



DNA Transcribed from Pfizer mRNA Vaccine Contains MUTANT gp130 Tumor Gene

Having fun BLASTing DNA Reverse Transcribed from Pfizer Vax



Igor Chudov
Feb 27

264

240



My [previous post](#) about a science [article](#) proving that Pfizer mRNA vaccine reverse transcribed into human DNA, has garnered enormous interest and lots of comments, many of which were incredible.

If you did not read it yet, PLEASE READ IT FIRST before reading this article. Otherwise you may get lost and not even realize the significance of how your loved ones' genetic code may have been reprogrammed. Here you go:



Igor's Newsletter

Worst Fears Realized: Pfizer mRNA Transcribes into DNA

A new study is out: Intracellular Reverse Transcription of Pfizer BioNTech COVID-19 mRNA Vaccine BNT162b2 In Vitro in Human Liver Cell Line. What it is saying is: lab studies show that mRNA vaccine DOES integrate itself into human cellular DNA. This means that a shot of Pfizer vaccine, taken even once, permanently changes the DNA of affected cells...

[Read more](#)

3 months ago · 263 likes · 325 comments · Igor Chudov

I decided to continue plodding along and see **what else we can uncover**, based on that [“Current Issues in Molecular Biology”](#) article:

Open Access Article

Intracellular Reverse Transcription of Pfizer BioNTech COVID-19 mRNA Vaccine BNT162b2 In Vitro in Human Liver Cell Line

by [Markus Aldén](#)¹ , [Francisko Olofsson Falla](#)¹ , [Daowei Yang](#)¹ , [Mohammad Barghouth](#)¹ ,
[Cheng Luan](#)¹ , [Magnus Rasmussen](#)² and [Yang De Marinis](#)^{1,*}

The article contains a **printout of genetic DNA code** that was detected in human cell DNA materials reverse transcribed from the mRNA vaccine.

Table 2. Sanger sequencing result of the BNT162b2 amplicon.

CGAGGTGGCCAAGAATCTGAACGAGAGCCTGATCGACCTGCAAGAACTGGGGAAGT
 ACGAGCAGTACATCAAGTGGCCCTGGTACATCTGGCTGGGCTTTATCGCCGGAAGTATG
 CCATCGTGATGGTACAATCATGCTGTGTTGCATGACCAAGCTGCTGTAGCTGCCTGAAGG
 GCTGTTGTAGCTGTGGCAGCTGCTGCAAGTTGACGAGGACGATTCTGAGCCCGTGCTGA
 AGGGCGTGAACTGCACTACACATGATGACTCGAGCTGGTACTGCATGCACGAATGCTA
 GCTGCCCTTTCCCGTCTGGGTACCCCGAGTCTCCCCGACCTCGGGTCCCAGGTATGC
 TCCACCTCCACCTGCCCCACTCACCACCTGTGCTAGTTCAGACACCTCCCAAGCACGC
 AGCAATGCAGCTCAAACGCTTAGCCTA

This is the DNA code
 That Pfizer Vaccine
 Reverse Transcribes
 in human cells
 like yours

So, I decided to check what is actually in this code above, is that just harmless junk or something more ominous. For that, I ran a [free NCBI "BLAST" tool](#) by copying and pasting the above genetic sequence in it. This is the same BLAST tool that @JikkyKjj used to show a Moderna "cancer patent" sequence on the most important, "furin cleavage site" of Sars-Cov-2. I wrote about that also:



Igor's Newsletter

Moderna Patented CANCER GENE is in Sars-Cov-2 "Spike Protein"

I did a little bit more digging into the topic of my article about genes from 2018 Moderna patent. I wrote about it yesterday, but kept reading and digging and found much more disturbing stuff than I expected. First, a recap: Sars-Cov-2 virus has a genetic insert that exists ONLY in Moderna...

[Read more](#)

4 months ago · 202 likes · 289 comments · Igor Chudov

Anyway, impressed with @JikkyKjj's discovery, I decided to do the same with the DNA code that Pfizer mRNA vaccine generates (reverse transcribes) into human cells. Turns out that I was the first to enter that sequence into the NCBI BLAST tool (because it took a while to analyze) and it now has a sequence ID of [1R3ZDZJY016](#).

And here are [the results](#). I annotated them to make it easier for you to see what is and is not interesting.

synthetic contig...	266	366	44%	16-96	100.00%	3759	MZ771338.1
synthetic contig...	266	366	44% <td>16-96</td> <td>100.00%</td> <td>3790 <td>MZ771338.1</td> </td>	16-96	100.00%	3790 <td>MZ771338.1</td>	MZ771338.1
synthetic contig...	335	335	52%	36-87	92.67%	3790	QK1120840.1
synthetic contig...	327	327	58%	56-85	89.53%	4217	MZ393689.1
synthetic contig...	327	327	58%	56-85	89.53%	4218	MZ393689.1
synthetic contig...	316	316	63%	16-81	85.76%	7488	MW408785.1
synthetic contig...	300	300	58%	16-76	87.60%	4115	MZ393688.1
Expression vec...	246	246	43%	16-60	89.64%	12445	MW506963.1
Expression vec...	246	246	43%	16-60	89.64%	10752	MW506962.1
Expression vec...	246	246	43%	16-60	89.64%	8866	MW506961.1
Expression vec...	246	246	43%	16-60	89.64%	8586	MW506960.1
Expression vec...	246	246	43%	16-60	89.64%	8586	MW506959.1
Expression vec...	246	246	43%	16-60	89.64%	8586	MW506958.1
Expression vec...	246	246	43%	16-60	89.64%	8586	MW506957.1
Expression vec...	246	246	43%	16-60	89.64%	8586	MW506956.1
Expression vec...	246	246	43%	16-60	89.64%	8586	MW506943.1

What is interesting – and I am not saying it is the only thing – is the **gp130 glycoprotein gene** that is **97% similar to the human gp130 glycoprotein gene**. The chance of that being a random coincidence, per BLAST tool, is
0.000000000000000000000000000000000000000000.

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Homo sapiens gp130 associated protein GAM mRNA, complete cds
Sequence ID: [AF072902.1](#) Length: 1317 Number of Matches: 1

Range 1: 1051 to 1192
GenBank
Graphics
Next Match
Previous Match

Score	Expect	Identities	Gaps	Strand
243 bits (131)	2e-59	138/142 (97%)	0/142 (0%)	Plus/Plus
Query 266	CTCGAGGCTGACTGTCATGCACGCAATGCTAGTCGCCCTTTCCGTCCTGGGTACCCGG	325		
Sbjct 1051	CTCAACCTTGGTACTGCATGCATGCACGCAATGCTAGTCGCCCTTTCCGTCCTGGGTACCCGG	1118		
Query 326	AGTCTCCCCGACCTCGGGTCCACAGGTATGCTCCCACTCCACACTGCGCCACTCACACAC	385		
Sbjct 1111	AGTCTCCCCGACCTCGGGTCCACAGGTATGCTCCCACTCCACACTGCGCCACTCACACAC	1176		
Query 386	TCTGCTAGTTCAGACACATCCC	407		
Sbjct 1171	TCTGCTAGTTCAGACACATCCC	1192		

Related Information
[Gene](#) - associated gene details
[GEQ Profiles](#) - microarray expression data
[PubChem BioAssay](#) - bioactivity screening

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TLE5

TLE family member 5, transcriptional modulator [*Homo sapiens* (human)]

Gene ID: 166, updated on 25-Jan-2022

Download Datasets

Summary

Official Symbol

TLE5

provided by HGNC

Official Full Name

TLE family member 5, transcriptional modulator

provided by HGNC

Primary source

HGNC:HGNC:307

See related

Ensembl:ENSG00000104964 MIM:600188; AllianceGenome:HGNC:307

Gene type

protein coding

RefSeq status

REVIEWED

Organism

Homo sapiens

Lineage

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo

Also known as

AES; GRG; ESP1; GRG5; AES-1; AES-2; Grg-5

Summary

The protein encoded by this gene is similar in sequence to the amino terminus of Drosophila enhancer of split groucho, a protein involved in neurogenesis during embryonic development. The encoded protein, which belongs to the groucho/TLE family of proteins, can function as a homooligomer or as a heterooligimer with other family members to dominantly repress the expression of other family member genes. Three transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Jul 2008]

Expression

Ubiquitous expression in heart (RPKM 135.6), spleen (RPKM 116.8) and 25 other tissues See more

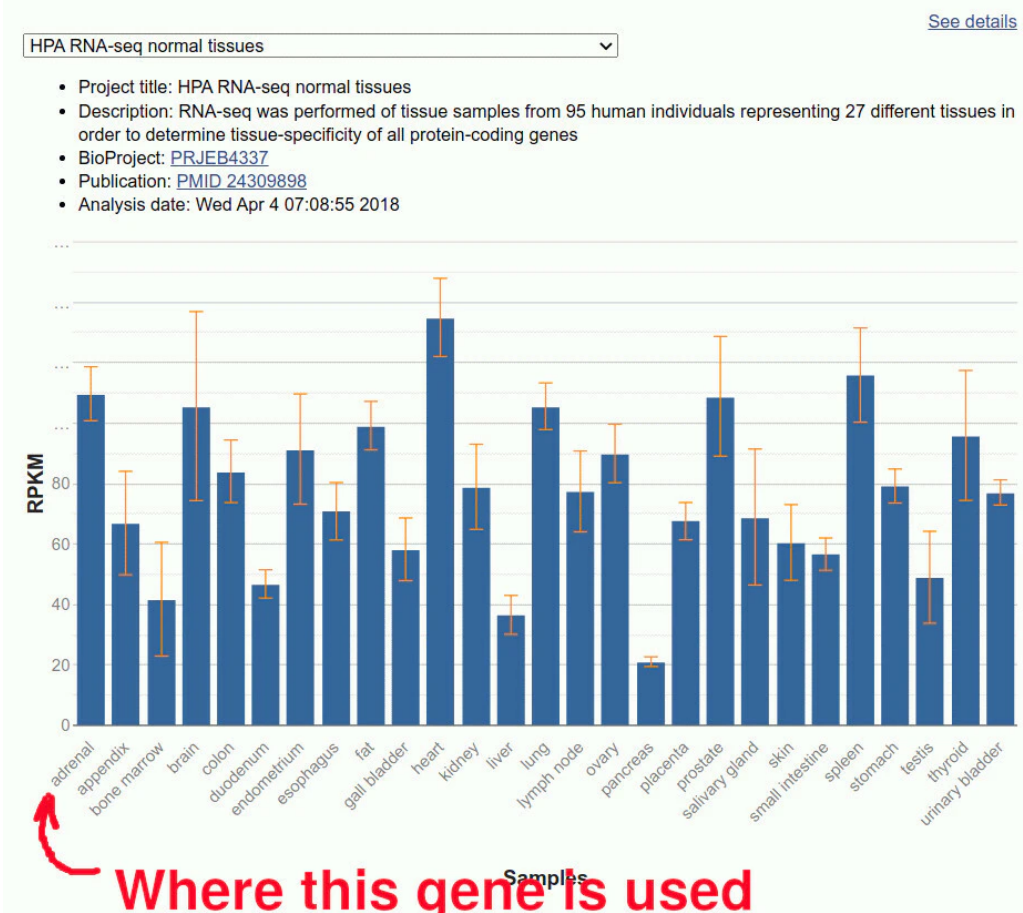
Orthologs

mouse all

NEW

Try the new Gene table

Try the new Transcript table



So, we have Pfizer Covid mRNA vaccine reverse transcribe to a MUTATED gp130 gene. Remember the 97% match? The 3% non-matches, the four red dots, are the mutations of the gp130 gene.

So, without looking at these specific mutations, what happens when gp130 gene

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> J Biol Chem. 2012 Apr 20;287(17):13743-51. doi: 10.1074/jbc.M111.349167.

Constitutively active mutant gp130 receptor protein from inflammatory hepatocellular adenoma is inhibited by an anti-gp130 antibody that specifically neutralizes interleukin 11 signaling **Liver Cancer**

Jan Sommer¹, Timo Effenberger, Elena Volpi, Georg H Waetzig, Marten Bernhardt, Jan Suthaus, Christoph Garbers, Stefan Rose-John, Doreen M Floss, Jürgen Scheller

Affiliations + expand

PMID: 22523320 PMCID: PMC3340202 DOI: 10.1074/jbc.M111.349167

Free PMC article

Abstract

Ligand-independent constitutively active gp130 mutants were described to be responsible for the development of inflammatory hepatocellular adenomas (IHCA). These variants had gain-of-function somatic mutations within the extracellular domain 2 (D2) of the gp130 receptor chain.

Please note that a question arises: gp130 mutations can cause liver tumor, and the entire experiment was performed on a line of immortal liver cancer cells. **Could it be that the original article picked up mutated gp130 from the Huh7 liver cancer cells?** If that is the case, if the DNA sequence is inherent to Huh7 line itself, it could invalidate a lot of conclusions that the original science article, as well as my own articles, were making.

However, the authors were diligent with controls and did NOT see the questioned DNA sequence that I am looking at, in the control cells that did NOT receive the Pfizer vaccine. In addition, the published DNA sequence contained Sars-Cov-2 genes (see BLAST results), so it does come from the effect of the vaccine, not the Huh7 culture cells.

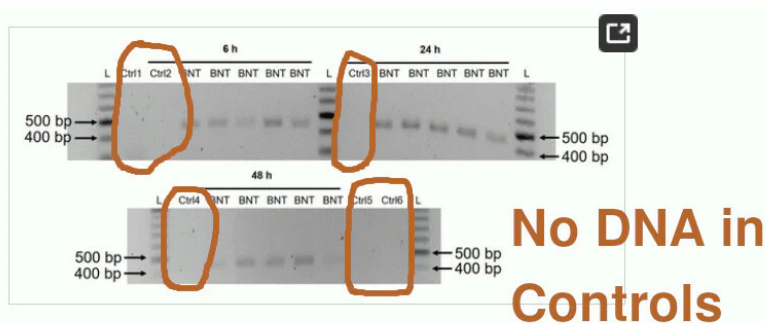


Figure 5. Detection of DNA amplicons of BNT162b2 in Huh7 cells treated with BNT162b2. Huh7 cells were treated without (Ctrl) or with 0.5 µg/mL of BNT162b2 for 6, 24, and 48 h. Genomic DNA was purified and digested with 100 µg/mL RNase. PCR was run on all samples with primers targeting BNT162b2, as shown in Figure 1 and Table 1. DNA amplicons (444 bps) were visualized on agarose gel. BNT: BNT162b2; L: DNA ladder; Ctrl1: cultured Huh7 cells; Ctrl2: Huh7 cells without BNT162b2 treatment collected at 6 h; Ctrl3: Huh7 cells without BNT162b2 treatment collected at 24 h; Ctrl4: Huh7 cells without BNT162b2 treatment collected at 48 h; Ctrl5: RNA from Huh7 cells treated with 0.5 µg/mL of BNT162b2 for 6 h; Ctrl6: RNA from Huh7 cells treated with 0.5 µg/mL of BNT162b2 for 6 h, digested with RNase.

I did perform some cursory checks, to the best of my ability, and the Huh7 line contains p53 mutations. but it does not seem like it contains gp130 mutations.

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So, keeping my fingers crossed, the mutated gp130 gene that I found, is a genuine finding of lab research, comes from the mRNA vaccine, and not a coincidental pickup from the Huh7 cells.

I am guessing that the authors were looking at liver cells specifically, because they knew where to look (that the mRNA delivery system delivers the lipid nanoparticles to the liver). Why did the authors pick liver cells? Maybe because they heard of this 4chan post from 2020, when NOTHING yet was known about the strange mRNA vaccines:



Anonymous

ID:CjVlc4Sa Wed 09 Dec 2020 04:22:55 No.295621351 [333 / 38 / 121]

View

Reply

Original

Report

Quoted By: >>295621805 >>295622149 >>295622168 >>295622241 >>295622293 >>295622302 >>295622410 >>295622483 >>295622603 >>295622774 >>295623062 >>295623469 >>295623736 >>295623741 >>295623779 >>295624089 >>295624289 >>295624304 >>295624495 >>295625215 >>295625376 >>295627306 >>295627673 >>295627827 >>295628182 >>295628849 >>295629650 >>295629933 >>295630160 >>295630241 >>295630390 >>295630940 >>295630981 >>295631051 >>295631178 >>295631283 >>295631296 >>295631786 >>295632341 >>295632357 >>295632419 >>295632739 >>295632768 >>295632904 >>295633435 >>295633483 >>295633848 >>295633868 >>295633918 >>295634022 >>295634536 >>295634636 >>295634910

1MIB, 756x547, pd.png

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I'm an industrial engineer at Moderna and the other one of us is a process development engineer. I'm sure the same thing is happening with Pfizer-BioNTech. It was hard to put things together based on the small quantities of additions happening in manual step (highly unorthodox for a continuous process production). The explanation we got was highly sensitive trade secret adjuvants being added. Digging in deeper showed how sensitive it actually was.

Most people's understanding of this novel vaccine type is that it works as follows:
1. Make mRNA coding for S protein
2. Make lipid nanoparticle delivery system
3. Profit

How it actually works from what we've uncovered:
1. Make mRNA coding for S protein
2. Make mRNA coding for mutant versions of CYP19A1 and CDKN1B in smaller amounts
3. Make sure that while delivery system for (1) mostly ends up in liver, most of (2) ends up in the gonads
4. Make sure form and quantity of additive upregulating LINE-1 reverse transcription activity makes it hard to detect among legit adjuvants
5. Effects from (2) integrated by (4) are recessive; mildly oncogenic effects in vaccine recipients unlikely to be noticed for many years
6. (5) recessive but since most of population vaccinated, in next generation female offspring have premature ovarian failure

(6) coincides with poor people being obsoleted by AI and robotics, so we didn't have to dig for motivation.
We've taken precautions but fear for our safety. So far I don't think we've raised suspicion, but can't be sure. Not sure what to do. Avoiding taking the vaccine makes us prime suspects for this leak.

We were Told it will Never Happen

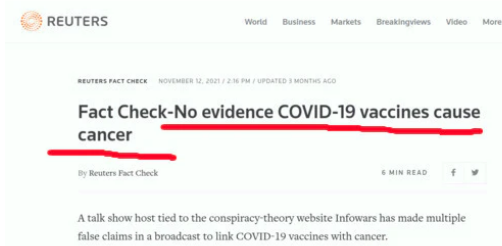
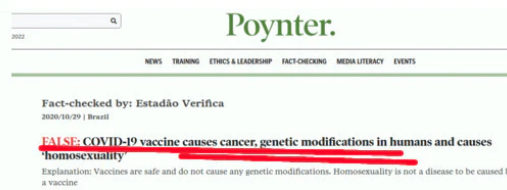
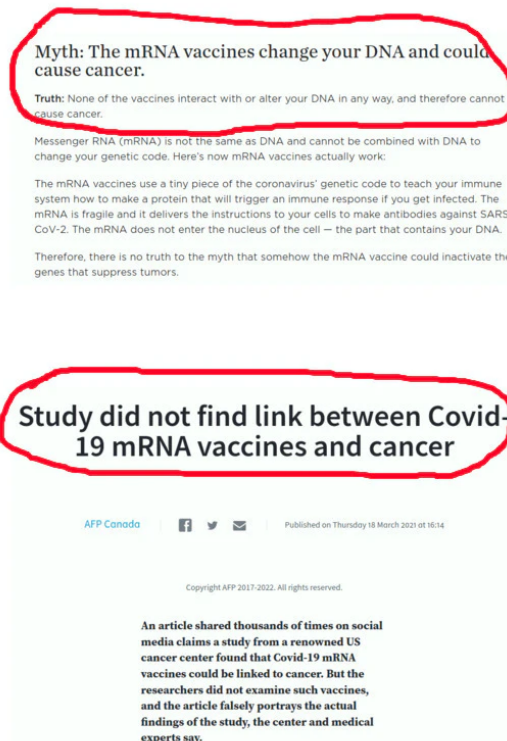
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https://igorchudov.substack.com/p/dna-transcribed-from-pfizer-mrna?s=r

6/10



Clarifications

The sequence of mutated gp130 genes, found in the DNA reverse transcribed from Pfizer Covid vaccine,

- Does not mean that it will NECESSARILY cause cancer
- The four “red dot” mutations listed, may be harmless
- Does not mean that it was added to Pfizer vaccine intentionally to cause harm
- Does not mean that it is even expressed as a gp130 protein, as expression of genes depends on cellular context
- What it DOES mean is that we need to look at this closely.

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Please repost this article in hopes that someone important will see it and authorities become concerned about the “unexpected” effects of mRNA Covid vaccines. Our

children are infected with it and we deserve to know what it does to them!

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↑ 52 ↓  **r/cancer** · Posted by u/Parisbruv 2 months ago

Diagnosed with rare liver cancer at 26.

Patient

Was diagnosed with fibrolamellar hepatocellular carcinoma today. I have a 12 cm mass on my liver. Currently sitting in the E.R trying to get admitted. Not sure why I'm posting this, guess I'm just still in shock. The cancer I have is 1/5,000,000. Just wondering why me yaknow?

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 **Potential-Biscotti26** · 2 mo. ago
NETs @ 19 | F(20)

totally get it. I'm 20 with a rare cancer. I asked and continue to ask the same thing every day. just take it one minute at a time. sending love! ❤️

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 **Parisbruv** OP · 1 mo. ago

Thank you so much. I wish you the very best luck with everything. You are strong

1 ↓ Reply Give Award Share Report Save Follow

 **Starshapedsand** · 2 mo. ago

I hear you. Fantastically rare brain cancer at 23. All that you can really do is to try to keep moving forward.

13 ↓ Reply Give Award Share Report Save Follow

 **Anna** @aanaaxo · 33m

Omg! My aunt got pfizer vax around February 2021 and in June she got liver cancer wtf.. i told my mom it was from the vax but they all didn't believe me..

 **Igor Chudov** @ichudov · 5h

Yesterday, I explained that mRNA vaccines do "reverse transcribe" into DNA in human cells.

Today, I ran the DNA sequence through BLAST, analyzed the genes they transcribe into, and found that they transcribe to a:

To a **MUTATED gp130 LIVER CANCER GENE.**

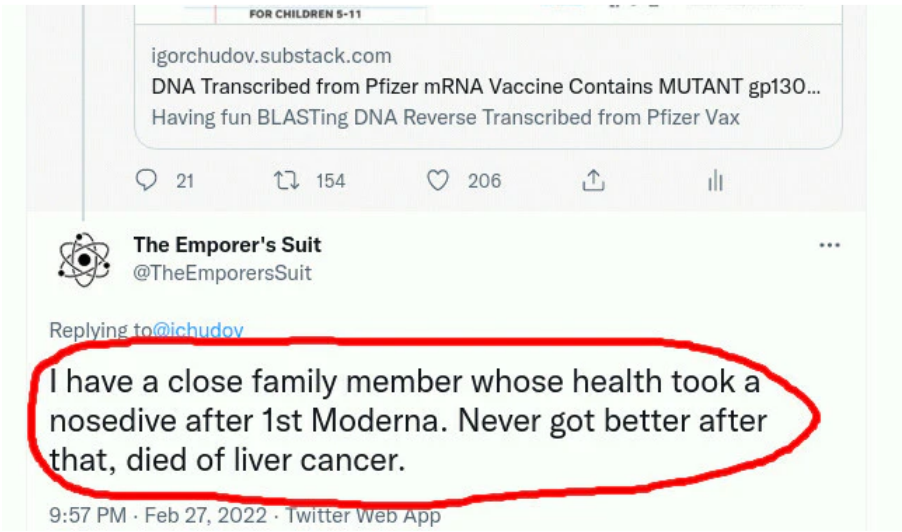
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 **Jeff Ferguson** Writes Economic Insights For All · Feb 28 · *edited Feb 28* ♥ Liked by Igor Chudov

I'm not going to lie, most of that goes right over my head. However what seems clear is injecting a major portion of the population with phenomenally complex synthetic genetic compounds absent a decade or more of careful testing was foolhardy in the extreme. And all for a virus which poses little to no danger for the great majority.

♡ 93 Reply Collapse

45 replies

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