

## Review Article

# Are fibrinaloid microclots a cause of autoimmunity in Long Covid and other post-infection diseases?

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It is now well established that the blood-clotting protein fibrinogen can polymerise into an anomalous form of fibrin that is amyloid in character; the resultant clots and microclots entrap many other molecules, stain with fluorogenic amyloid stains, are rather resistant to fibrinolysis, can block up microcapillaries, are implicated in a variety of diseases including Long COVID, and have been referred to as fibrinaloids. A necessary corollary of this anomalous polymerisation is the generation of novel epitopes in proteins that would normally be seen as ‘self’, and otherwise immunologically silent. The precise conformation of the resulting fibrinaloid clots (that, as with prions and classical amyloid proteins, can adopt multiple, stable conformations) must depend on the existing small molecules and metal ions that the fibrinogen may (and in some cases is known to) have bound before polymerisation. Any such novel epitopes, however, are likely to lead to the generation of autoantibodies. A convergent phenomenology, including distinct conformations and seeding of the anomalous form for initiation and propagation, is emerging to link knowledge in prions, prionoids, amyloids and now fibrinaloids. We here summarise the evidence for the above reasoning, which has substantial implications for our understanding of the genesis of autoimmunity (and the possible prevention thereof) based on the primary process of fibrinaloid formation.

## Introduction

Starting with analyses using the electron microscope (e.g. [1–7]), we observed anomalous structures in the fibrin networks of blood clots from individuals exhibiting inflammation arising from a variety of causes, including in a number of chronic diseases. These were originally referred to as ‘dense matted deposits’. We subsequently showed [8] that these ‘anomalous’ clots exhibited the properties of amyloids, in that they stained effectively, and in the same places [9], with stains such as thioflavin T [10] and the commercial oligothiophene Amytracker™ dyes known to stain amyloid forms of proteins [11,12]. Because these blood microclots based on fibrin and other entrapped molecules have this amyloid character, they are now referred to as ‘fibrinaloid’ microclots [13,14].

Many chronic diseases (that are usually considered noncommunicable) share a variety of observables such as inflammatory markers, iron dysregulation [15–18], hypercoagulability and hypofibrinolysis [19], and fibrinaloid microclots, along with considerable evidence that they may in fact have an infectious origin (e.g. [12,20–29]). This prevalence of fibrinaloid microclots is especially true of both acute and long COVID-19 [30–39].

A characteristic of amyloid proteins, including prion proteins (e.g. [40,41]), is that they retain the primary sequence of their normal, non-amyloid form but adopt a very different set of secondary structures (involving crossed beta-sheets [42–48]) and hence tertiary structure(s).

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An inevitable consequence of this ‘amyloid’ type of change in conformation, the details of which must also depend on the nature and concentrations of small molecules and metal ions present at the time of fibrinogen polymerisation, is the generation of novel epitopes of what are otherwise normal host proteins. This might then be thought to lead equally inevitably to the generation of autoantibodies, that may contribute to the symptoms associated with these diseases, and in particular to Long COVID. We here develop and assess the evidence for this idea.

## Multiple protein macro-conformations and amyloidogenesis

While it is well established that proteins, including enzymes, can adopt a great many isoenergetic conformations [49,50] or microstates, it had been widely assumed — following the famous protein refolding experiments of Anfinsen [51,52] — that the main, ‘ground’ macrostate adopted by a typical protein following its synthesis was also that of the thermodynamically lowest free energy. While this was necessarily an assumption (the total number of possible states is uncomputably high [53–56]), it was arguably the discovery of prion proteins [57–59] that showed that the assumption could demonstrably be false; stabler conformations of the ‘amyloid proteins’, i.e. ones of lower free energy, were indeed possible [60,61], and the ‘usual’ conformation was simply one of the more kinetically accessible [62]. Figure 1A is an illustration (adapted from [62]) of a thermodynamic model for the energetics of the conversion of a PrP protein in the PrP<sup>C</sup> conformation into PrP<sup>Sc</sup>. Protein interactions with other ligands may result in protein misfolding and has been shown to cause amyloidogenic changes to all kinds of proteins. Figure 1B is our interpretation of the structural changes in fibrin clots (plus entrapped molecules) in diseases such as Long COVID that exhibit them. Interactions between plasma proteins (mainly fibrinogen) and inflammatory molecules in circulation can result in plasma protein misfolding and have been shown to cause amyloidogenic changes to fibrinogen. This is illustrated by electron micrographs of fibrin clots (created by adding thrombin to platelet poor plasma). Although we are not aware of any experimental observations of the conversion in process, *ab initio* computer simulations [63–66] are beginning to provide a valuable indication of the precise mechanisms by which it may take place.

## Amyloidogenic proteins: prions

As is well known, the classical prion protein PrP normally exists in a relatively stable and ‘benign’ form known as PrP<sup>C</sup>, but can adopt a substantially more stable or ‘rogue’ and toxic [67] form (Figure 1A) known as PrP<sup>Sc</sup>, in which alpha-helices in the PrP<sup>C</sup> form are converted into (crossed) beta sheets [68]. PrP<sup>Sc</sup> can be ultra-stable; indeed its resistance to proteinase K digestion is often used in its assay [69–71], and essentially accounts for its heritability [72]. It is also relatively insoluble, a fact that has until recently hampered the determination of its structures [71,73–83], much as with other amyloids [84]. The chief problems caused by PrP<sup>Sc</sup> arise from the fact that it can itself catalyse (‘seed’ or ‘template’) the conversion of PrP<sup>C</sup> to further molecules of the membrane-disruptive PrP<sup>Sc</sup> [85], making the process of PrP<sup>Sc</sup> production autocatalytic, such that absolutely miniscule amounts of PrP<sup>Sc</sup> can be toxic [86–89].

## Mechanisms of fibril formation in prions and classical amyloid proteins

As illustrated in Figure 2 a fibril from a typical amyloidogenic protein [90–92] is ~7–12 nm in diameter; as templated by a single molecule of the ‘rogue’ form, soluble oligomer fibrils begin to form, and these assemble to form the insoluble rogue or amyloid form or aggregates that are observable e.g. by atomic force microscopy [93–97], or stainable by stains such as thioflavin T that are widely used to follow the process [98–108]. Fibrils formed by most amyloidogenic proteins are in the range 10–20 nm in diameter or lower, e.g. [109–114]).

We note here that in contrast with the classical prion and amyloid fibrils, the diameter of fibres in fibrinoid microclots is generally similar to the diameter of ‘typical’ healthy fibrin fibres in the range 80 to 110 nm [19,115–117], although it may be higher (e.g. in Alzheimer’s type dementia [115]) or lower (as in stroke [116]). That seen in most inflammatory diseases is lower [11], but necessarily involves multiple copies of the fibrinogen protein for the same length element.

## Multiple amyloid conformations and self-propagation

While it is recognised that amyloid proteins are much stabler than are their parent proteins, a very important feature of amyloid or prion proteins (especially from the present perspective) is that they can in fact adopt

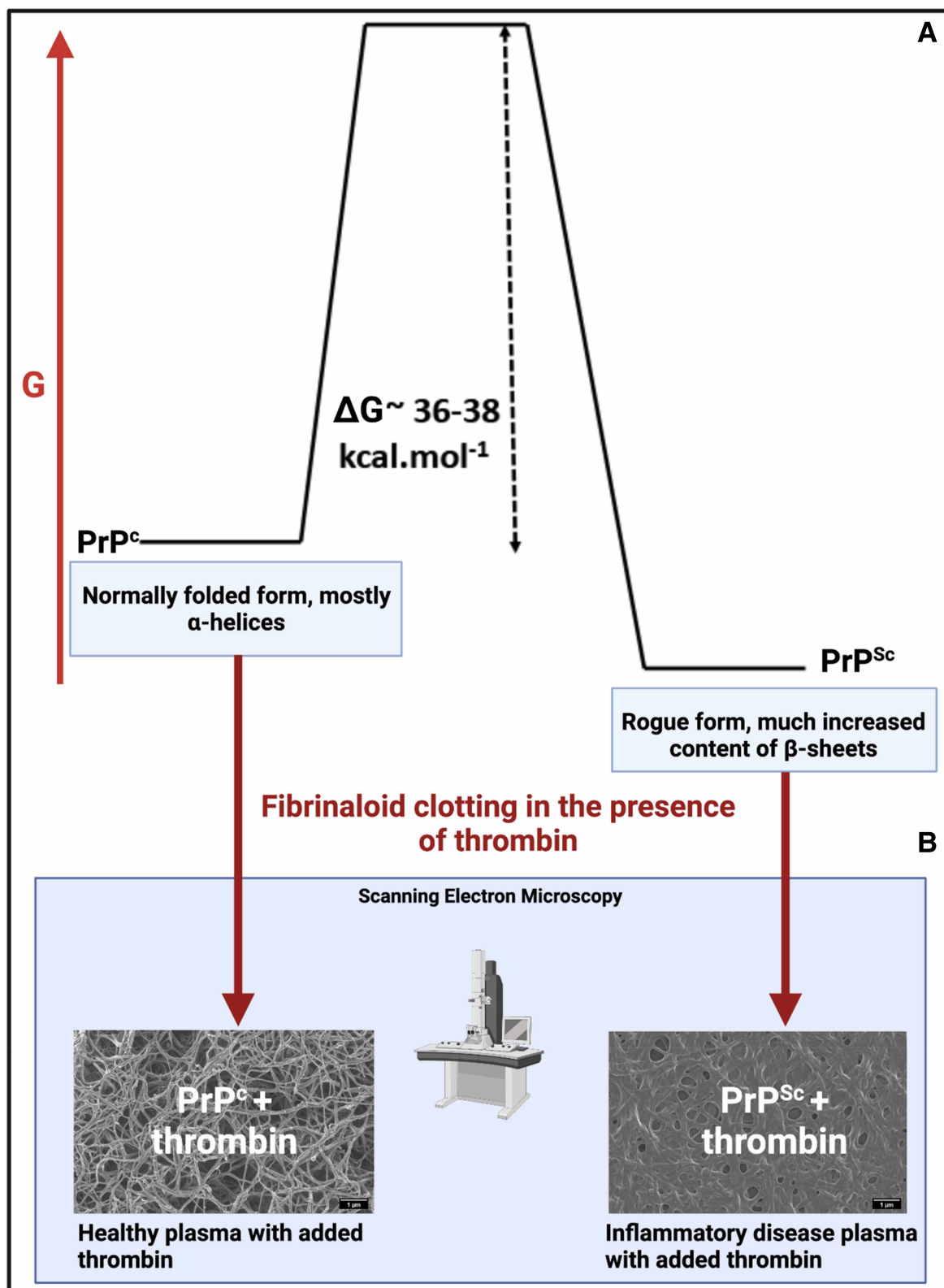


Figure 1. Illustration of the thermodynamics of prion proteins.

Part 1 of 2

(A) Illustration of a model for the energetics of the conversion of  $\text{PrP}^{\text{C}}$  sequences into  $\text{PrP}^{\text{Sc}}$  (adapted from [62]). (B) Protein-protein interactions may result in protein misfolding and has been shown to cause amyloidogenic changes to fibrinogen as

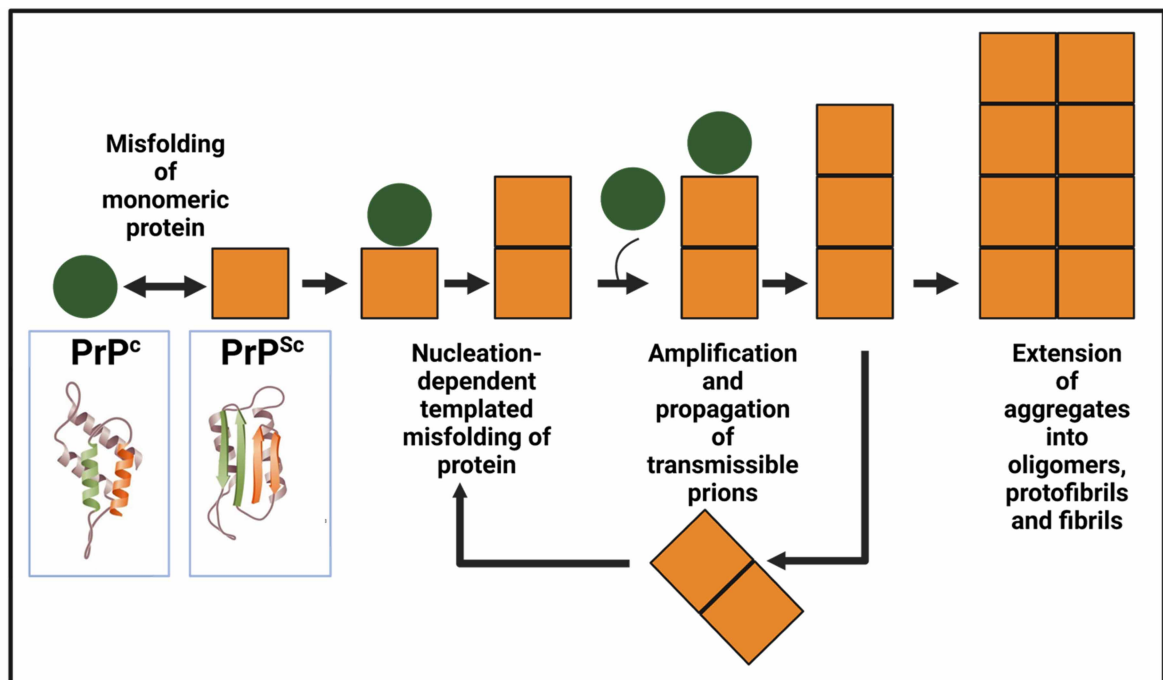
**Figure 1. Illustration of the thermodynamics of prion proteins.**

Part 2 of 2

illustrated by electron micrographs of fibrin clots (created by adding thrombin to the platelet poor plasma). Reprinted from an Open Access CC-BY 4.0 publication at [11], based on [62]. Created by BioRender.com.

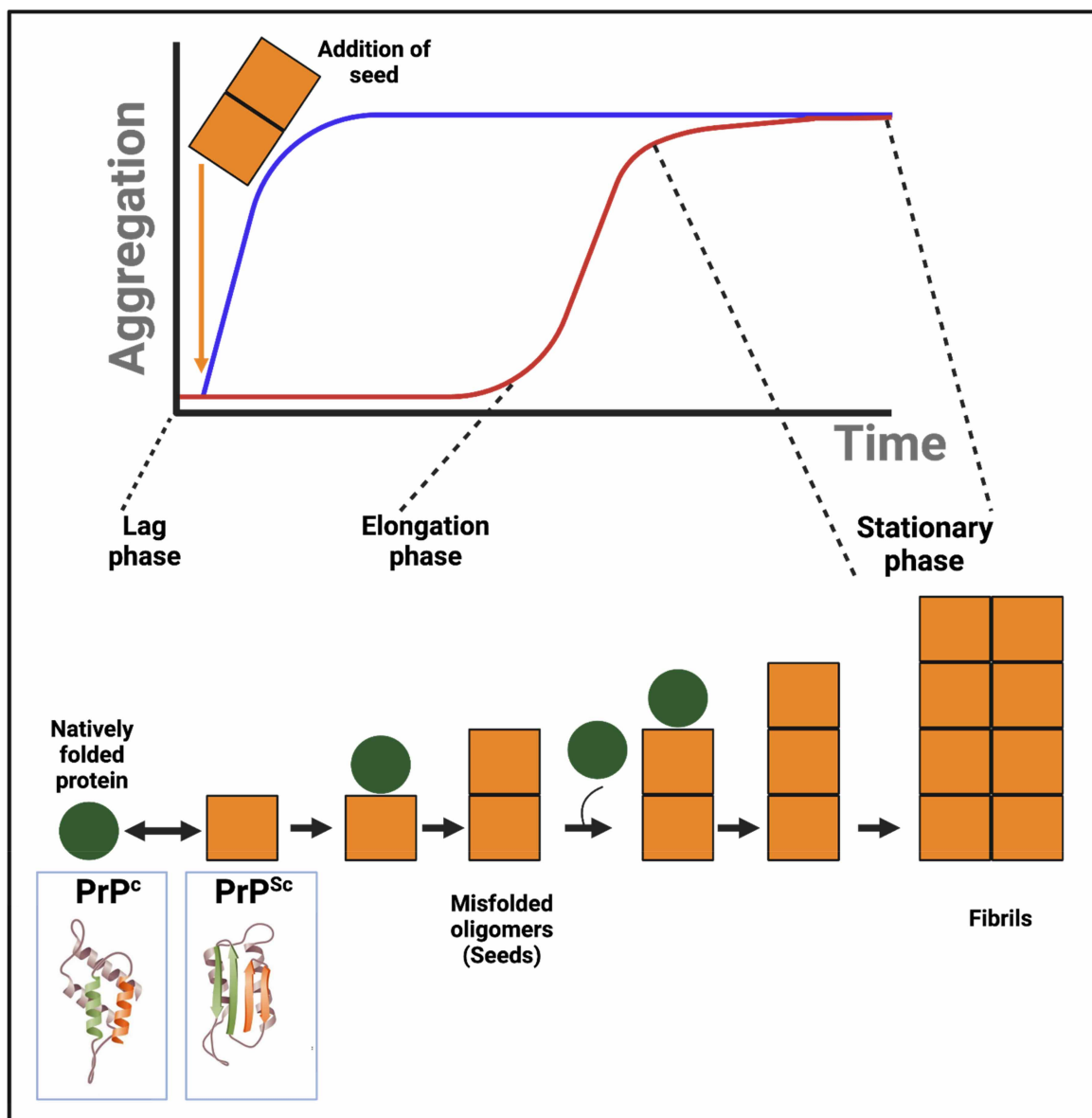
multiple stable states or conformations, sometimes referred to as ‘polymorphisms’ [118,119], ‘strains’ [120–122], or ‘subtypes’ [123], albeit they have the same sequence [46]. In effect the first molecule to convert into the rogue form acts as a ‘template’ to guide further molecules into a conformation with which it can pack, and that then catalyses further formation of the ultimately insoluble fibrils and aggregates. This has led to so-called ‘seed amplification’ (sometimes referred to as ‘quaking-induced conversion’) assays in which a seed molecule in the amyloid form effectively amplifies itself (Figure 3), thereby allowing the detection of tiny amounts of initial protein in a rogue conformation, whether for prions (e.g. [86,124–129]) or other amyloidogenic proteins such as the alpha-synuclein involved in Parkinson’s disease (e.g. [130–134]) or the tau aggregates that can accompany Pick disease [135] or Alzheimer’s dementia [136,137]. (We also note, although we do not pursue it here, that polymorphisms including amorphous and crystalline forms are also an extremely important and likely related feature of the structure and behaviour of both small pharmaceutical drugs (e.g. [138,139]) and organic but non-biological polymers and plastics (e.g. [140–142]).

It is generally the case [143] that they catalyse the production of their own specific conformations or aggregates (e.g. [45,61,76,77,81,85,144–170]). Thus, while an individual amyloidogenic protein also has a ‘set’ conformation, to which the host is presumably adapted and is seen as ‘self’, the amyloid forms (including in tauopathies [171–173]) can adopt a variety of individual and self-propagating [174–178] conformations, and thus, presumably, display a variety of novel and different epitopes depending upon which ‘polymorphism’ is produced.



**Figure 2. An illustration of a typical amyloidogenic ‘rogue’ protein folding illustrated by using a nucleation-dependent model of prion replication (adapted from [102]).**

PrP<sup>C</sup> converts into its infectious disease-associated isoform, which is PrP<sup>Sc</sup>. PrP<sup>Sc</sup> then induces nucleation-dependent misfolding in other PrP<sup>C</sup> molecules that in turn leads to amplification and propagation of transmissible prions. Growing aggregates extend into oligomers, protofibrils, and then fibrils that form the protein aggregates characteristic of disease. Created by Biorender.com.



**Figure 3. Seeding nucleation mechanism and amplification.**

Example given of of misfolded alphaSyn aggregates (Adapted from [132].) Created with BioRender.com.

Given that in many cases the starting (and of course finishing) protein sequences are the same, it is not precisely known in general what determines which polymorphisms are produced, but realistically it can only be because the starting molecules do in fact differ from each other by first having bound something else. For prions and amyloids, the most evidenced candidates for the ‘something else’ are small molecules [179–193], and/or metal ions [15,194–209] and/or anions [208,210,211]. In a certain sense this is little more than a recognition that allosteric interactions of small molecules with proteins (which are much more widespread than commonly recognised [212,213]) can change the conformation of the latter. The further general assumption, then, is that the closer the sequence and/or starting structure, the more likely it will self- or co-polymerise ([214], and see below).

In the case of fibrinogen, we know that amyloidogenesis into a variety of clot morphologies can be catalysed by the presence of miniscule amounts of bacterial cell wall components such as lipopolysaccharide [9,23,24,26,215,216,2724] or lipoteichoic acid [24], or the spike protein from SARS-CoV-2 [36] (which is itself amyloidogenic [217]) (Figure 4).

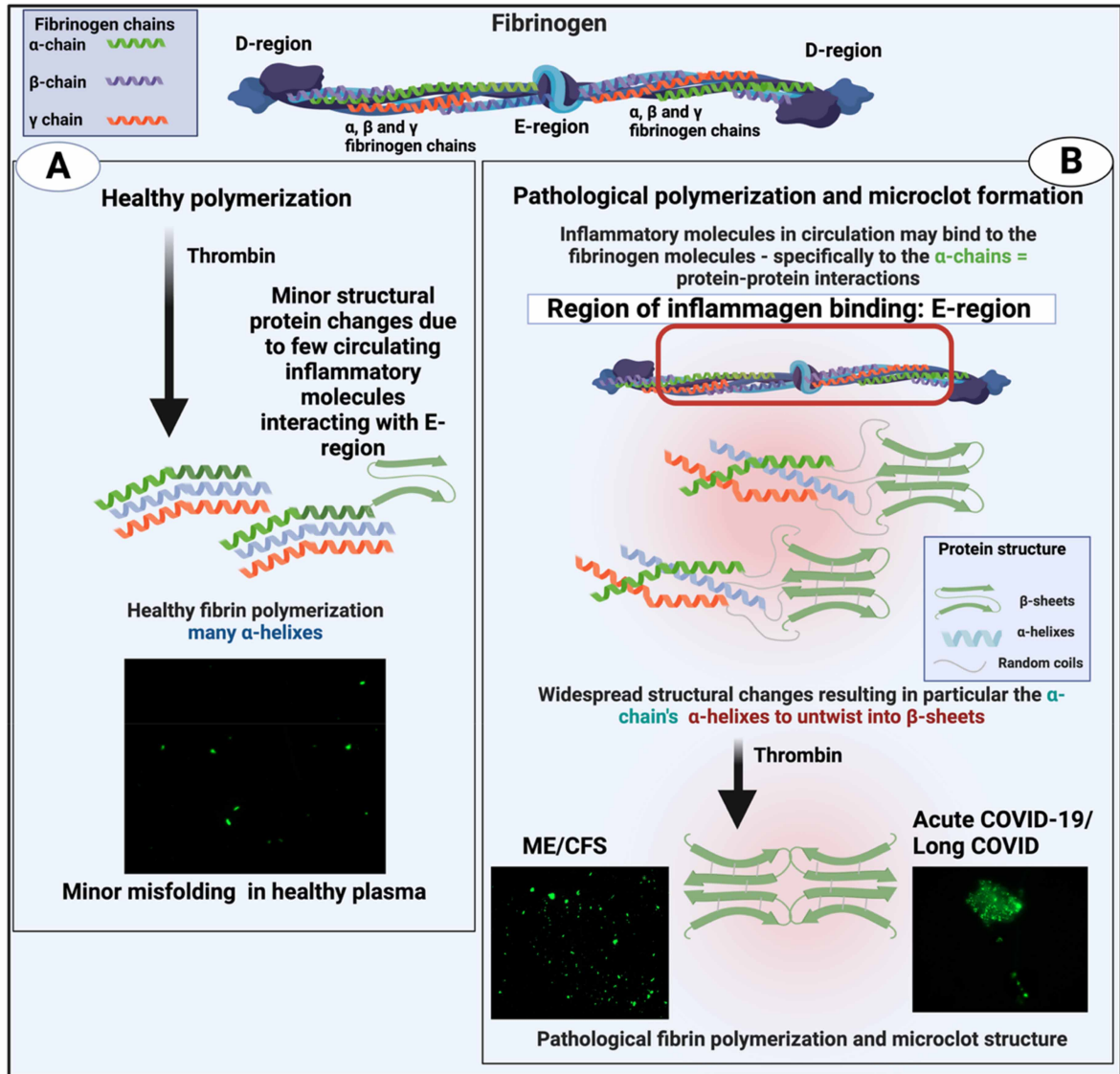


Figure 4. Misfolding of fibrinogen, result in a variety of pathological clot morphologies, catalysed by the presence of miniscule amounts of bacterial cell wall components such as lipopolysaccharide, lipoteichoic acid or the spike protein from SARS-CoV-2 (which is itself amyloidogenic).

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## Prionoids: a convergence of thinking on amyloidogenic proteins

Although in science a commonplace siloing means that parallel fields do not learn from each other as swiftly as they might, the fields of prions and non-prion amyloids do seem to be converging, as they come to recognise that the phenomena they study have many things in common (e.g. [102,218]). Note that as well as the classical amyloids (such as Abeta, synuclein, tau and so on involved in diseases known as amyloidoses) many other proteins can adopt amyloid forms, including lysozyme [219–225] and insulin [185,224,226–231]. These include multiple stable conformations of the proteins of interest that are insoluble and stainable by amyloid stains (and that differ from the 'benign', normal form), and the ability of a given rogue form to seed (however briefly [232], and ignoring post-translational modifications [233]), the propagation of forms similar to itself. This has led to the more general concept of prionoids [234–242] to describe this set of linked properties. As rehearsed

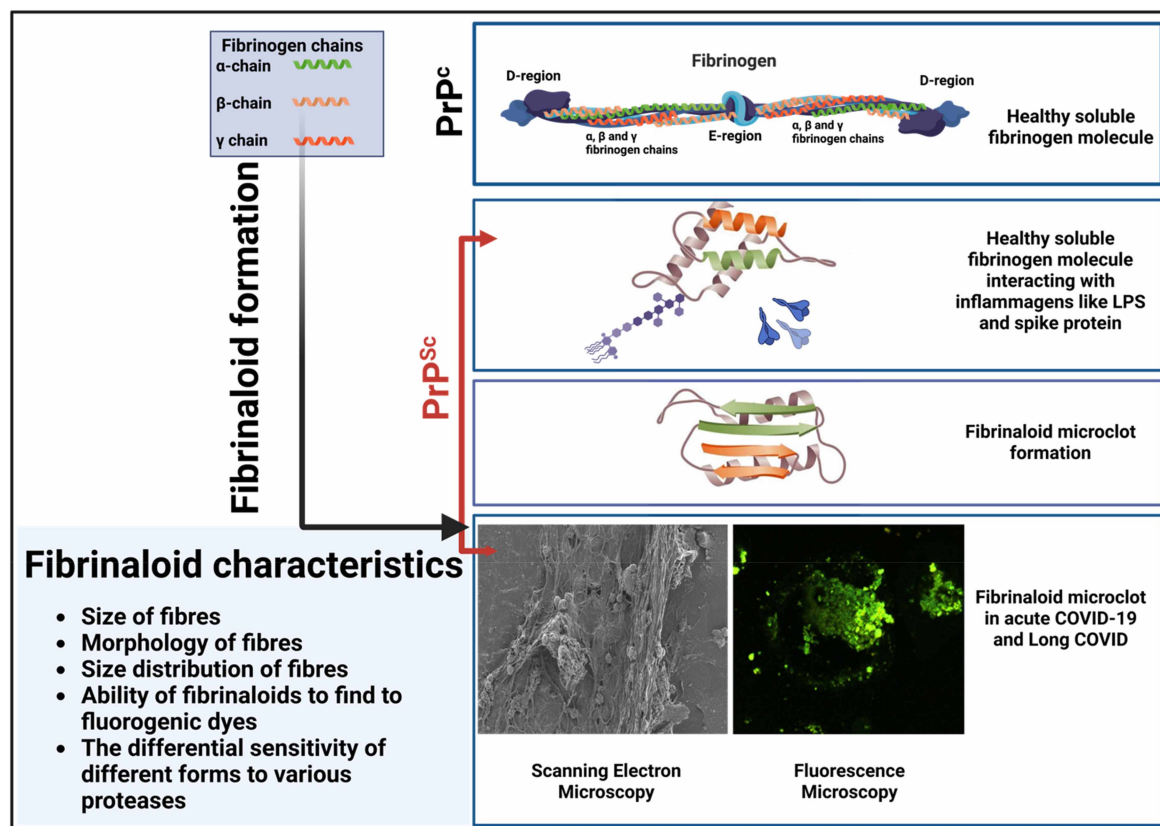


Figure 5. Features of fibrinaloid microclots (without the addition of thrombin).

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in detail elsewhere [11], these are also features common to the generation of fibrinaloid microclots (see Figure 5). We now begin to address the immunological consequences of such amyloidogenesis, starting with a brief section on autoantibodies.

## Autoantibodies

The classical function of immune systems is to discriminate self from non-self, or to detect ‘danger’ [243–245], and to arrange to produce either innate immune responses [246] or actual antibodies [247,248] against elements (usually epitopes of protein sequence or structure) that are considered foreign. In favourable cases the offending, exogenous invaders, usually microbes, are then suppressed or eliminated.

However, in the case of the adaptive immune response involving antibodies, usually mediated by B- and T-lymphocytes, an unwelcome phenomenon can occur: if the epitope possessed or (as we rehearse here) generated by the microbe is also shared by the host, the resultant autoantibody can also recognise this epitope and attack the host itself, causing an autoimmune disease that can share many of the characteristics of Long COVID and ME/CFS [249].

A well-worked example, described in detail by Ebringer [250–253] (and reviewed by us elsewhere [21]), involves members of the genus *Proteus* (viz *mirabilis* and *vulgaris*). These organisms are a common cause of urinary tract infections, especially in women, and can evoke substantial antibodies in patients who go on to develop rheumatoid arthritis. The relevant epitopes of *Proteus* are the amino acid sequences ESRRAL and IRRET; the former (e.g. in *Proteus* haemolysin and urease) mimics a ‘shared epitope’ EQR(K)RAA while the latter displays molecular mimicry with LRREI found in collagen XI of hyaline cartilage. The fact that these epitopes contain arginine doublets, which can be acted upon by peptidyl arginine deiminase, also provides a straightforward explanation for the early appearance of anti-citrullinated protein antibodies in patients with RA.

In a similar vein, SARS-CoV-2 elicits an array of autoantibodies [249,254–257], albeit the mechanisms and cross-reactivities towards the host are not yet well understood (though information is emerging in the related ME/CFS [258,259]). Of particular interest is the fact that ‘anti-ACE2 IgM is found in 27% of individuals with severe COVID-19, which can initiate complement binding and alter the permeability of vascular microvessel endothelium [260]’ [249]. However, our focus here is simply to suggest a particular mechanism of novel epitope creation that allowed ‘self’ sequences to become seen as non-self (as they are not normally exposed and thus able to elicit antibodies).

## Immunological responses to prion proteins

A chief premise of this review is that the anomalous folding of proteins in amyloid forms, and in particular of fibrinoids, leads to the display of novel epitopes (neoepitopes or neoantigens) that — unlike their parent protein, which is seen as ‘self’ — can induce autoantibodies that may also attack the normal form of the target. This has been anticipated for PrP<sup>C</sup> (‘We hypothesised that subtle conformational alterations of pathogenic PrP<sup>C</sup> variants could stochastically generate immunogenic neoepitopes, which in turn might elicit a protective humoral anti-PrP<sup>C</sup> immune response’ [261]). Some such anti-amyloid(ogenic) antibodies can be protective [262–268]. Consistent with the view that PrP<sup>Sc</sup> involves neo-epitope formation, antibodies can be found that react with PrP<sup>Sc</sup> and with aggregates of PrP<sup>C</sup> but not with soluble PrP<sup>C</sup> [269–272]. A particularly interesting example is the discovery that certain antibodies can cross-react with beta-amyloid and the prion protein [273], implying the existence of a common element. This is certainly true for small oligomers [274,275].

## Antigenic properties of amyloid forms of protein

The existence of autoantibodies following an infection is a commonplace, resulting from a molecular mimicry between the antigen and host antigens/targets (e.g. [21,250,276–279]). However, whether they are initially generated by an amyloid form of their target protein is not discussed because almost all studies fail to distinguish the conformation of the target antigen. This said, examples of autoantibodies that are selective for amyloid forms of amyloidogenic proteins include those for beta-amyloid [280,281], lysozyme [282], tau [283], transthyretin [284], and TSH receptor [285], as well as exogenous proteins such as fish beta-parvalbumin [286]. They may also be designed and selected for [287–289]. Of course there is also considerable interest in developing exogenous therapeutic antibodies against such targets (e.g. [290–295]), but these latter studies are beyond the present scope of this review.

## Interactions between different amyloid proteins; cross-seeding

That amyloidogenic proteins are typically capable of catalysing the production of amyloid homopolymers is both well known and has been discussed above. In some cases (where sequences differ) there is no cross-reactivity, i.e. there exists what amounts to a species specificity among prion proteins with regard to the PrP<sup>Sc</sup>-catalysed or -templated conversion of PrP<sup>C</sup> to PrP<sup>Sc</sup> [296–303]. The same can be true for antibodies against various prion forms [304].

More generally, though, the opposite kinds of phenomena (‘promiscuity’) have been found, namely within a given host or *in vitro* incubation there can be co-propagation of heterogeneous species [305,306], and such cross-reaction can depend on the anions present [210]. Thus, there is evidence for extensive amyloid-amyloid interactions [307], often referred to as a cross-seeding [308–316], in which the amyloid form of one protein induced amyloidogenesis of a different type of protein. This can often lead to a co-aggregation [317–322]. This can even occur with proteins not necessarily considered as classically amyloid, including proteins in the influenza virus [323]. Table 1 gives some other examples.

## Proteomics of amyloid aggregates

Of course at a trivial level, the production of (i) insoluble protein aggregates in a variety of amyloid diseases (e.g. Lewy bodies in Parkinson’s disease [333] and dementia [334]) and (ii) inclusion bodies during recombinant protein production [335] is well known. Certainly proteomics shows that a huge variety of heterogeneous molecules can be entrapped in such aggregates (e.g. [32,336–338]). Our interests here lie in some of the consequences, since the trapping of unfolded variants of any proteins may well lead to the generation of novel epitopes. Thus in recent proteomics studies of fibrinoids [32,338] we discovered that the clots contain various



**Table 1 Some examples of amyloidogenic biopolymers ('polymer 1') known to induce amyloid formation in others ('polymer 2') to which they are exposed ('crosstalk')**

Amyloidogenic polymer 1	Amyloidogenic polymer 2	Reference
Amyloid-beta	Islet amyloid polypeptide	[324]
	Alpha-synuclein	[325]
CsgA	Alpha-synuclein	[326,327]
Gut proteins	Alpha-synuclein	[328]
Insulin	Amylin	[329]
Islet amyloid polypeptide	Alpha-synuclein	[327,330]
Islet amyloid polypeptide	PrP	[331]
Serum amyloid A	Fibrin(ogen)	[319]
Alpha-synuclein	Tau	[332]

entrapped molecules. We found various clotting proteins, molecules involved in cellular functions and lipid metabolism that were both increased and reduced in the microclots. Interestingly, we also found numerous immunoglobulin molecules (or fragments thereof) that were found to be increased in the Long COVID sample compared with healthy samples.

## Consequences of cross-seeding – even further novel epitope creation

### Small molecules that bind to fibrinogen

Recognising that amyloids can adopt multiple, self-polymerising structures, and that this may depend on small molecules that were bound to fibrinogen before polymerisation, we here summarise what turns out to be fairly

**Table 2 Some small molecules known to bind to fibrinogen**

Small molecule	Nature of evidence	Reference (s)
Acebutolol	Biophysical binding assays; Binding and calculations	[347]; [339]
Benzothiazole	Fluorescence-based binding assays	[348]
Bilirubin	Binding assay	[349]
Clozapine	Binding assay, and structural changes in fibrin	[350]
Curcumin	UV/Vis spectroscopy; fluorescence quenching	[351]
Dihydro-alpha-lipoic acid	Binding assay and structural changes	[352]
Flavonoids	Spectroscopy, docking	[353]
Lipopolysaccharide and lipoteichoic acids	Amyloidogenesis	[8]
24dium-chain fatty acids	Calorimetric binding studies	[354]
Beta-oestradiol	Fluorescence-based binding assays	[355]
Penicillins	Calorimetric binding assays	[356]
Propranolol	Binding assay and calculations	[339,357]
Resveratrol	Binding assay	[358]
SARS-CoV-2 spike protein	Amyloidogenesis	[36]
Various, including bilirubin, resveratrol and dihydro-lipoic acid	Binding assays	[340]

We do not include those fluorogenic stains such as thioflavin T [10] and oligothiophenes [359] that stain the fibrinoid form.

considerable evidence (Table 2) that such small molecule binding to fibrinogen does indeed occur [339,340]. This would be consistent with the fact that typical pharmaceutical drugs are known to bind at least six separate target and off-target proteins [341–343], and have significant roles in affecting protein–protein interactions (e.g. [344–346]).

## Pharmacological approaches to inhibiting fibrinoid formation

Since the amyloid forms of proteins are normally more stable than are their soluble forms, it follows that they must function by raising the kinetic barrier to amyloid formation, by stabilising the native state [360] or by inhibiting folding intermediates in its formation [193]. Molecules known to inhibit various kinds of amyloid formation include L-DOPA [181], promethazine [361], cholic acid [184], and various halo-aromatic drugs [360]. Fibrinogen in its native form [362] is thus a reasonable target to avoid fibrinoid formation. It follows that at least some of those molecules in Table 2 might serve to stabilise the native state of fibrinogen and thereby inhibit fibrinoid formation, though as far as we know no screens for anti-fibrinoid formation have yet been performed. This seems to be a significant opportunity.

## Fibrin amyloids and how their structures may differ

As noted above, the structural biology of amyloids has lagged due to their insolubility, although it is certainly known even for homopolymers that different parallel or antiparallel cross-beta and macro-structures are formed [45,119,363]. Because fibrinogen is itself a heteropolymer, and the fibrinoid microclots entrap a great many other proteins [32,338], the details may be difficult to establish. As also mentioned above, the fibrinoid fibres have a substantially greater diameter than do those involved in the conventional amyloidoses. However, we recognise that at least four general properties of the fibres making up the fibrinoid microclots might be expected to differ between the different forms (see Figure 5):

- (i) the size, morphologies, and distribution in size of the fibrinoid microclots themselves
- (ii) the ability of the different fibrinoids to bind different molecules, including the fluorogenic ones commonly used to detect them (and where spectral differences may result [364–368])
- (iii) the differential sensitivity of different forms to various proteases (e.g. those caused by SARS-CoV-2 are most resilient [32,338]), as is established with the differential protease sensitivities of different prion forms [369]
- (iv) spectral properties of different dyes bound to the different microclots [364–366,370–373].

Since we know that both acute [374–376] and long COVID [33,39] can be ameliorated by suitable anticoagulants, without the addition of fibrinolytics, the question arises as to whether they may be orally available fibrinolytics [377] that could serve.

## Degradation of fibrinoids *in vitro* and *in vivo*

As also reviewed elsewhere [13,14], the enzymes nattokinase [378] (also active against spike protein [379]), serrapeptase [380,381] and lumbricase [382] have been shown to degrade fibrin clots (see also [229,230,383,384]). They would seem to have potentially useful roles, not least in removing any novel antigens appearing in fibrinoids.

## Concluding remarks and agenda

Much of this review involves the recognition that many (indeed likely most) proteins typically fold into kinetically stable but thermodynamically unstable states, and that under certain circumstances they can form stabler amyloids. This is true for prions, classical amyloids, and the more recently discovered fibrinoids in blood; it is also a hallmark of the proteins involved in energy transduction [385,386]. These conformations are radically different from the those of the ‘parent’ protein as synthesised; some amyloids can even then catalyse chemical reactions at significant rates [387–391]. Some of the conformations are particularly stable in the sense that they tend to catalyse homopolymerisation of the parent conformation; others are more promiscuous. This leads to a recognition that many infectious diseases involve fibrinoid formation en route to autoantibodies (albeit some are elicited by biomimicry directly [250,251,392,393]). Acceptance of the significance of autoantibody-driven inflammation in syndromes such as ME/CFS and Long COVID also implies that there may be value in testing

treatments (such as monoclonal antibodies [394] or small molecules) against TNF- $\alpha$  that are known to help in other autoimmune diseases like rheumatoid arthritis.

It is very likely that precisely which fibril conformations are formed depends on which small molecule and/or metal ligands may have pre-bound to the amyloids. Given the combinatorial explosion contingent upon making and testing multiple variants, the general sequence- and ligand-based rules are largely unknown, though the methods of synthetic biology [395] will allow us to begin to find out. A feature of note is that the modern and powerful computational folding algorithms such as AlphaFold [396–402] and RosettaFold [403–405] have been trained mainly or only on the native conformations of amyloidogenic proteins so at this stage (albeit they are non-deterministic [406]) they are unable to predict the structures of amyloids. Solving this would seem to be of high importance.

Our special focus is on the fibrinoid microclots that have been shown to entrap many other molecules, and that also contain a variety of autoantibodies. An important agenda item is thus to determine what these novel epitopes are, and to characterise the autoantibodies that they elicit. This may also hold out the hope that — whatever the autoantibody half lives — the removal of fibrinoid formation will lead to such autoantibody elimination.

### Competing Interests

E.P. is a named inventor on a patent application covering the use of fluorescence methods for microclot detection in Long COVID.

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### CRedit Author Contribution

**Douglas Kell:** Conceptualization, Resources, Funding acquisition, Investigation, Methodology, Writing — original draft, Project administration, Writing — review and editing. **Etheresia Pretorius:** Conceptualization, Resources, Data curation, Funding acquisition, Investigation, Visualization, Methodology, Writing — original draft, Project administration, Writing — review and editing.

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