

Review

Amyloid beta: structure, biology and structure-based therapeutic development

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Abstract

Amyloid beta peptide (A β) is produced through the proteolytic processing of a transmembrane protein, amyloid precursor protein (APP), by β - and γ -secretases. A β accumulation in the brain is proposed to be an early toxic event in the pathogenesis of Alzheimer's disease, which is the most common form of dementia associated with plaques and tangles in the brain. Currently, it is unclear what the physiological and pathological forms of A β are and by what mechanism A β causes dementia. Moreover, there are no efficient drugs to stop or reverse the progression of Alzheimer's disease. In this paper, we review the structures, biological functions, and neurotoxicity role of A β . We also discuss the potential receptors that interact with A β and mediate A β intake, clearance, and metabolism. Additionally, we summarize the therapeutic developments and recent advances of different strategies for treating Alzheimer's disease. Finally, we will report on the progress in searching for novel, potentially effective agents as well as selected promising strategies for the treatment of Alzheimer's disease. These prospects include agents acting on A β , its receptors and tau protein, such as small molecules, vaccines and antibodies against A β ; inhibitors or modulators of β - and γ -secretase; A β -degrading proteases; tau protein inhibitors and vaccines; amyloid dyes and microRNAs.

Keywords: amyloid beta peptide; amyloid precursor protein; Alzheimer's disease; neurodegenerative diseases; drug discovery

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Introduction

Alzheimer's disease is the most common type of dementia. It affects tens of millions of people worldwide, and this number is rising dramatically. The social and economic burden of Alzheimer's disease is high. The amyloid hypothesis^[1-3] proposes β -amyloid (A β) as the main cause of the disease and suggests that misfolding of the extracellular A β protein accumulated in senile plaques^[4] and the intracellular deposition of misfolded tau protein in neurofibrillary tangles cause memory loss and confusion and result in personality and cognitive decline over time. Accumulated A β peptide is the main component of senile plaques and derives from the proteolytic cleavage of a larger glycoprotein named amyloid precursor protein (APP). APP is a type 1 membrane glycoprotein that plays an important role in a range of biological activities, including neuronal development, signaling, intracellular transport, and other aspects of neuronal homeostasis. Several APP cleavage products may be major contributors to Alzheimer's

disease, causing neuronal dysfunction. Deposits of A β peptides are mainly observed in the region of the hippocampus and the neocortex as well as in the cerebrovasculature (CAA)^[5].

As A β peptides are the main components of senile plaques, understanding the structures and biochemical properties of A β will advance our understanding of Alzheimer's disease at the molecular level. A β monomers aggregate into different forms of oligomers, which can then form regular fibrils. The peptides share a common structural motif and aggregation pathway, providing a powerful conceptual framework for understanding the pathogenic mechanism and disease-specific factors. Here, we review the structure and biology of A β , which may constitute a core pathway for the growing number of neurodegenerative diseases, including Alzheimer's, Parkinson's, and Huntington's diseases, as well as structure-based drug discovery, which may contribute to the development of novel treatment strategies against different degenerative diseases.

Structure of the amyloid beta peptide Molecular architecture of APP and its proteolysis in the amyloidogenic pathway

The A β peptides are cleaved from the much larger precursor

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precursor APP. APP is an integral membrane protein expressed in many tissues, especially in the synapses of neurons, which plays a central role in Alzheimer's disease (AD) pathogenesis. APP consists of a single membrane-spanning domain, a large extracellular glycosylated N-terminus and a shorter cytoplasmic C-terminus. It is one of three members of a larger gene family in humans. The other two family members are the APP-related proteins (APLPs) APLP1 and APLP2^[6]. APP has been implicated as a regulator of synaptic formation and repair^[7], anterograde neuronal transport^[8] and iron export^[9]. It is produced as several different isoforms, ranging in size from 695 to 770 amino acids. The most abundant form in the brain (APP695) is produced mainly by neurons and differs from longer forms of APP in that it lacks a Kunitz-type protease inhibitor sequence in its ectodomain^[10]. APP isoform 695 is mainly expressed in neurons, whereas APP751 and APP770, which contain the Kunitz-type serine protease inhibitory domain KPI, are mainly expressed on peripheral cells and platelets^[11, 12] (Figure 1).

APP is best known as the precursor molecule cut by β -secretases and γ -secretases to produce a 37 to 49 amino acid residue peptide, $A\beta$ ^[13], that lies at the heart of the amyloid cascade hypothesis and whose amyloid fibrillar form is the primary component of amyloid plaques found in the brains of Alzheimer's disease patients. Human APP can be processed via two alternative pathways: amyloidogenic and nonamyloidogenic. APP is first cleaved by α -secretase (nonamyloidogenic pathway) or β -secretase (amyloidogenic pathway), generating membrane-tethered α - or β -C terminal fragments (CTFs). The cleavage of APP by α -secretase releases sAPP α from the cell surface and leaves an 83-amino-acid C-terminal APP fragment (C83). The production of sAPP α increases in response to electrical activity and the activation of muscarinic acetylcholine receptors, suggesting that neuronal activity

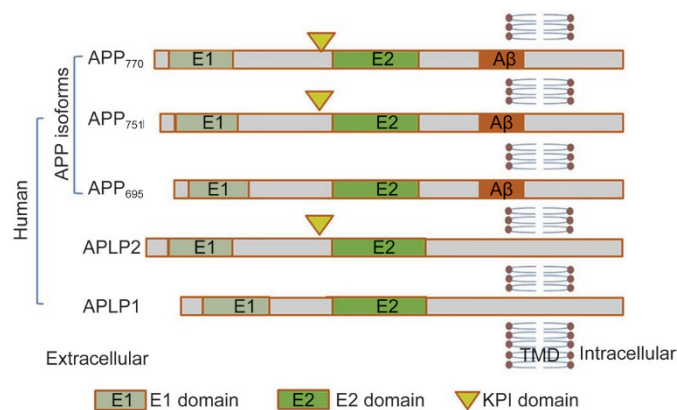


Figure 1. Molecular architecture of APP. Schematic representation of human APP isoforms and the APP-like proteins (APLP), APLP1 and APLP2. APP isoforms range in size from 695 to 770 amino acids. The most abundant form in brain is APP695, which lacks a Kunitz type protease inhibitor sequence in its ectodomain. APP751 and APP770 contain the Kunitz type serine protease inhibitory domain (KPI) are mainly expressed on the surface of peripheral cells and platelets.

increases the α -secretase cleavage of APP^[14]. Further processing involves the intramembrane cleavage of α - and β -CTFs by γ -secretase, which liberates the P3 (3 kDa) and $A\beta$ (4 kDa) peptides, respectively^[15, 16]. The amyloidogenic processing of APP thus involves sequential cleavages by β - and γ -secretase at the N and C termini of $A\beta$, respectively (Figure 2)^[17]. The 99-amino-acid C-terminal fragment of APP (C99) generated by β -secretase cleavage can be internalized and further processed by γ -secretase at multiple sites to produce cleavage fragments of 43, 45, 46, 48, 49 and 51 amino acids that are further cleaved to the main final $A\beta$ forms, the 40-amino-acid $A\beta$ 40 and the 42-amino-acid $A\beta$ 42, in endocytic compartments^[18, 19]. The cleavage of C99 by γ -secretase liberates an APP intracellular domain (AICD) that can translocate to the nucleus, where it may regulate gene expression, including the induction of apoptotic genes. The cleavage of APP/C99 by caspases produces a neurotoxic peptide (C31)^[20]. The β -site APP cleaving enzyme is abundant in neurons, which may accelerate the amyloidogenic processing pathway in the brain and impair neuronal survival. The three-dimensional structure of human γ -secretase was determined by single-particle cryo-electron microscopy in 2014^[21]. The γ -secretase complex comprises a horseshoe-shaped transmembrane domain, which contains 19 transmembrane segments (TMs), and a large extracellular domain (ECD) from the nicastrin subunit, which localizes immediately above the hollow space formed by the TM horseshoe. This structure serves as an important basis for understanding the mechanisms of γ -secretase function. The γ -secretase complex consists of four different proteins, presenilin, nicastrin, presenilin enhancer 2 and anterior pharynx-defective 1. Presenilin is activated by auto-processing to generate N- and C-terminal cleavage products that both contain aspartyl protease sites that together are required for the activity of the mature γ -secretase. Nicastrin, presenilin enhancer 2 and anterior pharynx-defective 1 are critical components of γ -secretase and may modulate enzyme activity in response to physiological stimuli^[22-24]. This unique cleavage process of APP provides essential targets for AD therapeutics^[25].

$A\beta$ monomer

$A\beta$ monomers aggregate into various types of assemblies, including oligomers, protofibrils and amyloid fibrils. Amyloid fibrils are larger and insoluble, and they can further assemble into amyloid plaques, while amyloid oligomers are soluble and may spread throughout the brain. The primary amino acid sequence of $A\beta$ was first discovered from extracellular deposits and amyloid plaques in 1984^[2]. The primary amino acid sequence of the 42-amino-acid $A\beta$ isoform $A\beta$ 42 is shown here (Figure 3A). $A\beta$ encompasses a group of peptides ranging in size from 37 to 49 residues. Amyloid plaques with $A\beta$ as the main component are most commonly found in the neocortex in the brain of Alzheimer's disease patients^[26].

$A\beta$ is commonly thought to be intrinsically unstructured and hence cannot be crystallized by common methods. Many studies therefore focus on optimizing conditions that can stabilize $A\beta$ peptides. The three-dimensional solution structure

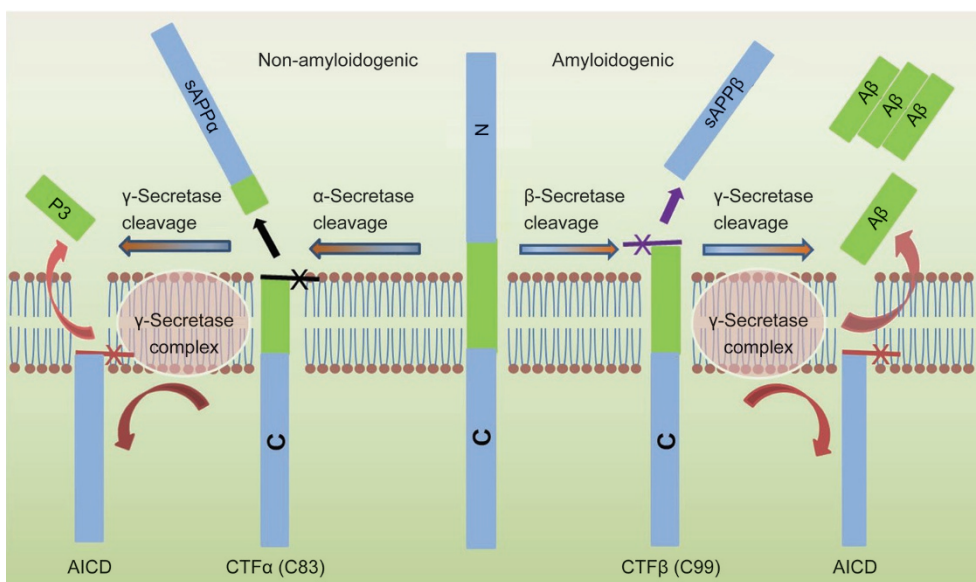


Figure 2. Human APP proteolytic pathways. Human APP proteolysis in the non-amyloidogenic pathway and amyloidogenic pathway. Non-amyloidogenic processing of APP refers to the sequential processing of APP by membrane bound α -secretases, which cleave within the A β domain to generate the membrane-tethered α -C terminal fragment CTF α (C83) and the N-terminal fragment sAPP α . CTF α is then cleaved by γ -secretases to generate extracellular P3 and the APP intracellular domain (AICD). Amyloidogenic processing of APP is carried out by the sequential action of membrane bound β - and γ -secretases. β -Secretase cleaves APP into the membrane-tethered C-terminal fragments β (CTF β or C99) and N-terminal sAPP β . CTF β is subsequently cleaved by γ -secretases into the extracellular A β and APP intracellular domain (AICD).

of different fragments of the A β peptide was determined using nuclear magnetic resonance (NMR) spectroscopy, molecular dynamic (MD) techniques and X-ray crystallography. Most structural knowledge about A β comes from NMR and molecular dynamics.

Early NMR-derived models of the solution structure of A β peptide (1-28) indicated that it folds into a predominately α -helical structure with β -sheet conversion in membrane-like media that may also occur during the early stages of amyloid formation in Alzheimer's disease^[27] (Figure 3B). It is the major proteinaceous component of amyloid deposits in Alzheimer's disease, where the side chains of histidine-13 and lysine-16 residing on the same face of the helix are in close proximity. The solution structure of A β peptide (1-40) suggests that the C-terminus of the peptide has an α -helix conformation between residues 15 and 36 with a kink or hinge at 25-27 in aqueous sodium dodecyl sulfate (SDS) micelles, while the peptide is unstructured between residues 1 and 14, which are mainly polar and likely solvated by water. The deprotonation of two acidic amino acids in the helix promotes a helix-to-coil conformational transition that precedes the aggregation of A β 1-40^[28] (Figure 3C). Solid-state NMR spectroscopy-derived models of the solution structure of A β peptide (10-35) show that in water^[29] (Figure 3D), the peptide collapses into a compact series of loops, strands, and turns without alpha-helical or beta-sheet structure. The van der Waals and electrostatic forces maintain its conformational stabilization. Approximately 25% of the surface is uninterrupted hydrophobic, and the compact coil structure is meta-stable, which may lead to a global conformational rearrangement and the formation of an

intermolecular beta-sheet secondary structure caused by fibrilization. The 3D NMR structures of A β peptide (8-25) and A β peptide (28-38) show two helical regions connected by a regular type I β -turn. A β peptide (25-35) is a highly toxic synthetic derivative of A β peptides. Researchers have used NMR and CD investigation of A β peptide (25-35) and fluoro-alcohols to scan its conformational properties. The peptide behaves as a typical transmembrane helix in a lipidic environment, forming fibrillar aggregates, which suggests a direct mechanism of neurotoxicity^[30,31].

NMR-guided simulations of A β peptides 1-40 (A β 40) and 1-42 (A β 42) also suggested very different conformational states^[32], with the C-terminus of A β 42 being more structured and residues 31-34 and 38-41 forming a β -hairpin that reduces the C-terminal flexibility, which may be responsible for the greater propensity of A β 42 than A β 40 to form amyloids. Replica exchange molecular dynamics studies suggested that A β 40 and A β 42 can indeed populate multiple discrete conformations, comprising α -helix or β -sheet conformers, and the structural states transition rapidly^[33]. More recent studies identified a multiplicity of discrete conformational clusters by statistical analysis^[34]. However, the most recent NMR structure of A β 40 shows significant secondary and tertiary structure^[35]. The hydrophobic C-terminal of the A β is critical in triggering the transformation from α -helical to β -sheet structure and plays a key role in determining the state of protein aggregation in Alzheimer's disease^[36].

Aggregation of A β into fibrils

Early proposals supported the so-called "amyloid cascade

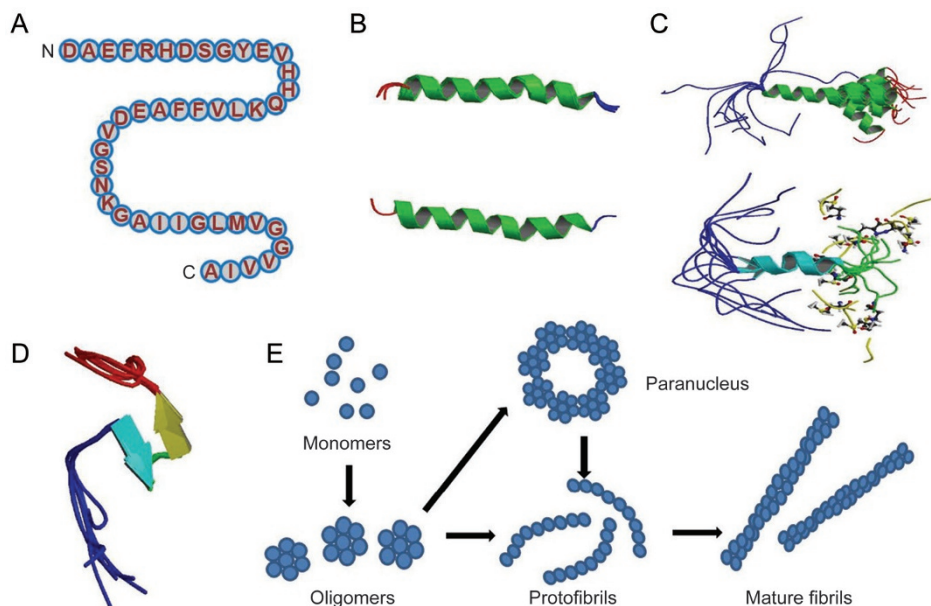


Figure 3. Structures of A β monomer, fibril and oligomers. (A) The primary amino acid sequence of the 42 amino acid A β isoform A β 42. A β encompasses a group of peptides ranging in size from 37–49 residues. (B) The structure of amyloid beta peptide (1–28), which forms a predominately alpha-helical structure that can be converted to a beta-sheet structure in membrane-like media (PDB code: 1AMC, 1AMB), it's the major proteinaceous component of amyloid deposits in Alzheimer's disease. The side chains of histidine-13 and lysine-16 residing on the same face of the helix are close. (C) Solution structure of amyloid beta peptide (1–40), in which the C-terminal two-thirds of the peptide form an alpha-helix conformation between residues 15 and 36 with a kink or hinge at 25–27 in aqueous sodium dodecyl sulfate (SDS) micelles with a bend centered at residue 12, while the peptide is unstructured between residues 1 and 14 which are mainly polar and likely solvated by water (PDB code: 1BA4, 1BA6). It collapsed into a compact series of loops, strands, and turns with no alpha-helical or beta-sheet structure. The van der Waals and electrostatic forces maintain its conformational stabilization. Approximately 25% of the surface is uninterrupted hydrophobic, and the compact coil structure is meta-stabled, which may lead to a global conformational rearrangement and formation of intermolecular beta-sheet secondary structure caused by fibrillization. (D) Amyloid beta peptide (10–35) forms a collapsed coil structure (PDB code: 1HZ3). It collapsed into a compact series of loops, strands, and turns with no alpha-helical or beta-sheet structure. The van der Waals and electrostatic forces maintain its conformational stabilization. Approximately 25% of the surface is uninterrupted hydrophobic, and the compact coil structure is meta-stabled, which may lead to a global conformational rearrangement and formation of intermolecular beta-sheet secondary structure caused by fibrillization. (E) Proposed pathway for the conversion of amyloid beta monomers to higher order oligomers, protofibrils and fibrils. A β monomers can form higher order assemblies ranging from low molecular weight oligomers, including dimers, trimers, tetramers, and pentamers, to mid-range molecular weight oligomers including hexamers, nonamers and dodecamers to protofibrils and fibrils.

hypothesis," which proposes that A β aggregation into plaques leads to neurotoxicity and dementia^[37] through common cytopathic effects that contribute to the pathogenesis of Alzheimer disease and other amyloidosis. While the A β peptide can rapidly aggregate to form fibrils that deposit into the amyloid plaques, which are found to be linked with Alzheimer's disease, later studies demonstrated that there is no direct correlation between amyloid plaques^[38] and the loss of synapses and neurons in brains with Alzheimer's disease^[39, 40]. Many pathways may lead to the peptide aggregation. Early studies indicated that the amyloid polypeptide is organized in a characteristic "cross β " pattern in a regular manner, in which adjacent chain segments are folded in an anti-parallel manner within the fiber lattice^[41]. Later research revealed that the peptide chains of β -strand segments run perpendicular to the long fibril, and the intermolecular hydrogen bonds of β -strands run parallel to the axis in a "cross β " structural pattern^[42].

Solid-state NMR measurements have shown that amyloid fibril "cross β " structures exist in two patterns: parallel and antiparallel. The crosslinking of A β peptides by tissue trans-

glutaminase (tTg) indicated that the A β fibril is a hydrogen-bonded, parallel β -sheet that defines the long axis of the A β fibril propagation^[43]. Specific amino acid contacts have implications for the overall fibril formation of the extended A β (10-35) and its stability, morphology and parallel organization^[44]. Multiple quantum (MQ) ¹³C NMR data indicate an in-register, parallel organization^[45]. These measurements, known as experimental EM, STEM, and solid-state NMR, suggest that the supramolecular structures of A β peptide (1-40) fibrils, A β peptide (10-35), and A β peptide (1-42) fibrils are organized as β -sheets^[46, 47]. As A β peptide aggregation pathways are determined by the primary amino acid sequence and the intermolecular interactions, later studies in the structural organization of disease-related amyloid fibrils have led to the identification of the exact register motif. In addition to the parallel pattern, several short peptide segments of A β can adopt an antiparallel pattern^[48]. Solid-state NMR spectroscopy indicates amyloid fibrils with a simple and intriguing structural motif^[49]. Site-directed spin labeling and electron paramagnetic resonance (SDSLEPR) spectroscopy for amyloid fibrils confirmed that this

parallel, exact register structural motif is highly conserved^[50-52]. Progress has been made by disulfide cross-linking within preformed fibrils, with results indicating that they are located proximally inside the hairpin turn. Residues 17 and 34 could be efficiently cross-linked by a disulfide bond, while residues 17/35 and 17/36 were not efficiently cross-linked in fibrils. Purified double mutant proteins consisted of disulfide-bonded monomers that were able to assemble into amyloid fibrils^[53]. The 17/35 residues on the C-terminal strand would need to flip 180 degrees to provide the structural flexibility allowing A β to assemble into at least two slightly different forms^[54-56]. These results are inconsistent with the hairpin model based on electrostatic interactions, with the exception of the side chains of Glu22 and Lys28^[57]. It is unclear whether small differences in the fibril structure are pathologically significant; however, the slight two-residue difference in A β 40 and A β 42 leads to great differences in their biophysical, biological, and clinical behaviors. The 3D structure of residues 15-42 of A β 42 adopts a double-horseshoe-like cross- β -sheet entity with maximally buried hydrophobic side chains, in which residues 1-14 are partially ordered and in a β -strand conformation, which is the more neurotoxic species, aggregates much faster, and dominates in senile plaque in Alzheimer's disease patients^[58]. Further studies reported that cognitive deficits appeared before plaque deposition or the detection of insoluble amyloid fibrils^[59, 60]. In contrast, the amount of oligomeric A β ^[61, 62] is increased in Alzheimer's disease brain extracts^[63], which is the basis for the A β oligomer hypothesis^[64-66], which posits that soluble A β oligomers rather than insoluble fibrils or plaques trigger synapse failure and memory impairment^[67], resulting in impaired brain function in the final stages of the disease.

A β oligomers

While amyloid fibrils are larger, insoluble, and assemble into amyloid plaques forming histological lesions that are characteristic of Alzheimer's disease, A β oligomers are soluble and may spread throughout the brain. The size distribution of A β oligomers is heterogeneous. There is a broad consensus for the preferential accumulation of a soluble high-molecular-weight species of approximately 100–200 kDa under relatively physiological conditions *in vitro*^[68-72]. A β monomers can form higher-order assemblies ranging from low-molecular-weight oligomers, including dimers, trimers, tetramers, and pentamers, to midrange molecular weight oligomers, including hexamers, nonamers and dodecamers, to protofibrils and fibrils (Figure 3E). In contrast to the fibril structure, relatively little is known about the structure of amyloid oligomers. Soluble oligomers prepared in the presence of detergents seem to feature substantial beta sheet content with mixed parallel and antiparallel character^[73]. The structural characterization of oligomers is complicated because their oligomeric states are more transient than fibrils, and preparing homogeneous populations of oligomers is difficult^[74]. They can be stabilized by detergents, which may help to alleviate this problem^[75]. There was little structural information on the oligomeric state of amyloid beta until 2010, when low temperature and low

salt conditions made it possible to isolate pentameric disc-shaped oligomers devoid of beta structure^[76]. Circular dichroism and infrared spectroscopy indicate that A β oligomers are extended coil or beta sheet structures^[63]. Hydrogen deuterium exchange analysis also indicates that they have a stable core, which is consistent with substantial beta sheet character, as 40% of the total backbone hydrogen bonds are resistant to exchange in the oligomeric conformation with a stable beta sheet secondary structure^[77]. In contrast, fifty percent of the backbone hydrogen bonds are resistant to exchange in the mature amyloid fibril, indicating that a small increase in main chain hydrogen bonding accompanies the transition to the fibrillar conformation^[78]. Computational studies suggest that A β oligomers form an antiparallel beta-turn-beta motif^[79]. The solution conformation of A β is of significant importance during self-assembly in water environments. The soluble peptide has no alpha-helical or beta-sheet character but adopts a collapsed coil structure^[80]. A particular conformation that forms ring-shaped pentamers and hexamers is stable by microsecond all-atom MD simulations^[81].

The relationship between oligomers and fibrils remains to be established. There seem to be some similar structural elements, as they both appear to be extended or beta sheet structures and both display similar amounts of main chain hydrogen bonding that is resistant to exchange. On the other hand, amyloid oligomers and fibrils appear to contain mutually exclusive and non-overlapping conformations recognized as generic antibody epitopes that are common to amyloids of different sequences^[74, 82]. Oligomers are a kinetic intermediate waxing at early times during the development of fibrils^[83]. Different types of soluble amyloid oligomers have a common structure and share a common mechanism of toxicity^[63]. It is also unknown whether the oligomer structures represent basic units of amyloid protein that then assemble into fibrils or are just in equilibrium with monomers, which directly form fibrils without intermediate oligomeric structure. Oligomers appear as spherical aggregates at early times and then elongate by the coalescence of spherical subunits with a "bead" appearance, forming the precursor of protofibrils on the pathway to mature fibers. The parallelism between A β monomers represents a key organizing principle for amyloid oligomers and may also serve as a common structural motif for amyloid fibrils^[71, 84]. Other studies suggest that the spherical oligomers simply dilute the A β monomer concentration and may be off-pathway intermediates^[85] or that both on-pathway and off-pathway concurrence is possible under special conditions^[69].

The structure of A β aggregate forms and the aggregation pathways remain challenging research issues, though considerable progress has been made recently. The interactions of A β with transition metals have revealed potential pathogenic interactions and structural consequences. Oligomers that may normally be embedded in the membrane bind to transition metals such as Cu, Zn and Fe^[86, 87]. Constitutively metal-bound senile plaques play a role in accelerating the aggregation of amyloid beta peptide^[88], and the expression of A β oligomers may, in turn, regulate metal transition homeostasis^[89-91].

NMR data have provided information on the structure of the $A\beta$ -(1-16)- Zn^{2+} complex in aqueous solution. The residues His(6), His(13), and His(14) and the Glu(11) carboxylate were identified as ligands that tetrahedrally coordinate the $Zn(II)$ cation^[92].

All these different structures have been generated in different environments and determined by different techniques. The special form of $A\beta$ structures may be not stable or may be stabilized only in a unique solution; they may be similar but not the same as each other; one structure may depict one representative form of $A\beta$, and all the forms of $A\beta$ may co-exist *in vivo*. $A\beta$ forms a myriad of structures in the monomeric and oligomeric states, all of which result in similar fibril structures. Amyloid fibrils of $A\beta$ form a parallel, in-register cross β -sheet structure. The accumulation of $A\beta$ into long, unbranched fibrils is a hallmark of the disease, as is the loss of neurons due to cell death in parallel with the $A\beta$ aggregation process. These new insights into the structures and aggregation pathways may help to uncover the mechanisms of amyloid pathogenesis in degenerative diseases, ultimately leading to new therapeutic strategies to prevent the formation of toxic aggregates (Table 1).

Biological function of amyloid beta

$A\beta$ production

Alzheimer's disease is characterized by abnormal accumulation of the $A\beta$ protein, which is important for memory and cognition, in the brain regions. $A\beta$ is a normal product of the cellular metabolism derived from the amyloid precursor protein (APP). APP is synthesized in the endoplasmic reticulum (ER) and then transported to the Golgi complex, where it completes maturation and is finally transported to the plasma membrane. Mature APP at the plasma membrane is cleaved by the successive action of the β -secretase and γ -secretase to generate $A\beta$ (Figure 2)^[93]. The newly generated $A\beta$ either is released to the extracellular space or remains associated with the plasma membrane and lipid raft structures. The binding of $A\beta$ to ganglioside GM1 in the lipid rafts strongly favors $A\beta$ aggregation^[94]. The binding of ApoE to $A\beta$ taken up by the cells through receptor-mediated endocytosis mediated by LRP (LDL receptor-related protein), and LDLR regulates aggregation but also the cellular uptake of $A\beta$ ^[95]. Endocytosed $A\beta$ also has access to other subcellular compartments through the vesicular transport system. Earlier studies pointed to $A\beta$ fibrils as the neurotoxic agent leading to cellular death, memory loss, and other AD characteristics. Over the last two decades, further investigation has suggested that oligomeric or prefibrillar species of the $A\beta$ peptide are the most damaging to neuronal cells. Soluble $A\beta$ can bind to numerous molecules in the extracellular space, including cell surface receptors, metals and cellular membranes.

$A\beta$ binding receptors

The extracellular accumulation of $A\beta$ in neuritic plaques and the binding of $A\beta$ to a variety of receptors appear to be the characteristic hallmarks of Alzheimer's disease. The binding

of $A\beta$ to a variety of receptors has been proposed as a cause for the neuronal toxicity: $A\beta$ oligomers were proposed to induce mitochondrial dysfunction and oxidative stress in AD neurons, resulting in a massive calcium influx and toxicity in neurons^[96]. Furthermore, soluble oligomeric $A\beta$ was proposed to be toxic through binding to a variety of receptors, including lipids, proteoglycans, and proteins, such as the $A\beta$ -binding p75 neurotrophin receptor (p75NTR), the low-density lipoprotein receptor-related protein (LRP), cellular prion protein (PrP^c), metabotropic glutamate receptors (mGluR5), α subunit containing nicotinic acetylcholine receptor ($\alpha 7nAChR$), N-methyl-D-aspartic acid receptor (NMDAR), β -adrenergic receptor (β -AR), erythropoietin-producing hepatoma cell line receptor (EphR), and paired immunoglobulin-like receptor B (PirB)^[97]. The $A\beta/A\beta$ receptor interactions are proposed to generate and transduce neurotoxic signals into neurons, causing cellular defects such as mitochondrial dysfunction and the ER stress response. In addition, some $A\beta$ receptors are most likely to internalize $A\beta$ into neurons to display distinct cellular defects (Figure 4).

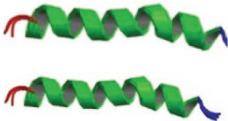
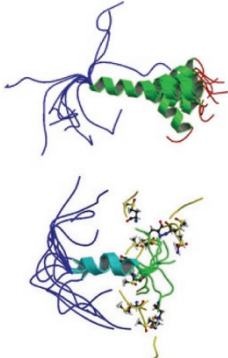


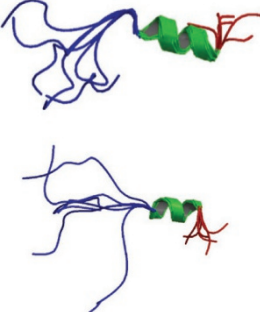

NMDAR and $\alpha 7nAChR$

NMDAR and $\alpha 7nAChR$ are both ion channel receptors. Several reports suggest that $A\beta$ interacts with NMDARs at post-synaptic terminals, and antibodies raised against the GluN1 or GluN2B subunit of NMDARs markedly block the binding of the $A\beta$ oligomer to neurons^[98, 99], indicating that $A\beta$ oligomers partially co-localize with the GluN2B subunits of NMDARs at the cell surface^[100]. Indeed, $A\beta$ directly or indirectly binds to NMDAR subunits to activate NMDAR, and thus $A\beta$ oligomers induce calcium dysregulation, neuronal death^[101], and synaptic dysfunction^[102, 103]. Moreover, $A\beta$ oligomers promote the endocytosis of NMDARs, which requires the activation of $\alpha 7nAChR$ signaling^[104]. The receptor $\alpha 7nAChR$ is another candidate $A\beta$ -binding receptor and binds to soluble $A\beta$ with high affinity^[105]. The $\alpha 7nAChR$ -expressing cells are susceptible to $A\beta$ -induced toxicity *in vitro*^[106], and it mediates $A\beta$ -induced tau phosphorylation via the ERK and JNK pathways^[107]. In a mouse model of AD, $\alpha 7nAChR$ may exacerbate AD pathology in a mouse model, while its deficiency may improve cognitive deficits and synaptic pathology^[108].


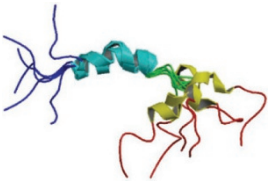
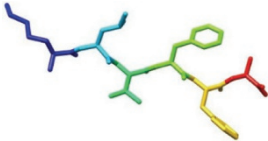
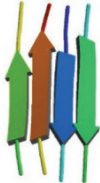
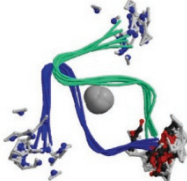

$A\beta$ binding p75 neurotrophin receptor (p75NTR)

The receptor p75NTR is a TNF family low affinity receptor for neurotrophins. $A\beta$ binds to both p75NTR monomers and trimers (Figure 4), which activates their intracellular signaling to induce apoptosis in human neuroblastoma cells. Early studies compared neuroblastoma cell clones that either did not express any of the neurotrophin receptors or had been engineered to express full-length or various truncated forms of the p75NTR^[109]. These studies showed that p75NTR binds to $A\beta$ via its extracellular domain, which directly signals cell death via its death domain. In fact, this signaling leads to the activation of caspase 8 and caspase 3 and to the production of reactive oxygen species (ROS) and cellular oxidative stress^[110]. In addition, $A\beta$ can interact synergistically with cytokines TNF α

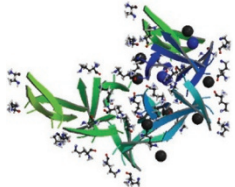
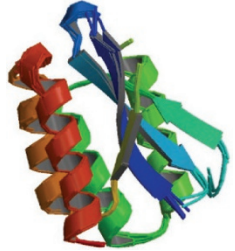
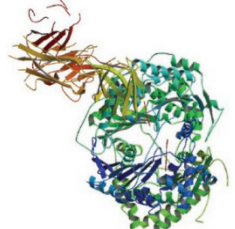
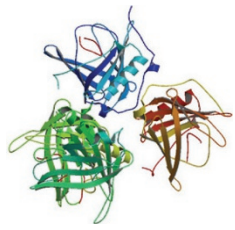
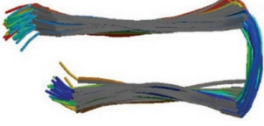
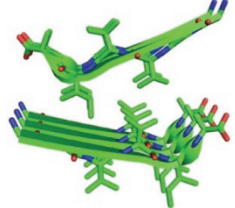
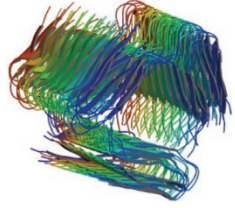
Table 1. Summary of A β structural studies.

Proteins and peptides	Structure	Characteristic	PDB code
A β 1-28		Monomer; NMR; In membrane-like media the peptide folds to form a predominately alpha-helical structure with a bend centered at residue 12.	1AMC 1AMB
A β 1-40 with Met(O)		Monomer; NMR; forms C-terminal alpha-helix; two acidic amino acids promote a helix-coil conformational transition.	1BA4 1BA6
A β 10-35		Monomer; NMR spectroscopy; A β collapsed into a compact series of loops, strands, and turns and the absence of alpha-helical or beta-sheet structure in water.	1HZ3
A β 1-42		Monomer; NMR; two helical regions encompassing residues 8-25 and 28-38, connected by a regular type I beta-turn.	1IYT
Two mutants (K16E, K16F) of A β 1-28		Monomer; NMR spectroscopy; the two mutations may stabilize the helix and also influence aggregation and fibril formation.	1BBJ 1BJC
Rat A β 1-28 and its interaction with zinc		Monomer; NMR spectroscopy; A helical region from Glu16 to Val24 exists; Arg13, His6, His14 residues provide Zn ²⁺ -binding sites; Zn ²⁺ -binding is more stable.	1NMJ

(To be continued)

Proteins and peptides	Structure	Characteristic	PDB code
A β 25-35		Monomer; CD and NMR; A β (25-35) is highly toxic and forms fibrillar aggregates.	1QWP 1QXC 1QYT
A β 1-42		Monomer; CD and Solution NMR; Alpha helix embedded in membrane, beta-sheet structures of amyloid fibrils	1Z0Q
A β 16-21		X-Ray; fiber-forming segments of A β . Self-complementing pairs of β -sheets termed steric zippers.	2Y29
A β 35-42		Polymorphic oligomers, protofibrils, and fibers; Homo tetramer-A4; β -sheets termed steric zippers.	2Y3L
A β 1-40		Rat homo dimer-A2; Solution NMR; zinc-binding domain formed by residues 1-16 of A β .	2LI9
A β 1-40		Monomer; Solution NMR; 3_{10} -helix from H13 to D23 and the N- and C-termini collapse against the helix.	2LFM

(To be continued)

Proteins and peptides	Structure	Characteristic	PDB code
A β 17-36		Homo 16-mer-A16; X-Ray; Crystallizes to form trimers that further assemble into oligomers; Trimers consist of three β -hairpins; Two trimers form hexamer; four trimers form dodecamer, and 5 dodecamers form an annular pore.	5HOW
A β 1-40 in complex with affibody protein Z (A β 3)		Homo trimer-A3; Solution NMR; Z(A β 3), nanomolar affinity, Bound A β (1-40) features beta-hairpin comprising residues 17-36	20TK
A β 1-40 in complex with Fab-bound human Insulin Degrading Enzyme (IDE)		Hetero trimer-ABC; X-Ray	4M1C
A β 1-40 complex with an engineered lipocalin (Anticalin H1GA)		X-Ray	4MVI 4MVK 4MVL
A β 1-42 fibrils		Homo pentamer-A5; Solution NMR; residues 18-42 form intermolecular parallel beta-strand-turn-beta-strand motif	2BEG
A β 37-42 fibrils		Homo tetramer-A4; X-Ray; a pair of beta-sheets, with the facing side chains of the two sheets interdigitated in a dry 'steric zipper'	2ONV
A β fibrils		Fibrils; solid-state NMR; the fibril backbone arrangement, stacking registry, and "steric zipper" core interactions	2MPZ

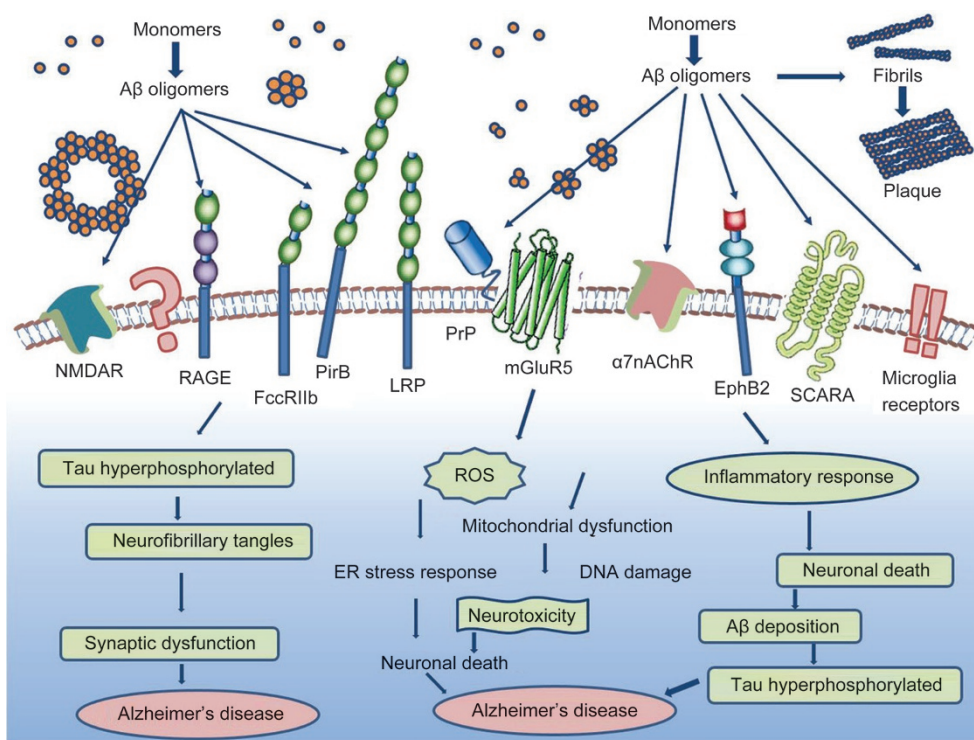


Figure 4. Biological functions of A β . A β monomers can form higher order assemblies ranging from low molecular weight oligomers (including dimers, trimers, tetramers, and pentamers) to midrange-molecular weight oligomers, high molecular weight oligomers, protofibrils fibrils and senile plaques. Soluble A β can interact with potential receptors and activate downstream pathways to generate reactive oxygen species, hyperphosphorylate Tau protein, and cause inflammatory responses, which may result in neuronal death and lead to Alzheimer's disease.

and IL1 β , which markedly strengthens the neurotoxic actions of A β /p75NTR signaling and potentiates neuronal damage. A β -bound p75NTR triggers cell death in the hippocampus of human Alzheimer's disease brains. Taken together, these findings indicated that p75NTR-expressing neurons endowed with receptors for proinflammatory cytokines might be the reason for the target selectivity of A β cytotoxic actions in Alzheimer's disease^[111,112].

Low-density lipoprotein receptor-related protein (LRP)

The low-density lipoprotein receptor-related protein (LRP), also known as alpha-2-macroglobulin receptor (A2MR), apolipoprotein E receptor (APOER) or cluster of differentiation 91 (CD91), is a protein receptor found in the plasma membrane of cells involved in receptor-mediated endocytosis. LRP1 is involved in various biological processes such as lipoprotein metabolism and cell motility, and pathologically in neurodegenerative diseases, atherosclerosis and cancer^[113].

LRP is a multifunctional cell surface receptor of more than 600 kDa in size with a single transmembrane-spanning domain. LRP has more than 20 identified ligands, many of which are localized to the central nervous system. The broad categories of these ligands include apolipoprotein E (apoE) and lipid-related ligands as well as protease and protease inhibitor complexes such as APP containing Kunitz proteinase inhibitor, α 2M, tissue plasminogen activator and plasminogen activator inhibitor 1 complexes, and others such as lactofer-

rin. Cholesterol is imported into neurons by apoE via LRP1 receptors. Starving neurons of cholesterol and malfunction of the neuronal cholesterol metabolism is thought to be a causal factor in Alzheimer's disease^[114]. In addition, over-accumulation of copper in the brain is associated with reduced LRP1-mediated clearance of A β across the blood brain barrier. This defective clearance may contribute to the buildup of neurotoxic A β ^[115]. Together, these studies support a critical role of the multifunctional receptor LRP in A β metabolism and Alzheimer's disease.

LRP also interacts with the amyloid precursor protein itself. LRP regulates APP trafficking and processing by different mechanisms. SorLA (also called SORL1, SORLA1, or LR11) is a neuronal apolipoprotein E receptor that can regulate the intracellular transport and processing of the APP in neurons. It alters the localization of APP to discrete intracellular compartments, resulting in a decrease of extracellular A β levels^[116]. LRP and LRP1B expression and endocytosis are thought to play opposing roles in APP endocytosis, resulting in increased APP processing to A β levels in the presence of LRP for a rapid fast endocytosis rate and decreased A β production in the presence of LRP1B for a slower endocytosis rate^[117].

PrP^C and mGlu5 receptors in astrocyte upregulation by A β

PrP^C is a glycosylphosphatidylinositol (GPI)-anchored membrane protein that can undergo a conformational change to an infectious, pathological state called scrapie prion protein

(PrP^{Sc}), which is linked to transmissible spongiform encephalopathies and causes terminal neurodegenerative disorders^[118]. PrP^c-binding ligands include the laminin γ 1-chain, Cu²⁺ ions and A β 42 oligomers^[119, 120], the latter of which binds PrP^c with high affinity^[121].

Metabotropic glutamate receptors (mGluR5) are members of the G-protein coupled receptor superfamily. mGluR5 has been specifically implicated in neurodegenerative diseases such as Alzheimer's disease, Parkinson's disease and Huntington's disease^[122-124]. The activation of mGluR5 has been shown to decrease the fragile X mental retardation protein (FMRP)-mediated translation repression of APP and to stimulate sAPP α secretion, which induces the β -secretase pathway and A β production. FMRP can stimulate neural pruning and synaptic plasticity, which results in neuroprotection under normal physiological conditions^[125]. More recently, mGluR5 has been suggested to be the primary co-receptor for both PrP^c and A β oligomers^[126] (Figure 4). The extracellular domain of mGluR5 interacts with both PrP^c and A β 42, which results in the activation of Ca²⁺ release from intracellular stores, thus promoting PKC translocation and ERK1/2 phosphorylation. A β 42 and PrP^c also activate mGluR5 to stimulate Fyn kinase-mediated APP protein translation.

Immune globulin receptors FccRIIb and PirB

Two immune globulin receptors, FccRIIb and PirB, originally believed to function exclusively in the immune system, were recently shown to play neuropathic roles as A β receptors in Alzheimer's disease brains^[97, 127, 128]. These two proteins show similarity in their structures and in the high binding affinity for A β oligomers. Both have immunoglobulin (Ig) domains in their extracellular domains and immunoreceptor tyrosine-based inhibitory (ITI) motifs in their intracellular domains. FccRIIb has two Ig domains and one ITI motif, whereas PirB has six Ig domains and four ITI motifs. FccRIIb interacts with low-molecular-weight oligomers via its second Ig domain, and PirB binds to high-molecular weight-oligomers via its first two Ig domains.

Other receptors

Other receptors, such as microglia receptors, are also involved in the amyloid cascade. Microglial membrane receptors bind A β and contribute to microglial activation and A β phagocytosis and clearance. These receptors can be categorized into several groups. The scavenger receptors (SRs) include scavenger receptor A-1 (SCARA-1), MARCO, scavenger receptor B-1 (SCARB-1), CD36 and the receptor for advanced glycation end product (RAGE)^[129]. The G-protein coupled receptor (GPCR) group includes formyl peptide receptor 2 (FPR2) and chemokine-like receptor 1 (CMKLR1)^[130], and the toll-like receptor (TLR) group includes TLR2, TLR4, and the co-receptor CD14^[131]. Functionally, SCARA-1 and CMKLR1 participate the uptake of A β , and RAGE is responsible for the activation of microglia and production of proinflammatory mediators in response to A β binding. CD36, CD36/CD47/ α 6 β 1-integrin, CD14/TLR2/TLR4, and FPR2 display functions in both A β

binding and microglia activation. In addition, MARCO and SCARB-1 exhibit the ability to bind A β and may be involved in the progression of Alzheimer's disease^[132].

A variety of microglia receptors are involved in A β clearance and in triggering an inflammatory response. Some receptors, including RAGE and NLRP3, are mainly implicated in the generation of an inflammatory response by triggering a signaling cascade that results in the production of proinflammatory mediators^[133]. Other receptors, such as SR-AI and TREM2, participate the clearance of A β by inducing internalization of A β fibrils. Complement receptors, Fc receptors, FPRL1/FPR2, CD36, and TLRs are involved in both A β clearance and the generation of inflammatory responses, while the microglia receptor CD33 seems to accelerate A β accumulation.

A β degradation

The production of A β is normally counterbalanced by several processes, including proteolytic degradation, cell-mediated clearance (which may itself involve proteolytic degradation), active transport out of the brain, and deposition into insoluble aggregates. A growing body of evidence suggests that proteolytic degradation is a particularly important determinant of cerebral A β levels and, by extension, of A β -associated pathology^[134]. The individual A β -degrading proteases neprilysin, endothelin-converting enzymes, insulin-degrading enzyme, plasmin and other A β -degrading proteases play important roles in A β degradation and Alzheimer's disease, although their relative importance remains to be established (Figure 5).

Neprilysin (NEP) is a 93-kDa zinc metallo-endopeptidase implicated in the degradation of a wide array of bioactive peptides^[135] and is the most efficient A β peptidase. It is a type 2 membrane glycoprotein with its active site located in the intraluminal/extracellular space, into which A β peptides are normally secreted^[136]. NEP is also localized to the early Golgi and endoplasmic reticulum and other subcellular compartments. Synthetic A β was first demonstrated to undergo proteolysis by NEP, and A β degradation was most strongly inhibited by a potent and selective inhibitor of NEP, thiorphan^[137]. The overexpression of NEP resulted in a lack of amyloid accumulation in APP transgenic mice, while the absence of NEP expression resulted in amyloid aggregation in APP transgenic mice^[138, 139]. These experimental and clinical observations, therefore, support the hypothesis that A β degradation and the development of idiopathic Alzheimer's disease may be greatly affected by the regulation of an aging-induced reduction of NEP activity.

Endothelin converting enzymes 1 and 2 (ECE1 and ECE2) are membrane-bound zinc metalloproteinases belonging to the same family as NEP (M13 family). While other members of the M13 family are capable of degrading A β in cell culture or *in vitro*^[140, 141], the addition of phosphoramidon, a known inhibitor of ECEs, can significantly elevate the secretion of A β into the medium of cultured cells. The overexpression of ECEs in cultured cells stably expressing APP led to a reduction of more than ninety percent in the level of secreted A β , and this effect was reversed by treatment with phosphoramidon. Taken together, the involvement of ECEs may play a causal role in

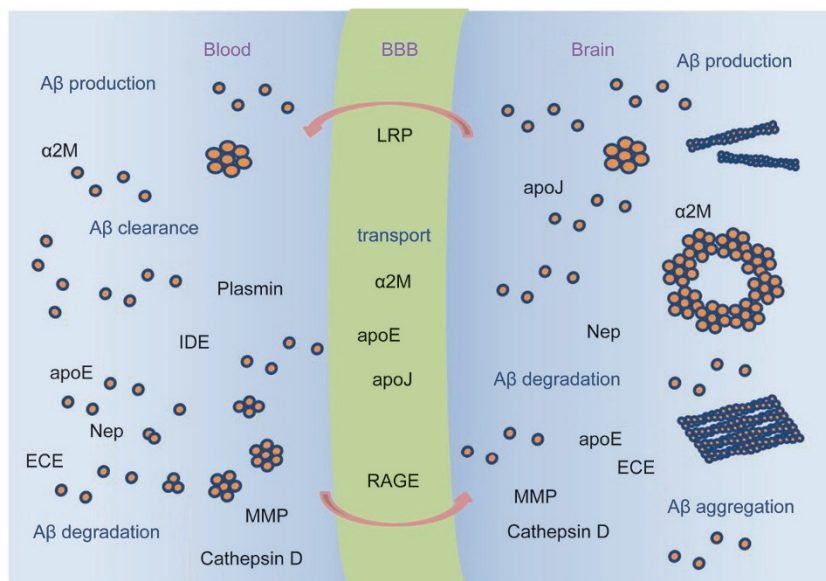


Figure 5. A β homeostasis involves production, aggregation, transport, degradation, and clearance. A β is produced in peripheral tissues and the CNS, where it can aggregate and form insoluble fibrils. Soluble A β can be transported across the BBB from blood to brain via RAGE, and from brain to blood via LRP. A β can also bind to transport proteins, eg, apoE, apoJ, α 2-macroglobulin (α 2M), which may influence A β sequestration as well as the form of its accumulation in brain. A β can be proteolytically degraded by the proteases Neprilysin (Nep), endothelin converting enzymes (ECE), insulin degrading enzyme (IDE), plasmin and other A β -degrading proteases (MMP, Cathepsin D), as well as by microglia-mediated degradation.

the degradation of A β ^[142].

Insulin-degrading enzyme (IDE) is a 110-kDa zinc metallo-endopeptidase that degrades a broad range of substrates, including insulin, glucagon, and amylin, along with a range of other bioactive peptides^[143], as well as the intracellular domain of APP^[144]. Early studies identified IDE as the first protease to degrade A β *in vitro* within crude brain homogenates^[145], and IDE was later identified independently as the major A β degrading component secreted into the medium by a range of cultured cells^[146]. Moreover, IDE might indirectly affect A β levels via its effects on AICD levels, which has recently been implicated in the transcriptional regulation of APP^[147] and neprilysin expression^[148-149].

Plasmin is a serine protease that is the ultimate effector in the fibrinolytic cascade. Plasmin can degrade and reduce the toxicity of both monomer and fibril A β ^[150-153].

Other candidate A β -degrading proteases remain to be identified. The matrix metalloproteases (MMPs) MMP2 and MMP9^[154, 155] have been shown to degrade A β *in vitro*. Angiotensin-converting enzyme is yet another metalloprotease that may play an important role in the pathogenesis of Alzheimer's disease and that has been shown to degrade A β *in vitro*^[156]. Cathepsin D, an aspartyl protease localized within lysosomes and endosomes, was identified as a major A β -degrading enzyme in brain homogenates^[157], and its expression level in the brain is altered in Alzheimer's disease^[158].

A β transport

In addition to degradation, A β released into the extracellular space can be transported between different compartments, such as from the brain to the blood or from the blood to the

brain, and can also be cleared by chaperones, such as apoE, which can affect A β metabolism after it is released by cells and influence A β aggregation, clearance, and transport^[159].

The carrier- and receptor-mediated transport of A β across the blood brain barrier (BBB) regulates brain A β levels^[160-165]. The concentration of soluble A β in the CNS, which is central to the formation of neurotoxic oligomeric A β species^[166] and vascular aggregated forms of A β , is critically influenced by A β transport exchange across the BBB. This transport process has been reported to be regulated by receptors, such as advanced glycation end products (RAGE)^[167], or the low-density lipoprotein receptor-related protein 1 (LRP1)^[168, 169]. Moreover, other receptors such as glycoprotein 330 (gp330/megalin)^[170] and P-glycoprotein^[171] may also contribute to the transport of A β across the BBB, and the A β -binding proteins α 2-macroglobulin, apoE and apoJ appear to influence this process^[172]. The levels and form of A β may be greatly determined by not only the vascular clearance and BBB transport of A β , proteolytic degradation^[173, 174], oligomerization, and aggregation but also by the production^[175, 176] and clearance of different forms of A β (fibrillar *vs* soluble) by other cells of the neurovascular unit, such as astrocytes^[177-179]. These activities may also play a major role in determining the brain accumulation and associated neuronal and vascular toxicity. Plasma A β levels may contribute more to Alzheimer's disease toxicity in cognitively normal elderly individuals^[180, 181]. Strategies to clear A β from the vascular system can reduce the A β levels and amyloid load in the CNS. These strategies include the use of an anti-A β antibody^[182-184], non-immune approaches with gelsolin, GM1^[185], sRAGE^[186] or soluble forms of LRP-1, sLRP-1 fragments^[187] and insulin-like growth factor I^[187]. Many receptors

are involved in inducing A β transport and clearance. Among them, RAGE is an influx transport receptor that binds soluble A β and mediates pathophysiological cellular responses^[188-190]. RAGE also mediates the transport of plasma A β across the BBB. LRP-1 functions as a clearance receptor for A β at the BBB^[191, 192] (Figure 5).

ApoE can regulate A β transport, clearance, and aggregation. ApoE is a 299-amino-acid lipid transport protein expressed as three different isoforms: apoE2, apoE3 and apoE4. E3 is the most common isoform, and E4 is responsible for a genetic predisposition to Alzheimer's disease, increasing the risk of Alzheimer's disease by approximately 3-fold more than the E3 allele, whereas E2 decreases AD risk^[193]. Glial cells such as astrocytes and microglia secrete apoE into the interstitial fluid (ISF) of the brain. When A β is secreted into the brain ISF, mostly by neurons, apoE-containing high-density lipoproteins (HDL) interact with A β and influence its clearance into cells via the endocytic LDL receptor family member LDLR. The binding of apoE/A β complexes to heparin sulfate proteoglycans (HSPG) can increase the retention of A β in the extracellular matrix of the brain and arterioles. This process may play a role in the development of cerebral amyloid angiopathy (CAA)^[194]. ApoE and A β have been shown to colocalize in detergent-insoluble glycolipid-rich membrane domains (DIGs), which may promote their interaction. In the ISF, apoE/A β interactions likely determine whether and when A β will aggregate. ApoE may also play a role in A β transport out of the brain via ISF/bulk flow, which can modulate both soluble and fibrillary A β clearance as well as transport and fibrillogenesis and, in doing so, plays an important role in Alzheimer's disease and CAA pathogenesis^[195].

A β forms and their toxicity

The different forms of A β include soluble A β , A β oligomer and A β present in amyloid plaques. In addition, a dynamic compartmentalization of the different types of A β may exist between plaques and soluble A β ^[196], and the different A β forms may contribute to neurodegeneration at different stages of the disease^[197]. A β has also been reported to form aggregates in two fundamental types of reactions: non-metal-dependent association and metal-dependent association. Non-metal A β aggregates form soluble oligomers and amyloid fibrils, while metal A β aggregates form ionically bridged aggregates, covalently crosslinked oligomers, and seeds for non-metal-dependent A β fibrillization^[198]. Accumulating A β first forms A β oligomers and gradually deposits as fibrils and senile plaques. In addition, tau protein becomes hyperphosphorylated in response to kinase/phosphatase activity changes mediated by A β aggregation, leading to the formation of neurofibrillary tangles (NFTs), neuronal and eventual synaptic dysfunction, and finally Alzheimer's disease (Figure 4). When the process of self-aggregation occurs on neuron membranes, it generates a toxic aldehyde called 4-hydroxynonenal and leads to lipid peroxidation, which can damage the function of ion-motive ATPases, glucose transporters and glutamate transporters. In turn, A β promotes depolarization of the syn-

aptic membrane, excessive calcium influx and mitochondrial damage, which impairs the ability of cells to conduct normal physiological activities^[79].

Furthermore, the aggregation of A β may also produce free radicals as ROS that react rapidly with proteins or lipids, resulting in the formation of "toxic" oxidized proteins and peroxidized lipids. Oxidized proteins are harmful to the membrane integrity and may also alter the sensitivity to oxidative modifications of enzymes such as glutamine synthetase (GS) and creatine kinase (CK), which are critical to neuronal function^[199, 200]. Peroxidized lipids can generate toxic products such as 4-hydroxy-2-nonenal (HNE) and 2-propenal (acrolein) that migrate to different parts of neurons and cause multiple harmful alterations to cellular activity. The deleterious functions associated with neuronal death include the inhibition of ion-motive ATPases and glial cell Na⁺-dependent glutamate transport, loss of Ca²⁺ homeostasis, and disruption of signaling pathways^[201-203]. In addition to proteins and lipids, oxidative stress induced by A β aggregation has also been reported to cause DNA oxidation, leading to DNA damage.

Sustained elevation of A β levels and continuous aggregation might also promote a chronic response of the innate immune system by activating microglia, which can lead to neuronal loss through direct phagocytosis. The immunological receptors that are activated by A β include toll-like receptor 2 (TLR2), TLR4, TLR6, and their co-receptors CD14, CD36, and CD47^[204, 205]. In addition, A β aggregation also causes inflammatory responses and the release of inflammation-related mediators, such as eicosanoids, chemokines, proinflammatory cytokines and complement factors, which can increase neuronal death and the loss of neuronal synapses and impair the clearance of A β and the neuronal debris mediated by microglia. In addition to the microglia driven neuroinflammatory response^[206], this processes is probably also mediated indirectly by regulating kinase/ phosphatase activity.

Moreover, when the A β precursor APP accumulates at the mitochondrial membrane, it blocks the translocation of inner mitochondrial metabolites and proteins, leading to disruption of the electron-transport chain and mitochondrial dysfunction, which may in turn increase excessive A β generation and result in greater toxicity in a feed-forward loop^[207, 208]. Excessive A β levels also activate the mitochondrial fission proteins Fis1 and Drp1, thereby inducing mitochondrial fragmentation^[209]. A β localized in the mitochondria can interact with the proapoptotic factors A β -binding alcohol dehydrogenase (ABAD) and cyclophilin D (CypD), resulting in increased neuronal cell death^[210]. Therefore, there may be a vicious feedback loop between increased A β production and mitochondrial dysfunction.

Extracellular deposits of fibrils or amorphous aggregates of A β peptide form plaques and diffuse deposits, while intracellular fibrillar aggregates of hyperphosphorylated and oxidated tau can form neurofibrillar tangles. These plaques and neurofibrillary tangles are deposited mainly in brain regions, such as the hippocampus, amygdala, entorhinal cortex, and basal forebrain, that influence memory and learning and emotional behaviors. A β can damage synapses and neurites, and plaque

deposits in brain regions reduce the number of synapses. A β specifically damages neurons that produce serotonin and nor-epinephrine or that employ glutamate or acetylcholine as neurotransmitters. After synthetic A β fragments were found to kill cultured neurons^[211], the chemical and cell biological bases for the synaptic dysfunction and death of neurons in Alzheimer's disease were reported by a series of studies. A β , particularly in its aggregating forms, can impair synaptic ion and glucose transporters, and electrophysiological studies have shown that A β impairs synaptic plasticity. Decreasing sAPP α levels can increase the resistance of neurons to oxidative and metabolic insults, which is consistent with sAPP α contributing to the demise of neurons, which is coincident with the increased production of A β in Alzheimer's disease^[212, 213]. Memory deficits correlate with the formation of A β oligomers, which appear relatively early in the process of A β deposition in APP mutant mice^[214]. Remarkably, the immunization of APP mutant mice with human A β 42 resulted in the removal of A β deposits from the brain and the reversal of cognitive deficits, adding to the evidence that A β deposition is a pivotal event in Alzheimer's disease^[215].

A β and Alzheimer's disease

The cause of most Alzheimer's cases is still unknown. Although it is characterized mostly by the formation of amyloid plaques in the brain, there are several other competing hypotheses regarding the cause of the disease.

The amyloid hypothesis proposed that the fundamental cause of the Alzheimer's disease is the deposits of extracellular A β peptides^[216]. Mutations in the human *APP* gene cause the development of amyloid plaques and Alzheimer's-like brain pathology, especially in early-onset familial Alzheimer's disease (EOFAD)^[217, 218]. Mutations in the human *APP* gene are close to the γ -secretase site and can increase the A β 42/A β 40-ratio. It is reported that mutations that alter residues C-terminal to the A β 42 site reduce cleavage efficiency and increase the A β 42/A β 40 ratio^[219]. AD-causing mutations also occur in the genes *PSEN1* and *PSEN2*. Mutations in the human *PSEN1* and *PSEN2* genes affect γ -secretase activity and can increase the A β 42/A β 40 ratio. Some early-onset families do not show mutations in *APP*, *PSEN1* or *PSEN2*. Several additional key proteins may be involved in γ - and β -secretase cleavage events, as well as in the hyperphosphorylation of tau and the development of neurofibrillary tangles^[65, 220]. Late-onset Alzheimer's disease (LOAD) is characterized by a pattern of interwoven genetic and non-genetic factors. These risk-factor genes each affect one or more of the known pathogenic mechanisms: increased A β production and aggregation; decreased A β clearance and degradation; increased inflammation; and resistance to γ -secretase activity, and thus lead to neurodegeneration in AD^[221]. Among these risk genes, for *APOE*, the alleles occurring at the *APOE* loci ϵ 2, ϵ 3 and ϵ 4 were tested and shown to be associated with increased risk of AD^[222, 223]. Other researchers have been led to suspect that non-plaque A β oligomers are toxic and might be the main cause of neurodegenerative disorders such as Alzheimer's disease^[224].

Non-A β hypothesis

The cause of most Alzheimer's cases is still unknown. Numerous reports on genetic evidence suggest that A β and its aggregation in senile plaques play an important role in the pathogenesis of AD. A β cleavage by β -secretase and γ -secretase from APP can result in oligomers that form higher-order fibrils, which then give rise to A β plaques. However, genetic causes only explain the small proportion (1% to 5%) of AD cases in which genetic differences have been identified^[225]. The dominant mutations in the genes *APP*, *PSEN1* and *PSEN2*^[226], which are implicated in AD pathology, are only present in a very small portion of Alzheimer's cases. It has also been reported that the accumulation of the more insoluble A β 42 over A β 40 is an important trigger for AD pathogenesis, while APP can alternatively be cleaved by α -secretase to generate non-plaque-forming extracellular peptides in the non-amyloidogenic processing pathway^[227]. Our previous studies have tested the effect of all 28 FAD-linked C99 mutations and found that most familiar Alzheimer's disease (FAD)-linked APP mutant proteins cause partial resistance to γ -secretase cleavage^[228]. Among them, only mutations that affect residues C-terminal to the A β 42 cleavage site (A β 42-53) markedly affect cleavage efficiency and increase the A β 42 production that leads to AD.

AD pathogenesis includes both A β -dependent and A β -independent mechanisms. There are still many doubts about the real pathogenesis of AD and the β -amyloid contribution to the onset of the disease. A β or A β oligomers or plaques are not solely responsible for the onset of the disease. More than 30 mutations responsible for FAD are localized in the APP gene; however, the "type London" APP mutations, causing only a slight increase in β -amyloid production, cause the onset of the pathology earlier than the "type Swedish" mutations, which induce a greater increase of the protein^[229], suggesting that there are other mechanisms involved in the onset of AD. In fact, the A β -independent mechanisms are mediated via APP, intracellular fragments and PS1 via the cellular processes, such as inflammation, oxidative stress and Ca²⁺ dysregulation, implicated in AD pathogenesis^[230]. Cdk5 may be influenced by or interact with both pathways, and its activation triggers DNA damage, cell cycle activation and neurodegeneration^[231]. Non-A β factors such as Tau and ApoE also contribute to AD pathology^[232]. All these pathways can lead to synaptic dysfunction, neurodegeneration and AD.

The senile plaques also do not seem to be an exclusive feature of Alzheimer's disease. They increase with age, even in healthy subjects, and the number of plaques in healthy controls is often comparable with the number found in age-matched affected individuals^[233]. Moreover, β -amyloid is physiologically produced in healthy brains during neuronal activity and is necessary for synaptic plasticity and memory^[234]. Furthermore, in the AD population, there is only a weak correlation between the number of senile plaques and the severity of the pathology. The cleavage of APP by γ -secretase produces some fragments called AICD (APP intracellular domain), which appear to play an important role in the onset of AD. In fact, it

is known that transgenic mice for AICD show tau phosphorylation and aggregation and decreased cell proliferation/survival, even in the absence of endogenous APP^[235]. High levels of AICD may also play an important role in the pathology in human brains^[236]. The challenges to the Amyloid Hypothesis of Alzheimer's Disease are sharply formulated^[237]. There are several other competing hypotheses, such as the cholinergic hypothesis, the tau hypothesis, and the hypothesis that some other environmental risk factors, may contribute additional causes of the disease.

The cholinergic hypothesis proposed that AD is caused by cholinergic effects such as reduced synthesis of the neurotransmitter acetylcholine, or the initiation of large-scale aggregation of amyloid and neuroinflammation^[238, 239]. Most currently available drug therapies are based on this hypothesis^[240].

The genetic heritability of Alzheimer's disease reveals that most AD is caused by mutations in one of the genes that encoding APP and presenilins 1 and 2^[241]. Most mutations in these genes increase A β 42 production. Environmental and genetic risk factors, such as the ϵ 4 allele of the apolipoprotein E (APOE)^[242], increase the risk of the disease by threefold. Mutations in the TREM2 gene make the risk of developing Alzheimer's disease several times higher^[243]. Other genes also appear to affect the risk, including *CASS4*, *CELF1*, *FERMT2*, *HLA-DRB5*, *INPP5D*, *MEF2C*, *NME8*, *PTK2B*, *SORL1*, *ZCWPW1*, *SIC24A4*, *CLU*, *PICALM*, *CR1*, *BIN1*, *MS4A*, *ABCA7*, *EPHA1*, and *CD2AP*^[244].

The tau hypothesis postulates that tau protein abnormalities initiate the disease cascade as hyperphosphorylated tau forms neurofibrillary tangles, leading to the disintegration of microtubules in brain cells^[245], which may result in dysfunction of the biological activity between neurons and later in the death of the cells.

Other hypotheses include such environmental risk factors as smoking and infection, and a neurovascular hypothesis has been proposed, suggesting that the blood-brain barrier is critical for brain A β homeostasis and regulates A β transport via the LRP receptor and RAGE, as mentioned before^[246]. These findings point to new therapeutic targets for AD.

A β and inflammation

A β peptides are the major components of the senile plaques present in Alzheimer's disease. Recent studies have shown that the soluble assemblies of A β also stimulate neuronal dysfunction and may play a prominent role in stimulating the proinflammatory activation of primary microglia^[247]. In the context of inflammation, compared to fibrillar assemblies, oligomer A β preparations induce greater or differential proinflammatory cytokine production by microglia and astrocytes *in vitro*^[248]. Indeed, studies in primary glia demonstrate that the oligomer A β -induced increase in proinflammatory cytokines, such as nitric oxide, NO, TNF α and TNF β secretion, occurs earlier and is greater than the increase induced by fibrillar assemblies of A β ^[249]. Thus, for different forms of A β , identifying their levels at different stages of AD, the inflammatory response they produce, and their underlying mechanisms

(eg, receptor mediated) may provide critical information for therapeutic development.

Other aspects of biology of A β

In addition to the key role in the pathology of AD, A β generated in the brain and peripheral tissues also function in many other aspects of biology. A β has been shown to be a ligand with various receptors, as mentioned in the previous section. It can also be transported between tissues and across the blood-brain barrier by complex trafficking pathways^[176] to destinations where it can induce and modulate proinflammatory activities in response to a variety of environmental stressors^[250, 251]. A β also functions similarly to a group of biomolecules collectively known as "antimicrobial peptides" (AMPs) that function in the innate immune system. It inhibits the growth of eight of 12 clinically important pathogens screened^[252] and acts as an anti-microbial peptide in several infection models including mice, *C elegans*, and cell culture models^[253]. This new function stands in stark contrast to current models of A β -dependent pathology and will play significant roles in the development of future AD treatment strategies.

Therapeutic approaches for the treatment of Alzheimer's disease

Drugs approved by the FDA

To date, only a total of five drugs developed to improve the symptoms of Alzheimer's disease have been approved by the FDA. It is important to note that a new drug, Namzaric (donepezil and memantine)^[254] was approved in 2014. The five drugs function by two different mechanisms. One is cholinesterase inhibition, which delays Alzheimer's disease by blocking hydrolysis of the critical neurotransmitter acetylcholine. This category of drugs includes donepezil (Aricept)^[255, 256], approved in 1996; rivastigmine (Exelon)^[255, 256], approved in 2000; and galantamine (Razadyne)^[257], approved in 2001. The other one is memantine (Namenda)^[258], approved in 2003, a non-competitive *N*-methyl-*D*-aspartate (NMDA) channel blocker that reduces the activity of the neurotransmitter glutamate, which plays an important role in learning and memory by binding to the NMDA receptor. Memantine can inhibit the prolonged influx of Ca²⁺ ions, particularly from extrasynaptic receptors, that forms the basis of neuronal excitotoxicity. It is an option for the management of patients with moderate to severe Alzheimer's disease. Namzaric is a combination of the two drugs to reduce the levels of both acetylcholine and glutamate (Table 2).

Novel therapeutic approaches for Alzheimer's disease

Researchers have identified several novel therapeutic approaches for Alzheimer's disease that focus on the reduction of amyloid oligomer levels. Methods that are currently under development include the inhibition of oligomerization using small molecule inhibitors, the neutralization of oligomeric species using immunotherapy, the overexpression of A β -degrading enzymes to control A β oligomer levels in the

Table 2. Summary of approved drugs for the treatment of Alzheimer's disease.

Name	Targets	Effects	Ref
Donepezil (Aricept)	Cholinesterase inhibitor	Blocks acetylcholine neurotransmitter	[255, 256]
Rivastigmine (Exelon)	Cholinesterase inhibitor	Blocks acetylcholine neurotransmitter	[350]
Galantamine (Razadyne)	Cholinesterase inhibitor	Blocks acetylcholine neurotransmitter	[257]
Memantine (Namenda)	NMDA receptor antagonist	Blocks glutamate neurotransmitter and improves learning and memory	[258]
Donepezil and Memantine (Namzaric)	Cholinesterase inhibitor and NMDA receptor antagonist	Blocks acetylcholine and glutamate neurotransmitters and improves learning and memory	[254]

brain, catalytic A β antibodies to hydrolyze specific aggregates, β -sheet breakers to break existing β -sheet structures, A β blockers to block amyloid channels, and therapies directed against the tau protein to lead to the partial reversal of brain pathologies. All these approaches are in preclinical research stages, and their therapeutic efficiency remains unknown.

Small molecule inhibitors

These molecules (2-amino-4-chlorophenol, 4-aminophenol, 4-aminoanisole, 3,4-dihydroxybenzoic acid, 2-hydroxy-3-ethoxy benzoaldehyde) block A β oligomerization or fibrillization^[259]. Fourteen naturally occurring polyphenolic compounds and polyphenol-containing black tea extracts inhibit the assembly of alpha-synuclein into multimeric oligomers, which are cytotoxic and share common structural elements with amyloid oligomers^[260, 261]. Polyphenols derived from red wine prevent A β oligomerization and attenuate cognitive deterioration. The main phenolic component of olive oil, oleuropein, has been shown to possess antioxidant^[262], anti-inflammatory^[263] and hypolipidemic activities^[264]. Small molecules (NQTrp, CINQTrp, coumarin, furosemide, D737) that inhibit A β aggregation^[265, 266] or remodel toxic soluble oligomers of A β ^[267] inhibit oligomer formation^[268-274] (Table 3).

Secretase inhibitors and modulators

Since β -secretase and γ -secretase are responsible for the

release of A β from the intracellular domain of APP, compounds that can partially inhibit the activity of either β - or γ -secretase have been extensively explored. β -Secretase inhibitors (eg, MK-8931, CTS21166) can block the first cleavage of APP inside the cell^[275, 276]. A novel orally active β -secretase inhibitor, AZD3293, was tested in phase II/III clinical trials by Astra Zeneca and Eli Lilly^[277]. γ -Secretase inhibitors can block the second cleavage of APP in the cell membrane and were expected to stop the subsequent formation of A β and its toxic fragments^[278]. One γ -secretase inhibitor, semagacestat, was a candidate drug for a causal therapy against Alzheimer's disease, originally developed by Eli Lilly and Élan, but is unfortunately being stopped as there is no effect in phase III clinical trials^[279]. An alpha-secretase agonist, EHT-0202^[276], biases APP processing towards the non-amyloidogenic pathway. A new γ -secretase modulator, CHF5074, showed a longer survival time for treated animals^[280]. Selective A β 42-reducing agents (eg, tarenflurbil) modulate γ -secretase to decrease A β 42 production in favor of shorter A β versions^[281] (Table 4).

Immunotherapeutic approach

Immunotherapy stimulates the host immune system to recognize and attack A β or produces antibodies that enhance the clearance of A β oligomers or plaques to prevent plaque deposition. Active or passive A β immunization can prevent A β oligomerization, which is why antibodies to A β can be used to

Table 3. Summary of small molecule inhibitors of amyloid oligomers for the treatment of Alzheimer's disease.

Name	Targets	Effects	Ref
2-Amino-4-chlorophenol	Blocks A β oligomerization and fibrillization	Blocks neurotoxicity	[259]
4-Aminophenol	Blocks A β oligomerization and fibrillization	Blocks neurotoxicity	[259]
4-Aminoanisole	Blocks A β oligomerization and fibrillization	Blocks neurotoxicity	[259]
3,4-Dihydroxybenzoic acid	Blocks A β oligomerization and fibrillization	Blocks neurotoxicity	[259]
2-Hydroxy-3-ethoxy benzoaldehyde	Blocks A β oligomerization and fibrillization	Blocks neurotoxicity	[259]
Resveratrol	Remodels soluble oligomers and amyloid fibrils into nontoxic species	Attenuates cognitive deterioration	[351]
NQTrp	Inhibits the fibrillization of amyloidogenic proteins	Reduces A β aggregation	[269, 270]
CINQTrp	Inhibits the fibrillization of amyloidogenic proteins	Reduces A β aggregation	[269, 270]
Coumarin	Inhibits A β aggregation	Prevents cognitive decline	[266]
Furosemide	Inhibits A β oligomerization	Increases the life span	[273]
D737	Inhibits A β formation	Prevents toxicity and ROS accumulation	[274]

Table 4. Summary of secretase inhibitors and modulators for the treatment of Alzheimer's disease.

Name	Targets	Effects	Ref
Semagacestat (LY450139)	γ -Secretase inhibitor	Reduces A β formation	[278]
CHF-5074	γ -Secretase modulators	Increases life span	[280]
MK-8931	β -Secretase inhibitor	Reduces A β levels	[275]
AZD3293	β -Secretase inhibitor	Reduces the production of A β	[277]
CTS21166	β -Secretase inhibitor	Reduce the amount of beta-amyloid	[276]
EHT-0202	α -Secretase agonist	Biases APP processing towards the non-amyloidogenic pathway	[276]
Tarenfluril	Modulates β -secretase to reduce A β 42 production	Potential treatment for Alzheimer's disease	[281]

decrease cerebral plaque levels. This decrease is accomplished by promoting microglial clearance and redistributing the peptide from the brain to the systemic circulation. Several epitopes of A β are exposed and available for antibody capture of the soluble peptides, while others are available for antibodies to bind with oligomers. One such A β vaccine is CAD106, currently in clinical trial^[265], which induced efficacious A β antibody titers of different IgG subclasses mainly recognizing the A β 3-6 epitope. The 20-amino-acid SDPM1 protein can bind to A β 40 and A β 42 tetramers and block subsequent A β amyloid accumulation. A β 42 immunization leads to the clearance of amyloid plaques in patients with Alzheimer's disease but does not prevent progressive neurodegeneration^[282]. A more recent study showed that programmed death 1 (PD-1) inhibitors, which are FDA-approved cancer drugs, may be effective in clearing A β plaques and improving cognitive performance in a mouse model of Alzheimer's disease^[283]. Anti-A β antibodies (solanezumab, gantenerumab, crenezumab, IVIG), which can bind soluble A β and improve cognitive performance, are currently in clinical trials^[165, 284, 285]. Solanezumab accommodates a large A β epitope (960 Å² buried interface over residues 16 to 26) that forms extensive contacts and hydrogen bonds to the

antibody, largely via main-chain A β atoms and a deeply buried Phe19-Phe20 dipeptide core Solanezumab and crenezumab both share identity with the A β KLVFF epitope^[286]. The human anti-A β monoclonal antibody, gantenerumab, binds A β plaques and targets the N-terminus and central portion of A β ^[287]. Intravenous immune globulin (IVIG) derived from human plasma contains IgGs that recognize conformational epitopes of A β fibrils and oligomers^[288]. Intravenous immunoglobulin G^[289] and 2E6^[290] bind to soluble A β and reduce amyloid aggregation (Table 5).

Anti-aggregation agents

Anti-aggregation agents^[291], such as apomorphine, can prevent A β peptides from aggregating or clear aggregates once they are formed^[292]. The hormone melatonin may be effective against amyloid by interacting with dimers of the soluble A β peptide and inhibiting their aggregation^[293-295]. The cannabinoid HU-210^[296] has been shown to prevent A β -induced inflammation^[297]. The endocannabinoids anandamide and noladin have also been shown to be neuro-protective against A β *in vitro*^[298]. Apomorphine^[299], melatonin^[300], and tannic acid^[301] can prevent A β aggregation. A number of small mol-

Table 5. Summary of immunotherapeutic approaches for the treatment of Alzheimer's disease.

Name	Targets	Effects	Ref
CAD106	A β vaccine	Inhibits A β oligomerization and cytotoxicity	[352]
SDPM1	A β antibody	Blocks subsequent A β amyloid aggregation	[353]
PD-1 inhibitors	T-cell-mediated autoimmune meningoencephalitis	Clears A β plaques and improves cognitive performance	[354]
Gantenerumab	Humanized monoclonal antibody to A β	Binds to aggregated A β and reduces A β plaques in the brain	[284]
Solanezumab	Humanized monoclonal antibody to A β	Binds to soluble A β and reduces amyloid load via peripheral sink mechanism	[182]
Crenezumab	Humanized monoclonal antibody to A β	Inhibits aggregation and promotes disaggregation	[284]
IVIG	Human polyclonal anti-A β antibody	Binds to A β and reduces neurotoxicity	[285]
Intravenous immunoglobulin G	Human immunoglobulin preparation containing endogenous polyclonal antibodies to A β	Primarily binds to soluble A β and reduces amyloid load via peripheral sink mechanism	[289]
2E6	Heterodimer of immunoglobulin light chain variable domains	Hydrolyzes A β peptides	[290]

ecules extracted from traditional Chinese herbal medicine have been shown to be capable of inhibiting A β aggregation. Among them, LJW0F2 purified from the flowers of *Lonicera japonica Thunb* could inhibit A β 42 aggregation and attenuate the cytotoxicity induced by A β 42 aggregation^[302]. Resveratrol, curcumin, EGb761, isoliquiritigenin, protocatechuic acid, atractylenolide III, chlorogenic acid, euphorbiafactor L3, euphorbiafactor L2, ganoderic acid D, and ganoderic acid DM extracts from Chinese herbal medicine can inhibit A β aggregation^[303, 304]. A series of substituted bisphenol A derivatives function as A β aggregation inhibitors and can inhibit neurotoxicity and increase cell viability^[305] (Table 6).

A β -degrading proteases (A β DPs)

A β can be degraded by a number of peptidases and proteinases, collectively known as A β -degrading proteases (A β DPs). A β -degrading proteases play an important role in A β degradation and may be a good target for the treatment of Alzheimer's disease. NEP has been reported to degrade A β oligomers that impair neuronal plasticity and cognitive function^[306]. Several close homologues of NEP, NEP2^[307] and human membrane metalloendopeptidase-like protein (hMMEL)^[308], are also implicated in the degradation of A β ^[308]. Members of the M13 family of zinc metalloproteases, endothelin converting enzymes ECE1, ECE2, and ACE, are also known to be endogenous regulators of A β levels^[142, 309]. The serine proteases plasmin, urokinase type and tissue type plasminogen activators (uPA and tPA, respectively) and acyl peptide hydrolase (APH) have been found to degrade A β both directly and indirectly^[150, 310-312]. Several cysteine proteases, including cathepsin D^[141], cathepsin B^[282, 313], BACE1^[283, 291], and BACE2^[314] are also involved in A β degradation (Table 7).

Therapies directed against the tau protein

Neurofibrillary tangles (NFTs) caused by hyperphosphorylated tau are an important pathogenic factor in Alzheimer's

disease, and the tau protein is therefore also an important biological target for innovative therapies. The inhibition of tau protein oligomerization and aggregation, tau phosphorylation, microtubule stabilization [epothilone D (BMS-241027), TPI-287]^[315], and the enhancement of tau degradation as well as tau immunotherapy (ACI-35^[275]) are all potential strategies for Alzheimer's disease therapy. The tau protein hyperphosphorylation inhibitor LMTX can facilitate the clearance of tau from the brain and reduce A β aggregation and has reached phase three clinical trials^[316]. The anti-tau AADvac1 vaccine is currently being investigated in phase II trials. AADvac1 has been reported to significantly improve neurobehavioral deficits and reduce neurofibrillary degeneration and mortality^[317]. Moreover, glycogen synthase kinase 3 beta (GSK-3 β) inhibitors, such as tideglusib and humulin R, can block the phosphorylation of tau protein and thus are potential drug targets for Alzheimer's disease^[318] (Table 8).

Other blockers

A drug that is currently under investigation is liraglutide (Victoza), which is typically used as a diabetes drug. Treatment with Victoza improved object recognition and spatial recognition and resulted in cognitive benefits. Other histological benefits include a reduced inflammatory response and an increase in the number of young neurons in the dentate gyrus, where the A β level was also found to be significantly reduced^[319]. The β -sheet breakers or blockers that are capable of binding A β consist of short synthetic peptides. They destabilize the β -sheet structure and inhibit the formation of A β oligomers or amyloids^[320, 321]. A β oligomers can form calcium channels in membranes. Calcium conductance through these channels can be blocked by compounds MRS2481 and MRS2485, which destabilize the β -sheet structure and decrease A β -promoted neuronal toxicity^[322]. Bexarotene might serve as another class of anti-Alzheimer compounds by efficiently preventing the cholesterol-dependent increase in calcium fluxes promoted by

Table 6. Summary of anti-aggregation agents for the treatment of Alzheimer's disease.

Name	Targets	Effects	Ref
Apomorphine	Prevents A β aggregation	Reduces cellular toxicity	[299]
Hormone melatonin	Inhibits A β aggregation	Reverts amyloid deposition	[300]
Cannabinoid HU-210	Blocks microglial activation	Prevents A β -promoted inflammation	[296]
Tannic acid	Binds A β fibrils	Inhibits A β aggregation and cytotoxicity	[301]
LJW0F2	Polysaccharide that blocks A β fibril formation	Reduces neurotoxicity	[302]
EGb761	Inhibits A β aggregation	Reduces neurotoxicity	[303]
Isoliquiritigenin	Inhibits A β aggregation	Reduces neurotoxicity	[304]
Protocatechuic acid	Inhibits A β aggregation	Reduces neurotoxicity	[304]
Atractylenolide III	Inhibits A β aggregation	Reduces neurotoxicity	[304]
Chlorogenic acid	Inhibits A β aggregation	Reduces neurotoxicity	[304]
Euphorbiafactor L3	Inhibits A β aggregation	Reduces neurotoxicity	[304]
Euphorbiafactor L2	Inhibits A β aggregation	Reduces neurotoxicity	[304]
Ganoderic acid D	Inhibits A β aggregation	Reduces neurotoxicity	[304]
Ganoderic acid DM	Inhibits A β aggregation	Reduces neurotoxicity	[304]
Substituted bisphenol A derivatives	Inhibit A β aggregation	Inhibit neurotoxicity and increase cell viability	[305]

Table 7. Summary of β -degrading proteases (A β DPs) for the treatment of Alzheimer's disease.

Name	Targets	Effects	Ref
NEP	Endogenous regulator of A β	Degrades A β oligomers	[306]
NEP2	Homologues of NEP	Degradation of A β	[307]
hMMEL	Homologues of NEP	Degradation of A β	[308]
ECE1	Endothelin converting enzyme	Endogenous regulator of A β	[142, 309]
ECE2	Endothelin converting enzyme	Endogenous regulator of A β	[142, 309]
ACE	Endothelin converting enzyme	Endogenous regulator of A β	[142, 309]
Plasmin	Serine protease	Degrades both monomeric and fibrillar forms of A β	[150, 355]
Acylpeptide hydrolase	Serine protease	Degrades secreted A β dimers and trimers	[356, 357]
Cathepsin D	Cysteine protease	Degradation of A β	[358]
BACE1	Cysteine protease	Degradation of A β	[291]
BACE2	Cysteine protease	Degradation of A β	[359]
Cathepsin B	Cysteine protease	Degradation of A β	[282]

A β in neural cells^[323]. Voltage-gated calcium channel blockers, such as verapamil, diltiazem, isradipine and nimodipine, protect cultured neurons from A β -induced toxicity and thus could be potential candidates for treating Alzheimer's disease^[324]. The 5-HT₆ receptor antagonist idalopirdine, in combination with a cholinesterase inhibitor, may also increase cognitive function^[325]. Huperzine A^[326, 327], 2,2',4'-trihydroxychalcone (TDC)^[328] and bis(7)-cognitin^[329] exhibit neuroprotective effects. Aagenin^[330] and clioquinol^[331] can inhibit A β deposition. Other inhibitors, such as the RAGE inhibitor azeliragon, the α 7-nAChR inhibitor encenicline and the calcium antagonist nilvadipine, can improve memory and could be further candidates for Alzheimer's disease therapeutics^[332-334] (Table 9).

Amyloid dyes

The traditional method of identifying amyloid fibrils in tissue sections is by the use of amyloid-staining dyes. The first of these dyes was Congo red^[335], whose staining is linked to the presence of the cross- β structure of fibrils. Other amyloid dyes include iodine-sulfuric acid^[336], thioflavin T or S^[337], crystal violet^[338], methyl violet^[339], BTA-1^[340], chrysamine G^[341], ANS (1-anilinonaphthalene-8-sulfonic acid)^[342], bisANS (4,4'-dianilino-1,1'-binaphthyl-5,5'-disulfonic acid)^[342], Nile red^[343], K114 ((*trans, trans*)-1-bromo-2,5-bis (4-hydroxystyryl) benzene)^[344],

FSB^[345], curcumin^[346], nanocurcumin^[346], and others. The thioflavin T staining method is widely used to identify and classify amyloid proteins in tissues. Specific BTA-1 binding to A β plaques inhibits A β aggregation and cytotoxicity, making it a good drug candidate for Alzheimer's disease^[340]. These amyloid dyes not only indicate the presence of mature amyloids but also function as a tool for dissecting their structure and the mechanism of amyloid formation. They bind selectively to A β in the human brain and blood vessels *in vitro*. They might thus lead to further compounds for the development of tracer agents for the *in vivo* diagnosis of Alzheimer's disease and of inhibitors of A β aggregation as a novel therapy for Alzheimer's disease (Table 10).

MicroRNAs

MicroRNAs (miRNAs) are a class of conserved endogenous small noncoding RNAs known to regulate the expression of complementary messenger RNAs involved in AD development^[347]. MiRNAs in the brain play an important role in A β generation, targeting the mRNAs of APP, β -secretase and γ -secretase and altering A β expression. MiRNAs may provide a novel therapeutic approach to the treatment of AD while also providing new insights into the etiology of this neurological disorder^[348]. A series of specific miRNAs can regulate APP

Table 8. Summary of novel therapeutic approaches directed against the tau protein for the treatment of Alzheimer's disease.

Name	Targets	Effects	Ref
LMTX	Inhibitor of tau hyperphosphorylation	Facilitates clearance of tau from the brain and anti-A β aggregation	[316]
Epothilone D (BMS-241027)	Microtubule stabilizer	Increases BBB permeability and microtubule stability	[315]
TPI-287	Microtubule stabilizer	Increases BBB permeability and microtubule stability	[315]
AADvac1	Tau active vaccination	Improves neurobehavioral deficits, and reduces neurofibrillary degeneration and mortality	[317]
ACI-35	Anti-tau vaccine	Stimulates the immune system to produce antibodies which target the tau protein	[275]
Tideglusib	GSK-3 β inhibitor	Blocks phosphorylation of tau protein	[318]
Humulin R	GSK-3 β inhibitor	Blocks phosphorylation of tau protein	[318]

Table 9. Summary of other blockers for the treatment of Alzheimer's disease.

Name	Targets	Effects	Ref
Liraglutide (Victoza)	A diabetes drug	Cognitive benefits, reduced inflammatory response and an increase of young neurons	[319]
β -Sheet breaker	Binds A β and destabilizes its structure	Inhibits oligomer or amyloid formation	[320, 321]
MRS2481	Small molecule blocker of Abeta channel	Protects neurons from A β induced toxicity	[322]
MRS2485	Small molecule blocker of Abeta channel	Protects neurons from A β induced toxicity	[322]
Bexarotene	Inhibits the binding of cholesterol to A β and prevents calcium-permeable amyloid pore formation	Anti-Alzheimer	[323]
Verapamil	Voltage-gated calcium channel blocker	Protects neurons from A β -induced toxicity	[324]
Diltiazem	Voltage-gated calcium channel blocker	Protects neurons from A β -induced toxicity	[324]
Isradipine	Voltage-gated calcium channel blocker	Protects neurons from A β -induced toxicity	[324]
Nimodipine	Voltage-gated calcium channel blocker	Protects neurons from A β -induced toxicity	[324]
Huperzine A	A novel lycopodium alkaloid	Neuroprotective effects	[326, 327]
Arctigenin	Inhibits A β production and promotes A β clearance	Ameliorates memory impairment	[330]
2,2',4'-trihydroxychalcone (TDC)	Represses beta-cleavage of APP and production of A β	Improves the memory impairment	[328]
Bis(7)-cognitin	Inhibition of AChE, NMDA receptor, nitric oxide synthase, and amyloid precursor protein/beta-amyloid cascade	Neuroprotective effects	[329]
Clioquinol	Inhibits metal-ion binding to A β	Inhibits A β deposition	[331]
Idalopirdine	5-HT ₆ receptor antagonist	In combination with a cholinesterase inhibitor may increase the cognitive function	[325]
Azeliragon	RAGE inhibitor	Mediates transport of the A β peptide into the brain	[332]
Encenicline	α 7-nAChR inhibitor	Restores memory function	[333]
Nilvadipine	Calcium antagonist	Cognition improvement	[334]

expression and serve as an ideal target for AD therapeutic drug design. Both miR-107 and miR-29 may potentially target the mRNA of BACE1, which is the key enzyme responsible for generating A β protein from APP^[349].

Conclusions

A β is the major component of senile plaques and partici-

pates in Alzheimer's disease progression through its neurotoxic effects. Identifying A β structures, biology, receptors and A β -based therapeutic approaches for the treatment of Alzheimer's disease therefore remains of paramount importance. In this review, we have addressed the different structures involved in A β accumulation and have discussed the current understanding of the biological function and neuro-

Table 10. Summary of amyloid dyes for the treatment of Alzheimer's disease.

Name	Targets	Effects	Ref
Congo red	Binds A β fibrils	Neuroprotective effects	[335]
Iodine-sulphuric acid	Binds A β fibrils	Inhibits A β aggregation and cytotoxicity	[336]
Thioflavin-T	Binds A β fibrils	Inhibits A β aggregation and cytotoxicity	[337]
Crystal violet	Binds A β fibrils	Inhibits A β aggregation and cytotoxicity	[338]
Methyl violet	Binds A β fibrils	Inhibits A β aggregation and cytotoxicity	[339]
BTA-1	Binds A β plaques	Inhibits A β aggregation and cytotoxicity	[340]
Chrysamine G	Binds A β deposits	Inhibits A β aggregation and cytotoxicity	[341]
ANS (1-anilino-naphthalene-8-sulfonic acid)	Binds A β fibrils	Inhibits A β aggregation and cytotoxicity	[342]
bisANS (4,4'-dianilino-1,1'-binaphthyl-5,5'-disulfonic acid)	Binds A β fibrils	Inhibits A β aggregation and cytotoxicity	[342]
Nile red	Binds A β fibrils	Inhibits A β aggregation and cytotoxicity	[343]
K114 ((<i>trans,trans</i>)-1-bromo-2,5-bis(4-hydroxystyryl)benzene)	Crosses the blood-brain barrier (BBB) and binds with amyloid plaques	Inhibits A β aggregation and inflammation	[344]
FSB	Binds A β deposits	Inhibits A β aggregation and cytotoxicity	[345]
Curcumin	Binds A β plaques	Detects A β plaques and as A β -specific antibody	[346]
Nanocurcumin	Binds A β plaques	Detects A β plaques and as A β -specific antibody	[346]

toxic role of A β and the potential receptors that interact with A β and mediate A β intake, clearance and metabolism. Identification of the key A β receptor under relevant physiological conditions and obtaining crystal structures of full-length A β in different states are critical for the development of new therapeutic agents.

Over the last decade, advances have been made in understanding the structures of A β peptide forms. A β peptide rapidly aggregates to form oligomers, protofibrils and fibrils that lead to the deposition of amyloid plaques. Different structural approaches, such as NMR spectroscopy, distance geometry, molecular dynamic techniques, and X-ray crystallography, have shown that the structural conversion of A β oligomers to fibrils involves the association of these loosely aggregated strands into α -helical and parallel β -sheet structures, as well as that the structural states transition quickly. Different signal transduction pathways are involved in A β expression, degradation, transport and clearance. The phosphorylation and activation of specific intracellular kinases represent common events in these signaling cascades, and these signaling molecules are potential targets for new Alzheimer's disease drugs.

Several therapeutic approaches for Alzheimer's disease target amyloid oligomers. Methods that are currently under development include the inhibition of A β oligomerization using small molecule inhibitors, the neutralization of oligomeric species using immunotherapy, the overexpression of A β -degrading enzymes in the brain, catalytic A β antibodies for hydrolyzing specific aggregates, β -sheet breakers for destabilizing existing β -sheet structure and A β blockers for blocking amyloid channels and thereby leading to the partial reversal of brain pathologies. The therapeutic targeting of microglia receptors implicated in the response to A β and their associated signaling pathways could reduce the inflammation associated with Alzheimer's disease. Tau protein inhibitors or vaccines and amyloid dyes that selectively bind A β and inhibit A β aggregation offer additional novel therapeutic approaches for the treatment of Alzheimer's disease.

We have summarized new progress in developing treatments targeting A β and its receptors. Existing Alzheimer's disease drugs only treat the symptoms of Alzheimer's disease; they do not decelerate or cure it. The last drug that was approved by the Food and Drug Administration for therapeutic Alzheimer's disease treatment was *namzaric* in 2014. In the last decade, several candidate drugs have failed to reach statistical significance in their primary outcomes. The drugs currently undergoing clinical trials are inhibitors of A β production and aggregation, A β antibodies and vaccines. Identification of the key physiological A β receptors and the determination of their crystal structures in complex with A β will play a critical role in mitigating Alzheimer's disease progression and symptoms.

Abbreviations

Amyloid beta (A β), amyloid precursor protein (APP), A β binding p75 neurotrophic receptor (P75^{NTR}), low-density lipoprotein receptor-related protein (LRP), cellular prion protein

(PrP^c), metabotropic glutamate receptor (mGluR5), α subunit-containing nicotinic acetylcholine receptor (α 7nAChR), *N*-methyl-*D*-aspartic acid receptor (NMDAR), β -adrenergic receptor (β -AR), erythropoietin-producing hepatocellular receptor (EphR), paired immunoglobulin-like receptor B (PirB).

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