Kevin McKernan 🙂

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May 19 • 19 tweets • 8 min read

Compounding error

Transcriptional error and Translational error.

The mRNA jabs use a RNA polymerase to synthesize mRNA from a DNA plasmid.
They replace U with m1pU.

The error rate jumps to 100-300 errors per million bases. That's 10-^3 -> 10-^4 error

biorxiv.org/content/10.110…

Improving the fidelity of uridine analog incorporation during in vitro transcription
In vitro transcribed synthetic messenger RNAs (mRNAs) represent a novel therapeutic modality and are currently being evaluated for a wide range of clinical indications. To overcome the inherent immuno…
https://www.biorxiv.org/content/10.1101/2022.04.12.488100v1

The vax is ~4200bp.
This is approximately 1 error in every vax molecule and you get injected with 40T.

This is a result of m1pU which is a low fidelity base. This low fidelity also impacts the next step of tRNA hybridization in translation.
This is compounding error.

Pfizer has mostly sold this base replacement as improving the magnitude and durability of expression.

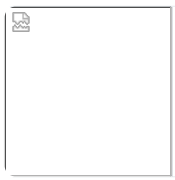
As with many things in biology, when you optimize for the magnitude of expression, you sacrifice fidelity.

Many think of variants as from the virus, not the vax
The virus has an ExoN gene to error correct the polymerase errors. These error correcting proteins don't like low fidelity bases like m1pU
In order maximize expression of m1pU they need sloppy enzymes

pnas.org/doi/10.1073/pn…

https://www.pnas.org/doi/10.1073/pnas.2106379119#fig03

pnas.org/doi/10.1073/pn…



https://www.pnas.org/doi/10.1073/pnas.2106379119#fig03

As for IVT polymerase error rate, I'd like to emphasize that the folks from New England Biolabs are no hacks when it comes to enzymology.

Their founder Rich Robert's won the Nobel prize for the discovery of restriction enzymes and they have been the gold standard for decades.

The problem is more pronounced with translation.
This model is changing only a few codons. Change them all I bet the error rate escalates.

pnas.org/doi/10.1073/pn…

https://www.pnas.org/doi/10.1073/pnas.1821754116#fig04

Add the transcriptional and translational compounded error and you have a combinatorial biochemistry problem on every injection.

This is why there is raw sequence data for vax lots in NCBI.
There is no peptide sequence of one of these mRNA libraries in NCBI.
Just smears on gels.

This is a highly variable prodrug.
The final drug has never been characterized.

There are 3D structures of protein translated from mRNA transcribed from a DNA construct without m1pU. Not relevant.
No m1pU.

There are also smeary antibody stained western blots.
Antibody stains are biased toward error free proteins. They don't tag the mutated ones.

Need to stain everything.

In summary, no mRNA injection should ever escape lot to lot sequence QC that is sensitive enough to find parts per thousand error. 40T molecules injected means small % error = billions of contaminants.
Protein sequencing of the final drug should be required.

To simplify, the error measured by Chen et al, suggests 1 error in every mRNA molecule. Poisson would imply some molecules have 2 and 3 errors and many have zero.

Now imagine you inject 40 Trillion molecules where each one is different.

The combinatorics are mind blowing.

The good news is that folk at BASE are starting to look at this problem with direct RNA sequencing with Oxford Nanopore (ONT). But the m1pUs look foreign to the ONT platform and get called as both a C and a T. It's unlikely this will have the accuracy to pick up 1:1K heteroplasmy

The bad news is, this should have been done and made public before injecting 1B people. Its pretty bleeding edge so I can see how it was overlooked but at the minimum ILMN sequencing could have measured the heteroplasmies. Probably need UMIs to discount the cDNA syn error.

But now that the camel has its nose in the tent and has feasted on the money machine.. It will be back for more.

For those doubting my assessment of the mfg process, BASE spells it out here. Maybe my purity expectations are too high but I'd be anlot less scrupulous if Pfizer/Moderna put any raw sequence live for lot to lot QC. Zero for the vax. Millions for the virus.

This preprint monitors the translation fidelity in PseudoU and m1PseudoU.

biorxiv.org/content/10.110…

Another one. I dont see an email address for this author.
jpands.org/vol27no2/hatfi…

Steven Hatfill – Wikipedia
https://en.wikipedia.org/wiki/Steven_Hatfill

• • •

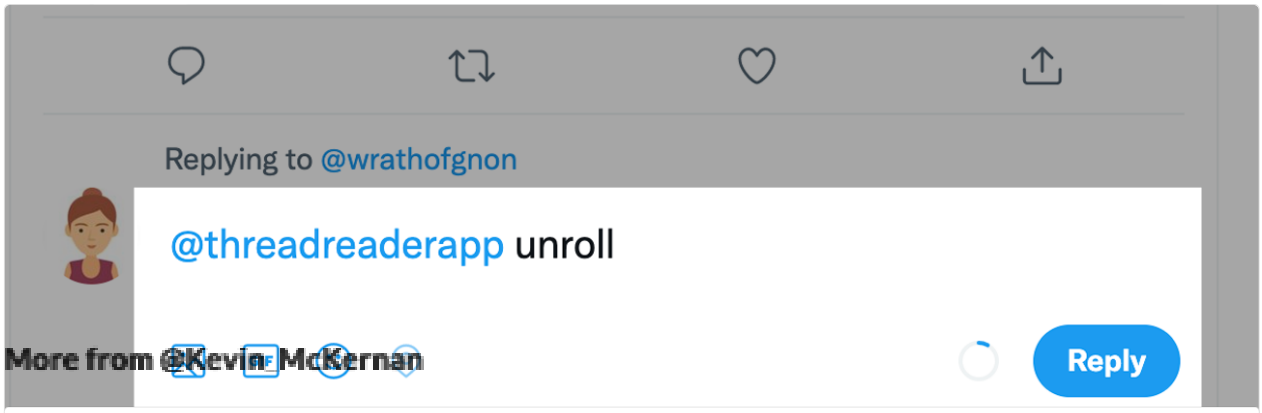
Josh Stylman
@jstylman

Jul 9

Friends, as many of you know, I've spent much of the last year railing about vaccine mandates and alerting people that we have not been given informed consent about the experimental gene therapy being injected into people across the globe. 🧵

At this stage, anyone who supports mandates has either been corrupted or brainwashed into believing these shots do something that they do not. This thread is focused on the possible risks that are being suppressed by those who shape the minds of the masses.

Let's start with VAERS, the reporting system overseen by the U.S. Government. As of today, there have been 2,191,417 reports of adverse events. That is more than all vaccines combined since they started keeping records of this 30+ years ago.



Kevin McKernan 🙂
@Kevin_McKernan

Aug 14

Franklins Tower

Read 4 tweets

Practice here first or read more on our help page!

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Aug 10

Just a reminder. Hotez continues to flamed journals with hatred toward vex skeptics that require military intervention.

Choice words to discriminate against people that question his holy wisdom.

Read 5 tweets

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Aug 5

Colonies from a cannabis flower. What are they? Toothpick into an 8 minute boil prep and we can PCR the ITS regions in an 1.5hours. 15minute TN5 transposon based rapid barcoding kit and we have DNA ready for Oxford Nanopore.

Agilent tape station used to quantify the PCR bands prior to TN5 transposition of the DNA barcodes.

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Aug 3

USB sized sequencer from ONT. This delivered 125,000 reads in a few hours. Great tool for 16S and ITS sequencing to ID unknown organisms.

~700bp ITS amplicons from various colonies isolated from cannabis flowers. You can get colonies identified same day. The only other methods that offer same day ID use protein mass spec.

These, unfortunately suffer in their ability to split closely related species as the protein sequence is often conserved while the DNA

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Jul 28

Spent the week in TwitoMo for a post Twitter claimed was a C19 violation. It clearly is not misinformation as documented below. anandamide.substack.com/p/twitmo

Upon appeal and upon informing them I'm in contact with several attorneys on the matter, they changed their tune. No longer is it C19 misinformation but the subjective "abusive behavior" claim has been made. This appeal occurred in 1 Biz day.

Can you spot the abusive content in the tweet?

Read 6 tweets

Kevin McKernan 🙂
@Kevin_McKernan

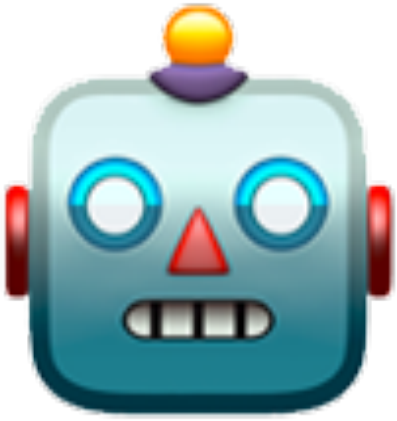
Jul 16

Spent the night in TwitMo once again for posting factually accurate information. @TwitterSupport should know Im in contact with @jlawrencenc as you have allowed the @NIH to post misinformation while penalizing the scientist who points it out.

You (@Twitter) are not qualified to weigh in on this debate. I have received over $32M in funding from NIH for genomics and constructing DNA sequencers. They posted factually incorrect information conflating natural RNA with NIH patented modifiedmRNAs genome.gov/12513210/2004-…

The above funding was to build the SOLiD sequencing which paid careful attention to modified nucleotides. The below funding was awarded to the company I founded. 5 genome centers were funded. Venter, Lander, Wilson, Gibbs, Agencourt. cummings.com/articles

Read 13 tweets



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