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Perez, 2020 Scientific Challenges

- None of the six proposed regions are identical at either the nucleotide or amino acid level with the corresponding HIV/SIV segmentsNone of the six peptides are related to identified immunosuppressive regions of HIV and SIV (Retroviral ISU Domains)The HIV gp41 Immunosuppressive (ISU) Domains sequence is KQLQARILAVERYLKDQQLLGG - this sequence does not match any of the sixFour of the six regions either perfectly or almost perfectly match corresponding peptides in multiple Pangolin CoVs - Perez did not account for Pangolin genomes in the paper

The next 2 pages are withheld in full citing (b)(1) and (b)(3) 50 USC 3024(i) and are not provided.

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Alternative Scenario

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Hypothetical Laboratory Origin of SARS-CoV-2

- WIV conducted a longitudinal studies to isolate a large number of bat Coronaviruses from multiple locations in China (2011-2015)WIV Developed Reverse Genetic System, assembled WIV1 full-length infectious clone, and created chimeric viruses exchanging the WIV1 spike gene with the spike gene from other bat Coronaviruses (2015-2017)WIV and other Chinese scientists conduct gain of function studies on SARS, MERS, IBV, and PEDV to insert furin cleavage sites demonstrating increased virulence of the chimeric virusesWIV conducted in vivo and in vitro studies to characterize the bank of bat CoronavirusesWIV conducted the live bat Coronavirus studies under BSL2 conditionsHypothesis: Between 2017 and 2019, WIV created a full-length infectious clone in pBAC-CMV using an unpublished bat Coronavirus genome as template (BatCoVX)Hypothesis: Between 2017 and 2019, WIV created chimeric Bat-CoV-X viruses using the pBAC-CMV-BCoVX backbone and swapping out key cassettes with other bat Coronaviruses (RBD, RBM, etc.) and adding additional features such as a furin cleavage siteHypothesis: In 2018-2019, WIV conducted in vitro and in vivo studies to characterize the BatCoVX chimeric viruses under BSL2 conditionsHypothesis: In mid-2019, one of the not fully characterized Bat-CoV-X chimeric viruses escaped from the WIV facilities and begins infecting civilians in the city of WuhanHypothesis: Starting in mid-2019 through present, WIV and other Chinese laboratories conduct studies to characterize the Chimerc BCoVX virus that escaped (now called SARS-CoV-2)WIV (Zhou et al., 2020) publishes the 2019-nCoV genome sequence showing relatedness to RaTG13 (a previously unpublished genome)BatCoVX likely highly related to RaTG13Hypothesis: Beginning in early 2020, WIV and other government controlled agencies begin to publish obfuscation information to drive the narrative that SARS-CoV-2 is of natural origin and resulted from natural recombinationRaTG13RMYN02Pangolin CoV's

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CONCLUSION

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Concluding Points

- WIV possesses a bank of Bat Coronavirus isolates WIV has scientists experienced in Coronavirology and Coronavirus Infectious Clone generation WIV Scientists generated chimeric SARS CoV and Bat CoV Spike genes to identify minimal Spike Receptor Binding Domain cassette that could transfer receptor binding specificity (Ren et al., 2008) WIV possesses an existing and published Coronavirus Reverse Genetics System (Zeng et al., 2016) utilizing their pBAC-CMV plasmid WIV has utilized the pBAC-CMV-WIV1 Full-length clone to generate chimeras with Bat CoV spike genes (Hu et al., 2017) WIV has BSL2/BSL3/BSL4 animal facilities WIV has multiple in vitro assays (apoptosis, IFN-B induction, etc.) to characterize their Bat Coronaviruses and chimeric Bat Coronaviruses WIV and other Chinese researchers have conducted Gain of Function studies in SARS, MERS, IBV, and PEDV to add Furin Cleavage Sites to CoV Spike protein The absence of a published progenitor virus for SARS-CoV-2 only indicates that it has not been published, not that it does not exist The genomic sequence of SARS-CoV-2 has Type IIS restriction sites that are consistent with being generated by the Golden Gate Cloning system utilizing the published pBAC-CMV plasmid The SARS-CoV-2 genome has several break points where homology jumps from Bat Coronaviruses to Pangolin Coronaviruses which is consistent with a synthesized chimeric virus The SARS-CoV-2 Spike protein similarity with RaTG13 and Pangolin CoV Spike proteins may also be explained by use of cassettes swapped into the base virus – these break points align with those identified by WIV scientists (Ren et al., 2008) There are no other published Betacoronaviruses that possess a Furin Cleavage Site in their Spike protein (RmYN02 does not have an insertion) Zeng et al., 2016 stated that "All experiments using live virus was conducted under biosafety level 2 (BSL2) conditions" which would make an accidental release of a pathogenic Bat CoV capable of binding human ACE2 more likely A chimeric virus comprised of segments from natural Bat CoV genomes would appear like a recombined virus

The molecular biology capabilities of WIV and the genome assessment are consistent with the hypothesis that SARS-CoV-2 was a lab-engineered virus that was part of a bank of chimeric viruses in Zhen-Li Shi's laboratory at WIV that escaped from containment

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BACK-UP SLIDES

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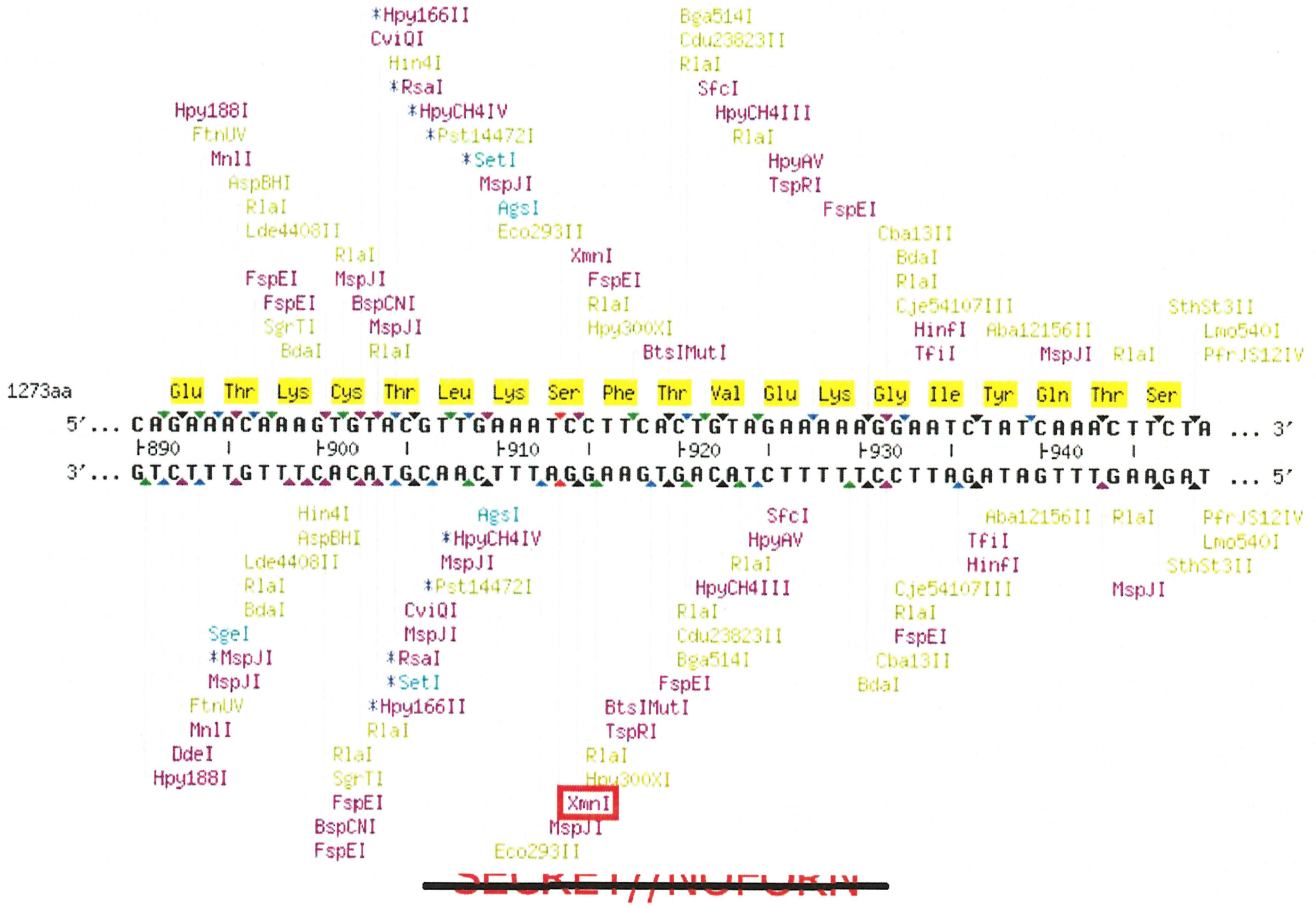
Nucleotide 914 Region



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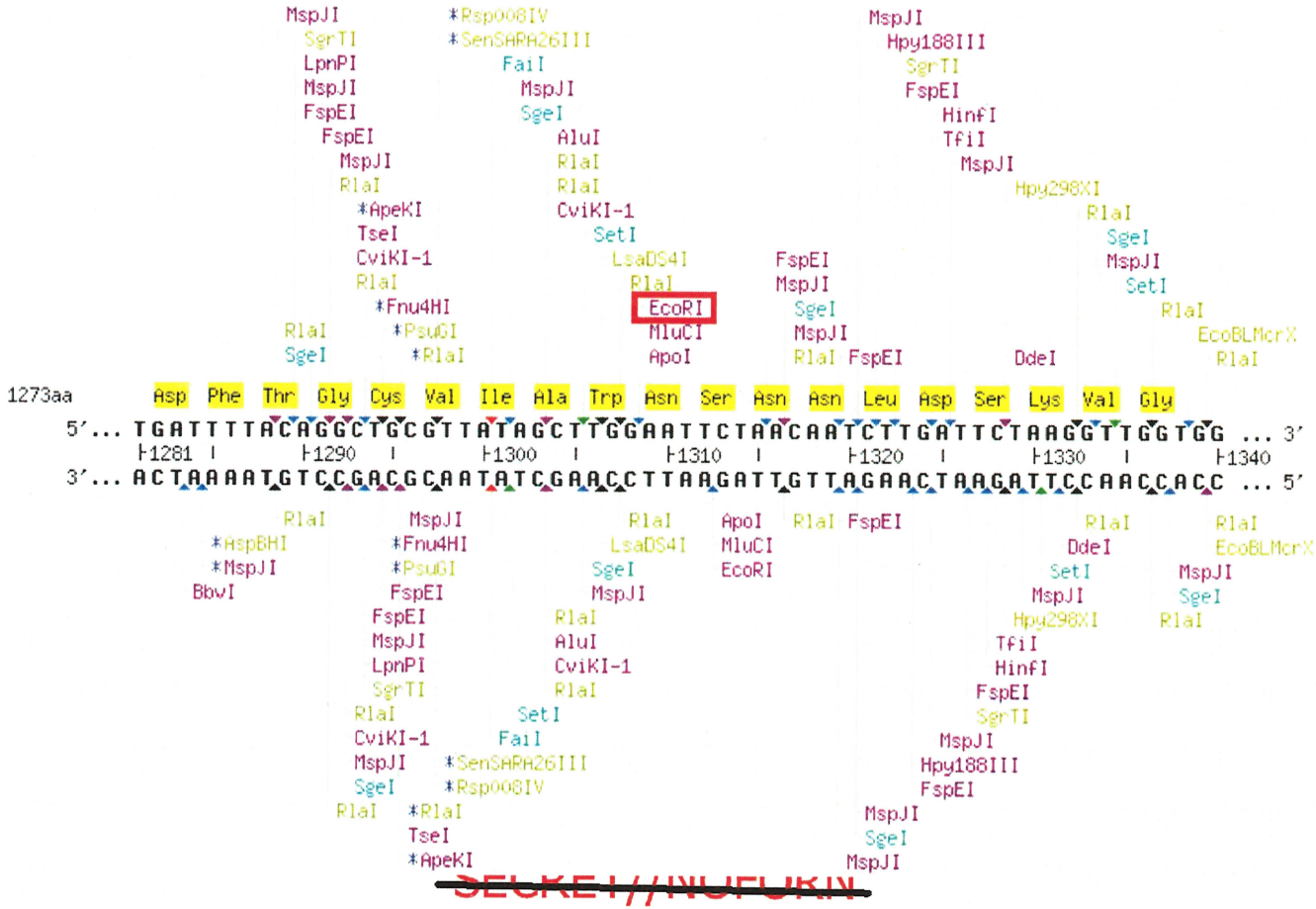
Nucleotide 1312 Region



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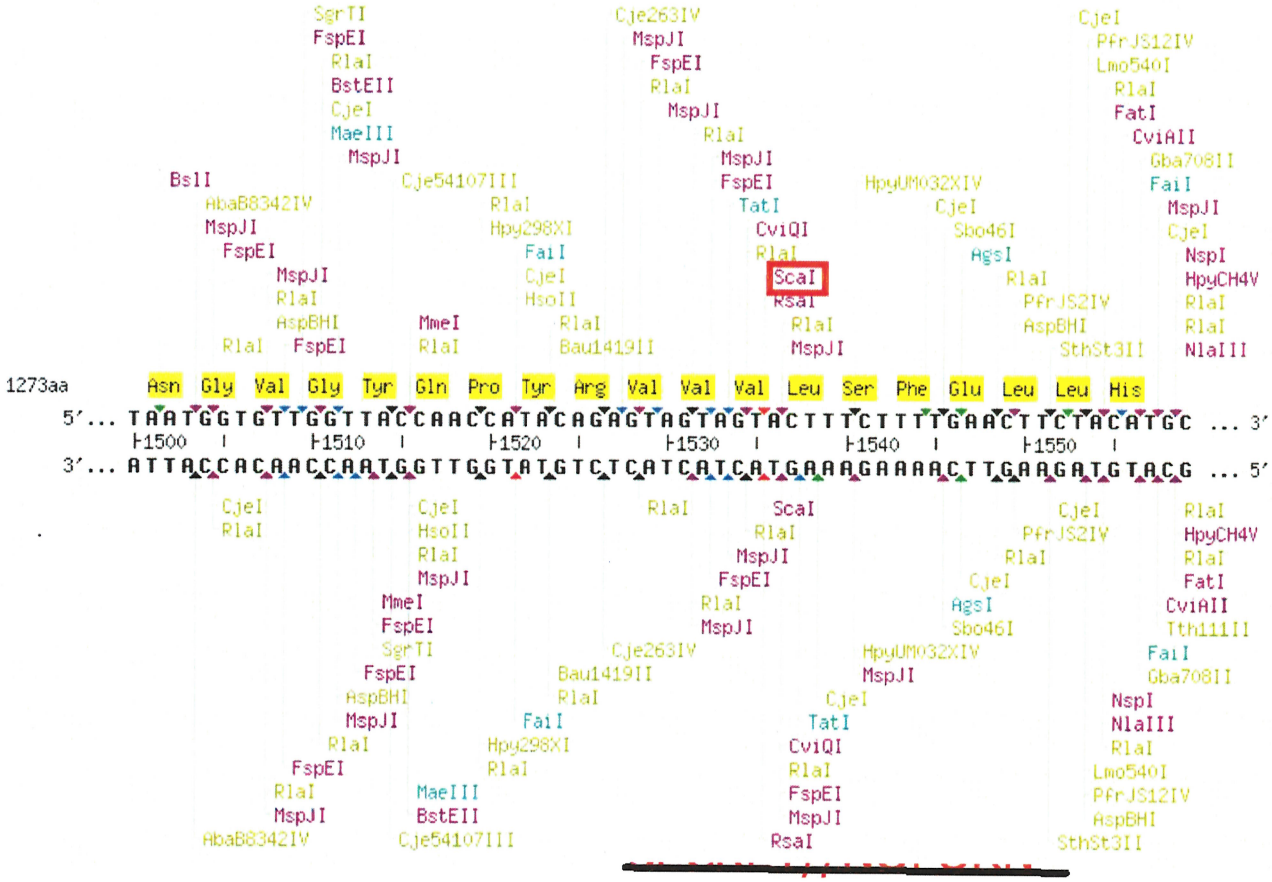
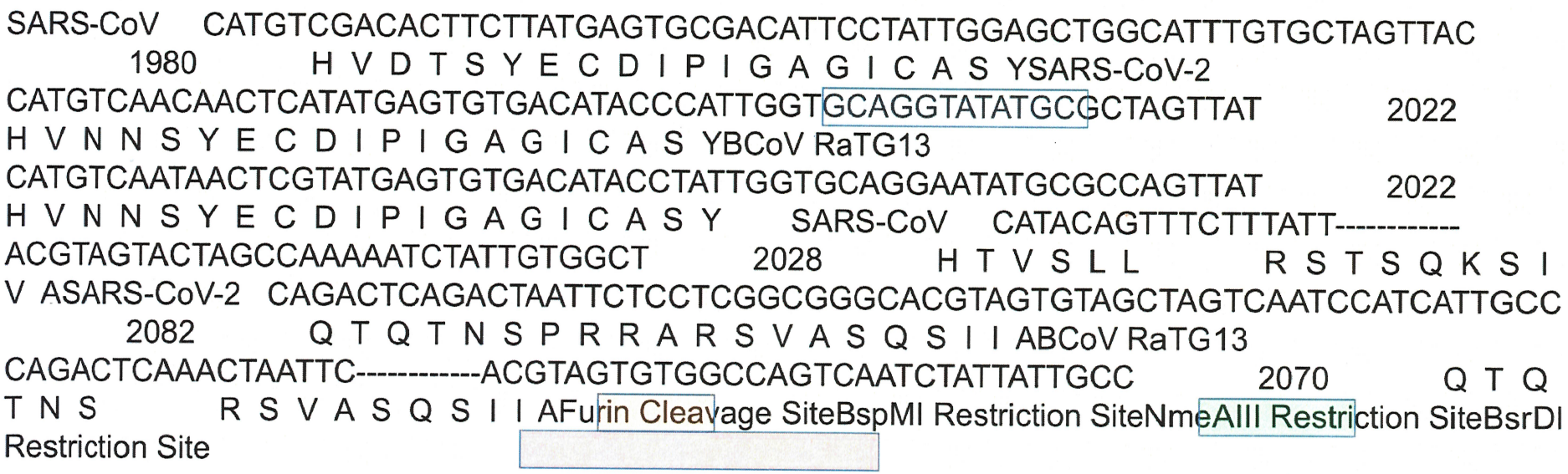
Nucleotide 1535 Region



~~[redacted]~~


SARS-CoV CATGTCGACACTTCTTATGAGTGCGACATTCCTATTGGAGCTGGCATTTGTGCTAGTTAC
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
CATGTCAATAACTCGTATGAGTGTGACATACCTATTGGTGCAGGAATATGCGCCAGTTAT 2022
H V N N S Y E C D I P I G A G I C A S Y SARS-CoV CATACAGTTTCTTTATT----------
ACGTAGTACTAGCCAAAAATCTATTGTGGCT 2028 H T V S L L R S T S Q K S I
V ASARS-CoV-2 CAGACTCAGACTAATTCTCCTCGGCGGGCACGTAGTGTAGCTAGTCAATCCATCATTGCC
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 SiteBspMI Restriction SiteNmeAIII Restriction SiteBsrDI
Restriction Site