

Advances in Amyloid- β Clearance in the Brain and Periphery: Implications for Neurodegenerative Diseases

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This review examines the role of impaired amyloid- β clearance in the accumulation of amyloid- β in the brain and the periphery, which is closely associated with Alzheimer's disease (AD) and cerebral amyloid angiopathy (CAA). The molecular mechanism underlying amyloid- β accumulation is largely unknown, but recent evidence suggests that impaired amyloid- β clearance plays a critical role in its accumulation. The review provides an overview of recent research and proposes strategies for efficient amyloid- β clearance in both the brain and periphery. The clearance of amyloid- β can occur through enzymatic or non-enzymatic pathways in the brain, including neuronal and glial cells, blood-brain barrier, interstitial fluid bulk flow, perivascular drainage, and cerebrospinal fluid absorption-mediated pathways. In the periphery, various mechanisms, including peripheral organs, immunomodulation/immune cells, enzymes, amyloid- β -binding proteins, and amyloid- β -binding cells, are involved in amyloid- β clearance. Although recent findings have shed light on amyloid- β clearance in both regions, opportunities remain in areas where limited data is available. Therefore, future strategies that enhance amyloid- β clearance in the brain and/or periphery, either through central or peripheral clearance approaches or in combination, are highly encouraged. These strategies will provide new insight into the disease pathogenesis at the molecular level and explore new targets for inhibiting amyloid- β deposition, which is central to the pathogenesis of sporadic AD (amyloid- β in parenchyma) and CAA (amyloid- β in blood vessels).

Key words: Amyloid- β clearance, Brain and periphery, Alzheimer's disease (AD), Cerebral amyloid angiopathy (CAA)

AMYLOID- β : A PEPTIDE INVOLVED IN TWO PATHOLOGIES - ALZHEIMER'S DISEASE (AD) AND CEREBRAL AMYLOID ANGIOPATHY (CAA)

Amyloid- β is generated during neuronal activity by the amyloid precursor protein (APP), a transmembrane protein [1, 2]. In non-pathological conditions, APP is first cleaved by α -secretase, preventing the formation of amyloid- β , and the subsequent carboxy-terminal fragment is then cleaved by γ -secretase [3], resulting in

non-aggregating products [4]. However, under pathological conditions, APP is first cleaved by β -secretase instead of α -secretase, and the subsequent γ -secretase cleavage results in the formation of soluble, monomeric amyloid- β . The most commonly reported soluble monomeric isoforms of amyloid- β are amyloid- β_{1-38} (<20%), amyloid- β_{1-40} (<80%), and amyloid- β_{1-42} (10%) [5, 6]. Amyloid- β_{1-40} is more likely to be deposited in the vascular walls, as seen in Cerebral amyloid angiopathy (CAA) [7], whereas amyloid- β_{1-38} is less likely to aggregate in either the vessel walls or the brain [8, 9]. Amyloid- β_{1-42} , with two extra amino acids, is more hydrophobic than amyloid- β_{1-40} , making it prone to forming insoluble aggregates that lead to plaque formation [10, 11]. These plaques differ in location, composition, and distribution. CAA plaques are perivascular and composed of amyloid- β_{1-40} , while parenchymal plaques are diffuse and composed of amyloid- β_{1-42} . CAA plaques increase

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the risk of hemorrhage, while parenchymal plaques contribute to cognitive decline in Alzheimer's disease (AD). Understanding these differences is essential for effective treatment strategies. These distinct plaque formations are considered major characteristics of AD and CAA, respectively [12, 13].

Amyloid- β in AD: risk factors and genetics

AD is a slowly progressive neurological disorder that poses significant health-care challenges in the twenty-first century [14, 15]. This disease is characterized by a range of symptoms, including memory loss, cognitive decline, personality changes, and impaired daily functioning. These symptoms are associated with the accumulation of extracellular amyloid- β (diffuse or insoluble plaques) and intraneuronal neurofibrillary tangles, which can trigger processes like necroptosis and ferroptosis, as well as neuroinflammation [16-18] (Fig. 1). Amyloid- β_{1-42} is the main component of amyloid plaques in AD brains, while amyloid- β_{1-40} is the main component of vascular amyloid deposits found in CAA

[19, 20]. The risk factors for developing AD include aging, sex, low educational and occupational status, low mental and physical activity, cardiovascular risk factors, hyperhomocysteinemia, smoking, obesity, and diabetes mellitus [19, 21]. Additionally, a typical hereditary risk factor for AD is apolipoprotein E (ApoE) gene mutation [22]. While sporadic AD, which is commonly referred to as late-onset AD, is seen in people over the age of 65 [23] and was previously thought to have no clear genetic component, recent Genome-Wide Association Studies have identified several genetic risk factors that are associated with the disease [24]. In contrast, early-onset familial AD, which affects those under the age of 65 [23], is caused by mutations in the presenilin-1 and 2 (PS1/PS2) and APP genes [25, 26]. The most common amyloid- β mutations that cause familial AD include English (H6R), A2V (A2V), Tottori (D7N), K16N (K16N), Osaka (E22 Δ), Flemish (A21G), Italian (E22K), Arctic (E22G), Dutch (E22Q), Iowa (D23N), Swedish (KM670/671NL), Piedmont (L34V), and Indiana (V717F) [27, 28]. The familial forms of AD are mostly noticeable by increased

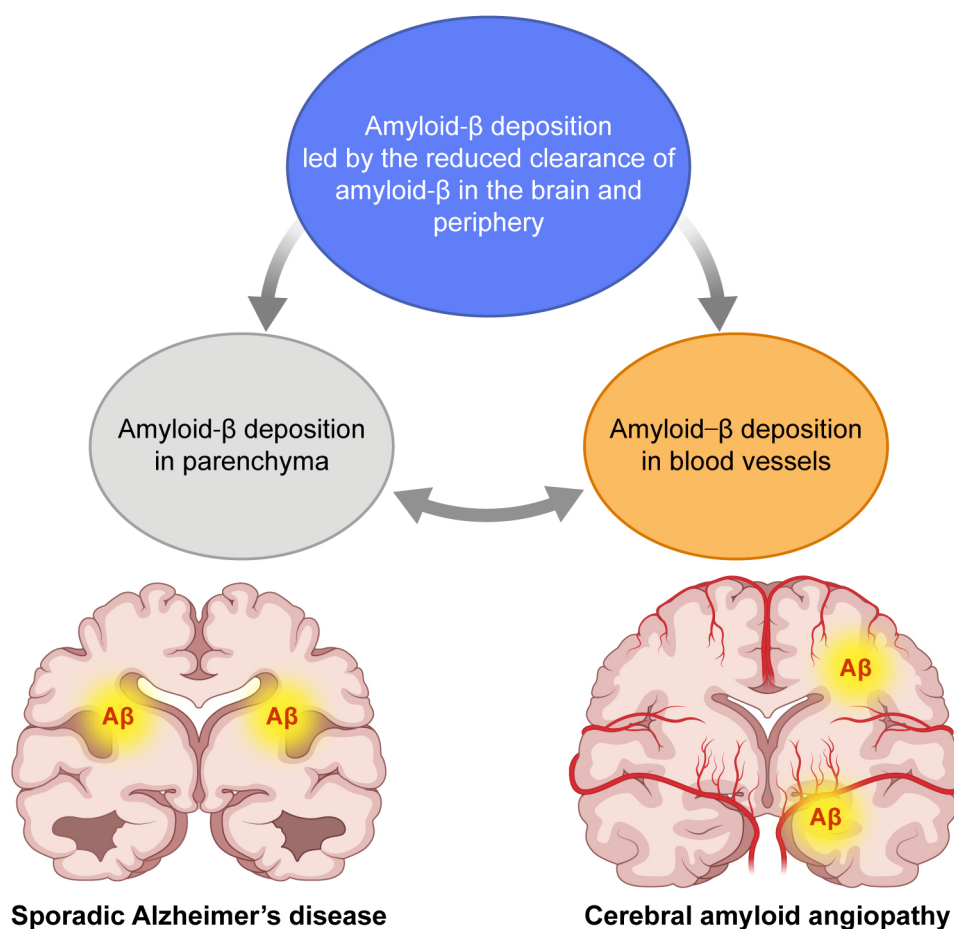


Fig. 1. Reduced clearance of amyloid- β in brain resulting in sporadic AD (amyloid- β deposition in parenchyma) and CAA (amyloid- β deposition in blood vessels).

kinetics of amyloid- β aggregation [27], which results in an early age of onset. Similarly, multiple mutations in amyloid- β sequence and other aggregation-prone proteins (ABri and Adan) are especially linked to early-onset aggressive forms of CAA and related to dementia with cerebral hemorrhage [19, 29].

Amyloid- β in CAA: risk factors and genetics

The main characteristic of CAA is the deposition of amyloid- β in the tunica media and adventitia of the arterioles and/or capillaries in the cerebral cortex and leptomeninges (Fig. 1) [30]. Amyloid- β_{1-40} is typically deposited in the vascular wall of CAA, while amyloid- β_{1-42} is primarily deposited in the senile plaques of AD. Depending on whether amyloid- β is present on cortical capillaries, sporadic CAA is divided into type 1 and type 2: CAA-type 1 is defined as the deposition of amyloid- β on cortical capillaries, but CAA-type 2 is not related with amyloid- β in the cortical capillaries [31]. Hereditary CAA is caused by Dutch, Arctic, Italian, Flemish, Iowa, Piedmont mutations in APP gene, Icelandic mutation in CST3 gene, and the British and Danish mutations in the ITM2B gene [19, 32]. CAA is recognized as a significant risk factor for “white matter hyperintensities” [33], and it occurs in 98% of AD patients, with roughly 75% of these cases categorized as severe CAA [34]. Furthermore, CAA is present in approximately 30% of non-demented elderly [34] and clinical studies have demonstrated a significant association between CAA and cognitive dysfunction [35, 36]. CAA is also closely linked to cerebral hemorrhage and weakens vascular walls as a result of amyloid deposits. Specific point mutations within the amyloid- β have been found including Iowa-type (D23N) and Dutch-type (E22Q), which cause familial forms of CAA [36].

The series of pathophysiological events that promote amyloid- β buildup in the brain and blood vessels are still not completely understood [37]. However, pathological, genetic, and functional studies suggest that the pathologies in both AD and CAA are driven by impaired amyloid- β clearance [12, 38]. Therefore, a deep understanding of amyloid- β clearance could lead to effective approaches to reduce excessive amyloid- β buildup in the brain and slow the progression of both AD and CAA [6, 39]. This review will focus on recent findings of amyloid- β clearance system in the body and try to explore potential interventional targets for future prevention and treatment of AD and CAA.

AMYLOID- β CLEARANCE IN THE BRAIN

The brain employs multiple mechanisms for amyloid- β clearance, which include both enzymatic and non-enzymatic pathways [40]. Recent studies have highlighted the potential therapeutic

benefits of targeting amyloid- β -degrading enzymes (A β DEs) in reducing amyloid- β pathology. Modulating the expression or activity of A β DE has been found to effectively regulate levels of amyloid- β and improve cognitive deficits in transgenic animal models [41, 42]. In parallel to the enzymatic pathway described later, the non-enzymatic clearance pathway of amyloid- β involves the active participation of glial cells (microglia and astrocytes), the blood-brain barrier, interstitial fluid bulk flow (perivascular drainage and the glymphatic system), and cerebrospinal fluid absorption clearance [40]. Disturbances in any of these clearance pathways can significantly contribute to the accumulation of amyloid- β in the brain. In this section, we will address recent progresses in both enzymatic and non-enzymatic mechanisms of amyloid- β clearance in the brain and explore the factors that contribute to the disruption of these pathways.

The role of enzymes in clearing amyloid- β in the brain

In the brain, both intracellular and extracellular amyloid- β are primarily degraded and cleared through the proteolytic machinery [40, 43]. To date, researchers have identified multiple amyloid- β -degrading proteases (A β DPs), numbering around 20 [44, 45]. These enzymes have an affinity for certain domains of the amyloid- β amino acid sequence, enabling them to cleave and convert amyloid- β proteins into shorter, less toxic forms [46-48]. The different categories of A β DPs include zinc metalloendopeptidase, thiol-dependent metalloendopeptidase, serine/cysteine proteases and matrix metalloproteinases and others as shown below (Fig. 2).

Zinc metalloendopeptidase

The majority of A β DPs currently recognized are zinc metalloproteases possessing the zinc-binding motif, and they can be categorized into the following groups [49].

Nephrilysin

Nephrilysin (NEP) is a plasma membrane glycoprotein belonging to the neutral zinc metalloendopeptidase family. It is also referred to as neutral endopeptidase-24.11, enkephalinase, common acute lymphoblastic leukemia antigen, or neutrophil antigen cluster differentiation antigen 10 (CD10) [50]. NEP is a major A β DP that can cleave both monomeric and oligomeric forms of amyloid- β in the brain and periphery [41, 51]. Its expression is found in vascular smooth muscle cells and pyramidal neurons in the cerebral vasculature and neocortex of the brain [52]. Several lines of evidence suggest that NEP plays a role in the pathology of AD and CAA [53, 54], indicating an inverse relationship between NEP activity and brain amyloid- β levels [55]. NEP deficiency caused by genetic factors results in abnormal amyloid- β accumulation in the brain [56,

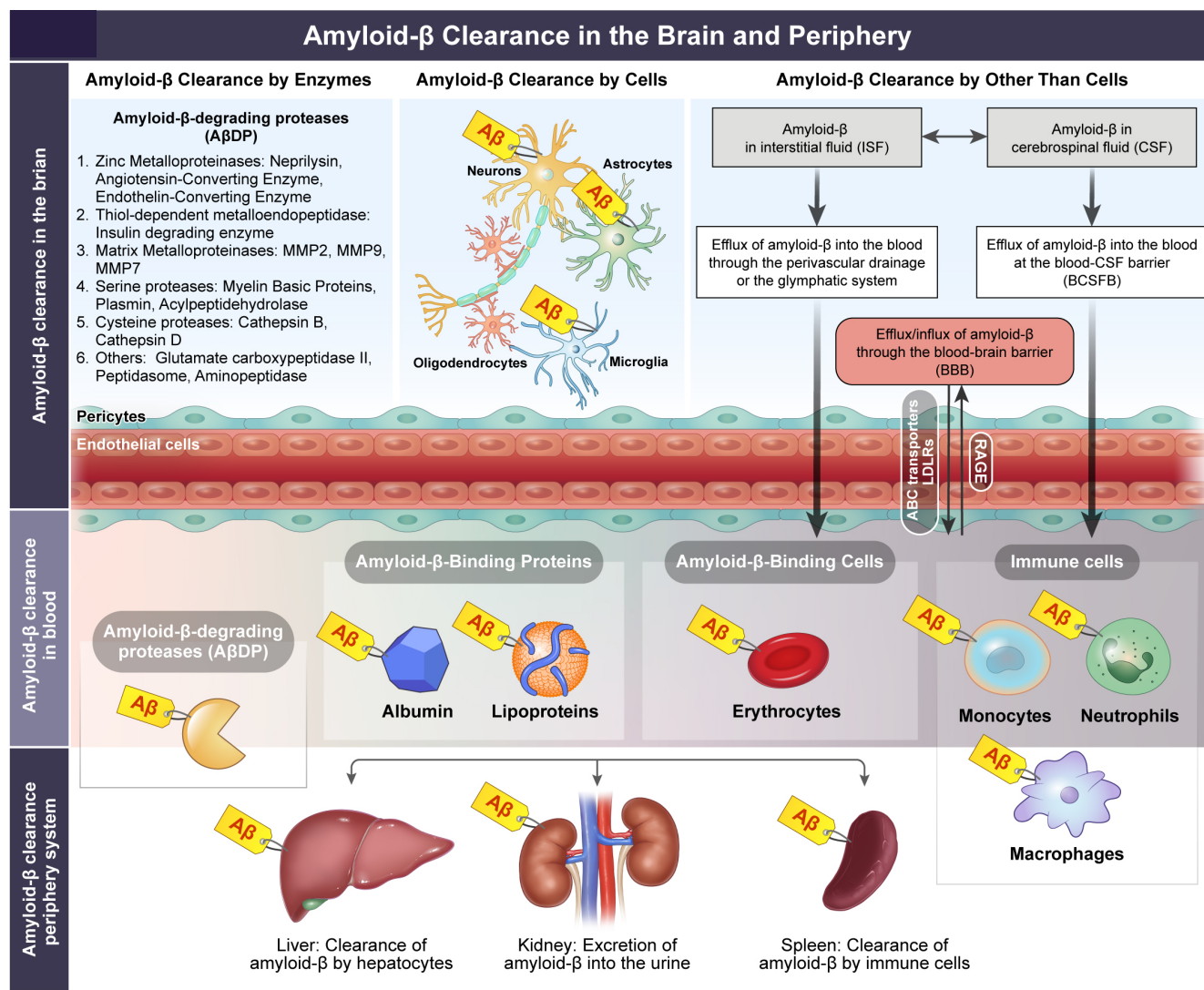


Fig. 2. Clearance mechanisms for amyloid- β in the brain and periphery. Central Clearance of amyloid- β in the brain. In the brain, amyloid- β clearance occurs through (1) enzymatic and (2) non-enzymatic pathways. Enzymatic clearance involves multiple amyloid- β -degrading enzymes (A β DPs) such as (i) zinc metalloendopeptidase, (ii) thiol-dependent metalloendopeptidase, (iii) serine protease, (iv) cysteine protease, and (v) matrix metalloproteinase. Non-enzymatic clearance mechanisms include clearance through (1) BBB, (2) cellular-mediated clearance involving (i) neurons, (ii) microglia, (iii) astrocytes, (iv) endothelial cells and (v) pericytes. (3) interstitial fluid (ISF) bulk-flow-mediated clearance through the perivascular drainage or the glymphatic pathway and (4) cerebrospinal fluid (CSF)-mediated clearance, which involves absorption into the circulatory system or the lymphatic system. Peripheral clearance of amyloid- β in blood or peripheral organs. In blood, amyloid- β is degraded or cleared by proteases, A β DPs, blood cells such as monocytes or neutrophils, or transported by carriers such as erythrocytes, albumin, and lipoproteins to peripheral organs, where it is degraded by macrophages in the spleen or hepatocytes or excreted via the liver or kidney. Abbreviations: BBB, blood-brain barrier; RAGE, advanced glycosylation end product specific receptor; CSF, cerebrospinal fluid; LRP1, Low density lipoprotein receptor-related protein 1, ISF, interstitial fluid; ABC transporters, ATP-binding cassette transporter; BCSFB, blood-CSF barrier.

57]. Conversely, increasing NEP expression and activity by direct injection [58] or overexpression in the brain or peripheral tissues [59-62] can significantly reduce amyloid- β burden and improve cognitive impairment [41, 63, 64].

Recent studies have also confirmed a correlation between NEP and amyloid- β degradation/clearance in AD and CAA [54, 65-67]. NEP has been found to metabolize not only amyloid- β_{1-40} and

a partial structure of amyloid- β (amyloid- β_{1-16}) but also a peptide segment generated by the breakdown of amyloid- β_{1-40} by insulin-degrading enzyme (IDE) [68]. Additionally, loading NEP into collagen hydrogels as a vehicle and delivering intranasally has been shown to clear plaques in a transgenic mouse model [69]. Together with the latest findings, it is evident that NEP is crucial for amyloid- β clearance, and its dysfunction significantly contributes

to amyloid- β accumulation in the body.

Angiotensin-converting enzyme

Angiotensin-converting enzyme (ACE; peptidyl-dipeptidase A; EC 3.4.1.5.1) is a widely expressed zinc metalloprotease in the body, including human brains where it is found in pyramidal neurons in the cortex and cerebral vasculature [70]. Several genetic, biochemical and cell biology studies have supported the idea that ACE plays an essential role in regulating amyloid- β metabolism [71, 72]. *In vitro* studies have demonstrated that ACE can cleave amyloid- β between Asp7 and Ser8, leading to inhibition of aggregation, deposition, fibril formation, and associated cytotoxicity of amyloid- β [47, 73, 74]. However, the effects of ACE on steady-state amyloid- β concentration in animals studies remain inconclusive. Although ACE-deficient mice and mice treated with ACE inhibitors did not consistently show changes [71, 75], there is a report that the treatment of transgenic mice with captopril, another ACE inhibitor, promotes amyloid- β_{1-42} deposition in the brain [76]. Overall, the effects of ACE on amyloid- β metabolism in animal studies are not fully understood [70].

More recently, molecular modelling and mass spectrometry studies have provided additional evidence of a strong interaction between ACE or N-domain of ACE and amyloid- β accumulation in the brain [77, 78]. Rocha et al. found a positive correlation between ACE levels and amyloid- β in AD patients, supporting the idea that ACE is linked to amyloid- β pathology [79].

The findings derived from both *in vitro* and *in vivo* studies reveal significant inconsistencies, presenting considerable challenges in scientific research. These discrepancies can be attributed, in part, to variations in the methods employed to measure ACE and the unique characteristics of the samples tested. Additionally, it is plausible that compensatory mechanisms involving other amyloid- β degrading enzymes, such as neprilysin, insulin-degrading enzyme, and endothelin-converting enzyme, may offset the observed acute reduction in ACE activity *in vivo*. Furthermore, insights gleaned from genetic studies may help elucidate the disparities surrounding ACE activity/levels in amyloid pathology. Notably, a comprehensive meta-analysis has demonstrated a robust correlation between the presence of an insertion (I) polymorphism within intron 16 of ACE and an increased risk of AD, while the deletion (D) variant appears to provide protection [76, 79-81].

Given the current inconsistencies and recent research findings, it is crucial to acknowledge the controversial role of ACE in amyloid- β clearance in the brain. It is strongly recommended to promote future research to address these existing disparities and to gain a clearer understanding of the specific function of ACE in clearing amyloid- β . Such insights could potentially prove valuable

in preventing the buildup of amyloid- β in the brain, which is a characteristic feature of conditions like AD [82] and CAA [83].

Endothelin-converting enzyme

The endothelin-converting enzymes (ECEs) are membrane-bound proteases that belong to M13 zinc metallopeptidases family. They are named after their ability to convert the inactive precursor big endothelin into the potent vasoactive peptide endothelin-1 [84]. Two types of ECE have been identified so far: ECE-1, which is found in both vascular and nonvascular cells in all organs [85], and ECE-2, which is predominantly expressed in the brain and neural tissues, including the cerebral cortex, cerebellum, and adrenal medulla [86]. The expression level and activity of ECE are strongly correlated with amyloid- β deposition and the onset of AD [85, 86]. Importantly, evidence from cultured cells and animal models has shown that amyloid- β is a physiologically significant substrate of ECE [86, 87]. For example, *in vivo* studies of ECE deficient mice (ECE-1 and ECE-2) have shown that both genotypes have higher amyloid- β levels than wild-type mice, indicating that these ECEs are A β DPs *in vivo* [86, 88]. Conversely, overexpression of ECE reduces amyloid- β deposition [87, 88]. *In vitro* studies have also found that ECE can hydrolyze amyloid- β at several sites [89].

In conclusion, the reviewed studies offer compelling evidence supporting the crucial role of ECE as a significant amyloid- β degrading enzyme in preventing the buildup of amyloid- β in the brain. Both *in vitro* and *in vivo* investigations have demonstrated that overexpression of ECE leads to reduced amyloid- β levels, while inhibiting ECE activity results in increased amyloid- β accumulation. These findings underscore the therapeutic potential of targeting ECE to modulate amyloid- β levels and potentially attenuate the progression of disease pathology. Further exploration of ECE and its enzymatic mechanisms holds promise in providing valuable insights into preventing the amyloid- β buildup observed in AD and CAA. By unraveling the intricate workings of ECE, we may unlock new avenues for intervention and contribute to the development of novel treatments aimed at mitigating the impact of amyloid- β pathology.

Thiol-dependent metalloendopeptidase

Thiol-dependent metallo-endopeptidase, also known as Pz-peptidase, endooligopeptidase A, collagenase-like peptidase, soluble metallo-endopeptidase and endopeptidase [90], is expressed in the brain [91] and play a crucial role in the degradation of small peptides, including glucagon, insulin, and atrial natriuretic peptide and amyloid- β [92, 93]. The highly conserved thiol metalloprotease insulin-degrading enzyme (IDE), which is one of the enzymes responsible for removing amyloid- β from the brain, is now con-

sidered a key component in the amyloid- β clearance process [91], as discussed below.

Insulin degrading enzyme (IDE, EC 3.4.24.56), also known as insulinase or insulysin, is a neutral thiol metalloprotease [94] found in several tissues, including skeletal muscle, skin, tongue, and testes [94, 95] and the brain [91, 96]. IDE is evolutionally conserved and developmentally regulated. Its physiological role encompasses several cellular functions as reviewed in Authier et al. [97]. IDE has been particularly well-known for degrading several peptides, including amylin, glucagon, calcitonin and atrial natriuretic peptide, as well as monomeric amyloid- β , which has been demonstrated by both *in vitro* and *in vivo* models [91, 98-101]. Notably, IDE expression levels and activity have been found to exhibit an inverse correlation with amyloid- β burdens in the brain [102, 103]. This finding is significant because hypofunction of IDE has been associated with defective neuronal and microglial regulation of amyloid- β , as well as deficits in memory in AD [104] and CAA [105] patients. Furthermore, genetic deletions of IDE in mouse brains have led to a significant increase in amyloidogenic amyloid- β [102]. Conversely, transgenic overexpression of IDE has been shown to significantly reduce levels of amyloid- β and amyloid plaque formation by over >50% in the brain [96, 106].

Several recent studies have extensively documented the significant role of insulin in amyloid- β clearance in the brain [42, 107, 108]. For instance, a recent study has focused on the catalytic role of IDE mutants (specifically, cysteine-free mutant cf-E111Q-IDE) in amyloid- β proteolysis/degradation, revealing that this mutant is exceptionally effective at breaking down amyloid- β peptides [106]. Additionally, Fu et al. found that microglia secrete IDE to partially degrade amyloid- β , which is inhibited by using a highly selective IDE inhibitor *in vitro* and *in vivo* [109, 110]. Moreover, Yamamoto et al. suggested that increased levels of IDE in the extracellular spaces of astrocytes aid in the degradation of soluble oligomeric and monomeric amyloid- β in the brain [111]. Taken together, these findings provide strong evidence that IDE plays a crucial role in amyloid- β clearance, and that its dysfunction significantly contributes to the accumulation of amyloid- β in the brain.

Matrix metalloproteinases

Matrix metalloproteinases (MMPs) are a family of nine highly homologous Zn²⁺-dependent endopeptidases that are capable of cleaving a wide range of extracellular matrix (ECM) proteins under health and disease conditions [112]. Almost 28 mammalian MMPs have been identified, sub-grouped into soluble matrix MMPs and membrane type MMPs (MT-MMPs) [113, 114]. Multiple MMPs including MMP2 and MMP9 [115, 116], have been reported in the degradation of both monomeric and fibrillar forms

of amyloid- β [115, 117]. Studies have shown a significant increase in amyloid- β levels in the brains of both MMP2 and MMP9 knock-out mice, highlighting the role of MMPs in amyloid- β catabolism [118, 119]. Previous studies have also discussed some special properties of MMPs and their impact on amyloid- β clearance [117]. Firstly, MMPs typically exist in an inactive form known as latent pro-enzymes, which can be activated through proteolytic processing [120]. Interestingly, a protease called extracellular matrix metalloproteinase inducer (EMMPRIN; CD147) has been identified as one of the enzymes responsible for activating MMPs through this mechanism. In cultured cells, EMMPRIN induction has been shown to decrease amyloid- β levels by activating multiple MMPs [121]. Secondly, the basal expression of MMPs is generally low, but it can be enhanced in response to pathological insults, including amyloid- β itself [122]. Supporting this observation, in transgenic mice expressing the amyloid precursor protein (APP), MMPs were found to be up-regulated in astrocytes located near amyloid deposits [119]. Furthermore, when a broad-spectrum MMP inhibitor called GM6001 was infused into the mice's brain ventricles (i.c.v.), it led to significant increases (approximately 50%) in both the steady-state levels and the half-life of interstitial fluid (ISF) amyloid- β [119].

Recent studies have shown a strong association between MMPs and AD [123] or CAA [124]. For example, Taniguchi et al. found that MMP7 is capable of degrading amyloid- β , inhibiting its aggregation and reversing amyloid- β pathology [125]. Additionally, a recent *in vitro* study has demonstrated that inhibiting MMP9 secretion from astroglia reduces the proteolytic clearance/degradation of amyloid- β [126].

In summary, the accumulating body of recent research provides compelling evidence supporting the critical involvement of MMPs in the degradation and clearance of amyloid- β . The activation and up-regulation of MMPs play key roles in amyloid- β metabolism. Notably, inhibiting MMPs leads to elevated amyloid- β levels, underscoring their significance in amyloid- β degradation. Consequently, targeting MMPs emerges as a promising therapeutic strategy for diseases characterized by amyloid- β accumulation, particularly AD and CAA.

Serine proteases

Serine proteinases represent the largest and most abundant class of mammalian proteinases, named as such because their active sites contain a serine residue essential for catalysis. These enzymes play significant roles in extracellular proteolysis, with optimal activity observed under neutral pH conditions [127].

Notable examples of this proteinase class include myelin basic protein (MBP), plasmin, and acylpeptide hydrolase, which will be

further discussed below [40].

Myelin basic proteins

Myelin basic proteins (MBP), comprising roughly 30% of all myelin protein, are crucial structural components of axonal myelin sheaths. MBP is recognized as a “membrane adhesion molecule”, tightly sealing the cytoplasmic components of the cell membrane bilayer in the densely packed myelin sheath [128, 129]. Additionally, similar to other naturally occurring “amyloid- β chaperone molecules (such as ApoE, apolipoprotein J, apolipoprotein A-1, α 1-anti-chymotrypsin, haptoglobin, transthyretin and gangliosides) in the CNS”, MBP also functions as a “novel chaperone”, capable of binding to both wild-type and Dutch/Iowa-type CAA mutant forms of amyloid- β , and therefore, inhibiting amyloid- β fibrillogenesis (with amyloid- β_{1-42} being more fibrillogenic than amyloid- β_{1-40}) in the brain [130, 131]. Detailed ultrastructural analysis revealed that MBP allows the assembly of oligomeric species but prevents their further assembly into fibrillar structures (protofibrils and amyloid fibrils) [130]. Furthermore, further analysis discovered that the N-terminal region of MBP contained the required amyloid- β binding domain, thereby inhibiting its assembly into fibrillar amyloid [132, 133]. Consistent with these findings, recent research indicates that purified MBP exhibits autocleavage activity, generating distinct peptide fragments [134]. Mei-Chen Liao and colleagues have reported that both purified human brain MBP and recombinant human MBP can effectively degrade amyloid- β_{1-40} and amyloid- β_{1-42} peptides. Moreover, MBP expressed in Cos-1 cells has demonstrated the ability to degrade exogenous amyloid- β_{1-40} and amyloid- β_{1-42} peptides. Additionally, purified MBP has been observed to degrade assembled fibrillar amyloid- β in vitro. Impressively, in situ experiments have shown that purified MBP can efficiently degrade parenchymal amyloid plaques and cerebral vascular amyloid in brain tissue obtained from amyloid- β precursor protein transgenic mice [128].

In conclusion, MBP serves as a unique chaperone, exerting inhibitory effects on amyloid- β fibrillogenesis and actively degrading amyloid- β peptides. Despite these compelling findings, our current knowledge regarding the role of MBP in amyloid- β clearance in the brain remains limited. Hence, we strongly encourage future research efforts aimed at unraveling the precise mechanisms underlying MBP-mediated amyloid- β clearance and developing strategies to enhance this process. Such investigations hold the potential to provide a valuable method for preventing the accumulation of amyloid- β in the brain, a phenomenon reported in conditions like AD and CAA. Through continued exploration in this area, we may unlock new insights into potential therapeutic targets and contribute to advancing the understanding and man-

agement of amyloid- β pathology.

Plasmin

Three functionally related serine proteases, including plasmin, urokinase-type plasminogen activator and tissue-type plasminogen activators, have been implicated in amyloid- β degradation [135]. Plasmin is the only one of these proteases that has been shown to directly degrade amyloid- β . Plasmin cleaves and degrades amyloid- β at multiple sites, preventing its aggregation into β -pleated sheets [135-137], which is critical for amyloid- β toxicity [138]. Notably, plasmin can degrade both aggregated and non-aggregated amyloid- β [139]. Several studies have highlighted the role of the plasmin in mediating amyloid- β degradation and preventing/blocking its neurotoxicity [135, 139, 140]. For example, purified plasmin has been shown to significantly decrease neurotoxicity induced by aggregated amyloid- β in neuronal cultured cells [136, 138]. Activation of plasmin has also consistently been shown to degrade amyloid- β , and the level of plasmin is reduced in aged brains [141]. Additionally, a significant correlation has been demonstrated between the proteolytic activity of plasmin and amyloid- β levels, suggesting that enhancing amyloid- β degradation/clearance by an increasing plasmin's proteolytic activity may be a viable therapeutic approach for lowering amyloid- β levels in the brain [135, 142].

Acylpeptidohydrolase

Acylpeptidohydrolase (APH) is a homomeric tetramer, which is a peptidase of approximately 75–80 kDa and belongs to the “prolyl oligopeptidase family”. It is expressed in numerous cells and organs, including the brain, liver, kidney, erythrocytes, and plasma [143, 144]. APH is thought to play a vital role in the catabolism of acetylated proteins and the subsequent removal of acetyl group [145]. Previous studies have suggested that APH is involved in the degradation of amyloid- β in SKNMC-neuroblastoma cells, indicating its importance in this process [143, 144]. *In vitro* studies also demonstrated that APH preferentially degrades monomeric and oligomeric forms of amyloid- β [144]. Interestingly, APH levels have been found to be significantly lower in aged brains compared to controls.

As far as we are aware, there is currently limited available data on the role of acylpeptidohydrolase in amyloid- β clearance within the brain. Consequently, we strongly advocate for future research efforts aimed at unraveling the precise mechanisms by which acylpeptidohydrolase mediates amyloid- β clearance. Such investigations hold the potential to pave the way for the development of strategies to enhance this clearance mechanism. By gaining a deeper understanding of acylpeptidohydrolase-mediated amyloid- β

clearance, we may discover valuable insights that could lead to the identification of novel therapeutic targets. This, in turn, may offer a promising avenue to prevent the accumulation of amyloid- β in the brain, a phenomenon frequently associated with conditions like AD and CAA. Through continued research in this area, we may eventually find innovative approaches to combat amyloid- β pathology and potentially ameliorate the progression of neurodegenerative diseases.

Cysteine proteases

Cathepsin B is a well-known member of cysteine proteases family and can function as either an exopeptidase or an endopeptidase. It is present in lysosomes of all cell types, participating in the degradation of proteins. Studies by Sun et al. [146] demonstrated that cathepsin B is involved in amyloid- β degradation in mice brain. Lysosomal cathepsin B is critical for the clearance of oligomeric amyloid- β peptide in microglia [147] and its upregulation enhances amyloid- β degradation in monocytes [148]. Using molecular modeling, Dhanavade et al. [149] found that cathepsin B is capable of cleaving amyloid- β peptide from the carboxylic end of Glu11. Cathepsin D, another aspartyl protease, is present in the majority of mammalian cells and functions to degrade internalized and endocytosed proteins, including amyloid- β peptide [150]. Monocytes from AD patients have been observed to show down-regulation of cathepsin D [151, 152]. Recently, Suire et al. found that genetic deletion of cathepsin D in mice leads to a significant accumulation of amyloid- β in lysosomes, indicating that extracellular amyloid- β is trafficked to lysosomes and its degradation is dependent on lysosomal A β DPs, such as cathepsin B and D [153-155].

Other miscellaneous enzymes

Glutamate carboxypeptidase II (GCPII) plays a crucial role in the degradation of several amyloid- β species (monomers, oligomers, and fibrils) in the brain. *In vitro* studies have shown that GCPII cleaves both amyloid- β_{1-40} and amyloid- β_{1-42} monomers. Moreover, GCPII not only inhibits the formation/synthesis of amyloid- β oligomers but also cleaves existing amyloid- β oligomers. GCPII is also known to degrade fibrils *in vitro* and reduce the plaque size in brain sections of transgenic mice [156]. Additionally, a mitochondrial amyloid- β -degrading protease called "peptidasome" has been identified and characterized in brain mitochondria, which has been reported to completely degrade amyloid- β [157-159]. Aminopeptidase, a family of enzymes that removes amino acid residues at the N-termini of proteins, has also been shown to contribute to N-terminal truncation of amyloid- β [160]. It efficiently degrades amyloid- β peptides (monomers, oligomers, and fibrils)

to prevent amyloid- β deposition in mammalian brains [161, 162].

The role of non-enzymes in clearing amyloid- β in the brain

Amyloid- β clearance by glial cells

The term "glia" was first coined by Virchow, referring to their ability to form "glue" in brain cells. Different types of glial cells have been recognized for their role in amyloid- β clearance, including astrocyte, microglia and oligodendrocyte [163]. In the human brain, glial cells make up about 50% of all cells [164]. Glial cells such as microglia and astrocytes can uptake amyloid- β and represent an additional functional pathway for amyloid- β degradation in the brain [165, 166].

On the other hand, strong evidence derived from fundamental molecular biology studies has also revealed that aberrant activation of glial cells can play a role in mediating neuroinflammation. This activation leads to the release of inflammatory mediators, such as inflammatory cytokines, complement components, chemokines, and free radicals. These factors collectively contribute to the production and buildup of amyloid- β , ultimately leading to the development of neurodegenerative conditions [167, 168].

The clearance of amyloid- β peptides by glial cells involves different mechanisms as described below.

Amyloid- β clearance by microglia

Microglia, a type of glial cells that make up 10~20% of glia cells in the brain and the spinal cord [169]. They serve as resident macrophages, equipped with numerous pattern recognition receptors that enable them to detect exogenous pathogen-associated molecular patterns (PAMPs) or endogenous danger-associated molecular patterns [109]. Microglia play vital roles in internalization and clearance of amyloid- β in the brain (Fig. 2). They interact with both soluble and fibrillar forms of amyloid- β in different ways. Soluble forms are taken up through macropinocytosis and LDLR (low density lipoprotein receptor)-related proteins mediated pathway, while fibrillar forms of amyloid- β interact with innate immune receptors of microglia, initiating intracellular signaling cascades and stimulating phagocytosis [170]. A wide range of innate immune receptors are involved in microglia-mediated amyloid- β clearance, including scavenger receptors, Toll-like receptors, purinergic G protein-coupled receptors, complement components and their associated receptors, and triggering receptor expressed on myeloid cells [46, 109]. The surface signaling receptor TREM2, found in microglia, can enhance the microglial phagocytosis of amyloid- β when increased expression is triggered by the presence of amyloid- β . However, the R47H mutation present in AD can impede TREM2's ability to recognize lipid ligands effectively,

resulting in failure to activate microglia and ultimately leading to amyloid- β deposition [171–173]. In addition, ATP-binding cassette transporter A7, mainly expressed in human microglial cells, regulates microglial phagocytic function to reduce amyloid- β deposition in the brain [171, 174]. In contrast to receptor-mediated amyloid- β phagocytosis, both receptor-mediated endocytosis (a biochemical and a mechanical process) and receptor-independent fluid-phase pinocytosis is also involved in the uptake and degradation of amyloid- β by microglia [109, 175–177]. Once internalized within cells, microglia rapidly traffic amyloid- β into intracellular degradation systems including autophagy, endosomal/lysosomal degradation, and ubiquitin–proteasome system, which prevent intracellular amyloid- β aggregation and accumulation, thus protecting against amyloid- β -associated neuropathology [46]. Additionally, microglia contribute to amyloid- β clearance by secreting A β DPs that degrade amyloid- β in the extracellular space, reducing its buildup in the brain [178, 179].

Amyloid- β clearance by astrocytes

In addition to microglia, stellate-shaped astrocytes also play a significant role in the metabolic functions of amyloid- β clearance [163, 180] (Fig. 2). Astrogliosis and astrocyte activation, similar to microgliosis, are closely related to amyloid- β pathogenesis [179, 181]. Notably, research has revealed that astrocytes are more proficient than microglia in removing amyloid- β , especially during the initial stages of AD [182, 183]. Mechanistically, both *in vivo* and *in vitro* studies have shown that astrocytes can release proteases, such as NEP, ACE, ECE-2 and MMP9, which aid in amyloid- β clearance in the brain [184, 185]. Additionally, astrocytes secrete kallikrein-related peptidase 7 (KLK7) and MMP membrane type-1 (MT1) [116, 186]. KLK7 protein can cleave amyloid- β within the central hydrophobic core, attenuating fibril formation and promoting the degradation of pre-formed fibrils [187]. The deletion of KLK7 in mouse brains resulted in an increased brain amyloid- β economy, supporting the notion that “KLK7-dependent amyloid- β degradation” activity is physiologically relevant in the catabolism of amyloid- β in brain [186]. Similarly, MT1 expressed in “reactive astrocytes” near amyloid deposits degrades exogenous amyloid- β and fibrillar amyloid- β *in vitro* [116].

Additionally, the endocytic and signaling receptor LRP1, along with its ligand ApoE, is widely recognized for its crucial involvement in the regulation of amyloid- β catabolism and APP processing [188, 189]. Chia-Chen Liu’s study provides compelling evidence for the significant involvement of astrocytic LRP1 in amyloid- β metabolism, as demonstrated in both *in vitro* and *in vivo* models. Deficiency of astrocytic LRP1 leads to impaired clearance of amyloid- β in the interstitial fluid (ISF) and worsened

amyloid- β deposition in the brains of APP/PS1 mice [190].

Astrocytes, among the various cell types in the brain, are also the primary contributors to the production of ApoE, generating the highest amounts of this protein [191]. Specifically, ApoE recycling plays a crucial role in regulating the expression of various cell surface proteins, particularly ABCA1 [192, 193]. The impaired recycling of ApoE4 results in the entrapment of ABCA1 within endosomes, preventing its localization to the cell surface [194]. This disruption in ABCA1 function is associated with decreased ABCA1-mediated cholesterol efflux activity and compromised amyloid- β degradation capacity. Remarkably, the enhancement of ABCA1 activity effectively restores amyloid- β degradation in cells treated with ApoE4 and concurrently reduces the aggregation of both ApoE and ABCA1 in mice’s brains [192, 194]. Furthermore, it is essential to recognize the critical role of the autophagy pathway in cellular homeostasis, facilitating the turnover of cell organelles and promoting the degradation of aggregated proteins in response to cellular stress [195]. A defective clearance of amyloid- β -generating autophagic vacuoles can create conditions favorable for amyloid- β accumulation in the brain, as evidenced by data indicating that increasing autophagy through rapamycin reduces amyloid burden *in vivo* [196]. Additionally, autophagy appears to play a role in the breakdown of amyloid- β by microglia [197], and astrocytes from transgenic AD models have shown strong expression of microtubule-associated protein light chain 3, suggesting the involvement of autophagy in amyloid- β internalization by these cells, providing a link between autophagy and phagocytosis [175, 198].

Consistent with these findings, the process of amyloid- β aggregation and fibrillogenesis initiates a deleterious cascade of events in astrocytes, impacting neuronal viability and functionality [199]. For instance, in an AD mouse model, reactive astrocytes exhibit metabolic and functional changes, resulting in the abnormal production of the neurotransmitter γ -aminobutyric acid (GABA) through the activity of monoamine oxidase B (MAO-B) in the putrescine-degradation pathway [200, 201], thereby contributing to memory impairment [200, 202]. Moreover, MAO-B generates toxic byproducts such as ammonia and H₂O₂ along this pathway, ultimately leading to neurodegeneration [201, 203].

Amyloid- β clearance via the blood-brain barrier

Amyloid- β can cross the blood–brain barrier (BBB) in both directions: from brain to blood (efflux) and from blood to brain (influx) (Fig. 2). The BBB is responsible for catabolizing the majority of amyloid- β (~75%) compared to interstitial fluid (ISF) bulk flow does (~10%, as explained below) [6]. Furthermore, the BBB has the ability to uptake and catabolize not only amyloid- β in the blood

but also amyloid- β that originates from the brain [204].

Receptor-mediated efflux of amyloid- β

Amyloid- β can travel from the brain to blood by (i) ATP-binding cassette transporters (ABC transporters) and (ii) LDLR family members, such as LRP1 [6].

The ABC transporter is one of the most common transmembrane proteins, which can be classified into subfamilies (A to G) based on sequence homology and functional similarity. These ABC transporters use energy generated through ATP hydrolysis to transport substrates across cell membranes and play an essential role in various physiological activities. Recent studies have suggested that ABC transporters are involved in amyloid- β clearance [152]. Among them, two ABC transporters, ABC transporter subfamily B member 1 (ABCB1, an efflux pump for xenobiotic molecules) and ABC transporter subfamily A member 1 (ABCA1 or Cholesterol Efflux Regulatory Protein (CERP), an efflux pump for cholesterol/phospholipids from cell membranes), have received considerable attention for their roles in amyloid- β clearance [205]. ABCB1 is directly involved in the export of amyloid- β into the bloodstream, while ABCA1 indirectly facilitates amyloid- β efflux transfer from the brain to blood via ApoE-dependent mechanisms [206]. It has been suggested that ABCA1 controls protein levels of ApoE and its lipidation state. A highly lipidated ApoE binds to amyloid- β (ApoE-amyloid- β interaction) more efficiently, diminishing its capacity to aggregate and making amyloid- β more accessible for transport at the neurovascular unit [205].

The LDLR family is a highly conserved family of receptors that bind to a wide range of ligands, including amyloid- β [207]. LRP1 is localized to neurons, glial cells, endothelial cells in the BBB, and epithelial cells in the blood-CSF barrier (BCSFB). Studies have shown that LRP1 binds to both amyloid- β_{1-40} and amyloid- β_{1-42} , either alone or in conjugated form with carrier proteins. Once bound, LRP1 can target amyloid- β for cellular degradation or facilitate its transcytosis [208], helping to transport amyloid- β out of the brain [209]. Furthermore, α 2-macroglobulin [210] and LDLR-related protein 2 (LRP2), also known as megalin, in combination with clusterin (ApoJ) can form a complex to regulate amyloid- β clearance across the BBB [6].

Receptor-mediated influx of amyloid- β

RAGE, the receptor for advanced glycation end products, is believed to be involved in the influx of amyloid- β into the CNS [211] (Fig. 2). Fang et al. reported that the RAGE-dependent signaling pathway regulates the cleavage of APP by β - and γ -secretases to generate amyloid- β , at least in part, through the activation of two specific enzymes, GSK3 β and p38 MAP kinase [212]. RAGE is

a multi-ligand receptor that interacts with a variety of ligands, including ^{125}I labeled amyloid- β (monomers, oligomers, and fibrils) [213]. Using an *in vitro* BBB model, Mackic et al. [214] demonstrated that RAGE interacts with amyloid- β followed by its subsequent cellular processing (endocytosis and transcytosis) in the circulation. In addition, recent studies reported that inhibition of RAGE or its interaction with amyloid- β suppresses amyloid- β accumulation in brain parenchyma in mice [215-217]. Ma et al. [218] also showed that upregulation of RAGE in the hippocampus or prefrontal lobe significantly contributed to the amyloid- β accumulation in animal brains [152]. However, more recently, numerous amyloid- β sequestering agents in the periphery (anti-amyloid- β IgG, serum amyloid P component, and soluble forms of both RAGE (sRAGE) and LRP1 (sLRP1)) are reported to inhibit its interaction with RAGE and therefore inhibit amyloid- β from entering the brain [6, 210, 219, 220].

Amyloid- β clearance via the interstitial fluid bulk flow

The brain and spinal cord contain two extracellular fluids, cerebrospinal fluid (CSF) and interstitial fluid (ISF) [70]. Previous studies have shown that CSF enters the interstitial space in the brain and exchanges or mixes with ISF. This suggests that proteins in ISF may also be transferred or cleared directly into the CSF via ISF bulk flow [221]. In fact, ISF bulk flow can remove proteins, such as amyloid- β from the interstitium via two possible pathways: (i) into the perivascular space or (ii) into the glymphatic system, as discussed below [70, 222].

Perivascular drainage

Previous animal studies have shown that perivascular routes are crucial for the clearance of amyloid- β from the brain (Fig. 2). A failure of this drainage pathway can cause amyloid- β to become trapped in the cerebral cortex and the walls of blood vessels [223], leading to the development of AD [70, 224] and CAA [70]. The lymphatic system serves as a secondary circulation system and closely resembles the blood-vascular system [222]. ISF bulk flow provides an effective clearance route for ISF-containing amyloid- β in the brain and cerebral vessels [70, 225], mostly consisting of perivascular drainage and glymphatic clearance. In perivascular drainage pathway, amyloid- β is eliminated from extracellular spaces by first entering into the capillary spaces before it drains along the walls of arteries in human brain [223]. Notably, if the direct entry of amyloid- β into the blood is either prevented or fails, this perivascular drainage becomes apparent [70] or when the level of NEP enzyme is reduced [52]. However, this route has been shown to be six times slower than amyloid- β absorption into the blood across the BBB [70, 226]. Several factors can influence the

perivascular drainage of amyloid- β , including ApoE* ϵ 4, arterial age, deposition of immune complexes, and arterial pulsation.

Glymphatic system

Recently, a novel pathway known as the “glymphatic pathway” has been discovered to contribute to the clearance waste, such as interstitial solutes, metabolites, amyloid- β , from the brain [6, 227]. The glymphatic system is a glial-dependent perivascular network that functions similar to a pseudo-lymphatic system in the brain [228]. The term “glymphatic” was coined based on two-photon imaging research [6, 222, 229], which emphasized the reliance on glial cells and functional similarity with the peripheral lymphatic system that helps to clear waste materials from the interstitial spaces between cells [222, 227]. According to this theory, CSF enters the paravascular spaces surrounding the brain’s penetrating arteries, combines with ISF and interstitial solutes in the parenchyma, and then leaves along the paravascular spaces of the brain’s draining veins. The glymphatic system contributes significantly to clearing amyloid- β from the brain, in addition to other wastes, more than was previously believed [227]. Supporting the idea, an increasing body of research has suggested a link between glymphatic dysfunction and decreased amyloid- β clearance in the brain [6, 227]. This relationship is influenced by several factors, including molecular size, arterial pulsation, aquaporin-4 (AQP4) expression and localization, and sleep [6].

The role of csf in clearing amyloid- β in the brain

The brain needs to eliminate proteins after their transport from the ISF into the CSF [6]. In particular, CSF, which is rich in amyloid- β , can be absorbed into the blood/circulation either through arachnoid villi [230] and the blood-CSF barrier (BCSFB), in the presence of amyloid- β transporters [209], or through the perivascular drainage pathways/perineural spaces and possibly meningeal lymphatics vessels, which empty into the lymphatic system [70, 222, 231]. However, the efficacy of either system to clear amyloid- β largely depends on several factors, including CSF production, BCSFB integrity and transporters, arachnoid villi resistance, and lymphatic absorption of the CSF [6].

TRANSPORT MECHANISMS OF AMYLOID- β BETWEEN THE BRAIN AND THE PERIPHERY

Brain-derived amyloid- β can be transported into the periphery for clearance through various routes, such as BBB [232, 233], BCSFB [214].

Similarly, the brain has evolved a distinct paravascular pathway that enables fluid exchange between the brain’s interstitial fluid

(ISF) and cerebrospinal fluid (CSF) without traversing the tightly regulated endothelial cell layer [222]. Numerous studies have demonstrated that a significant portion of cerebral amyloid- β is cleared through the transvascular route [234]. Additionally, emerging evidence suggests that the glymphatic system, which plays a crucial role in cerebral waste clearance, may also be vital for clearing amyloid- β [222]. Following the glymphatic system, the majority of CSF is believed to drain into the venous circulation through arachnoid granulations [235, 236].

On the other hand, how does amyloid- β originating in the periphery gain access to the brain’s regions? Several compelling lines of evidence support the notion that amyloid- β generated in the periphery can be transported into the brain, contributing to the development of amyloid pathology. For instance, a study demonstrated that the administration of peripherally applied amyloid- β -containing inoculates resulted in the deposition of cerebral amyloid- β , indicating that amyloid- β generated in the periphery can infiltrate the brain and contribute to amyloid pathology [237, 238]. Furthermore, the receptor for advanced glycation end products (RAGE) has been proposed as a primary transporter of amyloid- β from the systemic circulation into the brain through the blood-brain barrier (BBB). The upregulation of RAGE expression in both human and animal studies provides further support for this mechanism [215, 239]. Additionally, recent research findings suggest that platelets play a role in transporting amyloid- β from the systemic circulation into the brain [240]. These findings align with several recent reports demonstrating the contribution of circulating amyloid- β to cerebral amyloidosis. Collectively, these studies corroborate the notion that amyloid- β generated outside the brain can be transported from the periphery into the brain, leading to the development of central amyloid pathology [241-243].

This close relationship between the brain and the periphery concerning amyloid- β metabolism provides additional insight into the pathophysiology of diseases and may lead to new approaches for diagnosis and treatment of AD and CAA.

AMYLOID- β CLEARANCE IN THE PERIPHERY

Although the mechanisms of amyloid- β degradation/clearance in the periphery are not fully understood, available studies suggest that approximately 60% of brain-derived amyloid- β is cleared through transportation across the BBB to the periphery [244, 245]. In addition, a recent study demonstrated that brain-derived amyloid- β can be cleared in the periphery through a single peripheral system, resulting in an approximately 80% decrease in brain amyloid- β accumulation during parabiosis in humans and mice

[232]. This finding highlights the significant role of the periphery clearance system in clearing brain-derived amyloid- β and suggests that effective peripheral amyloid- β clearance could have a major impact on preventing amyloid- β accumulation in the brain. Multiple processes are likely involved in amyloid- β catabolism in the periphery, as explained below.

The role of peripheral enzymes in amyloid- β clearance

Several studies have reported that the expression and function of A β DPs in the brain to lower amyloid- β levels [246, 247]. Similarly, the expression and catabolic activity of these enzymes in the periphery have shown promising results [248]. Enzymes such as NEP, ECE, IDE and ACE have been found in the periphery and explored for their ability to degrade amyloid- β [249, 250]. These A β DPs have been found to bind to erythrocytes and degrade amyloid- β in plasma [248], human serum [251], skeletal muscle [232, 252, 253], and within the liver [254]. Furthermore, ECE-1 has been reported to degrade amyloid- β in the blood. The presence of ACE in blood and IDE in human CSF has been identified but their functional role in the amyloid- β metabolism remains unknown and requires future investigation [251].

The role of blood components in amyloid- β clearance

Amyloid- β from the brain can enter the bloodstream through various mechanisms [255-257]. Once in the blood, multiple components work together to clear circulating amyloid- β [103], including a wide range of amyloid- β -binding proteins such as lipoproteins and albumin, as well as amyloid- β -binding cells such as erythrocytes and immune cells [258].

Amyloid- β -binding proteins

An amyloid- β -equilibrium between blood and brain is maintained through a range of amyloid- β carrier proteins and receptors that facilitate transport and clearance of amyloid- β across the BBB [239, 248].

Human serum albumin, a most abundant protein in the blood, has been found to bind to amyloid- β (90% of amyloid- β_{1-40} and amyloid- β_{1-42}) [259, 260], including both amyloid- β monomers [261] and oligomers [262] (Fig. 2). Numerous studies have shown that human serum albumin targets both species [259] and inhibits amyloid- β fibrillization both *in vitro* [263] and *in vivo* [259, 264], supporting the peripheral sink hypothesis. This strategy is based on the idea that amyloid- β in the brain and periphery are in equilibrium and that reducing amyloid- β in the periphery can lead to a reduction of amyloid- β in the brain through passive diffusion down a concentration gradient [265, 266].

Amyloid- β -binding cells-erythrocytes

Amyloid- β -binding cells, such as erythrocytes, have been found to play a significant role in the transport and clearance of amyloid- β in peripheral organs [258] (Fig. 2). For example, erythrocytes facilitate the clearance of amyloid- β by relying on complement C3b-dependent adherence to complement receptor 1 on erythrocytes [171, 267]. Any alterations in the number and function of erythrocytes, or the decreased adherence to erythrocytes, may prevent amyloid- β from being transported and cleared in peripheral organs, eventually leading to amyloid- β accumulation in the brain. Recent studies also have found a significant association between amyloid- β and erythrocytes [268, 269]. For instance, Taylor et al. showed a new strategy in which immune complexes simultaneously capture amyloid- β and adhere it to erythrocytes via complement receptor 1 (CR1; CD35), promoting the rapid clearance of amyloid- β from the circulation and the brain [270].

Immune cells

Monocytes, lymphocytes, neutrophils, and macrophages are additional cell types that have been implicated in the clearance of amyloid- β peptides [258, 267, 271-273]. Just like glial cells and neurons in the brain clear amyloid- β by phagocytosis or endocytosis, amyloid- β in the periphery can also be phagocytosed in the blood by monocytes and neutrophils, as well as in tissues by macrophages [239, 274]. Monocytes in the blood are considered peripheral counterparts of microglia, and it has been shown that they are more effective at clearing amyloid- β clearance than microglia [257]. A recent study indicated that the receptors related with amyloid- β internalization (CD33, TLR2, TREM2, etc.) on blood monocytes are reduced in AD patients, implying that the capacity of monocytes to uptake and degrade amyloid- β is compromised, which contributes to an increase in amyloid- β level [50, 257].

Additionally, lymphocytes (including T cells, B cells, and natural killer cells) have been linked to amyloid- β clearance through immunoglobulin-mediated adaptive phagocytosis [239, 273, 275]. Multiple studies also have demonstrated that various types of cells derived from the peripheral system, including monocyte-derived microglia-like cells [276, 277], peripheral blood-derived microglia-like cells [278], CD11b-positive cells (predominantly monocytes) [279] and CD115-positive cells, can migrate from the bloodstream [280] into the brain to phagocytose amyloid- β peptides, potentially aiding in the prevention of amyloid- β accumulation [281].

BBB is a critical regulator of the entry of peripheral immune cells into the brain and their clearance of amyloid- β . Although the volume of blood is much larger than that of cerebrospinal fluid (CSF), the BBB limits the access of peripheral immune cells to the brain, which can affect their ability to clear amyloid- β . However, recent

research has highlighted the significant role of peripheral immune cells, particularly monocytes and macrophages, in amyloid- β clearance, particularly in the early stages of AD. Therefore, it is likely that peripheral clearance mechanisms play a crucial role in clearing soluble forms of amyloid- β that can traverse the BBB.

The role of peripheral organs in amyloid- β clearance

In the periphery, several tissues and organs are involved in amyloid- β peptide clearance, including the liver, kidney, and spleen etc. as discuss below [204, 232, 282, 283].

The role of the liver in clearing amyloid- β

The liver is a crucial metabolic organ that is responsible for synthesizing proteins, regulating metabolism, and detoxifying the body from harmful substances. Circulating amyloid- β is mainly cleared by either degradation in hepatocytes, which accounts for more than 60% of clearance, or excretion/catabolism in the bile (Fig. 2). A recent study indicated that people with liver cirrhosis have reduced liver-mediated amyloid- β clearance [284], and another study showed a significant association between hepatic function and plasma amyloid- β levels [285]. Although the molecular mechanisms governing hepatic amyloid- β uptake are not yet fully understood [286], multiple studies have revealed that transport proteins such as albumin, ApoJ, ApoE, transthyretin, and alpha-2-macroglobulin, which facilitate the degradation of amyloid- β in peripheral organs, particularly the liver, bind to amyloid- β after it is effluxed from the brain [103, 260, 287, 288]. To better comprehend the receptor-mediated amyloid- β uptake in the liver, it has been proposed that LRP1 is the major receptor involved in amyloid- β internalization [286, 289], followed by its degradation by several proteases found in the liver [254]. Although various receptors, such as SR-A and RAGE, are expressed in the liver [286], LRP1 has been identified as the primary receptor responsible for amyloid- β uptake in the liver [254]. Modulating LRP1 function in the liver, either pharmacologically or non-pharmacologically, has been shown to reduce amyloid- β buildup in the mouse brain [254, 290]. Similarly, insulin has been hypothesized to enhance liver-mediated amyloid- β clearance by inducing intracellular translocation of LRP1 to the plasma membrane in hepatocytes [285, 291].

The role of kidney in clearing amyloid- β

The kidneys are the body's primary excretory organs, responsible for regulating blood minerals to control metabolite levels [103]. Previous research has shown that protein uptake in the renal tubule is mediated primarily by two receptors, megalin and cubilin, expressed in renal tubular epithelial cells [292]. Megalin, also known as LRP2, has been suggested to transport amyloid- β

from the brain to blood across the BBB [293]. Recent studies have found that megalin-positive renal tubular epithelial cells in both humans and AD mice accumulate amyloid- β , suggesting that megalin may absorb amyloid- β from the urine [282]. Amyloid- β has also been detected in human urine samples [294], and animal experiments have shown that the kidney filtration removes amyloid- β from the blood into the urine [232, 295]. Renal failure can result in poor peripheral clearance of amyloid- β , as evidenced by an inverse relationship between serum amyloid- β levels and estimated glomerular filtration rate (eGFR) of renal function in chronic kidney disease patients [296, 297]. Human kidney donors have also shown reduced eGFR and the increased plasma levels of amyloid- β [298], demonstrating that the decreased renal function reduces amyloid- β clearance in the periphery. While the effect of renal dysfunction on amyloid- β burden in the brain is unknown, renal dysfunction has been associated with an increased risk of dementia [299]. Kidney transplantation can reduce amyloid- β deposition in the plasma [298], and hemodialysis may ameliorate amyloid- β deposition in the brains of CKD patients [300, 301].

Recent studies have provided further evidence for a strong association between kidney function and amyloid- β clearance [302]. For instance, Gronewold et al. have reported that reduced kidney function is linked to increased plasma amyloid- β level, which could contribute to cerebral amyloid- β accumulation [303]. Additionally, Tian et al. have found that amyloid- β levels in the blood of the renal artery were higher than in the blood of the renal vein [282], indicating that the kidney may participate in amyloid- β clearance by filtering it from the blood into the urine [239].

The role of spleen in clearing amyloid- β

The spleen is an organ that serves as a blood filter and performs important immunological functions, resembling a large lymph node. It stores blood and removes old erythrocytes and is composed of various immune cells, including monocytes/macrophages, which play a crucial role in the innate immune system [304]. Similar to other monocytes/macrophages in the body, the spleen is known to clear amyloid- β in the periphery [283, 305]. Recent research by Yu et al. has demonstrated that the spleen significantly contributes to the peripheral clearance of amyloid- β , with splenic monocytes and macrophages playing a significant role in this process. Conversely, splenectomy has been shown to increase amyloid- β accumulation and may accelerate the onset of AD [283, 306].

The role of other peripheral organs in clearing amyloid- β

Several studies have reported that the detection of amyloid- β deposits in non-neural tissues, such as skin, subcutaneous tissue, and

intestine in humans, and the gastrointestinal tract in animals such as dogs [307, 308]. The presence of circulating amyloid- β in the blood is thought to be the cause of these deposits, suggesting that these organs may participate in peripheral amyloid- β metabolism, as observed in many studies [309-311].

The skin, for example, is an immune organ [312], and it develops from the same ectodermal layer as the brain during embryonic development [312, 313]. Certain genes and molecular pathways linked to the mechanisms of neurodegenerative diseases modify their expression with progressing skin aging, possibly due to the shared ectodermal origin of the skin and nervous system [313]. BACE1 (β -secretase 1), an enzyme that degrades amyloid- β_{1-40} and amyloid- β_{1-42} , generates a shorter amyloid- β_{1-34} peptide [314], which has been identified in human skin and could serve as a possible marker of amyloid- β degradation [315]. Additionally, a study showed that the majority of the ^{125}I -labeled amyloid- β_{1-40} was detected in the skin with only a minor amount in the brain, demonstrating that amyloid- β produced in the brain can be cleared in the periphery [232]. Although basal keratinocytes have been shown to express high levels of amyloid- β precursor protein [316, 317], it is still unknown whether the amyloid- β deposits are caused by local skin cells or the circulating blood [103]. Sweat secretion is another potential mechanism for excreting amyloid- β , but it is unclear whether the skin contributes to the amyloid- β clearance. More research is needed to answer this question.

Similarly, the digestive system, which is a lymphatic organ, contains a substantial number of macrophages and other immune cells, suggesting that the gut may be capable of clearing amyloid- β . Many studies imply that the brain-gut-microbiota axis is implicated in the etiology of dementia-related disorders [318]. Therefore, exploring the possibility of the gastrointestinal system influencing peripheral amyloid- β metabolism is critical.

THERAPEUTIC STRATEGIES FOR CLEARING AMYLOID- β IN THE BRAIN AND THE PERIPHERY

At present, effective preventative or therapeutic medicines for AD and CAA are lacking. Over the years, various treatment approaches targeting amyloid- β in the brain, such as anti-amyloid- β therapy (including amyloid- β immunotherapy, secretase inhibitors, and amyloid- β aggregation inhibitors), have been developed and remain in use [319, 320]. However, most of these strategies have failed in clinical trials due to high costs, drug-drug interactions, food-drug interactions, and significant side effects, which impose a significant financial and social burden on society. To achieve the desired therapeutic outcomes of these complex and multifaceted diseases, we must consider different strategies tar-

geting amyloid- β in both the brain and periphery based on solid sources of information.

The accumulation of amyloid- β in the brain is largely caused by a reduction in A β DPs activity. Thus, increasing the expression levels of A β DPs would dramatically reduce amyloid- β buildup and associated pathologies. Strategies to translate A β DPs into therapeutic applications include enhancing A β DPs activity through the administration of compounds, gene therapy using genes encoding A β DPs, and cell therapies based on stem cell transplantation [40]. Additionally, non-enzymatic pathways (such as targeting microglial phagocytosis, photo-oxygenation [321, 322], BBB transporters, perivascular drainage etc.) should be improved to reduce the level of amyloid- β in the brain [171].

Besides mechanisms underlying the clearance of amyloid- β in the brain, peripheral intervention has also received much attention, with positive outcomes in reducing amyloid- β in the brain and the incidence of dementia. These peripheral approaches include managing cardiovascular risk factor [323], treating sleep-disordered breathing with sustained positive airway pressure [324, 325], lowering peripheral blood cholesterol levels by using statins [326, 327], plasma exchange programs [328], dialysis (peritoneal dialysis and hemodialysis) [329], improving the phagocytic ability/function of peripheral blood monocytes through proteolytic degradation [272, 305], targeting enzymes (NEP/ACE) processes [252, 253, 330], developing nanozymes [331], and various therapeutic agents targeting peripheral clearance of amyloid- β (such as inorganic nanoparticles, polymer nanoparticles and liposomes) [332-336]. In recent years, researchers have been investigating immunotherapy as a "gold standard strategy" to promote amyloid- β clearance, leading to an increased focus on development of anti-A β therapies [337-339]. However, amyloid-related imaging abnormalities (ARIA) are the major severe side effect associated with amyloid- β immunotherapy [340]. Despite the clinical therapeutic effects of anti-amyloid- β immunotherapies for Alzheimer's disease (AD), aducanumab and solanezumab have been shown to improve cognitive function, while aducanumab and bapineuzumab may also increase the risks of ARIA [341].

In addition to immunotherapy, non-immune approaches, such as peripheral amyloid- β -binding agents (e.g., gelsolin, GM1, sRAGE, sLRP fragments) [215, 335], blood cells, and protein [248, 265], have also made significant progress in disease prevention.

These findings suggest that both "central therapeutic strategies" in the brain and "systemic therapeutic strategies" may be helpful in reducing the amyloid- β burden in the brain and attenuating disease pathology. Therefore, a combination of both central and systemic therapeutic approaches may be necessary to effectively treat AD and CAA.

CONCLUSION

AD and CAA are often associated with each other, sharing the common factor of amyloid- β . The impaired clearance of amyloid- β peptide in the body is believed to contribute to the accumulation of central amyloid- β , leading to the pathogenesis of sporadic AD in the brain parenchyma and CAA in blood vessels. This review has highlighted the importance of clearing amyloid- β in the brain, which can be achieved through enzymatic or non-enzymatic pathways. Likewise, multiple mechanisms are involved in amyloid- β clearance in peripheral organs, such as immunomodulation, immune cells, enzymes, amyloid- β -binding proteins, and amyloid- β -binding cells. Therefore, it is recommended to investigate central therapeutic strategies targeting amyloid- β clearance in the brain and systemic therapeutic strategies targeting clearance mechanisms in peripheral organs to eliminate excess amyloid- β deposits. This approach will not only enhance our understanding of molecular mechanisms underlying both diseases but also provide new targets for inhibiting amyloid- β deposition in the pathogenesis of sporadic AD and CAA.

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