International Journal of Vaccine Theory, Practice, and Research
IJVTPR

A Closer Look at N1-methylpseudouridine in the Modified mRNA Injectables

Daniel Santiago RPh, PharmD

Pharmacist in Florida and member of the Editorial Board for *IJVTPR* sanshou1428@protonmail.com (ORCID https://orcid.org/0000-0001-5975-0592)

Abstract

Introducing 728 N1-methylpseudouridines into the spike coding sequence for SARS-CoV-2 has inevitably resulted in physical changes in the original SARS-CoV-2 coding sequence. These non-negligible physical changes include: (1) stereochemical alterations; (2) variations in molecular weight; and (3) changes in the nucleotide base count consisting of A, G, T(U, Ψ), C. Assuming only that things are going as planned by the inventors of the new technology, the physical changes in each of the 728 substitutions in the SARS-CoV-2 spike coding sequence, where a uridine is replaced with an N1-methylpseudouridine, engages the ribosome as it reads, interprets, and translates the modified mRNA spike coding sequence into a specific sequence of amino acids. Whatever the peptide/protein sequence turns out to be must set up a cascading series of downstream consequences from whatever adjustments occur in the largely unpredictable peptide/protein sequences being produced by the ribosome. The stereoscopic changes in moving from uridine to pseudouridine involve rotating the uracil ring structure 180º and shifting three carbon positions clockwise; then, the further modification of pseudouridine to N1-methylpseudouridine involves the introduction of a methyl group leading to even more noticeable changes in the stereochemical configuration. I also document physical changes in molecular weight and in base count. Such physical modifications must have cascading effects on interactions across all levels of the downstream peptide/protein products produced from the never before encountered sequences of nucleotides. Given such physical modifications, can the proteinaceous materials produced by the modified mRNA coding sequences lead to the production of effective antibodies against the SARS-CoV-2 spike protein? What can be expected from repeated exposures to these foreign modified mRNA sequences through multiple doses and subsequent booster injections? Empirical outcomes, it seems, get worse with each new dose rather than better.

Keywords: *modified mRNA spike coding sequence, N1-methylpseudouridine, pseudouridine, SARS-CoV-2 spike coding sequence*

Introduction

On December 11, 2020 the Pfizer COVID-19 product was approved for Emergency Use Authorization by the FDA (Maass, 2020), and on December 14, 2020 (Associated Press, 2022), the modified mRNA technology began to be introduced into the human genome through the first Pfizer and Moderna injectables. Other products, claiming different underlying technologies, in addition to the modified mRNA platform of Pfizer and Moderna, were deployed as well, but the leading products in the western nations are the ones I want to examine more closely. According to Pharmaceutical Technology (2024), COVID-19 injections from all the manufacturers world-wide months ago surpassed 13 billion in more than 5 billion people. A huge part of that injected population received the Pfizer and Moderna products supposedly coding a form of the SARS-CoV-2 spike protein. However, in every one of the billions of modified mRNA strings (Fleming, 2021, p. 99) — or perhaps as many as 10 trillion such strings (Tuuminen, 2024; Ulrich, 2024) — there were 728 substitutions of N1-methylpseudouridine (Nance & Meier, 2021). These modified coding strings were reportedly loaded into the lipid nanoparticles of the Pfizer and Moderna products in order to cloak them from the body's defense systems and to make them more stable and thus longer-lived (Nance & Meier, 2021). It was claimed, however, that the new technology would "naturally decompose" and would "not integrate into genomes" after injection. However Brogna et al. (2023), detected spike protein from the particular sequence coded in the injectables for up to 187 days after the injections were received by their study participants.[1] More specifically, they found "a double amino acid change" from the original SARS-CoV-2 spike protein "at position 986 and 987". At those positions "the amino acids lysine [one-letter code K] and valine [V] are both replaced by two proline amino acids [PP]" (Brogna et al., 2023, p. 2). They found spike proteins with the PPs "in 50% of the biological samples [from recipients of the injectables that they] analyzed" (p. 2). That sequence, they claimed, has never been seen in any of the so-called "wild-type" (Wt) sequences of which "[m]ore than 6,600,000 SARS-CoV-2 genomes have been sequenced" (p. 6). Brogna et al. called the modified synthetic coding sequence "PP". That sequence should also appear from injections of the modified coding sequences aimed at mutant-variants of the original SARS-CoV-2 virus (Bansal et al., 2021; Brogna et al., 2023; Brogna, Viduto, et al., 2023).

According to Steven Pelech, "From each genetically modified RNA molecule, it is feasible that hundreds of copies of the spike protein can be produced" (Pelech & Shaw, 2024, p. 252 in Chapter 12). Combining Pelech's prediction with the claim by Ulrich that every single dose of the Pfizer or Moderna products contains upwards of 10 trillion modified RNA molecules, the aberrant peptide/protein sequences in any given recipient of a single dose, could number in the hundreds of trillions. Oller and I suggested that the instability of the consequent products, likely to be long-lasting according to Brogna, et al. (2023), may partially or fully account for the strange whitish rubbery clots being found by clinicians in living recipients of the injectables, and by embalmers in the corpses of such recipients. Shaw and Pelech (2024) have written that the findings of the outspoken embalmers

[1] Because the study ended after 187 days from when the last injections were administered to its participants, it is not known for how long the spike protein from the injections could have been present if the study had been extended beyond 187 days. What is certain is that the spike protein coming from the shots was still present when the researchers stopped tracking the participants.

> have been confirmed in a survey that was prepared by Tom Haviland and Laura Kasner, which was sent to 30 state funeral director/embalmer associations and 800 funeral homes primarily in the USA to determine if they were seeing unusual blood clots in corpses. From 128 respondents: 68.75% had observed large whitish "fibrous" structures/clots in the corpses embalmed [A Midwestern Doctor, 2023]. Traditional "grape jelly" clots were reported by 66.4% of the respondents, especially in 2020, 2021, and 2022. In 2022, about 68.7% of the respondents observed large whitish, "fibrous" structures/clots, with 44% of the respondents finding these in cadavers 20% or more of the time. These clots were primarily found in the neck and legs. At the Canadian NCI Hearings on COVID-19, Laura Jeffrey noted that in her 27 years of experience as a funeral director, she [only] observed these unusual clots starting in the Spring of 2021, and had not seen these before in all of her years in the industry [Jeffrey, 2023].

Oller and I have written about the abundance of aberrant proteinaceous material in the bodily tubes of many of the recipients of injections of the experimental material (Santiago, 2022a, 2022b; Oller & Santiago, 2022; Santiago & Oller, 2023) and I have spoken about them in a readily available on-line Solari Report put together with the assistance of Ulrike Granögger (2023). Also, Mulroney et al. (2023) actually demonstrated empirically the kind of misreading of the modified mRNA that Oller and I wrote about. Our argument was based on open reading frames that could theoretically be impacted in multiple ways by the sort of "frameshifting" that Mulroney and 19 other colleagues demonstrated.

N1-methylpseudouridine (Ψ)

With the foregoing in mind, I want to focus attention on the modified nucleotide, N1-methylpseudouridine (Ψ). More specifically, I want to address the inevitable contribution that N1-methylpseudouridine (Ψ) substitutions for uridine make in the physical (1) steric arrangement, (2) molecular weight, and (3) nucleotide base counts. The targeted protein molecule is supposedly a recognizable variant of the original SARS-CoV-2 "wild-type" (Wt) spike protein of which millions have been sequenced. However, I will argue here that the synthetic PP-type sequences containing the N1-methylpseudouridine substitutions for uridine, must produce different downstream amino acid sequences, which in their turn must also, therefore, have different functional consequences than the original so-called Wt SARS-CoV-2 spike protein.

All of this can be effectively argued on the basis of the very simple lock-and-key principle of traditional pharmacology. If we change the molecular composition of the expected coding sequence in the mRNA delivered to the cell's ribosome, the aminos strung together in the protein(s), or whatever peptide fragments are produced in response to that coding sequence, must be impacted. Although no one can predict exactly what will happen in the 10 trillion cells which according to Ulrich (2024) are potentially commandeered in any given recipient of one of the Pfizer or Moderna products, what can be hypothesized is that the molecular changes progressing from uridine to pseudouridine to N1-methylpseudouridine — changes that I will document here in some detail — must be expected to cause countless problems in the body's deeply interconnected maintenance, repair, and defense systems as discussed by Oller (2022, pp. 229-260).

In what follows here, I will detail why I think disastrous outcomes are probably occurring on account of the many substitutions of N1-methylpseudouridine for uridine in the coding for the SARS-CoV-2 protein packaged in the billions, or trillions as the case may be, of lipid nanoparticles of the Pfizer and Moderna products. Perhaps the simplest and most explanatory way to account for

all the new COVID-19 diseases associated with the injectables is to merely examine the likely reasons for the production of a great variety of dysfunctional peptides along with whatever other foreign DNAs (Tuuminen, 2024), toxic lipid nanoparticles (Ulrich, 2024; Lee & Broudy, 2024), foreign toxic metals, etc. (Diblasi et al. 2024) happen to be contained in the injectables. All the confusion that such foreign entities create may well throw the body's defenses into a dysfunctional state and thay begin to attack the organelles, cells, tissues, and organ systems they are supposed to protect.

(1) Steric Changes from Uridine (U) to N1-methylpseudouridine (m1Ψ)

The modified nucleotide, N1-methylpseudouridine, is the basis of the issue at hand. The problem is to know how the modified mRNA, with 728 N1-methylpseudouridines (correctly designated as m1Ψ, but I will abbreviate this to just Ψ which is commonly used for designating pseudouridine, but that is not the way I am using it here) inserted in place of canonical uridines (U) will interact with the natural maintenance-repair-defense (Oller, 2022) systems of living recipients of the Pfizer and Moderna injectables (Oller & Santiago, 2022; Santiago & Oller, 2023). The substitutions must have a significant impact. If we consider the strings of sequences as directions written in a certain language but where the N1-methylpseudouridine substitutions have been made, then the 728 substitutions are something like taking out a meaningful word (or phrase) and replacing it in 728 different places, in a potentially meaningful discourse, with an unknown foreign word (or phrase) in each of those places. Normally, these kinds of substitutions in any language will impact the comprehensibility of the text in a disruptive manner. So why would that not occur in the instructions to the body's ribosomes about what sequences of aminos to place in the proteins that are to be constructed? All I want to do in this article is to show why the substitutions of N1-methylpseudouridine in 728 positions where a uridine is expected must tend to disrupt the shape, weight, and composition of the different proteins likely to be manufactured by the ribosomal systems of the body.

To be clear, a naturally prevalent archaeal nucleotide from single cell organisms, N1-methyl-pseudouridine — as supposedly contained in the COVID injectables, provided we accept at least that much of the doubtful mainstream narrative flowing from the proponents of the Pfizer and Moderna concoctions (Nance & Meier, 2021; Ulrich, 2024) — has no known natural role a human being. The leaps across biosignaling systems that are separated by many levels of processing from tRNA in a prokaryote (an Archaeal yeast) to the mRNA in an extremely complex eukaryote (*Homo sapiens*), is not likely to work well, to the extent that it works at all, at the higher eukaryote level.

Figure 1 (on the following page) illustrates certain steric changes necessary to transform uridine to N1-methylpseudouridine. At the top, I have pointed out that the chemical formula for uridine is $C_9H_{12}N_2O_6$ compared to $C_{10}H_{14}N_2O_6$ for N1-methylpseudouridine. If the intended protein structures were perfectly formed in pristine completeness during the rushed and inadequately supervised manufacturing process with the Pfizer and Moderna nanotechnology (Gutschi, 2022; Speicher et al., 2023) with no misreadings and no frame-shifts, antibodies to the spike proteins coded in the modified mRNA would still be stereoscopically so different from the "wild-type" SARS-CoV-2 spikes that the functions would have to be different as well. Moreover, recent research seems to show conclusively that differences between the virus and the DNA template using T7 bacteriophage polymerase for transcription into mRNA for the injectables is surprisingly error prone. Although the modified mRNA platform of Pfizer and Moderna requires that the mRNA packed into each of the 10 trillion or so lipid nanoparticles should be identical or almost identical on

each T7 replication, according to Bradley et al. (2022; 2024) that is not so for the SARS-CoV-2 "wild-type" spike and it also cannot be true for the PP spikes manufactured by Pfizer and Moderna. Given that each mRNA construct is supposed to be 4250 nucleotides in length, each manufactured modRNA likely has one or two errors in it before it even gets to the ribosomes to be translated into protein. The resulting trillions of peptides multiplied by the hundred or more replications of each coding sequence (according to Pelech and Shaw) in modified mRNA may generate some or all of the foreign tube clogging proteinaceous material being pulled from blood vessels, lymphatic ducts, and even respiratory tubes by clinicians and embalmers.

There must also be differences in molecular mass (as shown in section *2*) and in the base count (as shown in my section numbered *3*) for both the "wild-type" SARS-CoV-2 spike proteins and the various ribosome manufactured proteins in the Pfizer and Moderna injectables supposedly of the PP type according to Brogna, et al. (2023). We must predict from the mechanistic lock-and-key pharmacology that the use of the Pfizer and Moderna products being referred to can only disintegrate into chaos in the bodies of recipients of those hastily made concoctions.

The reader will notice that the steric changes visible in all three rows of Figure 1 take place above the pentagonal structure plainly visible in the first two rows of the chemical diagrams which pertain to the connection with the ribosome. That part is actually identical across all three rows of Figure 1. The significant changes take place in the upper portion, more or less the upper half of each molecular diagram, where the reader will see hexagonal structures containing two dark blue balls representing nitrogen atoms and four aqua colored balls representing carbon atoms. Together those six atoms make up the central structure of each molecule that must be modified to transform uridine to N1-methylpseudouridine.

Each of the diagrams in the leftmost column of Figure 1 represent the stereochemical structure of uridine. In the second column to the right, each diagram represents the intermediate transformation of the uracil component where the hexagonal ring at the top has been rotated 180° to achieve the structure seen in the second column from the left which is an intermediate form of uridine with the described uracil transformation on its way to becoming pseudouridine. Each diagram then in the third column from the left, shows the same hexagonal structure rotated clockwise by three carbon positions displacing the two nitrogen atoms so that they appear at the top of the hexagon and the two oxygen atoms are now in the rough orientation of an ell-shape at the right-hand side of the hexagon. Finally, to complete the transformation going from pseudouridine to N1-methylpseudouridine, a methyl group must be added in the form of the carbon atom that is attached to the leftmost nitrogen atom in the last column of Figure 1.[2]

In the bottom row of Figure 1, the van der Waal's force shapes are added to show the differences in the space theoretically occupied by the orbital sphere of each of the atoms in the distinct stereoscopic structures. The point is to show that the stereoscopy at each step is radically different in going from uridine to N1-methylpseudouridine. The expected result of those differences is that the

[2] Incidentally, I demonstrate all of these three-dimensional transformations with a physical ball and stick model in a video linked here.

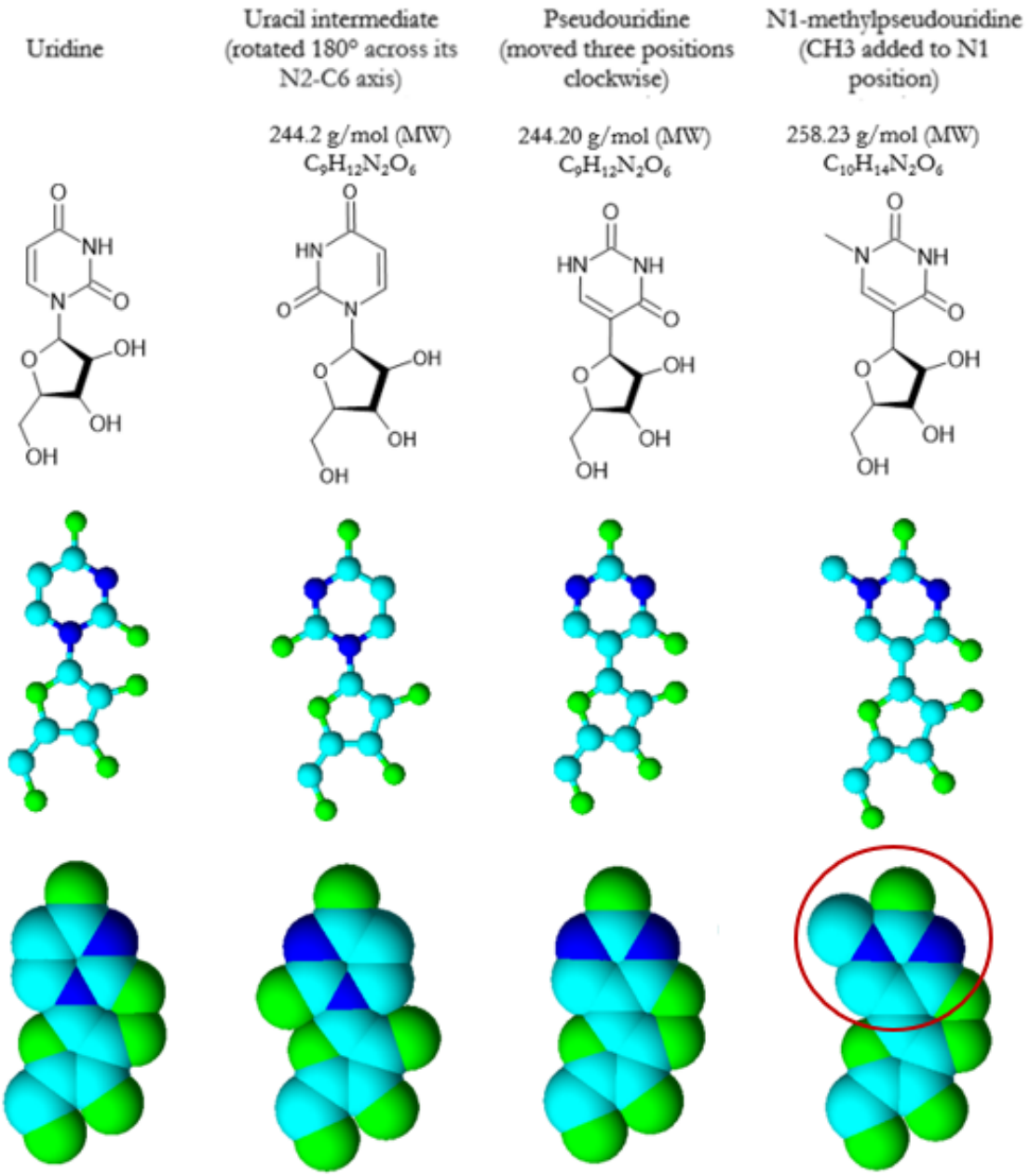

Figure 1. A series of chemical diagrams showing the transformation from uridine to N1-methylpseudouridine: the top row shows the traditional flat (two dimensional textbook chemical diagrams); the second row shows the three-dimensional ball-and-stick models; and the third row shows the three-dimensional van der Waals distance-dependent force interaction spaces theoretically occupied by the atoms involved. In the colored diagrams, aqua represents carbon; green, oxygen; and dark blue, nitrogen. The parts that are changing as the progression takes place from uracil to N1-methylpseudouridine are shown left to right across the page. Sources: PubChem, Uridine $C_9H_{12}N_2O_6$, CID 6029; Pseudouridine, $C_9H_{12}N_2O_6$, CID 15047; ACS, N1-Methylpseudouridine — American Chemical Society (acs.org). Drawn by the author with Molview.com and ChemSketch programs.

protein products constructed from strings of modified mRNA containing 728 of the N1-methylpseudouridine molecules substituted for natural uridines will be shocking to the maintenance, repair, and defense systems of every living body that encounters them. They may be regarded as threatening foreign material. At the same time, the strange foreign sequences being produced containing the PP, sequence rather than the KV sequence at positions 686 and 687, is not likely to provide a basis for the body's immune defenses to generate effective antibodies to attack, much less to dispatch, the "wild-type" SARS-CoV-2 spike protein. They can be expected to be sufficiently dissimilar, even if there are no shifts in the open reading frames that Oller and I predicted would be common, so that the new proteinaceous junk produced by the strangely modified mRNA coding sequences creates sufficient confusion to engender the kinds of disease conditions observed by Mead et al. and the auto-immunities predicted by Lyons-Weiler, and by Vojdani and his colleagues.

Given the differences between uridine and N1-methylpseudouridine, the question arises whether the conjugations required between the foreign spike coding sequence and the ribosomal interpretation leading to a string of aminos in a peptide or protein sequence will make any sense. Or will they be more-or-less meaningless junk proteins coming out of the translation from the modified mRNA to whatever peptides/proteins may be produced? My guess is in favor of meaningless proteins resulting in the whitish clots because the keys do not fit in the locks and the conjugations aimed for by the creators of the COVID-19 concoctions cannot occur. Figure 2 shows why I think this is so. In the top half the reader can see the chemical structure the left for the codon AUG, the canonical initiator of the vast majority of ordinary functional proteins in the human body, and in the right half of the top of that same figure the reader can see the Van der Waal's dynamic shape of that same structure. In the bottom half of Figure 2, at the left is given the standard chemical diagram for Adenosine, N1-methylpseudouridine, Guanosine (AΨG) which corresponds to the start codon in the foreign spike coding sequence of the modified mRNA of the Pfizer and Moderna products that may be creating problems with white clots. My theory about why this is happening is that the lock and key model completely breaks down between the top and bottom of Figure 2. The differences that guarantee the key will not fit in the lock, and vice versa, the lock cannot receive the key appropriately, are highlighted with the red circles that I have added to the top and bottom parts of the right-hand side of Figure 2. With a change of stereoscopy as large and evident as the one shown, will the ribosome be able to correctly interpret the START codon when it is so radically modified, not to mention all the other codon(s) that have incorporated the modified nucleotide(Ψ) as exhibited in Table 1?

(2) Molecular Weight Differences of U to Ψ

There exist significant differences in the amino acid sequences produced by the SARS-CoV-2 spike protein "CDS1" as shown in Figure 3 (below) at the left hand side as recorded by the National Library of Medicine (2020) and the modified mRNA for BNT162b2 as recorded with the World Health Organization (2020) as shown at the right hand side of Figure 3. The differences at the amino acid level begin immediately after the yellow highlighted portions where the last five highlighted aminos on both sides of the figure are the same, TSNFR, but all the ones to follow that are not highlighted are different. These differences are not negligible. The two proteins cannot possibly be the same or even similar. I discussed all this in my Solari presentation on November 21, 2023 (available at this link). Among the potentially crucial differences, are those in molecular weight.

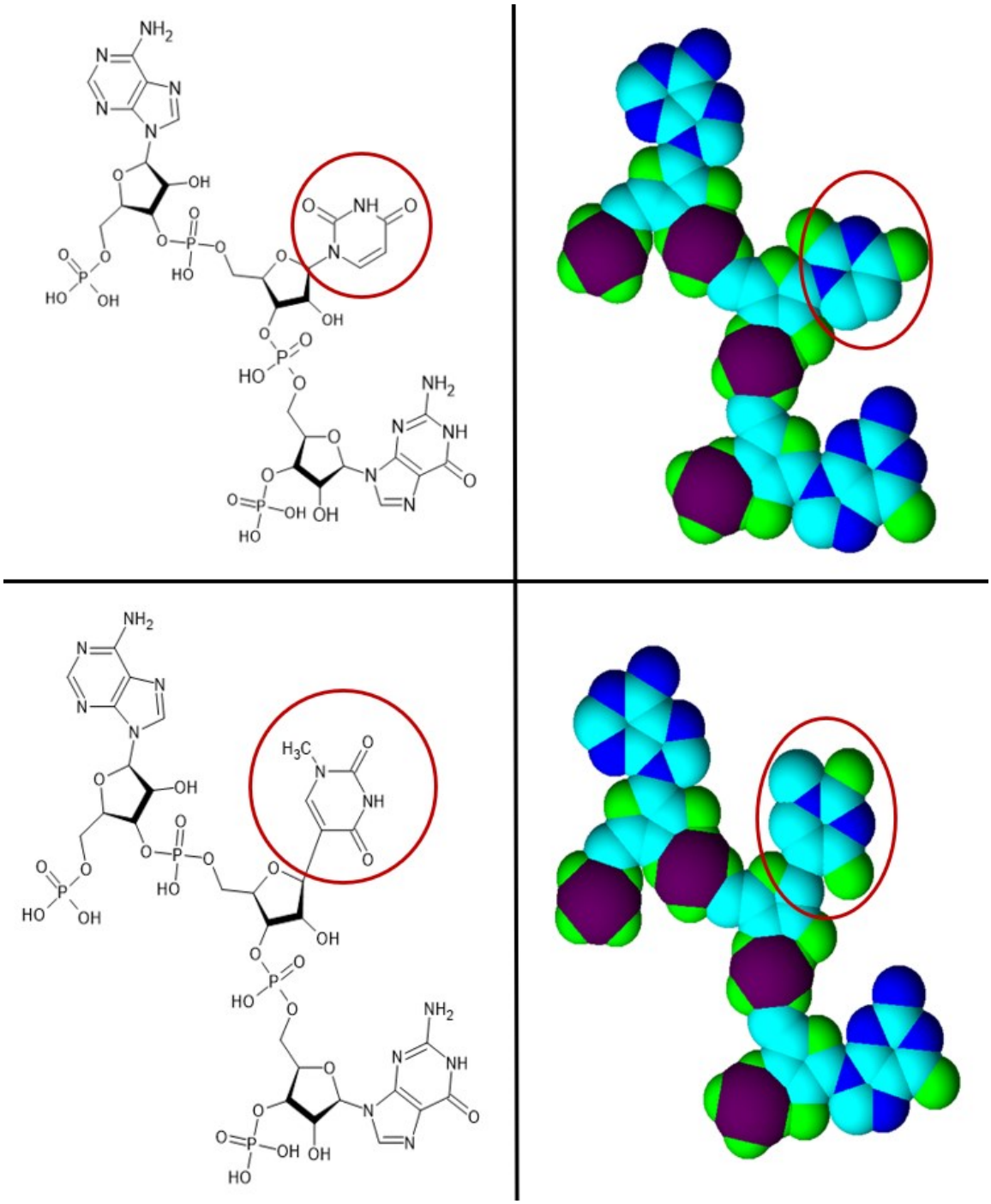

Figure 2. In the top half of this figure at the left is the chemical structure of the start codon AUG containing the canonical uridine encircled, and at the right in the top half is the Van der Waals dynamic stereoscopic shape of that same AUG with its uridine encircled. In the bottom half the chemical formula for the Am1ΨG with uridine replaced by the encircled N1-methylpseudouridine is shown at the left, and at the right the Van der Waals stereoscopic shape with the N1-methylpseudouridine also encircled. Drawn by the author with the Molview.com and ChemSketch programs.

https://doi.org/10.56098/5azda593

Severe acute respiratory syndrome coronavirus 2 Spike Protein CDS1

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDN
PVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSS
ANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLLAL
HRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGIYQTSNFRVQPTESI
VRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVR
QIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAGSTPCNGVEGFNC
YFPLQSYGFQPTNGVGYQPYRVVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDI
ADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGC
LIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMT
KTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSK
RSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQI
PFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISS
VLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQS
APHGVVFLHVTYVPAQEKNFTTAPAICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVN
NTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYI
WLGFIAGLIAIVMVTIMLCCMTSCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

BNT162b2 protein amino acid sequence

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVL
PFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCT
FEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLLALHRSYLTPGD
SSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGIYQTSNFRGSPPNPSCGSPISPICAPSA
RCSMPPDSPLCTPGTGSGSAIAWPTTPCCTTPPASAPSSATACPLPSTTCASQTCTPTASSGEMKCGRLPLDRQARSPTTTTSC
PTTSPAVLPGTATTWTPKSAATTITCTGCSGSPISPSSGTSPPRSIRPAAPLVTAWKASTATSHCSPTAFSPQMAWAISPTEWW
CASNCCMPLPQCAALRKAPISRTNATSTSTAPAPACQRATRSSCHSSSLAGISPIPQTPLEIPRHWKSWTSPLAASAECLSPLAP
TPAIRWQCCTRTTVPKCPWPFTPISHLHGGCTPPAAMCFRPEPAVSEPSTTIATSATSPSALESAPATRHRQTALGEPEAWPAR
ASLPTQCLWAPRTAWPTPTTLSLSPPTSPSAPQRSCLCPPRPAWTAPCTSAAIPPSAPTCCCSTAASAPSIEPQGSPWNRTRTP
KRCSPKSRSTRPLLSRTSAASISARFCPILASPASGASSRTCCSTKHWPTPASSSSMAIVWATLPPGIFAPRSLTDQCCLLCPMRS
PSTHLPCWPAQSQAAGHLEQAPLCRSPLLCRWPTGSTASEPRMCCTRTRSSPTSSTAPSARSRTAAAQQAPWESCRTWSTR
MPRHTPWSSSCPPTSAPSALCTISADWTLLRPRCRSTDSQADCRASRHTPSSSEPPRLEPLPIWPPPRCLSVCWARAREWTF
AARATTASLSLPLTAWCFCTHMCPLKRRISPPLQPSATTAKPTFLEKACSCPTAPIGSHSGTSTSPRSSPPTTPSCLATATSSALTIP
CTTLCSPSWTASKRNWTSTLRTTQAPTWTWAISAESMPASTSRKRSTGTRWPRITRASTCKNWGSTSSTSSGPGTSGWALS
PDLPSWSQSCCVAPAAVAARAVVAVAAAASSTRTILSPCRANCTTH

Figure 3. At left is the amino acid sequence for the wild-type SARS-CoV-2 spike protein from (National Library of Medicine, 2020) and at right is the amino acid sequence for BNT162b according to the International Nonproprietary Names, number 11889, filed with the World Health Organization (2020) for the messenger RNA encoding the full-length SARS-CoV-2 spike glycoprotein.

Technically speaking, the molecular mass is not the same as molecular weight (even though the numerical value is the same), M, of a chemical compound is defined as the ratio between the mass and the amount of substance (measured in moles) of any sample of the compound (Mills et al., 1993, p. 63). Although used interchangeably; the direct relationship is simply changing the units while keeping the numerical value the same. Having noted that difference, both interpretations are relevant here. I am focusing on in this section was suggested by L. Maria Gutschi, PharmD, in a question posed in a different presentation, one that I addressed during my Solari talk: namely, why is there a substantial molecular weight difference in the protein produced by the Sars CoV-2 versus the BNT162b2? The shifts are due to the substitution of the 728 uridines being replaced by N1-methylpseudouridines and the fact that some codons in the original SARS-CoV-2 spike coding sequencee were substituted by others, which are supposed to code for the same "amino acid" (Demongeot 2022) as seen in Table 1.

Table 1

Changes in the Codons from the Canonical Wild-Type SARS-CoV-2 Coding Sequence with Uridine to the Codons in the Modified mRNA BNT162b2 Coding Sequence with N1-methylpsuedouridine (with Unexplained Substitutions in the Highlighted Nucleotides in Different Codons Supposedly Calling for the Same Amino Acids)

Spike protein*	Sequence*											
Sars-Cov-2 (*VIRUS*)	CUU	GAC	AAA	GUU	GAG	GCU	GAA	GUG	CAA	AUU	GAU	AGG
	Leu	Asp	Lys	Val	Glu	Ala	Glu	Val	Gln	Ile	Asp	Arg
BioNTech BNT162b2 (*VACCINE*)	CΨG	GAC	CCΨ	CCΨ	GAG	GCC	GAG	GΨG	CAG	AΨC	GAC	AGA
	Leu	Asp	***Pro***	***Pro***	Glu	Ala	Glu	Val	Gln	Ile	Asp	Arg
	5- N1-methylpsuedouridines											

* World Health Organization: International Nonproprietary Names Programme. Messenger RNA Encoding the Full-Length SARSCoV-2 Spike Glycoprotein; 11889; 2020. Demongeot, J.; Fougère, C. mRNA COVID-19 Vaccines—Facts and Hypotheses on Fragmentation and Encapsulation. Vaccines 2023, 11, 40. https://doi.org/10.3390/ vaccines11010040

Table 2 on the next page shows that there are some significant shifts in molecular weight and that these modifications change the nucleotide base counts. The N1-methylpseudouridine (Ψ) nucleotide is heavier than the uridine (U) in every substitution and the resulting codons containing these substitutions must also increase in not only in weight but also in mass, and in stereoscopically measured size as well. Table 2 shows the types of shifts for every such substitution in the codons for each of the 20 canonical amino acids found in human proteins. There are exactly 37 codons in the entire table that contain at least one U and therefore are changed by the subtitution of one or more N1-methylpseudouridines. The physical changes we are talking about here are directly attributable to the N1-methylpseudouridines substituted for uridines. I have already pointed out the stereoscopic changes those substitutions must result in, and in Table 2, the weight differences produced by incorporating the stereoscopically different N1-methylpseudouridines nucleotides are shown to be substantial. For every such substitution there is a corresponding minimum weight increase of approximately 14.04 grams per mol in the codon affected.

In consideration of the hand-in-glove and key-in-lock metaphors, the most significant weight contrast between the natural codons containing uridine and the modified codons containing N1-

Table 2

The Amino Acids in Our Proteins with Their Molecular Weights, and the Codons with and without Ψ (N1-methylpseudouridine) Substituted for U (Uridine) Calling for an Amino Acid with Its Particular Molecular Weight*

Alanine-89.094	**Glycine-75.067**	**Methionine(Start)-149.211**	**Stop-307.2**
GCU 770.66	GGU 810.68	AUG 794.68	UAA** 778.68
GCΨ 784.70	GGΨ 824.72	AΨG 808.72	ΨAA 792.72
GCC 769.68	GGC 809.70		UAG*** 794.68
GCA 793.70	GGA 833.72	**Phenylalanine-165.192***	ΨAG 808.72
GCG 809.70	GGG 849.72	UUU 732.60	UGA† 794.68
		ΨΨΨ 774.72	ΨGA 808.72
Arginine-174.204	**His-155.157**	UUC 731.62	
CGU 770.66	CAU 754.66	ΨΨC 759.70	**Threonine-119.120**
CGΨ 784.70	CAΨ 768.70		ACU 754.66
CGC 769.68	CAC 753.68	**Proline-115.132**	ACΨ 768.70
CGA 793.70		CCU 730.64	ACC 753.68
CGG 809.70	**Isoleucine-131.175**	CCΨ 744.68	ACA 777.70
AGA 817.72	AUU 755.64	CCC 729.66	ACG 793.70
AGG 833.72	AΨΨ 783.72	CCA 753.68	
	AUC 754.66	CCG 769.68	**Tryptophan-204.229**
	AΨC 768.70		UGG 810.68
	AUA 778.68	**Serine-105.093**	ΨGG 824.72
Asparagine-132.119	AΨA 792.72	UCU 732.62	
AAU 778.68		ΨCΨ 759.70	**Tyrosine-181.191**
AAΨ 792.72	**Leucine-131.175**	UCC 732.62	UAU 755.64
AAC 777.70	UUA 755.64	ΨCC 744.68	ΨAΨ 783.72
	ΨΨA 783.72	UCA 754.66	UAC 754.66
Aspartic acid-133.103	UUG 771.64	ΨCA 768.70	ΨAC 768.70
GAU 794.68	ΨΨG 799.72	UCG 770.66	
GAΨ 808.72	CUU 732.62	ΨCG 784.70	**Valine-117.15**
GAC 793.70	CΨΨ 759.70	AGU 794.68	GUU 771.64
	CUC 730.64	AGΨ 808.72	GΨΨ 799.72
Cystine-121.15	CΨC 744.68	AGC 793.70	GUC 770.66
UGU 771.64	CUA 754.66		GΨC 784.70
ΨGΨ 799.72	CΨA 768.70		GUA 794.68
UGC 770.66	CUG 770.66		GΨA 808.72
ΨGC 784.70	CΨG 784.70		GUG 810.68
			GΨG 824.72
Glutamine-146.146	**Lysine-146.19**		
CAA 777.70	AAA 801.72		
CAG 793.70	AAG 817.72		
Glutamic acid-147.13			
GAA 817.72			
GAG 833.72			

*Molecular weight of each nucleotide in g/mol: Ψ=258.24, U=244.20, A=267.24, C=243.22, G=283.24.
** The most common STOP codon for humans calls for ochre in almost all bacteria (Belen & Puigbo, 2022).
*** Calls for tryptophan in the mitochondrial code of humans.
†Calls for the amino acid amber in most bacteria.

methylpseudouridine, as presented in Table 2, is observed in the transformation of the UUU codon to ΨΨΨ, which encodes for phenylalanine. This transformation is highlighted in yellow in Table 2. Aside from the alteration in the structural conformation of the contrasting codons, the change in molecular weight, measured in grams per mole (g/mol), is noteworthy. This discrepancy is mainly attributable to the presence of three additional methyl groups in each ΨΨΨ compared to the canonical UUU codon. The magnitude of this change can be partially assessed by comparing the molecular weights: UUU has a molecular weight of 732.60 g/mol, while ΨΨΨ has a molecular weight of 774.72 g/mol; similarly, UUC has a molecular weight of 731.62 g/mol, in contrast to ΨΨC, which has a molecular weight of 759.70 g/mol. Typically, the difference in molecular weight between these codons is within 1 g/mol; however, the modifications result in differences a lot greater than 1 g/mol. Specifically, the molecular weight difference between UUU and ΨΨΨ is 42.12 g/mol, while the difference between UUC and ΨΨC is 27.08 g/mol. Reiterating the central inquiry posed by the key-in-lock metaphor: will the two components continue to interact as intended, with the codon directing the synthesis of the amino acid, and will they still fit together to produce a standard phenylalanine molecule with a molecular weight of 165.192 g/mol? Spelling out some of the details, according to the National Center for Biotechnology Information (2024a) the molecular weight of a single uridine (U) nucleotide is approximately 244.20 g/mol. Consequently, the molecular weight of a sequence of three nucleotides (UUU), coding for phenylalanine is approximately 732.60 g/mol as shown in Table 2**.** Furthermore, a single Ψ nucleotide has an approximate weight of 258.24 g/mol (National Center for Biotechnological Information, 2024b). Therefore, the total molecular weight of a sequence comprising threeΨ nucleotides is calculated as 3 × 258.24 g/mol, resulting in a total of 774.72 g/mol. What rationale supports the assumption that the ribosome will interpret the sequence ΨΨΨ in the same manner as it does UUU, thereby incorporating phenylalanine into the nascent peptide or protein? Is it plausible for this unconventional codon, ΨΨΨ, to be recognized as calling for phenylalanine? In my opinion, the answer is no. If the codon determining the selection of a particular amino acid must align as precisely as a key fits a lock, there must exist some manner of successful communication between the codon and the corresponding amino acid. How can that communication occur if the key does not fit the lock, or if the hand does not fit the glove? Figures 2 presents the stereoscopic differences between the canonical AUG and the foreign AΨG and Figure 1 shows the the tranformation from U to Ψ.

The alterations resulting from the substitutions of N1-methylpseudouridine for uridine are likely to affect downstream interactions from the moment the modified mRNA is administered until the corresponding protein is synthesized and exerts its effects for the duration of its presence in the body. As Oller and I pointed out (2023) following (Nyström & Hammarström, 2022), as well as independently documented by Mead et al. (2024a, 2024b), the outcomes observed in human recipients of these injectables are noteworthy.

The overarching issue, which Oller and I pointed out in our 2023 paper about the abnormal clots, pertains to open reading frames within any given coding sequence typically derived from DNA and subsequently transcribed into mRNA. We illustrated that multiple start codons can exist, wherein the canonical AUG is altered to AΨG in the modified mRNA sequences. It is important to note that DNA can be interpreted from three potential starting points in both the 5' to 3' direction and its reverse complement, resulting in at least six possible initiation sites for each AUG or AΨG codon. This raises critical questions regarding the ribosome's interpretation of an AUG codon that has been converted to an AΨG codon. Also note that other codons in Table 1 are changed as well. The

question is, how many initiation sites will the ribosome use to commence the synthesis of a peptide or protein? Furthermore, what challenges does the ribosome face concerning the various modified STOP codons?

The question regarding the ribosomal mechanisms involved in peptide synthesis remains unanswered with the current technological capabilities for observation. Nevertheless, an analysis of the immediate and long-term effects of the injections administered to hundreds of millions, if not billions, of individuals in multiple doses indicates a generally negative trend that appears to be worsening over time. An increase in the number of doses correlates with a heightened risk. I propose that the molecular weight discrepancies associated with all the codons in the canonical "genetic code" that feature a uridine substituted by an N1-methylpseudouridine may have disruptive implications. Table 2 presents the notable differences in weight for each codon that contains one or more substitutions of N1-methylpseudouridine for uridine. For instance, when comparing the UUU codon, which as I said encodes for phenylalanine, with the ΨΨΨ substituted (foreign) codon, one must consider whether the ribosome will be able to appropriately interpret this change. In typical linguistic contexts, such a radical change to foreign terms would likely render the sequence unintelligible.

The assumption that substituting N1-methylpseudouridine for uridine would result in the same intelligible protein produced by the ribosome is unlikely for two primary reasons: First, it is generally observed that, an increase in the weight constant measured in kilodaltons, abbreviated commonly as kD, or kDa, correlates with an increase in particle radius. It is useful to keep in mind that one kilodalton is equal to 1,000 grams per mol, abbreviated commonly g/mol. The replacement of uridine with N1-methylpseudouridine alters the steric configuration as illustrated in Figures 1 and 2. Consequently, this modification necessitates a change in the lock-and-key fit. Nance and Meier (2021) posited that the incorporation of N1-methylpseudouridine leads to enhanced protein production and helps to evade the body's immune responses, a characteristic that uridine does not have in contrast to N1-methylpseudouridine. Second, substituting a modified nucleotide for the native nucleotide results in a change in the molecular weight of any codon, which potentially changes the call for some amino acid. A string of codons as long as the ones for SARS-CoV-2 spike protein, or the modified mRNA spike protein substitute in BNT162b2 (Figure 3) present significant interpretive difficulties to the body's systems. To enhance the understanding in molecular weight presented in Table 2, it is pertinent to examine the calculated molecular weight of the codon for AUG (coding for methionine), which corresponds to the canonical start codon that directed the ribosome to initiate protein synthesis. The molecular weight of the initiation complex, comprising AUG ($C_{29}H_{38}N_{12}O_{15}$), is approximately 794.681g/mol. This value is derived from the sum of the molecular weights of its constituent nucleotides: 267.24 g/mol for adenosine, 244.20 g/mol for uridine, and 283.241 g/mol for guanosine. In contrast the molecular weight of AΨG ($C_{30}H_{40}N_{12}O_{15}$) is calculated to be 808.721g/mol which includes 267.24 g/mol for adenosine, 258.24 g/mol for N1-methylpseudouridine, and 283.241 g/mol for guanosine. *This results in a difference of 14.04 g/mol on a molecular scale.* To consider these molecules as equivalent would be analogous to asserting the implausible notion that an increase in molecular mass of 14.04 kD does not correlate with an increase in the number of atoms. Such alterations are likely to influence the functional dynamics of the ribosome. Additionally, other codons exhibit even greater differences in molecular weight such as isoleucine, which has a difference of 28.08g/mol (AUU to AΨΨ).

Is it reasonable to expect that alterations in molecular weight and steric configuration may influence the loading and processing mechanisms (such as velocity and transfer of electrons) within the ribosome? The process of protein synthesis in the ribosome is contingent upon molecular interactions (Monroe et al., 2022). The presence of additional functional groups of the modified mRNA codon may impact the hydrogen bonding that the ribosome depends upon. Imagine a chain on a bike consisting of thousands of links with 728 changes in those links. Will the gear sprockets fit the new links enabling the user to pedal the bike? The observed increases in molecular weight are likely to be followed by biological outcomes never before seen in normal human mRNA processing.

(3) *Base Count Deviations from U to Ψ*

My third domain of comparison between uridine to N1-methylpseudouridine substitutions pertains to the base counts of nucleotides in the spike coding sequences in both the injectable formulations and the original "wild-type" SARS-CoV-2 spike protein coding sequences. In his seminal work on the "genetic code" Crick posited that "folding is simply a function of the order of the amino acids". That dictum became known as sequence hypothesis (Cobb, 2017). In normal cellular processes, messenger RNA (mRNA) plays a pivotal role in protein synthesis, as it transmits genetic information from DNA in the nucleus to the ribosomes in the cytoplasm. Ribosomes supposedly interpret the mRNA sequence one codon at at time and, with the assistance of other RNA molecules, translate it into amino acids, thereby enabling protein construction. The essential mRNA is synthesized during transcription and is specific to different species. Notably, the proportion of nucleotide bases exhibits significant variability within and across species (Hamilton et al. 1987). According to Hamilton and colleagues, the optimal context surrounding the start AUG sequence in yeast and mammalian mRNAs varies within and across these species and these differences influence the folding and, consequently the conformation of any given protein.

Proteins fold into intricate and dynamic three-dimensional conformations with their level of complexity deriving from the folding process, which is determined according to Crick's dictum, by their amino acid sequence. The short sequences of amino acids in any given protein are referred to loosely as "peptides". Strings of peptides are referred to as "polypeptides". Every well-formed protein has a unique polypeptide order allowing for the identification and characterization of the protein based on its molecular weight. Additionally, the molecular weight of the protein can be used to monitor biological processes and to assess alterations in protein structure such as the addition of the 728 modified N1-methylpseudouridines.

Table 3 summarizes the differences between coronavirus, BNT162b2 (Pfizer), and mRNA-1273 (Moderna) nucleotide base counts. A significant distinction is that none of the millions of sequenced coronaviruses incorporate any of the modified nucleotides known as N1-methylpseudouridines. The introduction of this atypical and foreign nucleotide into the modified mRNA sequence at a minimum of 728 locations is likely to result in the synthesis of various aberrant peptides. However, the nature of these peptides remains uncertain, including their

Table 3
Base Counts for the "Wild-Type" Spike Protein, for Various Coronaviruses, for BNT162b2 According to the World health Organization, BNT162b2 According to Researchers at Palo Alto Medical Center, and mRNA-1273 According to the Same Stanford University Center in Palo Alto, California

Base Count for Spike Protein	Coronavirus**	BNT162b2 (WHO)***	BNT162b2 Pfizer (Jeong et al., 2021)	mRNA-1273 Moderna (Jeong et al., 2021)
A	1125	915	916	852
T (Ψ)*	723	-1186	-730	-594
G	1272	728	993	1074
C	703	992	1186	1308

*N1-methylpseudouridine (Ψ) substituted for uridine.
** Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, co - Nucleotide - NCBI https://www.ncbi.nlm.nih.gov/nuccore/NC_045512.2 (accessed Feb 8, 2021).
*** World Health Organization. Messenger RNA Encoding the Full-Length SARS-CoV-2 Spike Glycoprotein. INN, 2020, 11889, Nance et al. (2021) supplementary; Jeong, D.-E., McCoy, M., Artiles, K., Ilbay, O., Fire, A., Nadeau, K., Park, H., Betts, B., Boyd, S., & Hoh, R. (2021). Assemblies-of-putative-SARS-CoV-2-spike-encoding-mRNA-sequences-for-vaccines-BNT162b2-and-mRNA-1273. GitHub, No. i, 0–3. PDF available here.

quantities, duration of production (potentially throughout the organism's lifespan), and their probable bioactive effects, which may disrupt normal biological processes and contribute to the onset of disease and mortality. We know from Brogna et al. that some of the modified mRNA molecules are producing synthetic spike proteins with PP in place of KV.

To the best of my knowledge, the majority of analyses conducted in this field utilize the canonical nucleotide uridine or its DNA counterpart, thymine, for any reported base counts. The software program known as "RNAfold" at this link will predict secondary structures from canonical single stranded RNA, or DNA sequences; however, it does not accommodate the inclusion of any modified nucleotides, such as N1-methylpseudouridine.

Discussion

Considering the three domains of chemical structure we have just explored — steric properties, molecular weight, and base count — we are forced to conclude that whatever proteins might be synthesized from the modified mRNA in the Pfizer and Moderna products, they are not likely to be equivalent to the SARS-CoV-2 spike protein. Consequently, these proteins cannot serve as suitable antigens for the spike protein SARS-CoV-2 "wild-type", or its numerous variants. Therefore, the biophysical chemistry underlying the mRNA technology platform, which is represented as a prophylactic vaccine producing system, is an experimental gene therapy destined by physical chemistry in all probability to be ineffective and harmful to its recipients. At its best it can only stimulate the body's defenses into a state of confusion that is destined to become exhaustion to the extent that the 10 trillion lipid nanoparticles succeed in delivering their modified mRNA strings to the ribosomal systems of the body. At its worst, the experiment can be expected to produce disease and death on a fairly wide scale proportionate to the number of doses of the injectables received.

Further evidence of the incompatibility of the mRNA technology as a "vaccine" can be found in the article by McKernan, Kyriakopoulos, and McCullough (2021). Figure 1 of their article reveals major differences in guanine cytosine nucleotides (GC content) in the SARs-CoV-2 (36%) vs BNT162b2 (53%) vs mRNA1273 (61%). The GC content is crucial to the hydrogen bonding the ribosomal systems depend on; a higher the GC content typically correlates with increased structural stability. In contrast, adenine-uracil connections are maintained by two hydrogen bonds. Notably, the incorporation of N1-methylpseudoruidine in place of the uridine (uracil) has an increased molecular

weight and a different steric conformation, due to the added methyl functional groups (-CH_3). Furthermore, when comparing mRNA sequences coding for spike protein of the coronavirus to those of BNT162b2/mRNA-1273, it can hardly be overemphasized that ***the virus sequence has no modified nucleotides***.

Revisiting the Lock-and-Key Model

The foundational basis for the lock-and-key model, also known as "molecular docking", leads to this question: if we change all the keys — the hundreds of billions or hundreds of trillions of new spike proteins represented in various protein sequences with the PP modification — against which the cells of persons who receive the injectables are supposed to generate locks in the form of antibodies — what can we expect? A simple way to conceptualize the essence of such an enzyme substrate interaction is to think of the enzyme as a lock, and the key as the substrate. According to the research of Brogna, et al. (2023), we must expect that whatever antibodies may be produced by the body's immune systems against any of the PP type spike proteins, will be quite different, and therefore ineffective against any "wild-type", Wt SARS-CoV-2 spike protein. Why would the new keys manufactured to fit new locks also just happen to fit the original locks presumably requiring considerably different keys?

Autoimmune Disorders and Pathogenic Priming

If a given protein sequence is not nearly identical to the original targeted "wild-type" SARS-CoV-2 spike protein, the antibodies produced may be attacking aberrant proteins while leaving the original SARS-CoV-2 spike to continue doing whatever damage it was doing beforehand. However, because the immune defenses of the recipient of the injectable material are deceived into attacking new foreign spike proteins — usurping resources supposedly needed to attack the "wild-type" spikes — something very much like what Lyons-Weiler has termed "pathogenic-priming" (Lyons-Weiler, 2020) and what others have called "antigenic cross-reactivity" (Vojdani et al., 2021; Vojdani & Kharrazian, 2020) is apt to occur leading to some form of "auto-immunity". What is more, the empirical findings of Mead et al. (2024a, 2024b) show that what ought to be expected is what is actually occurring.

In the great variety of autoimmune diseases, many of them novel COVID-19 forms that have never been seen before, that are occurring more rapidly and with greater severity than ever before, the bodily defense systems end up attacking and destroying the cells, tissues, and organ systems they were designed to defend. In this paper, I have shown why the many substitutions of N1-methylpseudouridine for the original uridine in the SARS-CoV-2 protein may be the main culprit playing havoc with the body's defense systems. Putting the whole argument in its simplest form, when antibodies (the locks) do not have the correct shape to latch onto and capture a real disease agent, they can in effect begin to attack anything that resembles it enough to be mistaken for it. If the lock, say it is the antibody to the original spike protein, the targeted "antigen", does not fit the spike protein key, or if it is fitted in a way that would enable it to latch onto other protein keys essential to bodily functions, auto-immunity will ensue.

Dysfunctional Proteinaceous Material

My predictions with Oller (2023) would account for many possible misreadings, not merely a singular frameshift in the canonical reading direction as discussed by Mulroney and his colleagues. Moreover,

it is evident from their research that, in principle, the open reading frames of the published coding sequences for the original SARS-CoV-2 spike, as well as mutant-variants of it, once they are converted to the modified mRNA with N1-methylpseudouridine substituted for uridine in 728 positions times all of the billions (or trillions) of sequences injected into every recipient (according to Ulrich, 2024), provide a plethora of invitations for the ribosomal systems commandeered by modified mRNA to potentially produce an even greater number of aberrant foreign and dysfunctional proteins. Whereas the specific amount of the dysfunctional proteinaceous material, and how long it takes for the body to produce it, and what symptoms it causes are all unknowns — given the findings of Brogna, et al. (2023) — it is possible that components of the proteinaceous clots being pulled out of recipients of the injectables can be traced back to the peculiar coding strings of modified mRNA in the injectables themselves.

It is doubtful, however, that any of the aberrant strings of proteinaceous material can have the advertised effect of causing the body's cells to produce antibodies specific to the original viral spike sequence rather than the unintended aberrant proteins instead. The Qatar national database and Cleveland clinic analysis acknowledged COVID-19 vaccine negative effectiveness, where the data indicated an increasing chance of COVID-19 infection with a greater number of doses (Chemaitelly, 2023, Shrestha, 2023). It is also unlikely that any of the foreign material being produced by the body's ribosomal systems will be harmless, much less that it could just accidentally serve some functional purpose. Whatever proteinaceous material is churned out by ribosomes trying to make sense of the modified mRNA strings must be contributing to, if is not in fact the main cause of the disastrous clotting that seems to be producing much of the chaos being reported, for example, by Mead et al. (2024a, 2024b).

Evolution of "Vaccine" Injections

Can all the foregoing be viewed as an evolutionary experiment? Evolutionary biology suggests that selection plays a role in the evolution of base composition, that is, in the arrangement of the coding sequences written in the vocabulary of the billions of nucleotides A, T (U), G, and C. In 2020, Ruggiero and Boissinot, discussed three lines of evidence that may contribute to base composition evolution. The authors indicated that

> ...base composition is one of the most fundamental properties of a DNA sequence because it profoundly affects a number of important functions such as efficacy of transcription, the secondary structure of DNA and RNA molecules, the codon usage as well as the amino acid composition of encoded proteins. All these aspects can potentially affect the reaction of retrotransposition and the overall replicative success of the element.

Reverse transcription has been documented by Aldén et al. (2022). The authors reported that the synthetic spike code has "124 sequences that are 100% identical to human genomic sequences and three sequences with only one nucleotide (nt) mismatch in 19–26 nts" (p. 1118). Furthermore, they showed novel sequences in liver cell DNA coming from the synthetic spike. The authors do not know if the spike protein can be reverse transcribed into the genome of the host, but they found it can be reverse transcribed into the DNA of liver cells by an endogenous reverse transcriptase enzyme coded by the long interspersed nuclear element-1 (LINE-1), which accounts for "~17% of the human genome" (p. 1115). This raises the question of whether these differences could influence biological processes, evolutionary patterns, and retrotransposition. The organization of the genome

regulates codon interpretation by the ribosome, methylation patterns, and overall genomic configurations.

Looking to Future Platforms

In November 2023, Japan approved a self-amplifying COVID vaccine (saRNA) known as Kostaive (Wayne & Blakney, 2024). It is essential to elucidate both the differences and commonalities between the COVID-19 mRNA vaccine (modified mRNA) and the COVID-19 saRNA. The modified mRNA technology uses cellular systems to induce the production of the spike protein, and potentially a range of other aberrant proteins, as Oller and I argued (as others also have), for an indeterminate duration. In contrast, the saRNA incorporates the necessary genes for replication and synthesis of the spike protein encoded by RNA, thereby establishing a more or less indefinite presence within the cell, potentially lasting at least for the lifespan of the cell itself. In essence, the self-amplifying RNA vaccine generates multiple copies of itself prior to the production of the intended protein. The saRNAs contain replicase genes that encode a polymerase complex which amplifies the mRNA-encoded sequence. The additional replicase genes may lead to an increased quantity of encoded "vaccine" mRNA within the cells, consequently resulting in heightened expression of the encoded protein relative to the primary dose.

The saRNA "vaccines" are based on alphaviruses, which are transmitted by mosquitos and other species and are associated with various medical problems, including arthritis (Adizie & Adebajo, 2014; also see Yıldız et al., 2024). The potential interactions of these saRNA within human biological systems raise significant concerns, akin to the proverbial opening of Pandora's box, particularly as modified nucleotides, such as 5-methylcytidine, may facilitate replication while reducing immunogenicity without compromising the power to replicate itself (Yıldız et al., 2024). A pertinent inquiry arises regarding the implications of this new platform for pregnancy. Gene expression does not adhere to the conventional model; developing oocytes and embryos use previously synthesized mRNA from the maternal genome during a phase when no new mRNAs are produced (Richter 1999). Instead, cells modulate gene expression by adjusting protein synthesis based on the stored mRNAs.

This complex regulatory interplay, wherein the embryo's immune defense systems gradually supplants the maternally conferred immune system, may be compromised by the introduction of both saRNA and modified mRNA technologies. Consequently, the effects of the modified nucleotide sequences present in the Pfizer and Moderna products discussed in this article may potentially exert an inhibitory influence on certain types of saRNA technologies (Yıldız 2024). The central question remaining is: What connections might exist between these phenomena emerging as unexpected new hazards?

Conclusion

In this essay, I have examined critical physical differences between uridine and N1-methylpseudouridine. The material differences between these two nucleosides result in varying functional properties and biological outcomes. The assumption of equivalency between them is unfounded and should not be regarded as plausible within the context of mammalian cell physiology. It is important to recognize that viruses exist at the boundary of life; they do not fit neatly into the categories of single-celled or multicellular organisms, nor do they qualify as cellular entities. Consequently, the application of N1-methylpseudouridine, derived from a unicellular

organism, into multicellular organisms such as humans and livestock poses significant risks and can be considered imprudent. My rationale for this assertion is grounded in biophysical principles, specifically: 1) differences in steric arrangement, 2) variations in observed molecular weight, and 3) discrepancies in the very vocabulary of base composition. Given these conflicts, it is reasonable to question whether the proteins and peptide fragments synthesized by the modified mRNA technology can be regarded as specifically targeted against the original SARS-CoV-2 spike protein. The increase in antibodies commonly seen after a person receives one or more doses of the modified mRNA injectables is probably not focused on the original SARS-CoV-2 spike protein. It is evidently more apt to result in collateral damage of the auto-immune kind than has been claimed by its mainstream proponents for reasons I have brought out in this article. So, my response to the question whether the multitude of antibodies appearing in vaccinated individuals are specifically targeted against any given SARS-CoV-2 variant, is "probably not". The shots are making the body's immune systems kick into high gear, but not necessarily in an efficient or safe manner.

Acknowledgments

The author is grateful for comments that helped improve this paper passed along by the Editor-in-Chief from Stephanie Seneff, PhD, and from Robert M. Davidson, MD, PhD. Whereas the author is also a member of the Editorial Board for the *IJVTPR*, except for approving some of the edits suggested by the editors, he was not involved in the decision to publish it. Any remaining errors are his own.

References

A Midwestern Doctor. (2023, January 18). Do the mysterious fibrous clots really exist? *The Forgotten Side of Medicine*. https://www.midwesterndoctor.com/p/do-the-mysterious-fibrous-clots-really

Adizie, T., & Adebajo, A. O. (2014). Travel- and immigration-related problems in rheumatology. *Best Practice & Research Clinical Rheumatology*, *28*(6), 973–985. https://doi.org/10.1016/j.berh.2015.04.006

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://doi.org/10.3390/cimb44030073

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 (Pfizer-BioNTech) 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

Bradley, C. C., Gordon, A. J. E., Wang, C., Cooke, M. B., Kohrn, B. F., Kennedy, S. R., Lichtarge, O., Ronca, S. E., & Herman, C. (2022). RNA polymerase inaccuracy underlies SARS-CoV-2 variants and vaccine heterogeneity. *Research Square*, rs.3.rs-1690086. https://doi.org/10.21203/rs.3.rs-1690086/v1

Bradley, C. C., Wang, C., Gordon, A. J. E., Wen, A. X., Luna, P. N., Cooke, M. B., Kohrn, B. F., Kennedy, S. R., Avadhanula, V., Piedra, P. A., Lichtarge, O., Shaw, C. A., Ronca, S. E., & Herman, C. (2024). Targeted accurate RNA consensus sequencing (tARC-seq) reveals mechanisms of replication error affecting SARS-CoV-2 divergence. *Nature Microbiology*, *9*(5), 1382–1392. https://doi.org/10.1038/s41564-024-01655-4

Brogna, C., Cristoni, S., Marino, G., Montano, L., Viduto, V., Fabrowski, M., Lettieri, G., & Piscopo, M. (2023). Detection of recombinant Spike protein in the blood of individuals vaccinated against SARS-CoV-2: Possible molecular mechanisms. *PROTEOMICS – Clinical Applications*, *17*(6), 2300048. https://doi.org/10.1002/prca.202300048

Brogna, C., Viduto, V., Fabrowski, M., Cristoni, S., Marino, G., Montano, L., & Piscopo, M. (2023). The importance of the gut microbiome in the pathogenesis and transmission of SARS-CoV-2. *Gut Microbes*, *15*(1), 2244718. https://doi.org/10.1080/19490976.2023.2244718

Chemaitelly H, Ayoub HH, Tang P, et al. Long-term COVID-19 booster effectiveness by infection history

and clinical vulnerability and immune imprinting: a retrospective population-based cohort study. The Lancet Infectious Diseases. 2023;23:816-27. https://doi.org/10.1016/S1473-3099(23)00058-0

Cobb, M. (2017). 60 years ago, Francis Crick changed the logic of biology. *PLOS Biology*, *15*(9), e2003243. https://doi.org/10.1371/journal.pbio.2003243

Demongeot, J.; Fougère, C. mRNA COVID-19 Vaccines—Facts and Hypotheses on Fragmentation and Encapsulation. Vaccines 2023, 11, 40. https://doi.org/10.3390/ vaccines11010040

Diblasi, L., & Sangorrin, M. (Directors). (2024, April 3). *Analysis on Covid-19 "vaccines" performed by Prof. Lorena Diblasi and Dr. Marcela Sangorrín* [Video recording]. https://odysee.com/@laquintacolumnainternational:7/Analysis-on-Covid-19-vaccines-performed-by-Prof-Lorena-Diblasi-and-Dr-Marcela-Sangorrín:1

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

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

Hamilton, R., Watanabe, C. K., & de Boer, H. A. (1987). Compilation and comparison of the sequence context around the AUG startcodons in Saccharomyces cerevisiae mRNAs. *Nucleic Acids Research*, *15*(8), 3581–3593. https://doi.org/10.1093/nar/15.8.3581

Jeffrey, L. (2023, April 2). Funeral director Laura Jeffery on post-vaccine embalming. *Canadian National Citizens Inquiry into COVID-19*. https://www.youtube.com/watch?v=kYxUS9YO2rE

Lee, Y., & Broudy, D. (2024). Response to Critics of Lee & Broudy (2024) on the Toxicity and Self-Assembling Technology in Incubated Samples of Injectable mRNA Materials. *International Journal of Vaccine Theory, Practice, and Research*, *3*(2), 1244.20-1244.29. https://doi.org/10.56098/aqgzye36

Lyons-Weiler, J. (2020). Pathogenic priming likely contributes to serious and critical illness and mortality in COVID-19 via autoimmunity. *Journal of Translational Autoimmunity*, *3*, 100051. https://doi.org/10.1016/j.jtauto.2020.100051

Maass, H. (2020, December 11). *10 things you need to know today: December 11, 2020*. Theweek. https://theweek.com/10things/954651/10-things-need-know-today-december-11-2020

McKernan, K., Kyriakopoulos, A., & McCullough, P. (2021). *Differences in vaccine and SARS-CoV-2 replication derived mRNA: Implications for cell biology and future disease*. https://doi.org/10.31219/osf.io/bcsa6

Mead, M. N., Seneff, S., Wolfinger, R., Rose, J., Denhaerynck, K., Kirsch, S., & McCullough, P. A. (2024a). COVID-19 modified mRNA "vaccines", Part 1: Lessons learned from clinical trials, mass vaccination, and the bio-pharmaceutical complex. *International Journal of Vaccine Theory, Practice, and Research*, *3*(1), 1112–1178. https://doi.org/10.56098/fdrasy50

Mead, M. N., Seneff, S., Wolfinger, R., Rose, J., Denhaerynck, K., Kirsch, S., & McCullough, P. A. (2024b). COVID-19 modified mRNA "vaccines", Part 2: Lessons learned from clinical trials, mass vaccination, and the bio-pharmaceutical complex. *International Journal of Vaccine Theory, Practice, and Research*, *3*(2), 1275-1344. https://doi.org/10.56098/w66wjg87

Mills, I., International Union of Pure and Applied Chemistry, & International Union of Pure and Applied Chemistry (Eds.). (1993). *Quantities, units, and symbols in physical chemistry* (2nd ed). Blackwell Scientific Publications ; CRC Press [distributor]. https://old.iupac.org/publications/books/gbook/green_book_2ed.pdf

Monroe, J. G., Mitchell, L., Deb, I., Roy, B., Frank, A. T., & Koutmou, K. (2022). *N1-Methylpseudouridine and pseudouridine modifications modulate mRNA decoding during translation* [Preprint]. Biochemistry. https://doi.org/10.1101/2022.06.13.495988

Mulroney, T. E., Pöyry, T., Yam-Puc, J. C., Rust, M., Harvey, R. F., Kalmar, L., Horner, E., Booth, L., Ferreira, A. P., Stoneley, M., Sawarkar, R., Mentzer, A. J., Lilley, K. S., Smales, C. M., von der Haar, T., Turtle, L., Dunachie, S., Klenerman, P., Thaventhiran, J. E. D., & Willis, A. E. (2023). N1-methylpseudouridylation of mRNA causes +1 ribosomal frameshifting. *Nature*, *625*(7993), Article 7993. https://doi.org/10.1038/s41586-023-06800-3

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

National Center for Biotechnology Information. (2024a). *PubChem Compound Summary for CID 6029, Uridine.* [Dataset]. https://pubchem.ncbi.nlm.nih.gov/compound/Uridine

National Center for Biotechnology Information. (2024b). *PubChem Compound Summary for CID 99543, 1-Methylpseudouridine* [Dataset]. https://pubchem.ncbi.nlm.nih.gov/compound/1-Methylpseudouridine

National Library of Medicine. (2020). *Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome* (1798174254; Version 2) [Dataset]. NCBI Nucleotide Database. http://www.ncbi.nlm.nih.gov/nuccore/NC_045512.2

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

Oller, J. W. (2022). *Human Anatomy and Physiology: An Introduction for Undergraduate Students of Speech-Language Pathology and Audiology* (3rd ed.). Sentia publishing. 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

Pelech, S., & Shaw, C. A. (2024). *Down the COVID-19 Rabbit Hole*. Skyhorse Publishing. https://www.amazon.com/Down-COVID-19-Rabbit-Hole-Independent/dp/1510779590

Pharmaceutical Technology. (2024, July 5). COVID-19 Vaccination Tracker: Daily Rates, Statistics & Updates. *Pharmaceutical Technology*. https://www.pharmaceutical-technology.com/covid-19-vaccination-tracker/

Richter JD. Cytoplasmic polyadenylation in development and beyond. Microbiol Mol Biol Rev. 1999 Jun;63(2):446-56. doi: 10.1128/MMBR.63.2.446-456.1999. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC98972/

Ruggiero, R. P., & Boissinot, S. (2020). Variation in base composition underlies functional and evolutionary divergence in non-LTR retrotransposons. *Mobile DNA*, *11*(1), 14. https://doi.org/10.1186/s13100-020-00209-9

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

Santiago, D., & Oller, J. W. (2023). Abnormal clots and all-cause mortality during the pandemic experiment: Five doses of COVID-19 vaccine are evidently lethal to nearly all Medicare participants. *International Journal of Vaccine Theory, Practice, and Research*, *3*(1), 847–890. https://doi.org/10.56098/ijvtpr.v3i1.73

Shrestha, N. K., Burke, P. C., Nowacki, A. S., Simon, J. F., Hagen, A., & Gordon, S. M. (2023). Effectiveness of the Coronavirus Disease 2019 Bivalent Vaccine. *Open forum infectious diseases*, *10*(6), ofad209. https://doi.org/10.1093/ofid/ofad209

Speicher, D., Rose, J., Gutschi, L., Wiseman, D., & McKernan, K. (2023). *DNA fragments detected in monovalent and bivalent Pfizer/BioNTech and Moderna modRNA COVID-19 vaccines from Ontario, Canada: Exploratory dose response relationship with serious adverse events.* https://www.researchgate.net/publication/374870815_Speicher_DJ_et_al_DNA_fragments_detected_in_COVID-19_vaccines_in_Canada_DNA_fragments_detected_in_monovalent_and_bivalent/figures

Sun, S., & Fu, J. (2018). Methyl-containing pharmaceuticals: Methylation in drug design. *Bioorganic & Medicinal Chemistry Letters*, *28*(20), 3283–3289. https://doi.org/10.1016/j.bmcl.2018.09.016

The Associated Press. (2022, December 14). *Today in History: December 14, 2020 U.S. COVID vaccinations begin*. AP News. https://apnews.com/today-in-history-december-14

Tuuminen, T. (2024). A GMO Experiment on Two-Thirds of the World's Population: Reaction to Ulrich's Commentary on Lee and Broudy (2024). *International Journal of Vaccine Theory, Practice, and Research*, *3*(2), 1244.11-1244.18. https://doi.org/10.56098/xncqaa94

Ulrich, A. S. (2024). No Nanobots in Vaccines — Just Lipids on the Loose: Commentary on Lee and Broudy (2024), "Real-Time Self-Assembly of Stereomicroscopically Visible Artificial Constructs in Incubated Specimens of

mRNA Products Mainly from Pfizer and Moderna: A Comprehensive Longitundinal Study." *International Journal of Vaccine Theory, Practice, and Research*, *3*(2), 1244.1-1244.10. https://doi.org/10.56098/7hsjff81

Walsh, D.J., Schinski, D.A., Schneider, R.A. *et al.* General route to design polymer

molecular weight distributions through flow chemistry. *Nat Commun* **11**, 3094 (2020). https://doi.org/10.1038/s41467-020-16874-6

Veenstra, T. D., Pauley, B., Injeti, E., & Rotello, R. J. (2022). *In vitro characterization of SARS-CoV-2 protein translated from the Moderna mRNA-1273 vaccine* (p. 2022.03.01.22271618). medRxiv. https://doi.org/10.1101/2022.03.01.22271618

Vojdani, A., & Kharrazian, D. (2020). Potential antigenic cross-reactivity between SARS-CoV-2 and human tissue with a possible link to an increase in autoimmune diseases. *Clinical Immunology (Orlando, Fla.)*, *217*, 108480. https://doi.org/10.1016/j.clim.2020.108480

Vojdani, A., Vojdani, E., & Kharrazian, D. (2021). Reaction of human monoclonal antibodies to SARS-CoV-2 proteins with tissue antigens: Implications for autoimmune diseases. *Frontiers in Immunology*, *11*, 617089. https://doi.org/10.3389/fimmu.2020.617089

Wayne, C. J., & Blakney, A. K. (2024). Self-amplifying RNA COVID-19 vaccine. *Cell*, *187*(8), 1822-1822.e1. https://doi.org/10.1016/j.cell.2024.03.018

World Health Organization. (2020). Messenger RNA Encoding the Full-Length SARS-CoV-2 Spike Glycoprotein. *International Nonproprietary Names*, *11889*.

Yıldız, A., Răileanu, C., & Beissert, T. (2024). Trans-amplifying RNA: A journey from alphavirus research to future vaccines. *Viruses*, *16*(4), Article 4. https://doi.org/10.3390/v16040503

Legal Disclaimer