

# Addressing the Yan report

In September 2020, the above claimed to **be** scientific evidence for SARS-CoV-2 being an engineered bioweapon 🤔 Zenodo granting it a Digital Object Identifier (DOI) made the report appear credible, despite a lack of peer review.

The Johns Hopkins University **made up for that lack** the same month, explaining why the report was unconvincing. But conspiratorial audiences 🤔🤔 value neither authority, nor being pointed to tonnes of reading material (can't blame them for the latter 😊).

They do value critical thinking, which only requires that **the core claim** be verified. Should it prove false, everything else can be dropped 🧑 What was the report's postulate, then, that sufficed for its authors to be able to seek asylum in 🇺🇸?

# Restriction enzymes around the spike's receptor binding motif

Mikolaj Raszek, PhD, was kind enough to elucidate, in [SARS-CoV-2 coronavirus origins alternative theories – do they hold up against science?](#), the core claim of the Yan report.



Two **restriction enzymes** (sequences bacteria use to slash viruses to bits, repurposed by humans to glue parts of different genomes together): **EcoRI** and **BstEII**. According to Yan et al, the sequence between them allowed to target mammals larger than 🦇🦇.


A SARS-CoV-2		EcoRI				
		W	N	S		
tataattata	aattaccaga	tgattttaca	ggctgcgtta	tagcttg	<b>gaa ttc</b>	taacaat
cttgattcta	aggttggtgg	taattataat	tacctgtata	gattgtttag	gaagtcta	aat
ctcaaacctt	ttgagagaga	tatttcaact	gaaatctatc	aggccggtag	cacacctt	gt
aatggtggtg	aaggttttaa	ttgttacttt	cctttacaat	catatgggtt	ccaacc	cact
aatggtggtt	<b>g gttacc</b>	aacc	atacagagta	gtagtacttt	cttttgaact	tctacatgca
	G Y Q					
	BstEII					

# Download the earliest known SARS-CoV-2 genome (1 of 2)

Yan et al's image caption cites the isolate **Wuhan-Hu-1** (isolate: a population of organisms having little genetic mixing with other organisms of the same species).

*Figure 5. Two restriction sites are present at either end of the RBM of SARS-CoV-2, providing convenience for replacing the RBM within the spike gene. A. Nucleotide sequence of the RBM of SARS-CoV-2 (Wuhan-Hu-1).*

Viewing [the isolate at NCBI Virus](#), the absolutely earliest accession (unique sequence identifier) is [MN908947.1](#), collected in Dec 2019  submitted 2020-01-05  released 2020-01-12.

That's 2 months until the World Health Organization would declare COVID-19 a pandemic  (2020-03-11).

# Download the earliest known SARS-CoV-2 genome 📄 (2 of 2)

In [the accession page](#), switching to the FASTA format (a text format often used for storing reference genomes) allows us to download the troublemaker's genome:

The screenshot shows the GenBank accession page for the 'Wuhan seafood market pneumonia virus' (GenBank: MN908947.1). A green circle with the number '1' highlights the 'FASTA' link. A warning message states: 'This sequence has been updated. See current version.' Below this, there are links for 'FASTA' and 'Graphics', and a 'Go to:' dropdown menu. Overlaid on the right is a 'Send to:' dialog box, which is highlighted with a green circle and the number '2'. The dialog box has three sections: 'Complete Record' (selected), 'Choose Destination' (with 'File' selected), and 'Download 1 item.' (with 'Format' set to 'FASTA'). A green circle with the number '3' highlights the 'Create File' button at the bottom of the dialog box.

~30k bases (a base is one of A, C, G, T) long? What a tiny genome. A human one is 3.1 billion bases, with a single cell taking up between 3.3 GB (reference genome, a measurement standard) and 70 GB (non-reference genome) of your hard drive 🙈

## Are EcoRI and BstEI *actually* there? 🔍👁️

- **Note:** Sequences identical to those listed **needn't** necessarily come from restriction enzymes - but let's simplify and humour that notion 🙌👩

You can open the downloaded SARS-CoV-2 genome in a text editor 📄, and search ( `Ctrl+f` / `Cmd+f` ) for the occurrences of the **EcoRI** sequence **GAATTC** yourself. If you fancy a dopamine rush, **stop reading and go ahead now** 😊

The **N** (= whichever base) in **BstEI**'s **GGTNACC** is a tad more problematic, though. If you can locate *regular expression mode* (look for a button marked `. *` ) 🙌, this hurdle can be cleared by inputting **GGT[ACGT]ACC**.

# Plotting EcoRI & BstEI sequence matches in the spike gene



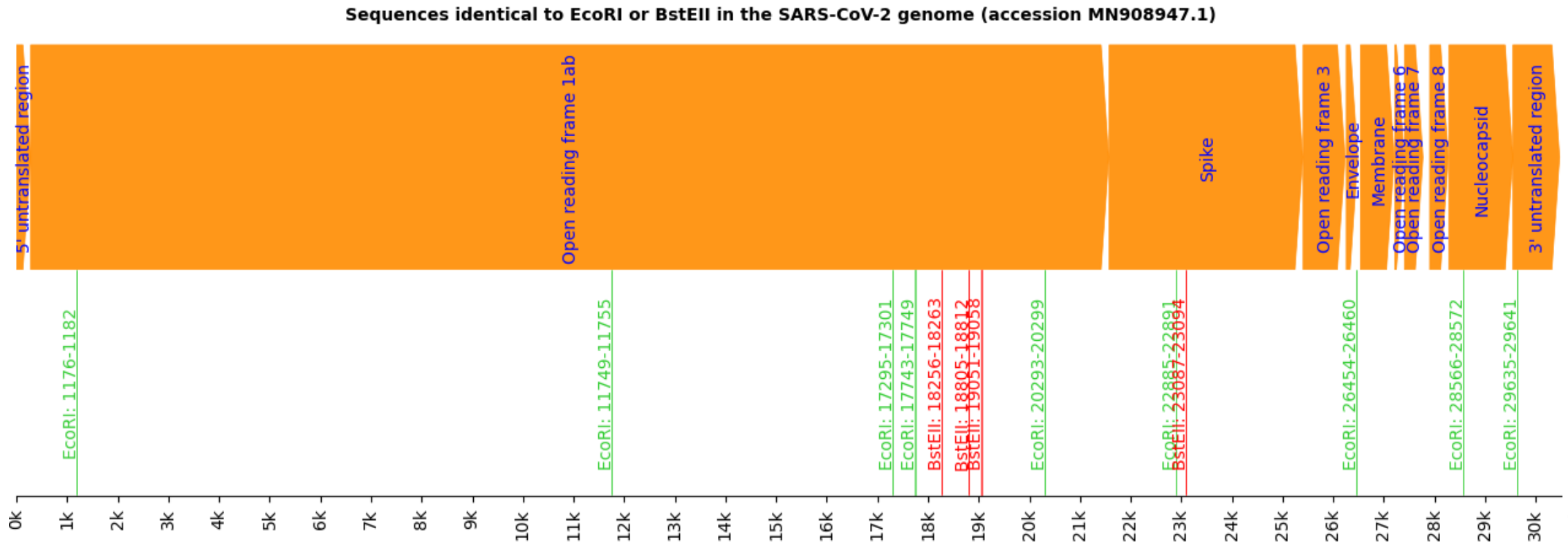
The accession MN908947.1 spike gene **does** contain sequence occurrences with 100% identity to EcoRI & BstEI, and that's at the **exact** coordinates specified by Yan et al 🎯

So far so good - let's look at the rest of the genome 🔍

# Plotting EcoRI & BstEI matches across the whole genome

But looking at **all the genes** (instead of just the spike), one seems to find more 'genetic modifications' than Yan et al bargained for 🤔

There's even an EcoRI match in the 3' untranslated region (nothing there ever becomes live proteins, hence there's no point in engineering the region).



# A restriction enzyme cornucopia? 🦄 Let's find out 🧑

*Bioinformatics Algorithms: An Active Learning Approach* gives the formula (search for `approximation`) for approximating the likelihood that a **k-mer** (word of size k) occurs in a text *by random chance alone* 🎲

The **lower** ⬇️ that likelihood, the **more probable** ⬆️ any bioengineering 🧬 ✂️ 🧬  
Customarily, values with `< 5%` chance of being randomly generated, are worthy of investigation.

[Click here](#) for the Python version of the approximation formula 🐍. Its code's been [tested](#), so should be reliable. Let's take it for a spin 🧶 🐱



## ✂ Theory vs practice: probabilities along the full genome 🧬


**1** A nice property of our approximation formula: if we seek the probability of **just a single occurrence**, any returned number `> 1.0` is the **expected occurrence count**.

**2** BstEII's middle character (GGT**N**ACC) can be anything, so BstEII is considered to have length 6 (the same length as EcoRI), instead of 7.

Restriction enzyme	Expected occurrences	Actual occurrences
EcoRI (GAATTC)	7.44	9 (...are Yan et al onto something?)
BstEII (GGT_ACC)	7.44	4 (...no they aren't)

No conclusive evidence either way yet 🧑🔬 Let's concentrate on the spike 👁👁

## Occurrence probabilities within the spike gene

The [accession page](#) informs us that the range of the "S" gene is 21579..25400, which makes for a length of 3821. Plugging this text length into our formula , we get:

```
In [3]: ProbabilityOfKmerOccurringNTimesInText(alphabet_size=4)(
...:      text_length=3821, kmer_length=6, kmer_occurrence_count=1
...: )
Out[3]: 0.931640625
```


There's a 93% probability of at least one sequence of length 6 (doesn't matter if it's EcoRI or BstEII) occurring, in a coronavirus spike gene of that length, just by random chance alone. How about the **joint probability of both of them occurring at once?**





## Conclusion

Since BstEI and EcoRI are considered the same length (after disregarding BstEI's arbitrary middle character, they're each 6 bases long), the joint probability of them occurring together in the spike is approximately  $93\% * 93\%$  :

```
In [4]: 0.931640625 * 0.931640625
Out[4]: 0.8679542541503906
```

➡ at least **86% of all coronaviruses** are going to have - in their spike protein gene - an EcoRI sequence occurring together with a BstEI sequence. Without the need for **any** genetic engineering 

Putting it differently: if SARS-CoV-2 was bioengineered   the way Yan et al suggested, then 17 in 20 coronaviruses occurring in nature **also were**. Why go through the trouble of bioengineering SARS-CoV-2, when nature has already done the work ?