

Review Article

Alpha-2-Macroglobulin, a Hypochlorite-Regulated Chaperone and Immune System Modulator

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Received 5 April 2019; Accepted 2 June 2019; Published 22 July 2019

Academic Editor: Sander Bekeschus

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Alpha-macroglobulins are ancient proteins that include monomeric, dimeric, and tetrameric family members. In humans, and many other mammals, the predominant alpha-macroglobulin is alpha-2-macroglobulin (α_2M), a tetrameric protein that is constitutively abundant in biological fluids (e.g., blood plasma, cerebral spinal fluid, synovial fluid, ocular fluid, and interstitial fluid). α_2M is best known for its remarkable ability to inhibit a broad spectrum of proteases, but the full gamut of its activities affects diverse biological processes. For example, α_2M can stabilise and facilitate the clearance of the Alzheimer's disease-associated amyloid beta ($A\beta$) peptide. Additionally, α_2M can influence the signalling of cytokines and growth factors including neurotrophins. The results of several studies support the idea that the functions of α_2M are uniquely regulated by hypochlorite, an oxidant that is generated during inflammation, which induces the native α_2M tetramer to dissociate into dimers. This review will discuss the evidence for hypochlorite-induced regulation of α_2M and the possible implications of this in neuroinflammation and neurodegeneration.

1. Structure and Function

α_2M is a secreted protein that is present at 1.5–2 mg mL⁻¹ and 1.0–3.6 μ g mL⁻¹ in human blood plasma and cerebral spinal fluid, respectively [1, 2]. The cage-like structure of α_2M (720 kDa) is formed by the assembly of four 180 kDa subunits into two disulfide-linked dimers, which noncovalently associate to complete the tetrameric quaternary structure of the protein [3]. A bait region that contains a large number of protease cleavage sites is responsible for the incredibly diverse range of proteases that interact with α_2M [4]. Cleavage of the α_2M bait region, which is in close physical proximity to a reactive thioester bond, results in covalent trapping of proteases within a steric cage [5]. This process involves a substantial conformational change that generates a compact tetrameric form [6] and reveals the binding site for the low-density lipoprotein receptor-related protein-1 (LRP1) [7, 8] (Figure 1(a)). For the purpose of this review, the compact tetrameric protease-bound form of α_2M is

referred to as transformed α_2M . Transformed α_2M (covalently bound to up to two protease molecules) is rapidly cleared from the circulation via LRP1-facilitated endocytosis (Figure 1(a)). As such, α_2M can efficiently inhibit a myriad of extracellular processes that are dependent on proteolysis.

Consistent with having an ancient origin in innate immunity, α_2M is a promiscuous protein that noncovalently binds to a diverse range of nonprotease ligands including cytokines [9, 10], growth factors [9–14], apolipoproteins [15], and misfolded proteins [16–20]. Many noncovalent ligands of α_2M including the Alzheimer's disease-associated $A\beta$ peptide [21], neurotrophins [14], and tumour necrosis factor-alpha (TNF- α) preferentially bind to transformed α_2M which is generated following the reaction of native α_2M with a protease or with small nucleophilic compounds that also target the α_2M thioester bond [6]. In these cases, it is proposed that transformed α_2M acts to limit the activities of noncovalently bound ligands by facilitating their disposal via LRP1 [10, 22] (Figure 1(a)). On the other hand, α_2M can control signalling

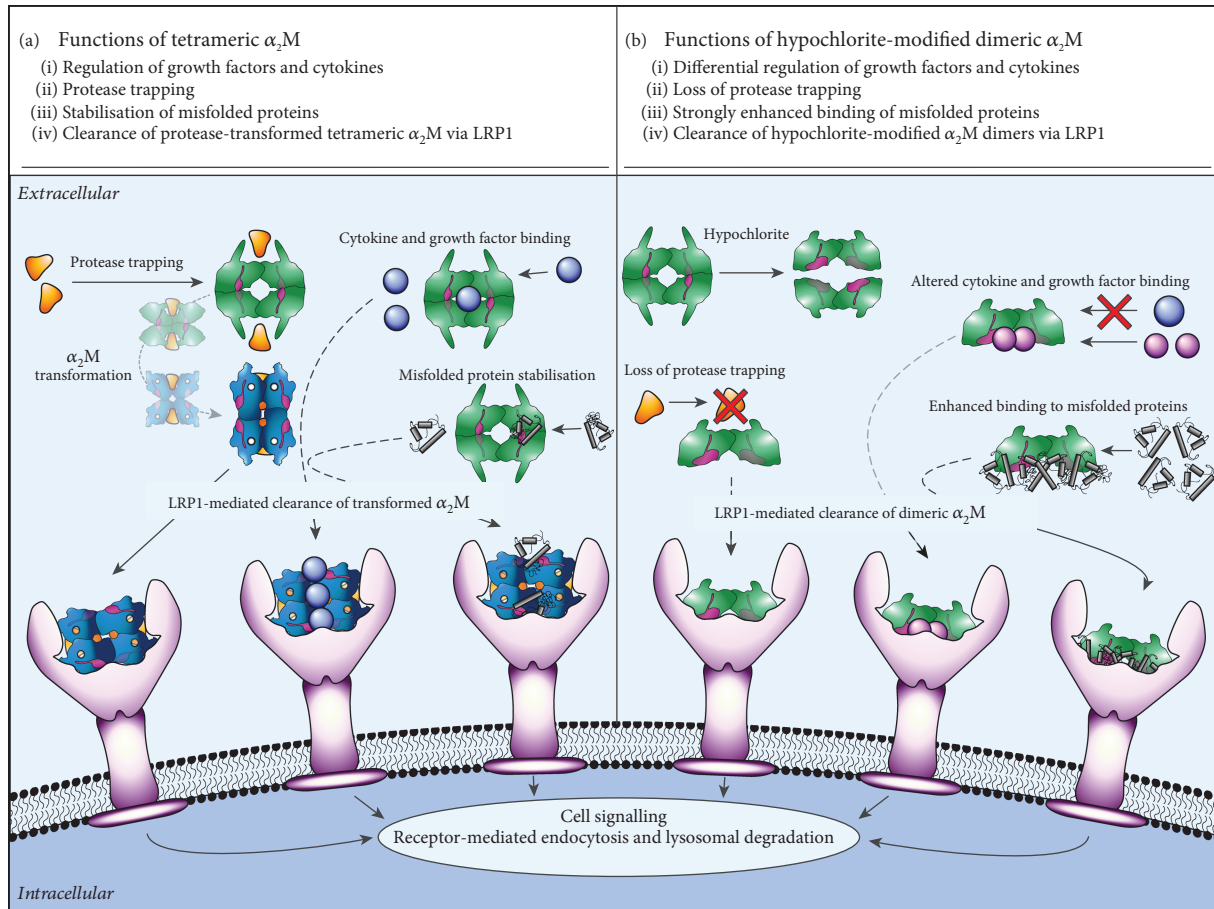


FIGURE 1: Schematic diagram showing the function consequences of hypochlorite-induced modification of α_2M . (a) Native α_2M , a tetramer (shown in green), is constitutively present in biological fluids and covalently binds to a broad range of proteases. Binding to proteases results in a conformational change that exposes the binding site on α_2M for LRP1, which is responsible for the clearance of the protease-transformed α_2M complex (shown in dark blue). α_2M also binds to a large number of noncovalent ligands including cytokines and misfolded proteins. In many cases, noncovalent binding of ligands occurs preferentially to the protease-transformed conformation (not shown). In the instance that native α_2M binds noncovalently to a nonprotease substrate, protease interaction is required to enable clearance of the complex via LRP1. (b) Reaction with hypochlorite induces the dissociation of the native α_2M tetramer into dimers. This process abolishes the protease-trapping activity of α_2M ; however, the binding to some cytokines (i.e., TNF- α , IL-2, and IL-6) and misfolded proteins is enhanced. On the other hand, the binding of α_2M to other noncovalent ligands (i.e., β -NGF, PDGF-BB, TGF- β 1, and TGF- β 2) is reduced. The dissociation of the native α_2M tetramer into dimers reveals the binding site on α_2M for LRP1. Therefore, α_2M dimers can facilitate the clearance of substrates in a protease-independent manner. N.B.: Inflammatory processes potentially elevate levels of protease-transformed α_2M and hypochlorite-modified α_2M dimers, concomitantly.

pathways via alternative mechanisms. For example, the binding of α_2M to phosphorylated insulin-like growth factor binding protein-1 abrogates its inhibitory effects on insulin-like growth factor-1 (IGF-1); therefore, in some scenarios, α_2M can potentiate growth factor signalling [13]. Another example whereby α_2M is reported to potentiate growth factor signalling involves the pronerve growth factor (pro-NGF), which induces the expression of TNF- α via stimulating the neurotrophin receptor p75 [11]. Although α_2M potentiates pro-NGF signalling *in vitro*, α_2M is reported to inhibit the activity of mature NGF by binding either to NGF or to Trk receptors [12, 23, 24].

The accumulation of misfolded proteins is inherently deleterious to living organisms and underlies the pathology of many human diseases including Alzheimer's disease,

Parkinson's disease, and motor neuron disease. α_2M is one of a small number of secreted proteins that are known to possess holdase-type chaperone activity, which is the ability to stabilise misfolded proteins and prevent their aberrant aggregation [16–20, 25]. The chaperone function of α_2M has been demonstrated *in vitro* using a broad range of misfolded clients including denatured globular proteins and aggregation prone, intrinsically disordered substrates (e.g., A β peptide and Parkinson's disease-associated alpha-synuclein). Furthermore, it has been shown that α_2M preferentially binds several plasma proteins *in situ* following experimentally-induced shear stress which causes plasma protein aggregation [18, 19]. The likely fate for complexes formed between native α_2M and misfolded proteins is clearance via LRP1 following interaction with a

protease [16, 22, 25–27] (Figure 1(a)). However, protease-transformed $\alpha_2\text{M}$ can also inhibit $\text{A}\beta$ aggregation via degrading the peptide because trapped proteases remain active following covalent binding to $\alpha_2\text{M}$ [18, 19]. The neuroprotective activity of $\alpha_2\text{M}$ against the toxicity induced by misfolded proteins has been demonstrated using several *in vitro* models [17, 25, 27, 28] and has also been demonstrated in rats directly injected with toxic $\text{A}\beta$ oligomers [29]. Taken together, the results of these studies support the conclusion that the functions of $\alpha_2\text{M}$ are broadly important to extracellular proteostasis.

2. $\alpha_2\text{M}$ and Neurodegenerative Diseases

Interest in the role of $\alpha_2\text{M}$ in Alzheimer's disease spans several decades. In part, this stems from early reports that polymorphisms in $\alpha_2\text{M}$ are associated with increased risk of Alzheimer's disease in some populations [30–36]. However, opposing results have also been presented [37, 38], and more recent genome-wide association studies have not found any association [39]. It has recently been reported that serum $\alpha_2\text{M}$ is elevated in men with preclinical Alzheimer's disease, which potentially represents a general response to neuronal injury [40]. The significance of elevated levels of $\alpha_2\text{M}$ is hard to determine, because aside from influencing $\text{A}\beta$ aggregation and clearance, there are many other relevant biological processes that $\alpha_2\text{M}$ potentially influences. For example, apolipoprotein E (ApoE) is an endogenous ligand of $\alpha_2\text{M}$ in blood plasma, and the binding of $\alpha_2\text{M}$ to the $\epsilon 4$ isoform (the strongest known genetic risk factor for Alzheimer's disease) is much less compared to the binding of $\alpha_2\text{M}$ to the $\epsilon 2$ and $\epsilon 3$ ApoE isoforms [15]. The functional importance of this interaction has yet to be solved.

There is strong evidence that native $\alpha_2\text{M}$ can inhibit the aggregation and toxicity of $\text{A}\beta$ peptide (the major constituent of extracellular plaques in Alzheimer's disease). Furthermore, the widely documented ability of $\alpha_2\text{M}$ to facilitate the clearance of the $\text{A}\beta$ peptide is central to its neuroprotective action [17, 25, 27–29]. $\alpha_2\text{M}$ is found colocalised with the $\text{A}\beta$ peptide in the brain in Alzheimer's disease [41, 42], which supports the idea that the LRP1-mediated clearance of $\alpha_2\text{M}$ - $\text{A}\beta$ complexes is impaired or overwhelmed. Similar to $\alpha_2\text{M}$, there are conflicting reports regarding an association between polymorphisms in LRP1 and the risk of Alzheimer's disease (reviewed in [43]). Given that the accumulation of the $\text{A}\beta$ peptide in the brain in Alzheimer's disease appears to be the result of a defect in clearance, rather than elevated production of the peptide [44], it is important to understand the contribution of $\alpha_2\text{M}$ to the clearance of the $\text{A}\beta$ peptide in greater detail.

Roles for $\alpha_2\text{M}$ in preventing or promoting neurodegeneration independent of Alzheimer's disease are less clear. Nevertheless, $\alpha_2\text{M}$ is reported to bind to a broad range of misfolded proteins including the infectious prion protein that is responsible for transmissible spongiform encephalopathies [45] and α -synuclein, the major constituent of misfolded protein deposits in Parkinson's disease [17]. In the case of the prion protein, it has been reported that binding to $\alpha_2\text{M}$ *in vitro* facilitates the conformational change in the

prion protein that is responsible for its infectious characteristics [45]. On the other hand, similar to the protective effect of $\alpha_2\text{M}$ on $\text{A}\beta$ toxicity, the binding of $\alpha_2\text{M}$ to α -synuclein is cytoprotective [17]. $\alpha_2\text{M}$ also potentially inhibits neurodegeneration by influencing the activity of neurotrophins such as NGF and pro-NGF or by inhibiting the activity of neurotrophin receptors directly [12, 23, 24]. The latter could have relevance in a range of neurodegenerative diseases including Alzheimer's disease, Parkinson's disease, and Huntington's disease in which aberrant neurotrophin signalling is implicated [46]. Moreover, the ability of $\alpha_2\text{M}$ to bind to proinflammatory mediators such as $\text{TNF-}\alpha$, IL-6, and IL-1 β [47–49] supports the idea that $\alpha_2\text{M}$ has generalised importance in controlling inflammatory processes including in the central nervous system.

3. Hypochlorite, a Novel Regulator of $\alpha_2\text{M}$ Functions

Hypochlorite (OCl^-) is a powerful oxidant that is produced by the action of the enzyme myeloperoxidase during inflammation. Myeloperoxidase is not detected in the brains of healthy individuals; however, in neuroinflammatory disorders, myeloperoxidase is generated by activated microglia and astrocytes [50–54]. Infiltrating monocytes/macrophages and neutrophils can also contribute to myeloperoxidase production in the brain [50, 55]. Although the reasons for this are unclear, myeloperoxidase-immunoreactivity is also detected in neurons in Alzheimer's disease [50, 51]. Interestingly, in a mouse model of Parkinson's disease, ablation of the myeloperoxidase gene is protective, which supports the conclusion that myeloperoxidase is a major contributor to the oxidative damage generated by pathological neuroinflammatory processes [56].

Hypochlorite production is primarily considered important for defence against invading microbes [57]. The effectiveness of hypochlorite as a microbicidal agent is linked to the potency with which hypochlorite damages proteins, inducing their misfolding [58, 59]. Given that reaction with hypochlorite is not specific to molecules of microbial origin, the generation of hypochlorite is associated with collateral damage to the host organism. As a result of aberrant inflammatory activity, hypochlorite-modified proteins accumulate in a large number of pathologies including Alzheimer's disease [51], atherosclerosis [60], kidney disease [61], rheumatoid arthritis [52] and in experimental animal models of Parkinson's disease [56] and multiple sclerosis [62]. Hypochlorite-induced modification can directly cause proteins to adopt immunostimulatory and cytotoxic properties. For example, hypochlorite-induced modification of apolipoprotein B-100, the major protein component of low-density lipoprotein particles, promotes macrophage foam cell formation and triggers platelet aggregation [63]. Additionally, hypochlorite-modified albumin is known to promote proinflammatory signalling [64], endothelial cell dysfunction [65], and apoptosis [66].

It is well-known that antioxidants are the first line of defence that protects the host from excessive oxidative damage during inflammation. However, evidence has emerged

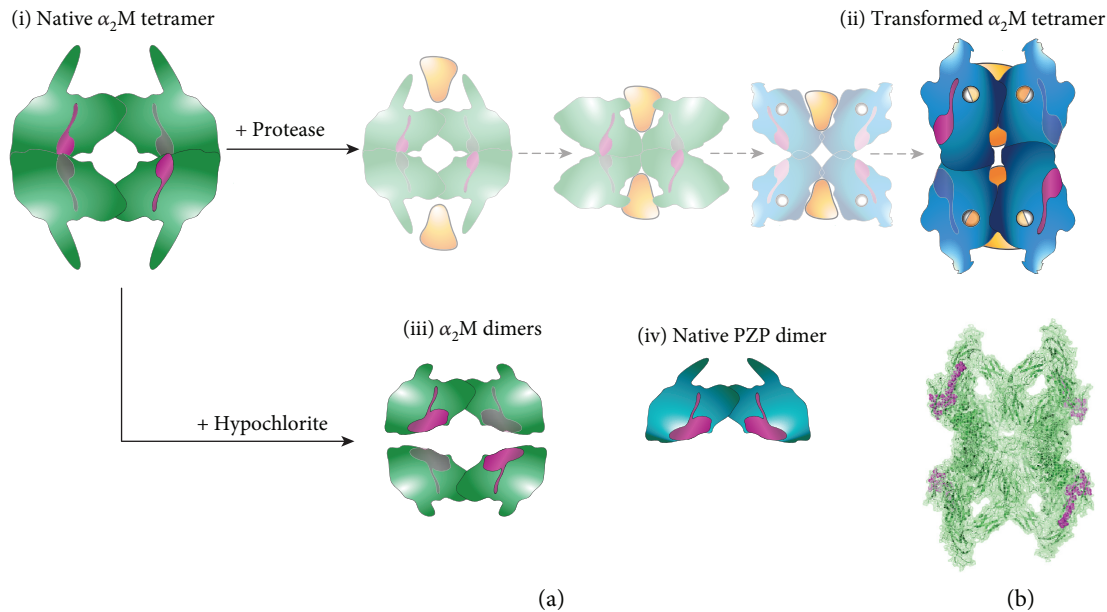


FIGURE 2: Theoretical model showing the binding sites for monomeric $A\beta$ on native α_2M and PZP. (a) The binding sites for monomeric $A\beta$ (magenta; centred at amino acids 1314–1365 according to [21]) are normally concealed at the noncovalent interface of the (i) native α_2M tetramer. (ii) Binding to proteases (yellow triangles) results in the partial opening of the noncovalent interface between α_2M dimers and exposes the binding sites for monomeric $A\beta$ on each subunit of transformed α_2M . (iii) The binding sites for monomeric $A\beta$ are also exposed by hypochlorite-induced dissociation of the native α_2M tetramer into dimers. (iv) Native PZP (a disulfide-linked dimer) shares 82.7% sequence identity with α_2M in the $A\beta$ binding region (magenta). The dimeric quaternary structure of native PZP results in surface exposure of the binding sites for monomeric $A\beta$. Although the binding sites for other misfolded proteins are not known, intuitively, they are also located at the normally buried hydrophobic interface of noncovalently associated α_2M dimers. (b) Image of the crystal structure of the transformed α_2M tetramer from PBD 4ACQ [3] with the binding sites for monomeric $A\beta$ shown in magenta, which is comparable to the model shown in (a (ii)). The crystal structures of native α_2M or hypochlorite-modified α_2M dimers have not been solved.

that supports the conclusion that specialised hypochlorite-inducible systems are also important. Around a decade ago, it was demonstrated that the activity of the bacterial chaperone Hsp33 is directly enhanced following reaction with hypochlorite and the chaperone activity of hypochlorite-modified Hsp33 protects bacteria from hypochlorite-induced death [59]. More recently, it has been demonstrated that reaction with hypochlorite induces the dissociation of the native α_2M tetramer into dimers that have dramatically enhanced chaperone activity compared to the native α_2M tetramer [25] (Figure 1(b)). The mechanism responsible for the enhanced chaperone activity of hypochlorite-modified α_2M dimers involves the exposure of the normally buried hydrophobic surfaces that are situated at the interface of noncovalently-associated dimers in the native α_2M tetramer [25] (Figure 2). It has been reported that methionine oxidation is largely responsible for the hypochlorite-induced dissociation of α_2M into dimers [67]; however, aromatic amino acids are also modified by physiologically relevant levels of hypochlorite [25, 68, 69]. The results of biophysical analyses show that physiologically-relevant levels of hypochlorite also alter the secondary structure of α_2M subunits [25, 68]. Precisely how hypochlorite-induced modification of the secondary structure of α_2M influences its functions is not known.

During inflammation, extracellular protease activity and the generation of hypochlorite are both elevated; therefore, it is plausible that protease-transformed α_2M

and hypochlorite-induced α_2M dimers are concomitantly generated *in vivo*. Hypochlorite-induced modification of native α_2M exposes its LRP1 binding sites ([25, 70]); therefore, during inflammation, α_2M and its cargoes are potentially cleared via two distinct mechanisms involving LRP1 (Figure 1(a): protease-transformed α_2M and Figure 1(b): hypochlorite-induced α_2M dimers). The dissociation constant for the binding of hypochlorite-modified α_2M to LRP1 is reportedly ~ 0.7 nM [70] compared to 40 pM–2 nM for the transformed α_2M [71]. Unlike native α_2M , reaction with hypochlorite does not induce transformed α_2M (generated using methylamine) to dissociate into dimers, and the resultant hypochlorite-induced damage reduces the binding of transformed α_2M to LRP1 [70]. Therefore, during inflammation, the generation of hypochlorite potentially enhances the delivery of hypochlorite-modified α_2M dimers that are generated from the native α_2M tetramer to LRP1, while impeding the delivery of transformed α_2M to the same receptor.

Although the chaperone activity of native α_2M is enhanced following hypochlorite-induced modification, similar levels of hypochlorite-induced modification abolish the protease trapping function of α_2M [72, 73]. Collectively, the evidence suggests that reaction with hypochlorite is a rapid switch that regulates the activities of α_2M during inflammation. Supporting this idea, it has been reported that hypochlorite-induced modification of α_2M also regulates its binding to cytokines and growth factors in a manner that increases its binding to TNF- α , IL-2, and IL-6 (involving

preferential binding to hypochlorite-induced α_2 M dimers) and decreases its binding to β -NGF, PDGF-BB, TGF- β 1, and TGF- β 2 *in vitro* [74] (Figure 1(b)). Furthermore, hypochlorite-induced dissociation of α_2 M enhances its cytoprotective effect against TNF- α *in vitro* [74]. Interestingly, it has been reported that the complement system, which includes several proteins that are closely related to α_2 M, is also activated by reaction with hypochlorite [75, 76]. Therefore, it is tempting to speculate that hypochlorite-induced regulation is a characteristic that is shared by this family of proteins.

Studies of the hypochlorite-induced regulation of α_2 M are currently limited to *in vitro* systems; however, using the specific marker for reaction with hypochlorite 3-chlorotyrosine, it has been shown that α_2 M is modified by hypochlorite in synovial fluid from inflamed joints [69]. Moreover, considering that hypochlorite levels are predicted to reach the low millimolar range in tissues during inflammation [77], it is plausible that hypochlorite-modified α_2 M dimers are generated in biological fluids during inflammation. Of the studies reporting an association between mutation in α_2 M and risk of Alzheimer's disease, one study has reported that there is a synergistic effect between polymorphisms in α_2 M and myeloperoxidase and an increased risk of Alzheimer's disease [36]. The results of the latter study support the idea that the functions of these two proteins might interrelate in a way that is important to neurodegeneration. It is not currently known if any of the other identified extracellular chaperones (e.g., clusterin and haptoglobin) might also have their activities regulated by hypochlorite-induced modification, but this is an area worthy of future investigation.

4. PZP, a Dimeric α_2 M-like Molecule

The major structural modification induced by reaction with hypochlorite that is responsible for functionally controlling α_2 M is the dissociation of the native α_2 M tetramer into dimers. Strikingly, many mammals are capable of generating large amounts of a dimeric α_2 M-like protein known as pregnancy zone protein (PZP). In humans, α_2 M and PZP share very high sequence homology in all domains (71% amino acid identity), with the exception of the bait region [4, 78]. As a result, the ability of PZP to inhibit proteases is much more restricted compared to that of α_2 M. Few *in vitro* studies have focused on characterising the functions of PZP; however, it has been proposed that PZP contributes to regulating glycodefin-A (a paracrine mediator in early pregnancy) and TGF- β 2 (important for embryonic development) [12, 79–81]. Consistent with this idea, PZP is usually lowly abundant in biological fluids but is markedly upregulated in pregnancy [82]. On the other hand, glycodefin-A and TGF- β 2 are also ligands for constitutively abundant α_2 M ([12, 79–81]); therefore, the precise importance of PZP as a modulator of these signalling pathways remains unclear. Similarly, several neurotrophins are shared ligands of PZP and α_2 M, but the precise biological importance of these interactions is not known [12]. Pregnancy-independent expression of PZP is widely reported in diseases such as Alzheimer's disease [83, 84], Parkinson's disease [85],

rheumatoid arthritis [86], Behcet's syndrome [87], psoriasis [88, 89], Chagas disease [90], viral infection [91, 92], inflammatory bowel disease [93], and cancers [94, 95]. The latter observations support the idea that the upregulation of PZP could be a general stress response that is related to chronic inflammation. This limits the usefulness of PZP as a diagnostic marker; however, the results of studies of lymphoma and arthritis patients suggest that PZP levels are potentially useful for monitoring disease progression [95, 96].

The ability of native tetrameric α_2 M to inhibit A β aggregation is restricted to binding to soluble A β oligomers formed early during the aggregation pathway [20]. In contrast, transformed α_2 M and hypochlorite-modified α_2 M dimers bind to monomeric A β [21, 25], presumably via the hydrophobic binding site (centred at amino acids 1314–1365) identified by [21] (Figure 2). Intuitively, surface exposure of this site contributes to the efficiency with which hypochlorite-modified α_2 M dimers inhibit A β amyloid formation compared to native α_2 M [25]. Similarly, the results of recent studies show that PZP binds to the monomeric A β peptide and prevents the aggregation of the A β peptide much more efficiently than native α_2 M [97]. Whether or not PZP contributes to the clearance of the A β peptide *in vivo* is currently unknown; however, it has been demonstrated that PZP levels are elevated in women with presymptomatic Alzheimer's disease and PZP is found colocalised with microglia around A β plaques in the brain in Alzheimer's disease [83, 84]. Combined, these observations suggest that PZP is likely to participate in A β homeostasis. Whether or not the role of PZP overlaps with or is discrete from that of α_2 M remains to be determined.

5. Concluding Remarks

α_2 M is a remarkably multifunctional protein that can influence a broad range of biological processes. Direct injection of α_2 M into inflamed joints has been shown to have protective effects in a rodent model of osteoarthritis ([98]); however, the efficacy and safety of this as a human therapy is not yet known. An alternative α_2 M-based anti-inflammatory strategy involves the oral administration of proteases, which is proposed to increase levels of transformed α_2 M in blood plasma [99, 100]. This strategy is clearly limited by the poor bioavailability of orally administered proteases, but this problem could potentially be overcome by the identification of bioavailable small molecule modifiers of α_2 M function.

Growing evidence suggests that hypochlorite-induced dissociation of α_2 M into dimers is a rapid switch that enhances the ability of α_2 M to facilitate the clearance of disease-associated misfolded proteins and proinflammatory cytokines during inflammation. This is potentially a broadly important process that occurs in response to inflammation, including in neurodegenerative disorders in which neuroinflammation is known to be an early event that precedes other pathological changes (reviewed in [101]). A deeper understanding of the physiological relevance of hypochlorite-induced α_2 M dimers has the potential to shed much needed light on the participation of α_2 M in controlling inflammatory processes and extracellular protein homeostasis during neuroinflammation.

Conflicts of Interest

The authors declare that there is no conflict of interest regarding the publication of this paper.

Acknowledgments

JHC is supported by an Australian Institute of Nuclear Science and Engineering (AINSE) postdoctoral award and an Australian Postgraduate Award (Commonwealth Government of Australia). This work was also supported by funding from the Australian Research Council (DP160100011 awarded to MRW), the National Health and Medical Research Council of Australia (APP1099991; awarded to ARW), and the Flinders Foundation (awarded to ARW).

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