# Mystery ORF genes in Covid Vaccine

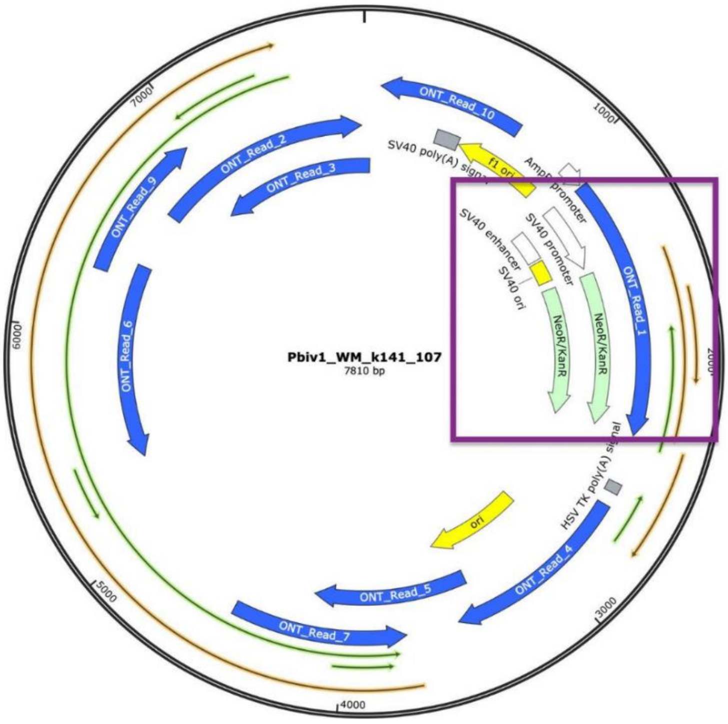
The following is taken from Spider webs in the Pfizer closet - by Anandamide (substack.com)

Pfizer failed to identify the 2nd largest ORF (Open Reading Frame) in the plasmid. This is the mystery ORF of 1252 amino acids described by Beaudoin et al. The protein sequence of the Mystery ORF is given below –

>Mystery_ORF_Under_Pfizer_Spike

MQYQLESSCVVQFHALQHGLRIVLVELAAAATATTALQAATAAGHATQHDCDHHDGNQSGDKAQPDVPGPLDVLLVLPQ
FLQVDQALVQILGHLVQPVDLFLDVHDAGIDSADIAQVHVGACVVLKVLVQFLFEAVQLGLQRVVHGIVHNADHDVAVAR
HEGVVGGDDLGLVEVPLCHEPMGAVGHEHAFSRKVGFAVVADGWSGGEILLLSGHICHVQKHHAVRGRLREAHQVVAL
AAKVHSLALAQHTLRHLGGGQIGRGSNLGGSDQLLGHVCLEALQSACDQSVDLHLGLRRVQSAQDIVQHRADGAELGGQ
LLDQGVQCLGIVVDHVLQLSQGACCAAQAVLDLADGAVELVGDQLLVLVQHILGHSDAVEPVGHLHSKGDLQSGACSKCP
AACDCAGQQGRCVLGDHLIGQQRRQHCQSVKLLGANQIPGGNVAQTIAILLDEAGVGQCHFVEQQVLDEAPLAGLARIGQ
NLAEIEAAEVLDRRGLVDLLHLGEHLLGVLVLFHGDPCQGSFQLGAEAAVLQQQVGALGGIAADVHGAVHAGLGHGHRQ
DLCGHADGEVGGDSDRVVGVGHAVLGAQRHCVGNDALAGHASGSPVALCLCLVAGADSSADGDVALVAIVHVLGSDQT
AGSGLKHIAAGGVHPPCRCQLIGVNGHGHFGTVHALVQHCHLIAGVGARGDHRHSAEAARGDVQDFQCLGISNGVCGIG
DIPAKLLEWQELLVALCQHAGAGQAVEVEVHAFVLHEIGAFLRAAHCGRGMQQFEAQHHHSVGLVAHAVCGPKAVGLQ
WEVAVHACHAVTRLVAGLIDLGGDVPLEGLQIGLPEQPVPVIVVAADFGVQLVAVPGNHTAGEVVGQLVVVVGDVACLSR
GNLPHFVSPDHEAVGVHVCEAQVVQLGRGHAVALECEEGGEVVQHGVVGHAIADPLPVPGVHRGESGGIEHLVEGAQIG
DIGEPHDGFGGLHPEVAGLVDALFHGEGLQGALCLAQRIQSTIHGVGDGAVLVVLQQEGSRLQVAHIVSGGTSCPSAAAIA
RCQVASVQGQQCLKPGDVDADGQIHQGFQSREALRQIPAEVDRGVLAVDLEVAVDVLKHELAQVLEVALLAFQVHQERL
GHVLEGAVVGAAVHPELAFHPALVVLVVVDVQEGVVAELELAHFDDHVGGVVHDQQALGLAVQCGAEDPASDDVGLLG
AGKVHPVVEGQHGVVESLGAIGAGDGVEPGHVAEERQEQVLGRVQHAGSEHLVGVVHASGKAVGV

ORFs are painted in Green and Gold in the plasmid map below.

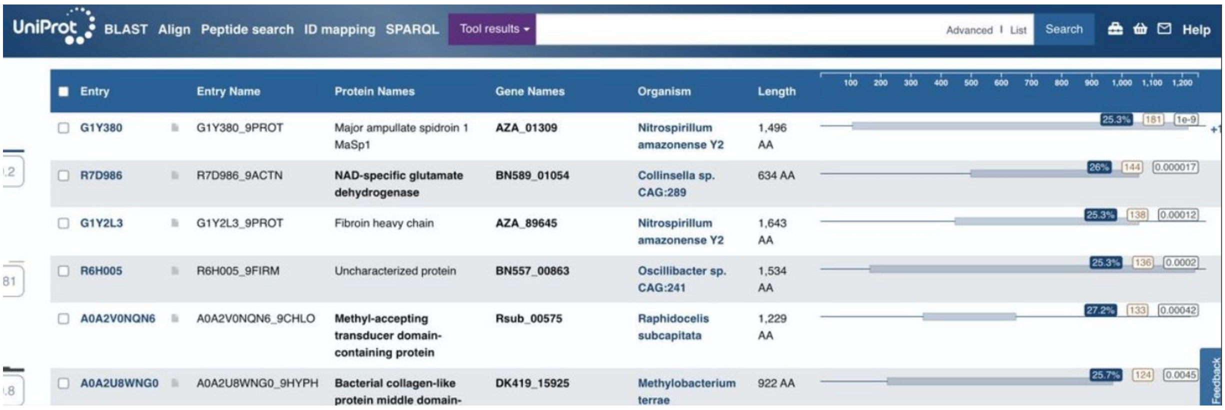


This large 1252 amino acid ORF was undisclosed and this violates FDA and WHO guidelines.

## Using Uniprot to Identify What this ORF Does

What is the Mystery ORF in Green on the opposite strand of Spike? Why was this ORF never disclosed **despite the WHO and FDA regulation claiming all ORFs need to be identified**? This seems like a major omission as FDA can't claim this is of no consequence if regulations demand all ORFs be disclosed.

Ananthamide found that the Mystery ORF's closest hit is to a protein involved in silk.



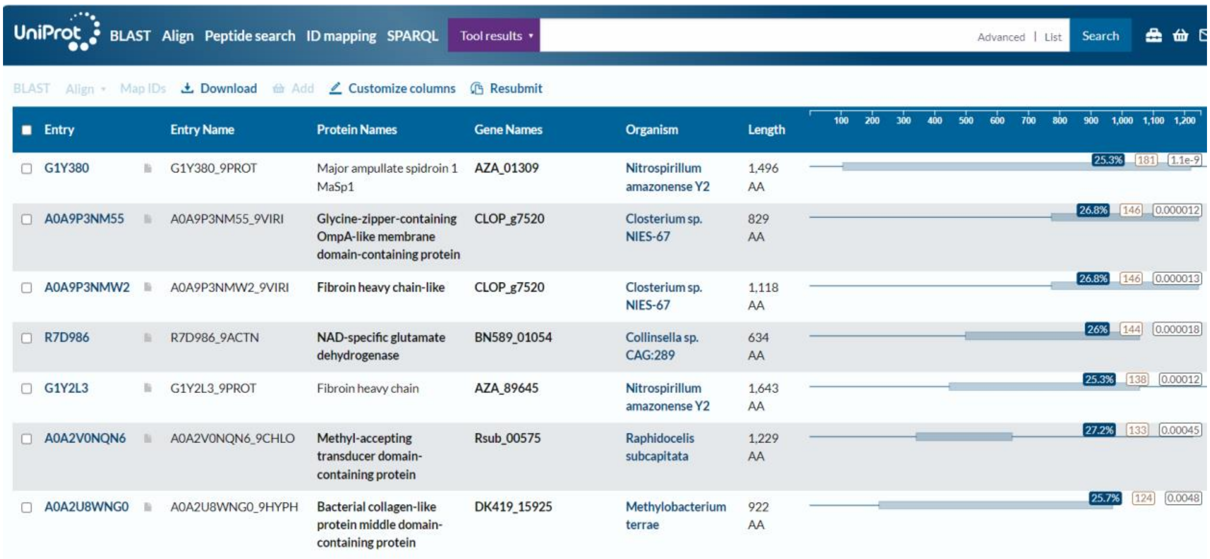
| Entry | Entry Name | Protein Names | Gene Names | Organism | Length | 100 200 300 400 500 600 700 800 900 1,000 1,100 1,200 |
|---|---|---|---|---|---|---|
| ☐ G1Y380 | G1Y380_9PROT | Major ampullate spidroin 1 MaSp1 | AZA_01309 | Nitrospirillum amazonense Y2 | 1,496 AA | 25.3% 181 1e-9 |
| ☐ R7D986 | R7D986_9ACTN | NAD-specific glutamate dehydrogenase | BN589_01054 | Collinsella sp. CAG:289 | 634 AA | 26% 144 0.000017 |
| ☐ G1Y2L3 | G1Y2L3_9PROT | Fibroin heavy chain | AZA_89645 | Nitrospirillum amazonense Y2 | 1,643 AA | 25.3% 138 0.00012 |
| ☐ R6H005 | R6H005_9FIRM | Uncharacterized protein | BN557_00863 | Oscillibacter sp. CAG:241 | 1,534 AA | 25.3% 136 0.0002 |
| ☐ A0A2V0NQN6 | A0A2V0NQN6_9CHLO | Methyl-accepting transducer domain-containing protein | Rsub_00575 | Raphidocelis subcapitata | 1,229 AA | 27.2% 133 0.00042 |
| ☐ A0A2U8WNG0 | A0A2U8WNG0_9HYPH | Bacterial collagen-like protein middle domain- | DK419_15925 | Methylobacterium terrae | 922 AA | 25.7% 124 0.0045 |

Other hits with lower E-values are to Collagen and Fibroin.

Ananthamide got no hits when he used blastP to search for this sequence in the NCBI database. It only showed up in UniProt.

I checked Uniprot to confirm Ananthamide's finding. I input the above sequence here – Tool results | UniProt

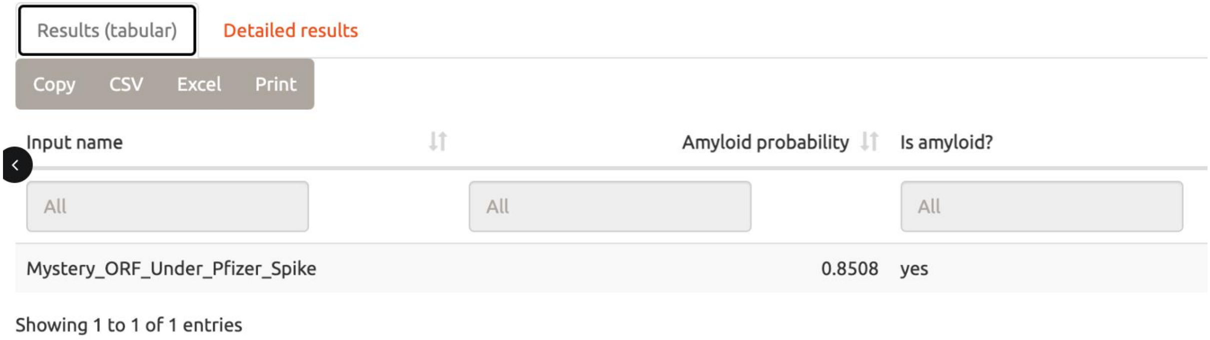
The top result was Spidroin as reported.



| Entry | Entry Name | Protein Names | Gene Names | Organism | Length | 100 200 300 400 500 600 700 800 900 1,000 1,100 1,200 |
|---|---|---|---|---|---|---|
| ☐ G1Y380 | G1Y380_9PROT | Major ampullate spidroin 1 MaSp1 | AZA_01309 | Nitrospirillum amazonense Y2 | 1,496 AA | 25.3% 181 1.1e-9 |
| ☐ A0A9P3NM55 | A0A9P3NM55_9VIRI | Glycine-zipper-containing OmpA-like membrane domain-containing protein | CLOP_g7520 | Closterium sp. NIES-67 | 829 AA | 26.8% 146 0.000012 |
| ☐ A0A9P3NMW2 | A0A9P3NMW2_9VIRI | Fibroin heavy chain-like | CLOP_g7520 | Closterium sp. NIES-67 | 1,118 AA | 26.8% 146 0.000013 |
| ☐ R7D986 | R7D986_9ACTN | NAD-specific glutamate dehydrogenase | BN589_01054 | Collinsella sp. CAG:289 | 634 AA | 26% 144 0.000018 |
| ☐ G1Y2L3 | G1Y2L3_9PROT | Fibroin heavy chain | AZA_89645 | Nitrospirillum amazonense Y2 | 1,643 AA | 25.3% 138 0.00012 |
| ☐ A0A2V0NQN6 | A0A2V0NQN6_9CHLO | Methyl-accepting transducer domain-containing protein | Rsub_00575 | Raphidocelis subcapitata | 1,229 AA | 27.2% 133 0.00045 |
| ☐ A0A2U8WNG0 | A0A2U8WNG0_9HYPH | Bacterial collagen-like protein middle domain-containing protein | DK419_15925 | Methylobacterium terrae | 922 AA | 25.7% 124 0.0048 |

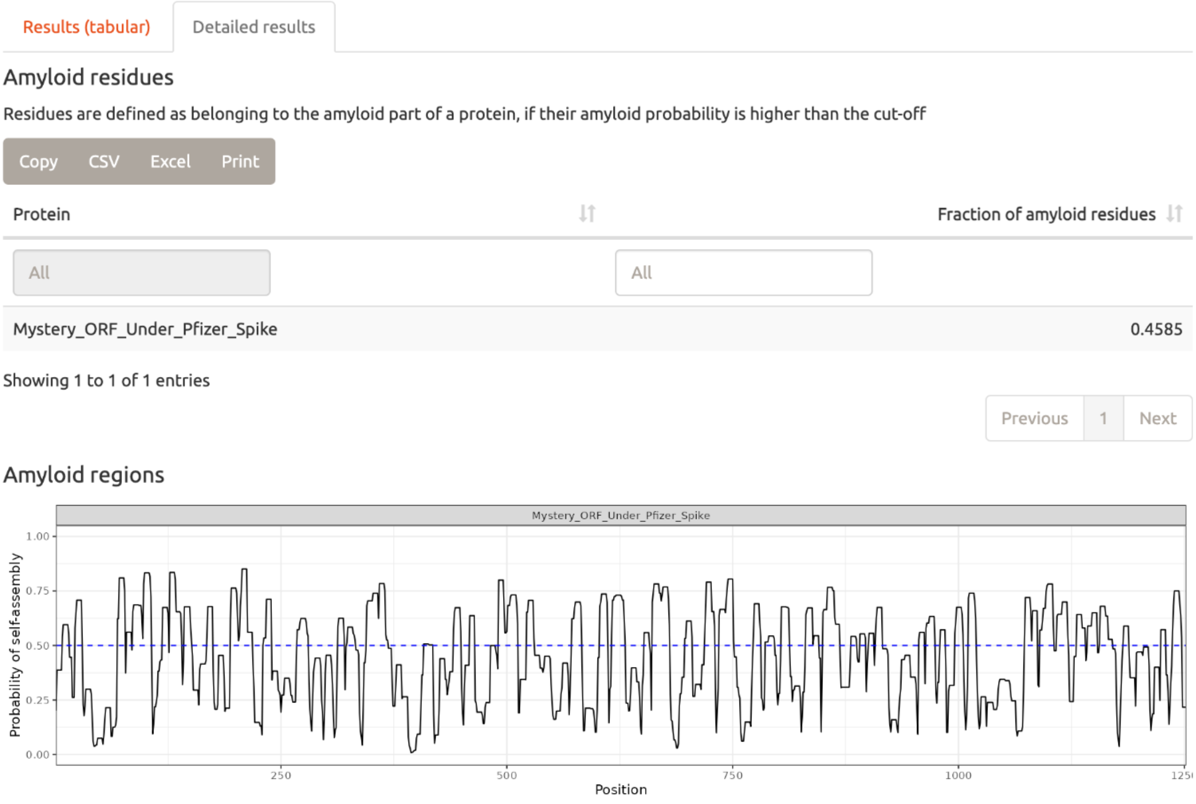
# Analysis of Mystery ORF Region Using AmyloGram Tool

AmyloGram (uni.wroc.pl) shows that this ORF sequence is amyloidogenic. If the cells lining blood vessels start manufacturing this amyloid, then the blood vessels will slowly fill with amyloid fibrils and the flow of blood will be gradually impeded.



| Input name | Amyloid probability | Is amyloid? |
|---|---|---|
| All | All | All |
| Mystery_ORF_Under_Pfizer_Spike | 0.8508 | yes |

Showing 1 to 1 of 1 entries



Amyloid residues

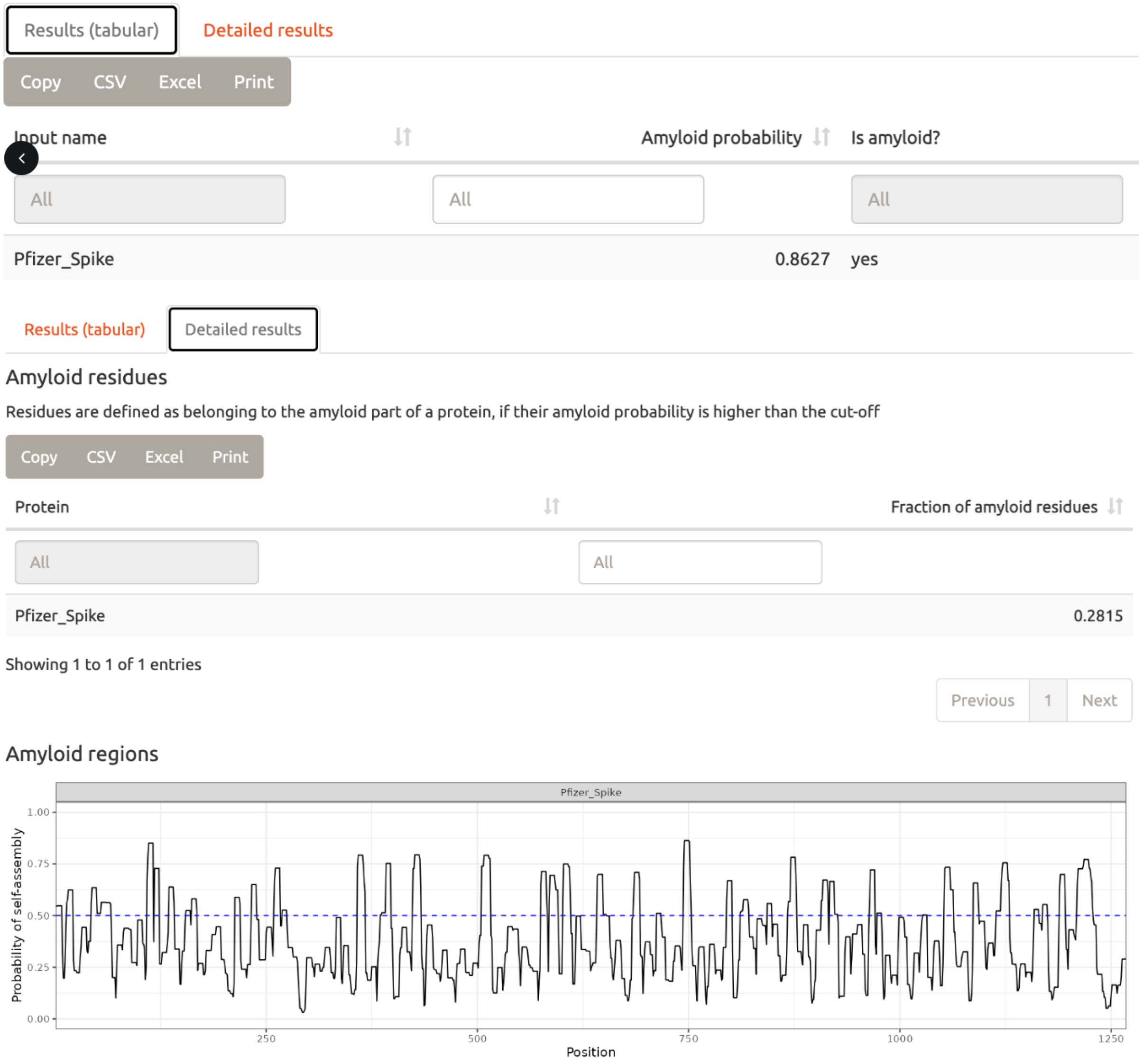
Residues are defined as belonging to the amyloid part of a protein, if their amyloid probability is higher than the cut-off

| Protein | Fraction of amyloid residues |
|---|---|
| All | All |
| Mystery_ORF_Under_Pfizer_Spike | 0.4585 |

Showing 1 to 1 of 1 entries

Amyloid regions

# Analysis of Pfizer Spike Region Using AmyloGram Tool



| Input name | Amyloid probability | Is amyloid? |
|---|---|---|
| All | All | All |
| Pfizer_Spike | 0.8627 | yes |

Amyloid residues

Residues are defined as belonging to the amyloid part of a protein, if their amyloid probability is higher than the cut-off

| Protein | Fraction of amyloid residues |
|---|---|
| All | All |
| Pfizer_Spike | 0.2815 |

Showing 1 to 1 of 1 entries

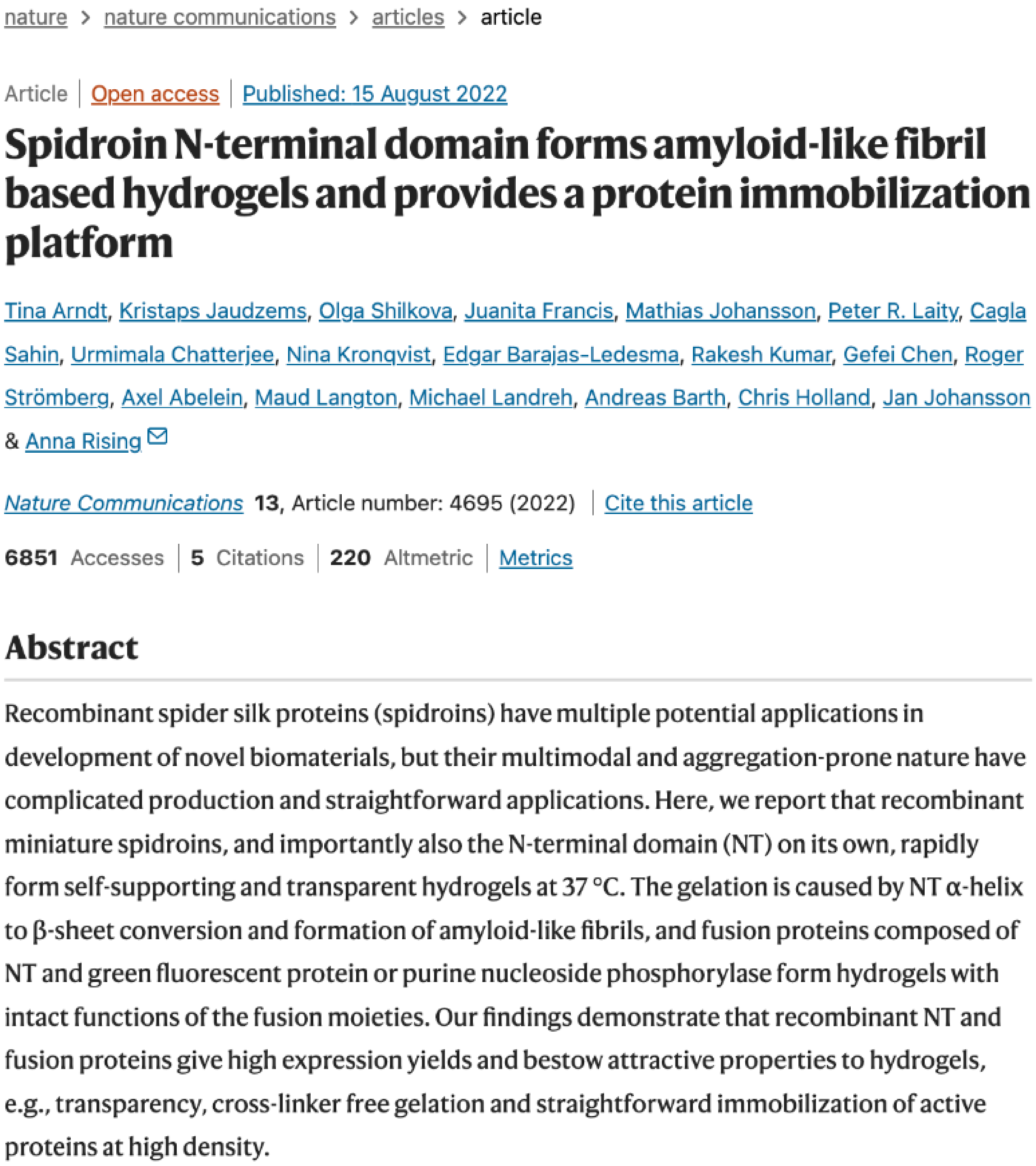
Amyloid regions

So BOTH the ORF sequence AND the SPIKE sequence will result in the production of amyloid. In other words – as surely as the vaccine RNA generates spike protein (its intended purpose), it will also generate amyloid (a hidden intended purpose?)

## Independent research confirms that Spidroin generates amyloid

Spider Silk Protein Forms Amyloid-Like Nanofibrils through a Non-Nucleation-Dependent Polymerization Mechanism - Qi - 2023 - Small - Wiley Online Library

Amyloidogenic nature of spider silk (wiley.com)



nature > nature communications > articles > article

Article | Open access | Published: 15 August 2022

# Spidroin N-terminal domain forms amyloid-like fibril based hydrogels and provides a protein immobilization platform

Tina Arndt, Kristaps Jaudzems, Olga Shilkova, Juanita Francis, Mathias Johansson, Peter R. Laity, Cagla Sahin, Urmimala Chatterjee, Nina Kronqvist, Edgar Barajas-Ledesma, Rakesh Kumar, Gefei Chen, Roger Strömberg, Axel Abelein, Maud Langton, Michael Landreh, Andreas Barth, Chris Holland, Jan Johansson & Anna Rising

*Nature Communications* **13**, Article number: 4695 (2022) | Cite this article

**6851** Accesses | **5** Citations | **220** Altmetric | Metrics

## Abstract

Recombinant spider silk proteins (spidroins) have multiple potential applications in development of novel biomaterials, but their multimodal and aggregation-prone nature have complicated production and straightforward applications. Here, we report that recombinant miniature spidroins, and importantly also the N-terminal domain (NT) on its own, rapidly form self-supporting and transparent hydrogels at 37 °C. The gelation is caused by NT α-helix to β-sheet conversion and formation of amyloid-like fibrils, and fusion proteins composed of NT and green fluorescent protein or purine nucleoside phosphorylase form hydrogels with intact functions of the fusion moieties. Our findings demonstrate that recombinant NT and fusion proteins give high expression yields and bestow attractive properties to hydrogels, e.g., transparency, cross-linker free gelation and straightforward immobilization of active proteins at high density.

Note that the spiridon sequence forms amyloid-like fibrils rapidly at 37 degrees Celsius. So it is highly amyloidogenic.

## Conclusion

Given the deliberate undisclosed inclusion of an amyloid producing sequence, as well as the inclusion of the spike sequence that is also amyloidogenic, there is a distinct possibility that amyloid formation may be an intended effect of the Covid vaccine.