

From: Carlson, Nils W.
Sent: Wednesday, March 1, 2023 12:03 PM
To: Williams, Brandon Kirk <williams312@llnl.gov>
Subject: FW: Logistical and Technical Exploration into the Origins of the Wuhan Strain of Coronavirus (COVID-19) - Harvard to the Big House

Since you asked here is paper I mentioned.

From: (b) (6) >
Sent: Wednesday, March 1, 2023 10:38 AM
To: (b) (6) >; Carlson, Nils W. <carlson18@llnl.gov>
Subject: Fw: Logistical and Technical Exploration into the Origins of the Wuhan Strain of Coronavirus (COVID-19) - Harvard to the Big House

----- Forwarded Message -----

From: (b) (6)
To: (b) (6)
Sent: Wednesday, March 1, 2023, 10:20:01 AM PST
Subject: Re: Logistical and Technical Exploration into the Origins of the Wuhan Strain of Coronavirus (COVID-19) - Harvard to the Big House

On Monday, June 7, 2021, 07:12:02 PM PDT, (b) (6) wrote:

<https://harvardtothebighouse.com/2020/01/31/logistical-and-technical-analysis-of-the-origins-of-the-wuhan-coronavirus-2019-ncov/>

Logistical and Technical Exploration into the Origins of the Wuhan Strain of Coronavirus (COVID-19)

Posted on [January 31, 2020](#) by [harvard2thebighouse](#)

An accessible and comprehensive YouTube summary of the report below by [a Professor of Neurobiology](#) at the University of Pittsburgh's Medical School [is available here](#). And you can read our takedown of Nature magazine's recent article [claiming COVID-19 definitely wasn't from a lab here](#).

[Read the peer reviewed research paper this article formed the base of, which was published by BioEssays here.](#)

This report is the product of a collaboration between [Dr. Karl Sirotkin](#), a retired professional scientist with dozens of peer-reviewed publications and 30 years of experience in genomic sequencing and analysis, who worked at the Theoretical Biology Division of the Los Alamos National Laboratory and later helped design several ubiquitous bioinformatic software tools, as well as [a former NSA counterterrorism analyst](#). It considers whether the Wuhan Strain of coronavirus (COVID-19) is the result of naturally emergent mutations against the possibility that it may be a bio-engineered strain – [directly altered by genetic manipulation, subject to artificially-guided evolutionary selection](#), or both – most likely released into the public by accident since [China's rate of occupational accidents is about ten-times higher than America's, and some twenty-times more than Europe's](#), the only other regions with high-level virology labs.

Raising the odds of an accidental release, researchers from China's only BSL-4 lab in Wuhan were reported to have particularly sloppy field research methods, [being both bled and peed on by local bats](#) that host coronaviruses remarkably similar to the Wuhan Strain COVID-19. And they've also been reported to smuggle used research animals out of their labs, [selling them for cash on the street](#). Perhaps unsurprisingly, in mid February the Chinese Ministry of Science sent out a directive to all its labs emphasizing the important of carefully handling bio-infectious agents [and alluding to slack oversight and past lapses](#), even mentioning coronaviruses specifically.

Mistakes may have been precipitated by the need to quickly finish research that was being rushed for [Johns Hopkins' Event 201](#) which was held this past October and meant to gameplan the containment of a global pandemic. Research may also have been hurried due to deadlines before the impending Chinese New Year – the timing of these events point to increased human error, not a globalist conspiracy. [Beijing has had four known accidental leaks of the SARS virus in recent years](#), so there is absolutely no reason to assume that this strain of coronavirus from Wuhan didn't accidentally leak out as well. This is unlikely to be a plot twist in one of the novels Tom Clancy wrote after he started mailing it in.

Simply and horribly, this is likely to become another Chernobyl or Fukushima – a catastrophic illustration of mankind’s hubris and intransigence clashing with Nature, as fate again reaps a once unimaginably tragic toll.

Given that this outbreak was said to begin in early winter [when most bat species in the region are hibernating](#) and the Chinese horseshoe bat’s habitat covers [an enormous swath of the region](#) containing scores of cities and hundreds of millions people, the fact that this Wuhan Strain of coronavirus, denoted as COVID-19, emerged in close proximity to the only BSL-4 virology lab in China, which in turn was staffed with at least two Chinese scientists – Zhengli Shi and Xing-Yi Ge – both virologists who had previously worked at an American lab which had already bio-engineered an incredibly virulent strain of bat coronavirus – the accidental release of a bio-engineered virus from Wuhan’s virology lab cannot be automatically discounted, especially when the Wuhan Strain’s unnatural genomic signals are considered.

UPDATE 2/14, 3:02am EST: [A probable smoking pre-print has been released](#), by the National Natural Science Foundation of China:

“In summary, somebody was entangled with the evolution of 2019-nCoV coronavirus. In addition to origins of natural recombination and intermediate host, the killer coronavirus probably originated from a laboratory in Wuhan.”

In a predictable turn, that article has been removed and both researchers have since deleted their profiles off of the ResearchGate site completely. Furthering the appearance of a cover-up, back on January 2nd, the Wuhan Institute of Virology’s director [sent out a memo forbidding discussion](#) of an “unknown pneumonia in Wuhan” after ordering the destruction of all related lab materials a day earlier, making it abundantly clear that the Chinese government knew about this outbreak long before they took any steps to contain it, or made any public announcement.

These propaganda efforts have been bolstered by possible collusion from American scientists, some of which is detailed below – but also most notably by one [Peter Daszak](#), who had been [publishing papers on coronaviruses alongside the primary Chinese person-of-interest](#), Zhengli Shi, for years. Perhaps most notably, Daszak is listed as a co-author in the paper [first documenting the isolation of a coronavirus from a bat](#) that targets the ACE2 receptor – just like COVID-19 – research done in Wuhan’s virology lab and supervised by Zhengli Shi, and led by a second suspect Chinese researcher who you’ll meet below. At best, Daszak is perhaps acting as

an unwitting agent of the Chinese government, but regardless holds an enormous conflict-of-interest. And if nothing else, it is wildly irresponsible to speak-out against the possibility that the virus got out of a lab when a natural origin has not been conclusively demonstrated.

[Daszak's statement in *The Lancet*](#) is either incompetence, or is meant to be a smokescreen for the wanton hubris and greed that have fueled the dual-use or “gain-of-function” research detailed below: As one possible related project which may have overlapped with this one, coronaviruses have been seen as [a viable vector for an HIV vaccine for years](#) – a project with [hundreds of millions of dollars dangling over it](#).

And unfortunately Daszak is far from alone, there are countless “journalists” mindlessly regurgitating statements from the Chinese government and the WHO with no effort to fact-check whatsoever, as well as “scientists” whose real job is running PR for pharmaceutical and research companies who have spent weeks serving China by making extraordinarily misleading and overconfident statements to the public about the origins and capabilities of this virus. As far back as 2015, Chinese labs were [reported to have been involved with dual-use gain-of-function research](#), mixing and matching viral genomes in the lab, research that accelerated after the Chinese military [made a massive push](#) to expand their biotechnological capabilities. And it should be noted that in 2018, the esteemed scientific journal *Nature* – which has published numerous articles speciously claiming this virus is definitely natural – was revealed to have [buckled to censorship demands from the Chinese government](#), killing over 1,000 articles to placate their Chinese partners.

Many involved in this dissimulation are effectively acting as agents of a foreign government, and they have left most Americans entirely unprepared for the tragedy that’s beginning to occur in our nursing homes and hospitals. If the idea that just *maybe* this thing came from a lab had been part of the national dialogue from the start – wouldn’t everyone have been much more cautious and open to social distancing and other limitations once the need arose?

And so being [an offshoot of this sort of vaccine program](#), possibly as a Red Team designed to build defenses and therapeutics against, is just one possible gain-of-function pursuit that would fit some of the unusual genomic and logistical picture below. Whether or not it was the exact target of the Wuhan lab’s genomic tinkering – the reality is millions of dollars of funding from multiple world governments have poured into this research, funding that’s dangled over these scientists as they’ve chased it like Icarus, this time not just risking their own lives – but hundreds of millions of others as well.

Subsequently, [we are calling for an immediate end to dual-use gain-of-function research](#).

– In 2002, [Stony Brook first assembled a DNA virus from scratch](#), building a polio-virus, and providing proof-of-concept for the creation, alteration, and manipulation of DNA-virus genomes. Two years prior, a separate team had already built a simpler RNA-virus from scratch – choosing to engineer a coronavirus from the ground up, [and even swapping out its vital spike-protein genes](#) to make it more infectious. A generation earlier, artificially enhancing selection by intentionally infecting countless series of lab animals with different viruses is understood to have created the H1N1 Swine Flu. Its Franken-genome has [a mysterious untraceable genetic parentage](#) and a [“clear unnatural origin,”](#) appearing to be the product of [“sequential passage in an animal reservoir”](#) which was determined by its vast genetic distance from any extant strain of flu, just like COVID-19 which also appears so distant from any related coronavirus that [it’s been placed in its own clade](#), an isolated branch way out on its own in the viral family tree – meaning it’s the lone example of its kind, and doesn’t clump together with all the other known coronaviruses. Although both the H1N1 Swine Flu and COVID-19 sprung into existence spontaneously, and were distant off-shoots of any other known strain of flu – so why is there a scientific consensus that the former leaked out of a lab, while many insist the latter is entirely natural?

– And so this strain of H1N1 became the poster-child for a moratorium against *gain-of-function* research – experimentation that seeks to increase a pathogen’s virulence, creating a more effective double-edged sword to counter and learn from. A ban that was in place for years, but was recently lifted by the American government. In the case of H1N1, it wasn’t a question of if it’d escaped from a research laboratory, only whether [it’d been designed as part of a weapons system, or been part of a vaccine trial](#).

– When a virus manages to infect a new species of host [it’s known as a zoonotic jump, a process that generally takes months or even years to complete](#). The first stage is when a virus infects one individual in a new host species, which is typically a dead-end the first time it happens since there’s no way for the virus to be adapted to a different species’ biology. The second stage of a zoonotic jump is when the virus manages to move from the first new host into more hosts of the new species, which results in some temporary transmission in a localized area – these are known as endemics and generally fizzle out the first few times they happen as the virus adapts to its new host species, and mutations win or lose the survival battle. The final stage, the only

time a zoonotic jump is considered complete, is when there's sustained host-to-host transmission in the new species. These zoonotic jumps have some predictable characteristics, the primary one is that adapting to a new host inevitably requires mutations that weren't optimal in the old host. And so the virus gets weakened as its initially attempting to jump into a new host species, which is why the above sequence of steps – one new host, a few new hosts that pass it among themselves temporarily, and then finally sustained transmission – takes at least several months if not years to play out, since a good bit of time is required for all three steps to occur. Viral trial-and-error is required for the virus to find the right mutations that will allow it to prosper in a new host species, it's never been known to just happen magically all at once.

– And so assuming that COVID-19 emerged naturally in a matter of weeks in the middle of a massive urban metropolis the size of New York City, when the host population of bats was hibernating anyways, requires completely ignoring everything we know about how viruses transfer between species. Not only was Wuhan's population not interacting with bats since they hardly interact with humans in urban situations to begin with, but any possible host bats were sleeping in their caves anyways. And not only would the circumstances of this transfer require rewriting the textbooks on zoonotic jumps if it occurred it all, but beyond that: supposedly not only did a zoonotic jump happen instantly without the necessary steps, but when it hit humans it was extraordinarily virulent from the start, something that's supposed to take an extensive amount of time to ever happen as mutations go through selective trial-and-error. This trial-and-error takes time and is why viruses have never made a zoonotic jump and been instantly virulent in a new host species like COVID-19 has been in humans. And in 2018, a study looking for past infections by bat coronaviruses in Wuhan [found no evidence whatsoever](#) that anyone there had ever been infected by one at all, making the idea that these viruses have been circulating there entirely absurd. Nothing we know about how viruses naturally make zoonotic jumps point to that happening here.

– Tinkering with viral genomes is not anything new, but is not something that has ever been fully embraced by the scientific community at large. About a decade ago, two separate research teams successful tweaked the genome of the H5N1 Bird Flu in just two spots and then passed it through ferrets until it became both airborne and pathogenic to mammals, creating a virus that [“could make the deadly 1918 pandemic look like a pesky cold.”](#) This involved selecting for a mutation that allowed the virus to access a receptor that's found in ferret lungs, and was alarming enough that the research was urged to be published without revealing the specific methods involved and data collected – however it appears that only the most technical details

were left out, and [most of the research is freely available](#). And studies [examining COVID-19's infectivity in ferrets](#) found that it spreads readily among them, and also appears airborne in that animal model, lending support to the idea that ferrets were used for serial passage. Further support for possibility that serial passage through lab animals played a role in the creation of COVID-19 [comes from an April 2020 pre-print](#), which found that coronaviruses that target the ACE2 receptor bind with ferrets cells more tightly than any other species except the tree shrew, which only scored about 2% higher. Tree shrews have also been used for serial viral passage, and [were promoted in a 2018 paper out of China](#) as a preferable host for laboratory serial passage since they're cheaper, smaller, easier to handle, and closer to humans evolutionarily and physiologically than ferrets. Pangolins however, formed a much weaker bond than either, and were clustered way down on the list along with a handful of other much more unlikely intermediate animal hosts.

– By 2015, Dr. Ralph Baric and his team at UNC were conducting research that was met with an enormous amount of concern, [they successfully created a “chimeric, SARS-like virus”](#) by altering the viral genome of a Chinese bat coronavirus's *spike-protein genes* – sequences that code for the spikes that poke out from surface of viruses and allow them to unlock entry into hosts, in this case making the bio-engineered coronavirus incredibly contagious. This research raised eyebrows since it was clearly dual-use gain-of-function research, a practice [banned in America from 2014 until December 2017 when NIH lifted the ban](#), specifically to allow research on this sort of virus. Looking at UNC's gain-of-function research on coronavirus spike-proteins, which received its funding just before the ban was implemented and was only allowed to go forward following a special review, a virologist with the Louis Pasteur Institute of Paris warned: *“If the [new] virus escaped, nobody could predict the trajectory.”*

– But then oddly, in late January right as the pandemic was blooming, Baric claimed in an interview that people [should be more concerned with the seasonal flu](#) – despite having personally overseen the controversial engineering of a hyper-virulent strain of batty coronavirus just a few years back, and having no possibly way of knowing COVID-19's clinical impact as early as January. Immediately discounting the burgeoning outbreak of an unknown coronavirus as a non-event seems particularly troubling for someone who'd trained two Chinese scientists on how to make hyper-virulent coronaviruses, especially when it's hard to imagine that Dr. Baric was unaware his past colleagues were now working at the Wuhan Virology Lab, the epicenter of the outbreak. Highlighting the dissembling absurdity of this statement, based on reporting from Who: the Wuhan Strain COVID-19 appears to be [thirty-four times more lethal than the seasonal flu](#). It should also be noted that several years prior to

tinkering directly with bat coronavirus spike-proteins, Baric orchestrated research that involved isolating a coronavirus from civets and then [passing it through mammalian ACE2 receptor cells](#) that were grown in the lab from kidney and brain samples – serial passage through host cell lines instead of entire hosts, which imparted a strong affinity for ACE2, and presumably created an airborne strain of coronavirus. And if cells derived from kidneys and brains were used for the serial passage development of COVID-19, that might help explain its affinity for attacking [the kidneys and brains](#) of its human hosts.

– Scientists have [expressed concern about China’s ability to safely monitor this BSL-4 lab](#) in Wuhan since it opened in 2017: *“an open culture is important to keeping BSL-4 labs safe, and he questions how easy this will be in China, where society emphasizes hierarchy. ‘Diversity of viewpoint, flat structures where everyone feels free to speak up and openness of information are important.’”* This lab is at most 20 miles from the wet market where the virus had been assumed to have jumped from animal to human. However the idea that a Chinese lab could have a viral sample escape is well-documented – as mentioned, [one lab in Beijing has had four separate incidents](#) of the SARS virus leaking out accidentally.

– Notably, the first three known cases from early December had [no contact with that market](#), and roughly one-third of the initial exposed cohort had [no direct ties to Wusan’s wild meat wet-market](#), the original presumptive source of the virus. And in mid February, reporting indicated that COVID-19’s patient zero [in fact had no connection at all with the wet-market](#). This is reinforced by the fact Chinese research has also concluded that COVID-19 [“may have begun human-to-human transmission in late November from a place other than the Huanan seafood market in Wuhan.”](#)

– Since its discovery, [scientists have been unable to fully determine the zoological origins of COVID-19](#), it was initially thought to have passed through snakes, but now all that’s agreed upon is that it’s mostly bat in origin. This inability to derive an exact zoological source is exactly what would be expected if the virus had been artificially engineered to target humans as UNC already has, this doesn’t prove an artificial nature – but it is consistent with one. Although there has been speculation that pangolins may have been the missing vector, the only data about the pangolin virome [wasn’t entered into NCBI’s system until late January](#), and couldn’t possibly have been collected [any earlier than late September 2019](#), and doesn’t fully answer the vector question anyways. And further research examining the regions of the genome that best show genetic heritage indicated it was [“very unlikely”](#) that similarities between their spike-protein

genomes of COVID-19 and pangolins, where they share the most similarities, was due to the virus passing through pangolins at all.

– As explained in *Nature*, COVID-19's Franken-genome combines a cornucopia of distinct genetic markers from each of the three other distinct branches of the coronavirus family tree, but is distinct enough from all of them that it in fact [forms its own clade](#). Along those same lines, a full-genome evolutionary analysis of COVID-19 published in *The Lancet* concluded, [“recombination is probably not the reason for emergence of this virus”](#) since it seems that the Wuhan Strain isn't a mosaic of previously known coronaviruses, but instead draws from distant, discrete parts of the coronavirus family tree – not how these viruses naturally evolve. Because even mixing and matching coronavirus genomes from every known zoological virus, scientists couldn't find any possible combination that would explain those regions of the Wuhan Strain's genome. *The Lancet* muses that a mysterious animal host could still be out there, however since they've already searched through every known possibility and been unable to find a match, another obvious explanation is that bio-engineering accounts for the inexplicable nucleotide signature of the Wuhan Strain's genome

– Early research found that [COVID-19 targets the ACE2 receptor](#), which seems to be distributed in roughly equal proportions across global populations, meaning this virus was not designed as an offensive weapon targeting one specific global population. Instead, it indicates that the Wuhan Strain was likely developed as part of a defensive dual-use gain-of-function project possibly linked to immunotherapy or vaccination programs – never meant to leave the lab, but meant to serve as a Red Team to fight back against. And counter-intuitively, researchers have pointed out that the most critical sections of the COVID-19's protein-spike genome [don't match the previously reported pattern that would be expected for optimal binding to the specific ACE2 receptors](#) found in mammals, which indicates that these particular segments wouldn't have been directly genetically engineered nucleotide-by-nucleotide to increase virulence.

– However this is exactly what researchers looking to design something for a “safe” vaccine candidate to target *would* engineer, and doesn't rule out a scenario where the virus was passed through a series of animal hosts in the lab. The research team in fact notes that its spike [“appears to be the result of selection on human or human-like ACE2 permitting another optimal binding solution to arise,”](#) failing to directly mention that the only other human-like receptors are found in ferrets and tree shrews – both of which have frequently been used for years [in vaccine trials for viruses with this sort of protein-spike](#), and is exactly how the H5N1 Bird Flu virus was altered to make it airborne. And so the Wuhan Strain's unique affinity for the

human ACE2 receptor, which [a pre-print reports to be 10 to 20 times greater than SARS](#), may be the exact type of vaccine-related accident that led to the moratorium on dual-use gain-of-function research in the first place, and caused scientists to call for the research around H5N1 to be partially sealed-off.

– The Wuhan Strain of coronavirus, COVID-19, appears to be transmissible even before its host shows any symptoms at all, making temperature-scanning at airports ineffective since hosts appear to be contagious for about a week before any symptoms emerge. This is in stark contrast with SARS, whose hosts weren't contagious until they were symptomatic, allowing for its relatively quick containment. This chart is not from a peer-reviewed source [but was claims to capture the comparative rates of infections](#) between recent outbreaks. A recent pre-print [now gives COVID-19 a rating of R4](#), meaning each host passes the virus on to four new victims, a rate significantly higher than any past global viral outbreak.

– The successful end results of [Baric's aforementioned bat coronavirus bio-engineering research at UNC that was critiqued for being too risky in 2015](#), was published the following year and described the successful bio-engineering of a highly-virulent coronavirus derived from bats which was achieved [by tinkering with its spike-protein genes](#). In this paper, researcher #8 is listed as one "Zheng-li Shi" who's listed as being attached to the *"Key Laboratory of Special Pathogens and Biosafety, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China."*

– Zhengli Shi seems to have returned to Wuhan at some point since 2016, specifically to the Wuhan Institute of Virology's [Disease Engineering Technical Research Center](#), since she then appears in this September 2019 paper on the human behaviors most likely to lead to bat-borne coronavirus exposure in southern China, and also [in the paper claiming that this coronavirus was bat in origin](#), which was peculiarly submitted [in coordination with the announcement of the outbreak](#). Very, [very peculiarly](#). She also appears [in this pending preprint on the current outbreak of COVID-19](#), just a small sample of the dozens of coronavirus-related papers she's published over a three decade career.

– Not only does Zhengli Shi provide a direct chain of expertise tying the already successful bio-engineering of a virulent bat-based coronavirus at UNC directly to the BSL-4 virology lab in Wuhan, but back in January 2014 she'd received a \$665,000 grant from NIH for a study titled *The Ecology of Bat Coronaviruses and the Risk of Future Coronavirus Emergence (NIAID R01 AI110964)* as well as \$559,500 more from USAID for a study titled *Emerging Pandemic Threats*

PREDICT_2China (Project No. AID-OAA-A-14-00102). Beyond this American funding specifically into viral diseases zoonotically transferring from animals to humans which would slipped in just before the ban, over the years she's also received around \$3 million in grants to study these zoonotic viruses from China and other countries, and has served on the editorial board of several virological research magazines. More of her research into the intersection of coronaviruses like the Wuhan Strain and their epidemic potential was funded by the U.S. Department of Defense, the U.S. Threat Reduction Agency, and U.S. Biological Defense Research Directorate of the Naval Medical Research Center.

– And so a scientist who's been prolifically involved with studying the molecular interaction of coronaviruses and humanity, spending decades and millions of dollars, and having even helped build a hyper-virulent coronavirus from scratch at UNC – just so happens to be working at the only BSL-4 virology lab in China that also just so happens to be at the epicenter of an outbreak involved a coronavirus that's escaping zoological classification, and has other unnatural characteristics that will be discussed below.

– Another Chinese virologist, Xing-Yi Ge, appears as an author on the 2016 UNC paper and is also attached to the lab in Wuhan. Previously in 2013, he'd been the very first scientist to [successfully isolated a SARS-like coronavirus from bats which targets the ACE2 receptor](#), just like our present virus, the Wuhan Coronavirus COVID-19 uses. And it turns out that sections of the Wuhan Strain's ACE2 receptor's genes are unique: they're almost identical to SARS's spike-protein genes – [despite the fact that almost none of the two coronavirus's genomes are similar anywhere else at all](#). Beyond that, although the Wuhan Strain's spike-protein genome [differs from SARS in four out of the five most important genomic spots that determine binding to the ACE2 receptor](#), they surprisingly don't effect the protein-spike's shape. And in an even bigger coincidence, these four spots also code for the outside region of the spike that allows entry into cells, and do not effect it either – allowing the Wuhan Strain to still use the ACE2 receptor to unlock cells while possibly gaining additional capabilities. The odds that this concordance was bio-engineered into the virus are several orders of magnitude more likely than for this to randomly have evolved in nature, and is exactly the sort of process used to make the H5N1 Bird Flu airborne and highly pathogenic.

– Numerous videos purportedly from inside hospitals in Wuhan depict a crisis that is far greater than the numbers released by China to date. There is widespread but unverified online reporting that Wuhan crematoriums have been running 24/7, which is consistent with [a recent peer-reviewed study that claims that as of January 25, Wuhan had over 75,000 infections –](#)

[when the official number was just 761](#). Chinese language social media also reflects a sense of panic and desperation that is highly discordant with the numbers being released by the Chinese government. Further evidence that far more lives were lost in Wuhan than the Chinese government is disclosing is provided by the fact that [some 21 million cell phone users](#) have somehow fallen of the map in China, as well as the long lines witnessed to collect loved ones' ashes in Wuhan, which alone is reported to have had [some 45,000 cremations](#). Additionally, the Chinese government repeatedly refused any direct assistance from the American CDC. (Further evidence that China is vastly downplaying this pandemic's severity: [Example 1](#). [Example 2](#). [Example 3](#). [Example 4](#). [Example 5](#). [Example 6](#).)

– Some of the dystopian carnage creeping across China may be due to the fact that much of China's population may have already been exposed to coronavirus infection via SARS or other less notorious strains, which would allow the Wuhan Strain COVID-19 to [use antibody-dependent enhancement \(ADE\) to much more efficiently enter into cells](#), and then become much more virulent since this enhancement hijacks the body's preexisting immune response to coronavirus infections and allows easier entry. However whether or not people have been exposed to a coronavirus infection before, once it's been circulating in a population for long enough the Wuhan Strain may be able to reinfect its own past hosts and use this molecular hijacking on antibodies left from its own previous infection to become far more virulent, regardless of whether or not someone has been exposed to other coronaviruses before COVID-19. And early reporting from Chinese doctors indicates that [re-infections of the Wuhan Strain are far more lethal than the first](#), which ADE could explain, as well as the fact that [between 5% and 10% of once "recovered" patients in Wuhan](#) have been showing up with fresh infections, since that phenomenon allows a virus to hijack the antibodies created by a previous infection to re-attack an old host.

– More evidence that ADE is occurring is its much higher affinity for the ACE2 receptor and far higher viral loads compared to SARS – both of these may be due at least in part to ADE allowing COVID-19 to much more efficiently bind to and enter cells. And another hint that the Wuhan Strain may be using ADE to more effectively attack its host is the fact that it [seems to be targeting its host's neurological systems](#), which is explored in depth below. A final clue is the fact that children seem to be far less effected by the Wuhan Strain COVID-19, a phenomenon that's found in Dengue Fever, which is one of the classic examples for ADE. And curiously Zhengli Shi, of UNC and Wuhan fame, [co-authored a 2019 paper](#) which used inert viral shells to figure out exactly how SARS, with its affinity to the ACE2 receptor just like COVID-19, was able to harness ADE to hijack white blood cells for enhanced cell entry. A gain-of-function extension

of this research would be exactly the kind of experiment that could've given birth to COVID-19, especially considering that 2019 paper managed to fine-tune the exact the concentration of antibodies that would best facilitate ADE.

– Another peculiar characteristic is COVID-19's similarities to HIV. And so [although another since-retracted pre-print noted several very short genomic sequences in COVID-19's spike-protein gene that look far more similar to sequences found in HIV than to other coronaviruses](#) – critics quickly pointed out that the shared homology didn't reach statistical significance. However a closer look at the data reveals that there were a few small shared genomic segments that, despite being physically separated from each other along each strand of DNA, all worked together to code for the Wuhan Strain's protein-spike's crucial receptor binding site. Something that is highly unlikely to have happened by chance. And despite most of its protein-spike being shared with SARS, these substituted segments weren't shared at all – nor were they found in any other coronavirus, and may well be related to previous research done in the Wuhan lab looking at [inserting HIV-like segments into coronaviruses that also target the ACE2 receptor](#). One possible reason for these HIV-like segments is that they were meant to be *epitopes*, or molecular flags meant to mark intruders for a vaccine to target – meaning the Wuhan Strain was built as a monster for a specific vaccine to hunt. It is mathematically possible for this to happen in nature – but only in a *ten-thousand bats chained to ten-thousand Petri dishes and given until infinity* sense. Alternatively, [this pattern could also be produced](#) by infecting a room full of ferrets or tree shrews with a bespoke coronavirus and [sifting through the wreckage for your genomic needle](#).

– Critics have brushed off the Wuhan Strain's shared homology with HIV as statistically insignificant, however clinical reporting indicates that the Wuhan Strain may be using this shared HIV homology to attack CD4 immune cells just like HIV does, as [an unusually high percentage of patients are showing low white blood cell counts](#), especially the sickest ones. This pathogenicity may well be due to the unique HIV-like genomics of the Wuhan Strain, as one white-paper by LSU's professor emeritus of Microbiology, Immunology, and Parasitology who's also a Harvard-educated virologist with a PhD in Microbiology and Molecular Genetics notes: ["This is the first description of a possible immunosuppressive domain in coronaviruses... The three key \[mutations\] common to the known immunosuppressive domains are also in common with the sequence from \[the spike-protein\]. While coronaviruses are not known for general immunosuppression of the style shown by HIV-1, this does not rule out immunosuppression at the site of active infection in the lung, which would prolong and potentially worsen infection at that site."](#) And early research has indicated that this unique region may make COVID-19 [up to](#)

[1,000 times more likely to bind to human cells than SARS](#), which could be due to either this homology or to ADE, or some combination of these or other factors.

– Even more troubling, a peer-reviewed study noted that one particular part of the Wuhan Strain’s spike-protein genome also wasn’t found in any of its relatives, [“and may provide a gain-of-function to \[COVID-19\] for efficient spreading in the human population.”](#) And according to that paper, this particular type of furin cleavage site makes similar viruses both more pathogenic and more neurotoxic. Additionally, this particular type of cleavage site is a hallmark of being passed through [a series of animal hosts in a lab](#). Evidence for the Wuhan Strain’s neurotoxicity arrived in late February, in a published paper which notes that [“the most characteristic symptom of COVID-19 patients is respiratory distress, and most of the patients admitted to the intensive care could not breathe spontaneously.”](#) Combined with the observation that “some COVID-19 patients also showed neurologic signs such as headache, nausea and vomiting,” this paper asserts that since SARS was found heavily concentrated in the brainstems of its autopsied victims, COVID-19 is also probably crossing the blood-brain barrier and killing its victims not just via pneumonia, but also [by causing neurological respiratory failure](#). Indicating that ADE may be occurring, but at a much faster rate than nature allows since reinfections of Dengue Fever that use ADE typically have years pass between them.

– And it should be noted that SARS – much ballyhooed as a close relative to the Wuhan Strain – [didn’t notable effect white blood cell counts](#). Additionally, clinical treatment guides [published online in late January by established Chinese medical sources](#) note the progressive reduction of white blood cells, as well as the importance of monitoring this decline. And reporting from Thailand indicates that [adding a cocktail of two different anti-HIV drugs](#) to the typical flu treatment regime seemed to effectively knock back the Wuhan Strain. Additionally, one of the only autopsies performed outside of China to date found that [the deceased had a severely depleted white blood cell count](#). These lowered counts may come from this shared similarity with HIV, or it could also be the result of ADE as well, since this phenomenon [primarily targets white blood cells for its hijackings](#) and may help explain why consecutive infections are so lethal.

– Nothing about COVID-19’S clinical presentation is typical, including the fact that one of the first signs of infection [seems to be losing your senses of smell and taste](#) without any other symptoms, something no other virus on earth is known to do to otherwise asymptomatic patients. Additionally, an unnaturally juiced-up ability to use ADE would also explain what our front-line medical workers are [observing in their patients](#): *“I’m seeing people who look*

relatively healthy with a minimal health history, and they are completely wiped out, like they've been hit by a truck. This is knocking out what should be perfectly fit, healthy people. Patients will be on minimal support, on a little bit of oxygen, and then all of a sudden, they go into complete respiratory arrest, shut down and can't breathe at all... That seems to be what happens to a lot of these patients: They suddenly become unresponsive or go into respiratory failure." This sort of sudden precipitous decline is exactly what would be expected if COVID-19's ability to use ADE had been accentuated in the lab, and would also explain the clinical observations that *"this severity of [acute respiratory distress] is usually more typical of someone who has a near drowning experience — they have a bunch of dirty water in their lungs — or people who inhale caustic gas. Especially for it to have such an acute onset like that. I've never seen a microorganism or an infectious process cause such acute damage to the lungs so rapidly. That was what really shocked me."* And also the following horrific account: *"Holy shit, this is not the flu. Watching this relatively young guy, gasping for air, pink frothy secretions coming out of his tube and out of his mouth. The ventilator should have been doing the work of breathing but he was still gasping for air, moving his mouth, moving his body, struggling. We had to restrain him. With all the coronavirus patients, we've had to restrain them. They really hyperventilate, really struggle to breathe. When you're in that mindstate of struggling to breathe and delirious with fever, you don't know when someone is trying to help you, so you'll try to rip the breathing tube out because you feel it is choking you, but you are drowning."*

– In a highly concerning turn, scientists [have noted that the Wuhan Strain can have a "striking" short term rate of mutation](#) which doesn't indicate an artificial origin but captures the unique threat posed by this coronavirus regardless of its providence, since a faster mutation rates makes it more likely this virus can dodge testing and neutralize vaccines. [Something there is already early evidence for](#). Further concerning are reports out of China that [even patients who appear cured still harbor COVID-19 in their system](#), and although the full implications of this are not yet known – none of them are good.

– One of the worst possible scenarios for COVID-19's mutation rate would be if it falls into the Goldilocks range that [would allow it to form mutant viral swarms](#): too many mutations will cause a virus to eventually implode, not enough allows host immune systems to catch-up, but if things are just right mutant swarms can form and spread across host populations, burrowing into host nervous systems and causing permanent neurological damage. Mutant swarms form when a virus produces mutationally-damaged copies of itself inside a host, some of which aren't infectious but find their way into the nervous system where they burrow in causing damage, and others that combine with complimentary broken copies inside host cells to

produce working infectious copies of the virus. So a host can not only become crippled with neurological issues, but also still be producing infectious copies of the virus. And it seems as if COVID-19 has many characteristics that indicate the potential to form mutant swarms: the “striking” mutation rate mentioned above and the fact a second widespread mutated strain seems to have already emerged in Washington State with many other isolated strains reported elsewhere, crossing between species is another factor and a dog in Hong Kong appears to have tested positive, the fact that the Wuhan Strain can infect not only the respiratory tract but feces as well – multi-organ involvement is [an important contributor to viral swarms](#), and finally the markedly viral load rate of COVID-19 compared to SARS – SARS produced a viral load several times lower which decreased over time, while COVID-19 produces [a “very high” viral load](#) that appears to increase over time and can peak several orders of magnitude higher than [SARS was measured to reach](#). And alarming evidence that this phenomenon is occurring emerged from a Chinese pre-print which noted that [over one-third of the roughly 200 patients studied has some neurological symptoms](#), with nearly half of the most severe patients exhibiting neurological issues. And further evidence for the possibility of both mutant swarms and ADE is witnessed by a study published in *Lancet*, which notes that the case fatality rate in Wuhan [could actually be as high as 20%](#) – the outbreak’s epicenter would be expected to have the highest rates of both phenomena as different variants of the Wuhan Strain infected and reinfected overlapping hosts.

– Another exceptional and atypical trait of the Wuhan Strain COVID-19 is that not only does it form its own clade, it’s calculated to have diverged from SARS and its other sister coronaviruses [some 260 years ago](#). And yet in all that time, while it every other branch of the coronavirus tree [was busy branching-off into countless variants](#), if it emerged naturally, COVID-19 somehow spent a quarter of a millennium as the lone known example of its clade, somehow not mutating into related lineages in all that time. Another simpler explanation is that this apparent hereditary distance and genetic uniqueness is the just the result of being altered in a lab. And although two distinct strains of COVID-19 have been identified, there’s no reason to believe this mutational differentiation happened before contact with humans in the winter of 2019. Additionally, when neutral sites, the specific points in the genome which most reliably show evolutionary change, were examined: [COVID-19 looks even more evolutionarily distant from any of its possible relatives](#), which would make sense if all that evolutionary distance was gained by artificially accelerated generational turn-over in a lab.

– Also giving credence to the idea that the Wuhan Strain was bio-engineered [is the existence of a patent application registered to a scientist from Wuhan that looks to modulate a coronavirus’](#)

[spike-protein genes](#) – the precise region altered by Zhengli Shi at UNC to make a hyper-virulent strain of coronavirus, and whose alteration and adaptation would explain the Wuhan Strain’s unusual behavior as discussed above.

– And curiously, the head of Harvard’s Chemistry Department, Dr. Charles Lieber, [was arrested in the midst of this outbreak on charges that he’d been accepting millions of dollars in bribes from the Chinese government](#). According to his charging documents, Dr. Lieber first went to the Wuhan University of Technology (WUT), in November 2011 to participate in a nanotechnology forum, which was when he was recruited into a bribery scheme that would net him several million dollars to “establish a research lab and conduct research at WUT,” which became known as “Joint Nano Key Laboratory,” as well as mentor and advocate for graduate students. By 2015, Dr. Lieber appeared to be fairly intimately involved with what seemed to begin as simply a nanotechnology lab, but now had shifted to involve biology as well, since he described visiting the lab multiple times per year “as we try to build up the nano-bio part of the lab.” Whether or not this nano-bio part of the Nano Key Laboratory is related to Wuhan’s BSL-4 virology lab isn’t clear, however if the Wuhan Strain was bio-engineered, technology classified as “nano-bio” would’ve almost certainly played a role.

Given the above facts, either:

– A coronavirus spontaneously mutated and jumped to humans at a wet market or deep in some random bat cave which just so happened to be 20 miles from China’s only BSL-4 virology lab, a virus with an unusually slippery never-before-seen genome that’s evading zoological classification, that may be as much as twenty-times more contagious than SARS and whose spike-protein region which allows it to enter host cells holds a unique HIV-like signature with the concomitant clinical response, that somehow managed to infect its patient zero who had no connection to this market, and then be so finely-tuned to humans that it’s gone on to create the single greatest public health crisis in Chinese history with approaching 100 million citizens locked-down or quarantined – also causing Mongolia to close its border with its largest trading partner for the first time in modern history and [Russia to ban Chinese citizens from entry into their country](#).

– Or, Chinese scientists failed to follow correct sanitation protocols possibly while in a rush leading up to an international virological conference and during their boisterous holiday season, something that had been anticipated since the opening of the BSL-4 lab and has happened at least four times previously, and accidentally released this bio-engineered Wuhan Strain – likely

created by scientists researching immunotherapy regimes against bat coronaviruses, who've already demonstrated the ability to perform every step necessary to bio-engineer the Wuhan Strain COVID-19 – into their population, and now the world. As would be expected, this virus appears to have been bio-engineered at the spike-protein genes which was already done at UNC to make an extraordinarily virulent coronavirus. [Chinese efforts to prevent the full story about what's going on from getting out](#) are because they want the scales to be even since they're now facing a severe pandemic and depopulation event. No facts point against this conclusion.

An immediate international moratorium on all dual-use gain-of-function research must be instated and all existing experimentation must be autoclaved, only greed and hubris have ever been served by attempting this type of genetic manipulation. Humanity does not need a vaccine against HIV derived from a coronavirus, nor do we need to be tinkering with genetic material that holds the potential to wipe a significant percentage of us off the face of the Earth.

Failure to embrace such a ban may effectively become a death sentence for our species, assuming we aren't already on our last mile.

[– Sign the petition to end gain-of-function research here –](#)

This article was produced independently of any governmental or other outside affiliation.

[Read more from the former NSA counterterrorism analyst here, and learn why social inequalities are the most likely source of sustained violence in America.](#)

[Find out about why a lot of what you think you know about evolutionary biology is wrong.](#)

Medium user [@siradrianbond](#) provided all information regarding Dr. Zheng-li's extensive grant funding.

From: Jamie Metzl <(b) (6)>
Sent: Friday, January 20, 2023 10:06 AM
To: Rakestraw, David J. <rakestraw1@llnl.gov>
Subject: Re: STEM Education

Thank you! Very interesting ideas. :-)

On Thu, Jan 19, 2023 at 6:40 PM Rakestraw, David J. <rakestraw1@llnl.gov> wrote:

Jamie,

Here are a couple items that I have thought about from a national security perspective:

- We need to establish a robust global surveillance system that includes metagenomic analysis of both environmental and clinical samples. The system must be able to identify changes in genetic background and ideally connect the genetic information to phenotype. Syndromic surveillance is insufficient as we must be able to detect biological threats that might have a long incubation period (e.g. HIV). This will require substantial scientific advancement in instrumentation and biological understanding. It will also require global cooperation to share information. The scientific and political challenges are equally grand.
- We need to establish the scientific capability to assess the risk involved with the introduction of novel genetically modified organisms (plants, animals, microbes) into the environment. We have been doing this routinely for decades without having the scientific tools to understand potential consequences.
- In the short term, we need to do a much better job of understanding the risks (malicious or unintended) associated with the use of existing biotechnology so that short-term resilience measures can be taken. Amazingly, this is not being done by organizations which have the capabilities to do it effectively. This is a very difficult problem and requires exceptional people with diverse scientific skills and the appropriate infrastructure. This cannot be accomplished effectively using traditional collection methods.

These are in the “scientific capabilities” category which is what I think most about. Obviously, there are so many general ethical discussions around genetic modification of humans. However, we know this is inevitable and in my opinion, society will eventually get to the place where **not** using of technology in reproduction will be considered unethical. That said, I do not know how to navigate the path between now and the future.

I look forward to reading your new book.

Dave

From: Jamie Metz [redacted] (b) (6)
Sent: Thursday, January 19, 2023 1:26 PM
To: Rakestraw, David J. <rakestraw1@llnl.gov>
Subject: Re: STEM Education

Thanks so much, David. I really appreciate this.

Coincidentally, I received your email just as I am at my desk wrestling with the final draft chapter of my next book, exactly exploring "what is to be done?" and feeling my ideas were not yet bold or creative enough.

The essential question I am asking is: what are the ten or so biggest and most important steps we should be taking now to increase the odds our newfound abilities to engineer life will have the best possible outcomes for the common good.

Thoughts?

Warmly,

Jamie

On Thu, Jan 19, 2023 at 3:49 PM Rakestraw, David J. <rakestraw1@llnl.gov> wrote:

Jamie,

I wanted to send you a separate note beyond the one you could forward to (b) (6)

I really appreciate the work you are doing on so many fronts. I hope you are able to continue the dialog you began with (b) (6). Advances in biotechnology are going to change our world in unforeseen ways in the coming decades and the S&T will create many challenges along with the remarkable benefits. I am grateful that we have thoughtful people leading the discussion and enhancing awareness.

I hope we can learn from the pandemic, but I am befuddled that there has not been a more dramatic shift in policy to address the existential risk associated “biology” – natural or synthetic. If we were told such an event was on the horizon, the entire planet would take dramatic steps to prepare. We seem to want to put this behind us and go back to normal. If I were in charge, I would be creating \$100B/year programs to prevent the next event that could be even more disruptive if we are not prepared. I would also recognize that the economic benefits that would also come from the technical advances would be the foundation for economic growth in the remainder of the century. (But I am not in charge, so I will work on educating the people that might make the decisions in the future.)

Sorry I could not say much on your questions related to SARS-CoV-2 origins. I am glad you are having this discussion with people. I think it is important.

In addition to connecting me with (b) (6) I appreciate your ideas about (b) (6) /ScienceforAmerica and (b) (6) Academy. All are good ideas. I only had emailed (b) (6) at OSTP so do not have his current email but will see if someone else here has it (there is also a generic email for scienceforamerica which I could try). The discussion reminded me that I should also contact (b) (6) as we made multiple trips to Russia together and he might also have some good input.

Thanks for your help.

Dave

From: Jamie Metzl <(b) (6)>
Sent: Saturday, January 14, 2023 9:31 AM

To: Rakestraw, David J. <rakestraw1@llnl.gov>
Subject: Re: STEM Education

Great. Would Thursday at 11 EST work for you?

On Sat, Jan 14, 2023 at 11:52 AM Rakestraw, David J. <rakestraw1@llnl.gov> wrote:

Jamie,

That would be great. Let me know a time that works for you. I am flexible. We are officially off on Monday but I will be working all day. My schedule is not too consumed by meetings so I can probably make time based on your schedule.

I need to be careful in discussing SARS-CoV-2 as you might expect from my previous job responsibilities.

Dave

Sent from my iPad

On Jan 13, 2023, at 6:14 PM, Jamie Metzler <jmetzler@llnl.gov> wrote:

Hi, Dave. Great hearing from you. I'd be delighted to discuss this with you further. While we are on the call, let's also discuss the pandemic origins issue.

Let's do it later next week.

With warm regards,

Jamie

On Fri, Jan 13, 2023 at 8:28 PM Rakestraw, David J. <rakestraw1@llnl.gov> wrote:

Jamie,

I continue to enjoy the updates you send out. It is great to see you making valuable contributions on so many topics. I really enjoyed your interview with (b) (6) a while back (I listened to all 4 hours in 55 minutes).

I have been working on a STEM education project the past few years. It exploits the sensors in smartphones to do hundreds of amazing investigations that I think are going to revolutionize physics education. You can check it out at: [Physics with Phones | Science and Technology \(llnl.gov\)](#). I have also attached a summary document that provides a little background and more importantly provides some examples of the kinds of investigations that the sensors enable.

If you are interested, I would welcome the chance to talk to you about this. I think it can really impact STEM education and provide a path toward bringing equitable opportunities to every student in the country. We know this is a huge issue and there are no rational ideas that are not cost prohibited. That fact that almost every student at the most disadvantaged high schools has a smart phone, means they can have conduct science investigations that are better than what are currently being done at the most elite colleges (I know because I am paying for my kids to go to them). It is rare that a commercial investment of the magnitude that supports the smartphone industry can not only advance the quality of the best educational practices, but had the potential to bring that advance to every student in the county (world). I have spent 80 hours a week on this for the past 3 years and have trained hundreds of HS teachers, had dozens of student interns evaluating the investigations, and am beginning to pilot some of the activities at Universities. The success and reception are compelling, and I am trying to figure the strategy to have the next level of impact.

You always have such a unique perspective on the most important societal challenges and communicating ideas. I would love to get your thoughts on the concept and how to scale the impact. It could even be a big new topic for you to champion. I believe it will be the most important work in my career.

Dave

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From: Jamie Metzl (b) (6) >
Sent: Wednesday, April 5, 2023 2:24 PM
To: Rakestraw, David J. <rakestraw1@llnl.gov>
Subject: Re:

Yes. I have been deeply involved in this ongoing and slightly insane saga. :-)

On Wed, Apr 5, 2023 at 4:44 PM Rakestraw, David J. <rakestraw1@llnl.gov> wrote:

Jamie,

I am sure you are all over this but just in case: [With new Nature study, scientists continue to debate SARS-CoV-2 origins | CIDRAP \(umn.edu\)](#)

Dave

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From: Jamie Metzl (b) (6)
Sent: Tuesday, March 14, 2023 9:00 AM
To: Rakestraw, David J. <rakestraw1@llnl.gov>
Subject: Re: Quick question

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On Tue, Mar 14, 2023 at 7:09 AM Rakestraw, David J. <rakestraw1@llnl.gov> wrote:

Jamie,

Glad you will stay in the fight.

Unfortunately, I cannot comment on any specific reports from the DOE. However, I feel very strongly about the exceptional quality of scientists we have at our DOE National labs and it is essential that we have such talented people working on our most important national security challenges.

Dave

From: Jamie Metzl (b) (6)
Sent: Monday, March 13, 2023 6:19 PM
To: Rakestraw, David J. <rakestraw1@llnl.gov>
Subject: Re: Quick question

Thanks so much, Dave. I really appreciate the kind words. Sticking with fights to the end has been kind of my thing since I was a little kid, so I imagine I will keep pushing. :-)

How much stock do you put in the shift in position by the department of energy? I feel like it's a pretty big deal and the low level of confidence reflects a hangover from the Iraq war intelligence failure rather than a real lack of confidence. Am I on track?

With warmest regards,

Jamie

On Mon, Mar 13, 2023 at 5:56 PM Rakestraw, David J. <rakestraw1@llnl.gov> wrote:

Jamie,

I finally got to watch the hearing today. I think you did your best to keep the committee focused. It is unfortunate that even though there seems to be uniform desire to follow the science, it is impossible for many to not spend most of their breath pushing political agendas. It was also unfortunate that so much time had to be wasted on (b) (6) background on an unrelated topic.

I am glad you have had the energy to keep up the fight. It has to be exhausting. I guess you have more experience being at the interface of science and politics. I got exhausted just listening to the 3-hour hearing. I hope that we can come together as a nation/world to prepare for a future where advances in biotechnology are going to result in dramatic changes to the world in very unpredictable ways. Unfortunately, I am not encouraged by our inability to come together on the relatively simple issue following such a catastrophic event that should have drawn us together.

Dave

From: Jamie Metz | (b) (6)
Sent: Saturday, March 4, 2023 2:09 PM
To: Rakestraw, David J. <rakestraw1@llnl.gov>
Subject: Quick question

Dave – can you give me your best estimate of how many scientists, in total, work for the US Department of energy. Does that make DOE the largest employer of scientists in the world? Great if you can reply quickly as I am working on my testimony. Thank you so much.--

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From: Jamie Metzl (b) (6)
Sent: Sunday, February 26, 2023 1:55 PM
To: Rakestraw, David J. <rakestraw1@llnl.gov>
Subject: Re: DoE Covid origins report

Fingers crossed. At very least, I'm glad you connected.

On Sun, Feb 26, 2023 at 2:41 PM Rakestraw, David J. <rakestraw1@llnl.gov> wrote:

Jamie,

Nothing available to public that I am aware of.

Discussion with (b) (6) was beneficial in helping to solidify some of my perspectives. He was very positive but also realistic about the challenges. He was going to digest the information and talk to a few people and then get back to me. He said to ping him after a few weeks which I did last week, but he has not responded yet. We will see what happens. I think he has enough information to decide if he has any more to offer in terms of help or engagement. As you know, he has a lot of irons in the fire so it may be difficult to expect more than the feedback I got from our initial meeting. Thanks for getting us together.

Dave

From: Jamie Metzl (b) (6)
Sent: Sunday, February 26, 2023 1:29 PM
To: Rakestraw, David J. <rakestraw1@llnl.gov>
Subject: Re: DoE Covid origins report

Are there any new materials connected to this finding that are available to the public?

Also, how did it go with (b) (6) ?

On Sun, Feb 26, 2023 at 12:53 PM Rakestraw, David J. <rakestraw1@llnl.gov> wrote:

It is critical that the nation assure we maintain the capabilities to understand and mitigate the increasing risks and range of threats associated with advances in biotechnology.

From: Jamie Metzl (b) (6)
Sent: Sunday, February 26, 2023 11:34 AM
To: Rakestraw, David J. <rakestraw1@llnl.gov>
Subject: DoE Covid origins report

Amazing!!!--

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