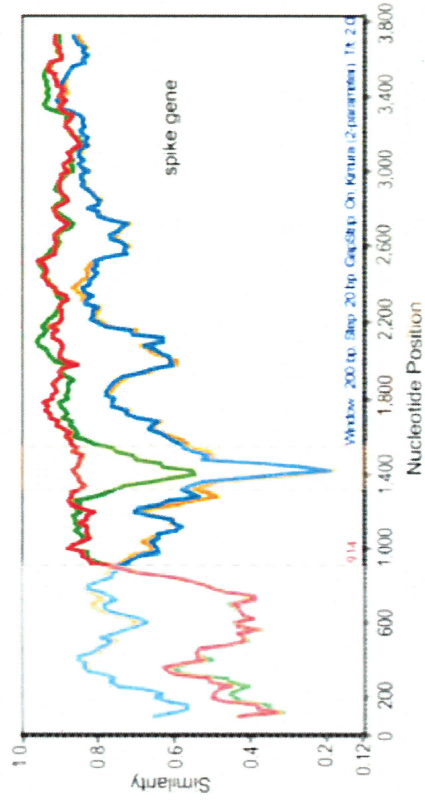


SARS-COV-2 SPIKE GENE SEGMENTS

QUERY: PANGOLIN-COV

- SARS-CoV-2_WIV02
- Bat CoV RaTG13
- Bat SARSr-CoV_ZC45
- Bat SARSr-CoV_ZXC21

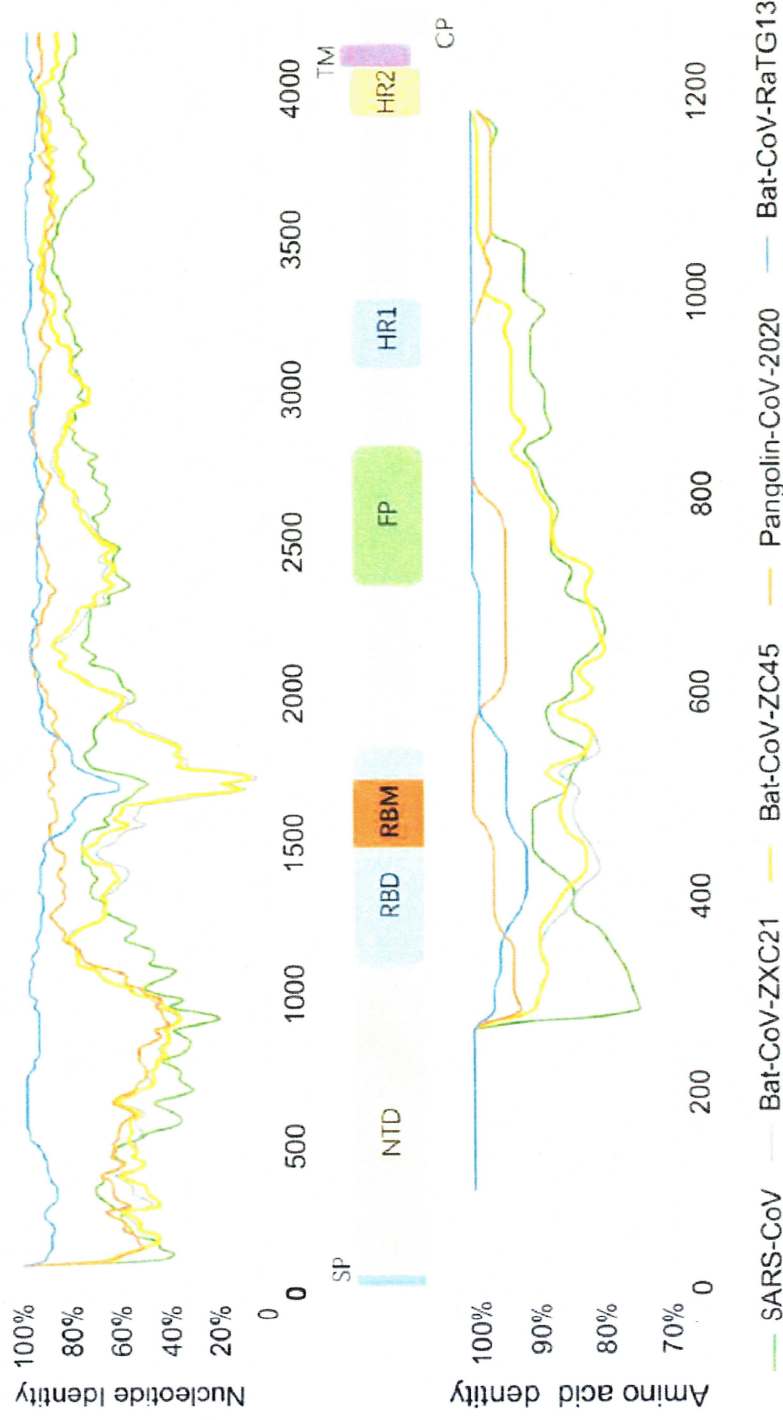


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SARS-CoV-2 SimPLOT

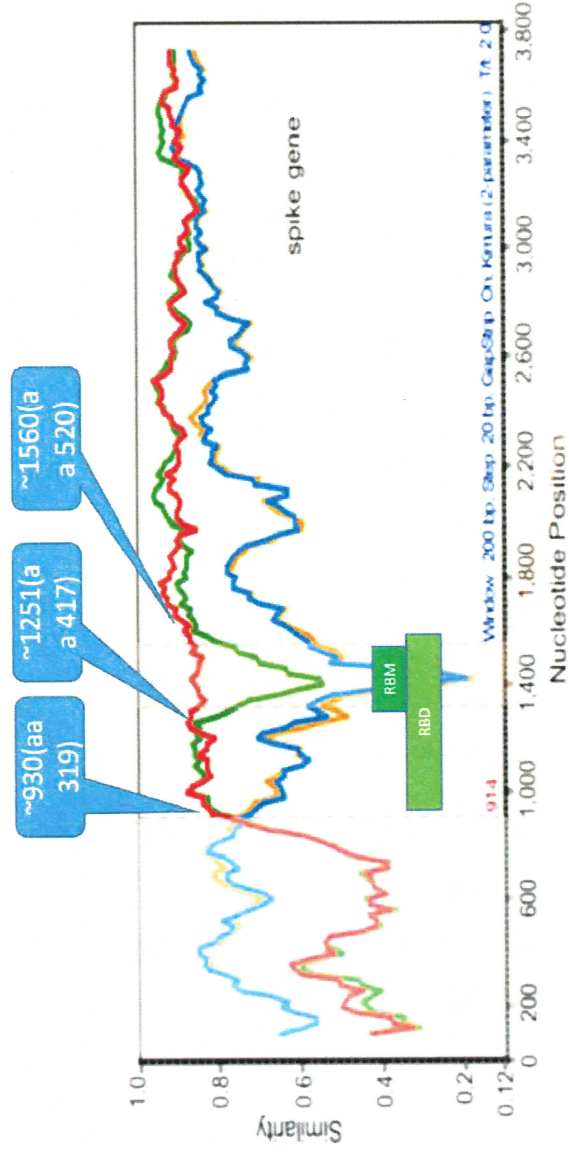


- "A recent study found that a human ACE2-binding ridge in SARS-CoV-2 RBD takes a more compact conformation compared with the SARS-CoV RBD; moreover, several residue changes in SARS-CoV-2 RBD may also enhance its human ACE2-binding affinity [13]. The core residues in RBM which may related to higher human ACE2-binding affinity than SARS-CoV are 100% identical between SARS-CoV-2 and CoV-Pangolin-2020. Therefore, pangolin-CoV-2020 (CoV-pangolin/GD) potentially recognizes human ACE2 better than the SARS-CoV."

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Minimal Receptor Binding Domain Cassette

- WIV scientists previously defined the minimal Receptor Binding Domain cassette that could functionally transfer ACE2 binding capability from one Spike protein to another SARS Nucleotide: 930-1554 SARS Amino Acid: 310-518 Receptor Binding Motif SARS Nucleotide: 1251-1482 SARS Amino Acid: 417-494 Homology cut points of SARS-CoV-2 coincide with WIV-identified borders of RBD and RBM



Furin Cleavage Site

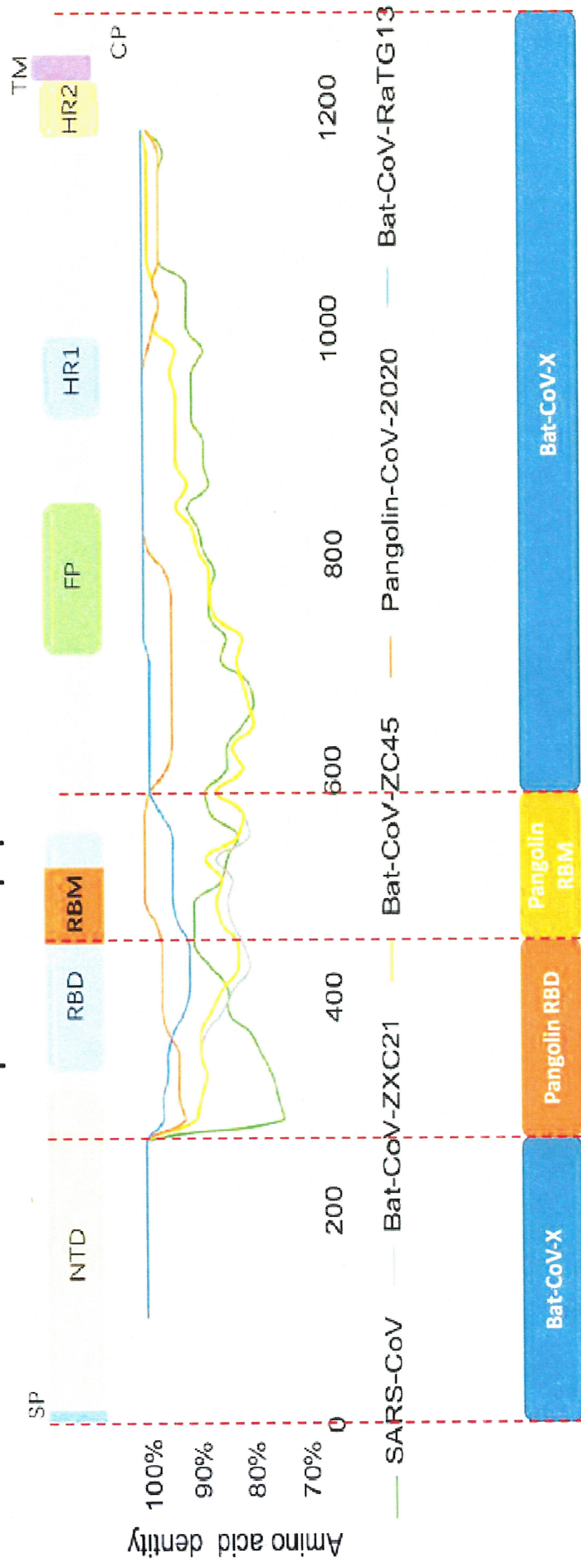
SARS-CoV CATGTCGACACTTCTTATGAGTGGGACATTCCCTATTGGAGCTGGCAATTTGTGCTAGTTAC
1980 H V D T S Y E C D I P I G A G I C A S YSARS-CoV-2
CATGTCAACAACTCATATGAGTGTGACATACCCATTGGTGCAGGTATATGCGCTAGTTAT 2022
H V N N S Y E C D I P I G A G I C A S YBCoV RaTG13
CATGTCAATAAAGTGTGAGTGTGACATACCTATTGGTGCAGGAATATGCCAGTTAT 2022
H V N N S Y E C D I P I G A G I C A S Y SARS-CoV CATAAGTTTCTTTATT-----
ACGTAGTACTAGCCAAAATCTATTGTGGCT 2028 H T V S L L R S T S Q K S I
V ASARS-CoV-2 CAGACTCAGACTAATTCTCCTCGGCGGCACGTAGTGTAGCTAGTCAATCCATCATTGCC
2082 Q T Q T N S P R R A R S V A S Q S I I ABCoV RaTG13
CAGACTCAAACTAATTC-----ACGTAGTGTGGCCAGTCAATCTATTATTGCC 2070 Q T Q
T N S R S V A S Q S I I AFurin Cleavage SiteNmeAIII Restriction Site

SARS-CoV-2 Furin Cleavage Site GC Content

- The percent GC of the furin cleavage site insert is 77% compared to ~40% of the surrounding DNA. Contains an NmeAIII restriction site. The other CoV's with FCS have a %GC of <55%

Virus	Nucleotide and Amino Acid Sequences																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
SARSCoV2 (47%)	G	G	T	A	T	A	T	G	C	G	C	T	A	T	A	G	A	C	A	C	T	C	A	G	A	C	T	A	A	T	T	C	T	C	A	G	A	C	T	A	T	G																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
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MERS-CoV (56%)	C	T	C	T	G	T	G	C	T	C	T	C	T	C	A	C	A	C	C	T	C	A	G	A	G	T	G	T	G	C	T	C	T	G	T	C	C	A	G	T	G	A	A	T	G	C	T	C	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C	T	T	G	C

SARS-CoV-2 Spike Appears to be a Chimera



Break points align with those identified by WIV Scientists in 2008 (Ren *et al.*, 2008)

RmYN02 a Red Herring

- Zhou et al., 2020 publish paper describing Bat CoV rmYN02Next generation sequencing was done on pooled bat samples to develop two genome sequences – RmYN01 and RmYN02. Claim that RmYN02 contains inserted nucleotides at the S1/S2 cleavage site. Assert that the SARS-CoV-2 FCS is therefore of natural origin. No virus is available for peer confirmation.

H		Polybasic cleavage site		O-linked glycan residues	
SARS-CoV-2 Numbering	667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693				
Consensus SARS-CoV-2	G A G I C A S Y Q T Q T N S P R R A R S V A S Q S I I				
RmYN02	G A G V C A S Y - - - N S S P - A A R - V G T N S I I				
RaTG13	G A G I C A S Y Q T Q T N S - - - R S V A S Q S I I				
ZC45	G A G I C A S Y H T A S I L - - - R S T S Q K A I V				
ZXC21	G A G I C A S Y H T A S I L - - - R S T S Q K A I V				
pangolin/MP789/2019	G A G I C A S Y Q T Q T N S - - - R S V S X A I I				
pangolin/GX/P5L/2017	G A G I C A S Y H S M S S F - - - R S V N Q R S I I				
SARS-CoV GZ02	G A G I C A S Y H T V S L L - - - R S T S Q K S I V				
RmYN01	G A G I C A S Y H T A S L L - - - R N T G Q K S I V				

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RmYN02 a Red Herring

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The next 3 pages are withheld in full citing (b)(1) and (b)(3) 50 USC 3024(i) and are not provided.

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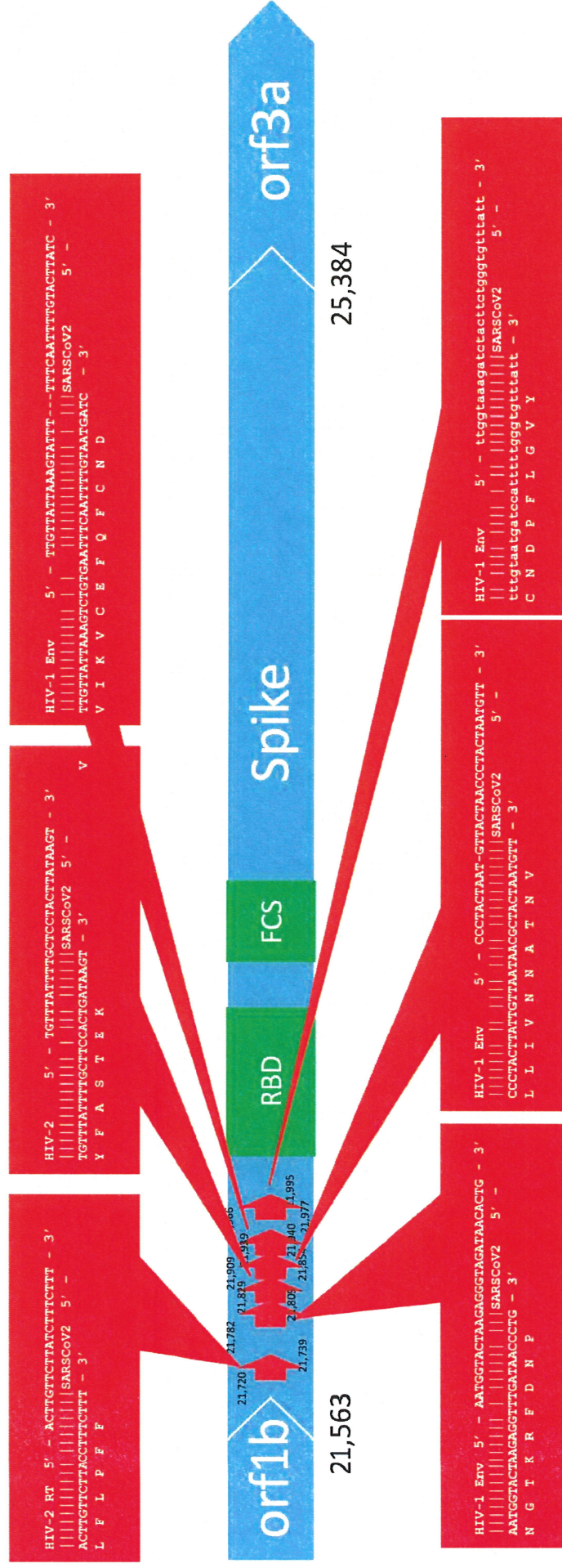
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HIV Epitopes

Perez, 2020

~~SECRET//NOFORN~~

HIV Sequences in the SARS-CoV-2 Spike Gene



Adapted from Perez, 2020

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