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# DNA Transcribed from Pfizer mRNA Vaccine Contains **MUTANT gp130 Tumor Gene**

Having fun BLASTing DNA Reverse Transcribed from Pfizer Vax



**Igor Chudov** Feb 27

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My <u>previous post</u> about a science <u>article</u> proving that Pfizer mRNA vaccine reverse transcribed into human DNA, has garnered enormous interest and lots of comments, may 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:



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### 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...

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I decided to continue plodding along and see what else we can uncover, based on that <u>"Current Issues in Molecular Biology" article:</u>



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

by ② Markus Aldén <sup>1</sup> ☑ <sup>1</sup> ☑ , ② Francisko Olofsson Falla <sup>1</sup> ☑ , ② Daowei Yang <sup>1</sup> ☑ , ② Mohammad Barghouth <sup>1</sup> ☑ , ② Cheng Luan <sup>1</sup> ☑ , ② Magnus Rasmussen <sup>2</sup> ☑ and ② Yang De Marinis <sup>1,\*</sup> ☑ <sup>1</sup> ☐

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.

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 <u>free NCBI "BLAST" tool</u> 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:



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

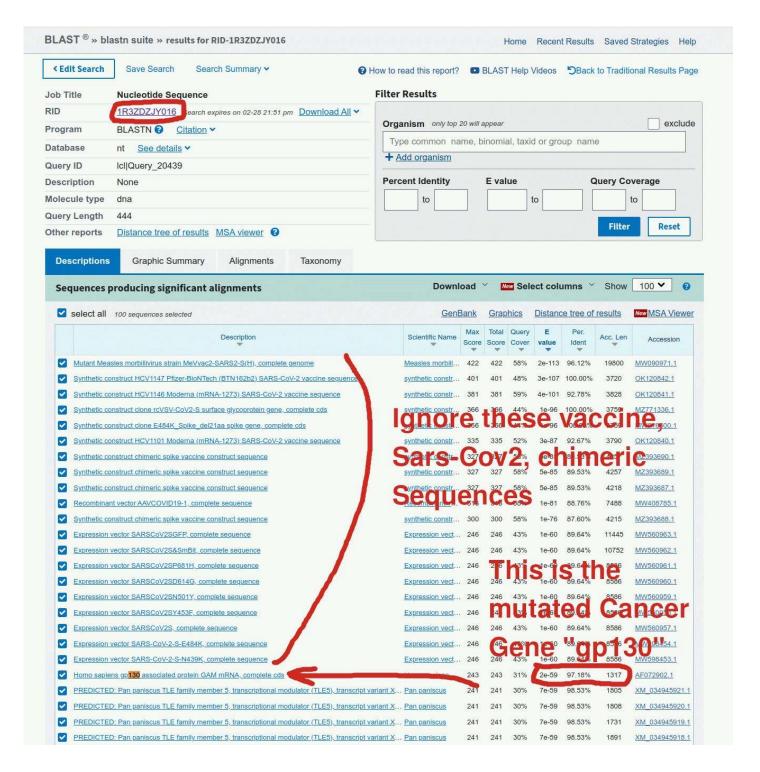
I did a little bit more digging into the topic of my article about genes from 2018 Moderna patent. I wrote about it yesterday, but kept reading and digging and found much more disturbing stuff than I expected. First, a recap: Sars-Cov-2 virus has a genetic insert that exists ONLY in Moderna...

### Read more

6 days 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 <u>1R3ZDZJY016</u>.

And here are <u>the results</u>. I annotated them to make it easier for you to see what is and is not interesting.

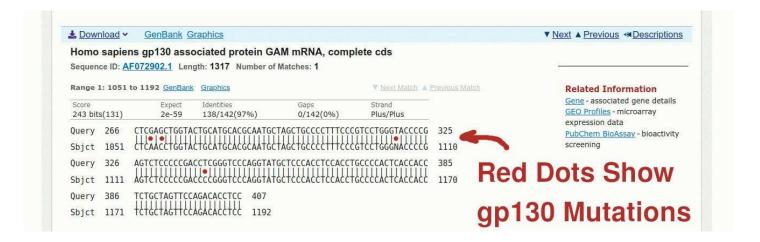


The first few results are from the usual suspects such as chimeric viruses, Sars-Cov-2 sequences, etc. It is understandable why we should ignore them — the chimeric viruses are pure lab constructs of unknown significance, and Sars-Cov-2 sequences are obviously there because the vaccine encodes Sars-Cov-2 spike protein. Those are "expected matches".

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

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### I clicked on it:



You can click on the "Gene" link to see what that gp130 gene is about:

### TLE5 TLE family member 5, transcriptional modulator [ Homo sapiens (human) ]

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

♣ Download Datasets



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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; Alliance Genome: 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 heteroologimer 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]

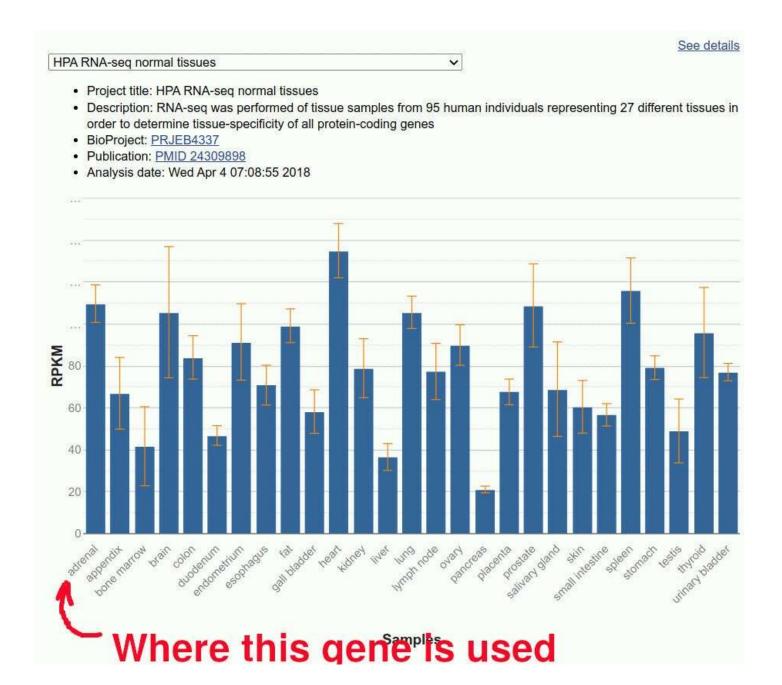
Expression Ubiquitous expression in heart (RPKM 135.6), spleen (RPKM 116.8) and 25 other tissues See

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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 mutates in general? Nothing good comes up and you can search for it too.

> 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 Sommer <sup>1</sup>, 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

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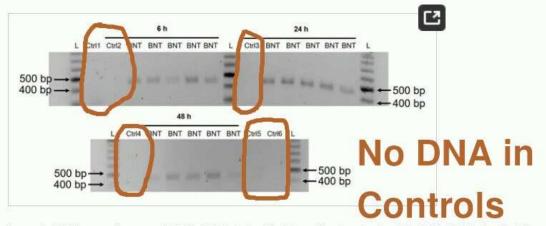
### **Abstract**

Ligand-independent constitutively active gp130 mutants were described to be responsible for the development of inflammatory hepatocellular adenomas (IHCAs). 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.

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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 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.

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:



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Anonymous ID:CjVlc4Sa Wed 09 Dec 2020 04:22:55 No.295621351

View Reply Original Report

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>>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

>>295632/39 >>295632/08 >>295632904 >>295633435 >>295633483 >>295634836 >>295634910

I'm an industrial engineer at Moderna and the other one of us is a process development engineer. I'm sure

[333 / 38 / 121]

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. Profi

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

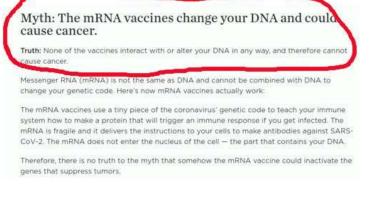
(6) coincides with poor people being obsoleted by Al and robotics, so we didn't have to dig for motivation.

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









# **Clarifications**

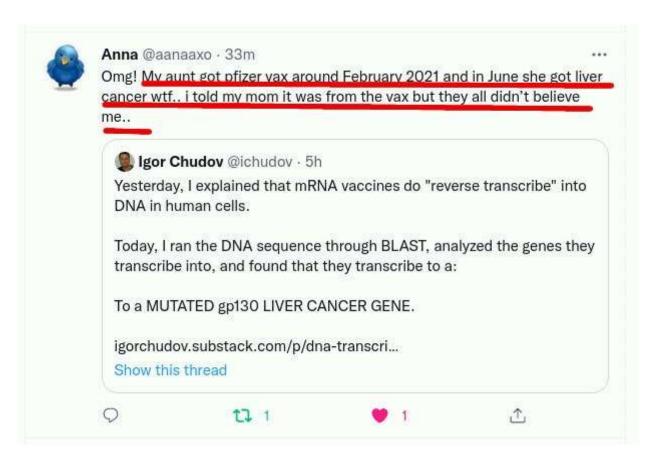
The sequence of mutated gp130 genes, found in the DNA reverse transcribed from Pfizer Covid vaccine,

- 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.

# **Please Share this Article**

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 injected with it and we deserve to know what it does to them!

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Jeff Ferguson Writes Economic Insights For All · Feb 27 · edited Feb 27 ♥ 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.  ○ 79 Reply							
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