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Abnormal Clots and All-Cause Mortality During the Pandemic Experiment: Five Doses of COVID-19 Vaccine Are Evidently Lethal to Nearly All Medicare Participants

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Abstract

Nyström and Hammarström (2022) found 7 segments in the bio-active SARS-CoV-2 spike protein that can produce abnormal proteinaceous (fibrinaloid) clots according to the Waltz algorithm. *In vitro* results confirmed the Waltz predictions. If the spike coding sequence was captured in the BNT162b2, Moderna, and other injectables, as claimed by the manufacturers, the clot producing segments are present in them too. Mainstream medical publications claim that SARS-CoV-2 infection can cause abnormal clotting, especially in "long COVID". Telling evidence from Medicare data shows a decreasing life expectancy with each dose of COVID-19 "vaccine" — 1 dose is worse than 0, and 2 worse than 1, etc. In Connecticut, 26,091 Medicare participants who died before December 31, 2022, but never took a COVID injection, on the average, survived 428 days after the middle of the pandemic period (July 27, 2020). By then nearly all of them must have been exposed to and/or infected by some SARS-CoV-2 variant — hence, the CDC urging to take the "vaccines". By contrast, 108,156 Medicare patients across the US who died before January 1, 2023, after just 1 dose of COVID-19 "vaccine", survived only 308 days — a loss of 119.9 days on the average. Connecticut participants, 23,248 of them, who received 2 to 5 doses, on the average, lost an additional 62 days of life-expectancy with each booster. It follows that 5 boosters times 62 days reduces the average remaining 308 days left-to-live after dose 1 by 310 days. So, nearly all the Medicare participants will have been dead for 2 days by booster 4 (dose 5). The upshot is that 5 doses, on the average, will kill all the Medicare participants who accept the advice of the CDC.[1] For 157,495 of the Medicare participants studied here — people supposedly most apt to benefit from COVID-19 injectables — days-left-to-live shrinks by 74 days, on the average, with each dose. It is also likely that the COVID-19 injectables are partly, maybe wholly, responsible for the unnatural clots found by treating physicians, pathologists, and embalmers in living and dead recipients of the experimental injectables. It is certain is that the injectables are increasing all-cause mortality across the globe.

Keywords: *amyloid disease, amyloidogenicity, abnormal clots, BNT162b2 contents, genetic therapies with XNAs, Medicare participants, Moderna, myocarditis, SARS-CoV-2 spike protein, synthetic nucleic acid, XNA*

[1] In the dataset from Connecticut, only 7 of 57,261 Medicare participants (7/57261 = 0.000122), or about 1.22 persons in 10,000 survived 5 doses during the experimental pandemic in order to take a 6th dose. Those who did so died, on the average, in 34 days. Only 1 participant survived 6 doses to receive a 7th and died within 69 days at the age of 68.

Introduction

There have been reports of extraordinary abnormal clots being removed from both living (Dong & Corson, 2022) and dead (Crowder & O'Looney, 2022; O'Looney et al., 2022; Trigoso, 2022) individuals who received one or more doses of a COVID-19 injectable, or some mix of more than one. By February 22, 2023 the *in vivo* experimental genetic therapy had already been administered in 13.29 billion doses — with 1,695,567 doses being added to the total in just one day in the still unfolding true narrative representation (see TNR-theory in Oller, 2014). When we started writing this paper, of the approximately 8 billion people on the planet, more than 5 billion (62.5% of the whole world's population) qualified as "fully vaccinated". To that growing number, on February 22, 2023, 1,266,689 persons were added in just one 24-hour period. By December 31, 2022 during the experimental pandemic period, in the US alone 665,886,823 doses had been administered to a population of fewer than 332,612,403 people.

As a result, the ongoing program of worldwide COVID-19 "vaccination" is by far the largest medical experiment in recorded history and it is still underway. Here, we first examine some of the background of the two-phase experiment. The first phase consisted of the experimental "pandemic" that, as we document, must be attributed to the accidental (or possibly intentional) release of the weaponized SARS-CoV-2 virus into the human population. The SARS-CoV-2 virus was artfully engineered in bioweapons laboratories mainly in the US and China to enhance its infectious powers first in mice, then ferrets, later bats, and finally in human beings through a highly bio-active "spike protein" (Yount, Denison, Weiss, & Baric, 2002; Menachery, Dinnon, Yount, . . . & Baric, 2019). We say it is "bio-active" because of the known interactions between DNA, RNA, and proteins in which the SARS-CoV-2 spike protein participates (Aldén et al. 2022; Kyriakopoulos et al. 2022; Lyons-Weiler, 2023). The second phase consisted of the ongoing effort to inject synthetic genetic materials into every person on the planet. As we examine the scope and outcomes of this two-phase experiment, we consider certain hypotheses about what factors precisely have resulted in the observed increase in all-cause mortality across the world, though we focus mainly in this paper, on the US population. We term the ongoing "pandemic" an "experiment" first and foremost because of the fact that the SARS-COV-2 virus was an experimental product of bioweapons research in various laboratories dating from prior to the development of SARS-CoV-1 (see Fleming, 2021; also Kennedy, Couey, & Rixey, 2023; Huff, 2022; Huff & Lyons, 2023).

As the facts of the true narrative concerning COVID-19 continue to materialize, the host of unpredicted consequences of the "directed evolution"/"gain-of-function" research planned by the defensive and offensive bioweapons experts (for documentation see Oller, 2021; Fleming, 2021; Huff, 2022) are being revealed on a daily basis in real clinical outcomes. Among the suspected causes of the emerging injuries and deaths summed up in the book, *Cause Unknown: The Epidemic of Sudden Deaths in 2021 and 2022* by Ed Dowd (2022), are the more than 13 billion injections of some COVID-19 "vaccine" each dose of which contains more than 13 billion exemplars of a synthetic nucleic acid posing as a natural "mRNA" coding for the SARS-CoV-2 spike protein (in the Pfizer and Moderna products). In the AstraZeneca version, the payload is estimated to contain as many as 50 billion exemplars of a synthetic "DNA" aiming purportedly to cause recipients to manufacture

billions more replicas of the SARS-CoV-2 spike protein.[2] This paper addresses the central clinical outcome question:

> *What is now pushing upward the abnormally high level of deaths from all-causes in the most heavily vaccinated populations of the world, especially in the USA?* [3]

Among the most likely suspected causes are the known components of the COVID-19 injections. The foremost suspects are the strings of synthetic nucleic acids that have been under development with the assistance of agencies within the US Department of Defense at a cost of hundreds of millions of US taxpayer dollars (Karikó, Ni, et al., 2004; Karikó, Muramatsu, et al., 2008; Sahin, Karikó, & Türeci, 2014; Pardi et al., 2015, 2018). Among the components suspected are the 728 m1Ψ nucleotides found in every complete xenonucleic acid (XNA) coding for SARS-COV-2 spike protein (Oller & Santiago, 2022; Santiago, 2022a, 2022b). Additionally, we know that the development of the COVID-19 injectables though supposedly rushed, was actually developed over an unprecedented lengthy time scale with vast sums of taxpayer money. Also, in spite of unsupervised manufacturing (Gutschi, 2022; Latypova, 2022b; Banoun, 2022, 2023), the whole experiment, still ongoing, has been undergoing research and development for at least three decades (Elzoghby, 2013; Dena & El-Sherbiny, 2022). That fact makes the ongoing experiment not only the most extensive and costly in recorded history, but it makes it also one of the longest vaccine programs in history. It is certainly not the shortest and fastest as has often been claimed in the mainstream media (Cohen, 2020; Ball, 2020; and Schelenz & Long, 2021 to cite only a few of thousands that come up on a Google search).

Abnormal Clotting as a Hallmark of the SARS-CoV-2 Spike Protein

According to the clinical observations, case studies, and written reports from front-line workers, the abnormal clots that have been seen clinically usually occur in people who have received at least a second dose of one of the experimental genetic injectables. Highly experienced embalmers including John O'Looney, Richard Hirschman, and Brenton Faithfull (O'Looney et al., 2022) have reported removing clots from about 50% to 70% of the corpses of recipients of one or more doses of the COVID-19 "vaccines". They report having seen normal blood clots previously in perhaps as many as 5% to 10% of the hundreds of bodies they embalmed before the worldwide distribution of COVID-19 "vaccines" began, but they report never having seen the kind being removed from recipients of the experimental COVID-19 injectables. The strange clotting phenomena, they report, only began to appear in corpses in 2021 and 2022 after the COVID-19 injectables began to be widely distributed.[4]

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[2] The numbers of exemplars of any particular synthetic nucleic acid cited here are from Fleming (2021, p. 99).
[3] Data from Europe have recently shown trends similar to the one we document for the US. All-cause mortality has increased in the UK (Santiago & Oller, 2022), and in Europe (Redert, 2023; Aarstadt & Kvitastein, 2023).
[4] Notably, some of the key researchers involved in developing the supposedly novel "mRNA" therapies for treating COVID-19, including Ralph Baric, Yount, and othes had commented as far back as 2002 (Yount, et al.) on the power of "genetic modifications of the entire coronavirus genome, particularly in the replicase gene" to enhance "transfection frequencies . . . 10- to 15-fold" (p. 11065). They commented that the mouse hepatitis virion "contains three or four virus proteins including a spike glycoprotein of ~180/90 kDa" which could help the engineers to understand "the replication strategy of coronaviruses"and then use that virion "as a model for pathogenesis, docking and entry, receptor usage,

Until recently, testimonials supporting the observations of the embalmers, which were also later confirmed by many medical practitioners who found abnormal clotting in living persons, could be found on a Telegram channel formerly dedicated exclusively to the abnormal post-vaccination "clotting" issues. However, that channel was taken down in 2022 only to be re-created under the new moniker — "Efectos Adversos de la Vacuna" [Adverse Effects of the Vaccine]. The many new testimonials now posted on Telegram in Spanish suggest a continuing and growing world-wide scope for the abnormal, often fatal, clotting phenomena in many recipients of COVID-19 injections.

In the meantime, the abnormal clotting phenomena are, it seems, almost exclusively represented in the mainstream medical/pharmaceutical publications as pertaining only to "long COVID" effects (Pretorius et al., 2021; Raveendran et al., 2021; Patterson et al., 2022; Grobbelaar et al., 2022; Hofer, 2022; McCafferty et al., 2022; Montano et al., 2022; Nyström & Hammarström, 2022). The living and dead persons with the abnormal clotting are regarded in the mainstream technical medical literature, and in the popular press, as victims of "long COVID". They have also been called "long haulers" (Rubin, 2022). However, the clinical outcomes in recipients of the experimental genetic therapies — for example, the BNT162b2 Pfizer product, as well as the other COVID-19 injectables — are well documented outside the mainstream medical publications in multiple reports by competent and independent observers (Crowder & O'Looney, 2022; Dong & Corson, 2022; McLernon, 2022; Trigoso, 2022). Also, independent researchers, as we document in this paper, have begun to link the abnormal clotting directly to the COVID-19 injectables, usually in recipients of two or more doses.[5]

Normal Blood Clotting Is Distinct

Normal blood clotting begins by converting the liquid blood to a gel. Then, with the addition of fibrinogen under the direction of an incompletely understood complex of many factors, the gel is transformed into a fibrinous blood clot (Weisel & Litvinov, 2017). The whole process is part of the

transcription, replication, polymerase function, and assembly and release" (p. 11065). Then, by 2019, those same researchers together with Menachery et al. extended their coronavirus gain-of function engineering to "bat coronavirus infection" observing that looking forward, their "results argue that both receptor binding and proteolytic cleavage of the spike are critical factors that must be considered for evaluating the emergence potential and risk . . . for future coronavirus emergence events in humans" (p. e01774-19).

[5] While the construction of the current paper was underway, the second author was motivated to join with the first when a fifth person among his own close relatives, those who willingly accepted one or more of the recommended doses of the COVID-19 injections, abruptly fell desperately ill or died suddenly with abnormal clotting. One individual in her 40s was diagnosed, soon after a "booster" injection with an acute Type 2 diabetes resulting in almost complete blindness and damage to both kidneys. Two deaths among the five were specifically attributed to clotting by attending physicians. One of the individuals who, in compliance with CDC recommendations took a COVID-19 "booster", subsequently experienced two distinct surgeries removing large clots from the same leg. The second clotting incident was fatal. On the recommendations of the treating physicians, the clotting was being treated with multiple blood thinners, and during the last brief hospitalization for the removal of a rapidly formed clot in the same leg from which a similar clot had been removed some weeks earlier, the patient died. The proximate cause of death was attributed to "internal bleeding" and a "ruptured spleen". For reasons to be explored in this paper, it is doubtful that the clotting could have been helped by the administration of the blood thinners, but the blood thinners may well have contributed to the uncontrollable internal bleeding that began soon after they were administered. In both of the clotting cases, the treating physicians seem to have misdiagnosed the underlying causes leading to death. Here, we examine tens of thousands of cases in multiple datasets.

thoroughly integrated normal maintenance-repair-defense systems of the human body (Oller, 2022). In cases of cuts, punctures, and other causes of bleeding, coagulation starts immediately after the damage to the lining inside the lumen of the injured blood vessel(s). Thrombin, an important component of this repair action, converts soluble fibrinogen into insoluble strands of fibrin. However, the abnormal clots being removed during the embalming process from the multitude of corpses of persons who had received more than one of the COVID-19 injections in most cases before expiring (O'Looney et al., 2022; Trigoso, 2022), and also from more than a few living persons — where the strange clots also are being found in surgeries, phlebotomies (the routine drawing of blood samples), or placement of peripheral intravenous (IV) cannulation (Dong & Corson, 2022) — the strange new clots appear to be radically larger and different in important ways from normal blood clots.

The differences have been remarked upon especially by embalmers (Crowder & O'Looney, 2022), but the abnormal characteristics of the fibrinous clots have also been noted by clinicians dealing with living patients (Dong & Corson, 2022; Thorp et al. 2022). The strange new clotting structures have a greater coherence and insolubility than ordinary blood clots. Stripped of any associated blood, they have a whitish callous-like coloration and, in corpses and cardiovascular procedures where they are observed, they are huge by comparison with normal blood clots.

Furthermore, they are apt to show up in arteries as well as in veins — a feature that is not seen with normal blood clotting at all. The abnormal clots are distinguished as well by the rapidity of their formation. Most importantly, their tangible toughness, and the consistency of their internal structure make them notably different from any ordinary blood clots (Crowder & O'Looney, 2022).

The differences in elasticity (stretchiness) and coherence (toughness) have been universally noted by embalmers and by clinicians who have extracted the abnormal clots from dead and living persons, respectively. One of the unnatural aspects viewed commonly only by embalmers is the extent to which the coherent abnormal clots occupy large portions of the branching vascular systems of veins and arteries throughout a corpse. The common vacuum equipment used by embalmers to remove the remains of bodily fluids from the cardiovascular system tends to breakdown because it clogs up with relatively small amounts of the large coherent fibrinous composites.

In living persons, by the time the abnormal clots are detected by a surgeon, a phlebotomist, or a nurse connecting an IV tube, the clots are thousands of times greater than the nanometer scale where fibrinogen begins its normal work to prevent uncontrolled internal or external bleeding after a severe bruise, puncture wound, or other injury. By the time the abnormal clotting associated with recipients of the COVID-19 injectables can be seen by clinicians, not to mention embalmers, the abnormal clots range from a millimeter up to a full centimeter or more in diameter, and in length they range from centimeters to a meter or more (Crowder & O'Looney, 2022; O'Looney et al., 2022).

As has already been suggested by Kell and Pretorius (2017) and by Nyström and Hammarström (2022) the abnormal fibrinous clots associated with the SARS-CoV-2 spike protein and with the synthetic "mRNA" spike proteins, the ones coded for in the XNA genetic therapies (the COVID-19

injectables), begin as tiny fibrils at a nanoscopic scale as shown in Figure 1 which is adapted from Nyström and Hammarström (2022). The fibrils seen in Figure 1 appear to be about 10 to 20 nanometers in diameter and up to 2000 nm (about 2 micrometers), or more, in length.

Table 1 lists all seven of the amyloidogenic segments in the SARS-CoV-2 spike protein receptor binding region, but Figure 1 shows only fibrils generated *in vitro* meeting all three of the "amyloid criteria" set by Nyström and Hammarström 2022. In particular, the fibrils had to stain yellow with thioflavin showing sigmoidal kinetics, red showing congophilicity, and they had to have a "fibrillar ultrastructure". Spikes 192, 601, and 1166 (each segment being named for the position in the full 1273 residue sequence of the spike protein of its first amino acid) met all these criteria and spike 192 in particular showed "exceptionally well-ordered fibrils" which were similar to the *in vitro* products when all 7 of the peptides in Table 1 were combined, as seen in the side-by-side comparison in Figure 2.[6]

Table 1

The 7 amyloidogenic segments identified *in vitro* in the SARS-CoV-2 spike protein receptor binding region by Nyström and Hammarström (2022) reported in "Amyloidogenesis of SARS-CoV-2 spike protein", *Journal of the American Chemical Society*, *144*(20), 8946 retrieved on March 5, 2023 at https://doi.org/10.1021/jacs.2c03925. Reprinted here as permitted by their Creative Commons 4.0 license. The notes *a* and *b* are theirs.

Peptide	Amino acid sequence[a]	MW (Da)[b]	pI	ThT kin	Congo Red	Ultrastructure
Spike192	FVFKNIDGYFKIYSKHTPIN	2431	9.4	+	+	fibril
Spike258	WTAGAAAYYVGYLQPRTFLLK	2389	9.5	-	+	fibril
Spike365	KKKGGGYSVLYNSASFSTFK	2169	10.0	-	+	amorphous
Spike532	NLVKNKCVNFNFNGLTGTGV	2139	9.3	+	+	amorphous
Spike601	GTNTSNQVAVLYQDVNCTEV	2155	3.7	+	+	fibril
Spike685	KKKRSVASQSIIAYTMSLGA	2139	10.5	-	-	ribbons
Spike1166	LGDISGINASVVNIQKEIDR	2141	4.6	+	+	fibril

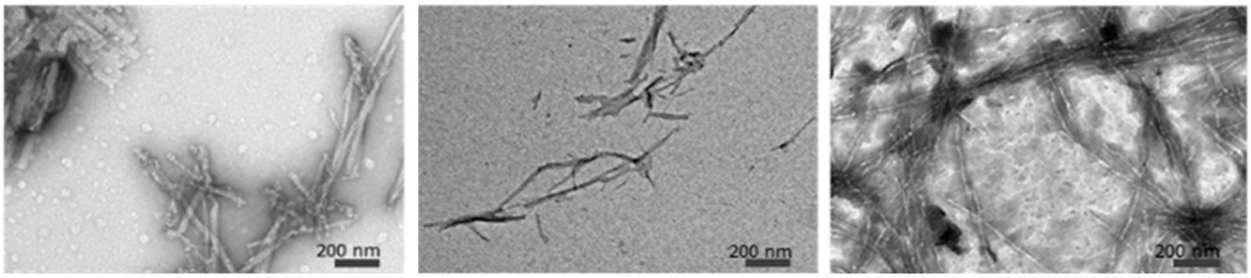
[a]Residues assigned in color indicate the amyloidogenic segments as predicted by WALTZ. Highlighted in gray are non-native amino acids introduced for solubility. [b]Theoretical mass.

The key finding is that the fibrils formed by the first of the seven amyloidogenic peptides in the sequence of amino acids comprising the SARS-CoV-2 spike protein receptor binding region (Table 1) would apparently have the power to cause the formation of the microclotting reported in the literature pertaining to the COVID-19 disease in both its acute and long-haul versions. We were able to confirm that spike 192 and spike 258 in Table 1 are in BNT162b2 "mRNA" (actually an XNA) coding for the spike protein in the Pfizer injectable according to the coding sequence published by Nance and Meier (2021). Government proponennts also said the "modified sequence" was included in the Moderna and the adenovirus DNA AstraZeneca injectables as well (Oller & Santiago, 2022).

In any case, the research of Nyström and Hammarström (2022) specifically implicates the SARS-CoV-2 synthetic spike protein as a possible source of abnormal clotting. Given that the lumen of

[6] It should also be noted here that spike 192 and the other amyloidogenic components in the injectables are supposedly enhanced in their power to generate proteinaceous fibrils by the unnatural mRNA coding that employs N1-methylpseudouridines in place of uridines (as stressed by the BNT162b2 and experimental genetic therapy proponents, Nance & Meier, 2021). If that is the case, the XNAs should be more apt than the original SARS-CoV-2 spike protein itself, to cause fibrinaloid clotting and all the disease conditions that it brings with it.

the smallest capillaries in the body is about 5 to 10 micrometers in diameter (Capillary, 2022), the fibrinous materials seen in Figure 1 and in Figure 2 are already large enough, if matted together, to impede the passage of red blood cells which are about 6 to 8 micrometers in their largest dimension (Red Blood Cell, 2019). Because the red blood cells are typically a little larger than the lumen of the capillary which they must squeeze through, the changing Zeta potential and electro-magnetic charge



(A) spike 192 (B) spike 601 (C) spike 1166

Figure 2. Fibrils formed *in vitro* by researchers Nyström and Hammarström (2022). The source of coding was the SARS-CoV-2 spike protein. That coding, according to Nance and Meier (2021), except for the 728 N1-methylpseudouridine insertions should be the same as found in the spike protein XNA of the BNT162b2 injectable. See Nyström, S., & Hammarström, P. (2022), Amyloidogenesis of SARS-CoV-2 spike protein, in the *Journal of the American Chemical Society*, *144*(20), 8945–8950. These micrographs are adapted from their figure 1 on page 8946, at https://doi.org/10.1021/jacs.2c03925. They are adapted and reprinted here as permitted by their Creative Commons 4.0 license.

inside the iron laden hemoglobin are believed critical (Davidson & Seneff, 2012) to enable the normal blood flow. Also, healthy red blood cells are round and flexible helping to enable the slide through the capillary lumen. However, the very small fibrinaloid formations seen in Figure 1 and 2, if present in matted clumps, would cause precisely the sort of

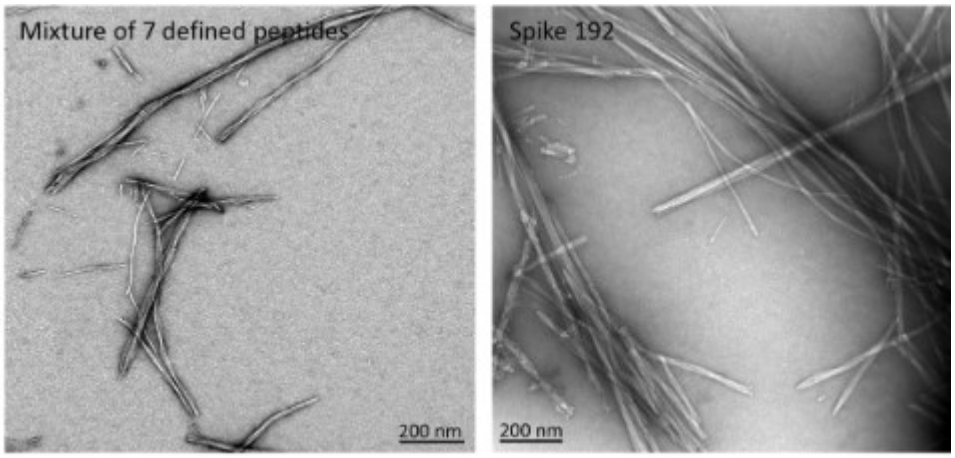


Figure 1. Side-by-side transmission electron microscopy (TEM) of fibrils obtained *in vitro* from a mixture of all 7 of the amyloidogenic segments in the receptor binding region of the synthetic SARS-CoV-2 spike protein (at left) with fibrils formed *in vitro* with the same procedure by spike 192 alone (at right) identified by Nyström and Hammarström (2022) and shown in their supplementary Figure 3S, items B and C, as discussed in "Amyloidogenesis of SARS-CoV-2 spike protein", *Journal of the American Chemical Society*, *144*(20), on page 8946 retrieved on March 5, 2023 at https://doi.org/10.1021/jacs.2c03925. Adapted and reprinted here as permitted by their Creative Commons 4.0 license.

cardiovascular disasters that are occurring increasingly according to McCullough (2023). It is mainly at the capillary level where the exchange of oxygen and nutrients for carbon dioxide and waste products takes place at the turn-around point from arteries carrying a load of oxygenated blood from the lungs going to veins carrying de-oxygenated blood back to the lungs. Fibrinaloid log jams at that level are certain to be problematic.

The logical question that we pose is whether the amyloidogenic segments, or the SARS-CoV-2 spike protein XNA as a whole, might be causing the abnormal clotting observed in both living and dead recipients of the BNT162b2 "vaccine" and its counterparts produced by the other known manufacturers of COVID-19 genetic therapies (specifically, AstraZeneca, Janssen, Moderna, Novavax, Pfizer, and Sanofi — all having been named in press conferences by President Donald

Trump in July and November of 2020a, 2020b). We also know now, based on multiple sources cited, for instance, in detail by Eyeinthesky (2022), that the Department of Defense funding for those companies, especially Moderna, supported research pertaining to synthetic "mRNA" and nanolipid delivery systems since at least 2012 (under the guidance of Katina Karikó). All of it has been traced back more or less directly to the US Department of Defense (Latypova, 2022c; Morris & Latypova, 2023)

Abnormal Clotting Precipitated by the SARS-CoV-2 spike protein

Now in the aftermath of COVID-19 it has become known that abnormal clotting is precipitated by the SARS-CoV-2 spike protein without any outside assistance from any XNA based COVID-19 "vaccine" (Ahmad et al., 2022; De Michele et al., 2022; Montano et al., 2022). This empirically established fact, together with mounting evidence of the strange clotting phenomena in recipients of the synthetic nucleic acid (XNA) component in the COVID-19 injectables, raises important questions about the potential impact of the artificial spike proteins created by billions of the XNA molecules in 13+ billions of doses in 5+ billions of recipients. We are referring specifically to the genetically engineered synthetic "mRNA", an XNA without question (Oller & Santiago, 2022; Santiago, 2022a, 2022b), that aims to code for the SARS-CoV-2 spike protein in the BNT162b2 injectable, and in its Moderna counterpart as well. The AstraZeneca DNA seeks to cause the production of the SARS-CoV-2 spike protein through a different genetic pathway (Nance & Meier, 2021).

With all that in mind, here are some of the inadequately addressed issues that arise:

- Perhaps the coagulating effects are being caused by spike proteins *in vivo* because of XNA molecules whether from a deceptive "mRNA" or "DNA" starting point. The XNAs are, in any case, designed to cause the production of multitudes (trillions) of SARS-CoV-2 spike proteins in COVID-19 "vaccine" recipients.
- The production of synthetic versions of the spike protein from SARS-CoV-2 (Nance & Meier, 2021) may be partly, or perhaps solely, responsible for the causation of the abnormal clotting being observed currently in the corpses as well as in the living bodies of recipients of the COVID-19 "vaccines".

- If the SARS-CoV-2 spike protein is already known to cause clotting of an abnormal, injurious, disease producing kind, it seems the XNA versions of that protein must also be prone to causing such abnormal clotting.
- Supposing that the XNAs in the lipid-nanoparticles can and do actually invade nucleated cells with whatever else the payload may contain, surely interactive effects must occur *in vivo*.
- In addition to whatever impact can be expected from the disclosed components of BNT162b2 discussed by Segalla (2023) in this journal (also by Banoun, 2023), additional impacts must be expected from whatever components though not previously acknowledged by the manufacturers that are being brought to light by microscopists across the world (Campra, 2021; Benzi Cipelli et al., 2022; Martín, 2022; Hughes, 2022; Latypova & Nixon; Nixon, 2023).

As Oller and Shaw (2019) argued, when the membranes guarding the deepest levels of genetic information in nucleated cells are compromised — as is the case according to recent studies showing that some components of the COVID-19 injectables can reverse transcribe into the recipient's DNA (Aldén et al., 2022) — metastatic conditions traditionally regarded as cancers can be expected to manifest or re-manifest suddenly, almost explosively. Similarly, rapidly developing prion-like conditions similar to the new Creutzfeldt-Jakob disease discussed in this journal by Perez, Chalmin-Moret, and Montagnier (2023) are consistent with the exploding plethora of disruptions that can be anticipated. Here is where the absurdity of predicting in advance and trying to prepare for the consequences of "directed evolution"/"gain-of-function" research leading to a pandemic such as COVID-19, as pointed out by Huff in his interview with Tony Lyons on March 1, 2023 at the Children's Health Defense website, becomes obvious. The combinatory possibilities explode to an irreducible complexity with even very small fragments of the synthetic nucleic acid strings. Whereas, for instance, Nyström and Hammarström (2022) are focussing attention on seven peptides (Table 1) that can be produced by strings as short as 5 nucleotides and as long as 21, the SARS-CoV-2 spike protein at 1273 nucleotides, is only a little more than 4% of the entire SARS-CoV-2 virus estimated at 29,870 nucleotides. Moreover, whatever protein/peptide sequences happen to be produced or injected can potentially interact with about 35,000 distinct proteins found in the human body, not to mention their potential interactions with the still greater complexities of the body's maintenance-repair-defense systems which are invoked in the transition from the laboratory context to living persons.

Although researchers Kell and Pretorius (2017) acknowledge the coagulopathies that are associated with the spike protein of SARS-CoV-2, they nonetheless seem to hold tightly to the severely constrained mainstream medical publication requirements. Those publications either assert or imply that more than 13 billion injections in more than 5 billion "fully vaccinated" recipients of the COVID-19 of injections to produce SARS-CoV-2 spike proteins *could not possibly have any causative role in the widespread abnormal clotting being observed in the world population*. Omitting many of the references embedded in the quoted remarks just below, here are some of the findings of Kell, Laubsher, and Pretorius (2022, pp. 540-541):

> Coagulopathies . . . especially the formation of extensive microclots *in vivo*, are a hallmark of both COVID . . . and long COVID . . . , and we have demonstrated that these microclots too are amyloid in character . . . . Importantly, the addition of purified, recombinant SARS-CoV-2 S1 spike protein to coagulation-competent normal plasma is sufficient to induce the formation of anomalous clots [Ryu et al. 2021] that adopt amyloid

> states that are also resistant to fibrinolysis [Grobbelar et al., 2021]. Note that the observations of the microclots in (platelet-poor) plasma are performed without the addition of exogenous thrombin; they are naturally there in the circulation of patients with both acute and long COVID. The size of these amyloid microclots, that can be observed microscopically and stained . . . are typically anywhere from 1–200 μm [oon their longest axis]; this means that they can effectively block up, and inhibit blood flow through, all kinds of microcapillaries, thereby strongly lowering the availability of oxygen in tissues. As expected, they consist mainly of fibrin, but also contain many other proteins, including α2-antiplasmin [Grobbelar et al., 2021] (and even the virus itself [Marfella et al., 2021]). They also have heightened pro-inflammatory activity and elicit fibrin autoantibodies [Ryu, et al., 2021] (and maybe others). Elements of at least some spike protein variants of SARS-CoV-2 can also stimulate (*in silico*) the amyloidogenic aggregation of serum amyloid A [Jana et al., 2021].

They not only follow the mainstream narrative in medical publications claiming, overtly at least, that the SARS-CoV-2 spike protein caused COVID-19 disease in all its forms (mild or fatal, short or long), but they go further to suggest that the COVID-19 coagulopathies may involve some of the same genetic precursors as the traditionally recognized amyloidogenic diseases such as Alzheimer's and the known prion diseases. They even suggest that the abnormal clotting associated with the spike protein may be causally involved in Parkinson's, Type 2 diabetes, rheumatoid arthritis, and autoimmunity in general (Kell & Pretorius, 2017, p. 25, Figure 9).

Homology Seems Central

All those disease conditions seem to involve near homologies in communications through the body's complex biosignaling systems. In this connection, we are reminded of the "pathogenic priming" theory of Lyons-Weiler (2021).[7] Even in ordinary experience, extreme similarities can cause mistaken identifications. We may mistake one twin or even a sibling for a different one. Or, similar sounding utterances may lead to false expectations in all sorts of real life contexts of experience. In biosignaling systems, close homologies also can confuse the body's maintenance-repair-defense systems into mistaking self-nucleic acids, proteins, cells, tissues, or even whole organ systems, for the disordered/diseased products of foreign agents that need to be attacked and destroyed, or at least quarantined for further analysis and observation. The reverse also seems possible. Genuine disease agents, such as the synthetic XNA posing as a native (self) mRNA, supposedly, according to relevant mainstream medical publications, can be mistaken for self-material and may be used to produce whole armies of invading SARS-CoV-2 spike proteins.

Such intentionally engineered mistakes — ones that end up conforming exactly to the formal requirements of pre-meditated lies (see Oller, 2014) — via the COVID-19 "vaccines" are being presented to the maintenance-repair-defense systems of the human body as if they were true representations of native bodily proteins. Yet these deliberate lies are the sole basis for the hoped for outcomes of the COVID-19 genetic therapies as spelled out in the mainstream narrative for Pfizer, Moderna, AstraZeneca, and the rest of the COVID-19 "vaccines". All of this messaging is promoted, for example, by Nance and Meier (2021) speaking on behalf of the US Department of Defense as we noted earlier (Oller & Santiago, 2022).

At any rate, the whole narrative behind the COVID-19 genetic therapies is predicated on the theory that the body can be deceived by synthetic nucleic acids into regarding foreign disease agents, such

[7] The importance of nearly homologous strings in complex biosignaling systems was also inadvertently noted by Yip et al. (2016) specifically in relation specifically SARS-coronavirus infections. They wrote that "anti-spike antibodies facilitate infection of SARS-CoVpp" (p.

as the XNA coding for SARS-CoV-2 spike protein, as native components of its own biosignaling systems. Kell and Pretorius (2017) explain the connection with the abnormal clotting associated with the SARS-CoV-2 spike protein as follows. They write that

> the finding [by Patterson et al., 2022] that S1 spike protein [the part from amino acid residues 14 through 685, in the full 1,273 amino acid sequence, that contains the receptor binding domain fusing with angiotensin-converting enzyme 2 (ACE2) thus enabling viral cell entry according to Huang et al. 2020] can itself persist in CD16+ Monocytes in PASC [post acute sequelae of COVID-19] for up to 15 months post-infection is highly relevant, as the amplification of trigger proteins to make microclots as part of the clotting mechanism[8] means that miniscule (and highly substoichiometric) amounts[9] . . . can suffice [Kell & Pretorius, 2017; Pretorius et al., 2016]. . . .

Given such a starting point in the SARS-CoV-2 spike protein coding sequence, Kell et al. claim that exceedingly small amounts ("substoichiometric" amounts) of the homologous sequence for an "epitope" of the fibrin producing peptide, at a ratio of 1 molecule to 100 million, may cause deadly diseases:

> The role of autoantibodies and biomimicry Autoantibodies [*sic*, their capital letter] are a feature of many chronic, inflammatory diseases, such as rheumatoid arthritis . . . and where the cross-reactive epitopes leading to "mimicry" by and of host protein targets are understood . . . . it has already been shown that both acute [Leonardi & Proenca, 2020; Woodruff et al., 2020] and Long COVID [Phetsouphanh et al., 2022] are accompanied by immunological dysfunction, and by novel antibodies [Proal & VanElzakker, 2021; Woodruff et al., 2020], including in the latter case to (an "abnormal" but unspecified form of) fibrin [Ryu et al., 2021]. We recognise that any change in the conformation of a protein can result in the generation of novel epitopes that can thereby lead to the production of novel antibodies; indeed the use of secondary antibodies in the detection of small molecules [Guntas et al., 2021] relies precisely on this fact. Although we consider that the more primary event is the generation of fibrinaloid microclots, we also recognise that they are likely to be able to change the natural conformation of many proteins that might normally present as harmless (seen as "self").

Chertow et al. (2021), about a year earlier, found in 37 of the 44 deceased patients on whom they performed complete autopsies that they had "acute pneumonia or diffuse alveolar damage at the time of death" (lines 232-333). Chertow et al. point out that the observed "diffuse alveolar damage showed clear temporal associations, with the exudative phase seen mainly within the first three weeks of infection and the fibrosing phase not seen until after a month of infection" (our Figure 3). Based on its distribution throughout the bodies of those who died with SARS-CoV-2 infection, the authors conclude: "Our data prove that SARS-CoV-2 causes systemic infection and can persist in the body for months" (lines 80-82):

> Overall, SARS-CoV-2 RNA was detected in respiratory tissue of 43/44 cases (97.7%); 160 cardiovascular tissue of 35/44 cases (79.5%); lymphoid tissue of 38/44 cases (86.4%); 161 gastrointestinal tissue of 32/44 (72.7%); renal and endocrine tissue of 28/44 cases (63.6%); 162 reproductive tissue in 17/40 cases (42.5%); muscle,

[8] We must insert here the objection that normal blood clotting is not "mechanical". It is not controlled by an "mechanism" that might be construed as some kind of automatic switch. It is certainly more than that. Insofar as it is understood at all, it is known to be under the direction of systems of communication that involve the delicate and highly articulated maintenance-repair-defense systems guided by holistic interactions of DNA, RNA, and protein signaling systems.

[9] The stoichiometric principle of chemistry holds that normal reactions will include proportionate amounts of input and output material (by mass). Usually the input and output ratio can be expressed a something close to a 1 to 1 distribution from start to finish. However, in the case at hand, the clotting process, Kell and Pretorius maintain, can be precipitated by a ratio of 1 triggering molecule to 100 million outcome molecules.

> skin, adipose, and peripheral nervous tissue 163 in 30/44 cases (68.2%); ocular tissue and humors of 22/28 cases (57.9%); and brain tissue in 164 10/11 cases (90.9%). . . .

The autopsy results of Chertow et al. demonstrate in actual cases how damage eventually marked by abnormal clotting, "fibrosing" as they describe it, begins before causing the kinds of fatal disease conditions widely attributed to the spike protein of the SARS-CoV-2 virus. In our view, the most important point to be borne in mind with respect to the abnormal clotting phenomena associated both with the original mRNA and with whatever synthetically produced SARS-CoV-2 spike proteins, or fragments, may be caused by the experimental XNA — in the BNT162b2, for instance, or in its Moderna, AstraZeneca, or other counterparts — is that there are exponentially many more ways for the disruptive and deceptive experimental injections to cause harm than to bring about hoped for benefits to recipients (Seneff & Nigh, 2021; Seneff, et al., 2022; Santiago, 2022a, 2022b; Perez, et al., 2023; Segalla, 2023).

In fact, as we noted earlier, the exploding range of possibilities rapidly becomes irreducibly complex, as implied by Huff in his 2023 interview with Lyons. The difficulty, as he explicitly said, makes

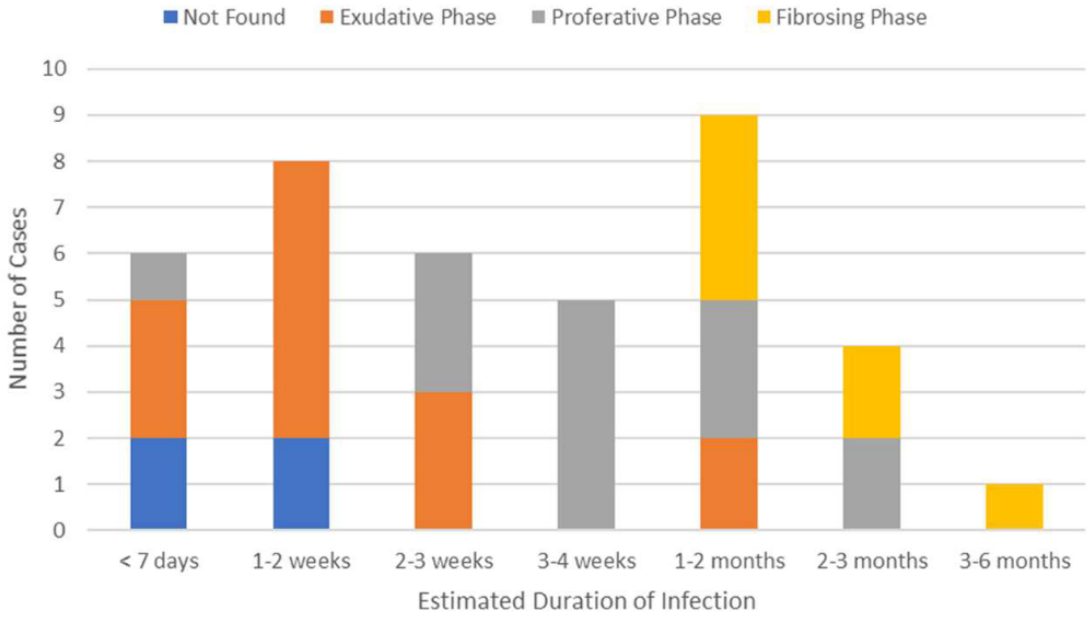


Figure 3. This is "Extended Data Figure 5" from Chertow et al. (2021), "*SARS-CoV-2 infection and persistence throughout the human body and brain* [Preprint]" https://doi.org/10.21203/rs.3.rs-1139035/v1 showing the "temporal association of diffuse alveolar damage in patients dying from COVID-19". The figure shows relatively early appearance of the "initial exudative phase of diffuse alveolar damage, while patients dying after prolonged illness are more likely to show organizing or fibrosing stages" (lines 839-843). Adapted and reprinted here as permitted by their Creative Commons 4.0 license.

government sponsoring of "directed evolution"/"gain of function" research for the purpose of predicting, preparing for, and heading off future pandemics before they happen, a special form of self-deception masquerading as thoughtfulness, as if the officials funding the research really believe it might work although they must know that it is a gamble guaranteed to lose every time it is attempted. The exponentially exploding combinatory possibilities in biosignaling systems

progressing upward from nucleotides to amino acids to proteins, organelles, cells, tissues, and organ systems shows all the claims by the Department of Defense about predicting pandemics in advance in order to get prepared to head them off with ready-made "vaccines" to be ludicrous. The proposition of the Department of Defense requires the acceptance of mathematical operations that amount to something like dividing a measured quantity by zero, or multiplying a real mass by infinity.

What Could Go Wrong?

In this paper we explore some of the ways for things to go wrong. Logically, commandeering the body's ribosomal protein producing systems in order to trick them into manufacturing billions of SARS-CoV-2 spike proteins seems exceedingly unlikely to enhance health and well-being while the probability that it will cause disorder, disease, and death is a virtual algebraic certainty. If the billions of synthetic "mRNAs" injected in every dose of BNT162b2, for example, are strategically cloaked so they will not be spotted out as "foreign, non-self" pathogens, can such deceptions lead to good outcomes?

Lies Do Not Fit the Context

For reasons explained in detail elsewhere with mathematical proofs that have stood the test of time in their minutest details (Peirce, 1897; Tarski, 1941, 1956; Sowa, 2011, 2017; Oller, 2014), in any meaningful sign system whatsoever, the formal structure of a deception is such that it artfully pretends to be a truthful, valid, and faithful representation of whatever facts it purports to represent (Oller, 2014). However, what qualifies all such representations as lies, is the strictly formal fact that they do not validly fit within all the formal constraints of whatever context into which they may be deliberately injected. Their sole reason for being is the specific intention of deceiving one or all interpreters concerning the material facts they purport to represent but do not quite report in all the requisite material details. It is important to note, however, that if the details of any false representation could be corrected so that it might come to fit all the formal requirements of the larger context in which it is contained in space and time, it would no longer be a lie. It would be transformed into a true narrative representation (TNR). Thus, the distinctiveness of lies in general is a strictly formal, logicomathematical fact. Opinions have no power to change or impact such formal relations in the slightest degree. Voting simply does not count when the questions are about ordinary TNRs as contrasted with fictions, errors, lies, nonsense, or completely erased representations.

Every XNA Coding for SARS-CoV-2 Spike Protein Is a Pack of Deceptions

In the instance of the synthetic XNA coding for the SARS-CoV-2 spike protein, every instance introduced in, say, the Pfizer BNT162b2 injectable, is supposed to consist of an exact replica of a string of pseudo-codons pretending to be ordinary self-produced mRNA authored by the body's native nuclear DNA.[10] In that respect each one of them is a lie to begin with. The SARS-CoV-2

[10] The exactness and completeness of the XNA string in every single instance, however, depends on the quality of the process by which the Pfizer (Moderna, AstraZeneca, or other genetically engineered product) has been produced. Here we concentrate on the strings supposedly incorporated into the XNA (the fake "mRNA") to produce a particular exact sequence of amino acids in the SARS-CoV-2 spike protein (also a fake, because the ones made by the XNA in the "vaccines" are only a small part of the full SARS-CoV-2 spike protein and do not represent the entire SARS-CoV-2 virus which they are designed to make the body think they actually are). The difference, as C. S. Peirce elegantly explained, is

virus itself, pretending to belong inside the cells, tissues, and organ systems of any human body is already a lie before it is transformed into any genetically modified XNA. However, when it is transformed into its XNA shape, coding for the 1273 amino acids of just the SARS-CoV-2 spike protein[11], it is modified to contain many additional lies embedded within itself. By simple combinatory logic we can show why those lies, billions of them in each dose of every genetically engineered injectable (Pfizer 13.1 billion, Moderna 13.1 billion, AstraZeneca 50 billion; according to Fleming, 2021, p. 99), must tend to increase exponentially over time into a multitude of multitudes of lies that rapidly reach a level of irreducible complexity (generalizing from proofs by Gregory Chaitin, 2004, 2007). Unless all of those lies can be expunged, corrected, or at least quarantined and ignored by the body's biosignaling systems, they must lead toward disorders, diseases, and the eventual catastrophic breakdown of the body's biosignaling systems which is death.

Bad Things Happen When Lies Are Mistaken for TNRs

The first layer of deception in the COVID-19 XNAs consists in the fact that the SARS-CoV-2 virus itself does not belong inside the human body. It is an invasive viral disease agent. Therefore, to get the body to regard any single instance of such an XNA as a native mRNA to deliver to its own ribosomal systems is a step toward disorder and disease. This level of deception, incidentally, seems to be the one that best qualifies the COVID-19 injectables as "vaccines" because all traditional vaccines prior to the COVID era, without any exceptions that we know of, aim to present some disease agent, or part of one, to the body in such a way as to make the maintenance-repair-defense systems think the body is being invaded by whatever the targeted agent(s) of the vaccine may be.[12] In that way, because of the homology between the targeted agent(s), and the active components in the vaccine whatever they may be, the body's communication systems are supposed to be trained up to deal more efficiently in the future with any real invasion by one or many targeted disease agents. The whole exercise is something like military training for genuine warfare where the training itself (vaccination) aims to be rigorous, may involve some risk of injury or even death, but is, hopefully,

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that between being something and merely representing something (in this instance, every instance of the XNA, perfectly well-formed by the manufacturers or not, is always pretending to be something that it is not. Moreover, it also pretends to represent something else, a normal bodily protein, when in fact, if it works as its designers intend for it to work, it represents a part of the supposed COVID-19 disease causing SARS-CoV-2 spike protein. Deceptions in the billions are involved from the beginning and can only be multiplied as the intended process moves forward across time. The question that arises is not whether corruption will occur but how severe that corruption can be expected to become.

[11] The full genome of the SARS-CoV-2 virus is known to consist of about 29,870 base pairs; according to a strain close to the alpha Wuhan variant isolated in northern Germany by Pfefferle et al. (2020).

[12] This stratagem defines what Jenner thought he had discovered with cowpox rendering people immune to smallpox. Again, it was a case of homology leading to mistaken identification. If indeed the smallpox virus is defeated by antibodies built to defeat cowpox, the deception may have had benefits. On the other hand, during the period when the CDC claims smallpox was eradicated, many other relevant changes in hygiene, waste disposal, refrigeration of food stuffs, and so forth were also accounting for huge reductions in disease across the board, smallpox being just one among many diseases that were waning. Moreover, contrary to the popular mythology of vaccination, relevant research specifically contrasting "smallpox" vaccinated populations against unvaccinated populations showed that the smallpox vaccine of Jenner was the source of the only pandemic outbreaks of smallpox during the time frame after his supposed prophylactic remedy was widely deployed.

much more apt to keep trainees alive during genuine warfare than if they had skipped the training exercises (i.e., if they had not been vaccinated).

COVID-19 "Vaccines" Commandeer Critical Communication Systems

The XNA strings of pseudo-codons in the COVID-19 injectables involve additional layers of deception with hoped-for hypothetical outcomes that cannot be guaranteed in advance by any stretch of the imagination. Among the deceptions that have been acknowledged in the lipid nanoparticle payload of the Pfizer BNT162b2 product, for instance, are the 728 N1-methylpseudouridine substitutions for the native uridines of the SARS-CoV-2 spike protein in every well-formed XNA contained in the injectable. Each of them is also a pretender, like the larger sequence in which it is contained. Each XNA is a lie containing a whole pack of additional lies. They are, in fact, lies multiplied by the number of XNAs pretending to be self-produced mRNAs coming from the body's own native DNA, and each well-formed XNA being multiplied by its own 728 embedded N1-methylpseudouridine substitutions for the native uridines that are no longer present in the pretending "mRNA" of the SARS-CoV-2 spike protein.[13] Even if each of those XNAs were manufactured to perfection (though we know they are not[14]), the lies they represent from the start, and the ones they contain within them, all of them designed to deceive the body's native maintenance-repair-defense systems, are incommensurably more likely to cause harm downstream than they are to bring about health and well-being (Seneff & Nigh, 2021; Seneff et al., 2022).

Methods and Results

In this section our purpose is to present some analyses of clinical data emerging from the ongoing worldwide COVID-19 experiment. Although we did not design the experiment, we are in as good a position as any researchers to examine and analyze the emerging clinical findings. In our analysis, we choose to focus attention on the most reliable data accessible in the US concerning one of the larger and one of the more vaccinated populations in the world. We are not suggesting that the findings here will generalize perfectly to the whole world, but the size of the US population and the numbers of deaths occurring over the time frame to be examined closely must nonetheless be indicative of what is happening in the larger worldwide experiment, especially in the developed/industrialized nations most heavily impacted by the injectables. Certainly, there is no reason to expect that the

[13] Each XNA, according to Nance and Meier (2021) who credit the research of Sahin, Karikó, & Türeci (2014), deploys its 728 contained lies to cloak itself from the body's maintenance-repair-defense systems while the whole string purports to be ordinary self-produced mRNA on its way to a ribosomal system to produce the pretend / fake self-protein which it encodes. However, Karikó's research must have begun sometime prior to her 2004 publication about pseudouridine (Karikó, Ni, et al., 2004).

[14] Documents recently obtained through Freedom of Information Act filings and other reliable sources show that none of the COVID-19 injectables are manufactured anywhere close to perfection (Gutschi, 2022; Latypova, 2022b; Segalla, 2023; Banoun, 2023). The shoddy manufacturing was apparently only one of the consequences of unregulated creation of the BNT162b2 product and its counterparts produced by other pharmaceutical companies.

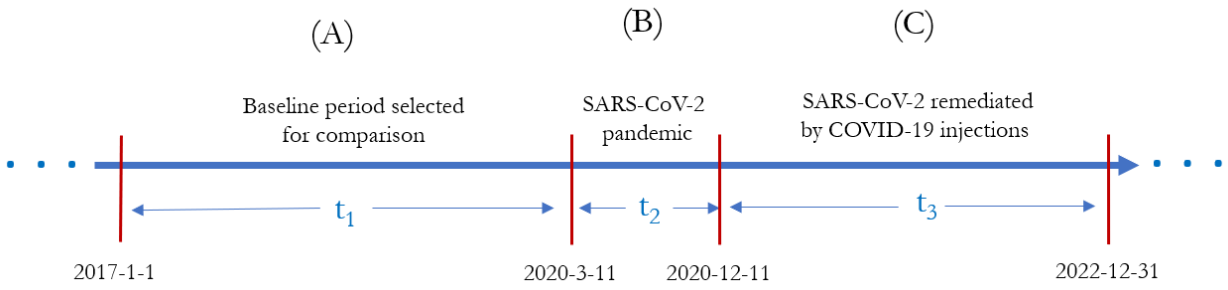

Figure 4. Timeline showing segments to be contrasted in the Results section of this paper. (A) Segment t_1 begins January 1, 2017 and ends 167 weeks later with the announcement of the onset of the worldwide pandemic by Tedros A. Ghebreyesus, Director-General of the World Health Organization on March 11, 2020. The reason for including that segment is to provide a baseline of all-cause mortality against which to compare the two phases of the worldwide experimental pandemic in phases one and two as represented in time segments t_2 and t_3.

COVID-19 "vaccines" should be less harmful, safer, more efficacious, etc., in other parts of the world than they are in the country that allegedly spends more than any other on "health" care (Masters, 2009; Belk & Belk, 2020). Also, though we would like to be able to do a more complete analysis looking at roughly the same time segments leading up to and including both phases of the ongoing experiment for the whole world, in seeking to put together comparable data for all the world population we found that the quality and coverage is sadly deficient. The World Health Organization claims to have worldwide data but we found it to be too sparse for the purposes we had in mind. Therefore, we will concentrate on data from checked sources for the US to establish a baseline and then to evaluate all-cause mortality during both phases of the ongoing pandemic experiment.

The timeline of interest throughout the remainder of this paper is the one shown in Figure 4. Our focus is on the three distinct time segments marked off between 2017-1-1 (year-month-day) and 2022-12-31. Segment (A), t_1, serves to find a baseline (average weekly rate) of all-cause mortality against with compare segments (B), t_2, and (C), t_3. (B), t_2, is the time from the onset of the pandemic up to the introduction of the COVID-19 injectables on December 14, 2020. Time segment (C), t_3, begins when the COVID-19 injectables are introduced to quench the pandemic. Given that our criterion for comparing the time segments in question is all-cause mortality as reported to the US Centers for Disease Control, we have not included the first three months of 2023 in order to be relatively certain that the deaths reported during the compared time segments are fully up-to-date.[15] While the primary symptoms of interest are the abnormal clotting observed in both living and dead persons, we apply the standard of all-cause mortality to test the hypotheses to be detailed below. All those hypotheses are tested specifically against all-cause mortality, adjusted to the standard of deaths

[15] The CDC warns users of the Wonder site that provisional data "are lagged by an average of 1–2 weeks". Therefore, to make sure the comparisons of all-cause mortality in each of the three time segments are comparable, all of the weeks of 2023 up to the time of this writing are excluded from the analyses reported below.

per one hundred thousand of the persons who were alive during each respective time segment. For population estimates, we have relied on those supplied by the US Census Bureau.[16]

Phase One of the Worldwide Pandemic-Experiment

The first phase, was the "gain-of-function"/"directed evolution" (artificially speeded up) production of the SARS-CoV-2 virus itself. It is, in fact, unlikely that any such virus would have ever emerged by itself if left to natural causes — i.e., without human intervention and technology. We set aside the question of whether the virus was either deliberately or accidentally released into the world population from an epicenter in Wuhan, Hubei Province of China leading to the COVID-19 "pandemic". Regardless, according to Huff and Lyons (2023), the announced pandemic[17] which marked the beginning of the pandemic experiment, may have begun some days or possibly weeks prior to the opening of the pre-Olympic 2019 CISM [Conseil Internationale du Sports Militaire] Military World Games on October 11, 2019. If the reports from athletes are to be trusted, it seems the city of Wuhan was already in some kind of "lockdown" mode with Chinese authorities wearing masks and hazmat suits keeping the athletes quarantined to the "Olympic type" village prepared for them before the games were officially opened. Judging from the fact that some, perhaps many, of the 9,308 athletes who competed (Wikipedia, 2023) returned home with the COVID-19 disease, it seems likely that the pandemic began in Wuhan early in September 2019 but not later than the first week in October 2019. Otherwise, given the approximate 6-day incubation period judging from the Chinese data (Wassie et al., 2020), it seems the virus would have had insufficient time to spread to the athletes and infect some of them prior to the conclusion of the games on October 27, 2019.

Given the foregoing facts, it may be supposed that the first stage of the worldwide experimental pandemic began near the middle or end of September, 2019. Huff supposes, therefore, that the entry of the SARS-CoV-2 virus into the human population was known to insiders prior to the convening of "Event 201" at Johns Hopkins University on October 18, 2019. He notes that the convocation itself featured various representatives of key entities, agencies, and individual stakeholders to the "gain-of-function" research that led to the accidental escape, or the intentional release, whichever it may have been. What is well-known by now and not a subject of any reasonable debate is that SARS-CoV-2 was a laboratory produced, weaponized virus (see Fleming, 2021; also Huff, 2022; Huff & Lyons, 2023). Therefore, it is reasonable to think of the propagation in human subjects as a bioweapons experiment, whether intentional or accidental. Whereas we do not claim any credit or responsibility for the design of the experimental SARS-CoV-2 weaponized virus, we have no reason whatever to doubt the documentary evidence showing that the "virus" produced was a product of "gain-of-function"/"directed evolution" research. It was developed over more than

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[16] Other sources were consulted, such as Our World in Data in addition to the CDC Wonder system, but the Wonder system provided consistent population estimates only through 2016, whereas the US Census Bureau estimates are based on the same system throughout the timeline of interest.

[17] On January 9,2023, an interview between Clayton Morris and Alexandra (Sasha) Latypova revealed on the basis of documents obtained by following the requirements of the Freedom of Information Act that the entire "pandemic" (as suggested also by Huff, 2022; Huff & Lyons, 2023) was a form of theater where the actors on stage, e.g., the would-be poster-child, a little 13 year-old girl who was so severely injured in the "clinical trials" that the segment that was supposed to be used at the Super Bowl LVII on February 12, 2023 was pulled. Critical documentary evidence from validated sources are discussed here.

two decades with the involvement of multiple teams of researchers in the US and China (Fleming, 2021; Huff, 2022). The main basis for the SARS-CoV-2 infective agent, we can say without fear of being contradicted, was a deliberately constructed experimental product developed in various bioweapons laboratories.

Phase Two of the Worldwide Pandemic Experiment

The second phase of the pandemic experiment, involved the advanced preparation, beginning about three decades before the COVID-19 "pandemic" by ostensibly trying to produce various remedial COVID-19 "genetic therapies" for the possible future pandemic. These would be presented to the public as "warp-speed produced vaccines" but we now know they had been under development and were already at an advanced design stage before the "pandemic" was announced to the public worldwide. Much of this has come from Huff and Lyons (2023) and from other sources that Huff has validated with his own firsthand insider information backed up by ample documentation from sources we have already cited.

The official start of the second phase of the worldwide experiment, at any rate its public part, began with the distribution of genetic therapies, marketed as a whole new generation of "vaccines" promising to prevent severe COVID-19 disease and to reduce deaths in recipients (as documented extensively by Kennedy, 2021). That development, we now know, thanks to discoveries from the Freedom of Information Act, and from investigations of patents and contracts underlying them, showing the government funding of "gain-of-function" research over many years (see Latypova, 2022c; Morris & Latypova, 2023) was owed to the US Department of Defense (see Huff, 2022). It was grounded in sponsored research by Karikó and colleagues dating back more than a decade earlier than 2013 (Karikó, Ni, et al., 2004; Karikó, Muramatsu, et al., 2008).

The documentation (Fleming, 2021; Huff, 2022; Huff & Lyons, 2023) shows, that the COVID-19 genetic therapies that were supposedly rushed into production to halt the pandemic and return the whole world to normalcy were actually being developed decades before the World Health Organization announced on March 11, 2020 that a worldwide "pandemic" was underway. In fact, documents that have recently come to light show that hundreds of millions of doses of the genetic remedies for the "pandemic" were already in production by December, 2019 (Huff & Lyons, 2023), well before the WHO even announced the existence of any "pandemic". Perhaps the most damning document of all is one showing that the US Department of Defense had issued a subcontract dated November 12, 2019 to Labyrinth Global Health, Inc., specifically calling for "COVID-19 research" a full month before the supposed virus was even named (Reese, 2023), and four months prior to the lockdown that occurred in the US after the March 11, 2020 announcement by the WHO that a worldwide pandemic was underway. The contract in question was part of a much larger one with Black and Veatch — a company deeply tied to the US military from World War I forward, but especially during and following the Manhattan Project of World War II ("Black & Veatch", 2023) leading to the nuclear bombs dropped on Hiroshima and Nagasaki. Until the penetration of biology to the nanometric level of molecules, atoms, and beyond, the military industrial entities of the world seemed to direct public fear and attention to nuclear weapons. Now, the world's worst nightmares seem to be about biological threats and the transhumanist revolution that seems to be looming on

the horizon (see, for instance, Bostrom, 2003, 2005; Broudy & Kyrie, 2021; Kyrie & Broudy, 2022a, 2022b; and their references).

Hypotheses to Be Tested Using Data from Emerging Clinical Outcomes

Regarding the still ongoing two-phase worldwide pandemic experiment, we seek to test three alternative hypotheses with respect to the abnormal clotting phenomena and the associated disease conditions that were already emerging in phase one of the ongoing experiment. We draw the reasonable inference that the "fibrosing" pointed out in autopsies of dead victims of COVID-19 disease by Chertow et al. (2021; see Figure 3 above), together with the diffuse distribution of the SARS-CoV-2 virus not only in the lungs, liver, vasculatory system, kidneys, heart tissue, and the brain, in all probability, must be involved in causing the cascading series of biosignaling injuries leading to whatever increase in all-cause mortality has actually occurred from t_1 to the remaining segments of the time frame spelled out in Figure 4.

From here forward we keep the SARS-CoV-2 spike protein and its genetically engineered versions in the COVID-19 "vaccines" in the background until we come to our **Discussion** and **Conclusions** sections. All the while, however, we also have in mind, as Segalla (2023; see his discussion in English here) has pointed out, that the lipid nanoparticles used to deliver whatever unannounced ingredients the BNT162b2 and Moderna injectables may contain, are injurious on their own. Therefore, it would be irresponsible and incautious not to test the alternative hypotheses that we formulate explicitly in this section of our paper.

The null hypotheses concerning the mean rate, μ, of all-cause mortality per 100,000 population for each of the time segments of interest, if there were no impact from the two-phase worldwide pandemic experiment, can be summed up as follows:

$$H_0: \mu_{t1} = \mu_{t2} = \mu_{t3}$$

However, there are three alternative hypotheses to be tested. The first alternative is the unsurprising expectation that the standardized weekly pre-pandemic mean of all-cause mortality per 100,000 persons in the US population distributed over a comparable time frame prior to the worldwide exposure to SARS-CoV-2 should be less than the standardized weekly mean during the pandemic:

$$H_{A1}: \mu_{t1} < \mu_{t2}, \text{ at an } \alpha < 0.0001$$

We set a stringent significance (α) level at $p < 0.0001$ for H_{A1} (and for the subsequent alternative hypotheses) because the stakes are life and death. H_{A1} merely asserts that after the onset of the worldwide pandemic all-cause mortality up to the time when the COVID-19 vaccines were introduced, SARS-CoV-2 and whatever consequences the declared pandemic brought with it (e.g., lockdowns, social distancing, masks, increased fear and stress, suicides of desperation, loss of life from comorbidities, businesses that failed, etc.) must have logically caused an increase in all-cause mortality above the previous baseline before the announcement of the pandemic.[18]

[18] Other factors that are literally coming to light and the electro-magnetic frequnecies at distinct wavelengths that can, like the microwaves in everyone's kitchen, be tuned to particular molecular entities from water molecules to virions, bacteria, and brain cells. Certain metals and carbon-based composites (Jernigan & Joseph, 2005; Jernigan et al. 2021; Yanowitz, 2022) have been implicated along with the strange abnormal clots discussed above in this paper.

Next, a slightly more interesting alternative hypothesis concerns the downturn in all-cause mortality as people in the US were supposedly benefiting — according to the government-approved CDC, Department of Defense, etc., narrative — from 1 to 7 doses of the COVID-19 injectables. According to promoters of the injectables, the administration of hundreds of millions of doses in the US should have caused a return of all-cause-mortality in the US population toward (if not all the way back to) the standardized weekly mean of all-cause mortality at the μ_{t1} baseline before the pandemic began in t_2. H_{A2} takes into consideration the difference between the baseline all-cause mortality mean μ_{t1} prior to the pandemic minus the mean μ_{t2} in order to estimate what should be expected once the curative/preventative COVID-19 vaccines were widely distributed during t_3. H_{A2} takes account of the expectation/promise that the COVID-19 vaccines would move the mean of all-cause mortality, after they are injected into more than half the world population and from 67% to 79% of the US population, back in the direction of the pre-pandemic baseline of t_1. According to the public narrative the whole basis for creating the COVID-19 experimental "vaccines", and for injecting more than 13.2 billion doses of them into more than 5.1 billion people worldwide at a cost of trillions of dollars (Pharmaceutical Technology, 2023) was to stop the pandemic attributed to the spike protein of the SARS-CoV-2 virus. More specifically, the genetic therapies provided in the experimental COVID-19 "vaccines" were intended to commandeer the ribosomal systems of recipients causing them to produce the offending SARS-CoV-2 spike protein on the theory that the immune systems of recipients would attack the virus and thus return impacted populations to the neighborhood of the former baseline of all-cause mortality during the pre-pandemic period often referred to as "normalcy" in the mainstream media (Economist Group, 2021; Administration for Community Living, 2022; Brennan, 2023). With that in mind, H_{A2} can best be stated as follows:

$$H_{A2}: (\mu_{t3} - (\mu_{t2} - \mu_{t1})) \approx \mu_{t1}, \text{ at an } \alpha < 0.0001$$

There is one additional alternative hypothesis, actually consisting of a series contained within the scope of H_{A2} provided it should turn out to be true. This latter series, which we loosely refer to as H_{A3}, follows from the assumption that multiple doses of COVID-19 injectables should be more effective in returning the recipient groups, all else being equal, to the mean all-cause mortality before the two-phase experiment began. If so, the following series of inequalities should be true across the board where the greater than symbol ">" is taken to mean that all-cause mortality should decrease from zero doses to the *n*th booster — more doses working better than fewer doses in returning the population toward (if not to) normalcy:

$$H_{A3}: 0 \text{ dose} > 1 \text{ dose } \mu_{t3} > 2 \text{ dose } \mu_{t3} > 3 \text{ dose } \mu_{t3} \ldots > 7 \text{ dose } \mu_{t3}$$

In other words, in accord with the mainstream narrative, H_{A3} asserts that, all else being equal, significant increases in longevity (lowering of all-cause-mortality) should follow with each additional dose of a COVID-19 vaccine received by any randomly selected sample of persons in the population. However, based on our review of the background literature on abnormal clotting phenomena in the first part of this paper, there is a completely opposite version of H_{A3} in which the symbol ">" is read to mean that each additional dose beyond the first will increase all-cause mortality for any random sample of the population (i.e., will reduce the time remaining to live) making recipients worse off instead of better off — as Seneff and Nigh (2021) and also Seneff, et al. (2022) have been arguing. In what follows we will rigorously test both of those versions of the sequence, the one that favors the mainstream narrative and the one that refutes it.

RESULTS: CLINICAL OUTCOMES OF THE PANDEMIC EXPERIMENT

For any given segment of time, the underlying formula for standardized reporting of all-cause mortality is the following:

$$(all\ deaths/target\ *\ population)\ \text{X}\ 100{,}000 = all\ cause\ mortality\ per\ hundred\ thousand\ people$$

The critical data points in the formula consist of the ratio inside the parentheses at the left side. Deaths need to be accurately recorded, and the size of the population during the time frame at issue must also be estimated with reasonable accuracy.

In the first part of the analysis that follows, for population estimates we have relied on the US Census Bureau for each of the segments of time in question (see footnote 11), and for the record of deaths we have used data from the Centers for Disease Control and Prrevention (2023). Multiplying the result of the quantity in the parentheses on the left side of the equation times 100,000 merely converts the ratio to a standard form enabling comparisons, say, between all-cause mortality across populations of different sizes, for instance, the whole US population compared against a smaller or larger population, component of the whole population, or a randomly selected sampler of persons within the larger population or some subcomponent of it. In what follows we look first to the whole US population to test H_{A1} and H_{A2}, and then, to test $H_{A3,}$ we rely on a sample of Medicare participants who received only one dose of COVID-19 vaccine to compare with random samples drawn from the state of Connecticut who received none or from 2 to 5 doses of COVID-19 vaccine.

Column (F) in Table 2 reports the mean of weekly all-cause mortality for the whole US population (as recorded by the CDC during each of the time periods specified in column A) — where rows 5, 6, and 7 correspond to data from the entire US population for t_1, t_2, and t_3 of Figure 4. To make the weekly rate more interpretable, column (B) in Table 2 converts the raw weekly mean number of deaths in each time segment to a standardized weekly mean per 100,000 persons. It is worth noting that the US population from week-to-week during the entire time period segmented into three parts in Figure 4 — pre-pandemic baseline period (t_1), pandemic period (t_2), and experimental vaccine administration period (t_3) — must consist in a large proportion of instances of the very same individuals. In fact, they are very nearly the same people in the time segments on either side of t_2. (excepting those who died previously, or immigrated into the US, or were born during the time frame).

According to the US Census Bureau's Population Clock (on March 20, 2023 shown just below as Figure 5), the population in the US is increasing by one newborn child every 9 seconds on the average, and by one immigrant every 32 seconds. At the same time the population is being decreased by one death every 10 seconds. The absolute difference in the population from one time segment to the next, therefore, amounts to approximately 2.37% of the total population from year-to-year as seen in Table 3 (on the following landscape page). This means that from year-to-year, we can estimate that about 97.6% of the people are *the same individuals as those who were present in the preceding year*. As a result, the comparisons of greatest interest with respect to the hypotheses stated earlier come very close to meeting the required assumptions for a repeated-measures design except for the fact that the people who end up dead can only die once. Nevertheless, the exposure to SARS-CoV-2 during t_2 happened to about 97.6% of the people who were present during t_1 and who will still be

Table 2
All-Cause Mortality in the United States Annualized in Each of the Various Time Segments Leading up to and Including the Worldwide Pandemic Experiment inRows (6) and (7)

(A) Time Segment (Year-Month-Day)	(B) All-Cause Mortality per 100,000 People in the USA	(C) Total Unadjusted All-Cause Mortality (Raw) for Time Segment	(D) Population During Time Segment †	(E) Total All-Cause Mortality during the Time Segment Made Proportional to a 52 Week Year ‡	(F) Mean All-Cause Mortality per Week for the Time Segment in Question
(1) 2011 thru 2015 all weeks	821.5	12,994,778	1,581,910,672	2,598,956	49,980
(2) 2016 all weeks	849.3	2,744,248	323,127,513	2,744,248	52,774
(3) 2017 all weeks	864.5	2,810,988	325,147,121	2,810,988	54,057
(4) 2018 all weeks	867.8	2,839,074	327,167,434	2,839,074	54,598
(5) 2019 all weeks thru week 11 of 2020	879.1	3,505,841	329,158,518	2,893,710	54,826
(6) 2020-3-21 thru 2020-12-5 Pandemic before Any COVID-19 Vaccines)	1011.8	2,451,254	331,511,512	3,354,348	64,507
(7) 2020-12-12 thru 2022-12-31 Pandemic After COVID-19 Vaccines	1023.7	7,072,106	332,612,403	3,405,088	65,482

† In row 1 of this column, the CDC summed the population estimate for the 5 years at its Wonder Bridged-Race Population Estimates website. Their estimate for those 5 years agrees closely with the US Census Bureau total "resident" US population estimate at 1,582,997,300, based on the July 1 date for each year. Given that the July 1 date falls at the middle of each calendar year, and is the evident standard applied by the CDC in calculating annualized all-cause mortality for the US population, in rows 2-6 we use the mid-point estimates from the US Census Bureau for each of the time segments in question.

‡ Here in data column 4, if the time segment is greater than a full year (as in rows 1, 4, and 6) or less than a full years (as in row 5 marking the 38 weeks of the experimental pandemic prior to the administration of any COVID-19 vaccines), the CDC weekly average all-cause mortality as reported in March 2023 (column 5) is multiplied by 52 to obtain an annulaized (standard) rate for the whole of the time segment in question. Then, to obtain the crucial all-cause mortality per million people (column 1), so the comparisons are exactly as fair as the accuracy of the US CDC and Census Bureau data allows them to be, we simply divide the total unadjusted all-cause mortality in column 3 by the median population estimated by the US Census Bureau for the time frame in question to obtain the criterial annualized all-cause mortality for the time segment in question as reported in in column 1.

present during t_3. As a logical consequence it follows that we are in each of the time periods at issue largely comparing apples with apples as the expression goes. Approximately 97.6% of the people who came into the experimental pandemic during t_2 remained in place for whatever challenges or benefits the COVID-19 injections might add into the mix during time segment t_3. It follows that the near homogeneity of the population variance should only be affected by environmental and/or governmental changes impacting almost a large percentage, or all, of the population because the affected population itself consists of about 97.6% the self-same individuals for the segments on either side of the middle segment, t_2, consisting of phase-one of the experimental pandemic. Except for the fact that people can only die once, the transition from phase-one to phase-two conforms to the requirements of a repeated-measures design in which members of a population are compared only against themselves with respect to some treatment such as the introduction of the virus in the transition from t_1 to t_2 or the introduction of the COVID-19 injections at the transition from t_2 to t_3. Otherwise, all else must remain approximately the same across the time segments — more particularly, except for a relatively small percentage of persons who are new to the population or who have left due to migration or death, the population across the three time segments is 97.6% the same as shown in Table 3.

Figure 5. Components of population change according to the US Census Bureau and its World Population Clock.

It is also known with mathematical certainty from the central limit theorem (Pólya, 1920; Le Cam, 1986) that the sampling distribution for sizes above about 25 individuals will be normally distributed and have a standard deviation equal approximately to the square root of the standard deviation of any given actual sample of that size (i.e., the standard error of measurement). When the numbers reach into the tens of thousands the stability of estimates, all else being equal, is assured. The upshot of the numbers in Figure 5 and Table 3 is to say that the statistical estimates of means, variances, and the contrasts needed to test the various hypotheses stated above can be counted on in what follows here for the requisite reliability to definitively answer the implicit and explicit statistical questions posed.

Table 3
Estimating the Proportion of the US Population Remaining the Same in the Three Time Segments of Figure 4.

Estimated births per annum at 1 every 9 seconds	3,504,000
Immigrants per annum at 1 every 32 seconds	985,500
Deaths per annum at 1 every 10 seconds	3,153,600
Estimated total change in persons per annum in the US population	7,643,100
Estimated proportion of the total population that changes each year	2.37%
Estimated proportion of the population remaining the same across all time segments in Figure 4	**97.63%**

Also, the design of the pandemic experiment as laid out in Figure 4 above reduces the typical complexity of CDC and Our World in Data reports (often dividing time segments into weeks, days, or even hours, multiplied by as many as 11 age groups from 0 years to 80+ years) into a simple three segment comparison format that can be easily understood. The crucial components of the design are the independent variables which are well-known and ubiquitous: they consist of (1) the SARS-CoV-2 virus (plus whatever it brought with it, lockdowns, masks, social distancing, fear, stress, business failures, loss of employment, suicides, etc.) during t_2, on the one hand, and of (2) the COVID-19 injections during t_3 on, the other hand. It follows that all the assumptions that need to be met in order to test the various null and alternative hypotheses, indeed are satisfied and the powerful and extraordinarily simple statistic known as Welch's *t*-test (2023) is supremely applicable. It is a generalization of the long-standing Student's *t*-test, but is more robust than a one-way analysis of variance which might be applied to assess the impact of the independent variables. Welch's *t*-test is specifically adapted to problems with samples that have unequal numbers of cases and unequal variances as do all of the contrasts in what follows.

According to the mainstream published medical researche, essentially all the "excess deaths" in the category of all-cause mortality during the period designated in Figure 4 as t_3 must be attributed to SARS-CoV-2 or its variants. However, SARS-CoV-2 (and whatever it brought with it) is the only ubiquitous independent variable in t_2. Similarly, the only ubiquitous independent variable that is added to a substantial majority of the whole population living during t_3 consists of the newly introduced COVID-19 injectables that were administered to between 60 and 79 percent of the entire US population during the time frame at issue. The fact that the COVID-19 "vaccines" were not present at all during t_2 guarantees that whatever beneficial change the injections might have brought to bear must register independently of the purportedly negative impact of the SARS-CoV-2 bioweapon and whatever stress factors it brought with it to the whole population. However, during t_3, because the impact of the injectables is added only to a portion of the population in 1 to 7 doses, independent samples of each of the impacted groups contrasted with those not impacted, should produce a significant and measurable impact. If the mainstream narrative is true, each dose, on the average, all else being held equal, should enhance the longevity of the recipients. If the narrative is false and the injectables are doing harm, each additional dose should increase all-cause mortality in the impacted group. In fact, if the mainstream narrative about returning the whole population to "normalcy" is correct, the mean all-cause mortality expressed as μ_{t3} ought to be about as much less than μ_{t2}, as μ_{t1} is than μ_{t2}. If the injectables are working as intended, they should cause a return toward, if not all the way back to, the baseline of all-cause mortality during t_1. At any rate, whatever benefits or injuries hundreds of millions of doses of the COVID-19 injectables brought with them should be measurable and substantial in contrasts of samples from t_2 to t_3. In particular, those people only exposed to SARS-CoV-2 and its accompanying stress factors across both phases of the experimental pandemic, should either be measurably worse off (according the mainstream narrative) or better off according to Seneff et al. and those who regard the COVID-19 injectables as a bad idea.

Alternative Hypothesis One (H_{A1})

With all the foregoing in mind, Table 4 reports Welch's *t*-test examining the predicted contrast between t_1 and t_2. The test applied is the one-tailed variety because SARS-CoV-2 and whatever other

stress factors it brought with it during t_2 can only be expected to increase all-cause mortality. Because there is nothing during the t_1 time frame that is remotely comparable to SARS-CoV-2, the stress factor that differentiates the two time frames (t_1 from t_2) is an independent variable not impacting t_1 at all. Incidentally, the introduction of the stress factors associated with the experimental pandemic in t_2 requires the assumption that the variances across samples from those time frames should be unequal. More particularly, as is confirmed in the analyses to follow, increasing stress on the population being sampled can only be expected to cause greater variability in the all-cause mortality statistic.

Table 4
Two-Sample Welch's *t*-test Contrasting t_2 Against t_1 Assuming Unequal Variances and Testing H_{A1} that the COVID-19 Pandemic Would Significantly Increase All-Cause Mortality in the US

	Pandemic (t_2)	*Baseline All-Cause Mortality (t1)*
Mean	64506.68	54825.77
Variance	33962289	12786896
Observations	38	167
Hypothesized Mean Difference	0	
df	44	
t Stat	9.827899	
P(T<=t) one-tail	5.69E-13	
t Critical one-tail	4.057435	

Looking to the results in the first line of Table 4, the probability that an increase of approximately 9,680.9 deaths could be added to the weekly 54825.77 average from t_1 to get to the weekly average of 64,506.68 deaths by chance during t_2 is estimated at approximately 5.69 in 10^{-13}. In other words, it has virtually zero likelihood of ever occurring by chance. This result suggests that the magnitude of the problems that the weaponized SARS-CoV-2 brought with it were both significant and substantial.

Table 5
Two-Sample Welch's *t*-test Assuming Unequal Variances and Testing H_{A2} that the COVID-19 Injectables in t_3 Would Return the US toward the Pre-Pandemic Level of All-Cause Mortality in the US Making It Substantially Lower than in the Pandemic Period t_2 with No Vaccines Available

	Vaccine Period of the Pandemic (t_3)	*Pandemic without the COVID-19 Vaccines (t_2)*
Mean	65482.46296	64506.68421
Variance	75887381.73	33962289.41
Observations	108	38
Hypothesized Mean Difference	10,000	
df	97	
t Stat	-7.14230086	
P(T<=t) one-tail	8.48 E-11	
t Critical one-tail	3.87	

Such a contrast cannot occur by chance. Therefore, the null hypothesis that $\mu_{t1} = \mu_{t2}$ can be ruled out and H_{A1} that $\mu_{t1} < \mu_{t2}$, at an $\alpha < 0.0001$ must be accepted.

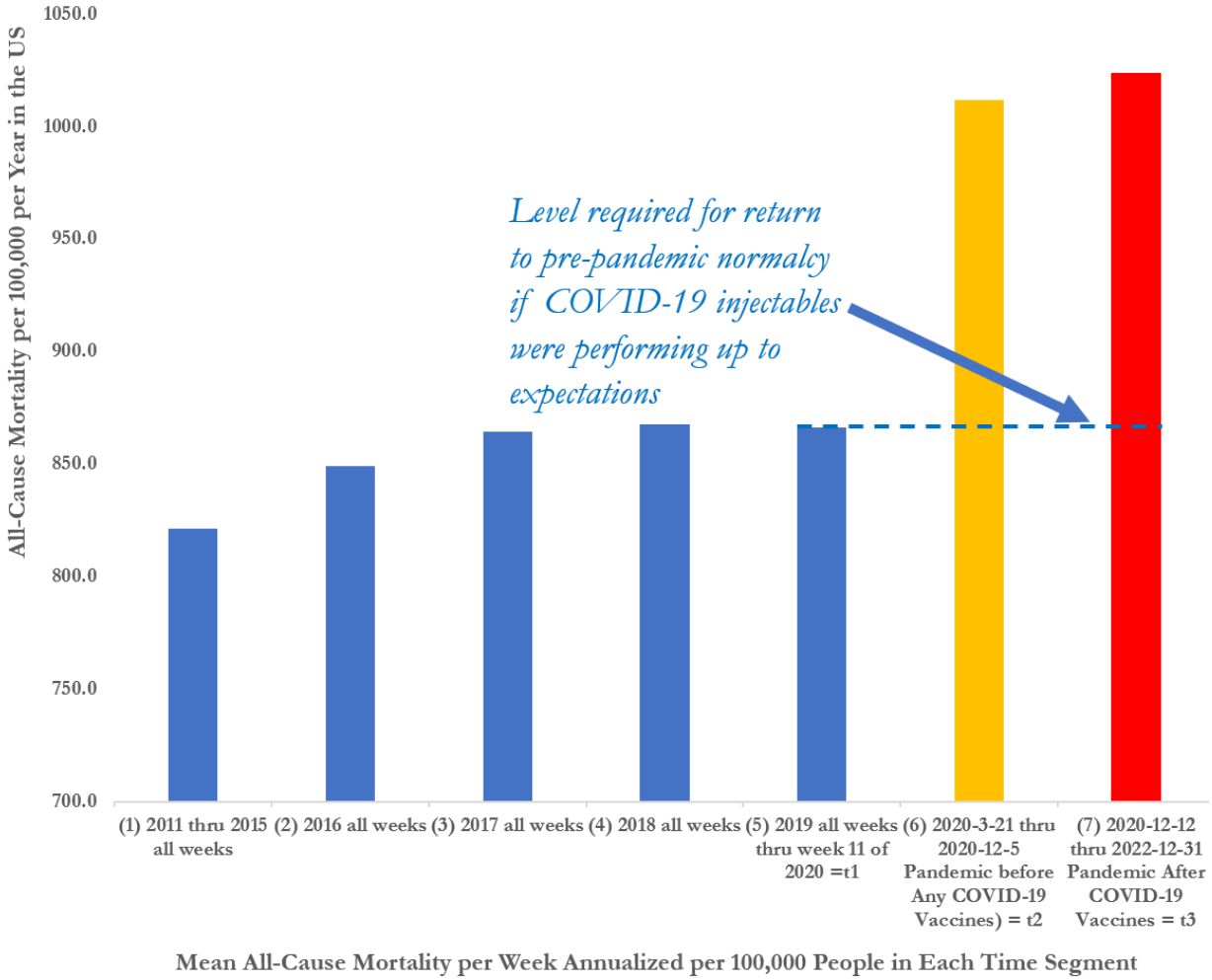

Figure 6. All-cause mortality per 100,000 people in the US appears on the vertical axis whereas the time segments leading up to and including the worldwide pandemic experiment are charted on the horizontal. Blue bars show weekly all-cause mortality per year per 100,000 persons for (1) the years 2011-2015, (2) 2016, (3) 2017, (4) 2018, (5) 2019 through the 11 weeks of 2020 up to the announced onset of the COVID-19 pandemic by the WHO, (6) the official time segment occupied by the pandemic itself up to the time when the vaccines were introduced, and (7) represents the time period combining whatever SARS-CoV-2 variants were still circulating along with the injectables.

Next we consider H_{A2}. Table 5 reports the two-sample Welch's *t*-test. Again, because the directionality and approximate magnitude of the predicted return to normalcy once the COVID-19 injectables were administered to more than half the world, and more than 70 percent of the people in the US, was measured and known prior to the application of this test, Table 5 uses a one-tailed Welch's *t*-test and the results are contrary to the government-sponsored narrative. What we find is that, instead of returning to normalcy with the multi-trillion dollar phase-two of the worldwide

experiment, the COVID-19 injections increased the level of all-cause mortality during the pandemic, t_2, and at a probability level that not only rules out the null variant of H_{A2} but makes the case that the COVID-19 vaccines are doing more harm than good, as predicted some months ago by Seneff and Nigh (2021) and also by Seneff, et al. (2022).

The injectables are doing essentially the same level of harm as the weaponized virus and its stress factors during the pandemic period, t_2, and rather than calming the situation back to (or even towards) normalcy, the injections have elevated all-cause mortality.

Another way to look at the data from Table 5 is offered in Figure 6. If the COVID-19 injectables were working to return the world to pre-pandemic normalcy, we should expect a drop of the red bar at the right-hand side of Figure 6 back to (or at least significantly towards) the level of all-cause mortality during the baseline period defined at t_1. But instead, not only do the injectables perform much like the SARS-CoV-2 virus along with whatever other stress factors it brought with it (lockdowns, fear, etc.), they exceed the level of damage done in the pandemic phase of the experiment by actually increasing the mean all-cause mortality across the entire US population.

Finally, we turn to H_{A3}. In Table 6 we present data from samples of Medicare participants drawn either from the whole population in the US, or from the State of Connecticut. Notably these are people who must usually be 65 years of age or more to enter that program. The data in Table 6 refers to about 157,495 Medicare participants who died on or before December 31, 2022.

To show the generalizability of the Medicare data, it must be noted that, all else being held equal, comorbidities owed to cumulative injuries, diseases, and the like make the Medicare segment of the US population more susceptible to additional stress factors than any younger and healthier segment of the population. In the CDC promoted narrative, it has therefore been argued that the people in the Medicare program should be prioritized to make them first to receive COVID-19 vaccines. Whereas US Medicare participants are more vulnerable to comorbidities, we have evidence that the impact on the COVID-19 injectables generalizes across the board to younger people. In the UK during weeks 34-52 in 2021 and weeks 1-12 in 2022, Oller and Santiago (2022) found a nearly perfect correlation $r = 0.99881$ between all-cause mortality ($N = 31,437$) across all age groups in 10-year increments from 0 to

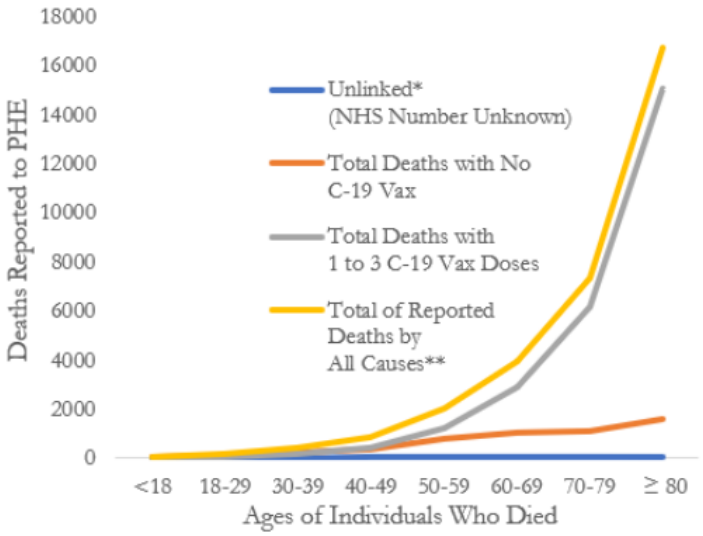

Figure 7. Deaths reported to Public Health England for Weeks 34-52 (excluding week 51) in 2021 and for Weeks 1-12 of 2022 for 16,724 persons who tested positive for COVID-19 within 60 days before they died. The total deaths with 1 to 3 doses of COVID-19 correlated with total deaths reported from all causes at 0.99881.

above 80 for persons who died in a hospital reported to Public Health England and 26,013 of whom died after for 1 to 3 doses of COVID-19 vaccine. Figure 7 graphs the observed correlation in the yellow and gray lines. That almost perfect correlation between vaccine dosage and mortality across all age groups reporting deaths from all causes to Public Health England demonstrates substantial generalizability across similar populations worldwide. Given that the correlation is nearly perfect across all age groups, it follows that more vulnerable people impacted by the pandemic experiment are not exceptional. The differential impact of the pandemic with all its stresses during t_2 as contrasted with t_3 when the COVID-19 injections were added into the mix in hundreds of billions of doses must generalize to the population at large.

To assure the reliability of reporting of relevant deaths to the CDC, we marked the end of t_3 (as shown in Table 2) at December 31, 2022.[19] Given that 665,886,823 doses of Emergency Use Authorized COVID-19 "vaccines"from Johnson&Johnson, Moderna, Novavax, and Pfizer/BioNTech (Pharmaceutical Technology,

Table 6
Days Left-to-Live for Persons on Medicare Who Died After Exposure to SARS-CoV-2 and After Zero to Five Doses of COVID-19 Vaccine

Number of Doses	Mean of Days Left-to-Live	Standard Deviation	Variance	Number of Cases
Zero†	427.84	12.34	121.11	26091
One‡	307.90	186.66	34842.20	108155
Two ¤	247.22	10.60	112.47	14356
Three	198.62	118.62	14071.40	7474
Four	112.43	72.53	5260.18	1211
Five	58.63	51.25	2626.21	207

† The "Zero" group consists of 26,090 Connecticut Medicare participants who were almost certainly exposed to SARS-CoV-2 virus at least by the midpoint of the pandemic, July 27, 2020, but who chose not to accept any COVID-19 vaccinations. The people in this sample nonetheless died before January 1, 2023. However, during the pandemic experiment, Connecticut had 689,572 Medicare participants (HelpAdvisor.com, 2023). Given the greater life-expectancy of the "Zero" dose group, the number of days left-to-live for that group must be substantially under-estimated. Therefore, the contrast in Figure 8 between the "Zero" and "One" groups must be greater than it appears to be there because many more of the "Zero" dose people will have survived into 2023 and beyond, than those who received one or more doses of the COVID-19 injections. Incidentally, the correlation between days to survive and proportion of the population represented in the various Connecticut samples of this table is 0.989. The Medicare particiants seem to have increasingly perceived the consequences of taking the shots as the pandemic experiment progressed.

‡ The "One" dose group in the Connecticut data seemed to omit people who received a free vaccination outside the Medicare system. This inference is based on the fact that 6,366 more people were reported as having received "Two" doses (14356) than were reported as receiving only "One" (7911). To correct that logical problem, for the data charted in Figure 7, we calculateed mean days left-to-live for the 108,155 Medicare cases from the whole US who died on or before December 31, 2022. These records were available to us in the same dataset thanks to Steve Kirsch (2023a, 2023b).

¤ As noted, in this Connecticut Medicare dataset nearly twice as many people were reported as receiving a second dose than who were recorded as receiving a first.

[19] The early termination of our reckoning to compare the three time periods of the two phase experiment was on account of the lag between death and reporting to the CDC. We were able to check the weekly deaths recorded in two distinct databases on a week by week basis and the records we are using in this report from the CDC seem to be reliable.

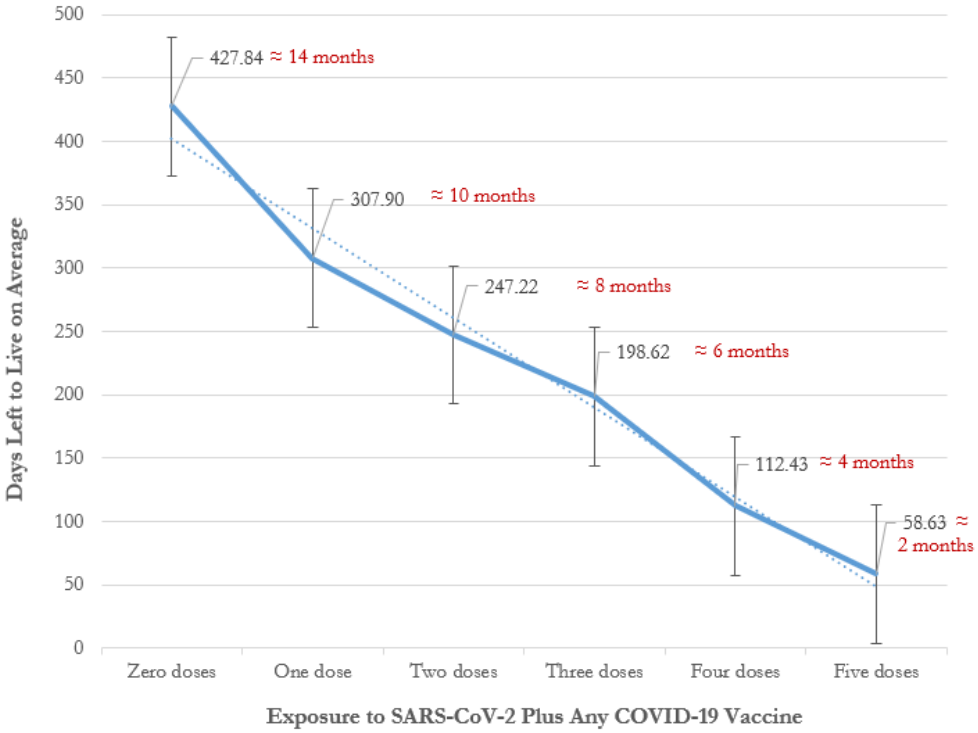

Figure 8. Average number of days left-to-live for persons who died before January 1, 2023 and who were exposed to both the SARS-CoV-2 virus and stresses of the pandemic (t_2) plus whatever number of doses of the COVID-19 vaccine they received during t_3.

March 11, 2023) were administered to the entire US population during the 814 days from December 14, 2020 to December 31, 2022, we should be able to find a measurable effect from t_2 to t_3 attributable exclusively to the COVID-19 injectables. The effect of the experimental SARS-CoV-2 virus, stress, lockdowns, etc. during t_2 should be markedly impacted by an independent effect of the COVID-19 injectables administered only in t_3. True, other factors during t_3 may interact with the billions of injections, but no such interaction is possible in t_2, so any interaction must also show up in t_3 as a distinct (orthogonal, completely independent, contribution of the COVID-19 injections). This follows with irrefutable logic on account of the fact that the population of people impacted contains 97.6% of the same individuals from the prior time period. They are being compared only against themselves. Therefore, the other factors in either time frame must be as either equivalent or, if not, as impacting the same people across the time segments so that the only measurable difference in all-cause mortality must be attributed to the introduction of the injectables.

On December 14, 2020, the first day of vaccine availability in the US, 4,824 doses were administered and on the last day of t_3, December 31, 2022, there were 38,069 doses administered (according to Our World in Data, March 11, 2023). Given such widespread exposure the supposedly beneficial

The two data sources, CDC and Our World in Data, correlated at 0.999999798. The total difference in reporting showed 331 more persons recorded by the CDC than by Our World in Data.

impact of the COVID-19 "vaccines" added on top of any continuing negative impact from SARS-CoV-2 and its variants, a substantial reduction in all-cause mortality should have appeared during t_3.

The expected effect — according to the almost universal narrative supported by the CDC and the mainstream press — would be a return to (or at least towards) the pre-pandemic "normalcy" during t_1 (Economist Group, 2021; Administration for Community Living, 2022; Brennan, 2023). If that promise were true, the red bar in Figure 6 (above) should drop significantly toward (if not all the way to) the level of the horizontal broken line in that figure. It should have fallen back toward the pre-pandemic level of all-cause mortality. It did not.

With that in mind, finally, we come to H_{A3} which, by the mainstream promises, predicts an increase in life expectancy with each additional dose of COVID-19 vaccine. We find the opposite. Table 6 and the results graphed in Figure 8 tell the tale. There is a significant reduction of life expectancy, averaging 74 days, from zero doses of COVID-19 vaccine to one, two, and so forth up to five doses. Persons surviving beyond a 5th dose were so few (only about 1 in 10,000; actually 8 of 57,261, only 1 of whom survived to take a 7th dose) that they are not included or shown in Figure 8. On the average, Medicare patients who refused all COVID-19 injectables (all of whom died), according to the Medicare records summarized in Table 6 and graphed in Figure 8 (see the top two entries), survived 119.94 days longer than those who took just one dose of the COVID-19 "vaccine".[20] According to the alternative hypothesis at issue, H_{A3}, the life expectancy of persons surviving the pandemic during t_2 should — if all other factors are held the same as they are when the people sampled are 97.6% the very same individuals — be increased by each dose of COVID-19 vaccine received during t_3. This is what we should expect if the mainstream narrative were true. However, the Medicare data summarized in Table 6 and graphed in Figure 8 demolishes that theory.

Table 7
Welch's *t*-Test Assuming Unequal Variances: Two-Samples Consisting of 14,356 Medicare Participants Who Received Two Doses of COVID-19 Vaccine Contrasted with 7,473 Connecticut Participants Who Received Three Doses of COVID-19 Vaccine

	Two Doses of COVID-19 Vaccine	***Three Doses of COVID-19 Vaccine***
Mean Days to Live	247.22	198.62
Variance	28084.12	14069.90
Observations	14,356	7,473
Hypothesized Mean Difference	0	
df	19,892	
t Stat	24.80	
P(T<=t) one-tail	4.3454E-134	
t Critical one-tail	3.72	

Each new dose, on the average, shortens the time left-to-live by 74 days for the average independent samples. The patients in the Medicare system are supposedly the most in need and most likely to benefit from getting all the injections available and recommended by the CDC. That, is not true, however. The Medicare data analyzed here, irrespective of any other factors (age, income, multiple comorbidities, etc.) are almost certain to die sooner from one dose than none, sooner from two than one, and so forth. Hardly anyone in the Medicare system can survive the first five doses in order to

[20] Throughout this section we are relying on Medicare data available on the website of Steve Kirsch (2023a, 2023b) to anyone wishing to analyze it. We also include in our **Suplementary Files**, all of the data we have used in this paper.

receive a sixth. In the Medicare data at hand, only 7 people of 57,261 individuals in the data set (see **Supplementary Data Files**), were willing and able to take six doses of any COVID-19 vaccine. They died, on the average within 34 days of that sixth dose. Only one person in the entire dataset (a 68-year-old person) survived the first six doses to take a seventh before dying within 69 days. The reason, according to the dotted trend line of Figure 8, is that the CDC recommended 7 doses of the vaccine are sufficient to reduce the life expectancy of recipients, on the average, by more than the number of days they would have had left-to-live even if they had taken no doses of the injectable(s) at all (74 X 6 = 444 days; 16.16 days longer than the average time left to live, 427.84 days, for people who took zero doses).[21]

To keep things simple and non-redundant, although we tested every contrast in Figure 8 with the supremely relevant and applicable Welch's *t*-test for samples with unequal sample-sizes and unequal variances, we only need to report the result for the smallest contrast at issue to establish that all the adjacent contrasts in Figure 8 are significant at a level that is more significant even than 4.34 raised to the negative 134th power (see the next to last line in Table 7). Any event with such a remote level of probability cannot ever be expected to occur at all by chance. The number of repeat experiments required to produce such a result, in theory, would be many orders of magnitude greater than the estimated number of particles in the universe which comes to about 10^{80} (Heile, 2018).

In fact, that smallest contrast in Figure 8, between two doses and three, is significant at a probability level approximating absolute zero. It leaves no remaining likelihood at all that any finite number of repetitions of the pandemic experiment would accidentally occur, strictly by chance, producing a contrast as large as the one observed. Given that the contrast showing a loss 48.6 days left-to-live when Medicare participants opted to get a third dose of COVID-19 vaccine is the smallest one in the whole series, every component of the H_{A3} series of alternatives must be accepted and every null counterpart of H_{A3} must be rejected. The hypothesis predicting a measurable negative impact of each successive dose of COVID-19 vaccine on life expectancy of recipients must be accepted.

Each additional dose of COVID-19 vaccine — all else being held equal by virtue of the fact that there is no reason to expect that sicker or older, or otherwise more prone-to-die persons are more likely to get another dose of COVID-19 vaccine than people who are healthier, younger or less prone to die, etc. — on the average, shortens the life expectancy of the Medicare participant receiving it. Each successive shot diminishes the remaining lifespan of persons like the thousands of Medicare participants in the data set examined here, on the average, by 74 days per dose received.

DISCUSSION

For some time now a few outspoken medical doctors of distinction such as Peter McCullough — one of the most published MDs of the world and one of the most sought after editors, practitioners, researchers, and theoreticians in mainstream medicine — have been warning that the worldwide pandemic experiment has resulted in millions of cases of myocarditis. According to more than 200 mainstream peer-reviewed papers that McCullough referred to in March 2022 (see and hear him here), myocarditis was being diagnosed at a rate of about 4 cases per million per year prior to the introduction of the COVID-19 injectables. During the worldwide pandemic experiment, the

[21] As one of us noted in an earlier paper (Santiago, 2022b), getting successive doses of COVID-19 vaccine is like playing Russian Roulette. Before the sixth, much less seventh pull of the trigger, the spin will have landed on an non-empty chamber, and as Kirsch (2023a) put it: "Game Over".

number of cases that have occurred worldwide, according to the mainstream research literature as early as a year ago, already accounted for about 25,000 million cases in recipients of two or three doses of any one of the marketed COVID-19 vaccines. He estimates that during the pandemic experiment period about 500 cases per million per year were occurring in male athletes in peak physical condition who were between the ages of 18 to 24 years. We ourselves find it interesting that McCullough, a distinguished MD, cited the world's formerly most "notorious" and now perhaps most admired tennis champion, Novak Djokovic, to bolster his (McCullough's) case and public appeal.

Notably, Djokovic was banned from the Australian Open 2023 because of newly created laws there requiring "foreigners to be vaccinated". He was already there but refused to take any COVID-19 vaccine and was deported. Against enormous pressure, eight months after McCullough's citation of the tennis champion who refused to be injected, by November 2022, Djokovic won back the right to play in the 2023 tournament (Nivison, 2022). To top it off, not only was he courageous in refusing the COVID-19 vaccine, as McCullough also noted, but Novak Djokovic came back on January 29, 2023 to win the Australian Open for the 10th time. He did it, moreover, playing the final match against Stefanos Tsitsipas in straight sets (ABC News January 15, 2023), in spite of the fact that Djokovic had a radiographically documented three-centimeter tear in his left hamstring. In doing so, Djokovic replaced the second best player, Nadal Rafael, to take the top ranking in the world, and tying Nadal's record of 22 Grand Slam wins (Gonzalez, February 1, 2023).[22]

McCullough also cited several mainstream documents in the medical research literature to make his case about circulatory problems brought on by the COVID-19 vaccines a little more than a year ago. For example, Mansanguan et al. (2022)[23] estimated 23,000 serious cardiac issues per million and LePessec et al. (October 24, 2022 cardio online, Switzerland) set the number at 28,000 per million. During the two phases of the pandemic experiment (t_2 and t_3) as specified in Figure 4 above, we have suggested multiple factors: first, whatever is in the COVID-19 injectables, but also variants of other disease agents, evolved mutants of the initial SARS-CoV-2 bioweapon, lockdowns, sudden inaccessibility to healthcare, and the like.

In December 2022, a little more than a month before Djokovic would defy all odds to win the Australian Open 2023, but several months after McCullough's reference to the 200-plus mainstream

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[22] We are grateful to Australian, Gerry Brady, Doctor of Medicine (retired) University of Queensland, Australia, with 30 years of patient focused clinical experience, and now the renowned Publisher and Editor of BOOM Finance and Economics for reviewing this paper and for commenting particularly on this section. Among his many contributions to the ongoing discussion is "COVID Under Question Cross Party Enquiry by Members of the Australian Senate and Federal Parliament 23rd March 2022". See some of the relevant videos here.

[23] McCullough does not mention the fact that to get into the mainstream medical literature — an arena that he and his colleagues in the editorial business must know as well as the rest of us who consult it know — it is necessary to include some prominent but absolutely false statements such as the following in the second and third sentences of the opening paragraph in the introduction to the work by Mansanguan et al.: "Clinical trials have revealed that the vaccine's *efficacy is 95% and its safety profile is good, similar to that of other vaccines* [we omit four citations given here to support what is a known falsehood that we have emphasized in red italics]. Systemic reactions to the vaccine, which were usually *mild and transient* [our emphasis of the part of this half-truth that is known to be false] have been reported more commonly among the younger population and more often after the second dose". In the last part of the quotation, we omit three supporting citations in support of the part of which actually happens to be true. It is true that "systemic reactions" are more common for these injectables after a second dose and especially so in younger people.

papers showing serious cardiological issues in well-known young athletes who, for whatever reasons did not refuse the COVID-19 injections, Polykretis and McCullough (2022) wrote:

> From January 2021 to the time of writing [this paper published December 22, 2022], 1598 athletes suffered cardiac arrest, 1101 . . . with deadly outcome. Notably, in a 38-years timespan (1966-2004), 1101 athletes under the age of 35 died (~29/years) due to various heart-related conditions, 50% of whom had congenital anatomical heart disease and cardiomyopathies and 10% had atherosclerotic heart disease with early onset.

It is true that all kinds of factors make young athletes, males in particular, more susceptible to cardiac events because of pushing themselves to the limits of extreme exertion not only in competitions but also in training. Therefore, it is no surprise that catastrophic cardiac-related events can occur in that group of people who are notably in far better physical condition than most non-athletes and the general population at large. However, McCullough and his co-author Polykretis had to examine a 38-year span of time to find 1101 athletes who ostensibly died of exertion-induced cardiac stress. If we assume their research is approximately correct, COVID-19 injections have produced 1101 lethal outcomes during slightly more than 24 months in t_3 of the worldwide pandemic experiment — since the "emergency authorization" of the "safe and effective" COVID-19 "vaccines" with a "safety profile similar to that of other vaccines" — the COVID-19 vaccines have increased the likelihood of athletes dying suddenly by a factor of 19 times. That factor is estimated from the 38 years of 1966 up to 2004 times the 12 months of all those years divided by the 24 months of t_3 during the vaccination phase of the worldwide pandemic experiment when McCullough and Polykretis were writing their paper.

Deaths from all causes, the unassailable best index to measure outcomes in the worldwide pandemic experiment, have increased on the average by more than 10,000 persons per week since the pandemic experiment began. The primary cause of all those deaths can be linked to the abnormal fibrinaloid (proteinaceous but unprecedented) clots we documented in the first part of this paper. Our statistical analyses of some very large datasets in the second part show that the "emergency authorized" COVID-19 injectables did not return all-cause mortality to its pre-pandemic baseline but actually raised it somewhat *above the level of the pandemic itself prior to the release of the "safe and effective" COVID-19 vaccines*. Mainstream medical publications keep saying that the COVID-19 injections are "similar to other vaccines" (e.g., see Mansanguan et al., 2022) in spite of the fact that the very spotty and under-used Vaccine Adverse Event Reporting System (Lazarus et al., 2010) shows them to be more injurious and lethal during the first two years of their existence than all the vaccines of recorded history put together across the whole period of VAERS record keeping (Santiago, 2022b; Nass, 2023).

Excess deaths are increasing and the abnormal clots discussed in the first part of our paper are probably the central causative factor. John Campbell, an MD in the UK (December 29, 2022) and Meryl Nass an MD in the US (March 19, 2023) have documented the increase in deaths from all-causes. They suggested that in March 2020 the weekly average was up by 197 persons above the baseline but by October 2022 they estimated an increase of 1,564 per week based on UK data. By February 11, 2023, Campbell (February 11, 2023) accentuated his concern about rising rates of all-cause deaths. As long ago as October 7, 2022, Joseph Ladapo, MD and Florida Surgeon General released an analysis showing an 84% increase in the relative incidence of cardiac related death among males 18-39 years old within 28 days following a COVID-19 mRNA injection. Our analysis of CDC and US Census Bureau data throughout the pandemic experiment period from its start on

March 11, 2020 up to December 31, 2022 showed an average increase in all-cause mortality for the whole US population at above 10,000 persons per week throughout the whole period.

Conclusion

The CDC, US Census Bureau, and Medicare data presented here show that the worldwide pandemic experiment not only raised the US weekly all-cause death rate by more than 10,000 persons per week but the administration of more than 635 million doses of COVID-19 injectables to well over half the US population only made things worse. The expensive remedy only moved the all-cause mortality index higher. Pressuring people to accept one or more doses of the COVID-19 injectables not only did not return the all-cause death rate to its pre-pandemic baseline, it made things worse just as Seneff and Nigh (2021) and Seneff, et al. (2022) predicted. Moreover, tens of thousands of recorded deaths in Medicare participants from all 50 US states and from Connecticut, during the period of the experiment after the COVID-19 injectables were marketed, reveal that life expectancy for injected Medicare participants (people supposedly in the age bracket most needing protection from infectious viruses, etc.) fell in a nearly straight line from an average of about 307.9 days after one dose to about 58.6 days after five doses. Life expectancy for Medicare patients was shortened on the average by 74 days with each dose of COVID-19 injectable fluid (whatever is in it). Unfortunately, on the sixth dose, the average life expectancy according to the Medicare data is already 16.16 days past zero.

References

Aarstad, J., & Kvitastein, O. A. (2023). Is there a Link between the 2021 COVID-19 Vaccination Uptake in Europe and 2022 Excess All-Cause Mortality? *Romania*, *40*, 19328838. link here

Administration for Community Living. (2022, July 14). *As US Returns To Pre-Pandemic Normalcy, People Who Are Disabled, Immunocompromised Remain Forgotten. | ACL Administration for Community Living*. https://acl.gov/news-and-events/news/us-returns-pre-pandemic-normalcy-people-who-are-disabled-immunocompromised

Ahmad, F., Kannan, M., & Ansari, A. W. (2022). Role of SARS-CoV-2 -induced cytokines and growth factors in coagulopathy and thromboembolism. *Cytokine & Growth Factor Reviews*, *63*, 58–68. https://doi.org/10.1016/j.cytogfr.2021.10.007

Aldén, M., Olofsson Falla, F., Yang, D., Barghouth, M., Luan, C., Rasmussen, M., & De Marinis, Y. (2022). Intracellular reverse transcription of Pfizer BioNTech COVID-19 mRNA vaccine BNT162b2 in vitro in human liver cell line. Current Issues in Molecular Biology, 44(3), 1115–1126. https://www.mdpi.com/1467-3045/44/3/73/htm?s=09

Ambati, B. K., Varshney, A., Lundstrom, K., Palú, G., Uhal, B. D., Uversky, V. N., & Brufsky, A. M. (2022). MSH3 homology and potential recombination link to SARS-CoV-2 furin cleavage site. *Frontiers in Virology*, *2*. https://www.frontiersin.org/articles/10.3389/fviro.2022.834808

Australian Open. (2023). In *Wikipedia*. https://en.wikipedia.org/w/index.php?title=2023_Australian_Open&oldid=1142611717

Ball, P. (2020). The lightning-fast quest for COVID vaccines—And what it means for other diseases. *Nature*, *589*(7840), 16–18. https://doi.org/10.1038/d41586-020-03626-1

Banoun, H. (2022). Current state of knowledge on the excretion of mRNA and spike produced by anti-COVID-19 mRNA vaccines; possibility of contamination of the entourage of those vaccinated by these products. *Infectious Diseases Research*, *2022;3(4):22*. https://doi.org/10.53388/IDR20221125022

Banoun, H. (2023). mRNA: Vaccine or gene therapy? Regulatory issues. Preprint available at https://www.researchgate.net/profile/Helene-

Banoun/publication/368720208_mRNA_vaccine_or_gene_therapy_Regulatory_issues/links/63f72a585749505945378ab2/mRNA-vaccine-or-gene-therapy-Regulatory-issues.pdf

Bansal, S., Perincheri, S., Fleming, T., Poulson, C., Tiffany, B., Bremner, R. M., & Mohanakumar, T. (2021). Cutting Edge: Circulating exosomes with COVID spike protein are induced by BNT162b2 (PfizerBioNTech) vaccination prior to development of antibodies: A novel mechanism for immune activation by mRNA vaccines. *Journal of Immunology* (Baltimore, Md.: 1950), 207(10), 2405–2410. https://doi.org/10.4049/jimmunol.2100637

Belk, D., & Belk, P. (2020). *The Great American Healthcare Scam: How Kickbacks, Collusion and Propaganda Have Exploded Healthcare Costs in the United States*. https://www.goodreads.com/book/show/53126475-the-great-american-healthcare-scam

Benzi Cipelli, R., Giovannini, F., & Pisano, G. (2022). Dark-field microscopic analysis on the blood of 1,006 symptomatic persons after anti-COVID mRNA injections from Pfizer/BioNtech or Moderna. *International Journal of Vaccine Theory, Practice, and Research*, *2*(2), 385–444. https://doi.org/10.56098/ijvtpr.v2i2.47

Black and Veatch. (2023). In *Wikipedia*. https://en.wikipedia.org/w/index.php?title=Black_%26_Veatch&oldid=1139871360#History

Blaylock, R. L. (2022). The COVID-19 "vaccines": What is the truth? *International Journal of Vaccine Theory, Practice, and Research*, *2*(2), 595–602. https://doi.org/10.56098/ijvtpr.v2i2.57

Bostrom, N. (2003). Human genetic enhancements: A transhumanist perspective. *Journal of Value Inquiry*, *37*, 493–506. https://heinonline.org/HOL/LandingPage?handle=hein.journals/jrnlvi37&div=54&id=&page=

Bostrom, N. (2005). In defense of posthuman dignity. *Bioethics*, *19*(3), 202–214. https://doi.org/10.1111/j.1467-8519.2005.00437.x

Brand, R. C., Klootwijk, J., Planta, R. J., & Maden, B. E. (1978). Biosynthesis of a hypermodified nucleotide in Saccharomyces carlsbergensis 17S and HeLa-cell 18S ribosomal ribonucleic acid. *The Biochemical Journal*, *169*(1), 71–77. https://doi.org/10.1042/bj1690071

Brennan, M. (2023). *In U.S., 47% Do Not Expect Return to Pre-Pandemic Normalcy*. https://news.gallup.com/poll/471953/not-expect-return-pre-pandemic-normalcy.aspx

Broudy, D., & Kyrie, V. (2021). Syllogistic reasoning demystifies evidence of COVID-19 vaccine constituents. *International Journal of Vaccine Theory, Practice, and Research*, *2*(1), 149–171. https://doi.org/10.56098/ijvtpr.v2i1.32

Brown, C. M., Vostok, J., Johnson, H., Burns, M., Gharpure, R., Sami, S., Sabo, R. T., Hall, N., Foreman, A., Schubert, P. L., Gallagher, G. R., Fink, T., Madoff, L. C., Gabriel, S. B., MacInnis, B., Park, D. J., Siddle, K. J., Harik, V., Arvidson, D., … Laney, A. S. (2021). Outbreak of SARS-CoV-2 infections, including COVID-19 vaccine breakthrough infections, associated with large public gatherings—Barnstable County, Massachusetts, July 2021. *Morbidity and Mortality Weekly Report*, *70*(31), 1059–1062. https://doi.org/10.15585/mmwr.mm7031e2

Buzhdygan, T.P.; DeOre, B.J.; Baldwin-Leclair, A.; Bullock, T.A.; McGary, H.M.; Khan, J.A.; Razmpour, R.; Hale, J.F.; Galie, P.A.; Potula, R.; et al. The SARS-CoV-2 spike protein alters barrier function in 2D static and 3D microfluidic in-vitro models of the human blood-brain barrier. Neurobiol. Dis. 2020, 146, 105131.

Campbell, John. (2022, December 29). *Dr. John Campbell uses RUMBLE to call for JAB halt*. https://mole.substack.com/p/dr-john-campbell-uses-rumble-to-call

Campbell, John. (2023, February 16). *Germany leads Western nations in "massive" excess death spike since COVID jab rollout: Data - LifeSite*. https://www.lifesitenews.com/news/germany-leads-western-nations-in-massive-excess-death-spike-since-covid-jab-rollout-data/

Campra, P. (2021, June 28). *Graphene oxide detection in aqueous suspension: Observational study in optical and electron microscopy*. https://www.docdroid.net/rNgtxyh/microscopia-de-vial-corminaty-dr-campra-firma-e-1-fusionado-pdf

Capillary. (2022). In *Wikipedia*. https://en.wikipedia.org/w/index.php?title=Capillary&oldid=1102901466

Centers for Disease Control and Prevention, National Center for Health Statistics, National Vital Statistics System, Mortality. (2017). *National Vital Statistics System, Mortality: Compressed Mortality File 1999-2016 on CDC WONDER Online Database, released June 2017. Data are from the Compressed Mortality File 1999-2016 Series 20, 2016, as compiled*

from data provided by the 57 vital statistics jurisdictions through the Vital Statistics Cooperative Program. Accessed at http://wonder.cdc.gov/cmf-icd10.html on Mar 9 2023 2:09:36 PM. CDC. http://wonder.cdc.gov/cmf-icd10.html on Mar 9 2023 2:09:36 PM

Centers for Disease Control and Prevention. (2023, March 22). *Excess Deaths Associated with COVID-19*. https://www.cdc.gov/nchs/nvss/vsrr/covid19/excess_deaths.htm

Chaitin, G. J. (2004, November 4). *Irreducible Complexity in Pure Mathematics*. ArXiv.Org. https://doi.org/10.48550/arXiv.math/0411091

Chaitin, G. (2007). The halting probability omega: Irreducible complexity in pure mathematics. *Milan Journal of Mathematics*, *75*(1), 291–304. https://doi.org/10.1007/s00032-006-0064-2

Chertow, D., Stein, S., Ramelli, S., Grazioli, A., Chung, J.-Y., Singh, M., Yinda, C. K., Winkler, C., Dickey, J., Ylaya, K., Ko, S. H., Platt, A., Burbelo, P., Quezado, M., Pittaluga, S., Purcell, M., Munster, V., Belinky, F., Ramos-Benitez, M., … Kleiner, D. (2021). *SARS-CoV-2 infection and persistence throughout the human body and brain* [Preprint]. In Review. https://doi.org/10.21203/rs.3.rs-1139035/v1

Chesnut, W. M. (2023, January 3). Massive discovery: Known in 2007: expressing the viral spike protein alone induces endoplasmic reticulum stress: an explanation for emerging heterogeneous pathologies [Substack newsletter]. *WMC Research*. https://wmcresearch.substack.com/p/massive-discovery-known-in-2007-expressing?utm_medium=email

Cheung, C. Y., Poon, L. L. M., Ng, I. H. Y., Luk, W., Sia, S.-F., Wu, M. H. S., Chan, K.-H., Yuen, K.-Y., Gordon, S., Guan, Y., & Peiris, J. S. M. (2005). Cytokine Responses in Severe Acute Respiratory Syndrome Coronavirus-Infected Macrophages In Vitro: Possible Relevance to Pathogenesis. *Journal of Virology*, *79*(12), 7819–7826. https://doi.org/10.1128/JVI.79.12.7819-7826.2005

Cohen, S. (2020, December 10). *The fastest vaccine in history*. https://www.uclahealth.org/news/the-fastest-vaccine-in-history

Cohn, B. A., Cirillo, P. M., Murphy, C. C., Krigbaum, N. Y., & Wallace, A. W. (2022). SARS-CoV-2 vaccine protection and deaths among US veterans during 2021. *Science (New York, N.Y.)*, *375*(6578), 331–336. https://doi.org/10.1126/science.abm0620

Crowder, S., & O'Looney, J. (2022, November 2). *Exclusive: Undertaker explains "mysterious" clotting phenomenon!* Louder with Crowder. https://rumble.com/v1r2ts2--live-daily-show-louder-with-crowder.html

Davidson, R. M., & Seneff, S. (2012). The initial common pathway of inflammation, disease, and sudden death. *Entropy*, *14*(12), 1399–1442. https://doi.org/10.3390/e14081399

De Michele, M., d'Amati, G., Leopizzi, M., Iacobucci, M., Berto, I., Lorenzano, S., Mazzuti, L., Turriziani, O., Schiavo, O. G., & Toni, D. (2022). Evidence of SARS-CoV-2 spike protein on retrieved thrombi from COVID-19 patients. *Journal of Hematology & Oncology*, *15*(1), 108. https://doi.org/10.1186/s13045-022-01329-w

Dena, A. S. A., & El-Sherbiny, I. M. (2022). Chapter 21—Biological macromolecules for nucleic acid delivery. In A. K. Nayak, A. K. Dhara, & D. Pal (Eds.), *Biological Macromolecules* (pp. 479–490). Academic Press. https://doi.org/10.1016/B978-0-323-85759-8.00021-X

Dong, Y., & Corson, A. (2022, September 18). *Fibrous clots, foreign matter in blood after COVID jabs: Is there a way to detox?* Www.Theepochtimes.Com. https://www.theepochtimes.com/fibrous-clots-foreign-matter-in-blood-after-covid-jabs-is-there-a-way-to-detox_4738079.html

Dowd, E. (2022). *Cause Unknown: The Epidemic of Sudden Deaths in 2021 and 2022*. Children's Health Defense. https://www.target.com/p/cause-unknown-children-s-health-defense-by-ed-dowd-hardcover/-/A-87479317

Economist Group. (2021, June 30). *The Economist launches "normalcy index" to quantify the return of pre-pandemic life in 50 countries*. https://www.economistgroup.com/group-news/the-economist/the-economist-launches-normalcy-index-to-quantify-the-return-of-pre-pandemic

Elzoghby, A. O. (2013). Gelatin-based nanoparticles as drug and gene delivery systems: Reviewing three decades of research. *Journal of Controlled Release, 172*(3), 1075–1091. https://doi.org/10.1016/j.jconrel.2013.09.019

Event 201, a pandemic exercise to illustrate preparedness efforts. (2019, October 18). Johns Hopkins Bloomberg School of Public Health, World Economic Forum, & Bill and Melinda Gates Foundation. https://centerforhealthsecurity.org/event201/

Eyeinthesky. (2022, March 17). *Sponsored by DARPA - the development of mRNA bioweapons—Labeled as "vaccines"—Part I*. Telegraph. https://telegra.ph/Sponsored-by-DARPA---the-development-of-mRNA-bioweapons---labeled-as-vaccines---Part-I-03-17

Fleming, D. R. M. (2021). *Is COVID-19 a Bioweapon? A Scientific and Forensic Investigation*. Skyhorse. https://www.simonandschuster.com/books/Is-COVID-19-a-Bioweapon/Richard-M-Fleming/Children-s-Health-Defense/9781510770195

Fraiman, J., Erviti, J., Jones, M., Greenland, S., Whelan, P., Kaplan, R. M., & Doshi, P. (2022). Serious adverse events of special interest following mRNA COVID-19 vaccination in randomized trials in adults. *Vaccine*, *40*(40), 5798–5805. https://doi.org/10.1016/j.vaccine.2022.08.036

Gonzalez, Isabel. (2023, February 2). *Novak Djokovic won 2023 Australian Open despite hamstring tear, tournament director says*. CBSSports.Com. https://www.cbssports.com/tennis/news/novak-djokovic-won-2023-australian-open-despite-hamstring-tear-tournament-director-says/

Gore, M. E. (2003). Adverse effects of gene therapy: Gene therapy can cause leukaemia: no shock, mild horror but a probe. *Gene Therapy*, *10*(1), 4–4. https://doi.org/10.1038/sj.gt.3301946

Grobbelaar, L. M., Kruger, A., Venter, C., Burger, E. M., Laubscher, G. J., Maponga, T. G., Kotze, M. J., Kwaan, H. C., Miller, J. B., Fulkerson, D., Huff, W., Chang, E., Wiarda, G., Bunch, C. M., Walsh, M. M., Raza, S., Zamlut, M., Moore, H. B., Moore, E. E., … Pretorius, E. (2022). Relative Hypercoagulopathy of the SARS-CoV-2 Beta and Delta Variants when Compared to the Less Severe Omicron Variants Is Related to TEG Parameters, the Extent of Fibrin Amyloid Microclots, and the Severity of Clinical Illness. *Seminars in Thrombosis and Hemostasis*, *48*(7), 858–868. https://doi.org/10.1055/s-0042-1756306

Gundry, S. R. (2021). Observational findings of PILSs cardiac test findings for inflammatory markers in patients receiving mRNA vaccines. *Circulation*, *144*, A10712. https://doi.org/10.1161/circ.144.suppl_1.10712

Guntas, G., Mansell, T. J., Kim, J. R., & Ostermeier, M. (2005). Directed evolution of protein switches and their application to the creation of ligand-binding proteins. *Proceedings of the National Academy of Sciences*, *102*(32), 11224–11229. https://doi.org/10.1073/pnas.0502673102

Gutschi, M. (Director). (2022, November 2). *Quality issues with mRNA Covid vaccine production*. https://www.bitchute.com/video/muB0nrznCAC4/

Harpaz, R., DuMouchel, W., Van Manen, R., Nip, A., Bright, S., Szarfman, A., Tonning, J., & Lerch, M. (2022). Signaling COVID-19 Vaccine Adverse Events. *Drug safety*, *45*(7), 765–780. https://doi.org/10.1007/s40264-022-01186-z

Heile, F. (2017, October 8). *How many particles are there in the universe? - Quora*. https://www.quora.com/How-many-particles-are-there-in-the-universe

HelpAdvisor.com. (2023). *Connecticut Medicare Eligibility and Enrollment*. https://www.helpadvisor.com/medicare/connecticut

Hofer, U. (2022). Clotting and SARS-CoV-2 entry. *Nature Reviews Microbiology*, *20*(6), Article 6. https://doi.org/10.1038/s41579-022-00729-6

Hughes, D. A. (2022). What is in the so-called COVID-19 "vaccines"? Part 1: evidence of a global crime against humanity. *International Journal of Vaccine Theory, Practice, and Research*, *2*(2), 455–586. https://doi.org/10.56098/ijvtpr.v2i2.52

Huff, A. G. (2022). *The Truth about Wuhan: How I Uncovered the Biggest Lie in History*. Publisher: Skyhorse (December 6, 2022). https://www.simonandschuster.com/books/The-Truth-about-Wuhan/Andrew-G-Huff/9781510773882

Huff, A. G., & Lyons, T. (2023). *The Truth about Wuhan with Dr. Andrew Huff*. https://live.childrenshealthdefense.org/chd-tv/shows/good-morning-chd/the-truth-about-wuhan-with-dr-andrew-huff/

Irrgang, P., Gerling, J., Kocher, K., Lapuente, D., Steininger, P., Habenicht, K., Wytopil, M., Beileke, S., Schäfer, S., Zhong, J., Ssebyatika, G., Krey, T., Falcone, V., Schülein, C., Peter, A. S., Nganou-Makamdop, K., Hengel, H., Held, J., Bogdan, C., Überla, K., … Tenbusch, M. (2023). Class switch toward noninflammatory, spike-specific IgG4 antibodies after repeated SARS-CoV-2 mRNA vaccination. *Science immunology*, *8*(79), eade2798. https://doi.org/10.1126/sciimmunol.ade2798

Jana, A. K., Greenwood, A. B., & Hansmann, U. H. E. (2021). Presence of a SARS-CoV-2 Protein Enhances Amyloid Formation of Serum Amyloid A. *The Journal of Physical Chemistry B*, *125*(32), 9155–9167. https://doi.org/10.1021/acs.jpcb.1c04871

Jernigan, D. A., Hart, M. C., Dodd, K. K., Jameson, S., Farney, T., Jernigan, D. A., Hart, M. C., Dodd, K. K., Iii, S. W. J., & Farney, T. (2021). Induced native phage therapy for the treatment of lyme disease and relapsing fever: A retrospective review of first 14 months in one clinic. *Cureus*, *13*(11). https://doi.org/10.7759/cureus.20014

Jernigan, D. A., & Joseph, S. (2005). Illuminated physiology and medical uses of light. *Subtle Energies & Energy Medicine Journal Archives*, *16*(3), Article 3. https://journals.sfu.ca/seemj/index.php/seemj/article/view/59

Kampf, G. (2021). The epidemiological relevance of the COVID-19-vaccinated population is increasing. *The Lancet Regional Health - Europe*, *11*, 100272. https://doi.org/10.1016/j.lanepe.2021.100272

Karikó, K., Ni, H., Capodici, J., Lamphier, M., & Weissman, D. (2004). mRNA is an endogenous ligand for toll-like receptor 3. *The Journal of Biological Chemistry*, *279*(13), 12542–12550. https://doi.org/10.1074/jbc.M310175200

Karikó, K., Muramatsu, H., Welsh, F. A., Ludwig, J., Kato, H., Akira, S., & Weissman, D. (2008). Incorporation of pseudouridine into mRNA yields superior nonimmunogenic vector with increased translational capacity and biological stability. *Molecular Therapy: The Journal of the American Society of Gene Therapy*, *16*(11), 1833–1840. https://doi.org/10.1038/mt.2008.200

Kell, D. B., & Pretorius, E. (2017). Proteins behaving badly. Substoichiometric molecular control and amplification of the initiation and nature of amyloid fibril formation: Lessons from and for blood clotting. *Progress in Biophysics and Molecular Biology*, *123*, 16–41. https://doi.org/10.1016/j.pbiomolbio.2016.08.006

Kell, D. B., Laubscher, G. J., & Pretorius, E. (2022). A central role for amyloid fibrin microclots in long COVID/PASC: Origins and therapeutic implications. *Biochemical Journal*, *479*(4), 537–559. https://doi.org/10.1042/BCJ20220016

Kennedy, R. F., Jr. (2021). *The Real Anthony Fauci: Bill Gates, Big Pharma, and the Global War on Democracy and Public Health*. Skyhorse Publishing. https://www.simonandschuster.com/books/Thimerosal-Let-the-Science-Speak/Robert-F-Kennedy/9781632206015

Kennedy, R. F., Jr., Couey, J. J., & Rixey, C. (2022). New Analysis of COVID Virus Suggests Fauci and Baric's Fingerprints on Pandemic Bug • Children's Health Defense. *The Defender*. https://childrenshealthdefense.org/defender/covid-pandemic-nih-unc-fauci-baric/

Kirsch, S. (2023a, February 9). EXCLUSIVE: Stunning new data pulled from the Medicare database shows how each shot increases your risk of death [Substack newsletter]. *Steve Kirsch's Newsletter*. https://stevekirsch.substack.com/p/exclusive-stunning-new-data-pulled?publication_id=548354&isFreemail=true

Kirsch, S. (2023b, February 25). GAME OVER: Medicare data shows the COVID vaccines increase your risk of dying [Substack newsletter]. *Steve Kirsch's Newsletter*. https://stevekirsch.substack.com/p/game-over-medicare-data-shows-the?isFreemail=true

Kyriakopoulos, A. M., Nigh, G., McCullough, P. A., & Seneff, S. (2022). Mitogen activated protein kinase (MAPK) activation, p53, and autophagy inhibition characterize the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) spike protein induced neurotoxicity. *Cureus*, *14*(12), e32361. https://doi.org/10.7759/cureus.32361

Kyrie, V., & Broudy, D. (2022a). Cyborgs R Us: The bio-nano panopticon of injected bodies? *International Journal of Vaccine Theory, Practice, and Research*, *2*(2), 355–383. https://doi.org/10.56098/ijvtpr.v2i2.49

Kyrie, V., & Broudy, D. (2022b). Hiding in plain sight: technocratic tyranny behind a medical mask. *Propaganda in Focus*. https://propagandainfocus.com/hiding-in-plain-sight-technocratic-tyranny-behind-a-medical-mask/

Ladapo, J. A. (2022, October 7). *State Surgeon General Dr. Joseph A. Ladapo Issues New mRNA COVID-19 Vaccine Guidance*. Florida Department of Health. https://content.govdelivery.com/accounts/FLDOH/bulletins/3312697

Latypova, A. Sasha. (2022a, June 10). Did Pfizer perform adequate safety testing for its COVID-19 mRNA vaccine in preclinical studies? Evidence of scientific and regulatory fraud. *Doctors for COVID Ethics*. https://doctors4covidethics.org/did-pfizer-perform-adequate-safety-testing-for-its-covid-19-mrna-vaccine-in-preclinical-studies-evidence-of-scientific-and-regulatory-fraud/

Latypova, A. Sasha. (2022b, October 5). *Very Bad Manufacturing Practices—What We Know To Date*. https://www.bitchute.com/video/BGIqC6ufcyjF/

Latypova, A. Sasha. (2022c, December 28). The role of the US DoD (and their co-investors) in the "COVID countermeasures" enterprise [Substack newsletter]. *Due Diligence and Art*. https://sashalatypova.substack.com/p/the-role-of-the-us-dod-and-their?publication_id=870364&isFreemail=true

Latypova, A. Sasha, & Nixon, D. (2023, January 14). Pfizer Under Microscope—Dr. David Nixon [Substack newsletter]. *Due Diligence and Art*. https://sashalatypova.substack.com/p/pfizer-under-microscope-dr-david

Le Cam, L. (1986). The Central Limit Theorem around 1935. *Statistical Science*, *1*(1), 78–91. https://www.jstor.org/stable/2245503

le Pessec, G. (2022, August 26). *Incidence non négligeable des myocardites après 3ème dose de vaccin à ARN messager anti-COVID 19 [Significant incidence of myocarditis after 3rd dose of anti-COVID 19 messenger RNA vaccine]*. European Congress of Cardiology, Barcelona, Spain. https://www.cardio-online.fr/Actualites/A-la-une/ESC-2022/Incidence-non-negligeable-myocardites-apres-3-dose-vaccin-ARN-messager-anti-COVID-19

Lee, W. S., Wheatley, A. K., Kent, S. J., & DeKosky, B. J. (2020). Antibody-dependent enhancement and SARS-CoV-2 vaccines and therapies. *Nature Microbiology*, *5*(10), Article 10. https://doi.org/10.1038/s41564-020-00789-5

Leonardi, A. J., & Proenca, R. B. (2020). Akt-Fas to Quell Aberrant T Cell Differentiation and Apoptosis in Covid-19. *Frontiers in Immunology*, *11*. https://www.frontiersin.org/articles/10.3389/fimmu.2020.600405

Lyons-Weiler, J. (2023, January 7). Harvard Study: Free Spike Protein - Not Bound by Antibodies - Detected in the Blood of Adolescents and Young Adults Who Developed Post-mRNA Vaccine Myocarditis [Substack newsletter]. *Popular Rationalism*. https://popularrationalism.substack.com/p/harvard-study-free-spike-protein?publication_id=475124&isFreemail=true

Mansanguan, S., Charunwatthana, P., Piyaphanee, W., Dechkhajorn, W., Poolcharoen, A., & Mansanguan, C. (2022). Cardiovascular manifestation of the BNT162b2 mRNA COVID-19 vaccine in adolescents. *Tropical medicine and infectious disease*, *7*(8), 196. https://doi.org/10.3390/tropicalmed7080196

Marfella, R., Paolisso, P., Sardu, C., Palomba, L., D'Onofrio, N., Cesaro, A., Barbieri, M., Rizzo, M. R., Sasso, F. C., Scisciola, L., Turriziani, F., Galdiero, M., Pignataro, D., Minicucci, F., Trotta, M. C., D'Amico, M., Mauro, C., Calabrò, P., Balestrieri, M. L., … Paolisso, G. (2021). SARS-COV-2 colonizes coronary thrombus and impairs heart microcirculation bed in asymptomatic SARS-CoV-2 positive subjects with acute myocardial infarction. *Critical Care*, *25*(1), Article 1. https://doi.org/10.1186/s13054-021-03643-0

Martín, R. D. (2022). Identification de possibles micro-technologie et structures artificielles dans le vaccin de Pfizer par microscopie optique: Analyse au microscope optique et reportage photo [Identification of possible micro-technology and artificial structures in the Pfizer vaccine by optical microscopy; Light microscope analysis and photographic report]. *University of Seville, Spain*, 34. here

Masters, R. D. (2009). Cost and effectiveness in American health care: Paying for a new Mercedes and getting a clunker. *International Journal of Health Science*, *2*(3), 221–226. http://cabdirect.org/abstracts/20093322686.html;jsessionid=A8F8043BEA30437909DC035D31413AD6

Maurer-Stroh, S., Debulpaep, M., Kuemmerer, N., de la Paz, M. L., Martins, I. C., Reumers, J., Morris, K. L., Copland, A., Serpell, L., Serrano, L., Schymkowitz, J. W. H., & Rousseau, F. (2010). Exploring the sequence determinants of

amyloid structure using position-specific scoring matrices. *Nature Methods*, *7*(3), Article 3. https://doi.org/10.1038/nmeth.1432

McCafferty, C., Lee, L., Cai, T., Praporski, S., Stolper, J., Karlaftis, V., Attard, C., Myint, D., Carey, L. M., Howells, D. W., Donnan, G. A., Davis, S., Ma, H., Crewther, S., Nguyen, V. A., Van Den Helm, S., Letunica, N., Swaney, E., Elliott, D., … Monagle, P. (2022). Fibrin clot characteristics and anticoagulant response in a SARS-CoV-2-infected endothelial model. *EJHaem*, *3*(2), 326–334. https://doi.org/10.1002/jha2.407

McCullough, P. (2023, March 23). *Dr. Peter McCullough Raises the Alarm on Vaccine-Induced Myocarditis [VIDEO]*. Red Voice Media. https://www.redvoicemedia.com/video/2022/03/dr-peter-mccullough-raises-the-alarm-on-vaccine-induced-myocarditis/

Miller, N. Z. (2015). *Vaccines Are They Really Safe and Effective?* (1 edition). New Atlantean Press.

Menachery, V. D., Dinnon, K. H., Yount, B. L., McAnarney, E. T., Gralinski, L. E., Hale, A., Graham, R. L., Scobey, T., Anthony, S. J., Wang, L., Graham, B., Randell, S. H., Lipkin, W. I., & Baric, R. S. (2019). Trypsin treatment unlocks barrier for zoonotic bat coronavirus infection. *Journal of Virology*, *94*(5), e01774-19, /jvi/94/5/JVI.01774-19.atom. https://doi.org/10.1128/JVI.01774-19

Montano, M., Ryu, J. K., Sozmen, E. G., Dixit, K., Matsui, Y., Liu, Y., Helmy, E. W. A., Deerinck, T. J., Yan, Z., Schuck, R., Thomas, R., Pico, A. R., Ellisman, M. H., Akassaglou, K., & Greene, W. (2022). SARS-CoV-2 spike binds fibrinogen-inducing abnormal inflammatory blood clots. *Topics in Antiviral Medicine*, 9–9. https://pesquisa.bvsalud.org/global-literature-on-novel-coronavirus-2019-ncov/resource/pt/covidwho-1880599

Morris, C., & Latypova, A. (Sasha) (Directors). (2023, January 9). *Sasha Latypova interviewed by Redacted with Clayton Morris*. https://www.bitchute.com/video/Zscb24uOFmwE/

Nance, K. D., & Meier, J. L. (2021). Modifications in an Emergency: The Role of N1-Methylpseudouridine in COVID-19 Vaccines. *ACS Central Science*, *7*(5), 748–756. https://doi.org/10.1021/acscentsci.1c00197

Nass, M. (2023, March 19). Western Australia releases vaccine safety data: Adverse events reported for covid vaccines 24x higher than for non-covid vaccines [Substack newsletter]. *Meryl's COVID Newsletter*. https://merylnass.substack.com/p/western-australia-releases-vaccine?publication_id=746368&isFreemail=true

Nivison, A. (2022, November 16). *Novak Djokovic will be granted visa to play in 2023 Australian Open*. CBSSports.Com. https://www.cbssports.com/tennis/news/novak-djokovic-will-be-granted-visa-to-play-in-2023-australian-open/

Nixon, D. (2023). *Background—Dr David Nixon—1*. https://drdavidnixon.com/

Nyström, S., & Hammarström, P. (2022). Amyloidogenesis of SARS-CoV-2 spike protein. *Journal of the American Chemical Society*, *144*(20), 8945–8950. https://doi.org/10.1021/jacs.2c03925

Olesen, K., Felding, T., Gjermansen, C., & Hansen, J. (2002). The dynamics of the Saccharomyces carlsbergensis brewing yeast transcriptome during a production-scale lager beer fermentation. *FEMS Yeast Research*, *2*(4), 563–573. https://doi.org/10.1111/j.1567-1364.2002.tb00123.x

Oller, J. W. (2010). The antithesis of entropy: Biosemiotic communication from genetics to human language with special emphasis on the immune systems. *Entropy*, *12*(4), 631–705. https://doi.org/10.3390/e12040631

Oller, J. W. (2014). Biosemiotic entropy: Concluding the series. *Entropy*, *16*(7), 4060–4087. https://doi.org/10.3390/e16074060

Oller, J. W. (2021). Weaponized pathogens and the SARS-CoV-2 pandemic. *International Journal of Vaccine Theory, Practice, and Research*, *1*(2), 172–208. https://doi.org/10.56098/ijvtpr.v1i2.16

Oller, J. W. (2022). *Human Anatomy and Physiology* (3rd ed.), https://www.researchgate.net/publication/368752719_Human_Anatomy_Physiology

Oller, J. W., & Santiago, D. (2022). All cause mortality and COVID-19 injections: Evidence from 28 weeks of Public Health England "COVID-19 vaccine surveillance reports." *International Journal of Vaccine Theory, Practice, and Research*, *2*(2), 301–319. https://doi.org/10.56098/ijvtpr.v2i2.42

Oller, J. W., & Shaw, C. A. (2019). From superficial damage to invasion of the nucleosome: Ranking of morbidities by the biosemiotic depth hypothesis. *International Journal of Sciences*, *8*(06), 51–73. https://doi.org/10.18483/ijSci.2069

O'Looney, J. (2021, November 13). British Funeral Director Tells RFK, Jr. About Fear, Propaganda and COVID Vaccine Deaths During Early Days of Pandemic. *Children's Health Defense*. https://childrenshealthdefense.org/defender/rfk-jr-podcast-john-olooney-fear-propaganda-covid-vaccine-deaths/

O'Looney, J., Hirschman, R., & Faithfull, B. (2022, October 11). *Funeral Directors & Embalmers Unite to Expose A Day in the Death of Life—Counterspin Media*. https://ugetube.com/watch/tJorwmSg5i6FVOd

Our World in Data. (2023, March 11). *Daily COVID-19 vaccine doses administered*. Our World in Data. https://ourworldindata.org/grapher/daily-covid-19-vaccination-doses

Pardi, N., Hogan, M. J., Porter, F. W., & Weissman, D. (2018). mRNA vaccines—A new era in vaccinology. *Nature Reviews Drug Discovery*, *17*(4), Article 4. https://doi.org/10.1038/nrd.2017.243

Pardi, N., Tuyishime, S., Muramatsu, H., Karikó, K., Mui, B. L., Tam, Y. K., Madden, T. D., Hope, M. J., & Weissman, D. (2015). Expression kinetics of nucleoside-modified mRNA delivered in lipid nanoparticles to mice by various routes. *Journal of Controlled Release*, *217*, 345–351. https://doi.org/10.1016/j.jconrel.2015.08.007

Park, J.; Park, M.-S.; Kim, H.J.; Song, T.-J. Association of Cerebral Venous Thrombosis with mRNA COVID-19 Vaccines: A Disproportionality Analysis of the World Health Organization Pharmacovigilance Database. Vaccines 2022, 10, 799. https://doi.org/10.3390/vaccines10050799

Parr, C. J. C., Wada, S., Kotake, K., Kameda, S., Matsuura, S., Sakashita, S., Park, S., Sugiyama, H., Kuang, Y., & Saito, H. (2020). N 1-Methylpseudouridine substitution enhances the performance of synthetic mRNA switches in cells. *Nucleic Acids Research*, *48*(6), e35. https://doi.org/10.1093/nar/gkaa070

Patterson, B. K., Francisco, E. B., Yogendra, R., Long, E., Pise, A., Beaty, C., Osgood, E., Bream, J., Kreimer, M., Heide, R. V., Guevara-Coto, J., Mora, R., & Mora, J. (2022). *SARS-CoV-2 S1 protein persistence in SARS-CoV-2 negative post-vaccination individuals with long COVID/PASC-like symptoms* [Preprint]. In Review. https://doi.org/10.21203/rs.3.rs-1844677/v1

Perez, J.-C., Moret-Chalmin, C., & Montagnier, L. (2023). Emergence of a new Creutzfeldt-Jakob Disease: 26 cases of the human version of Mad-Cow Disease, a few days after a COVID-19 injection. *International Journal of Vaccine Theory, Practice, and Research*, *3*(1), 727–770. https://doi.org/10.56098/ijvtpr.v3i1.66

Pfefferle, S., Huang, J., Nörz, D., Indenbirken, D., Lütgehetmann, M., Oestereich, L., Günther, T., Grundhoff, A., Aepfelbacher, M., & Fischer, N. (2020). Complete genome sequence of a SARS-CoV-2 strain isolated in northern Germany. *Microbiology Resource Announcements*, *9*(23), e00520-20. https://doi.org/10.1128/MRA.00520-20

Pharmaceutical Technology. (2023, February 23). Covid-19 Vaccination Tracker. *Pharmaceutical Technology*. https://www.pharmaceutical-technology.com/covid-19-vaccination-tracker/

Phetsouphanh, C., Darley, D. R., Wilson, D. B., Howe, A., Munier, C. M. L., Patel, S. K., Juno, J. A., Burrell, L. M., Kent, S. J., Dore, G. J., Kelleher, A. D., & Matthews, G. V. (2022). Immunological dysfunction persists for 8 months following initial mild-to-moderate SARS-CoV-2 infection. *Nature Immunology*, *23*(2), Article 2. https://doi.org/10.1038/s41590-021-01113-x

Pólya, G. (1920). Über den zentralen Grenzwertsatz der Wahrscheinlichkeitsrechnung und das Momentenproblem [About the central limit theorem of the probability calculation and the moment problem]. *Mathematische Zeitschrift*, *8*(3–4), 171–181. https://link.springer.com/content/pdf/10.1007/BF01206525.pdf

Polykretis, P., & McCullough, P. (2022). Rational harm-benefit assessments by age group are required for continued COVID-19 vaccination. *Scandinavian Journal of Immunology*. https://doi.org/10.1111/sji.13242

Pradhan, P., Pandey, A. K., Mishra, A., Gupta, P., Tripathi, P. K., Menon, M. B., Gomes, J., Vivekanandan, P., & Kundu, B. (2020). *Uncanny similarity of unique inserts in the 2019-nCoV spike protein to HIV-1 gp120 and Gag* [Preprint]. Evolutionary Biology. https://doi.org/10.1101/2020.01.30.927871

Pretorius, E., Mbotwe, S., Bester, J., Robinson, C. J., & Kell, D. B. (2016). Acute induction of anomalous and amyloidogenic blood clotting by molecular amplification of highly substoichiometric levels of bacterial lipopolysaccharide. *Journal of The Royal Society Interface*, *13*(122), 20160539. https://doi.org/10.1098/rsif.2016.0539

Proal, A. D., & VanElzakker, M. B. (2021). Long COVID or Post-acute Sequelae of COVID-19 (PASC): An Overview of Biological Factors That May Contribute to Persistent Symptoms. *Frontiers in Microbiology*, *12*. https://doi.org/10.3389/fmicb.2021.698169

Raveendran, A. V., Jayadevan, R., & Sashidharan, S. (2021). Long COVID: An overview. *Diabetes & Metabolic Syndrome*, *15*(3), 869–875. https://doi.org/10.1016/j.dsx.2021.04.007

Red Blood Cell. (2019). In *Wikipedia*. https://en.wikipedia.org/w/index.php?title=Red_blood_cell&oldid=925073357

Redert, A. (2023). *Causal effect of covid vaccination on mortality in Europe*. https://www.researchgate.net/publication/368777703_Causal_effect_of_covid_vaccination_on_mortality_in_Europe

Reese, G. (Director). (2022, March 10). *Klaus Schwab & Hunter Biden Connected To Ukraine Bio-Labs*. https://www.bitchute.com/video/egzoOM7EcP31/

Rubin, R. (2020). As their numbers grow, COVID-19 "long haulers" stump experts. *JAMA*, *324*(14), 1381–1383. https://doi.org/10.1001/jama.2020.17709

Ryu, J. K., Sozmen, E. G., Dixit, K., Montano, M., Matsui, Y., Liu, Y., Helmy, E., Deerinck, T. J., Yan, Z., & Schuck, R. (2021). SARS-CoV-2 spike protein induces abnormal inflammatory blood clots neutralized by fibrin immunotherapy. *Biorxiv*, 2021–10. https://doi.org/10.1101/2021.10.12.464152

Sahin, U., Karikó, K., & Türeci, Ö. (2014). mRNA-based therapeutics—Developing a new class of drugs. *Nature Reviews Drug Discovery*, *13*(10), Article 10. https://doi.org/10.1038/nrd4278

Santiago, D. (2022a). A partial answer to the question posed by David A. Hughes, PhD, in the article: "What is in the so-called COVID-19 'vaccines'? Part 1: evidence of a global crime against humanity." *International Journal of Vaccine Theory, Practice, and Research*, *2*(2), 587–594. https://doi.org/10.56098/ijvtpr.v2i2.56

Santiago, D. (2022b). Playing Russian Roulette with every COVID-19 injection: The deadly global game. *International Journal of Vaccine Theory, Practice, and Research*, *2*(2), 619–650. https://doi.org/10.56098/ijvtpr.v2i2.36

Schelenz, R., & Long, Z. (2021, May 19). *The COVID vaccine came out super quickly. Here's why it's safe. | University of California*. https://www.universityofcalifornia.edu/news/covid-vaccine-came-out-super-quickly-heres-why-its-safe

Schwab, C., Domke, L. M., Hartmann, L., Stenzinger, A., Longerich, T., & Schirmacher, P. (2022). Autopsy-based histopathological characterization of myocarditis after anti-SARS-CoV-2-vaccination. *Clinical research in cardiology : official journal of the German Cardiac Society*, 1–10. Advance online publication. https://doi.org/10.1007/s00392-022-02129-5

Segalla, G. (2023). Chemical-physical criticality and toxicological potential of lipid nanomaterials contained in a COVID-19 mRNA vaccine. *International Journal of Vaccine Theory, Practice, and Research*, *3*(1), 787–817. https://doi.org/10.56098/ijvtpr.v3i1.68

Seneff, S., & Nigh, G. (2021). Worse than the disease? reviewing some possible unintended consequences of the mRNA vaccines against COVID-19. *International Journal of Vaccine Theory, Practice, and Research*, *2*(1), 38–79. https://doi.org/10.56098/ijvtpr.v2i1.23

Seneff, S., Nigh, G., Kyriakopoulos, A. M., & McCullough, P. A. (2022). Innate immune suppression by SARS-CoV-2 mRNA vaccinations: The role of G-quadruplexes, exosomes, and MicroRNAs. *Food and Chemical Toxicology*, *164*, 113008. https://doi.org/10.1016/j.fct.2022.113008

Pharmaceutical Technology. (2023, March 11). COVID-19 Vaccination Tracker: Daily Rates, Statistics & Updates. *Pharmaceutical Technology*. https://www.pharmaceutical-technology.com/covid-19-vaccination-tracker/

Shrestha, Patrick C. Burke, Amy S. Nowacki, James F. Simon, Amanda Hagen, Steven M. Gordon (2022-preprint). Effectiveness of the coronavirus disease 2019 (COVID-19) bivalent vaccine. medRxiv 2022.12.17.22283625; doi: https://doi.org/10.1101/2022.12.17.22283625

Syed, A. K. (2021, December 28). How to BLAST your way to the truth about the origins of COVID-19 [Substack newsletter]. *Arkmedic's Blog*. https://arkmedic.substack.com/p/how-to-blast-your-way-to-the-truth

Tartof, S. Y., Slezak, J. M., Fischer, H., Hong, V., Ackerson, B. K., Ranasinghe, O. N., Frankland, T. B., Ogun, O. A., Zamparo, J. M., Gray, S., Valluri, S. R., Pan, K., Angulo, F. J., Jodar, L., & McLaughlin, J. M. (2021). Effectiveness of mRNA BNT162b2 COVID-19 vaccine up to 6 months in a large integrated health system in the USA: A retrospective cohort study. *The Lancet*, *398*(10309), 1407–1416. https://doi.org/10.1016/S0140-6736(21)02183-8

Thomas, S. J., Moreira Jr, E. D., Kitchin, N., Absalon, J., Gurtman, A., Lockhart, S., Perez, J. L., Pérez Marc, G., Polack, F. P., & Zerbini, C. (2021). Safety and efficacy of the BNT162b2 mRNA COVID-19 vaccine through 6 months. *New England Journal of Medicine*, *385*(19), 1761–1773. https://doi.org/10.1056/NEJMoa2110345

Thorp, J. A., Rentz, T., Northrup, C., Lively, C., Breggin, P., Bartlett, R., & et al. (2022). Patient betrayal: The corruption of healthcare, informed consent and physician-patient relationships. *The Gazette of Medical Sciences* 3(1), 46-69. https://www.doi.org/10.46766/thegms.medethics.22021403

Trigoso, E. (2022, September 2). *Embalmers Have Been Finding Numerous Long, Fibrous Clots That Lack Post-Mortem Characteristics*. Www.Theepochtimes.Com. https://www.theepochtimes.com/embalmers-have-been-finding-numerous-long-fibrous-clots-that-lack-post-mortem-characteristics_4696015.html

Trump, D. (2020a, July 27). *Remarks by President Trump in Press Briefing on COVID-19 – The White House*. https://trumpwhitehouse.archives.gov/briefings-statements/remarks-president-trump-press-briefing-covid-19/

Trump, D. (2020b, November 13). *Remarks by President Trump During an Update on Operation Warp Speed – The White House*. https://trumpwhitehouse.archives.gov/briefings-statements/remarks-president-trump-update-operation-warp-speed/

Tuvali, O., Tshori, S., Derazne, E., Hannuna, R. R., Afek, A., Haberman, D., Sella, G., & George, J. (2022). The Incidence of Myocarditis and Pericarditis in Post COVID-19 Unvaccinated Patients -A Large Population-Based Study. *Journal of clinical medicine*, *11*(8), 2219. https://doi.org/10.3390/jcm11082219

United States Census Bureau. (2023, March 10). *United States Population Growth by Region*. https://www.census.gov/popclock/data_tables.php?component=growth

United States Census Bureau>> (n.d.). *Population Estimates and Projections*. Census.Gov. Retrieved March 20, 2023, from https://www.census.gov/data/developers/data-sets/popest-popproj.html

United States Department of Health and Human Services (US DHHS), Centers for Disease Control and Prevention (CDC), National Center for Health Statistics (NCHS), Bridged-Race Population Estimates, United States July 1st resident population by state, county, age, sex, bridged-race, and Hispanic origin. Compiled from 1990-1999 bridged-race intercensal population estimates (released by NCHS on 7/26/2004); revised bridged-race 2000-2009 intercensal population estimates (released by NCHS on 10/26/2012); and bridged-race Vintage 2020 (2010-2020) postcensal population estimates (released by NCHS on 9/22/2021). Available on CDC WONDER Online Database. Accessed at http://wonder.cdc.gov/bridged-race-v2020.html on Mar 10, 2023 2:06:55 PMVaccine Tracker. (2022, October 6). More Than 12.7 Billion Shots Given: Covid-19 Tracker. *Bloomberg.Com*. https://www.bloomberg.com/graphics/covid-vaccine-tracker-global-distribution/

Wan, Y., Shang, J., Sun, S., Tai, W., Chen, J., Geng, Q., He, L., Chen, Y., Wu, J., Shi, Z., Zhou, Y., Du, L., & Li, F. (2020). Molecular Mechanism for Antibody-Dependent Enhancement of Coronavirus Entry. *Journal of Virology*, *94*(5), e02015-19. https://doi.org/10.1128/JVI.02015-19

Wassie, G. T., Azene, A. G., Bantie, G. M., Dessie, G., & Aragaw, A. M. (2020). Incubation period of severe acute respiratory syndrome novel coronavirus 2 that causes coronavirus disease 2019: A systematic review and meta-analysis. *Current Therapeutic Research, Clinical and Experimental*, *93*, 100607. https://doi.org/10.1016/j.curtheres.2020.100607

Weisel, J. W., & Litvinov, R. I. (2017). Fibrin Formation, Structure and Properties. In D. A. D. Parry & J. M. Squire (Eds.), *Fibrous Proteins: Structures and Mechanisms* (pp. 405–456). Springer International Publishing. https://doi.org/10.1007/978-3-319-49674-0_13

Welch's *t*-test. (2023). In *Wikipedia*. https://en.wikipedia.org/w/index.php?title=Welch%27s_t-test&oldid=1132254179

Wikipedia (2023). 2019 Military World Games. In *Wikipedia*. https://en.wikipedia.org/w/index.php?title=2019_Military_World_Games&oldid=1136296333

Woodruff, M. C., Ramonell, R. P., Lee, F. E.-H., & Sanz, I. (2020). Clinically identifiable autoreactivity is common in severe SARS-CoV-2 Infection. *MedRxiv*, *10*. https://doi.org/10.1101/2020.10.21.20216192

Yanowitz, S. (Director). (2022, April 20). *Evidence of self-assembling structures in C19 injection vials*. https://www.bitchute.com/video/e9mvTko2Ts0T/

Yip, M. S., Leung, H. L., Li, P. H., Cheung, C. Y., Dutry, I., Li, D., Daëron, M., Bruzzone, R., Peiris, J. S., & Jaume, M. (2016). Antibody-dependent enhancement of SARS coronavirus infection and its role in the pathogenesis of SARS. *Hong Kong Medical Journal = Xianggang Yi Xue Za Zhi*, *22*(3 Suppl 4), 25–31. https://hub.hku.hk/handle/10722/234335

Yount, B., Denison, M. R., Weiss, S. R., & Baric, R. S. (2002). Systematic assembly of a full-length infectious c[coronavirus]DNA of mouse hepatitis virus strain A59. *Journal of Virology*, *76*(21), 11065–11078. https://doi.org/10.1128/JVI.76.21.11065-11078.2002

Supplementary Files (Source Data for Statistical Analyses)

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