Do Covid19 modified mRNA jabs Pose a Risk of Creating Harmful Proteins or Prions ?

Jean-Claude Perez

Biomathematics; **Luc Montagnier Foundation**,

https://montagnier.net/flm/fr/accueil/

jeanclaudeperez2@gmail.com

https://orcid.org/0000-0001-6446-2042

ABSTRACT.

In COVID-19 mRNA vaccines, natural uracil bases are replaced with modified pseudouracil. This study investigates the potential consequences of this modification on protein synthesis. Occasionally, ribosomes may overlook these modified bases, leading to a shift in the reading frame of the genetic code. We examine the spike protein in the context of these shifted reading frames and identify the resulting proteins. Our analysis focuses on the potential formation of prion-like or amyloidogenic proteins due to this frame-shifting process.

INTRODUCTION.

Investigating Unintended Consequences in COVID-19 mRNA Vaccines: Frame Shifts and Potential Prion Formation.

Recent studies have raised concerns about the stability and safety of mRNA in COVID-19 vaccines. Mulroney et al. (2023) reported that N1-methylpseudouridylation, a modification in the RNA of these vaccines, can lead to unpredictable shifts in the ribosomal reading frames. This alteration potentially impacts how the RNA sequence is translated into proteins.

Additionally, the late Luc Montagnier's final work (Perez et al., 2023) highlighted a concerning trend. Among 26 cases studied, individuals developed a rapid form of Creutzfeldt-Jakob disease, leading to death within months post-vaccination. This research posited a link between this outcome and a prion-like region in the

spike protein of mRNA vaccines. Intriguingly, our previous research (Perez et al., 2021) identified this prion region in the Wuhan strain of the virus, which was the basis for the vaccine development. However, this region seems to have vanished in the Omicron variant.

In this study, we aim to explore the presence of unintended proteins resulting from frame shifts during RNA codon reading. We will also investigate whether these unintended proteins exhibit prion-like functions, which could have significant implications for vaccine safety and efficacy.

METHODS.

Identifying Unintended Proteins and Prion Functions in COVID-19 mRNA Vaccines.

The primary goal of this study is to explore the potential emergence of inappropriate proteins resulting from ribosomal frame-shifting over modified uracil bases within the mRNA structure of COVID-19 vaccines. Additionally, we aim to investigate the presence and characteristics of potential prion functions within these proteins.

To identify protein homologs of these unintended proteins, we will utilize the Basic Local Alignment Search Tool for Proteins (BLASTP), available at https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE=Proteins .

This tool will allow us to input altered spike protein sequences and analyze them against established protein databases to uncover any similarities with known protein structures.

For the assessment of prion-like characteristics in the identified proteins, we will employ the Prion-Like Amino Acid Composition (PLAAC) tool, accessible at https://plaac.wi.mit.edu/ This analysis will help

determine if the unintended proteins possess prion-like properties, which could have significant implications.

The spike protein sequence used as a basis for the vaccine development is derived from the Severe Acute Respiratory Syndrome Coronavirus 2 isolate Wuhan-Hu-1, with the NCBI Reference Sequence being NC_045512.2. Our analysis will focus on the potential alterations in this sequence due to the skipping of modified uracil bases by ribosomes. Given the unpredictable nature of this skipping, the study will consider the combinatorics of possible sequence shifts.

The research will particularly focus on two main scenarios of sequence alteration. The first, which is not the primary focus, involves the preservation of the regular reading frame but the emergence of stop codons leading to truncated spike proteins. The more critical scenarios for our study involve the spike sequence being read with a shift by either one or two bases, interpreted according to the second and third reading frames of the codons, respectively.

Data analysis and interpretation will concentrate on these last two scenarios, aiming to identify the presence of unintended proteins and evaluate any prion-like features they might possess. Such an approach is crucial for a comprehensive understanding of the potential unintended consequences of mRNA vaccine administration, thereby contributing significantly to the ongoing discourse on vaccine safety and effectiveness. All analyses will be conducted using publicly available sequences and tools.

RESULTS.

Summary:

Our investigation focused on the implications of ribosomal frame-shifting over pseudo-uridine bases in the mRNA sequence of COVID-19 vaccines. This study delves into the potential emergence of unintended proteins and prion functions as a result of these shifts.

Detailed results:

1. One-Base Shift in Codon Reading Frame

1.1 Alteration of the Prion Region in the Spike Protein:

• Analysis revealed that a one-base shift in the reading frame due to ribosomal skipping on a pseudo-uridine base leads to significant changes in the prion region of the spike protein. Despite the shift, amino acids such as asparagine (N) and glutamine (Q), which are highly associated with prion functions, remained prevalent. This suggests that the prion nature of the spike protein is retained even with the frame shift.

Here the region PRION of Wuhan

REGIONPRIONWUHAN
TATCAGGCCGGT**AGCACA**CCTTGTAATGGTGTT**GAA**GGTT
TTAATTGTTACTTTCCTTT**A**CAATCATAT**GGT**TTC**CAA**CCC
ACT**AAT**GGTGTTGGT**CAC**CAACCATACAGAGTA

Here the region PRION of OMICRON

REGIONPRIONOMICRON
TATCAGGCCGGT**AACAAA**CCTTGTAATGGTGTT**GCA**GGTT
TTAATTGTTACTTTCCTTT**AAA**TCATAT**AGT**TTC**CGA**CCC
ACT**TAT**GGTGTTGGT**CAC**CAACCATACAGAGA

example of PRION region codons and amino acids in OMICRONSA3; there are 5 amino acids Q or N well known to be PRION like amino acids.

Figure1. the Prion region

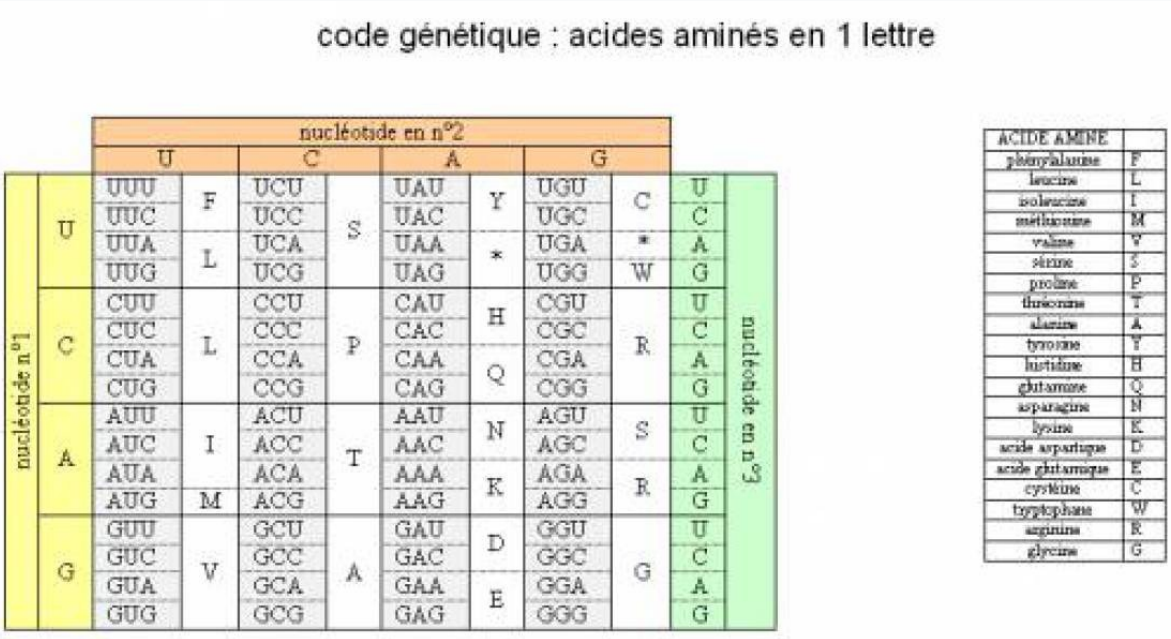

Figure2. Genetic code

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 Emergent Proteins from the One-Base Shift:

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__ELSTTQYDPLQPELD
S
FKEELDKYFKNHTSRC_FR_HLWH_CFSCKHSKRN_PPMRLPRI_

Third protein ==>
MNLSSISKNLESMSSI_

WPWYIWLGFIAG
LIAIVMVTIMLCYDQLL_LSQGLLFLWILLQI__RRLSQCSKESNYITHK

Upon shifting the reading frame by one base, our analysis identified three distinct proteins.
These proteins, arising from an error in ribosomal reading, include sequences homologous to fragments of the original spike protein. The proteins identified are:

- **MISALLMSMDSFVIRGDEVRQIAPGQTGKIADYL_ITR_FYRLRYSLEF_**
- **MISFHVLTKLREVQIDRLITGRLQSLQTYVTQQLISCRNQSFC_**
- **MNLSSISKNLESMSSI_**

Particularly, the third protein showed a notable homology to a hypothetical protein from Nematocida sp. AWRm77, suggesting intriguing implications for further study.

hypothetical protein NECID01_1208 [Nematocida sp. AWRm77]

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

Range 1: 66 to 77GenPeptGraphicsNext MatchPrevious 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. Two-Base Shift in Codon Reading Frame

2.1 Proteins Emerging from the Third Reading Frame:

The translation of the spike protein sequence offset by two bases revealed a different protein profile. The protein of interest, emerging from this shift, was identified as **MQQSFVAIWQFLYTIKPCFLE_**. This protein demonstrated similarities to certain nuclease family proteins and a domain-containing protein from Longitalea arenae.

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 chinchillae]	Parabacteroides chinchillae	34.1	34.1	57%	21	75.00 %	968	WP_103982177.1
Select seq gb|MDR1938841.1|	PD-(D/E)XK nuclease family protein [Tannerellaceae bacterium]	Tannerellaceae bacterium	34.1	34.1	57%	21	75.00 %	968	MDR1938841.1
Select seq ref|WP_099465130.1|	PD-(D/E)XK 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 GenPept Graphics 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 GenPept Graphics 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 GenPept Graphics 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 GenPept Graphics 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 GenPept Graphics 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
```

Download GenPept Graphics Next Previous Descriptions

unnamed protein product [Naegleria fowleri]

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

Range 1: 91 to 105 GenPept Graphics Next Match Previous 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
```

Download GenPept Graphics Next Previous Descriptions

M23 family metallopeptidase [Treponema sp.]

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

Range 1: 33 to 45 GenPept Graphics Next Match Previous 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
```

DownloadGenPeptGraphicsNextPreviousDescriptions

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
```

Naegleria fowleri Homology Concern

Our findings also uncovered a striking homology with Naegleria fowleri, commonly known as the "brain-eating amoeba." This discovery raises several concerns:

- The presence of Naegleria fowleri traces could be linked to the uninterpreted pseudo-uridine bases in the ribosome, a scenario increasingly probable considering the widespread use of mRNA protein injections since 2021.
- The resurgence of this disease has been noted concurrently with COVID-19 vaccine rollouts,

particularly highlighted in regions like Texas and Pakistan : see particularly

In Texas : https://www.kut.org/energy-environment/2023-09-21/brain-eating-amoeba-infection-naegleria-fowleri-natural-water-swimming-austin-texas In Pakistan : (Shehroze Tabassum et al., 2022) .

- Future mRNA vaccine developments, expected to continue in 2024, may also perpetuate this issue due to the ongoing issue of skipped pseudo-uridine bases.

This study's results underscore the importance of further exploration into the unintended consequences of mRNA vaccine components, particularly in the context of potential pathogen-like protein creation and prion functions.

2.2 Detection of a Hypothetical Prion Function:

- Using PLAAC for prion function analysis, a slight prion function was detected at the beginning of the MQQSFVAIWQFLYTIKPCFLE_ sequence. This was primarily attributed to the presence of two consecutive amino acids QQ, which are indicative of potential prion activity.

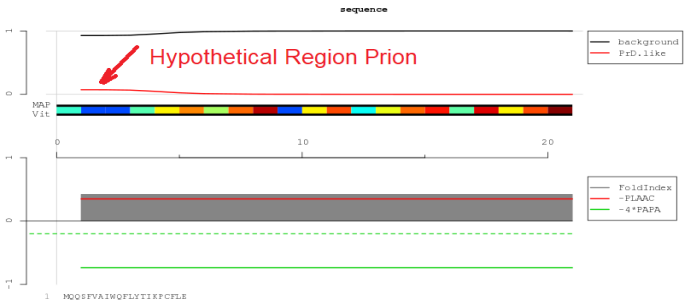

Figure3. Potential Prion region in MQQSFVAIWQFLYTIKPCFLE_

DISCUSSION & CONCLUSION REFINEMENT.

Our investigation, while focusing on a limited subset of possible unintended proteins resulting from mRNA COVID-19 vaccinations, has revealed noteworthy findings that merit serious consideration. The scope of potential off-target proteins is vast, yet even within our constrained analysis, significant observations have been made.

Observations of Parasitic Proteins

A notable aspect of our study is the identification of parasitic proteins, many of which were discovered post-2020. This timeline coincides with the widespread administration of COVID-19 vaccines. The emergence of these proteins during the same period suggests a possible link to the vaccine's mRNA technology and its unintended consequences.

The Implications of a Potential Prion Region

Our analysis identified not only unknown proteins but also the presence of a potential prion region. This finding is particularly concerning due to the inherent risks associated with prion diseases and their impact on neurological health. The discovery of a prion-like sequence within the altered spike protein emphasizes the need for rigorous examination of mRNA vaccine components and their long-term effects.

The Pervasive Use of Pseudo-Uridine Technology

The use of pseudo-uridine technology in mRNA vaccines has been universal, affecting billions of inoculations and encompassing various iterations of the vaccine, including those targeting both the original Wuhan strain and the subsequent Omicron variant. This widespread application raises concerns about the broad impact of any unintended protein creation across different vaccine batches and formulations.

CONCLUSION.

The findings of our study, while preliminary, highlight the critical need for comprehensive research into the full spectrum of potential off-target effects of mRNA COVID-19 vaccines.
The detection of unknown proteins and prion-like regions, particularly in the context of a technology as widespread as pseudo-uridine modification, calls for a cautious approach. It underscores the importance of ongoing monitoring and evaluation of vaccine safety, especially as new formulations are developed and deployed globally.
The potential implications for public health are significant, warranting continued vigilance and investigation into the molecular intricacies and long-term effects of these novel medical interventions.

ACKNOWLEDGEMENTS.

Thanks for discussions at the neurologist **Dr Claire Moret Chalmin** co-authored with me the posthumous article by **Luc Montagnier** on prions and new form of Creutzfeldt Jakob.

We thank **Dr Kevin McCairn** for an initial peer review and corrections of this article.

Kevin W McCairn's Lab

Institution: Korea Brain Research Institute

https://youtu.be/55lnmanIlVk?si=ue4QiIlkC1P3kUza

REFERENCES.

(Mulroney et al, 2023) Mulroney, T.E., Pöyry, T., Yam-Puc, J.C. et al. N1-methylpseudouridylation of mRNA causes +1 ribosomal frameshifting. Nature 625, 189–194 (2024).

(Perez et al, 2023) Emergence of a New Creutzfeldt-Jakob Disease: 26 Cases of the Human Version of Mad-Cow Disease, Days After a COVID-19 Injection. (2023). *International Journal of Vaccine Theory, Practice, and Research* , *3*(1), 727-770. https://doi.org/10.56098/ijvtpr.v3i1.66

(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.
Published online 2014 May 13. doi: 10.1093/bioinformatics/btu310
PMCID: PMC4147883
PMID: 24825614
PLAAC: a web and command-line application to identify proteins with prion-like amino acid composition .

(Shehroze Tabassum et al.) Shehroze Tabassum et al. Increasing cases of Naegleria fowleri during the time of COVID 19; an emerging concern of Pakistan Int J Surg. 2022 Sep; 105: 106881. Published online 2022 Sep 6. doi: 10.1016/j.ijsu.2022.106881
PMCID: PMC9444334PMID: 36075555