The Myth of the Blind Watchmaker

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The Myth of the Blind Watchmaker: A Legacy of Collateral Damage

Preface & Prologue

This summary has been placed on ResearchGate to serve as a record for posterity, in order to begin raising awareness about the conclusions it contains. A fuller and more formal analysis will ultimately replace it, just as this is replacing the initial 4-page document published on 4/9/2022.

Many will find the 4/9/2022 livestream[i] between Dr. Jonathan Couey and I very helpful for clarity on some details; however, this updated version covers far more ground. A topical bibliography with more than 200 references[ii] is also available on ResearchGate. An unofficial *companion article by Arkmedic*[iii] from 4/10/2022 remains highly relevant.

This work remains, unequivocally, the most important thing I've ever written. It attempts merely to synthesize the efforts of DRASTIC and numerous other independent researchers with whom I've collaborated directly [the left-hand column below], as well as the outstanding research of those scientists who've fought against the censorship and false narratives that obscured their findings:

Jonathan Couey
Johanna Deinert
Kevin McCairn
Rossana Segreto
Ah Khan Syed [pseud]
Jack Ward [pseud]
Dayou Zhang
Igor Chudov

Fernando Castro-Chavez
Angus Dalgleish
Richard Fleming
Luc Montagnier
Jean-Claude Perez
Steven Quay
Birger Sorenson
Walter Chesnut

My findings and conclusions on scientific censorship are based on several thousand hours of individual research. The findings related to the HIV inserts in general, gp120, the furin cleavage site and other aspects of the SARS-CoV-2 genome are the product of those listed above, or others referenced in the endnotes.

The implications are profound, and profoundly disturbing; the scale of the response to the first draft and livestream has clearly shown me that my intuition about their importance was correct. I've published them here, now, because the evidence has become so overwhelming that I can't, in good conscience, withhold these conclusions from the public. In short:

- Dr. Fauci & others knew, based upon the suspicious elements of the SARS-CoV-2 genome, that the virus had ***almost certainly*** been manipulated
- They knew that such manipulations likely came from pseudovirus & insertion techniques very familiar to US & Chinese viral vaccine & therapeutic/MCM programs
- They immediately took steps to censor and control public & scientific discussions related to the HIV inserts and FCS, respectively; these actions are more properly viewed as ***obstruction of justice***
- This had major implications for both the ***early response*** to the pandemic [FCS] and the ***long-term impact*** on global public health [the HIV inserts and 'Long COVID' sequelae]

Without hesitation, I would testify under oath to the veracity of the evidence in support of these conclusions. They involve implications that are horrific regardless of which scientists, from which country, may have been responsible for creating SARS-CoV-2. I propose the list of questions that follows on behalf of the victims of the COVID-19 pandemic, who cannot ask them themselves. I promise you, however, that all of them are waiting to hear the answers.

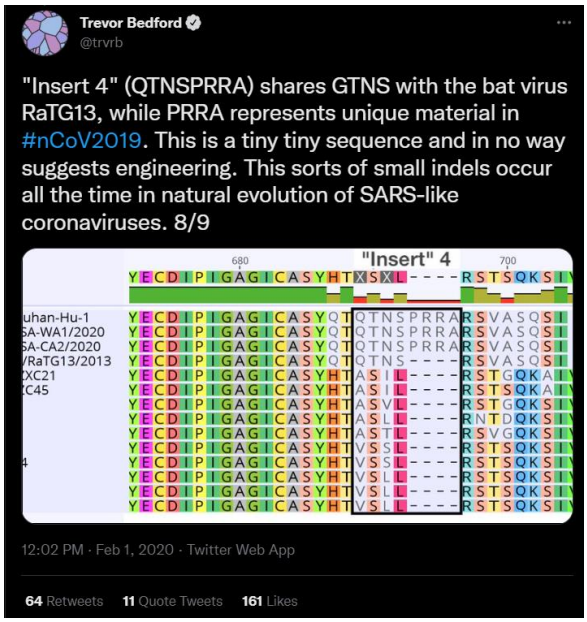
Semper Fidelis,

Charles H. Rixey

1 week to slow the spread [of uncomfortable narratives]: 1/29/2020 – 2/4/2020

On January 31st, 2020, an 80-page book titled *Analysis of Wuhan Coronavirus: Déjà vu* was published as a free download on Amazon's Kindle service. This was the first English-language publication to discuss the existence and implications of the FCS [the only prior reference was a Chinese research paper published as a pre-print on 1/21/2020 to the ChinaXiv server]. Gallaher's first mention of the FCS came 2 days earlier, in a post on the Virology.org professional message board.[iv]

Also on January 31st, a 9-page scientific article titled "Uncanny similarity of unique inserts in the 2019-nCoV spike protein to HIV-1 gp120 and Gag" was uploaded to the pre-print server *bioRxiv*. The authors, a group of researchers from India, listed a set of 4 short segments they'd discovered within the then-2019-nCoV spike protein's genome that matched portions of HIV-1 – the virus responsible for AIDS.



That same day, Trevor Bedford [an expert in viral evolutionary dynamics][v] began tweeting in response[vi] to the paper's claims, and Anthony Fauci and Jeremy Farrar called for an emergency teleconference to be held the next day – a Saturday – with leading scientists & public officials from four countries. By Monday afternoon, a second teleconference had been held,[vii] with GOF-implicated scientists, Trevor Bedford, Anthony Fauci, Tom Inglesby, Gigi Gronvall and more attending at the request of Kelvin Droegemeier, the Presidential Science Advisor for President Trump and the director of the White House Office of Science & Technology Policy; the stated purpose of the event was to "combat misinformation"[viii] surrounding the origin of the 2019-nCoV virus.

One of the speakers was David "Chris" Hassell, senior science advisor to Robert Kadlec, Assistant Secretary for Preparedness & Response [AS/PR] at the Department of Health & Human Services; Hassell was also the chair of the P3CO oversight committee created in 2017 to review gain-of-function research involving Potential Pandemic Pathogens. Together, this group reached the decision to construct a specific narrative, meant to silence any inquiries that might travel down a path that implicated many of the most prominent virologists and vaccinologists in the world.

> "They made a decision, almost a P.R. decision, that they were going to push one point of view only" and suppress rigorous debate. They argued they did it in defense of science, but it was antithetical to science."[ix]
>
> - Robert Redfield, Director of the US CDC, 2018-2021 (from Eban, 2022)

"This is a tiny tiny sequence and in no way suggests engineering"

Trevor Bedford's tweet [pictured above] of 2/1/2020 argued that "Insert 4 (QTNSPRRA) shares GTNS with the bat virus RaTG13, while PRRA represents unique material in #nCoV2019. This is a tiny tiny sequence and in no way suggests engineering." It's hard to overstate how disingenuous his statement was, especially since the internet archive shows that Bedford had been active on the message board during the period between Gallaher's first post on 1/29/2020 and Bedford's 2/1/2020 tweet.

The existence of the Furin Cleavage Site [FCS] couldn't be suppressed, because its crucial role in increasing the infectiousness of respiratory pathogens was widely understood[x] within the international scientific community. However, the existence of the FCS was **not highlighted** by ***any*** of the scientists or public health officials convened by Anthony Fauci and Jeremy Farrar on 2/1/20 until the final publication of "The Proximal Origin of SARS-CoV-2" on 3/17/2020 – in which the potentially unnatural origin of the FCS was roundly rejected, and its relevance for infectivity [as compared to the ACE2 receptor] was minimized.

Much of what has been done to combat the pandemic – especially here in the United States – has been the opposite of what would've been recommended, if all of the information available to Dr. Fauci by February 1st 2020[xi] been publicly known. Collateral damage from the decision to withhold this information can be grouped into 6 primary topics:

1 & 2-COVID's origin & Censorship of it:

Dr. Fauci and a few other senior scientists knew instantly that the discovery of HIV spike inserts[xii] within the SAR-CoV-2 viral genome made it almost impossible for the virus to be natural;[xiii] mixing elements of HIV-1's spike protein with CoV sequences and/or backbones[xiv] [or *vice versa*] has been part of HIV-1/CoV vaccine research[xv] since at least 2006[xvi] [at least 2007 for the WIV[xvii], and at least as recently as 2018[xviii]]. They knew[xix] about the Furin cleavage site [FCS] – the single biggest genomic contributor to SARS-CoV-2's ability to become a pandemic virus[xx] – yet didn't share that information[xxi] with the rest of the world, even though medical professionals in particular needed to be warned.

3 & 4-Non-Parmaceutical Interventions [NPI] & Early Treatments:

They suppressed early treatments that were already available – including the very fusion inhibitors implicated by the high homology [similarity]between the fusion peptides of HIV & SARS-like coronaviruses[xxii] – even after a pioneer in the field recommended their use so early in the outbreak.[xxiii] As a career Marine in the field of CBRN defense, I know that early treatment & prophylaxis are ***vital*** for WMD mitigation plans[xxiv] – why wouldn't this be the case during a pandemic?

5 & 6-Vaccine Development & Implications of the FCS/HIV Inserts:

The QTNSPRRA that encodes for the FCS ***forms the bookends of the HIV gp120 motif – a feature that may be the reason SARS-CoV-2 can infect human T-cells***. Ignoring the need for early research into the antigenic implications of the HIV inserts – and ignoring the potential risks of including the complete spike sequence ***within most SARS-CoV-2 vaccine prototypes***, directly contributed to many of the issues associated [or soon to be associated] with "***Long COVID.***"

Continuing to suppress research and discussion that questions the viability of the mRNA platform & prototypes – given their partial epitope coverage and high recombination traits – as well as the decade of prior failed attempts to produce a vaccine that overcame these challenges, will only exacerbate the Long COVID challenges.

The true legacy of Anthony Fauci – the implications of censorship of Intelligent Design

These questions are valid ***regardless of who created the SARS-CoV-2 virus, or for what purpose it was created***. The magnitude of their implications is such that simply refusing to answer them should itself be considered ***obstruction of justice.***

A) Key Questions & Considerations [sorted by topic]:
   a. The origin of SARS-CoV-2
      i. Why did Dr. Fauci react to the announced discovery of HIV-like inserts in the 2019-nCoV genome by immediately moving to neutralize the subject?
      ii. He'd previously spent almost 4 decades being the world's foremost advocate for HIV-1/AIDS research – why would he not embrace the challenge of a capstone pandemic with an HIV connection?
      iii. Especially now, when we're learning about how SARS-CoV-2 can infiltrate the immune system[xxv] [and so can his VRC-designed vaccines]?
      iv. Why did the US intelligence community report called the Biden Report [both the original announcement & the de-classified 'full' document] on the origin of the SARS-CoV-2 virus make no mention of the CIA's connections to EcoHealth Alliance via the USAID, or the DEFUSE documents that were found stored within a folder on JWICS, a shared, top-secret intelligence server?
      v. Why did Anthony Fauci & Kelvin Droegemeier withhold highly relevant information about gain-of-function research connections between the WIV & the NIAID from President Trump's administration, and potentially President Biden's as well?
   b. Scientific censorship
      i. Why did Anthony Fauci, Francis Collins & Jeremy Farrar immediately act to curtail research[xxvi] [including pressuring the authors of *Pradhan et al* to withdraw their paper] into the potential lab origin of SARS-CoV-2, despite their own significant concerns?
      ii. Why did Anthony Fauci & Kelvin Droegemeier – the ***Presidential Science Advisor*** – withheld *virtually* everything from President Trump[xxvii] and his team related to US-funded gain-of-function research being conducted with the Wuhan Institute of Virology?
      iii. Why was Bill Gallaher removed from any mention within *Proximal Origin*?[xxviii] His *Déjà vu* book was the ***only*** citation from the Virological.org version of 2/16/2020[xxix] that was removed from the final version, published on 3/17/20 in *Nature Communications*.
         1. This is despite the fact that Gallaher's arguments regarding the origin of the FCS and the SARS-CoV-2 virus itself were copied ***almost verbatim*** from his book or the virological.org posts that discussed his findings.
      iv. Why was Gallaher's advice on therapeutics[xxx] ignored/suppressed?[xxxi]
      v. Censorship[xxxii]/Narrative[xxxiii] & Top 6 journals,[xxxiv]
   c. Non-pharmaceutical interventions [NPI's]
      i. Why did Anthony Fauci and the other attendees of the 2/1 teleconference not warn the rest of the world of the existence[xxxv] and implications of the FCS?
      ii. Why did Anthony Fauci continuously push back on President Trump's travel ban throughout the latter part of January, 2020, during this period of silence?
      iii. Further, why has the aerosol[xxxvi]/airborne transmission[xxxvii] of the virus been largely ignored by the WHO[xxxviii] and most public health agencies?

d. Early treatments
   i. Why did Anthony Fauci, BARDA, AS/PR push Remdesivir but not other anti-viral drugs; specifically fusion inhibitors,[xxxix] which had been invented in the US[xl] and showed strong potential[xli] in 2 decades' worth of *in silico*,[xlii] *in vitro*[xliii] & *in vivo*[xliv] studies on Class 1 viruses including HIV-1/2 and CoV's?
   ii. Robert Garry recently informed us that Vitamin D is critical for our T-Cell response,[xlv] which is one of the bodily systems hit hardest[xlvi] during a severe COVID-19 infection. [Why didn't Anthony Fauci et al ***ever*** recommend/include Vitamin D as a prophylactic/early treatment [or weight loss, exercise or healthier diets]]?
   iii. Why was Bill Gallaher's note on the Chinese use of chloroquine[xlvii] [to block the virus from using endosomal entry, especially in the lungs] during the Wuhan outbreak never specifically addressed [pictured below]?

> ***[UPDATE: There are reports that the anti-malarial drug Chloroquine is being used to treat nCoV2019. Chloroquine acts by increasing the pH of endosomes. As described above, Ujike et al.(2008)warned that peptide inhibitors of HR2 would not block the virus from using endosomal entry as a bypass pathway. The use of Chloroquine would imply that the alternate entry pathway is indeed an issue that Chloroquine is intended to inhibit.]***
>
> In terms of "off the shelf", those are the only such drugs known to exist that have potential in inhibiting nCoV2019 without further development.

   iv. Why was Remdesivir targeted for approval for the treatment of late-stage COVID-19 infection, when its mechanism targets the virus itself – which has already inflicted its damage by that point in the infection? Ralph Baric & Mark Denison – who helped create and test it – reiterated this point in February 2020.[xlviii]
   v. Why didn't we look at antivirals besides Remdesivir? You know, like…. fusion peptide inhibitors, for instance?
   vi. Why issue an EUA for an FDA-approved medication like Hydroxychloroquine? What was so dangerous about Drs. prescribing ***anything*** off-label?
   vii. China had a potent pan-CoV inhibitor *prior* to the COVID-19 outbreak in Wuhan [EK1, published on 4/1/2019]; they literally pointed this out several times in Jan-Feb 2020, before announcing an ***even more effective*** fusion inhibitor [EK1C4] on 3/30/2020.
   viii. Some have suggested that SARS-CoV-2 is a Live Attenuated Vaccine [LAV] reverting to its original form, something seen with LAV's with Dengue Fever. However, that makes no sense – why would China need an antidote for a vaccine/vaccine trial?

e. Deformed Consent: Vaccine development
   i. Why did the VRC drop the SARS-CoV-2 spike into their mRNA backbone before its immunogenicity/risks were understood? Apart from the HIV inserts, Bill Gallaher described 1 such immunosuppressive domain, LQPRTFLLKYNENGTITDAVD, with similarity to strains of Ebola and HIV1.[xlix]

ii. Why did Dr. Fauci, the VRC, BARDA, and FDA remain silent about the poor results of previous studies involving mRNA and other CoV vaccine attempts in animals – especially those of Ralph Baric?[l]
iii. Why was the DoD forced to universally vaccinate our active-duty troops with a partial-epitope-coverage[li] spike protein vaccine less than 3 years after DARPA rejected[lii] a very similar proposal – **in bats**?[liii]
iv. Why were the vaccines mandated for many Americans just as evidence of escape was emerging *c.* Fall 2021?
v. Why universally vaccinate ALL troops when the long-term effects of the mRNA method are unknown – much less the long-term antigenic effects of the SARS-CoV-2 spike itself?[liv] Why risk the operational readiness of the ***entire*** American military by transfecting all troops with a 'leaky' vaccine?
vi. Why are Dr. Fauci et al still silencing any discussion of the potential immune suppression of the vaccines,[lv] and stalling the clinical trial data from Pfizer[lvi] et al? The potential implications of massive immune damage[lvii] supersede any FDA deliberations about follow-on booster shots.

f. Why is the QTNSPRRA sequence that contains the furin cleavage site ***so*** important – and ***so*** unique?
i. First, the insert should be viewed as two distinct 4 protein/12-nt segments, since they actually form the book-ends of the full gp120;[lviii] the latter half is the PRRA that is more commonly referred to as the "Furin cleavage site." This particular FCS motif cannot function without the QTQTNS that precedes it.[lix]
ii. When viewed as a group, the full set of 4 HIV inserts **appears to form a functional gp120 sequence** that can infect T-cells, thus being the worst possible thing anyone could add to an mRNA transfection that can only stimulate antibody responses. No other than the WIV itself just published a study demonstrating t-cell infection by spike proteins;[lx] thus, the wild & vaccine spikes teach our cells to literally manufacture spikes with HIV-like antigens. Why would this be a desirable outcome for a transfecting coronavirus vaccine?
iii. Why would extra steps be taken to stabilize the immunogenic elements of the spike, including QTNSPRRA, which serves as an SEB toxin[lxi] & contained the FCS?[lxii]
iv. Furthermore, why would so much faith be placed in the use of lipid nanoparticles to convey spike proteins that already exhibited broad tropism[lxiii] via the FCS?
v. Why would a prion-like domain be conserved[lxiv] within the vaccine's genome[lxv] at all? There is ***no*** reason to risk transfecting ***any*** part of ***any*** genome that could trigger amyloidogenesis[lxvi] – the creation and thus buildup of amyloid plaques which drives the emergence of **Parkinson's Disease**, **Alzheimer's Disease** and **Creutzfeldt-Jakob Disease** [colloquially referred to as Mad Cow Disease], etc.
    1. Can this amyloidogenesis be systemic? Is this related to the seemingly irrational objection to Zinc, or to Vitamin D?
vi. The viral genome appears to be attempting to revert [de-attenuate] away from the FCS & HIV inserts,[lxvii] further evidence that those mutations didn't occur naturally.
vii. Why does the region of the FCS match a reverse complement sequence[lxviii] from Moderna, who partnered with the NIAID's Vaccine Research Center [VRC] to produce an mRNA vaccine?
viii. Why do the forward and reverse primers for PCR for SARS-CoV-2 match those of Ralph Baric's previous constructs[lxix] SARS-CoV-M15, SARS-CoV-Rs3367 & **SHC014-CoV-MA15**?

ix. The virus gains the functions of an efficient FCS AND a potentially effective antidote target with the appropriate peptide fusion inhibitor[lxx] [dozens of proposed compounds, targeting various sequences of the SARS-CoV-2 spike protein, have been developed or are currently being studied].[lxxi] In December, Chinese scientists reported that their EK1C4 inhibitor also helps reduce the risk of Antibody-Dependent Enhancement.[lxxii]

x. As with previous coronaviruses, Antibody-Dependent Enhancement [ADE][lxxiii] is a realistic possibility, as Robert Malone himself also pointed out[lxxiv] in early March of 2020.

xi. The FCS increases the ability of the virus to infect via the inhalation route, which has the added benefit of lowering the bar for the size of the viral load needed for an infectious dose.[lxxv]

xii. Jean-Claude Perez & Luc Montagnier [who was awarded the 2008 Nobel Prize in Physiology or Medicine for his discovery of the HIV-1 virus in 1983] showed that the location of the PRRA insert within the SARS-CoV-2 genome ***was already an optimal cleavage site BEFORE this insertion***.[lxxvi]

xiii. As oxygen levels decrease[lxxvii] [hypoxia] in the lungs, furin expression increases,[lxxviii] which can contribute to rapid declines in patient disposition as a snowball effect. This also plays a role in reducing the suppression of cancerous cells.[lxxix]

xiv. Even mild hypoxia [~10% reduction] was enough to allow SARS-CoV-2 to pass through the Blood-Brain Barrier [BBB].[lxxx]

xv. The existence of many arginine residues within a small region that contains the FCS follows the pattern associated with the mechanism known as binding of cell penetrating peptides.[lxxxi] The goal of building up a high cumulative positive charge[lxxxii] is to enhance cell affinity towards the virus.[lxxxiii] SARS-CoV-2's ability to utilize the human sodium channel ENaC[lxxxiv] is unlikely to be fortuitous.

> Cumulative data suggests that the general method of action of this chimeric virus includes membrane components other than the ACE2 receptor, which may explain clinical evidence of its infectivity and pathogenicity. Data shows the nonspike receptor binding domain dependent phagocytic general method of action to be specifically related to cumulative charge from insertions on the SARS-CoV-2 spike (see Fig. 1) poised to form salt bridges with attachment receptors. This suggests that attachment to such previously reported membrane proteins has been enhanced directly due to the basic and positive charged inserts in the spike protein together with other basic and positive charged amino acid substitutions enabling formation of salt bridges with the receptor CLEC4M/DC-SIGNR or, indirectly, by the additional salt bridges formed between the positive charged amino acids and negative charged phospholipids on the cell membrane.

xvi. How would someone investigate a SARS-like CoV's ability to infiltrate dendritic cells via the DC-SIGN pathway, as stated in the DEFUSE proposal?[lxxxv] The virus best known for utilizing this pathway is… HIV-1:

> parental strain. *N-linked glycosylation:* Some glycosylation events regulate SARS-CoV particle binding DC-SIGN/L-SIGN, alternative receptors for SARS-CoV entry into macrophages or monocytes[76,77]. Mutations that introduced two new N-linked glycosylation sites may have been involved in the emergence of human SARS-CoV from civet and raccoon dogs[77]. While the sites are absent from civet and raccoon dog strains and clade 2 SARSr-CoV, they are present in WIV1, WIV16 and SHC014, supporting a potential role for these sites in host jumping. To evaluate this, we will sequentially introduce clade 2 disrupting residues of SARS-CoV and SHC014 and evaluate virus growth in Vero cells, nonpermissive cells ectopically expressing DC-SIGN, and in human monocytes and macrophages anticipating reduced virus growth efficiency. We will introduce the clade I mutations that result in N-linked glycosylation in rs4237 RBD deletion repaired strains, evaluating virus growth efficiency in HAE, Vero cells, or nonpermissive cells ± ectopic DC-SIGN expression[77]. *In vivo*, we will evaluate pathogenesis in transgenic hACE2 mice.

[i] The DRASTIC Report with Charles Rixey: They added gp120 from HIV-1 and they have the antidote," archived on *Bitchute*, originally streamed on 4/9/2022 on GigaOhm Biological's Twitch page.
[ii] (PDF) 20220514 - The Myth of the Blind Watchmaker - Topical Bibliography.pdf (researchgate.net)
[iii] Ah Kahn Syed, "Absolute proof: The Gp-120 sequences prove beyond all doubt that "COVID-19" was man-made," *Substack*, 4/10/2022.
[iv] William R. & Andrew D. Gallaher, "Analysis of Wuhan Coronavirus: déjà vu [findings on 1/29, 1st edition on 2/1]," *Virological.org*, 2/1/2020.
[v] Trevor Bedford, Ph.D, from the Fred Hutchinson Institute website, 5/1/2022.
[vi] Trevor Bedford, "https://twitter.com/trvrb/status/1223337991168380928?s=20&t=GjdGSZ8PbXB7fTscIxLAGw," *Twitter*, 1/31/2020.
[vii] Charles Rixey, Who Watches The Watchmen? - Fauci's "Noble Lie" Exposed," *Zero Hedge*, 7/24/2021.
[viii] Volume 11 of Ralph Baric's emails, "Baric-Emails-2.17.21.pdf," *US Right-To-Know Biohazard FOIA collection*, pages 115-133, 2/17/2021.
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[xvii] Zheng-Li Shi *et al*, "Difference in Receptor Usage between Severe Acute Respiratory Syndrome (SARS) Coronavirus and SARS-Like Coronavirus of Bat Origin," *Journal of Virology*, 12/12/2007.
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[xx] Vineet Menachery et al, "Furin Cleavage Site Is Key to SARS-CoV-2 Pathogenesis," *BioRxiv*, 8/26/2020.
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[xxii] Yossef Kliger & Erez Levanon, "Cloaked similarity between HIV-1 and SARS-CoV suggests an anti-SARS strategy," *BMC Microbiology*, 6/1/2003.
[xxiii] https://virological.org/t/analysis-of-wuhan-coronavirus-deja-vu/357/4
[xxiv] See numerous unclassified but restricted US & NATO Joint Publications on CBRN defense, mitigation, hazard prediction, consequence management, etc [I am well-versed in the technical aspects of these publications, as a former Instructor & Curriculum Developer at the United States Marine Corps CBRN School in Fort Leonard Wood, Missouri.
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[xxvi] Charles Rixey, Glenn Beck & Jason Buttrill, "Crimes or Cover-Up? Exposing the World's Most Dangerous Lie," *The Blaze TV*, 11/17/2021.
[xxvii] Charles Rixey, Glenn Beck & Jason Buttrill, "Crimes or Cover-Up? Exposing the World's Most Dangerous Lie," *The Blaze TV*, 11/17/2021.
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[xxxi] In *Déjà vu*, Gallaher described fusion peptide inhibitors, protease inhibitors, chloroquine to protect the endosomal pathway in lung cells, potential immunosuppressive portions of the SARS-CoV-2 spike protein that should be avoided in any vaccines, etc.
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[xlv] Jay Kolls & Robert Garry, "Role of the T cell vitamin D receptor in severe COVID-19," *Nature Immunology*, 12/20/2021.
[xlvi] Sonia Andre *et al*, "T cell apoptosis characterizes severe Covid-19 disease," *Nature Cell Death & Cell Differentiation*, 1/22/2022.
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