Amyloidosis and the COVID Vaccine

By Craig Paardekooper

PART A : Observations of amyloidosis by embalmers and funeral homes

Dr Vaughn - spike protein creates FIBRIN that is resistant to being broken down. See.... CEO of MedHelp Clinic, Alabama, Dr. Vaughn

Several undertakers and embalmers are speaking out regarding the discovery of rubbery amyloid clots within the veins of the vaccinated - sometimes of considerable length and resistant to breakdown by enzymes. These amyloid clots obstruct the infusion of embalming fluids.

Dr John Campbell Amyloid clots are a real phenomenon following C19 vax - occurring in 20% of corpses in the UK. John Campbell has received 250 samples of these clots. This is a completely new pathology since the jab rollout. See.... Dr John Campbell

Major Tom Haviland : USA Airforce These amyloid clots consist of amyloid protein, fibrin and platelet. They stretch like a rubber band. These clots are almost certainly the cause of death. The amyloid clots occur on the venous AND the arterial side of the body - ordinary clots are usually restricted to the venous side. These clots are in the 6 to 10 inch range - though some can be up to 2 ft long. Ordinary clots look and feel like jelly and dissolve in your hands. In comparison these amyloid clots are much tougher, rubbery, elastic and longer lasting. The amyloid clots grow to large size - blocking blood supply - they fill the entire blood vessel - taking its shape - like a cast. They appear to grow without limit.

During 2020 44 embalmers saw these clots, but the incidence of these clots exploded in 2021. (In both cases, the spike protein is associated with the clot formation.) In 2022 about 30% of corpses contained these amyloid clots. In 2023 the percentage decreased to 20%. Embalmers have never seen this phenomenon before.

A fifth to a third of corpses have these clots. 20-30% of all people dying! In addition there has been a great increase in the incidence of traditional jelly clots and micro-clotting.

A survey was sent to 50 national undertakers associations, and to 1700 funeral homes. 197 out of 269 embalmers were still observing these clots in 2023. See.... Major Tom Haviland's survey

John O'Looney - undertaker. See.... John O Looney

Yet another embalmer speaks out. See.... Embalmer speaks out

Laura Jeffery - Director of Canadian funeral home for 37 years. See.... Laura Jeffrey

Brenton Faithfull - undertaker. See.... Brenton Faithful

Brenton Faithfull - undertaker - 95% of deaths are vaccinated and dying within 2 weeks of the jab. See.... Brendon Faithful

Dr Peterson Pierre - undertakers reporting deaths of vaccinated. See.... Dr Peterson Pierre

Wesley - undertaker. See.... Wesley

Richard Hirschman - undertaker. See.... Richard Hirschman

Richard Hirschman - undertaker. See.... Richard Hirschman Interview with Conservative Daily

Nicky King - Embalmer. See.... Nicky King

Funeral Directors and Embalmers Unite. See.... Funeral Directors and Embalmers

Physicians and embalmers reveal shocking vaccine injuries. See.... Physicians and embalmers

Wallace Hooker - Embalmer and funeral director testifies to white amyloid clot formation in vaccinated. See.... Wallace Hooker

Hooker is a funeral director for the independent Family and Friends Funeral Home in Wingate, Indiana with over 30 years experience. Hooker serves on the advisory board of Worsham College of Mortuary Science, is a member of the BIE (British Institute of Embalmers) and board member of the North American Division. He also travels around the nation providing lectures to other embalmers on perfecting the process and navigating unusual problems. Hooker confirmed an increase in strange blood clots in the past two years, not just witnessed by himself but by other morticians from across the nation who send him photographs.

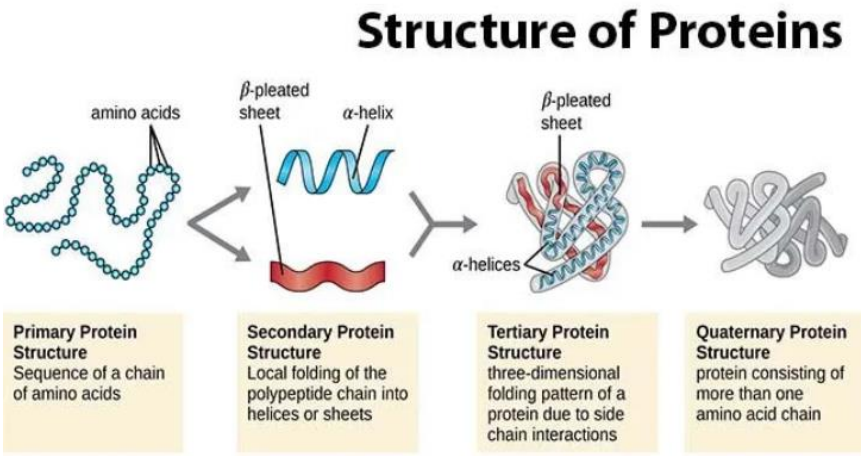
“I have lectured four times so far this year," Hooker said. "I am asking questions and showing pictures of these clots in my Power-point, and routinely, everywhere I lecture, people say they are seeing these clots, and have not seen them prior to COVID.”

Anna Foster - Embalmer speaks out about amyloid clot formation in vaccinated. See.... Anna Foster

Part B : The Nature of Amyloid

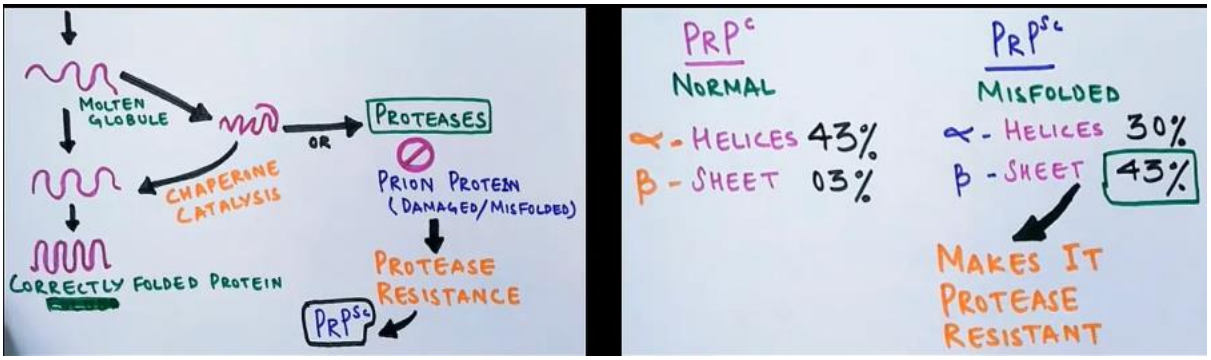
What is a prion ?

All proteins are a string of aminoacids that fold locally to form alpha helixes or beta sheets. These then fold 3-dimensionally to give the protein its shape. A prion is a misfolded protein and they are associated with neuro-degenerative diseases like Alzheimer's disease. Prions cause other proteins to misfold around them



3. Why are prions resistant to being broken down ?

Prions are resistant to being broken down (proteolysis) by proteases. In normal proteins 43% are alpha helixes and only 3% are beta sheets. However prions have far fewer alpha helixes (30%) and far more betasheets (43%). The betasheets are very compact and this makes them resistant to proteases.



There are misfolded proteins in our bodies all of the time. If a protein is misfolded then the body deals with this in one of two ways – chaperones refold it properly, or it is destroyed by proteases. However, prions are misfolded proteins that form beta-sheets, and these are not broken down by proteases.

4. What is amyloidosis ?

Amyloidosis comprises diseases that result from protein aggregation of fibrous proteins called amyloids. the beta-sheet alignment that gives the fibrils their visual appearance.

Rambaran RN, Serpell LC. Amyloid fibrils: abnormal protein assembly. Prion. 2008;2(3):112-117. doi:10.4161/pri.2.3.7488.

Part C : The SARS-nCoV-2 spike contains amyloidogenic peptides

Amyloidogenesis of SARS-CoV-2 Spike Protein - https://pubs.acs.org/doi/10.1021/jacs.2c03925

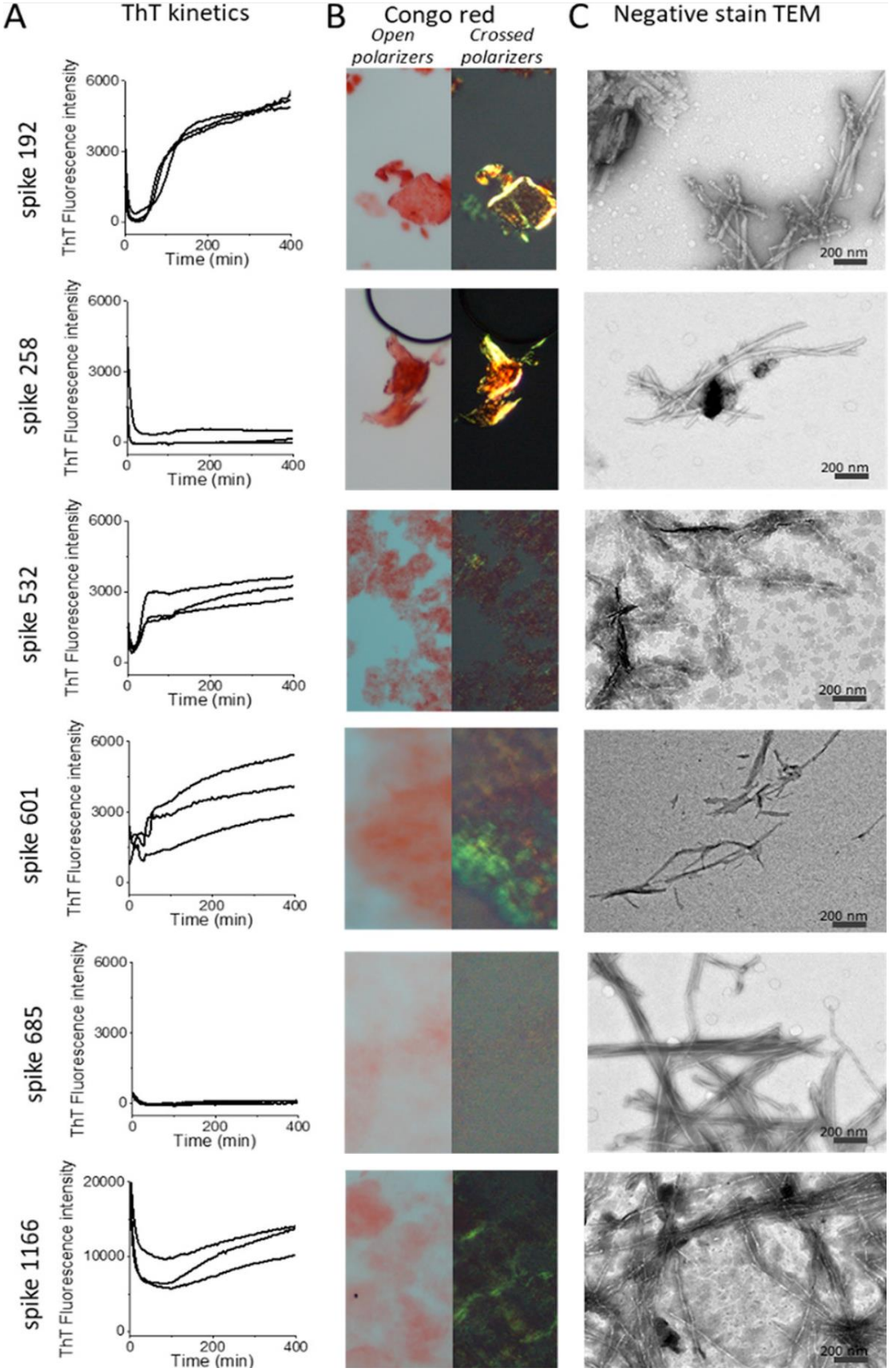
The protease neutrophil elastase (NE), which is overexpressed at sites of inflammation, cuts the spike protein into smaller pieces. 7 of these smaller pieces are highly amyloidogenic. They produce amyloid deposits. These amyloid deposits don't get broken down, and they disrupt the normal functioning of cells and tissues.

> *"Amyloid fibril assays of peptide library mixtures and theoretical predictions* ***identified seven amyloidogenic sequences within the S-protein. All seven peptides in isolation formed aggregates during incubation at 37 °C****. Three 20-amino acid long synthetic spike peptides (sequence 192–211, 601–620, 1166–1185) fulfilled three amyloid fibril criteria: nucleation dependent polymerization kinetics by ThT, Congo red positivity, and ultrastructural fibrillar morphology.* ***Full-length folded S-protein did not form amyloid fibrils****, but amyloid-like fibrils with evident branching were formed during 24 h of* ***S-protein coincubation with the protease neutrophil elastase*** *(NE) in vitro. NE efficiently cleaved S-protein, rendering exposure of amyloidogenic segments and accumulation of the amyloidogenic peptide 194–203, part of* ***the most amyloidogenic synthetic spike peptide****. NE is overexpressed at inflamed sites of viral infection."*
>
> *"Neither NE nor SARS-CoV-2 S-protein incubated alone formed fibrils (Figure 2G–H). Fibrils were found only after co-incubation of the two proteins"*

Peptide	Amino acid sequence[a]	MW (Da)[b]	pI	ThT kin	Congo Red	Ultrastructure
Spike192	FVFKNIDGYFKIYSKHTPIN	2431	9.4	+	+	fibril
Spike258	WTAGAAAYYVGYLQPRTFLLK	2389	9.5	-	+	fibril
Spike365	KKKGGGYSVLYNSASFSTFK	2169	10.0	-	+	amorphous
Spike532	NLVKNKCVNFNFNGLTGTGV	2139	9.3	+	+	amorphous
Spike601	GTNTSNQVAVLYQDVNCTEV	2155	3.7	+	+	fibril
Spike685	KKKRSVASQSIIAYTMSLGA	2139	10.5	-	-	ribbons
Spike1166	LGDISGINASVVNIQKEIDR	2141	4.6	+	+	fibril

[a]Residues assigned in color indicate the amyloidogenic segments as predicted by WALTZ. Highlighted in gray are non-native amino acids introduced for solubility.
[b]Theoretical mass.

Seven amyloidogenic sequences distributed over the entire S-protein were identified and named according to the starting position in the S-protein (Figure S2, Supporting Information). All but one (Spike365) of the predicted sequences are in β-sheet conformation in the SARS-CoV-2 Spike cryo-EM structure in its closed state. (1) The C-terminal part of the protein (Spike1166) is not resolved in the structure.

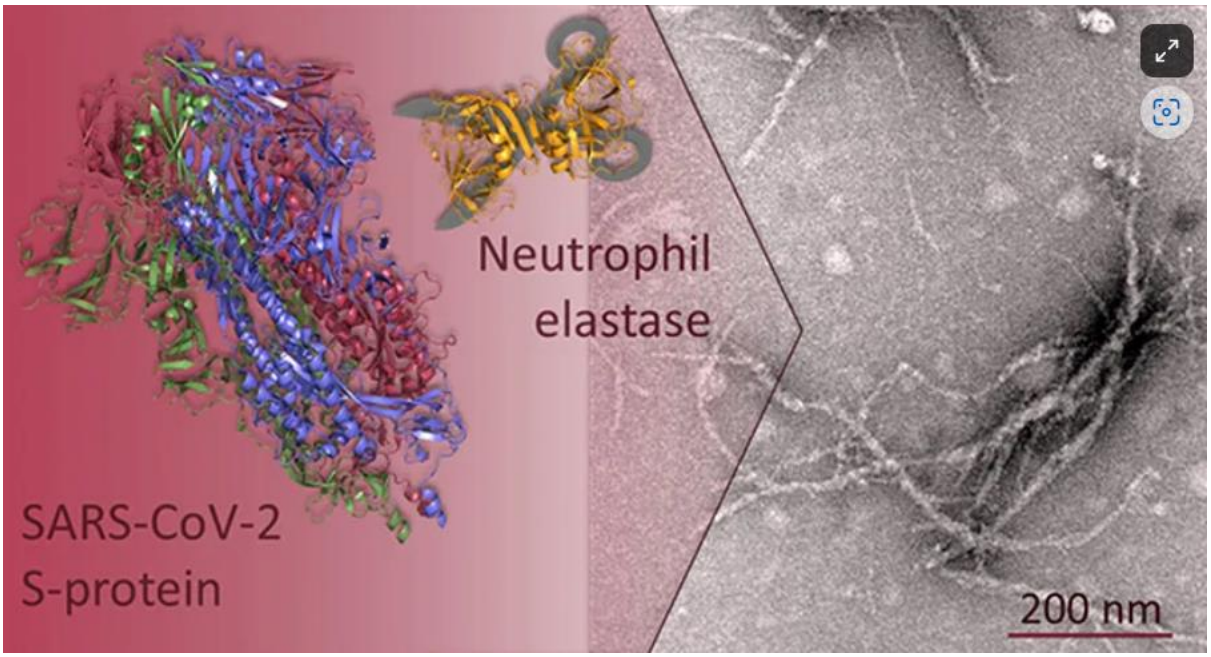


"Fibrils from most of the synthetic peptides were detected within a few hours by at least one assay (Table 1, Figure 1). Spike192, Spike601, and Spike1166 fulfilled all our amyloid criteria: sigmoidal ThT kinetics, Congophilicity, and fibrillar ultrastructure (Figure 1, Table 1). Spike192 formed exceptionally well-ordered fibrils comparable to a mix of all peptides (Figures 1C and S3C)."

As you can see from the charts above, fibrils resulting from spike regions 192, 601 and 1166 show strong growth, which was ongoing at the end of the study.

These amyloid fibrins induced a resistance to breakdown of clots –

"The addition of 10 µg/mL amyloid fibrils formed from a mix of the seven spike peptides (Table 1, Figure S3) during fibrin formation decreased the fibrinolysis (Figure 4C). Furthermore, the addition of 2% fibrils (from 1 mg/mL stock, total 20 µg/mL) of Spike192 and 194–203 increased persistent plasmin indigestible fibrin (Figure 4 D). As expected, the more amyloidogenic Spike192 induced more plasmin resistant fibrin clots than did Spike194–203."



Study author Per Hammarstrom says

"When the spike protein is cut up, it produces the exact piece of protein which, according to the researchers' analysis, is most likely to produce amyloid. This enzyme is released in large quantities from one type of white blood cells, neutrophils, which are released early on during infections such as COVID-19. When the researchers mixed pure spike protein with this enzyme, called neutrophil elastase, unusual fibrils were produced."

"We have never seen such perfect, but scary, fibrils as these ones from the amyloid-producing SARS-CoV-2 spike protein and pieces thereof. The fibrils starting from the full-sized spike protein branched out like limbs on a body. Amyloids don't usually branch out like that. We believe that it is due to the characteristics of the spike protein."

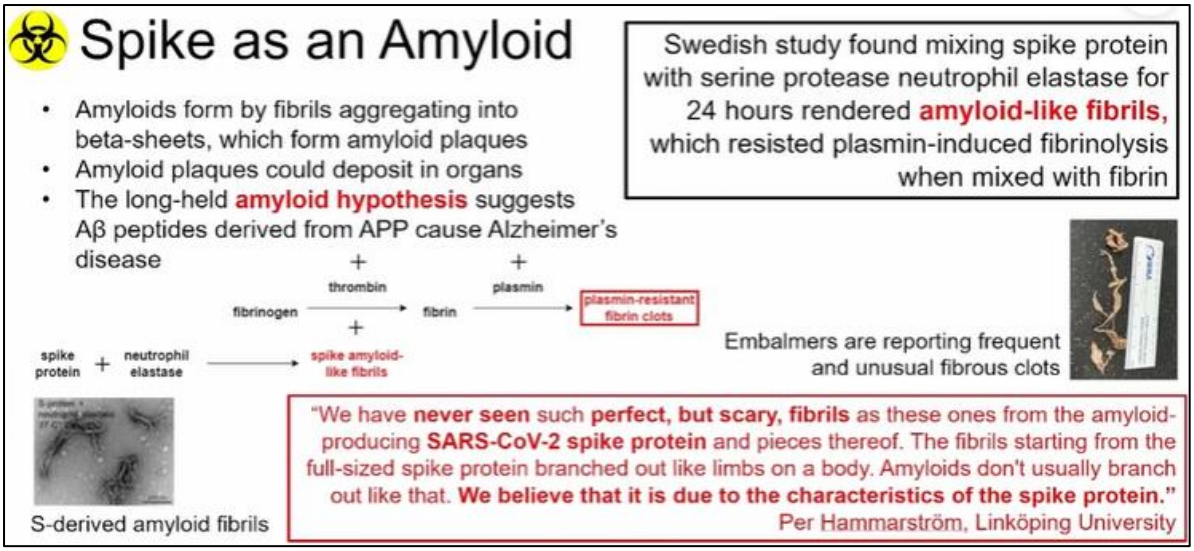
Study author Sofie Nystrom explained to Medical News Today:

"Under normal circumstances, when we get an injury, fibrinogen that we have in our bloodstream is transformed into fibrin to form clots. To prevent 'over-clotting,' there is another blood component, plasmin, that will dissolve the fibrin clots when there are enough and ultimately get rid of all fibrin when it is not needed anymore."

"Our experiment shows that if fibrin is formed in the presence of spike amyloid, the plasmin cannot totally remove the fibrin clots"

"Our finding that the SARS-CoV-2 Spike protein can form amyloid when cut by neutrophil elastase is probably an important piece in the puzzle for many unsolved questions related to COVID-19 infection."

See also - https://liu.se/en/news-item/mojlig-mekanism-bakom-gatfulla-symtom-vid-covid-19-upptackt



See also Amyloid and Hydrogel Formation of a Peptide Sequence from a Coronavirus Spike Protein | ACS Nano

It has been shown repeatedly in the literature that prion-like domains or peptides exist in the spike protein of SARS-nCoV-2 and these are specific to SARS-2.

*** Tetz G, Tetz V. Prion-like Domains in Spike Protein of SARS-CoV-2 Differ across Its Variants and Enable Changes in Affinity to ACE2. Microorganisms. 2022; 10(2):280. https://doi.org/10.3390/microorganisms10020280.

Misfolded Proteins - SUZANNE GAZDA M.D. (suzannegazdamd.com)

*** Neurotoxic amyloidogenic peptides in the proteome of SARS-COV2: potential implications for neurological symptoms in COVID-19 | Nature Communications

Highly efficient intercellular spreading of protein misfolding mediated by viral ligand-receptor interactions | Nature Communications

Part D : Amyloid plaques are associated with diseases

Amyloidosis is a universal hallmark of

- CJD
- Alzheimer's
- Parkinson's
- Dementia
- Type II Diabetes

Covid 19 vaccine is unique in having a high proportional reporting ratio for all of these. See Safety Signal - https://howbad.info

The number of Creutzfeldt-Jacob Disease (CJD)/prion disease reports in VAERS since the deployment of the COVID-19 injections has far surpassed the background rate for the U.S. for the year.

> *"There are 59 reports of CJD and prion diseases in VAERS to date (June 10, 2022). The background rate of CJD in the United States is 1/1M per year. Since the population of the U.S. as of June 6, 2022 is ~334M5, then we would expect no more than 334 cases of CJD reported. If we consider an extraordinarily low under-reporting factor (URF)6 of 6, then we have already surpassed the background expected number of cases reported by 20 reports. If we use the calculated URF of 31 as referenced in (2), then we have 1,829 cases of prion diseases (CJD) in the U.S., to date. And this is just data from VAERS. And this is just in the context of the COVID-19 shots. ~589M doses of the COVID-19 injections (Moderna, Pfizer and Janssen) have been doled out in the States as of June 6, 2022. This means that we are seeing ~3.1 incidents of prion diseases/CJD per million Americans - 3 times the background rate. Already."*
> Jessica Rose

Cases of CJD in temporal proximity to COVID vax

Prion diseases are no joke - by Jessica Rose (substack.com)

COVID-19 RNA Based Vaccines and the Risk of Prion Disease (scivisionpub.com)

(PDF) COVID19 injection dose-effect on dynamics of Creutzfeldt-Jakob disease (researchgate.net)

Part E : Proportional Reporting Ratios

Safety Signal is available at https://howbad.info

Arterial effects of amyloidosis

You can use Safety Signal to search for each of these symptoms associated with the amyloid clots to see which vaccines generate a high proportional reporting ratio. The arterial location of amyloid clots makes them distinct from blood clots that are mainly located on the venous side of the body.

- Amyloidosis
- Arterial catheterisation
- Arterial occlusive disease
- Arterial stenosis
- Arterial thrombosis
- Coronary arterial stent insertion
- Embolism arterial
- Peripheral arterial occlusive disease
- Pulmonary arterial hypertension
- Pulmonary arterial pressure

Biomarkers for amyloidosis

You can use Safety Signal to search for each of these biomarkers associated with the amyloid clots to see which vaccines generate a high proportional reporting ratio

- D-Dimer
- Light chain analysis
- Blood alkaline phosphatase
- Blood creatine
- Troponin T
- Troponin I
- Brain natriuretic peptide
- Blood fibrinogen

Diseases associated with amyloidosis

You can use Safety Signal to search for each of these diseases associated with the amyloid clots to see which vaccines generate a high proportional reporting ratio

- Brain Fog
- CJD
- Alzheimer's
- Parkinson's
- Dementia
- Type II Diabetes
- Disorientation
- Memory loss

https://newsnetwork.mayoclinic.org/discussion/what-is-amyloidosis-and-10-signs-you-might-have-it/

Part F : Mystery ORF genes in Covid Vaccine code for Amyloid

So far, we have seen evidence of a high incidence of amyloid clotting reported by embalmers since the rollout of the COVID vaccines. We have also seen experimental evidence that the COVID spike protein rapidly generates amyloids in the presence of neutrophil enzyme. Thirdly we have seen that COVID vaccines have a high proportional reporting ratio for symptoms associated with amyloidosis.

A question arises as to how these adverse effects came to be associated with the Covid vaccines, and why the vaccines have not been suspended pending an investigation.

When we look at the RNA sequence within the COVID vaccine, we find that other genes have been added besides the gene for the spike protein, and these genes were kept hidden from the public.

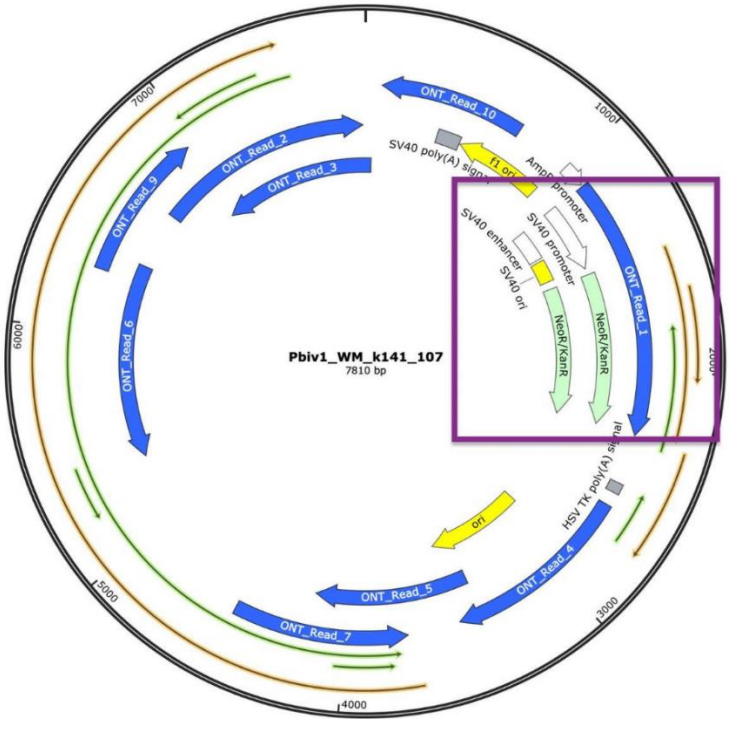
The following is taken from Spider webs in the Pfizer closet - by Anandamide (substack.com)

Pfizer failed to report the 2nd largest sequence in the RNA. This is the mystery ORF of 1252 amino acids described by Beaudoin et al. The protein sequence is given below –

>Mystery_ORF_Under_Pfizer_Spike

MQYQLESSCVVQFHALQHGLRIVLVELAAAATATTALQAATAAGHATQHDCDHHDGNQSGDKAQPDVPGPLDVLLVLPQFLQVDQALVQIL
GHLVQPVDLFLDVHDAGIDSADIAQVHVGACVVLKVLVQFLFEAVQLGLQRVVHGIVHNADHDVAVARHEGVVGGDDLGLVEVPLCHEPMG
AVGHEHAFSRKVGFAVVADGWSGGEILLLSGHICHVQKHHAVRGRLREAHQVVALAAKVHSLALAQHTLRHLGGGQIGRGSNLGGSDQLLG
HVCLEALQSACDQSVDLHLGLRRVQSAQDIVQHRADGAELGGQLLDQGVQCLGIVVDHVLQLSQGACCAAQAVLDLADGAVELVGDQLLVL
VQHILGHSDAVEPVGHLHSKGDLQSGACSKCPAACDCAGQQGRCVLGDHLIGQQRRQHCQSVKLLGANQIPGGNVAQTIAILLDEAGVGQCH
FVEQQVLDEAPLAGLARIGQNLAEIEAAEVLDRRGLVDLLHLGEHLLGVLVLFHGDPCQGSFQLGAEAAVLQQQVGALGGIAADVHGAVHAG
LGHGHRQDLCGHADGEVGGDSDRVVGVGHAVLGAQRHCVGNDALAGHASGSPVALCLCLVAGADSSADGDVALVAIVHVLGSDQTAGSGL
KHIAAGGVHPPCRCQLIGVNGHGHFGTVHALVQHCHLIAGVGARGDHRHSAEAARGDVQDFQCLGISNGVCGIGDIPAKLLEWQELLVALCQ
HAGAGQAVEVEVHAFVLHEIGAFLRAAHCGRGMQQFEAQHHHSVGLVAHAVCGPKAVGLQWEVAVHACHAVTRLVAGLIDLGGDVPLEGL
QIGLPEQPVPVIVVAADFGVQLVAVPGNHTAGEVVGQLVVVVGDVACLSRGNLPHFVSPDHEAVGVHVCEAQVVQLGRGHAVALECEEGG
EVVQHGVVGHAIADPLPVPGVHRGESGGIEHLVEGAQIGDIGEPHDGFGGLHPEVAGLVDALFHGEGLQGALCLAQRIQSTIHGVGDGAVLVV
LQQEGSRLQVAHIVSGGTSCPSAAAIARCQVASVQGQQCLKPGDVDADGQIHQGFQSREALRQIPAEVDRGVLAVDLEVAVDVLKHELAQVL
EVALLAFQVHQERLGHVLEGAVVGAAVHPELAFHPALVVLVVVDVQEGVVAELELAHFDDHVGGVVHDQQALGLAVQCGAEDPASDDVGL
LGAGKVHPVVEGQHGVVESLGAIGAGDGVEPGHVAEERQEQVLGRVQHAGSEHLVGVVHASGKAVGV

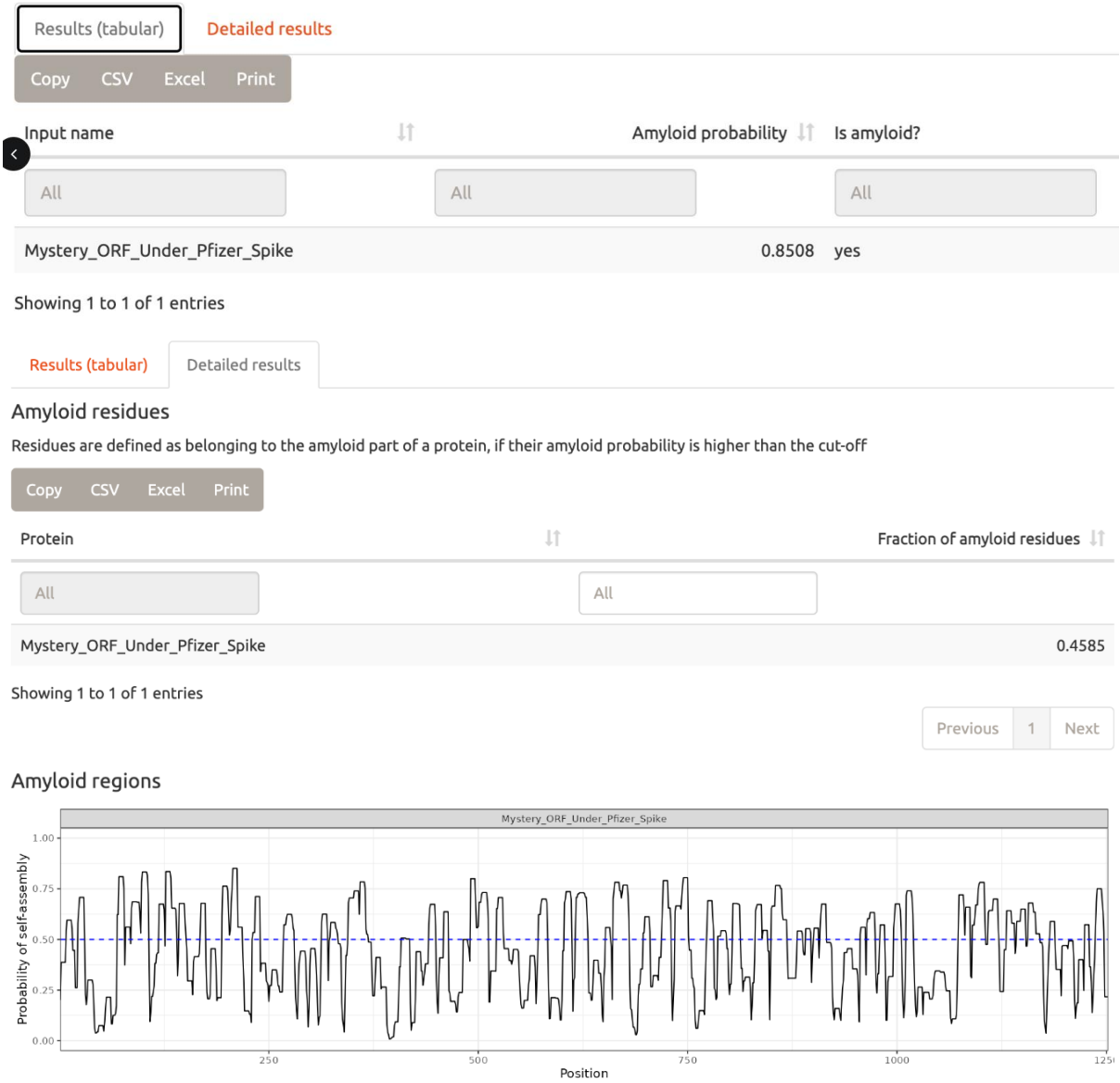
ORFs are painted in Green and Gold in the plasmid map below.



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

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.



The probability that the ORF sequence will generate amyloid is 0.8508 (1 is absolute certainty)

The percentage of the ORF sequence that is amyloid residue is 45.85%

Analysis of Pfizer Spike Region Using AmyloGram Tool

Results (tabular) Detailed results

Copy CSV Excel Print

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

Results (tabular) Detailed results

Amyloid residues

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

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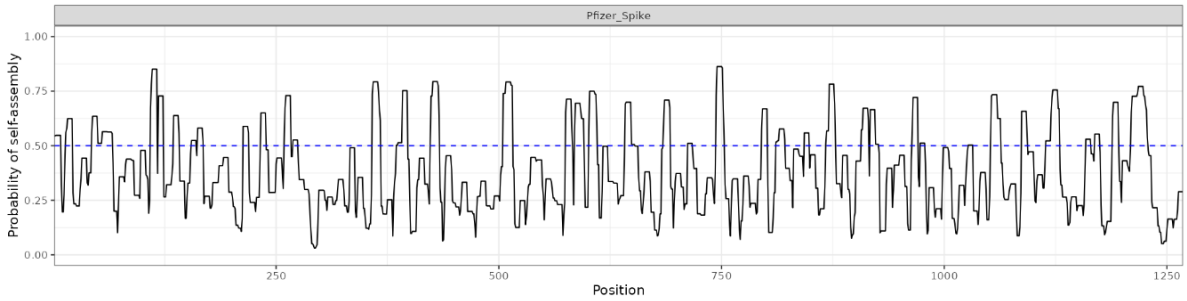
Protein	Fraction of amyloid residues
All	All
Pfizer_Spike	0.2815

Showing 1 to 1 of 1 entries

Previous 1 Next

Amyloid regions



The probability that the SPIKE sequence will generate amyloid is 0.8627 (1 is absolute certainty)

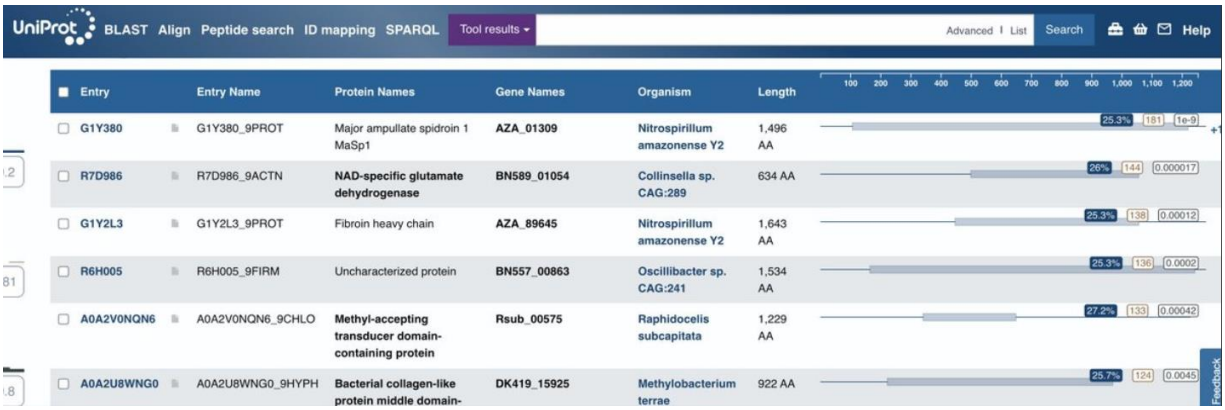
The percentage of the SPIKE sequence that is amyloid residue is 28.15%

(Note that the breakup of the SPIKE protein into amylogenic residues when exposed to neutrophil elastase will further increase both the probability and percentage of amyloid formation)

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?)

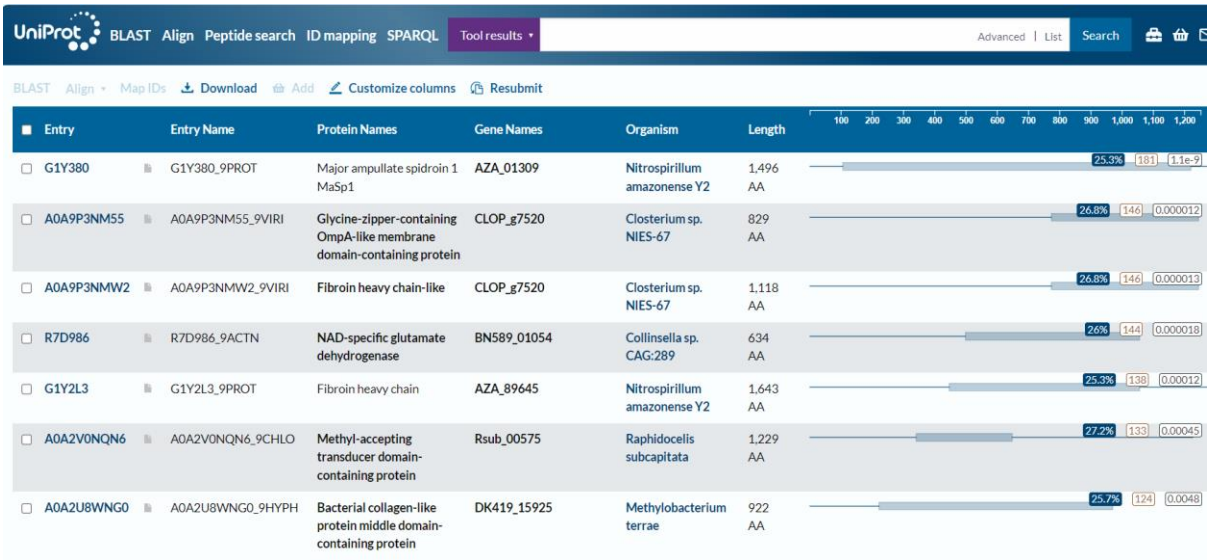
Using Uniprot to Identify What this Sequence Does

Anandamide found that the Mystery ORF's closest hit is to a protein involved in spider silk – called Spidroin. Other hits with lower E-values are to Collagen and Fibroin. Anandamide 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 Anandamide's finding. I input the above sequence here - Tool results | UniProt

The top result was Spidroin as reported.



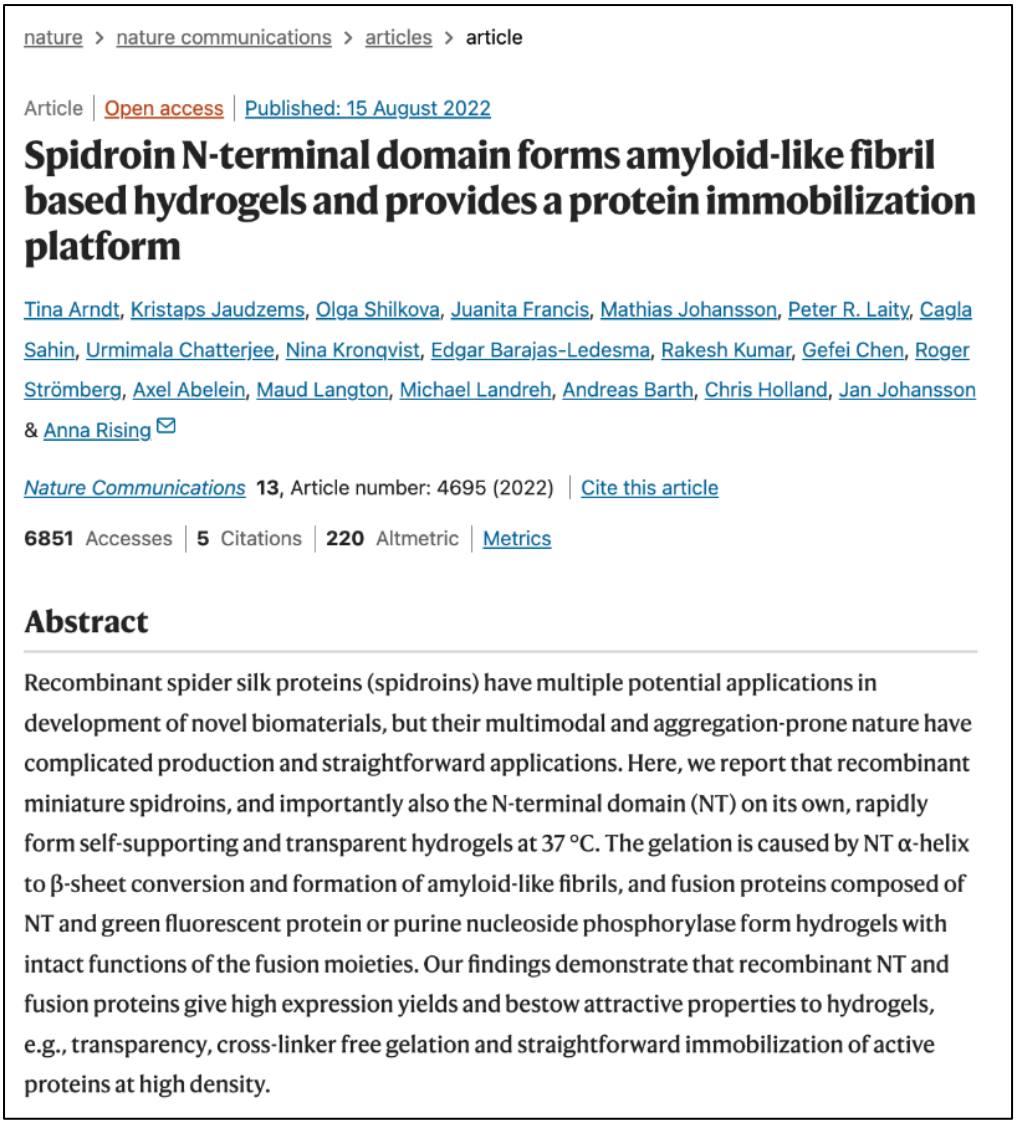
Curiously the Spidroin protein codes for natures toughest silk fibre, comparable in tensile strength to that of steel or Kevlar. The RNA sequence is also similar to that of other fibrous materials – fibrin and collagen.

When blood vessel lining is exposed to the vaccine, the RNA codes for the Spike, but also codes for fibres akin to spider silk, fibrin and collagen. The result is that endothelial cells begin to exude the tendrils of a fibrous mesh.

In addition, Spidroin is well known to be highly amyloidogenic.

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 Spidroin sequence forms amyloid-like fibrils rapidly at 37 degrees Celsius.

A Reasonable 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.

Despite these dangers, the failure of governments to withdraw or suspend the vaccine, or to investigate or even acknowledge the risk, means that harms can no longer be considered an accident. It looks as if a conscious decision has been made to allow and encourage a harmful protocol.

Branding the COVID vaccine a success, governments plan to replace more traditional vaccines with RNA ones, and childhood vaccination continues unabated.