

# Case Study: SARS-CoV-2

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# Identification of SARS-CoV-2

ORIGINAL ARTICLE BRIEF REPORT

## A Novel Coronavirus from Patients with Pneumonia in China, 2019

Na Zhu, Ph.D., Dingyu Zhang, M.D., Wenling Wang, Ph.D., Xingwang Li, M.D., Bo Yang, M.S., Jingdong Song, Ph.D., Xiang Zhao, Ph.D., Baoying Huang, Ph.D., Weifeng Shi, Ph.D., Roujian Lu, M.D., Peihua Niu, Ph.D., Faxian Zhan, Ph.D., et al., for the China Novel Coronavirus Investigating and

### VIRAL GENOME SEQUENCING

RNA extracted from bronchoalveolar-lavage fluid and culture supernatants was used as a template to clone and sequence the genome. We used a combination of Illumina sequencing and nanopore sequencing to characterize the virus genome. Sequence reads were assembled into contig maps (a set of overlapping DNA segments) with the use of CLC Genomics software, version 4.6.1 (CLC Bio). Specific primers were subsequently designed for PCR, and 5'- or 3'-RACE (rapid amplification of cDNA ends) was used to fill genome gaps from conventional Sanger sequencing. These PCR products were purified from gels and sequenced with a BigDye Terminator v3.1 Cycle Sequencing Kit and a 3130XL Genetic Analyzer, in accordance with the manufacturers' instructions.

# Identification of SARS-CoV-2

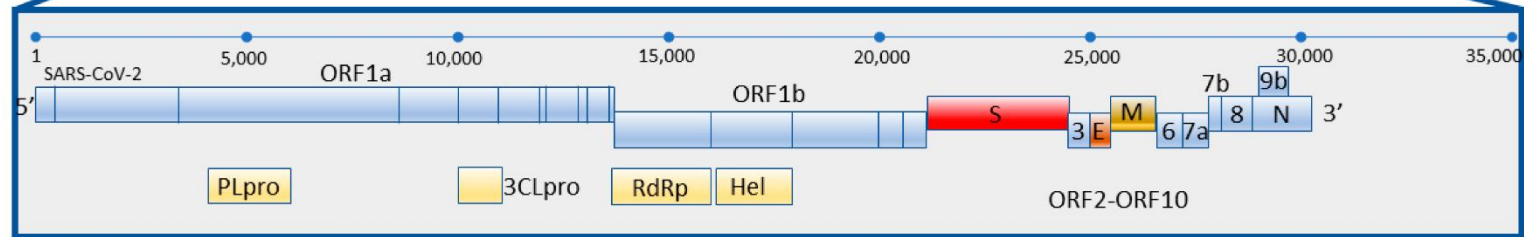
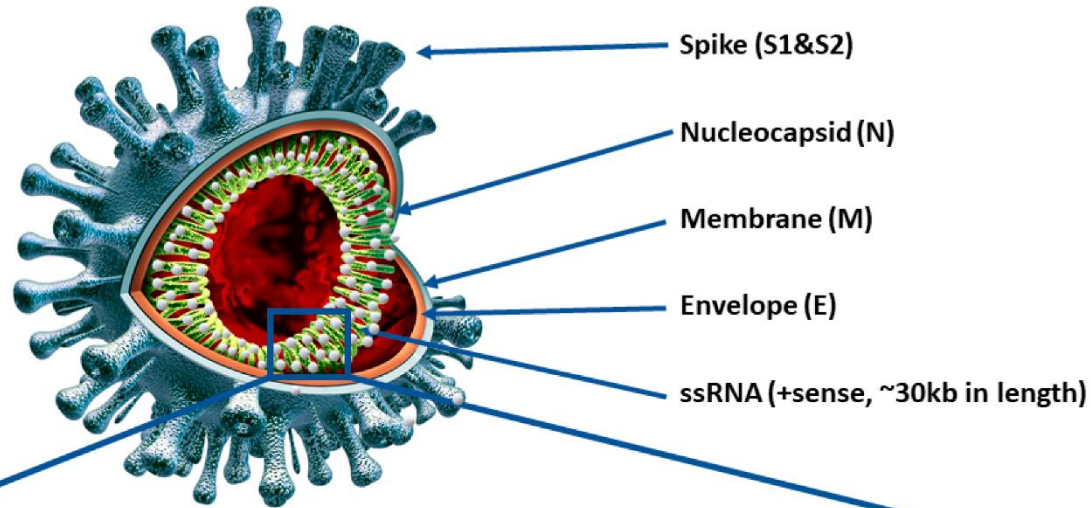
ORIGINAL ARTICLE BRIEF REPORT

## A Novel Coronavirus from Patients with Pneumonia in China, 2019

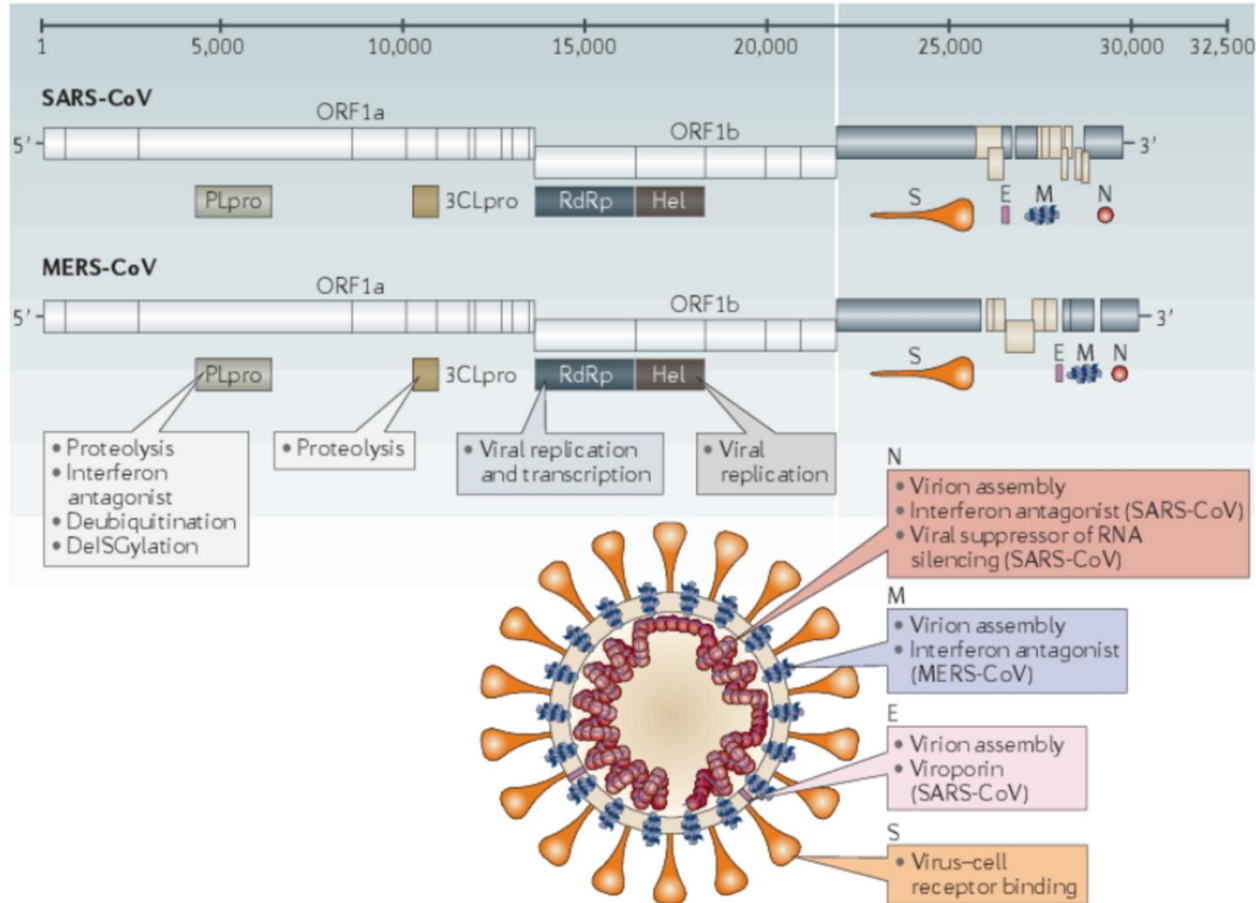
Na Zhu, Ph.D., Dingyu Zhang, M.D., Wenling Wang, Ph.D., Xingwang Li, M.D., Bo Yang, M.S., Jingdong Song, Ph.D., Xiang Zhao, Ph.D., Baoying Huang, Ph.D., Weifeng Shi, Ph.D., Roujian Lu, M.D., Peihua Niu, Ph.D., Faxian Zhan, Ph.D., et al., for the China Novel Coronavirus Investigating and

RespiFinderSmart22kit. RNA extracted from bronchoalveolar-lavage fluid from the patients was used as a template to clone and sequence a genome using a combination of Illumina sequencing and nanopore sequencing. More than 20,000 viral reads from individual specimens were obtained, and most contigs matched to the genome from lineage B of the genus betacoronavirus — showing more than 85% identity with a bat SARS-like CoV (bat-SL-CoVZC45, MG772933.1) genome published previously. Positive

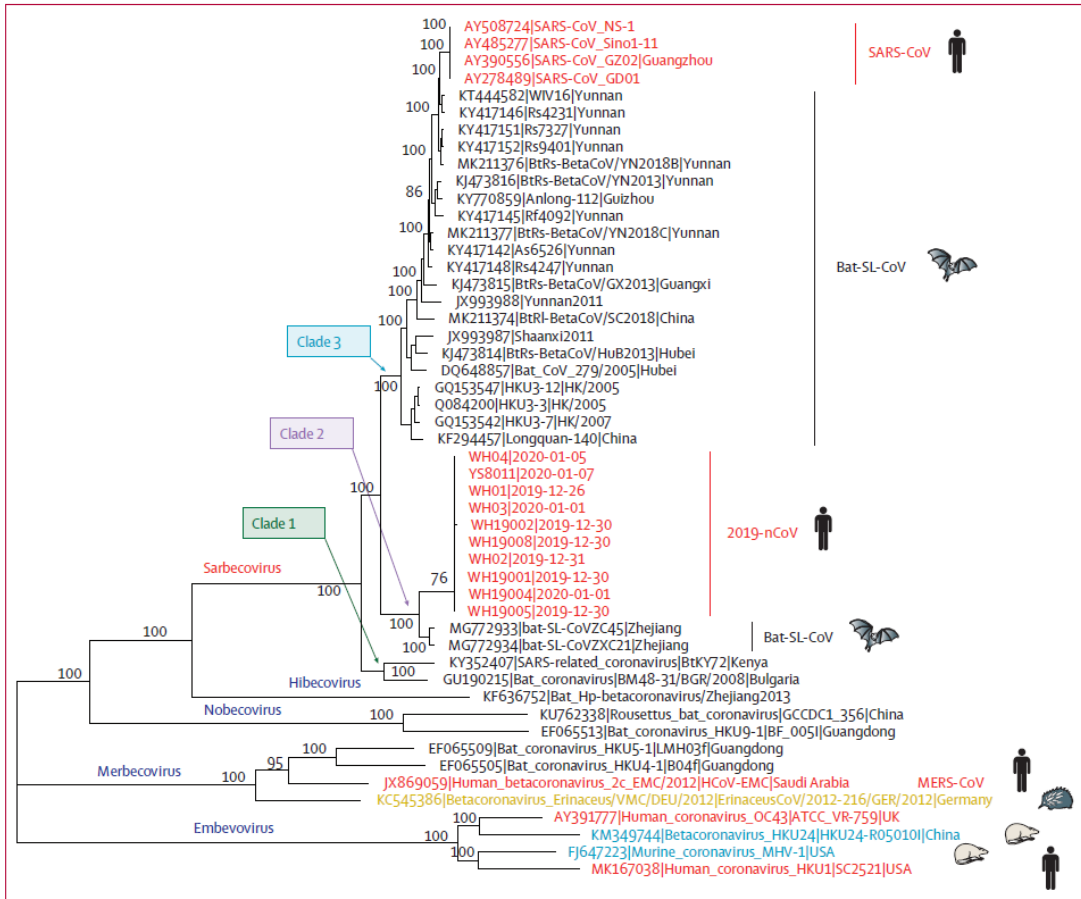
# Genomic structure



# SARS-CoV-2 proteins



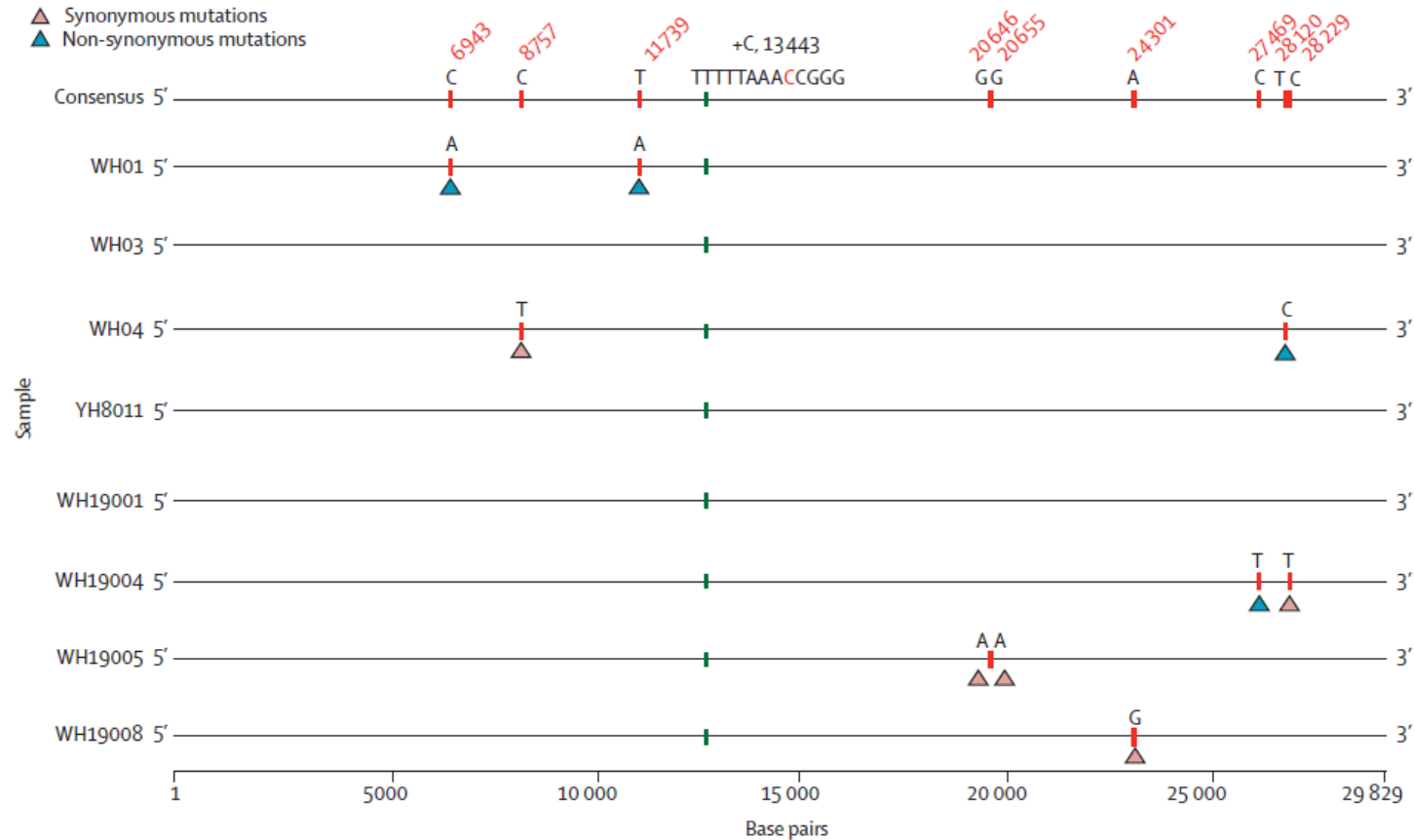
# Phylogenetic analysis of SARS-CoV-2



## Phylogenetic analysis

Sequence alignment of 2019-nCoV with reference sequences was done with Mafft software (version 7.450).<sup>21</sup> Phylogenetic analyses of the complete genome and major coding regions were done with RAXML software (version 8.2.9)<sup>22</sup> with 1000 bootstrap replicates, employing the general time reversible nucleotide substitution model.

# SARS-CoV-2 variants





# Drug repurposing for SARS-CoV-2

CLUSTAL O(1.2.4) multiple sequence alignment

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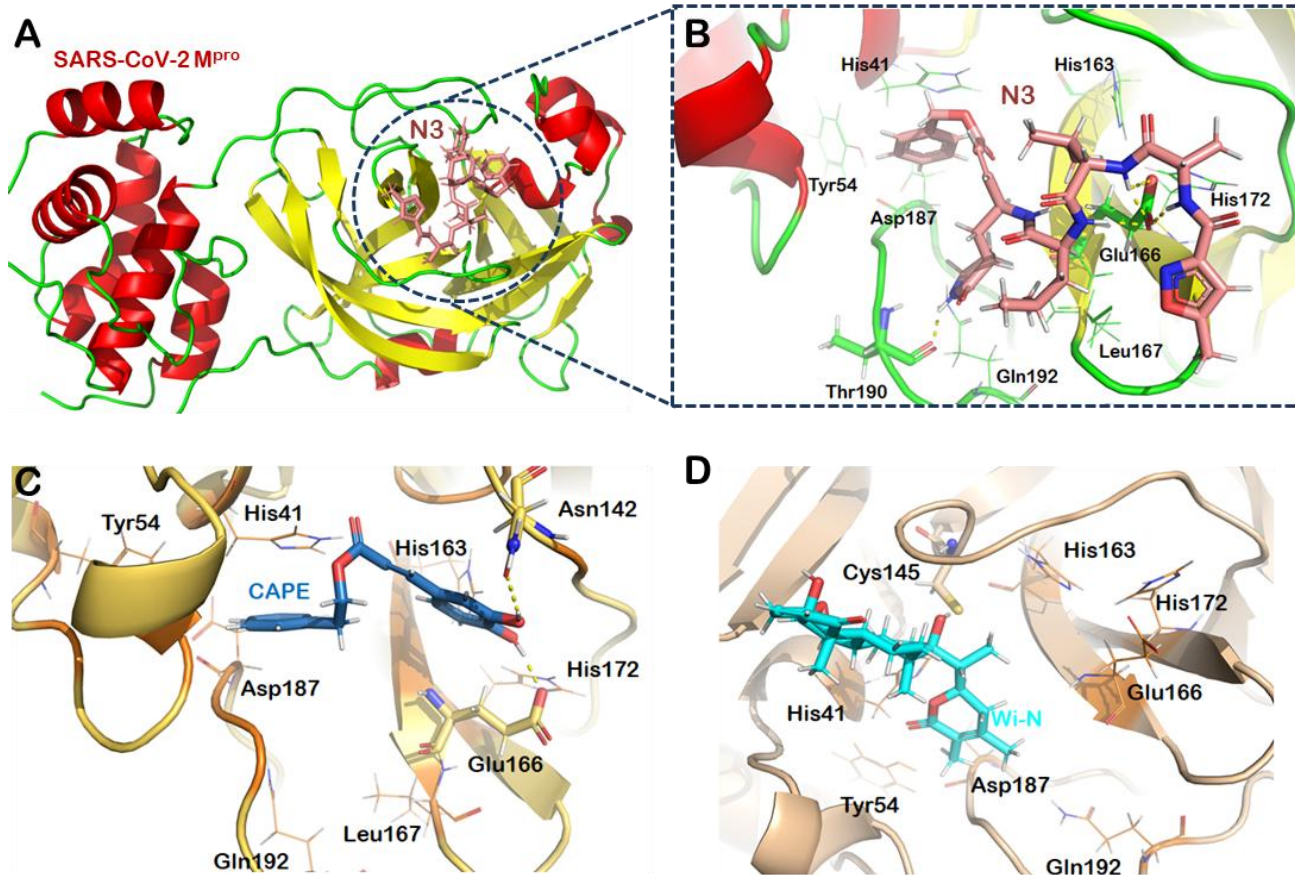
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3D23:B|PDBID|CHAIN|SEQUENCE      -----ASSGIVKMVSPTSKEIPCIVSVTYSMTLNLGLWLDKVCYCPRICTSSNNPEPD 55
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3IWM:A|PDBID|CHAIN|SEQUENCE      YEDLLIRKSNHNSFLVQ---AGNVQLRVIGHSMQNCVLLRLKVDTSNPKTPKYKFVRIQPGQ 110
3D23:B|PDBID|CHAIN|SEQUENCE      YSALLCRVTLGDFTIM---SGRMSLVVSYQMGCVLTVSLQNPYTPKYTFGNVKPGE 112
5WKK:A|PDBID|CHAIN|SEQUENCE      YDALLISMTNHSFSVQKHIGAPANLRVVGHAMQGTLLKLTVDVANPSTPAYTFTTVKPGA 120
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:
3TLO:A|PDBID|CHAIN|SEQUENCE      SFNIIACYEGIASGVFGVNLRTNFTIKGSFINGACGSPGYNVRNDGTVEFCYLHIEIGS 169
1P9S:A|PDBID|CHAIN|SEQUENCE      GFNIIACYDSCAQGVFGVMRTNWTIRGSFINGACGSPGYNLIN-GEVEFYVHIEIGS 168
6LU7:A|PDBID|CHAIN|SEQUENCE      TFSVLACYNGSPSGVYQCAMPNFTIKGSFLNGSCGSGVFNIDY-DCVSFCYHMEIPT 169
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3D23:B|PDBID|CHAIN|SEQUENCE      TFTVLAAYNGRPQGAHVTRMSYTIKGSFLCGSCGSGVYVLTG-DSVKFYVHMEIPT 171
5WKK:A|PDBID|CHAIN|SEQUENCE      AFSVLACYNGRPTGFTTVMRPNYTIKGSFLCGSCGSGVYTKEG-SVINFCYHMEIPT 179
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6LU7:A|PDBID|CHAIN|SEQUENCE      GVAIGTDLEGHFYGPFVDQTAQAAGTDTITVNVLAWLYAAVINGDRWFLNRFITTLND 229
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3D23:B|PDBID|CHAIN|SEQUENCE      ELAPSDVYQQLAGV--- 302
5WKK:A|PDBID|CHAIN|SEQUENCE      EFTPFDVVRQIMGVVMQ 313
                                     * : : * : * :
:
3TLO: HCoV-NL63
1P9S: HCoV-229E
3D23: HCoV-HKU1
GLU7: SARS-CoV-2
3IWM: SARS-CoV
5WKK: MERS-CoV

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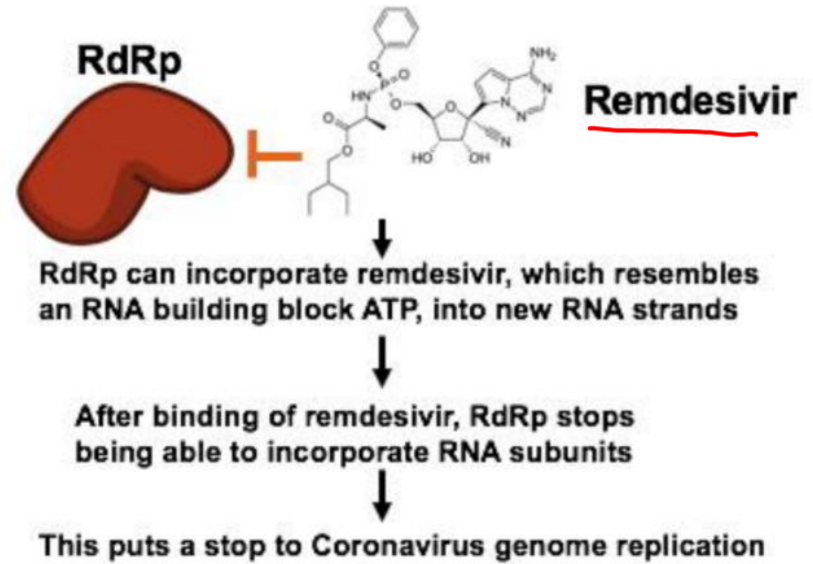
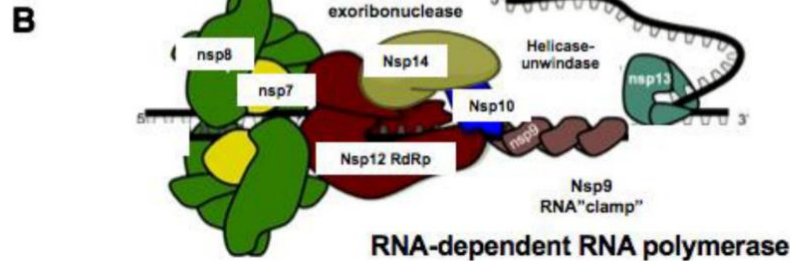
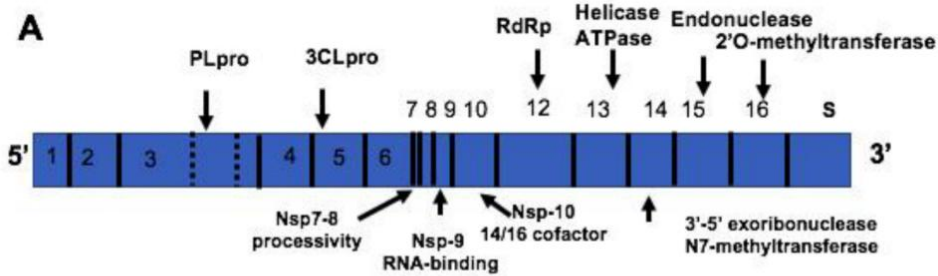
Multiple sequence alignment of Main protease enzyme of various human coronaviruses, including SARS-CoV-2



# Drug repurposing for SARS-CoV-2

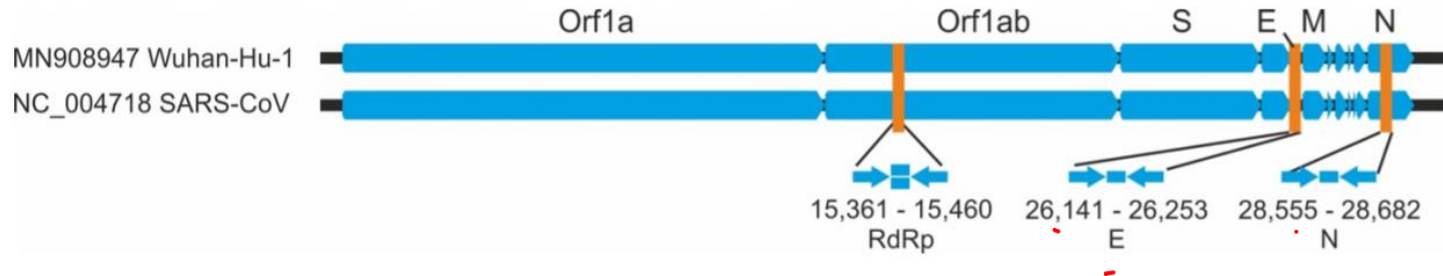


# Remdesivir against RdRp

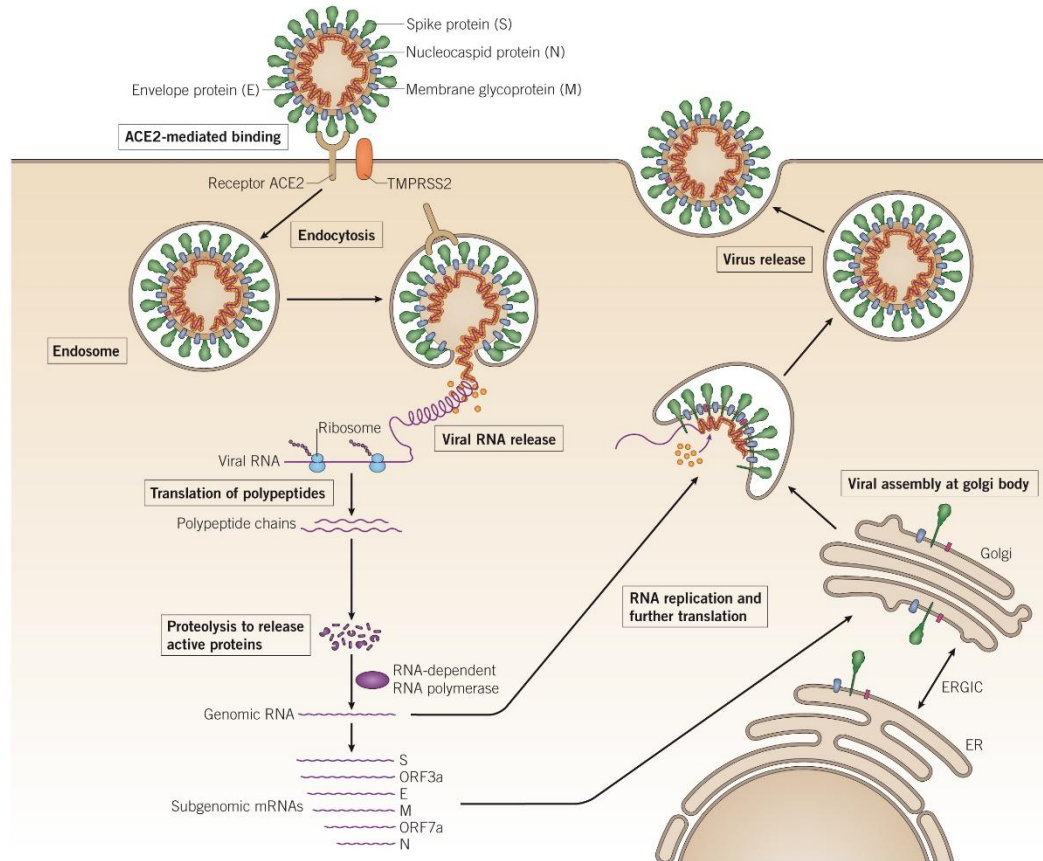


# RTPCR test for SARS-CoV-2

**First line screening assay: E gene assay**  
**Confirmatory assay: RdRp gene assay**  
**Additional confirmatory assay: N gene assay**



# Transmission of SARS-CoV-2

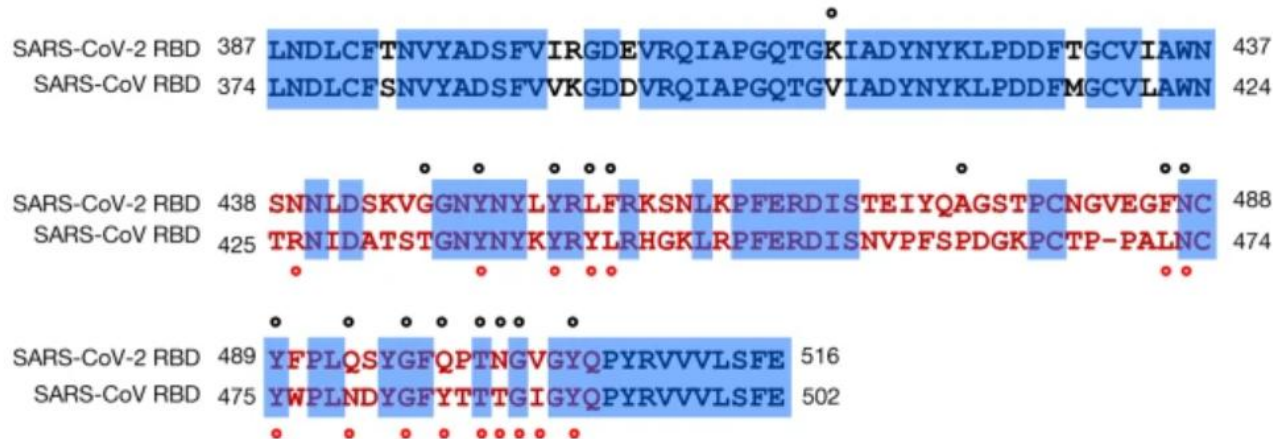


# Transmission of SARS-CoV-2

## Structure of the SARS-CoV-2 spike receptor-binding domain bound to the ACE2 receptor

[Jun Lan](#), [Jiwan Ge](#), [Jinfang Yu](#), [Sisi Shan](#), [Huan Zhou](#), [Shilong Fan](#), [Qi Zhang](#), [Xuanling Shi](#), [Qisheng Wang](#),  
[Linqi Zhang](#) ✉ & [Xinquan Wang](#) ✉

*Nature* **581**, 215–220 (2020) | [Cite this article](#)



Sequence alignment of the SARS-CoV-2 and SARS-CoV RBDs.