Do Covid19 injections with modified RNA risk generating inappropriate parasite proteins and prions?

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ABSTRACT.

Injection technology mRNA COVID19 substitutes to the natural Uracile bases of the modified pseudo Uracile bases. These modified bases are sometimes ignored by the ribosome which skips them, thus causing a shift in the codon reading frame. Here we analyze the Spike protein when it is read following the second or third reading frame of the codons. We then discover parasitic proteins that we analyze, some of which may have the property of Prion or amyloid.

INTRODUCTION.

On the one hand, it has just been demonstrated (Mulroney et al, 2023) that the basics U modified RNA Covid19 injections provoke in a way unpredictable and erratic frame shifts reading while translating of the RNA sequence in protein, more precisely, N1-methylpseudouridylation of mRNA causes +1 ribosomal frameshifting. On the other hand, in (Perez and al, 2024), the final posthumous article by Luc Montagnier explores the emergence of a form dazzling Creutzfeldt Jakob driving, for the 26 cases studied, death a few months after the injection. The article suggests that this causal relationship effect could result from the presence of a Prion region in the Spike protein of MRNA injections. Curiously we let's demonstrate in (Perez et al, 2021) that this Prion region present in there WUHAN strain (having served as matrix for injections), and in all variants a completely disappeared in the Omicron variant. In this article we will search therefore the presence of hypotheticals unwanted proteins due to these shifts in the frameworks of reading RNA codons. But we will search also the presence of possible Prion functions in these Unwanted proteins.

METHODS.

The objective of this article is the search for hypothetical inappropriate proteins which would result from the ribosaumes hopping on certain modified U bases of the RNA injections.

For this purpose we use BLASTP to search for these protein homologs (https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGEproteins).

For the search for possible Prion functions of these unwanted proteins we use PLAAC (content://com.android.chrome.FileProvider/offline-cache/3b230c18-c4ff-421c-aa5e-ee728276c09e.mhtml).

The sequence of the Spike which served as a matrix for the injections is as follows

Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
NCBI Reference Sequence: NC_045512.2
CDS 21563..25384
 /gene="S"
/locus_tag="GU280_gp02"
/gene_synonym="spike glycoprotein"
/note="structural protein; spike protein"
/codon_start=1
/product="surface glycoprotein"
/protein_id="YP_009724390.1"
/db_xref="GeneID:43740568"

It is unknown which U bases are skipped by ribosaumes. The combinatorics of shifted sequences is therefore infinite.

However there are 3 major configurations of sequence evolution due to these alterations:

A first case that we do not analyze is the one where the regular reading frame would be preserved but where the disappearance of a U base would cause stop codons like UAA or UAG to emerge, thus producing fragments of modified and truncated Spike.

The second scenario concerns the reading of the Spike sequence shifted by one base and therefore read according to the second reading frame of the codons.

The third scenario concerns the reading of the Spike sequence shifted by two bases and therefore read according to the third reading frame of the codons.

It is these last 2 cases that we will analyze.

RESULTS.

Summary:

1/ The shift of one base in the reading frame of the codons due to the jump of the ribosaumes on a pseudo Uridine base.

1.1 What happens to the Prion region of the Spike?

1.2. What proteins emerge from this one-base shift in the codon reading frame?

2/ The shift of two bases of the reading frame of the codons due to two jumps of the ribosaumes on pseudo Uridine bases.
2.1. Which proteins emerge from reading according to the third reading frame?
2.2. The detection of a hypothetical Prion function.

Detailed results:

1/ The shift of one base in the reading frame of the codons due to the jump of the ribosaumes on a pseudo Uridine base.

1.1 What happens to the Prion region of the Spike?

In the article (Perez et al, 2023) a prion region in the spike of the injections. What happens to this region if we shift it by one base following the failure of translation of a pseudo Uricil towards the beginning of the Spike protein?

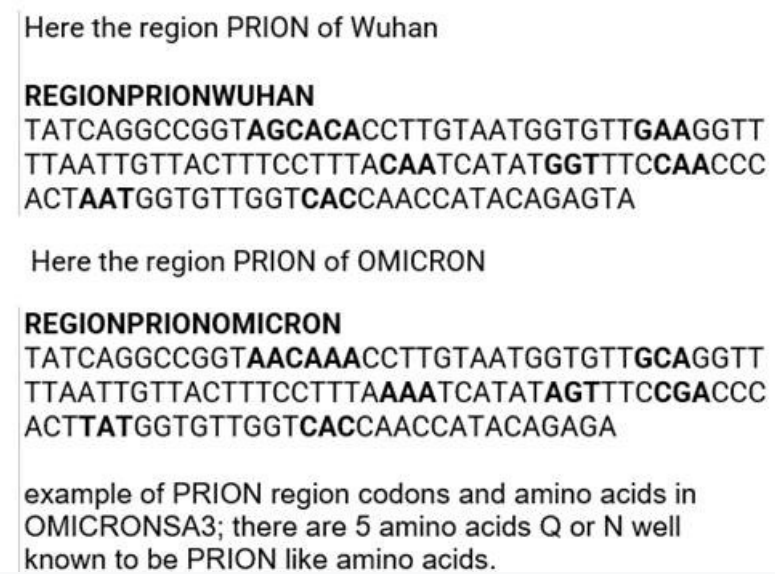

Figure1. the Prion region

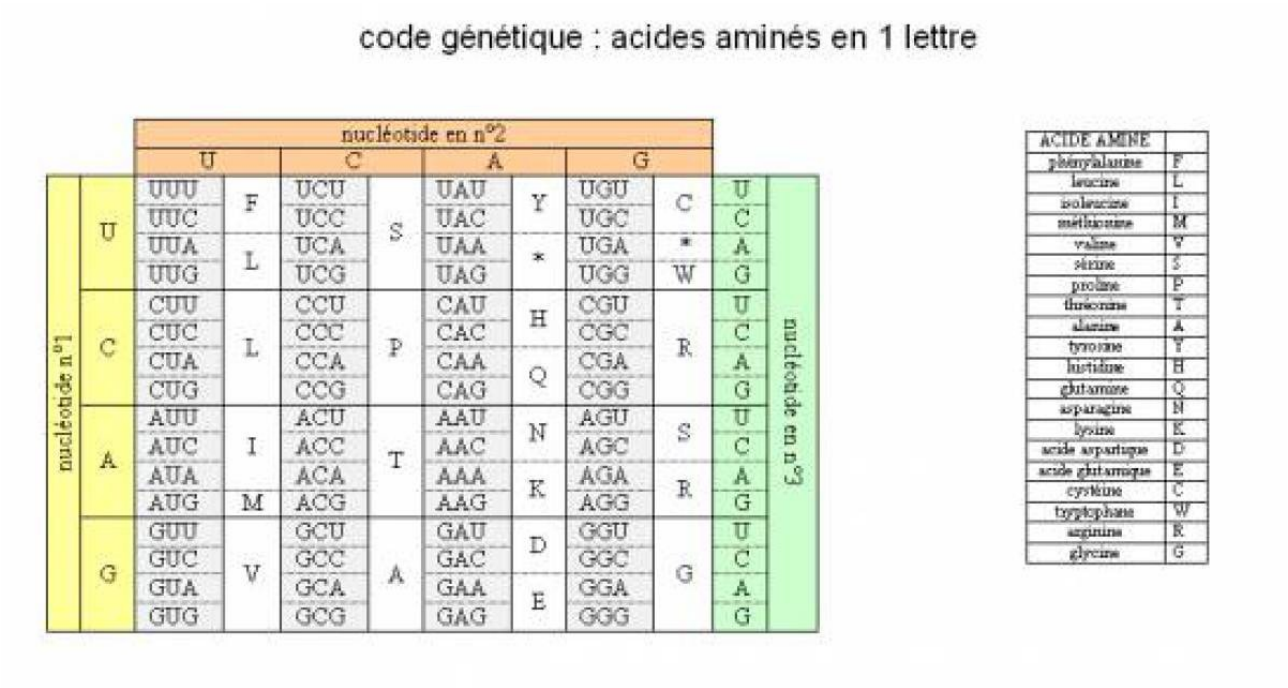

Figure2. Genetic code

Remember that the amino acids promoting Prion function are in descending order:

N (Asn. asparagine) ###

Q (Gln. glutamine) ###

these are the 2 amino acids that most promote Prion function.

Then come

Y H M S... #

etc...

ATC. I
AGG. R
CCG. P
GTA. V
GCA. A
CAC. H. #
CTT. L
GTA. V
ATG. M. #
GTG. V
TTG. L
AAG.
GTT. V
TTA. L
ATT. I
GTT. V
ACT. T
TTC. F
CTT. L
TAC. Y
AAT. N. ###
CAT H. #
ATG. M. #
GTT. V
TCC. S. #

```
AAC.  N. ###
CCA.  P
CTA.  L
ATG. M. #
GTG. V
TTG. L
GTC. V
ACC. T
AAC. N. ###
CAT. H. #
ACA. T
GAG. E
```

We see that by the presence of N amino acids, the Prion nature remains active despite the shift in the codon reading frame. On the contrary, the shift of 2 bases completely eliminates the Prion nature.

1.2. What proteins emerge from this one-base shift in the codon reading frame?

Result after shifting the codon reading frame by one base:

```
CLFFLFYCH_SLVSVLILQPELNYPLYTNSFTRGVYYPDKVFRSSVLHSTGLVLTFLFQCYLVPCYTCLWDQW
YRGLITL
 SYHLMMVFILLPLRSLT_RGWIFGTTLDSKTQSLLIVNNATNCY_SL_ISIL__SIFGCLLPQKQQVGWKVSSE
 FILVRIIALLNMSLSLLMDLEGKQGNFKNLREFVFKNIDGF_NIF_AHAY_FSA_SPSGFFGFRHW_ICQ_VLT
 SLGFKLYLLYIEVITPGDSSSGWTAGAAAYYVGYLQPRFSIKI__KWNHYRCCRLCT_PSLRQSVR_NPSL_KK
 ESIKLLTLESNQESIVRFPNITNLCPFGEVFNATRFICLCLEQEENQQLCC_LFCPI_FRHFPLLSVMECLLLN
 _

First Protein ==>
MISALLMSMDSFVIRGDEVRQIAPGQTGKIADYL_

ITR_FYRLRYSLEF_QS_F_GWVIIITCIDCLGSLISN
 LLREIFQLIYQAGSTPCNGVEGFNCYFPLQSYFPTH_WCWLPTIQSSSTFF_TSTCQQLFVDLKSLLIWLKTNV
 SISTSMLTGTGVLTESNKKFLPFQQFGRDI_HY_CCP_STDT_DS_HYTMFFWWSVL_HQEQILLTRLLFFIRM
 LTAQVPVAIHADQLTPTWRVYSTGSNVFNTCRLFNRG_TCQQLI_V_HTHWCVYALVIRLRLILLGGHVV_LV
N
 PSAYTMSLGAENSVAYSNNSIAIPTNYY_CYHRNSTSVYDQDISRLYNVHVVIQLNAAIFCCNMAVFVHN_T
VL

 TGIAVEQDKNTQEVFAQVKQIYKTTN_RFWWF_FFTNITRSIKTKQEVLLKIYFSTK_HLQMLASSNNMVIA
GD
 IAARDLICAQKFNGLTVLPPLLR_NDCSIHFCTVSGYNHFWLDLWCVLHYKYHLLCKWLIGLMVLELHRML
YEN
 QKLIANQFNSAIGKIQDSLSHSKCTWKTSRCGQPKCTSFKHAC_NLAPILVQFQVF_

Second protein ==>
MISFHVLTKLREVQIDRLITGRLQSLQTYVTQQLISCRNQSFC_
```

SCCY_NVRVCTWTIKELIFVERAIILCPSLSQHLMV_SSHVTYVPAQ
EKNFTTAPAICHDGKALSS_RCLCFKWHTLVCNTKEFL_TKSLLQTTHLCLVTVML__ELSTTQYDPLQPELDS
FKEELDKYFKNHTSRC_FR_HLWH_CFSCKHSKRN_PPMRLPRI_

Third protein ==>
MNLSSISKNLESMSSI_

WPWYIWLGFIAG
LIAIVMVTIMLCYDQLL_LSQGLLFLWILLQI__RRLSQCSKESNYITHK

The 3 unwanted proteins resulting from a ribosome error on a single Uracil pseudo are:

MISALLMSMDSFVIRGDEVRQIAPGQTGKIADYL_ITR_FYRLRYSLEF_

MISFHVLTKLREVQIDR
LITGRLQSLQTYVTQQLISCRNQSFC_

MNLSSISKNLESMSSI_

The first 2 proteins are homologous to fragments of Spike.

Focus on the third and last protein:

hypothetical protein NECID01_1208 [Nematocida sp. AWRm77]

Sequence ID: KAI5190913.1 Length: 371 Number of Matches: 1

Range 1: 66 to 77 GenPept Graphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
35.4 bits(76)	3.4	10/12(83%)	11/12(91%)	0/12(0%)

```
Query  1   MNLSSISKNLES  12
          M+LS ISKNLES
Sbjct  66  MDLSTISKNLES  77
```

hypothetical protein NECID01_1208 [Nematocida sp. AWRm77]

GenBank: KAI5190913.1
Identical Proteins FASTA Graphics
Go to:

```
LOCUS       KAI5190913               371 aa            linear
PLN 13-JUL-2022
DEFINITION  hypothetical protein NECID01_1208 [Nematocida sp.
AWRm77].
ACCESSION   KAI5190913
VERSION     KAI5190913.1
DBLINK      BioProject: PRJNA579982
            BioSample: SAMN13280735
DBSOURCE    accession JALPNA010000071.1
KEYWORDS    .
SOURCE      Nematocida sp. AWRm77
  ORGANISM  Nematocida sp. AWRm77
            Eukaryota; Fungi; Fungi incertae sedis;
Microsporidia; Nematocida.
REFERENCE   1  (residues 1 to 371)
  AUTHORS   Wadi,L. and Reinke,A.W.
```

```
  TITLE     Comparative genomic analysis of nematode-infecting
microsporidia
  JOURNAL   Unpublished
REFERENCE   2  (residues 1 to 371)
  AUTHORS   Wadi,L. and Reinke,A.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2022) Molecular Genetics,
University of Toronto,
            661 University Ave, MaRS Centre, West Tower 16th
floor, Toronto, ON
            M5G 1M1, Canada
COMMENT     ##Genome-Assembly-Data-START##
            Assembly Date          :: 01-SEP-2021
            Assembly Method        :: ABySS v. 2.0.2
            Assembly Name          :: ncid_AWRm77
            Genome Representation  :: Full
            Expected Final Version :: Yes
            Genome Coverage        :: 3073.99x
            Sequencing Technology  :: Illumina NovaSeq
            ##Genome-Assembly-Data-END##
            Method: conceptual translation.
FEATURES             Location/Qualifiers
     source          1..371
                     /organism="Nematocida sp. AWRm77"
                     /strain="AWRm77"
                     /isolation_source="spores"
                     /host="Caenorhabditis sp. 8"
                     /db_xref="taxon:2670344"
                     /country="USA: Stow, Massachusetts"
                     /collection_date="2017"
     Protein         1..371
                     /product="hypothetical protein"
```

2/ The shift of two bases of the reading frame of the codons due to two jumps of the ribosaumes on pseudo Uridine bases.

2.1. Which proteins emerge from reading according to the third reading frame?

Here is the translation of the Spike offset by one base.
Only one protein will be retained here, starting with a methionine M and ending with a Stop codon.

VCFSCFIATSL_SVC_SYNQNSITPCTLILSHVVFITLTKFSDPQFYIQLDLFLPFF
SNVTWFHAIHVSGTNGTEV__PCPTI__WCLFCFH_EV_HNEAGFLVLL_IRRP
SYLLLITLLMVIKVCEFQFCNDPFLGVYYHKNNKLDGK_VQSLF_CE_LHF_ICL
SAFLWTLKENRVISKILGNLCLRILMVFKIYSKHTPINLVRDLPQGFSALEIGRFA
NRY_HH_VSNFTCFT_KLFLLVILLQVGQLVLQLIMWVIFNLGFLLKYNENGTITD
AVDCALDPLSEKVYVEILHCRKRNLSNF_L_SPTNNLLLDFLILQTCALLVKFLTP
PDLSVYAWNRKRISNCVADYSVLYNSAIFHF_VLWSVSY_IK_SLLY_CLCIHL_L
EVMKSDKSLQGKLERLLIIYKLPDDFTGCVIAWNSNNLDSKVG_L_LPV_IV_EV
_SQTF_ERYFN_SIRPVAHLVMVLKVLIVTFLYNHMFQPTNGVGYQPYRVVVLS
FELLHASNCLWT_KVY_FG_KQMCQFQLQW_QAQVFLLSLTKSFCLSNNLAET
LDTTDAVRDPQTLEILDITPCSFGGQCYNTRNKYF_PGCCSLSGC_LHRSLLLF

MQINLLLLGVFILQVLMFFTRAGCLIGAEHVNNSYECDIPIGAYMR_LSDSD_FS
SAGT_CS_SIHHPTLCHLVQKIQLLTLITLLPYPQITISVTTEILPVSMTKTSVDCT
MYIW_FN_

First protein ==>
MQQSFVAIWQFLYTIKPCFLE_

LLNKTKTPKKFLHKSNKFTKHPIKDFGGFNFSQILPDPSKPSKRSY_RSTFQQS
DTCRCWLHQTIW_LPVILLLETSFVHKSLTALLFCHLCSDEMIAQYTSALLAGTI
TSGWTFGACCITNTICYANGL_V_WYWSYTECSMRTKN_LPTNLIVLLAKFKTH
FLTASALGKLQDVVNQNAQALNTLVKT_LQFWCNFKCFK_YPFTS_QS_GKCK
LIG_SQADFKVCRHM_LNN_LAAEIRASANLAATKMSECVLGQSKS_FLWKGL
SSYVLPSVSTSWCSLLM_LMSLHKKRTSQLLLPFVMMEKHFPREGVFVSNGT
HWFVTQRNFYEPNHYYRQHICVW_L_CCNRNCQQHSMILCNLN_THSRRS_I
NILRIIHHDVDLGDISGINASVVNIQKEIDRL_GCQEFK_ISHRSPRTWKV_AVYK
GHGTFG_VL_LA_LP__W_QLCFAMTSCCSCLKGCCSCGSCCKFDEDD_ASA
QRSQITLHIN

Let's look for possible homologs of this wild protein

MQQSFVAIWQFLYTIKPCFLE_

Here are the closest existing protein homologies to this wild protein:

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession	
Select seq gb|QNK64972.1|	MFS transporter [Pedobacter sp. PAMC26386]	Pedobacter sp. PAMC26386	35.0	35.0	71%	11	73.33 %	388	QNK64972.1
Select seq ref|WP_102409550.1|	PD-(D/E)XK nuclease family protein [Parabacteroides bouchesdurhonensis]	Parabacteroides bouchesdurhonensis	34.1	34.1	57%	21	75.00 %	960	WP_102409550.1
Select seq ref|WP_118319173.1|	PD-(D/E)XK nuclease family protein [Parabacteroides bouchesdurhonensis]	Parabacteroides bouchesdurhonensis	34.1	34.1	57%	21	75.00 %	960	WP_118319173.1
Select seq ref|WP_103982177.1|	PD-(D/E)XK nuclease family protein [Parabacteroides	Parabacteroides chinchillae	34.1	34.1	57%	21	75.00 %	968	WP_103982177.1

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
	chinchillae] PD-(D/E)XK							
Select seq gb|MDR1938841.1|	nuclease family protein [Tannerellaceae bacterium] PD-(D/E)XK	Tannerellaceae bacterium	34.1	34.1	57%	21	75.00 %	968	MDR1938841.1
Select seq ref|WP_099465130.1|	nuclease family protein [Parabacteroides provencensis]	Parabacteroides provencensis	34.1	34.1	57%	21	75.00 %	968	WP_099465130.1
Select seq ref|WP_205514649.1|	DUF262 domain-containing protein [Longitalea arenae]	Longitalea arenae	34.1	34.1	95%	21	65.00 %	1034	WP_205514649.1
Select seq emb|CAG4716923.1|	unnamed protein product [Naegleria fowleri]	Naegleria fowleri	33.7	33.7	71%	30			

MFS transporter [Pedobacter sp. PAMC26386]

Sequence ID: QNK64972.1 Length: 388 Number of Matches: 1

Range 1: 296 to 308 GenPeptGraphics Next Match Previous Match

Related Information
AlphaFold Structure-3D structure displays

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
35.0 bits(75)	11	11/15(73%)	11/15(73%)	2/15(13%)

```
Query   6    VAIWQFLYTIKPCFL   20
             VAIW FLY   PCFL
Sbjct   296  VAIWGFLYA--PCFL   308
```

Download GenPeptGraphics Next Previous Descriptions

PD-(D/E)XK nuclease family protein [Parabacteroides bouchesdurhonensis]

Sequence ID: WP_102409550.1 Length: 960 Number of Matches: 1

Range 1: 160 to 171 GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
34.1 bits(73)	21	9/12(75%)	10/12(83%)	0/12(0%)

```
Query   2    QQSFVAIWQFLY   13
             QQSF A+WQ LY
Sbjct   160  QQSFLAVWQILY   171
```

Download GenPeptGraphics Next Previous Descriptions

DUF262 domain-containing protein [Longitalea arenae]

Sequence ID: WP_205514649.1 Length: 1034 Number of Matches: 1

Range 1: 700 to 716 GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
34.1 bits(73)	21	13/20(65%)	14/20(70%)	3/20(15%)

```
Query  2    QQSFVAIWQFLYTIKPCFLE  21
            QQSF A W+FLY I P  LE
Sbjct  700  QQSFYALWHFLYYI-P--LE  716
```

DownloadGenPeptGraphicsNextPreviousDescriptions

unnamed protein product [Naegleria fowleri]

Sequence ID: CAG4716923.1Length: 298Number of Matches: 1

Range 1: 91 to 105GenPeptGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
33.7 bits(72)	30	12/16(75%)	12/16(75%)	2/16(12%)

```
Query  6    VAIWQFLYTIKPC-FL  20
           VAIWQ L TI PC FL
Sbjct  91   VAIWQIL-TISPCIFL  105
```

DownloadGenPeptGraphicsNextPreviousDescriptions

M23 family metallopeptidase [Treponema sp.]

Sequence ID: MCL2411156.1Length: 344Number of Matches: 1

Range 1: 33 to 45GenPeptGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
33.7 bits(72)	30	10/13(77%)	10/13(76%)	3/13(23%)

```
Query  5    FVAIWQFL---YT  14
            FVAIWQFL   YT
Sbjct  33   FVAIWQFLTRRYT  45
```

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uncharacterized protein FDP41_004512 [Naegleria fowleri]

Sequence ID: XP_044561326.1Length: 624Number of Matches: 1

- See 1 more title(s) See all Identical Proteins(IPG)

Range 1: 417 to 431GenPeptGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
33.7 bits(72)	30	12/16(75%)	12/16(75%)	2/16(12%)

```
Query  6    VAIWQFLYTIKPC-FL  20
           VAIWQ L TI PC FL
Sbjct  417  VAIWQIL-TISPCIFL  431
```

2.2. The detection of a hypothetical Prion function.

The analysis of this parasite protein by PLAAC highlights a slight Prion function at the beginning of the sequence due mainly to the presence of 2 consecutive

amino acids QQ.

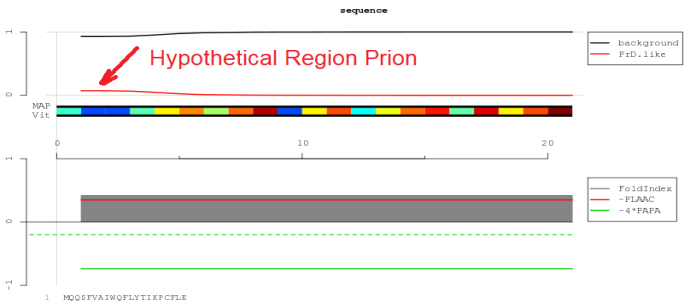

Figure3. Potential Prion region in MQQSFVAIWQFLYTIKPCFLE_

DISCUSSION & CONCLUSION.

What we have just demonstrated here constitutes very little compared to the infinity of potentially possible undesirable proteins.

Although we have only retained a small number of parasitic proteins, we note that a good part of them have a collection date after 2020, a period when Covid injections had already been put in place. These unwanted proteins could therefore result from this period of injections.

Finally, if with such a limited selection of proteins, we already obtain on the one hand unknown proteins, and on the other hand a potential Prion region, this gives us an idea of the potential risk of these injections, and this, whatever are the batches of vaccines.

Indeed, pseudo Uridine technology has been universally used in the billions of injections inoculated but also in successive versions of the vaccine, including the last one targeting the WUHAN and Omicron strains.

REFERENCES.

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(Perez et al, 2021) Perez, J. C., Lounnas, V., & Montagnier, M. (2021). THE OMICRON VARIANT BREAKS THE EVOLUTIONARY LINEAGE OF SARS-COV2 VARIANTS. *International Journal of Research -GRANTHAALAYAH*, *9*(12), 108–132. https://doi.org/10.29121/granthaalayah.v9.i12.2021.4418

(Lancaster et al, 2014) Alex K Lancaster et al

Bioinformatics. 2014 Sep 1; 30(17): 2501–2502.

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PMCID: PMC4147883

PMID: 24825614

PLAAC: a web and command-line application to identify proteins with prion-like amino acid composition .