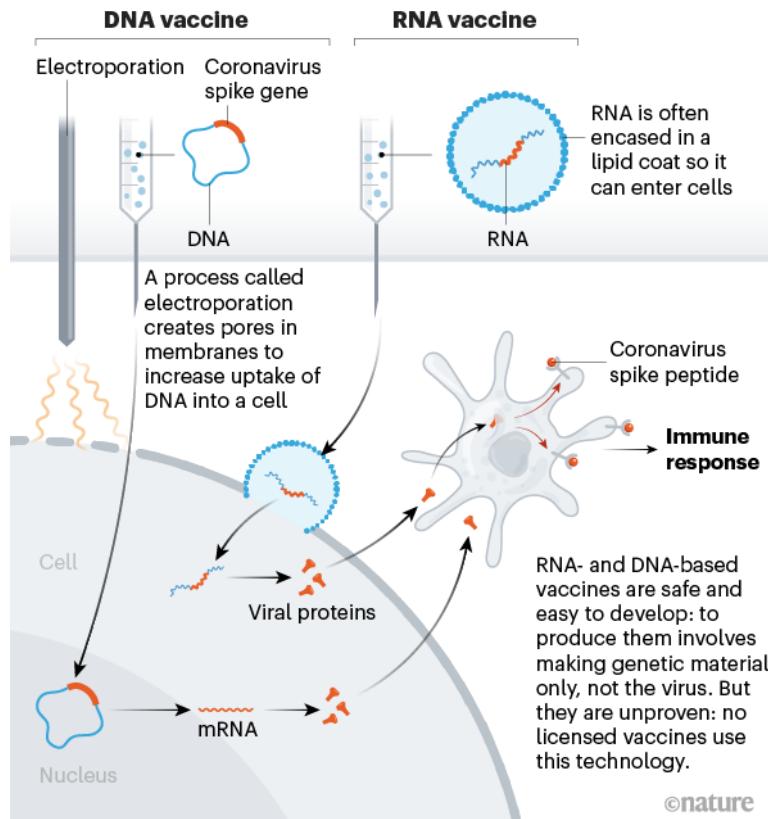
Non-replicating viral vector (such as adenovirus)

No licensed vaccines use this method, but they have a long history in gene therapy. Booster shots can be needed to induce long-lasting immunity. US-based drug giant Johnson & Johnson is working on this approach.

Sputnik V - two adenovirus vectors with Spike protein- rAd26-S + rAd5-S

Vakcíny II

NUCLEIC-ACID VACCINES

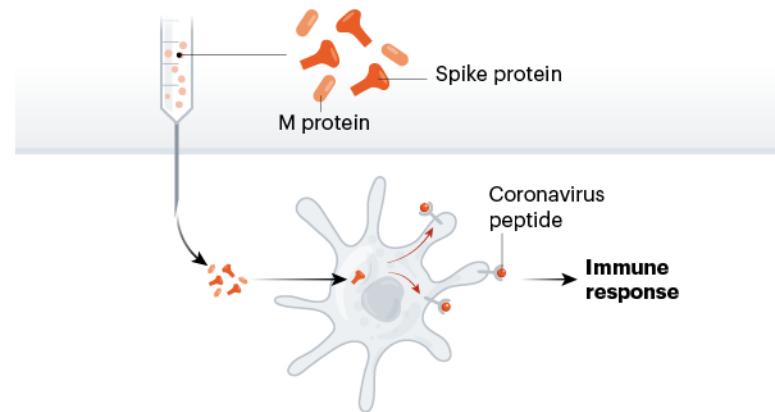


Pfizer-BioNtech – mRNA for Spike protein
Moderna - mRNA-1273 for Spike protein

PROTEIN-BASED VACCINES

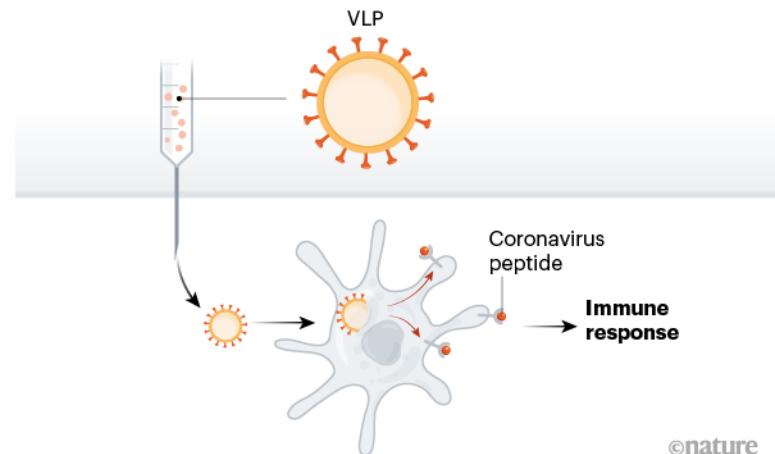
Protein subunits

Twenty-eight teams are working on vaccines with viral protein subunits — most are focusing on the virus's spike protein or a key part of it called the receptor binding domain. Similar vaccines against the SARS virus protected monkeys against infection but haven't been tested in people. To work, these vaccines might require adjuvants — immune-stimulating molecules delivered alongside the vaccine — as well as multiple doses.



Virus-like particles

Empty virus shells mimic the coronavirus structure, but aren't infectious because they lack genetic material. Five teams are working on 'virus-like particle' (VLP) vaccines, which can trigger a strong immune response, but can be difficult to manufacture.



©nature

Leading vaccines

| Developer | How It Works | Phase | Status |
|---|--------------|-------|--|
|  Pfizer-BioNTech | mRNA | 3 | Approved in U.S., other countries. Emergency use in many countries. |
|  Sinopharm | Inactivated | 3 | Approved in China, Bahrain. Emergency use in many countries. |
|  Oxford-AstraZeneca | ChAdOx1 | 2 3 | Approved in Brazil, India. Emergency use in many countries. |
|  Sinovac | Inactivated | 3 | Approved in China. Emergency use in many countries. |
|  Moderna | mRNA | 3 | Approved in U.S., Canada, Switzerland. Emergency use in many countries. |
|  Novavax | Protein | 3 | Approved in Canada, South Korea. Emergency use in several countries. |
|  Bharat Biotech | Inactivated | 3 | Approved in India. Emergency use in other countries. |
|  Johnson & Johnson | Ad26 | 3 | Approved in Canada. Limited in U.S. Emergency use in many countries. |
|  Baylor-Biological E | Protein | 3 | Emergency use in India, Botswana. |
|  Gamaleya | Ad26, Ad5 | 3 | Approved in Russia. Emergency use in many countries. |

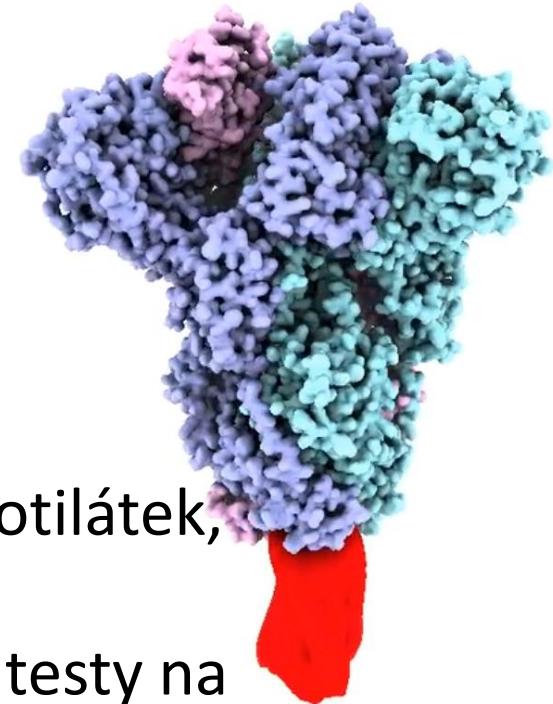
Zamítnuté vakcíny – zvláštní zmínka

ABANDONED



CSL

- Opuštěna 10.12.2020
- Na křečcích fungovala skvěle
- Fáze I – červenec 2020 – skvělé, hodně protilátek, žádné závažné vedlejší účinky
- Ale pak – dobrovolníci začali mít pozitivní testy na HIV, aniž by HIV virus měli
- Důvod: Aby udrželi S protein ve správném tvaru – drželi ho na místě pomocí „molecular clamp“ – ke kterému použili segment HIV proteinu – a ten chytaly protilátkové testy na HIV



Summary

Závěry

- Máme už docela dobrou představu ohledně struktury a funkce drtivé většiny proteinů SARS-CoV-2
- Vede to k návrhu léčiv a vakcín
- Sledováním mutací můžeme odhalit, které protilátky už na nové varianty nebudou plně fungovat
- Bohužel ani po nákaze tolika lidí stále má virus i v rámci RBD domény kde mutovat...

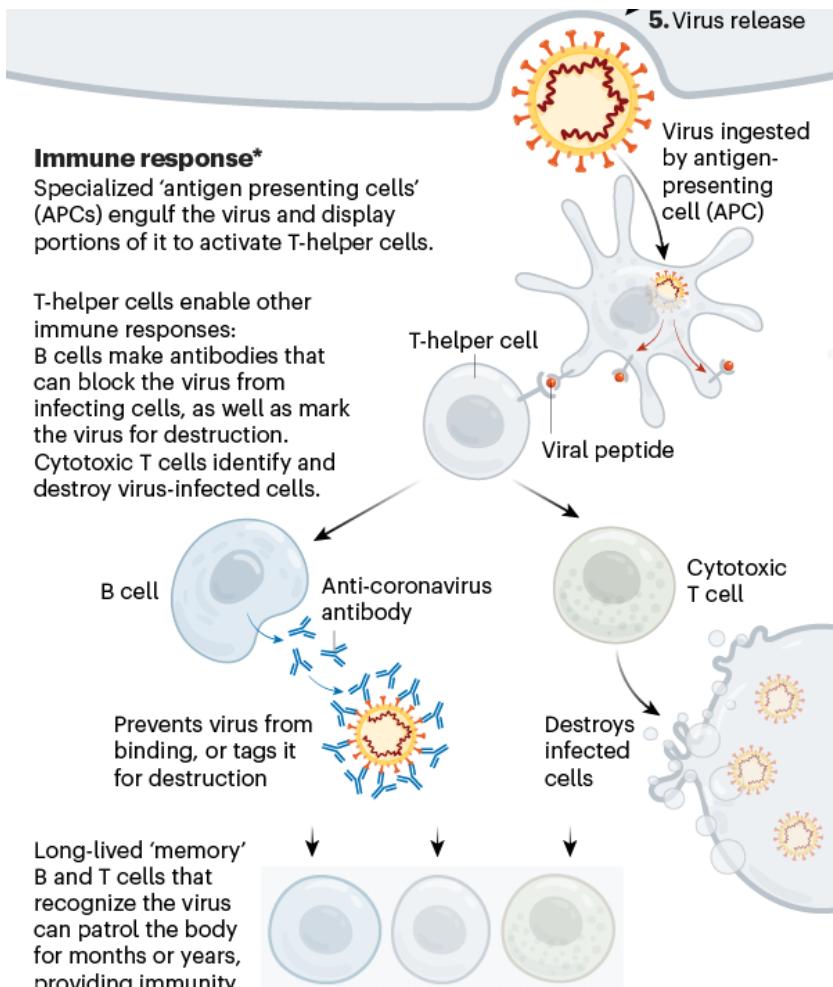
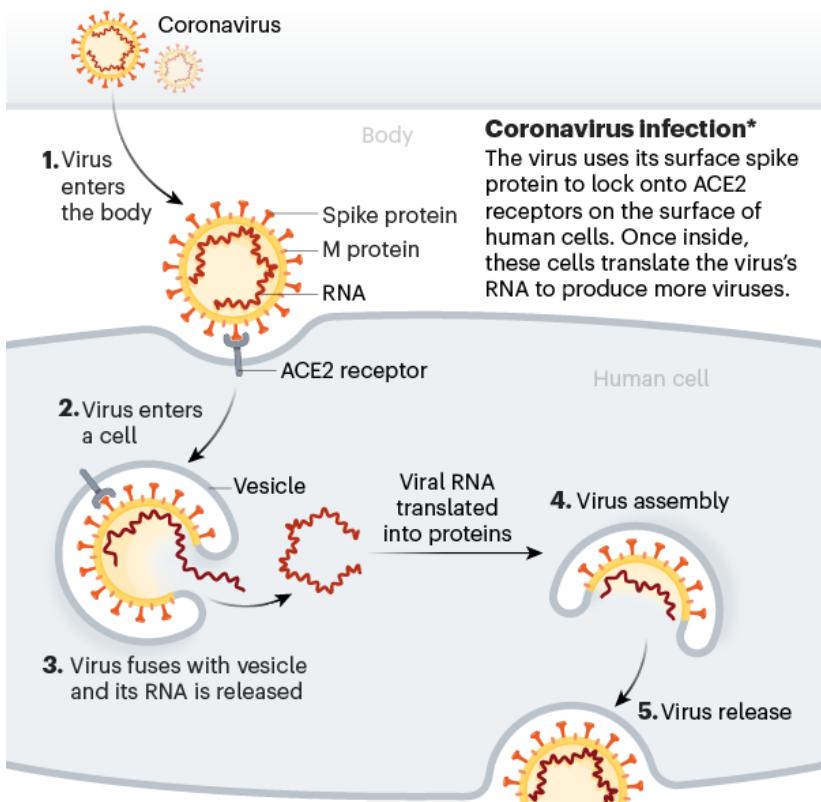
Zdroje

- virus.img.cas.cz
- covid19dataportal.org
- pdb101.rcsb.org/teach/covid-19
- pdb101.rcsb.org/sci-art/goodsell-gallery
- swissmodel.expasy.org/repository/species/2697049
- ebi.ac.uk/pdbe/covid-19
- [http://home.sandiego.edu/~josephprovost/Biochem
Covid Teaching.html](http://home.sandiego.edu/~josephprovost/Biochem_Covid_Teaching.html)

Imunita

VACCINE BASICS: HOW WE DEVELOP IMMUNITY

The body's adaptive immune system can learn to recognize new, invading pathogens, such as the coronavirus SARS-CoV-2.



*Simplified

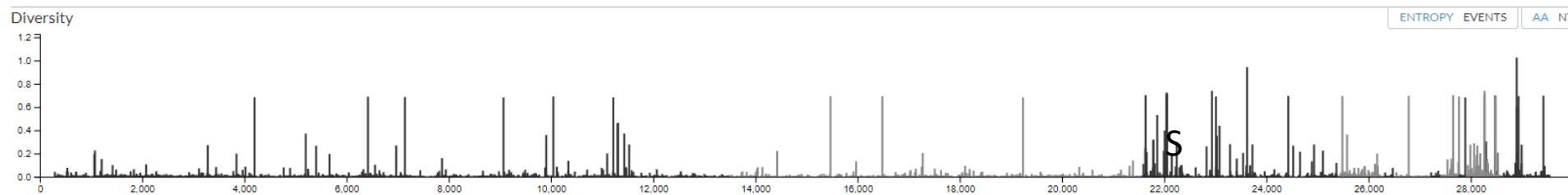
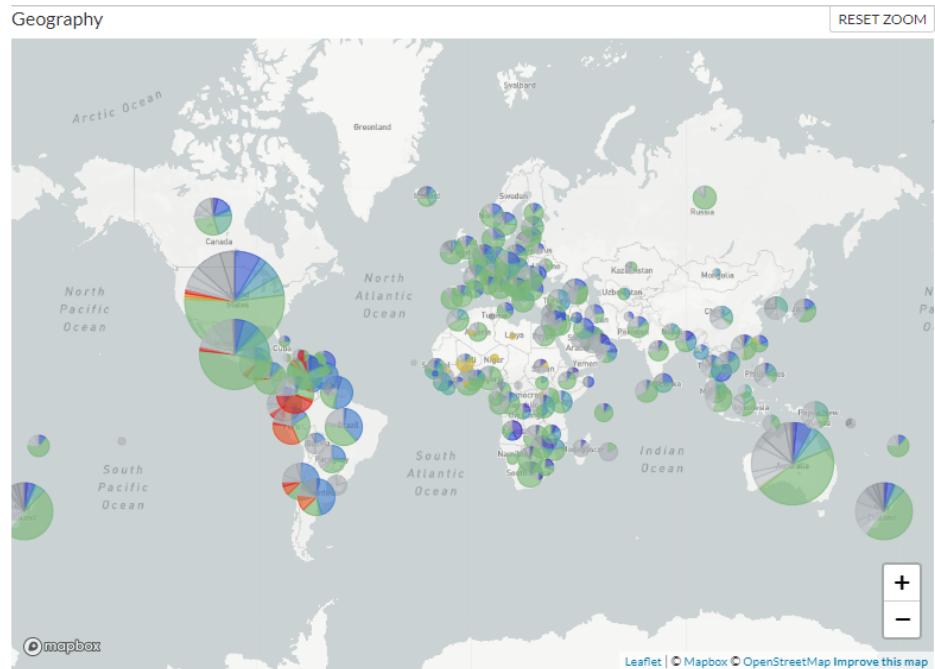
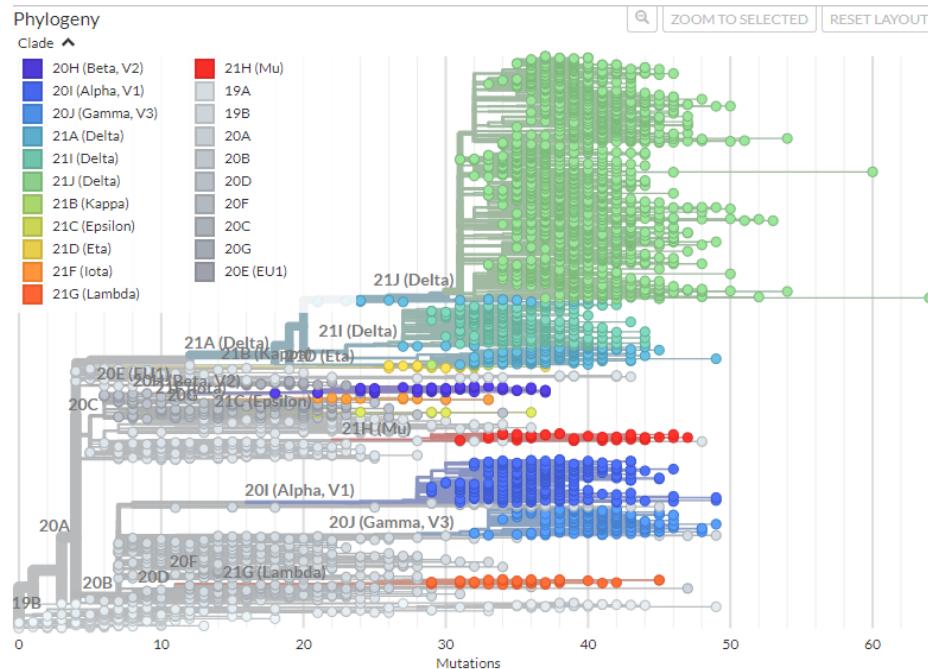
©nature

Genomy SARS-CoV-2

Genomic epidemiology of novel coronavirus - Global subsampling

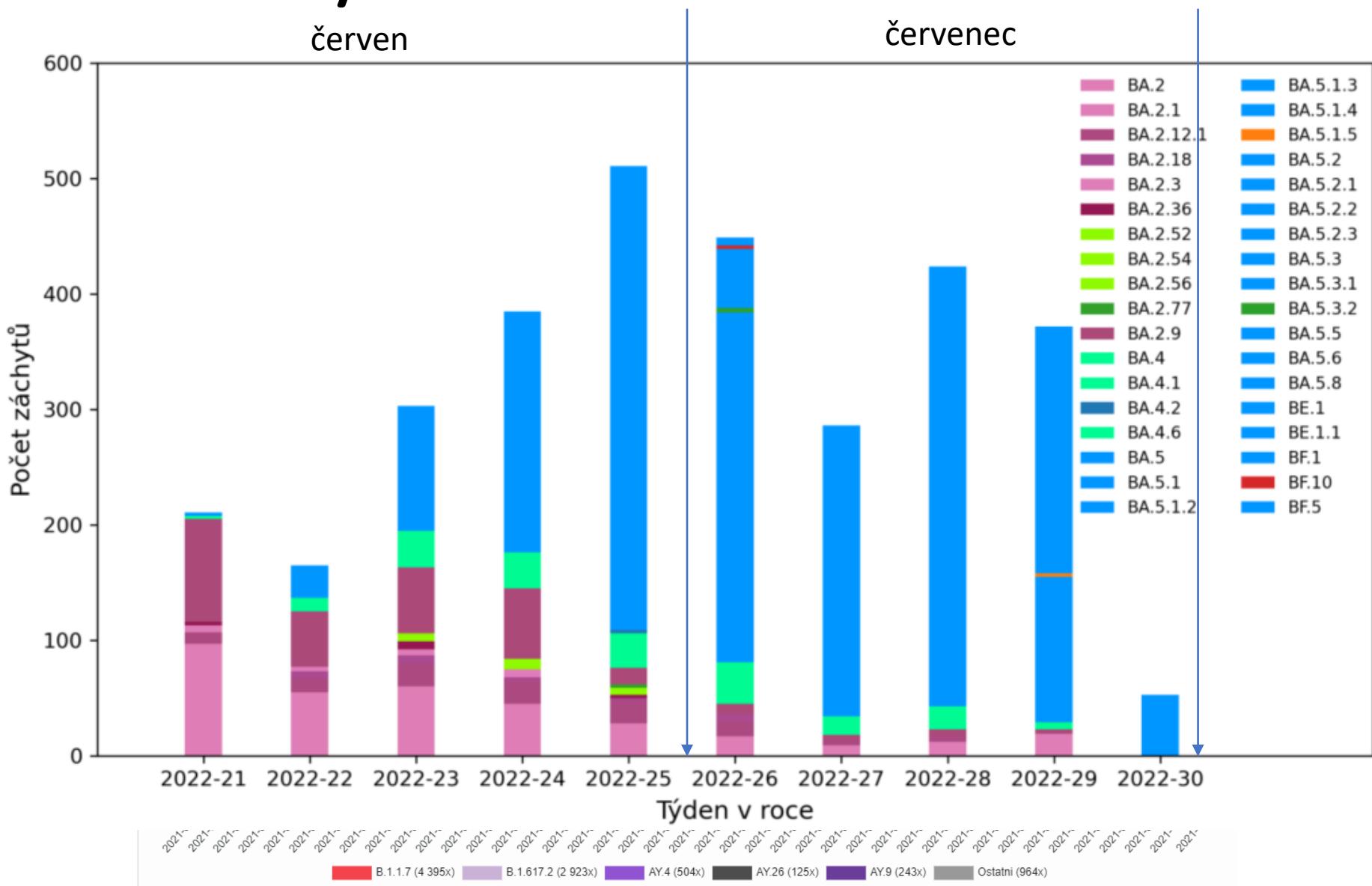
Built with nextstrain/ncov. Maintained by the Nextstrain team. Enabled by data from [GISaID](#).

Showing 3572 of 3572 genomes sampled between Dec 2019 and Oct 2021.

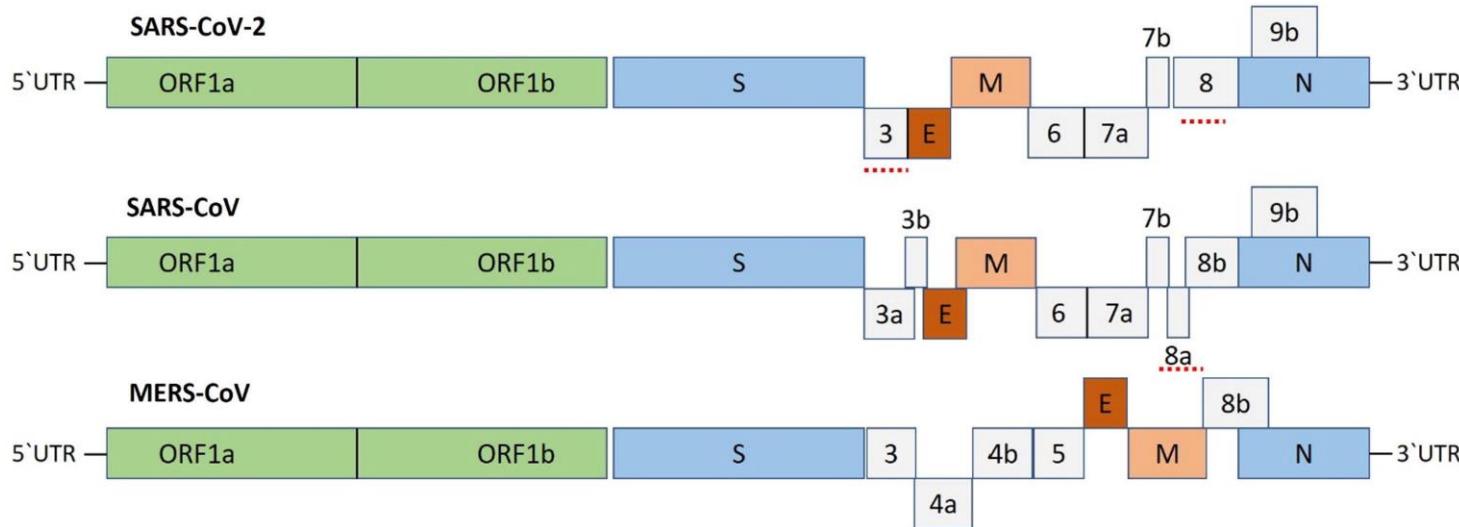
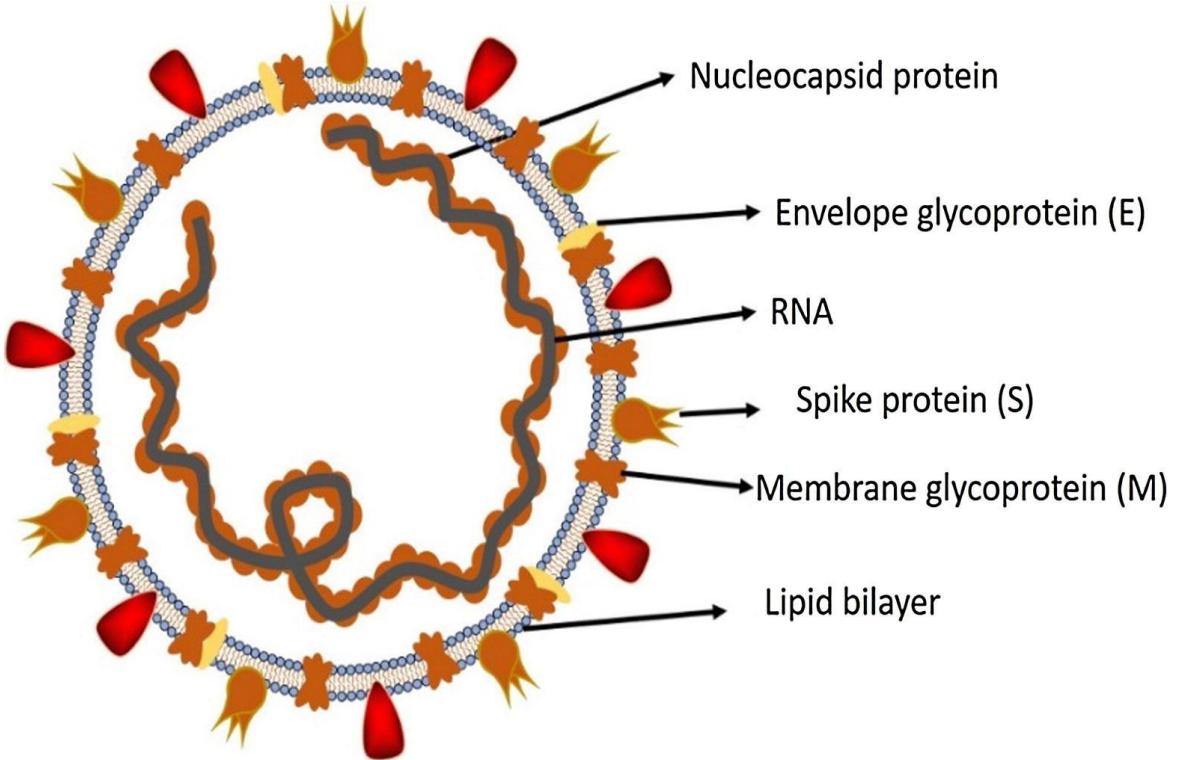


<https://nextstrain.org/ncov/global?m=div>

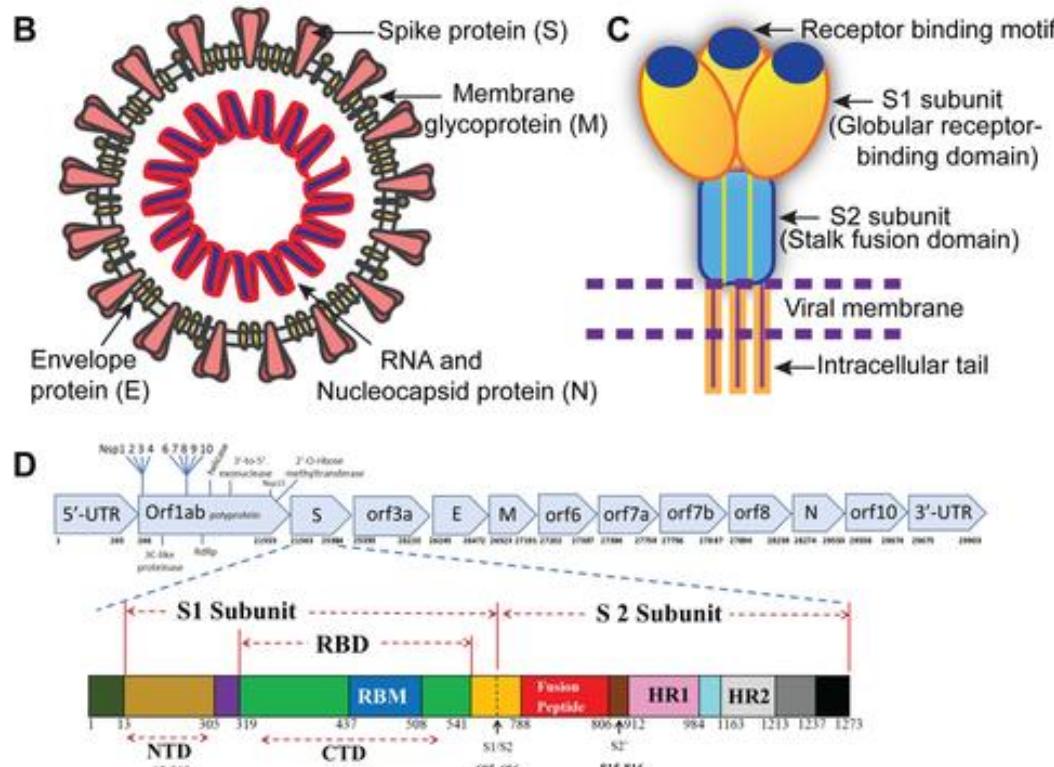
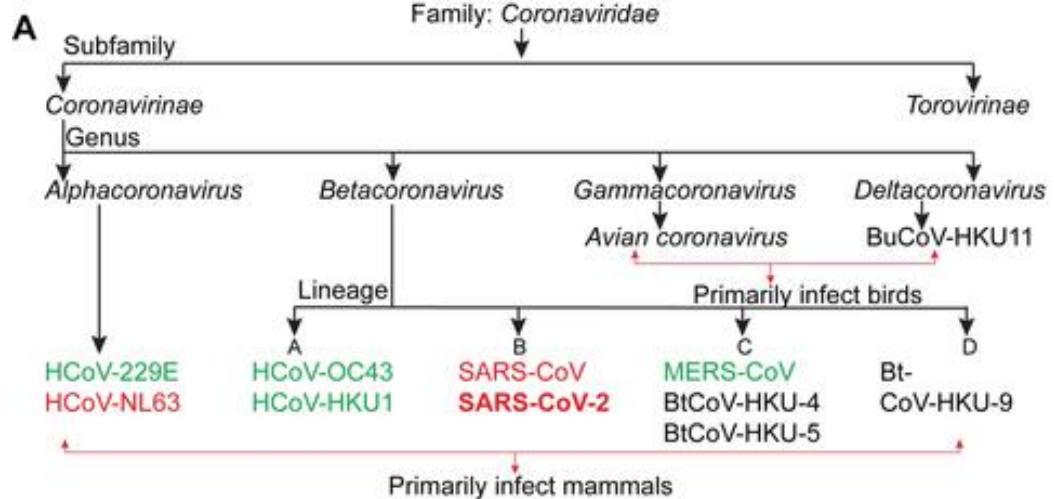
Varianty v ČR



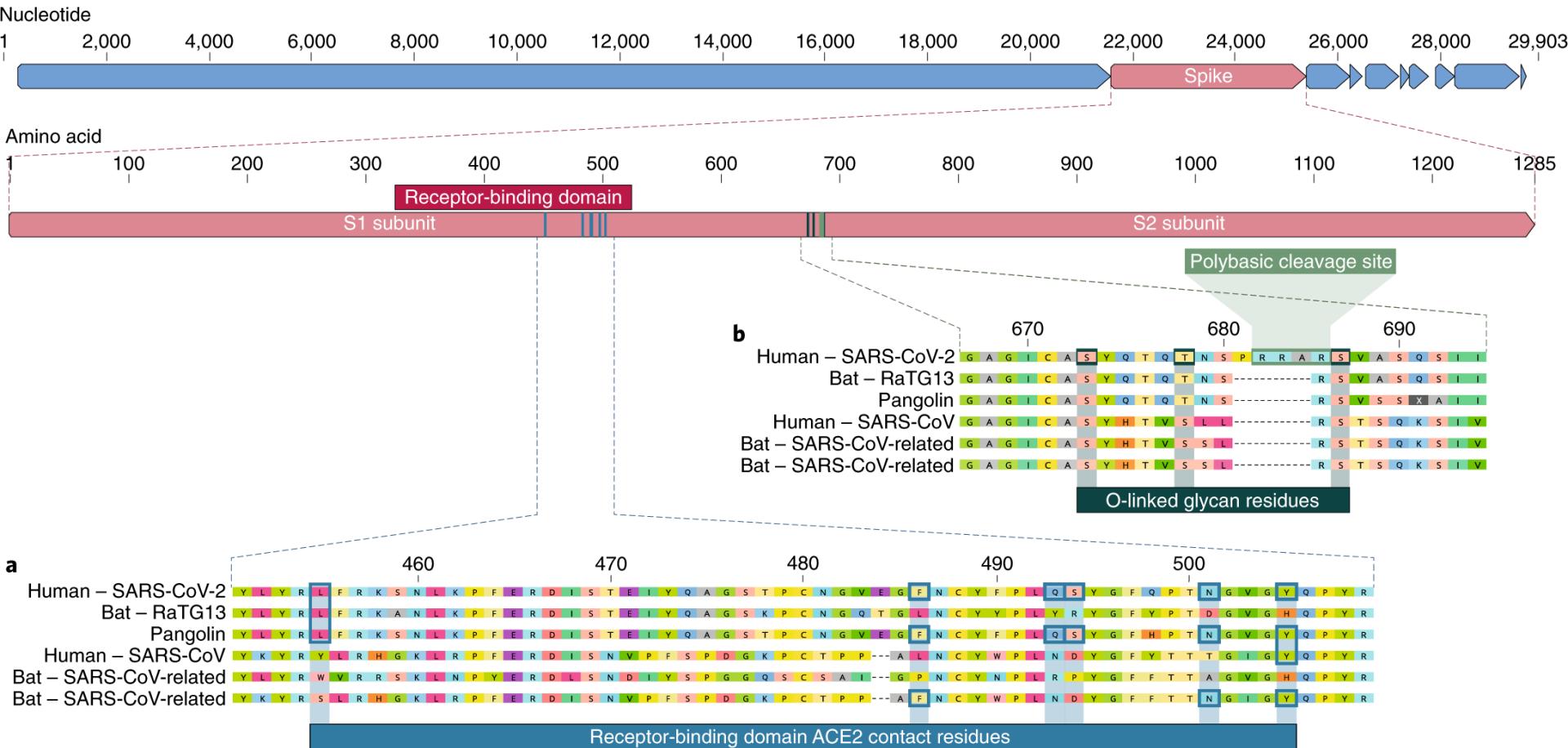
SARS, MERS, COVID-19 “parts list”



Klasifikace a struktury koronavirů



Spike Protein



Detail komplexu proteinů viru

Nsp3 -- a multidomain protein that includes RNA-binding domains, a membrane-anchoring domain, and the papain-like protease

Nsp4 and 6 -- membrane-spanning proteins that remodel the ER membrane

Nsp5 -- main protease that cuts the viral polyproteins into functional pieces

Nsp7, 8 and 10 -- proteins involved in organizing the replicase complex

Nsp12 -- RNA-directed RNA polymerase creates new viral RNA strands

Nsp13 -- helicase separates strands in an RNA double helix

Nsp14 -- guanine N7-methyltransferase includes an exoribonuclease involved in proofreading

Nsp15 -- uridylate-specific endoribonuclease breaks RNA, the function of which is still under study

Nsp16 -- 2'-O-methyltransferase is involved in formation of the RNA cap

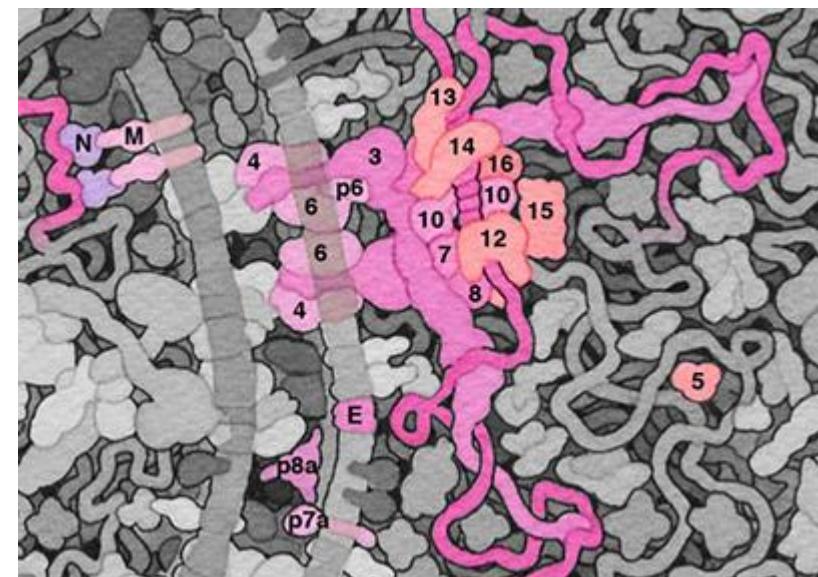
Three structural proteins are also shown:

Nucleocapsid (N) condenses the viral genomic RNA

Membrane (M) protein works with N to package the RNA into the virion

Envelope (E) is involved in the process of budding

sizes and shapes of each protein are based on current structural information, but the arrangement within the complex is largely speculative:



Several accessory proteins (p6, p7a, and p8a) are also shown. These are dispensable for replication of the virus, but are involved in the virulence of infection.