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Review

# Reproductive Aging, FSH, APO Proteins, and Alzheimer's Disease: Endocrine Mechanisms Linking Ovarian Decline to Neurodegeneration

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## Abstract

Alzheimer's disease (AD) disproportionately affects women, with risk increasing sharply during and after the menopausal transition. While declines in estrogen have traditionally been emphasized, emerging evidence suggests that elevations in follicle-stimulating hormone (FSH) may represent a critical and underappreciated driver of neurodegenerative vulnerability. This review synthesizes current evidence linking reproductive aging to AD pathobiology, with a focus on endocrine, metabolic, and inflammatory mechanisms. We examine how sustained FSH elevation interacts with key molecular pathways implicated in AD, including C/EBP $\beta$ - $\delta$ -secretase signaling, mitochondrial dysfunction, impaired glucose metabolism, and disruptions in autophagic and lysosomal clearance. These processes converge to promote amyloid- $\beta$  accumulation, tau pathology, and chronic neuroinflammation. In parallel, FSH influences apolipoprotein biology - particularly ApoE - through effects on lipid metabolism, protein lipidation, and clearance dynamics, thereby modulating both amyloid kinetics and inflammatory responses in an isoform-dependent manner. Reproductive aging is further characterized by systemic shifts in vascular integrity, blood-brain barrier function, and immunometabolic regulation, all of which may amplify susceptibility to neurodegenerative processes. Importantly, these upstream disturbances precede classical pathological hallmarks, reframing amyloid and tau accumulation as downstream manifestations of broader regulatory failure. Collectively, this work positions FSH not merely as a biomarker of ovarian decline, but as an active endocrine mediator of neurodegeneration. Targeting FSH signaling and its downstream pathways may therefore represent a promising and mechanistically grounded approach for mitigating AD risk, particularly in women.

**Keywords:** FSH; Alzheimer's disease

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## Introduction

Alzheimer's disease (AD) is a progressive neurodegenerative disorder and the leading cause of dementia worldwide, representing a growing public health challenge. In the United States, approximately one in nine individuals aged 65 years and older (10.8%) are affected, with an annual incidence of 1,275 new cases per 100,000 persons (Zhang et al., 2024). Clinically, AD is characterized primarily by amnesic cognitive impairment. Early manifestations may include depression, anxiety, social withdrawal, and sleep disturbances, which progressively evolve into severe memory loss, neuropsychiatric symptoms (e.g., hallucinations and delusions), and behavioral dysregulation. In some cases, non-amnesic presentations occur, involving impairments in visuospatial processing, language, executive function, or motor coordination.

AD is broadly categorized into familial and sporadic forms. Familial AD (FAD), accounting for approximately 1-5% of cases, is typically driven by autosomal dominant mutations in amyloid precursor protein (APP), presenilin 1 (PS1), and presenilin 2 (PS2), with onset often occurring between 30 and 65 years of age and characterized by rapid progression (Liu et al., 2019). In contrast, sporadic or late-onset AD (SAD), which comprises over 95% of cases, generally manifests after age

65 and arises from a complex interplay of genetic susceptibility, environmental exposures, and comorbid conditions (Fedele, 2023; Suresh et al., 2023).

The primary risk factors for late-onset AD include advanced age, female sex, and apolipoprotein E (APOE) genotype (Riedel et al., 2016). Women account for nearly two-thirds of individuals living with AD in the United States, with most cases emerging after age 65 (Alzheimer's Disease and Dementia, 2024). Reproductive aging appears to contribute significantly to this increased vulnerability, reflecting coordinated changes in endocrine and neurobiological systems. Declines in circulating estrogen and progesterone, alongside alterations in gonadotropins and hypothalamic signaling peptides (e.g., FSH, LH, GnRH), are associated with measurable changes in brain structure and function. Lower bioavailable estrogen levels have been linked to increased risk of global cognitive decline and impaired verbal memory (Laughlin et al., 2010; Zsido et al., 2019). Peri- and postmenopausal women also exhibit accelerated rates of cognitive decline compared to men, as well as greater reductions in hippocampal volume (Mosconi et al., 2018). Additionally, vasomotor symptoms such as nocturnal hot flashes have been associated with impaired memory performance and elevated biomarkers of amyloid pathology (Maki et al., 2008; Thurston et al., 2024).

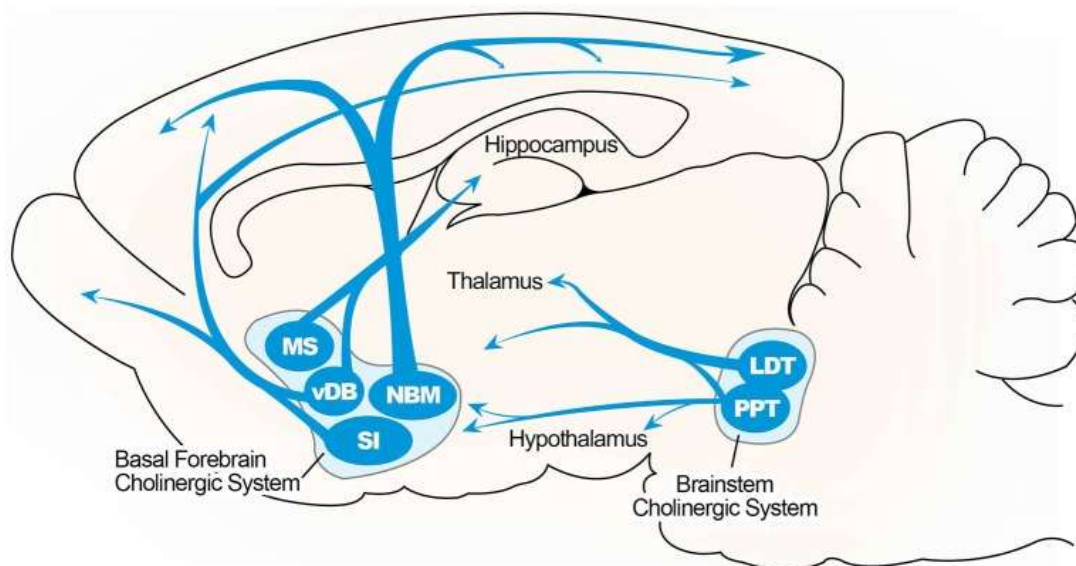
Importantly, reproductive aging is accompanied by a broader spectrum of hormonal perturbations beyond estrogen decline. Among these, progressive elevation of follicle-stimulating hormone (FSH) has emerged as a potentially significant contributor to age-related pathology. Elevated FSH levels have been associated with a range of chronic conditions, including AD, osteoporosis, cardiovascular dysfunction, and metabolic disturbances (Lizneva et al., 2019). These observations suggest that FSH may function not only as a compensatory marker of ovarian insufficiency, but also as an active endocrine driver of systemic aging processes. Accordingly, this review examines the mechanistic pathways through which sustained elevations in FSH may contribute to downstream pathological changes relevant to AD.

Overview of Canonical Cellular Alterations Underlying Neurodegeneration in Alzheimer's Disease

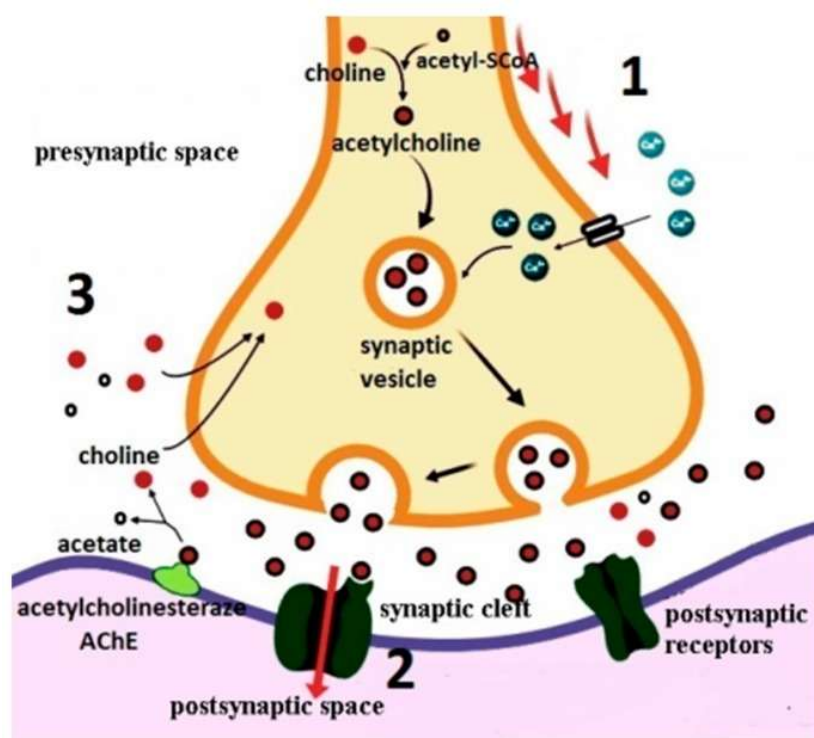
### *Cholinergic Hypothesis*

The cholinergic hypothesis represents one of the earliest frameworks proposed to explain AD pathogenesis. It posits that selective degeneration of cholinergic neurons in the nucleus basalis of Meynert (NBM) leads to reduced choline acetyltransferase (ChAT) activity, impairing acetylcholine synthesis and disrupting cortical cholinergic transmission (Berry & Harrison, 2023). This loss of cholinergic integrity is accompanied by increased deposition of senile plaques in affected cortical regions (Rodríguez et al., 2010; Serrano-Pozo et al., 2011). Collectively, this model highlights a strong association between basal forebrain cholinergic dysfunction and the cognitive deficits characteristic of AD (Hampel et al., 2019). Cholinergic neurons within the NBM, as well as those in the medial septum and diagonal band of Broca (MS/DBB), are particularly vulnerable to degeneration in this context (Schmitz et al., 2018).

Acetylcholine (ACh) is produced in cholinergic neurons through the enzymatic conversion of choline and acetyl-coenzyme A by choline acetyltransferase (ChAT). Once synthesized, ACh is transported into synaptic vesicles by the vesicular acetylcholine transporter (VACHT) and released into the synaptic cleft in response to presynaptic depolarization. In the synaptic space, ACh interacts with both muscarinic and nicotinic receptors (mAChRs and nAChRs) on postsynaptic cells to facilitate signal transmission (Paul et al., 2022). Termination of signaling is achieved through rapid enzymatic breakdown by acetylcholinesterase (AChE), generating choline, which is subsequently reclaimed by the presynaptic neuron for reuse (Berry & Harrison, 2023; Stanciu et al., 2019). Disruptions in ChAT expression or function reduce ACh availability, weakening cholinergic signaling. Such impairments affect multiple physiological processes governed by this system, including cognitive function, attentional regulation, motor control, and sleep-wake dynamics (Walczak-Nowicka & Herbet, 2021).



**Figure 1.** Cholinergic projections arise from basal forebrain nuclei - including the medial septum (MS), vertical limb of the diagonal band of Broca (vDB), nucleus basalis of Meynert (NBM), and substantia innominata (SI) - which send widespread projections to the hippocampus, thalamus, olfactory bulb, and cortical regions. In parallel, cholinergic neurons of the pontomesencephalon - specifically the laterodorsal tegmental nucleus (LDT) and pedunculopontine tegmental nucleus (PPT) - project to the hindbrain, thalamus, hypothalamus, and basal forebrain, contributing to the regulation of arousal and behavioral state. *Adapted from Paul et al. (2015).*



**Figure 2. Acetylcholine release and synaptic signaling.** Schematic of cholinergic neurotransmission showing (1) Ca<sup>2+</sup>-dependent release of acetylcholine (ACh) from presynaptic vesicles, (2) binding of ACh to postsynaptic receptors to induce depolarization, and (3) enzymatic breakdown of ACh by acetylcholinesterase (AChE) with subsequent reuptake of choline into the presynaptic neuron. *Adapted from Stanciu et al., (2019).*

## A $\beta$

C/EBP $\beta$  acts as an upstream transcriptional regulator of  $\delta$ -secretase, also known as asparagine endopeptidase (AEP; LGMN), linking inflammatory signaling to proteolytic pathways implicated in AD (Luo et al., 2025). Increased C/EBP $\beta$  activity elevates AEP expression, facilitating cleavage of APP at N585 and tau at N368, thereby generating fragments with increased aggregation potential (Wu et al., 2020). APP, a type I transmembrane glycoprotein, undergoes sequential processing in the amyloidogenic pathway via  $\beta$ -secretase followed by  $\gamma$ -secretase, a multiprotein complex in which PS1 or PS2 functions as the catalytic core. This cleavage produces A $\beta$  peptides of varying lengths, most notably A $\beta$ 40 and A $\beta$ 42. The latter, due to its more hydrophobic C-terminal region, exhibits a greater tendency to adopt  $\beta$ -sheet conformations and self-assemble into fibrillar aggregates that form the structural basis of senile plaques (Lin et al., 2019).

A $\beta$  has remained a central feature of AD models, supported in part by genetic evidence from familial disease. Mutations in APP on chromosome 21 are associated with autosomal dominant AD, and individuals with Down syndrome - who possess an additional copy of APP - consistently develop early-onset pathology (Wiseman et al., 2015). Similarly, APP duplications increase disease risk, whereas variants associated with reduced A $\beta$  production have been linked to preserved cognitive aging (Castellani et al., 2025). Rare cases of Down syndrome lacking APP triplication do not exhibit early pathological changes, reinforcing the importance of APP gene dosage. However, extrapolation of these findings to sporadic AD remains complicated by the broader genetic alterations present in trisomy 21 (Castellani et al., 2025).

Mutations in PS1 and PS2 further support a role for amyloidogenic processing in familial disease, although PS1-associated cases often display distinct pathological features, raising questions regarding their direct relevance to sporadic AD (Heilig et al., 2010). Across both familial and sporadic forms, insoluble A $\beta$  species are consistently elevated relative to cognitively normal individuals (van Helmond et al., 2010; Wang et al., 1999). Nevertheless, whether A $\beta$  accumulation alone is sufficient to account for the full clinical and pathological spectrum of AD remains an area of ongoing debate (Castellani et al., 2025).

Despite these uncertainties, A $\beta$  deposition remains a consistent feature of disease, and plaque formation - along with broader alterations in A $\beta$  metabolism - remains closely associated with disease progression. As emphasized throughout this review, however, A $\beta$  accumulation occurs within a broader network of upstream regulatory disturbances. Accordingly, while A $\beta$  remains central to the disease landscape, its precise position within the temporal and mechanistic hierarchy of AD is considered in greater detail elsewhere (Castellani et al., 2025; Riku et al., 2025).

## Tau

Tau is a microtubule-associated protein predominantly localized to neuronal axons, with lower expression in dendrites, the soma, and glial cells (Sinsky et al., 2021; Wei et al., 2022). Its structure includes multiple phosphorylation sites distributed across the N-terminal region, C-terminal domain, and microtubule-binding repeats. Under physiological conditions, tau phosphorylation is tightly controlled through coordinated kinase and phosphatase activity, a balance required for maintaining microtubule stability and normal neuronal function (Noble et al., 2013).

Disruption of this regulatory equilibrium results in excessive phosphorylation, reducing tau's affinity for microtubules and promoting its detachment (Bjørklund et al., 2019; Almansoub et al., 2019). Detached tau undergoes conformational changes and redistributes from axons to the somatodendritic compartment, where it forms soluble oligomeric species. These intermediates can further assemble into paired helical filaments (PHFs) and eventually neurofibrillary tangles (NFTs), which accumulate within neuronal cell bodies and dendrites as defining pathological features of tauopathies (Lo et al., 2020; Robbins et al., 2021).

Tau pathology spreads along synaptically connected networks, impairing synaptic transmission and axonal transport prior to overt tangle formation. This progressive dissemination, characterized by Braak staging (Therriault et al., 2022), reflects a network-based propagation that precedes synaptic

loss, axonal degeneration, and neuronal death, ultimately driving cognitive decline (Lo et al., 2020; Wu et al., 2017; Yin et al., 2021). Notably, the extent of tau pathology shows a stronger association with memory impairment and neurodegeneration than amyloid burden (Doering et al., 2024; Iaccarino et al., 2017; Lamontagne-Kam et al., 2023).

In addition to phosphorylation, tau undergoes diverse post-translational modifications - including truncation, glycosylation, glycation, acetylation, methylation, and sumoylation - that modulate its structural properties, aggregation behavior, and intracellular trafficking (Alquézar et al., 2021). Many of these modifications occur on lysine residues and influence protein turnover. Ubiquitination of lysine residues typically targets tau for proteasomal degradation; however, competing modifications such as acetylation or methylation can inhibit ubiquitin attachment, thereby impairing clearance and promoting accumulation (Luo et al., 2014; Kontaxi et al., 2017). Consistent with this, lysine 254 (K254) is preferentially methylated in fibrillar tau, suggesting that site-specific methylation may hinder degradation and contribute to the persistence of pathogenic species (Thomas et al., 2012).

As discussed in subsequent sections, accumulation of tau and A $\beta$ , along with disruptions in neurotransmission, arise as downstream consequences of upstream perturbations that are further amplified by age-related and reproductive aging-associated changes.

## Endocrine Drivers of Female-Related Alzheimer's Disease Vulnerability

### *Follicle-Stimulating Hormone and Its Role in Alzheimer's Disease Pathogenesis*

The menopausal transition is marked by a decline in circulating estradiol (E2) alongside a sustained rise in FSH (Muhammad, 2025). This endocrine shift has traditionally been linked to the increased prevalence of AD in women; however, emerging evidence suggests that elevated FSH may play a more direct role in shaping neurodegenerative risk than estrogen loss alone (Scheyer et al., 2018; Nerattini et al., 2023; Wood Alexander et al., 2025).

Elevated FSH has been shown to engage inflammatory, lipid, and neuronal signaling pathways that favor amyloid accumulation and downstream neurodegenerative processes (Wang et al., 2026). In clinical cohorts of older women, circulating FSH levels stratify with disease severity, with the highest concentrations observed in individuals with AD, intermediate levels in those with mild cognitive impairment, and the lowest levels in cognitively normal individuals (Wang et al., 2026; Short et al., 2001). Higher FSH levels are associated with increased cerebral A $\beta$  burden and poorer cognitive performance, whereas circulating estradiol does not demonstrate comparable associations across disease stages (Wang et al., 2026).

Notably, the relationship between FSH and amyloid burden persists within diagnostic groups, indicating that FSH tracks pathological progression independently of clinical classification. Consistent with this, individuals with higher amyloid deposition exhibit correspondingly elevated circulating FSH levels. Together, these findings position FSH as both a potential biomarker and an active endocrine contributor to disease progression, with effects that appear to extend beyond those attributable to estrogen decline alone.

### *Convergent Pathways of Ovarian and Neurobiological Aging*

Aging of the ovary and the brain has traditionally been viewed as parallel but independent processes; however, increasing evidence suggests that these trajectories are mechanistically linked and converge on shared systems-level dysfunction. Reproductive aging is now understood not as an isolated ovarian event, but as a broader neuroendocrine and immunometabolic transition involving coordinated changes across endocrine, immune, metabolic, and mitochondrial networks (Muhammad, 2025). Within this framework, ovarian decline and neurobiological aging reflect interconnected manifestations of systemic dysregulation rather than discrete processes.

Both ovarian and neural tissues undergo a shift toward chronic, low-grade inflammation with age. In the ovary, inflammatory signaling contributes to follicular depletion, impaired

steroidogenesis, and reduced oocyte quality. In the brain, similar inflammatory pressures manifest as microglial priming and astrocytic reactivity, often emerging well before overt neurodegeneration. These changes are not restricted to higher-order cognitive regions, but also involve neuroendocrine centers such as the hypothalamus. Age-related hypothalamic inflammation is characterized by progressive microglial activation and neuronal dysfunction (Tang & Cai, 2013; Kermath et al., 2013; Muhammad, 2025; Zhang et al., 2013), with consequences that extend beyond reproductive regulation. Indeed, hypothalamic deterioration has been linked to impairments in both cognition and physical function (Zhang et al., 2013). Mechanistically, reductions in GnRH signaling - partly driven by IKK $\beta$ /NF- $\kappa$ B-mediated pathways - have been associated with neuronal loss in both the hypothalamus and hippocampus, a key site of vulnerability in AD (Zhang et al., 2013). Together, these findings support inflammaging as a shared upstream process linking reproductive decline with increased susceptibility to neurodegeneration.

In parallel, aging is accompanied by a gradual decline in cellular maintenance systems critical to both ovarian and neural function. Mitochondrial dysfunction, oxidative stress, and impaired autophagic clearance are consistently observed across both tissues, alongside increases in pro-inflammatory extracellular vesicle populations. These disruptions are particularly consequential in metabolically active cells, where sustained energy demands require efficient turnover of damaged proteins and organelles. Over time, failure of these systems leads to the accumulation of dysfunctional mitochondria, lipid peroxidation products, and misfolded proteins - features common to both ovarian aging and neurodegenerative pathology.

Hormonal changes intersect with these processes in a context-dependent manner. While acute gonadotropin signaling supports adaptive responses in reproductive tissues, chronic elevations - particularly of FSH - may exert maladaptive effects in non-gonadal systems. These include modulation of inflammatory pathways, vascular function, and cellular metabolism, all of which contribute to neurobiological aging. In this context, menopause is increasingly viewed not simply as an endocrine endpoint, but as a neuroimmune transition shaped by the integration of hormonal, metabolic, and inflammatory signals that collectively influence systemic aging trajectories.

## The Role of APOE Variants in AD Pathobiology

Genetic variation in APOE is one of the strongest modifiers of AD risk. Carriage of a single  $\epsilon$ 4 allele increases risk approximately two- to three-fold, while homozygosity is associated with an estimated ten- to twelve-fold increase (Ayton & Bush, 2021). ApoE protein is consistently localized within neuritic plaques, and  $\epsilon$ 4 carriers exhibit greater cerebral A $\beta$  accumulation relative to non-carriers (Baek et al., 2020). Experimental evidence supports multiple mechanisms through which APOE4 exacerbates amyloid pathology, including altered APP processing that may increase A $\beta$  production, facilitation of A $\beta$  aggregation through interactions with soluble and fibrillar species, and impaired clearance via disrupted glial uptake, enzymatic degradation, and reduced vascular efflux (Koutsodendris et al., 2022; Serrano-Pozo et al., 2021; Troutwine et al., 2022).

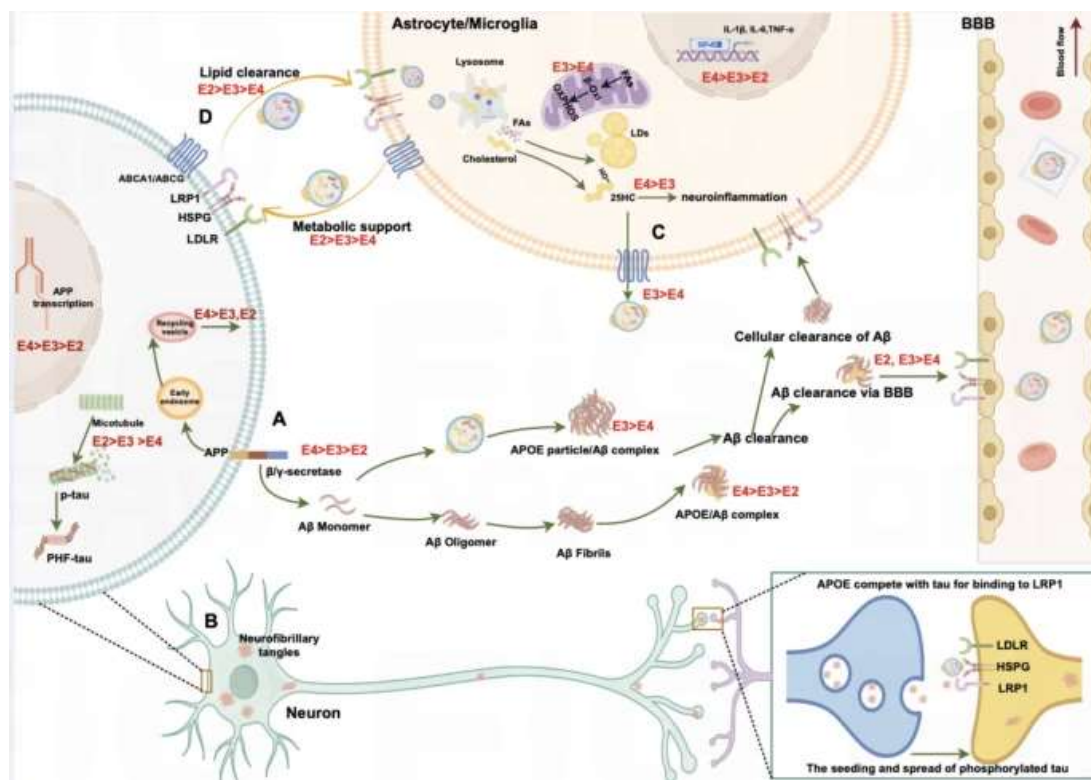
Within the CNS, ApoE functions as the primary lipid transport protein, mediating cholesterol redistribution among astrocytes, microglia, and neurons (Belaidi et al., 2025). Through its role in maintaining membrane composition, supporting lipid-dependent signaling, and facilitating clearance of neurotoxic substrates - including A $\beta$  - ApoE is central to neuronal integrity and brain homeostasis (Islam et al., 2025; Ioannou et al., 2019). Humans express two alleles drawn from three major isoforms -  $\epsilon$ 2,  $\epsilon$ 3, and  $\epsilon$ 4 - which differentially influence disease susceptibility. Epidemiological data indicate that risk is lowest in  $\epsilon$ 2 carriers, approximately neutral in  $\epsilon$ 3 carriers, and markedly elevated in individuals carrying one or more  $\epsilon$ 4 alleles, with particularly pronounced effects observed in women (Stuchell-Brereton et al., 2023; Sun et al., 2023).

ApoE contributes to A $\beta$  clearance through both vascular and cellular pathways. At the blood-brain barrier, ApoE binds A $\beta$  to form complexes that interact with lipoprotein receptors on the abluminal surface, including LDL receptor-related protein 1 (LRP1), the low-density lipoprotein receptor (LDLR), and very-low-density lipoprotein receptor (VLDLR) (Kanekiyo et al., 2013; Ruiz et

al., 2005). ApoE2 and ApoE3 preferentially facilitate A $\beta$  transport through LRP1-dependent pathways, which are characterized by rapid internalization and efficient transcytosis into the circulation. In contrast, ApoE4 biases A $\beta$  trafficking toward VLDLR-mediated routes with slower clearance kinetics, resulting in prolonged retention within the brain and increased propensity for plaque formation (Deane et al., 2008).

In addition to vascular clearance, A $\beta$  is removed through cellular uptake by glial populations, where it is frequently internalized in complexes with ApoE and trafficked to lysosomes for degradation (Liu et al., 2025). Within these compartments, proteases such as neprilysin and insulin-degrading enzyme (IDE) facilitate peptide breakdown. The efficiency of this pathway is strongly influenced by the lipidation state of ApoE (Chen et al., 2025). Lipid-rich ApoE - regulated in part by ATP-binding cassette transporter A1 (ABCA1) - more effectively supports A $\beta$  uptake and degradation, whereas poorly lipidated ApoE exhibits reduced clearance capacity (Jiang et al., 2008).

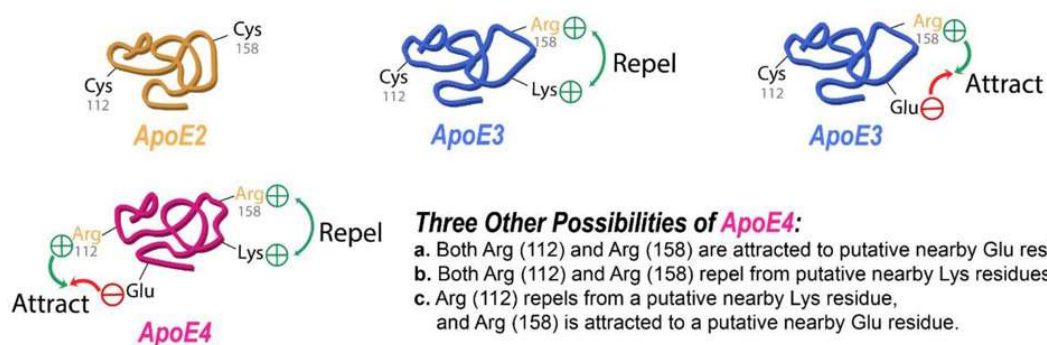
The three major ApoE isoforms differ at amino acid positions 112 and 158, where cysteine-to-arginine substitutions distinguish their biochemical properties. ApoE2 contains cysteine at both positions, ApoE3 contains cysteine at position 112 and arginine at 158, and ApoE4 contains arginine at both sites (Stuchell-Brereton et al., 2023). Structurally, ApoE comprises an N-terminal region (residues 1-167) organized into a conserved four-helix bundle, a flexible hinge region (residues 168-205), and a C-terminal domain (residues 206-299). While the helical bundle is well characterized and structurally consistent across studies (Frieden & Garai, 2013; Wilson et al., 1991; Grimaldi et al., 2024), the conformation and positioning of the hinge and C-terminal domains remain less clearly defined.



**Figure 3. Isoform-dependent ApoE regulation of A $\beta$  clearance kinetics and context-specific tau pathology.** Collectively, ApoE4 disrupts multi-compartment A $\beta$  clearance kinetics, leading to impaired A $\beta$  turnover, prolonged brain retention, and enhanced neuroinflammatory signaling. However, the relationship between ApoE isoforms and tau pathology is more context-dependent and does not strictly follow the canonical AD risk hierarchy. In primary tauopathy models (e.g., TauP301L and PSP), ApoE2 promotes greater tau aggregation and hyperphosphorylation than ApoE3 and ApoE4 (ApoE2 > ApoE3 > ApoE4). In contrast, in the presence of amyloid- $\beta$  - as in Alzheimer's disease - ApoE4 appears to exacerbate tau-mediated neurodegeneration, likely

through indirect mechanisms linked to impaired A $\beta$  clearance and heightened inflammatory signaling. *Adapted from Liu et al., 2025.*

A widely cited explanation for the functional divergence of ApoE isoforms is the “domain interaction” model (Mahley et al., 2009). In ApoE4, substitution of cysteine with arginine at position 112 alters intramolecular electrostatic interactions within the helical bundle, promoting a distinct folding conformation. The presence of positively charged arginine residues modifies local charge distributions and interactions with neighboring residues, reshaping the protein’s tertiary structure. These conformational changes influence key functional properties, including lipid-binding capacity, receptor engagement, susceptibility to proteolysis, and intracellular trafficking. Importantly, such structural differences are also thought to impact autophagic processing and the handling of A $\beta$  and other protein substrates, thereby linking ApoE isoform-specific properties to downstream cellular dysfunction.



**Figure 4. Structural conformations of apolipoprotein E (apoE) isoforms.** Schematic representation of the distinct conformational differences among apoE2, apoE3, and apoE4, illustrating how amino acid substitutions at key positions alter intramolecular interactions. Replacement of cysteine residues with positively charged arginine residues - particularly in apoE4 - modifies electrostatic interactions within the protein, promoting domain–domain interactions between the N-terminal and C-terminal regions. In contrast, apoE2 and apoE3, which retain cysteine at these positions, exhibit reduced intramolecular interaction and adopt more flexible conformations. These structural differences influence lipid binding, receptor interactions, and isoform-specific functional properties relevant to disease risk. *Adapted from Butterfield and Mattson (2020).*

In addition to alterations within the four-helix bundle, structural and sequence differences in other regions of APOE further shape its functional behavior. Variations outside the core bundle - particularly within the hinge and C-terminal domains - can modulate lipid binding, receptor interactions, oligomerization, and intracellular trafficking. These non-four-helix contributions to ApoE function and dysfunction have been considered elsewhere (Stuchell-Brereton et al., 2023). Historically, APOE4 has been described as adopting a characteristic “closed” conformation, in which the N-terminal domain (NTD) and C-terminal domain (CTD) are in close physical proximity. Early biochemical and structural studies proposed that this intramolecular domain interaction shields residues within the NTD that are critical for binding to the low-density lipoprotein receptor (LDLR), thereby impairing receptor-mediated lipid transport and clearance (Stuchell-Brereton et al., 2023). This domain interaction model became a dominant framework for explaining ApoE4-associated functional deficits.

However, APOE exhibits substantial conformational plasticity, owing to intrinsically disordered and flexible segments distributed throughout the protein (Frieden et al., 2017). More recent biophysical studies suggest that the “closed” conformation attributed to ApoE4 may arise preferentially under conditions that promote protein oligomerization, including certain experimental contexts and pathological states (Stuchell-Brereton et al., 2023). As such, NTD-CTD proximity may not represent a stable or obligatory feature of monomeric ApoE4, but rather an emergent property of

higher-order assemblies that becomes relevant after oligomer formation. Nonetheless, the hinge region plays a central regulatory role by competing with the CTD for interactions with the four-helix bundle. Specific contacts involving the N-terminal tail and the four-helix bundle can bias interaction preferences toward either the hinge or the CTD, dynamically shaping ApoE conformational states.

In addition to effects on protein conformation, ApoE isoform differences also shape vulnerability to oxidative chemical modification. The brain is particularly susceptible to oxidative stress due to its high polyunsaturated fatty acid content, elevated oxygen consumption, and the presence of redox-active transition metals such as Fe<sup>2+</sup> and Cu<sup>+</sup>, which catalyze reactive oxygen species formation (Cobley et al., 2018). Under these conditions, lipid peroxidation generates reactive aldehydes such as 4-hydroxynonenal (HNE), which covalently modify proteins through Michael addition reactions with nucleophilic residues, particularly cysteine, histidine, and lysine (Milkovic et al., 2023). These adducts introduce carbonyl functional groups (aldehydes or ketones) onto proteins, forming so-called protein carbonyls-stable oxidative modifications widely used as biomarkers of oxidative reactions and molecular aging (Gonos et al., 2018; Milkovic et al., 2023; Weber et al., 2015).

ApoE2 and ApoE3 contain cysteine residues that provide thiol nucleophiles capable of sequestering electrophilic lipid peroxidation products, thereby limiting their diffusion and secondary damage to proteins and membranes (Abeer et al., 2023). In contrast, ApoE4 lacks these cysteine residues at key positions, reducing its capacity to neutralize reactive aldehydes and increasing susceptibility to oxidative protein modification (Abeer et al., 2023; Butterfield & Mattson, 2020). This deficit is further compounded by impaired glutathione-dependent redox buffering, as cysteine availability is rate-limiting for glutathione synthesis (Hara et al., 2017). Consistent with this, individuals with mild cognitive impairment and Alzheimer's disease exhibit reduced glutathione levels and lower GSH/GSSG ratios, reflecting compromised antioxidant defenses (Bermejo et al., 2008).

Understandably, a substantial body of work demonstrates that ApoE isoforms differentially modulate A $\beta$  pathology. Carriers of the  $\epsilon$ 4 allele exhibit increased cerebral A $\beta$  deposition, earlier amyloid positivity, and a more rapid accumulation of A $\beta$  burden over time (Liu et al., 2017). Historically, efforts to explain APOE-dependent Alzheimer's disease risk focused primarily on differences in plaque load, however; this framework proved insufficient, as plaque burden correlates poorly with synaptic dysfunction and cognitive decline (Xia et al., 2024). Instead, converging evidence indicates that soluble, early-stage A $\beta$  assemblies - rather than mature plaques - are the species most closely linked to neuronal toxicity and cognitive impairment (Xia et al., 2024).

**Accordingly**, the role of fibrillization warrants careful interpretation. Although fibril formation ultimately contributes to plaque deposition, it can also mitigate acute neurotoxicity by sequestering highly diffusible, synaptotoxic oligomeric species into relatively inert fibrillar assemblies (Verma et al., 2015). Thus, the pathological relevance of fibril growth kinetics does not depend simply on whether elongation is accelerated or delayed, but on how aggregation dynamics govern the abundance, persistence, and clearance of intermediate A $\beta$  species. These intermediates - rather than mature fibrils - are now widely recognized as the principal drivers of synaptic dysfunction, neuroinflammation, and disease progression (Liu et al., 2025). Importantly, although APOE2 and APOE3 inhibit fibril elongation more strongly than ApoE4, this does not result in greater neurotoxicity. Instead, these isoforms tend to promote more ordered aggregation pathways and facilitate more efficient clearance of early A $\beta$  assemblies (Dasadhikari et al., 2025). In contrast, APOE4 preferentially stabilizes disordered, poorly cleared A $\beta$  intermediates, extending their lifetime and amplifying their synaptotoxic and pro-inflammatory effects (Xia et al. 2024).

**Using** single-molecule imaging and ex vivo brain-derived aggregates, Xia et al. (2024) demonstrated that ApoE does not simply modulate plaque deposition or the structure of mature fibrils. Instead, ApoE transiently associates with A $\beta$  during the earliest stages of aggregation, forming highly populated yet short-lived APOE-A $\beta$  co-aggregates that critically shape aggregation pathways, toxicity, and clearance behavior (Verghese et al., 2013; Xia et al., 2024). Although only 1-5% of A $\beta$  particles are physically associated with APOE, these co-aggregates account for approximately 20-50%

of the total A $\beta$  mass, indicating that they represent disproportionately large and biologically consequential intermediates rather than rare byproducts.

**Table 1. Structural and functional hierarchy of amyloid- $\beta$  aggregation states and their relevance to Alzheimer's disease.** This table summarizes the progressive aggregation states of amyloid- $\beta$  (A $\beta$ ), spanning from soluble monomeric peptides to insoluble extracellular plaques, and highlights their distinct structural, biochemical, and pathological characteristics. Early-stage species, particularly soluble oligomers, are highly dynamic and exhibit the greatest neurotoxicity, with strong associations to synaptic dysfunction and cognitive decline. Intermediate assemblies such as protofibrils represent transitional forms with significant pathogenic potential. In contrast, mature fibrils and plaques are structurally stable end-products of aggregation that, while defining histopathological features of Alzheimer's disease, show weaker correlations with clinical symptoms. Collectively, the table emphasizes that A $\beta$  toxicity is not solely dependent on aggregate presence, but is critically influenced by aggregation state, solubility, and molecular dynamics.

Term	Scale	Structure	Solubility	Stability	Primary Biological Relevance	Toxicity	Relationship to AD
<b>Monomers</b>	Molecular	Single A $\beta$ peptides	Soluble	Unstable	Baseline physiological state	Low	Not directly pathogenic
<b>Early-stage aggregates (oligomers)</b>	Molecular-nanoscale	Small, flexible clusters (dimers, trimers, etc.)	Soluble	Transient	Synaptic signaling disruption, membrane interaction	<b>Highest</b>	Best correlate with cognitive decline
<b>Protofibrils</b>	Nanoscale	Elongated, partially ordered assemblies	Semi-soluble	Intermediate	Transitional species between oligomers and fibrils	High	Contribute to early pathology
<b>Mature fibrils</b>	Nanoscale-microscale	Highly ordered $\beta$ -sheet polymers	Insoluble	Stable	Structural end-products of aggregation	Moderate-low	Build plaques but are not main toxic species
<b>Plaques</b>	Tissue-level	Macroscopic extracellular deposits of fibrils + cellular debris	Insoluble	Very stable	Histopathological hallmark	Variable	Poor correlation with symptoms

Importantly, the formation and behavior of these co-aggregates are strongly dependent on ApoE isoform and lipidation state. In ApoE4 homozygotes, a substantially greater fraction of A $\beta$  exists in co-aggregated form compared with ApoE3 carriers, with approximately 80% of these assemblies containing non-lipidated ApoE. Rather than influencing the final fibrillar end state, APOE acts upstream by stabilizing or destabilizing early, toxic A $\beta$  intermediates that drive synaptic dysfunction, membrane disruption, and neuroinflammatory responses. Consistent with this model, mature A $\beta$  fibrils do not retain ApoE and are functionally indistinguishable regardless of which APOE isoform was present during aggregation. This indicates that ApoE does not exert its pathogenic effects by shaping plaque structure itself. Instead, ApoE modifies Alzheimer's disease risk by regulating the structure, persistence, Further evidence of this can be gleaned from the work of Xia et al (2024), who demonstrated that lipidated ApoE-A $\beta$  co-aggregates are cleared more efficiently by glial cells and elicit a comparatively attenuated inflammatory response. In contrast, non-lipidated ApoE4-A $\beta$  co-aggregates are cleared less effectively and induce a strongly pro-inflammatory glial phenotype. This sustained inflammatory environment further compromises the clearance of additional A $\beta$  species, establishing a self-reinforcing cycle that promotes progressive A $\beta$  accumulation over time.

These findings provide a mechanistic explanation for the heightened Alzheimer's disease risk conferred by ApoE4, which is less efficiently lipidated in vivo than ApoE2 or ApoE3. Reduced lipidation increases the likelihood that ApoE4 participates in the formation of toxic, poorly cleared co-aggregates rather than in protective, clearance-facilitating assemblies. Consistent with this, genetic deletion of ABCA1-a key regulator of ApoE lipidation-exacerbates amyloid plaque deposition, whereas ABCA1 overexpression enhances ApoE lipidation, reduces cerebral A $\beta$  burden, and improves cognitive outcomes in transgenic Alzheimer's disease models (Wahrle et al., 2008; Tate et al., 2024).

### *Differential Hormonal Regulation of Apolipoprotein E*

The functional units of the ovaries are the follicles, each consisting of an oocyte surrounded by specialized somatic cells, including granulosa and theca cells. These structures serve both endocrine and gametogenic roles, supporting steroid hormone and peptide synthesis as well as oocyte survival, growth, maturation, and eventual release for fertilization. Ovarian follicles are broadly classified into preantral and antral stages. Preantral follicles include primordial, intermediate, primary, and secondary follicles and collectively represent approximately 90-95% of the total follicular population in mammals (Smitz & Cortvrindt, 2002; van den Hurk & Zhao, 2005). As folliculogenesis progresses, follicles transition into the antral stage, where they can be further categorized based on size and developmental status into tertiary and preovulatory follicles. Being an abundantly expressed lipoprotein, not only is in the central nervous system, or by the liver, but also in mammalian ovarian tissue (Corraliza-Gomez et al., 2019; Oriá et al., 2020). Although ApoE is best known for its role in mediating cholesterol transport from peripheral tissues to the liver for metabolism, it also plays a critical role in reproductive physiology.

ApoE contributes to cholesterol trafficking within ovarian follicles, where it supports steroidogenesis by facilitating cholesterol availability to steroidogenic cells (Oriá et al., 2020). Cholesterol uptake by ovarian thecal and granulosa cells depends in part on ApoE, either through participation in lipoprotein-receptor complexes or via lipid endocytosis pathways (Getz et al., 2009). Structurally, ApoE is a key component of several lipoprotein particles, including VLDL remnants, a subclass of high-density lipoproteins (HDL) involved in reverse cholesterol transport, and chylomicrons that carry dietary lipids absorbed from the intestine (Kockx et al., 2018). Through these roles, ApoE serves as a molecular link between lipid metabolism, ovarian steroid hormone production, and systemic metabolic regulation.

ApoE production in ovarian cells is under direct hormonal control and shows a strong dependence on FSH signaling. Early in vitro studies demonstrated that exposure of rat granulosa cells to FSH (50 ng/mL) resulted in an approximately two-fold increase in ApoE secretion compared with cells maintained under FSH-free conditions (Driscoll et al., 1985). Mechanistically, this effect was mediated through activation of intracellular cyclic AMP (cAMP) signaling, as treatment with exogenous cAMP similarly enhanced ApoE release. These findings indicate that ApoE expression in granulosa cells is responsive to cAMP-dependent endocrine pathways downstream of FSH receptor activation. Consistent with these experimental observations, age-associated increases in circulating apolipoprotein E levels have also been reported in vivo in women, supporting a link between reproductive aging, increased gonadotropin signaling, and ApoE regulation (Von Wald et al., 2010).

### *Metabolic and Lipid Regulation of Apolipoprotein E*

It is well established that both AD and reproductive aging are associated with extensive alterations in cellular metabolism and mitochondrial function (Muhammad, 2025; Spina et al., 2025; Wang et al., 2025; Xu et al., 2025). One of the most prominent consequences of impaired mitochondrial activity - particularly reduced oxidative phosphorylation (OXPHOS) - is the disruption of key components required for mitochondrial homeostasis, including proteins within the electron transport chain such as complex I. Beyond energetic deficits, emerging evidence suggests that mitochondrial dysfunction exerts broader regulatory effects on cellular signaling pathways, including those governing lipid metabolism and apolipoprotein expression. Notably, ApoE appears to be particularly sensitive to shifts in mitochondrial and metabolic state.

ApoE expression is highly responsive to cellular metabolic stress. Work by Wynne et al. (2023) demonstrates that disruption of mitochondrial electron transport - whether through genetic manipulation of mitochondrial solute carriers (e.g., SLC25A family members such as SLC25A1) or through pharmacologic and genetic inhibition of electron transport chain complexes I, III, or the copper-dependent complex IV - elicits robust upregulation of ApoE across multiple cell types (Wynne et al. 2023). This response is especially pronounced in human glial cells, which represent the primary source of ApoE within the central nervous system (Wynne et al., 2023; Wang et al., 2026).

Importantly, ApoE induction is not restricted to conditions of overt mitochondrial respiratory failure. Mutagenesis of the mitochondrial carnitine transporter SLC25A20 increases ApoE expression despite preserved oxidative phosphorylation and intact respiratory chain subunit abundance. Similarly, disruption of ATP citrate lyase (ACLY) - a cytosolic enzyme critical for acetyl-CoA production - also elevates ApoE levels (Wynne et al. 2023). Therefore, ApoE upregulation likely reflects an adaptive program linked to mitochondrial dysfunction, altered lipid and acetyl-CoA metabolism, and potentially mitochondria-initiated inflammatory signaling. While such responses may initially support membrane repair and metabolic homeostasis, they may become maladaptive in the aging brain, particularly in carriers of the ApoE4 isoform.

Under more canonical physiological conditions, ApoE expression is also regulated through sterol-sensitive transcriptional pathways. Reductions in neuronal cholesterol availability promote the formation of oxysterols, which activate the astrocyte-enriched liver X receptor (LXR) pathway (Wang et al., 2021). LXR functions as a ligand-activated nuclear receptor that induces the expression of genes central to cholesterol homeostasis, including ABCA1 and ApoE (Staurenghi et al., 2021). Together, these proteins facilitate the formation of HDL-like particles and mediate cholesterol transport within the brain (Lindner & Gavin, 2024). In parallel, peroxisome proliferator-activated receptor gamma (PPAR $\gamma$ ) contributes to ApoE upregulation in astrocytes, linking APOE expression to broader metabolic programs involving glucose metabolism and insulin sensitivity (Tyagi et al., 2011; Qi et al., 2021).

Beyond sterol signaling, lipid availability itself further modulates ApoE expression and processing. Oleic acid, a monounsaturated fatty acid that is esterified into triacylglycerols (TAGs) and stored in lipid droplets under conditions of excess, has been shown to alter APOE dynamics. Specifically, oleic acid exposure reduces intracellular levels of heavily glycosylated ApoEE while promoting its secretion (Huang et al., 2004). Chronic exposure enhances ApoE release from astrocytes, with a disproportionately greater increase observed for the ApoE4 isoform (Lindner et al., 2022). This hypersecretion is likely driven by impaired degradation of ApoE4 and increased interactions between ApoE4 and TAG-rich lipid droplets.

#### *A Note on Other Apolipoprotein Variants*

Hormonal perturbations associated with aging - particularly those influencing apoE dynamics - occur alongside broader age-related declines in multiple apolipoprotein species. Using data-independent acquisition (DIA) proteomics, McCoy et al. (2025) demonstrated that circulating apolipoproteins, including ApoA-I, ApoA-IV, ApoB-100, ApoC-I, ApoC-IV, ApoD, ApoE, and ApoM, decline significantly with age in postreproductive female mice.

Several of these apolipoproteins have established relevance to neurodegenerative processes. For example, ApoA-I can bind A $\beta$  and has been implicated in modulating its aggregation and clearance; accordingly, circulating ApoA-I levels are significantly reduced in individuals with Alzheimer's disease compared to healthy controls (Tong et al., 2022). Restoration of ApoA-I levels following ovarian tissue transplantation was associated with improved cognitive performance, reduced inflammatory signaling, and decreased gliosis in aged mice (McCoy et al., 2025).

Additional apolipoproteins exhibit similar patterns. ApoC-IV and ApoD both decline with age and are restored following transplantation of young ovarian tissue (McCoy et al., 2025). Notably, loss of ApoD function increases susceptibility to oxidative stress, elevates brain lipid peroxidation, and impairs locomotor and learning capacity, whereas ApoD overexpression confers protective effects, enhancing survival and limiting oxidative damage (Ganformina et al., 2008).

Importantly, these restorative effects appear largely independent of follicular content. Both follicle-containing and follicle-depleted ovarian tissue transplants returned circulating apolipoprotein levels in aged mice to profiles resembling those of young animals, while also improving cognitive outcomes and attenuating gliosis (McCoy et al., 2025). In parallel, these interventions suppressed circulating FSH levels to those observed in young, reproductively active mice (McCoy et al., 2025; Uilenbroek et al., 1978). These effects occur alongside reductions in

circulating FSH, supporting a model in which endocrine aging contributes to both altered lipid transport biology and neurodegenerative vulnerability. However, whether FSH directly regulates the synthesis of apolipoproteins beyond ApoE remains to be determined.

## Stepwise Neurobiological Dysregulation Driven by Elevated FSH in Alzheimer's Disease

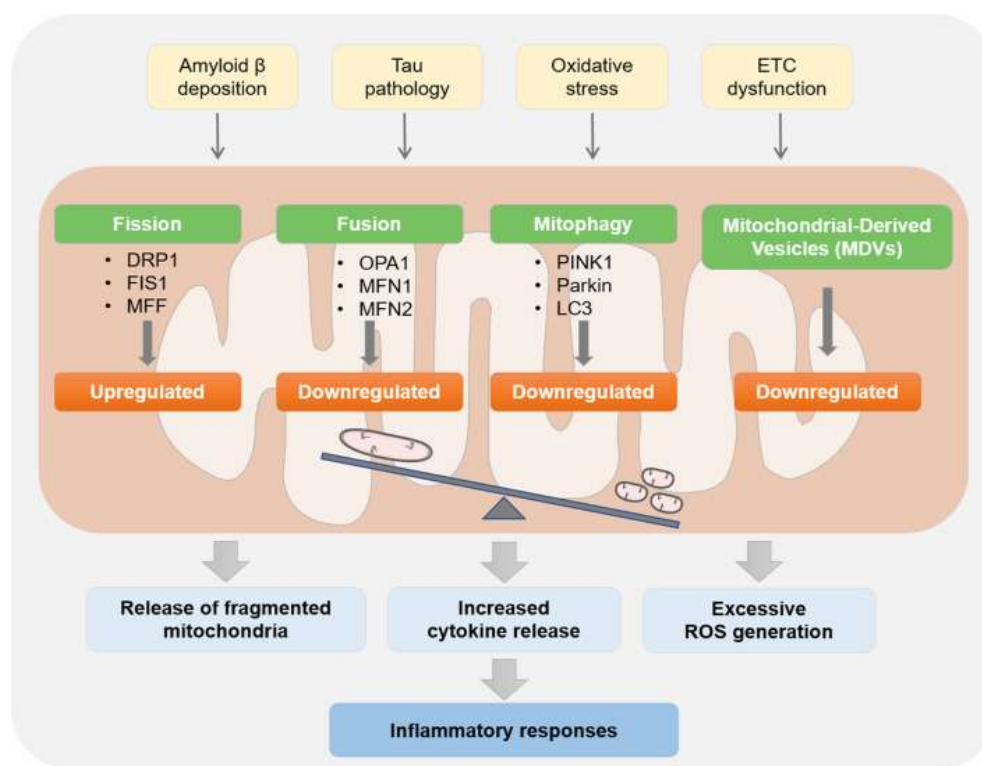
*Elevated FSH Disrupts Oxidative Phosphorylation (OXPHOS) in Aging Neurons, Shifting Cellular Energetics Toward Dysfunction*

Impairments in glucose metabolism and oxidative phosphorylation are well-established features of AD, consistently documented across both experimental and clinical settings. These deficits are routinely observed using fluorodeoxyglucose positron emission tomography (FDG-PET), which reveals characteristic patterns of cerebral hypometabolism in affected individuals (Christodoulou et al., 2026). Among the pathways implicated in this dysfunction, the C/EBP $\beta$ - $\delta$ -secretase signaling axis has emerged as a key contributor, with FSH acting as a positive regulator of this pathway (Xiong et al., 2023). C/EBP $\beta$ , a stress-responsive transcription factor upregulated with aging and in AD, disrupts neuronal glucose utilization by interfering with insulin signaling (Tsukada et al., 2011). Specifically, C/EBP $\beta$  suppresses FOXO1 activity and inhibits Akt (protein kinase B), a central mediator of insulin-dependent glucose uptake. Because Akt signaling is required for efficient glucose transport and downstream metabolism, its inhibition induces a functional insulin-resistant state within neurons (Gabbouj et al., 2019). As a result, brain cells are unable to effectively utilize glucose despite adequate substrate availability, directly contributing to the hypometabolic profile observed on FDG-PET imaging in AD. Notably, the metabolic effects of FSH extend beyond the central nervous system, influencing processes such as adipogenesis and cardiovascular function in both men and women, suggesting broader systemic consequences of dysregulated FSH signaling (Kim et al., 2026).

Beyond its effects on glucose utilization, the C/EBP $\beta$ - $\delta$ -secretase pathway further compromises cellular energetics by targeting key regulators of mitochondrial function. Activation of this axis promotes degradation of nicotinamide phosphoribosyltransferase (NAMPT), leading to depletion of nicotinamide adenine dinucleotide (NAD<sup>+</sup>) (Li et al., 2025), an essential cofactor for mitochondrial respiration and energy production. Upstream regulation of C/EBP $\beta$  provides an additional layer of relevance in aging. C/EBP $\beta$  is physiologically induced by gonadotropins, including follicle-stimulating hormone FSH and LH, where it regulates genes involved in steroidogenesis and inflammatory signaling, such as steroidogenic acute regulatory protein (StAR) and prostaglandin-endoperoxide synthase 2 (PTGS2/COX-2) (Sirois & Richards, 1993; Duffy et al., 2019). Under normal conditions, LH surges produce transient increases in C/EBP $\beta$  that support tightly regulated periovulatory transcriptional programs. However, in the context of aging, sustained elevations in gonadotropins-particularly chronic exposure to FSH can drive persistent activation of C/EBP $\beta$  (Zaidi et al., 2024). Such prolonged induction may shift signaling away from adaptive, temporally restricted responses toward sustained inflammatory and proteolytic activity. Correspondingly, both ApoE4 and FSH have been shown to additively activate the C/EBP $\beta$ - $\delta$ -secretase pathway, promoting proteolytic processing of amyloid precursor protein (APP) and tau, and thereby enhancing amyloid- $\beta$  accumulation and neurofibrillary tangle formation (Xiong et al., 2022; Xiong et al., 2023; Zaidi et al., 2024).

Importantly, the hypometabolic state observed in AD is not necessarily a primary event, but may instead be preceded by a phase of heightened mitochondrial activity and neural hyperexcitability (Christodoulou et al., 2026; Naia et al., 2023). During these early stages, C/EBP $\beta$ -dependent signaling can transiently enhance mitochondrial output - partly through increased transcriptional activity at the TFAM promoter - thereby supporting mitochondrial biogenesis and oxidative capacity in response to elevated cellular demand (Sierra-Magro et al., 2023). Concurrently, C/EBP $\beta$ -mediated suppression of FOXO1 and REST disrupts inhibitory neuronal programs, particularly within GABAergic circuits, leading to reduced inhibitory tone and aberrant network

excitation (Mattson M. P. 2020; Xia et al., 2022). This state of hyperexcitability is consistent with early hypermetabolic signals detected in preclinical and prodromal stages of AD (Christodoulou et al., 2026; Naia et al., 2023)



**Figure 5. Convergent drivers and consequences of mitochondrial perturbation in Alzheimer's disease.** Amyloid- $\beta$  deposition, tau pathology, oxidative stress, and electron transport chain (ETC) impairment. These stressors disrupt mitochondrial quality control by promoting excessive fission (e.g., DRP1, FIS1, MFF upregulation) while suppressing fusion (OPA1, MFN1/2), mitophagy (PINK1, Parkin, LC3), and mitochondrial-derived vesicle (MDV) formation. The resulting imbalance favors mitochondrial fragmentation, reduced turnover of damaged organelles, and accumulation of dysfunctional mitochondria. *Adapted from Li et al., (2022).*

However, sustained activation of this pathway appears to shift the system toward metabolic failure. Chronic C/EBP $\beta$  activity - together with persistent Akt inhibition and progressive mitochondrial damage - promotes the accumulation of dysfunctional mitochondria and reduces overall metabolic efficiency (Shaerzadeh et al., 2014; Yu et al., 2014; Wang et al., 2025). As mitochondrial quality control mechanisms become compromised, this initially compensatory hypermetabolic state transitions into overt hypometabolism (Naia et al., 2023; Christodoulou et al., 2026). The downstream consequences of this metabolic shift are both multifaceted and self-reinforcing. Impaired oxidative metabolism promotes cytosolic acidification and lactate accumulation, which in turn disrupt lysosomal acidification and autophagic flux (Chen et al., 2022; Hagihara & Miyakawa, 2024; Wang X et al., 2025). These alterations contribute to lysosomal swelling, autophagosome accumulation, and impaired clearance of cellular debris (Quick et al., 2023). In parallel, these metabolic disturbances sustain microglial activation and inflammatory signaling, further amplifying neurodegenerative processes (Jung et al., 2025; Wu et al., 2025). The mechanisms by which metabolic perturbations bias microglial cells toward pro-inflammatory phenotypes are beyond the scope of this review; however, readers are referred to prior work for a more detailed treatment of this topic (Ball et al., 2025; Shaikh & Nicholson, 2009).

*FSH-Mediated Enhancement of ApoE4 as a Barrier to Autophagy: Implications for Proteinopathy*

During folliculogenesis, FSH is generally regarded as a regulator of autophagy, acting in a context-dependent manner through the PI3K-AKT-mTOR signaling axis. Under basal conditions, FSH activation of AKT-mTOR promotes cell growth and suppresses autophagy (Liu et al., 2023). However, as follicles progress to the antral and pre-ovulatory stages, rapid cellular proliferation and metabolic demand create localized hypoxic microenvironments. Under these conditions, FSH signaling intersects with hypoxia-inducible pathways, leading to dynamic modulation of mTOR activity. Specifically, transient activation of mTOR is followed by a relative decline in its activity as hypoxia stabilizes HIF-1 $\alpha$ , shifting the balance toward autophagy induction via an FSHR-mTOR-HIF-1 $\alpha$ -dependent mechanism (Zhou et al., 2017). This transition allows follicular cells to maintain metabolic homeostasis despite increased energetic and oxidative stress. Functionally, autophagy plays a critical protective role in follicular survival. Impairment of autophagic pathways leads to intracellular waste accumulation, compromised cellular integrity, and depletion of the primordial follicle pool (Gawriluk et al., 2011; Wu et al., 2015; Song et al., 2015; Zhou et al., 2017). Accordingly, stress-induced upregulation of autophagy during later stages of folliculogenesis likely represents an adaptive mechanism that preserves follicular viability under conditions of heightened metabolic demand.

The downstream consequences of enhanced FSH signaling appear to be highly context-dependent and may diverge significantly in the central nervous system. These differences are largely determined by tissue-specific coupling of FSHRs to distinct intracellular signaling pathways. In classical endocrine tissues such as the ovary, FSHR predominantly couples to G $\alpha$ s proteins, leading to increased cAMP production and activation of protein kinase A (PKA). This signaling cascade integrates with Akt-mTOR pathways to promote cell survival and growth (Casarini & Crépieux., 2019). In contrast, neuronal FSHR signaling may preferentially engage alternative G-protein pathways, including G $\alpha$ i-mediated signaling. Rather than promoting a cAMP-driven anabolic program, this coupling activates downstream kinases such as Akt, ERK1/2, and SRPK2, resulting in upregulation of the transcription factor C/EBP $\beta$ . Following phosphorylation, SRPK2 translocates to the nucleus, where it contributes to activation of  $\delta$ -secretase (also known as AEP). This protease cleaves APP and tau into aggregation-prone fragments, thereby promoting amyloid- $\beta$  accumulation and tau pathology (Li et al., 2024). Thus, a consequence of FSH up-regulation is the production of protein metabolites that the cells are unable to clear, including A $\beta$ , tau, and ApoE (especially APOE4).

Consequently, the accumulation of autophagic vesicles within dystrophic neurites is a well-established feature of Alzheimer's disease, reflecting impaired autophagosome-lysosome fusion and defective degradation of autophagic cargo (Nixon et al., 2005; Nixon & Yang, 2011; Zhang et al., 2022). Consistent with this, experimental models show elevated levels of LC3-II, indicative of stalled or incomplete autophagosome turnover (Yang et al., 2011; Zhang et al., 2022). Notably, ApoE4 carriers exhibit a pronounced accumulation of autophagic vesicles, suggesting that this isoform further exacerbates impairments in autophagic flux (Sohn et al., 2021). One proposed mechanism involves FSH-mediated induction of ApoE4 nuclear localization, where it interferes with transcriptional regulation of autophagy by binding to coordinated lysosomal expression and regulation (CLEAR) motifs. In vitro studies indicate that ApoE4 competes with transcription factor EB (TFEB) for occupancy at these elements - including SQSTM1, MAP1LC3B, and LAMP2 - thereby suppressing TFEB-driven expression of lysosomal and autophagy-related genes (Parcon et al., 2018).

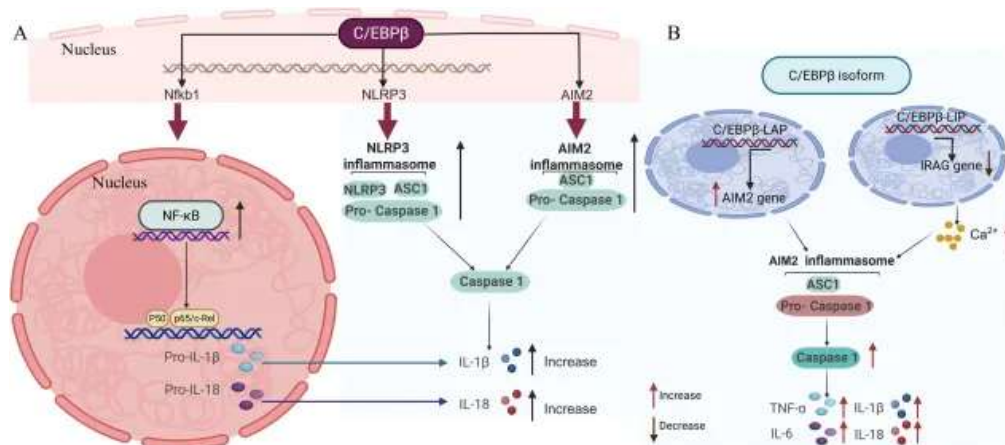
Additionally, aberrant autophagosome accumulation has been shown to precede amyloid plaque formation, indicating that autophagic dysfunction represents an early pathogenic event rather than a secondary consequence of amyloid deposition (Yu et al., 2005). Experimental induction or inhibition of macroautophagy in neuronal cells produces parallel changes in autophagic vesicle abundance and amyloid- $\beta$  production (Yu et al., 2005). Impaired PS1 function promotes mTORC1 activation, which suppresses TFEB-mediated autophagy and lysosomal biogenesis in brain cells (Reddy et al., 2016), while PS2 mutations further inhibit autophagosome - lysosome fusion (Fedeli et al., 2019). Importantly, the efficiency of autophagic and lysosomal pathways declines with advancing age even in individuals without presenilin mutations or complete loss of function, further increasing

vulnerability to disrupted protein homeostasis later in life (Beckman et al., 2020; Lim et al., 2024; Shen et al., 2007; Thakur & Ghosh, 2007).

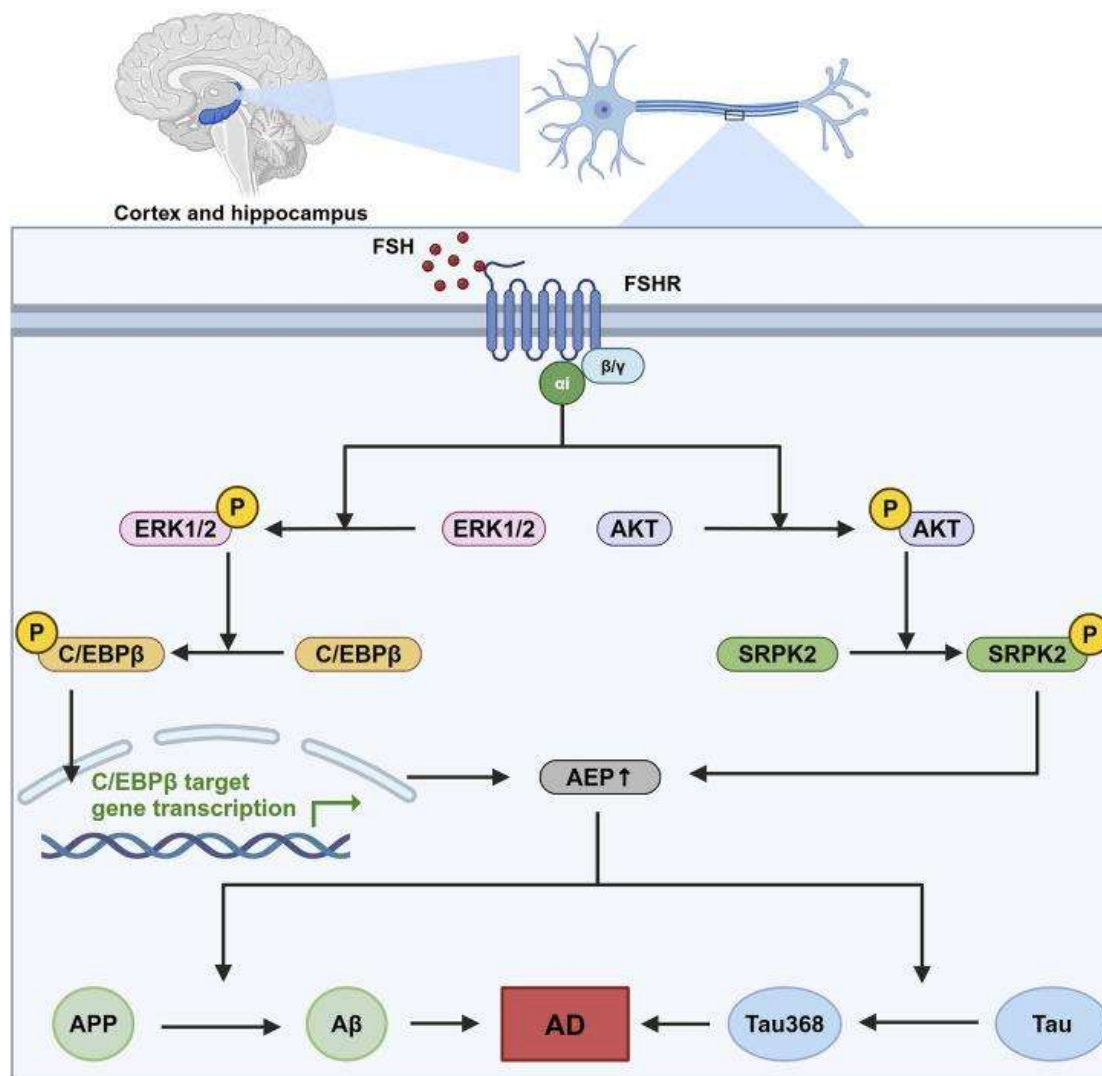
#### *FSH-Mediated Augmentation of Glial Activation in Alzheimer's Disease*

C/EBP $\beta$  serves as a central regulator of inflammatory signaling. Numerous pro-inflammatory genes contain consensus C/EBP $\beta$  binding sites, and both macrophages and glial cells exhibit marked upregulation of C/EBP $\beta$  in response to inflammatory stimuli (Wang et al., 2025). Consistent with this role, C/EBP $\beta$ -deficient brains display reduced expression of pro-inflammatory genes and attenuated neurotoxic effects of activated microglia (Straccia et al., 2011; Yao et al., 2024). Moreover, loss of C/EBP $\beta$  activity confers neuroprotection in experimental models of ischemic and excitotoxic injury, underscoring its contribution to neuroinflammatory damage (Wu et al., 2023).

C/EBP $\beta$  plays a central role in regulating genes involved in inflammasome activation (Wang, J. et al., 2025). Inflammasomes - particularly the NLRP3 complex - are activated by a range of cellular stressors, including misfolded protein aggregates, oxidative stress, and mitochondrial dysfunction (Wu, D. et al., 2022; Baragetti et al., 2020; Hamilton & Anand, 2019; Halliday & Mallucci, 2015; Jones et al., 2021). Within this context, C/EBP $\beta$  directly regulates the transcription of key inflammasome components by binding to their promoter regions. Notably, C/EBP $\beta$  has been shown to upregulate expression of NLRP3, a core structural component of the inflammasome complex (Ma et al., 2018; Chen, J. et al., 2021). It similarly enhances expression of AIM2, a cytosolic DNA sensor that forms a caspase-1-activating inflammasome (Hornung et al., 2009; Zou et al., 2023). Through these actions, C/EBP $\beta$  contributes to the priming phase of inflammasome activation, increasing cellular sensitivity to downstream activating signals. In addition to its direct transcriptional effects, C/EBP $\beta$  functions synergistically with other inflammatory transcription factors, most notably NF- $\kappa$ B, to amplify cytokine production (McClure et al., 2016). NF- $\kappa$ B is a well-established regulator of inflammatory gene expression, and its cooperation with C/EBP $\beta$  enhances transcriptional output at shared target loci. For example, both factors bind to adjacent promoter regions of IL-1 $\beta$  and IL-18, driving coordinated upregulation of these cytokines (Ma et al., 2018).



**Figure 6. C/EBP $\beta$ -dependent transcriptional regulation of inflammasome activation and pro-inflammatory signaling.** This figure illustrates the role of C/EBP $\beta$  as a central transcriptional regulator linking upstream inflammatory cues to inflammasome activation. In panel A, C/EBP $\beta$  cooperates with NF- $\kappa$ B to induce expression of key inflammasome components, including NLRP3 and AIM2, promoting assembly of ASC-containing complexes, activation of caspase-1, and subsequent maturation of IL-1 $\beta$  and IL-18. In panel B, distinct C/EBP $\beta$  isoforms differentially regulate inflammasome gene expression, thereby modulating downstream inflammatory responses through calcium-dependent signaling and cytokine production. Collectively, the figure highlights C/EBP $\beta$  as a key integrator of transcriptional control and innate immune activation, coordinating inflammasome pathways implicated in neuroinflammation and neurodegenerative disease. Adapted from Wang, J., et al. (2025).



**Figure 7. FSH-FSHR signaling as a driver of amyloidogenic, tau-directed, and inflammatory pathology in Alzheimer's disease.** FSH binding to FSHR in cortical and hippocampal neurons activates G $\alpha$ i-dependent ERK1/2 and AKT signaling, leading to phosphorylation of C/EBP $\beta$  and SRPK2. These pathways upregulate asparagine endopeptidase (AEP), promoting cleavage of APP and tau into aggregation-prone species (A $\beta$ , Tau368). These products further activate microglial and inflammasome signaling, amplifying cytokine production and sustaining neuroinflammation. Collectively, this axis links elevated FSH to proteolysis, inflammation, and accumulation of neurotoxic substrates in AD. *Adapted from Li et al., (2024).*

Despite the lack of evidence concerning microglial expression of FSH-receptors, considering the regulatory influence of FSH on C/EBP $\beta$ , it follows that elevated FSH signaling may directly promote microglial activation through C/EBP $\beta$ -dependent and related inflammatory pathways. Consistent with this, accumulating evidence indicates that FSH acts as a positive modulator of neuroinflammatory processes and glial activation. To directly assess these effects, Xiong et al. (2023) developed an Alzheimer's disease mouse model using ovariectomy to disrupt endogenous sex hormone balance, while maintaining physiological estrogen levels through replacement. Under these conditions, FSH elevation was associated with increased accumulation of Alzheimer's disease-related markers in the brain, including A $\beta$  and hyperphosphorylated tau (Tau368), indicating that FSH may promote disease pathology independently of estrogen.

Importantly, A $\beta$  and hyperphosphorylated tau act as reciprocal amplifiers of neuroinflammation. A $\beta$  facilitates microglial recruitment and clustering within plaque-dense regions

(Gao et al., 2023) and induces activation of the NLRP3 inflammasome, leading to the release of apoptosis-associated speck-like protein containing a CARD (ASC) aggregates. These ASC specks can bind A $\beta$ , further promoting its aggregation and propagation (Venegas et al., 2017). In parallel, chronic activation of microglia and astrocytes enhances amyloidogenic APP processing and upregulates tau-directed kinases, including glycogen synthase kinase-3 $\beta$  (GSK-3 $\beta$ ), thereby accelerating tau hyperphosphorylation, synaptic dysfunction, and neurodegenerative spread (Chen & Yu, 2023; Zhang et al., 2021). Further supporting a causal role, treatment with FSH-neutralizing antibodies has been shown to reduce A $\beta$  accumulation and tau pathology in experimental models, reinforcing the contribution of FSH signaling to Alzheimer's disease progression (Xiong et al., 2022).

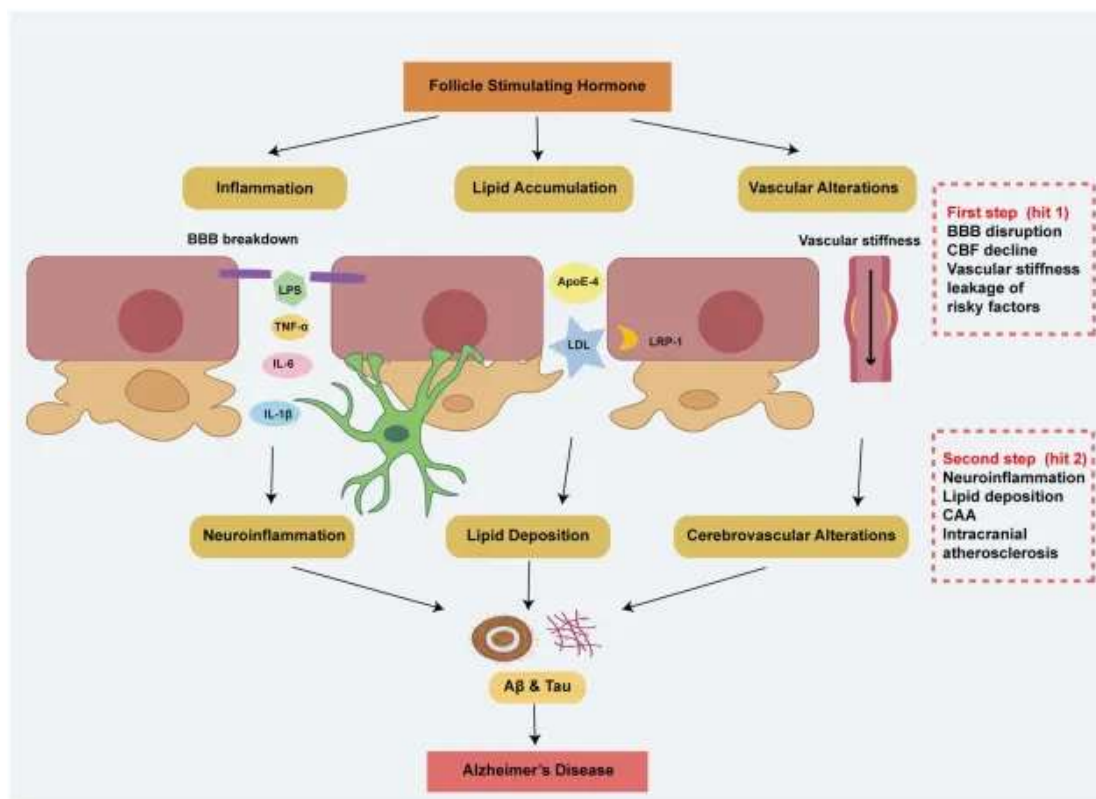
#### *FSH-Mediated Disruption of the Blood-Brain Barrier*

The blood-brain barrier (BBB) is formed by specialized brain endothelial cells connected by tight junctions and supported by perivascular cell populations, including pericytes, astrocytes, microglia, and oligodendrocytes. Together, these components tightly regulate molecular exchange between the circulation and the central nervous system, restrict the entry of neurotoxic substances, and maintain neural homeostasis (Kim et al., 2025).

Circulating FSH levels are inversely associated with vascular compliance, such that higher FSH concentrations correlate with increased arterial stiffness and endothelial dysfunction (Ferretti et al., 2018; Laakkonen et al., 2021; Wang et al., 2026; Xue et al., 2025). Experimental and clinical studies further indicate that elevated FSH promotes vascular calcification and progressive loss of arterial elasticity, contributing to age-related vascular remodeling (Li et al., 2024; Roelofs et al., 2022). In parallel, FSH has been shown to disrupt endothelial junctional integrity by altering the expression of adherens junction proteins, including E-cadherin and V-cadherin, thereby increasing vascular permeability (Kolnes et al., 2020; Rocca et al., 2024).

Beyond its effects on peripheral vasculature and neural cells (Xue et al., 2025), emerging evidence suggests that FSH can also influence cerebrovascular function (Alkhalifa et al., 2023; Wilson et al., 2008). Because BBB integrity depends on adherens and tight junction mechanisms shared across vascular beds, FSH-mediated disruption of endothelial junctional signaling observed in peripheral tissues may extend to the BBB. Such destabilization would be expected to increase permeability, facilitating the entry of inflammatory mediators, lipids, and circulating factors into the brain parenchyma.

In addition to adherens junction disruption, BBB impairment may also arise through FSH-associated alterations in gap junction signaling. In a mouse model, ovariectomy followed by treatment with a gonadotropin agonist (leuprolide acetate) resulted in increased expression of connexin-43 and enhanced Evans blue dye extravasation into the brain, indicating elevated BBB permeability (Wilson et al., 2008). Notably, BBB dysfunction is now recognized as an early feature of Alzheimer's disease, emerging prior to overt neurodegeneration and clinical symptoms (Alkhalifa et al., 2023).



**Figure 8. FSH-mediated contributions to blood–brain barrier dysfunction and cerebrovascular pathology.** Elevated FSH promotes blood-brain barrier (BBB) disruption, vascular stiffness, and reduced cerebral blood flow (CBF) through inflammatory signaling, lipid dysregulation, and structural vascular changes. These alterations facilitate the entry of peripheral risk factors into the brain, amplifying neuroinflammation, cerebral lipid accumulation, cerebral amyloid angiopathy (CAA), and intracranial atherosclerosis. Collectively, these processes contribute to the development of Alzheimer’s disease-like pathology. *Adapted from Xue, Y., et al. (2025).*

Astrocyte aging represents an additional layer of vulnerability. Aged astrocytes exhibit reduced capacity to support neuronal function and maintain homeostasis, and have been identified as a strong cellular predictor of Alzheimer’s disease risk (Bronzuoli et al., 2019; Cohen & Torres, 2019; Monterey et al., 2021). Given that astrocytic endfeet provide near-complete coverage of the cerebral vasculature (Mathiisen et al., 2010), age-related astrocytic dysfunction is likely to further compromise BBB stability. Consistent with this, aging itself is associated with progressive increases in BBB permeability, with older women demonstrating greater BBB vulnerability than younger individuals (Goodall et al., 2018; Knox et al., 2022).

### **Integrative Mechanistic Framework: How Reproductive Aging in Biological Females Reconfigures Alzheimer’s Disease Risk**

The biological features commonly associated with AD, as with many age-related disorders, are not unique to individuals who meet diagnostic criteria for the condition. Although amyloid- $\beta$  accumulation, tau pathology, and  $\alpha$ -synuclein aggregation are central to the pathobiology of neurodegenerative diseases such as Alzheimer’s disease, Parkinson’s disease, and dementia with Lewy bodies, these same molecular alterations are also observed during normative aging (Sengupta & Kaye 2022). Indeed, postmortem studies have repeatedly identified amyloid plaques and tauopathy, of varying degrees, in cognitively normal for older adults and even middle aged carriers (Krishnadas et al., 2022; Morris et al., 2010; Pletnikova et al., 2008; Sengupta & Kaye 2022). Moreover, the proteins involved in these processes are produced constitutively throughout life, yet the majority

of individuals never develop clinical neurodegenerative disease (Pearson et al., (1999). Thus, pathology does not arise simply from protein presence, but from failures in the regulatory systems that govern protein folding, trafficking, clearance, and cellular context, which are commonly aberrant among various neurodegenerative conditions outside of the one subject to this review (Jamerlan, A., & Hulme, J. (2026).

The earliest indicators of impending neurodegeneration - often preceding measurable cognitive impairment - include impaired proteostatic and autophagic clearance, altered cellular metabolic activity (Gazestani et al., 2023), chronic microglial activation (Li et al., 2018), increased blood-brain barrier permeability, and astrocytic dysfunction. Collectively, these upstream disturbances compromise cellular homeostasis, inflammatory regulation, and metabolic support well before overt neuronal loss becomes evident (Li et al., 2018). In this context, classical pathological hallmarks such as amyloid- $\beta$  and tau accumulation, autophagosome buildup, and progressive neuronal degeneration are more accurately understood as downstream consequences of sustained regulatory failure rather than primary initiating events. With these points in mind, it is prudent to consider factors that pre-emptively perturb these aspects of the condition at an early stage so that the risk of disease progression may be mollified.

In the United States, the majority of AD cases occur in women, suggesting that female-specific biological factors contribute meaningfully to disease risk, progression, and severity. Consistent with this, women - particularly those carrying the ApoE4 allele - tend to exhibit earlier onset and more severe clinical manifestations of AD. Notably, approximately 40-60% of AD cases involve at least one ApoE4 allele, underscoring its substantial contribution to the overall disease burden (Pires & Rego, 2023). Beyond its role in AD, ApoE4 may also influence responses to other conditions associated with reproductive aging. For example, female APOE4 carriers appear to be at increased risk for treatment resistance in the context of menopausal symptoms, including vasomotor instability and sleep disturbances (Muhammad, 2025). These observations suggest that ApoE4 may interact with endocrine aging processes in ways that extend beyond classical neurodegenerative pathways.

Although this review focuses on mechanisms underlying increased AD risk in women, it is important to note that age-related increases in FSH are also observed in men, albeit to a lesser extent (Kim et al., 2024). This raises the possibility that FSH-related mechanisms may contribute to neurodegenerative processes across sexes, and warrants further investigation into the role of FSH in AD pathophysiology in male populations.

## **Endocrine and Metabolic Targets: Translational Opportunities in Alzheimer's Disease**

Although a wide range of pharmacologic agents are currently used in the clinical management of AD - including cholinesterase inhibitors, NMDA receptor antagonists, and more recently developed anti-amyloid therapies (Zhang et al., 2024) - a comprehensive evaluation of these treatments is beyond the scope of this review. Instead, the present work focuses specifically on mechanisms linking reproductive aging to AD pathophysiology, with particular emphasis on endocrine transitions, gonadotropin signaling, and their downstream effects on inflammation, metabolism, and cellular homeostasis. Within this framework, emerging therapeutic strategies targeting these upstream, system-level processes - such as modulation of FSH signaling - are discussed as potential avenues for intervention. This approach is intended to complement, rather than replace, existing treatment paradigms by highlighting underexplored biological drivers that may contribute to disease susceptibility and progression in women.

### *Therapeutic Targeting of FSH in Alzheimer's Disease*

Given the emerging role of FSH in modulating AD risk and pathology, therapeutic targeting of FSH signaling represents a promising avenue for intervention. Preclinical studies demonstrate that ovariectomy induces AD-like pathology and cognitive deficits in female ApoE4 knock-in mice, effects

that are significantly attenuated by treatment with FSH-neutralizing antibodies. These interventions reduce amyloid burden, mitigate hippocampal and cortical neurodegeneration, and improve cognitive performance (Xiong et al., 2022; Xiong et al., 2023). Subsequent work has reinforced these findings, showing that disruption of FSH signaling - either through FSHR knockout or antibody-mediated blockade - improves spatial learning and recognition memory in experimental models (Korkmaz et al., 2025; Pallapat et al., 2025). Despite these encouraging results, FSH-targeted therapies remain in the preclinical stage, although efforts toward translation into human trials are currently underway (Pallapat et al., 2025).

#### *Hormone Therapy and Estrogen Receptor Modulation*

The use of menopause hormone therapy (MHT) for the treatment of menopausal symptoms and its effects on cognition and dementia risk remains an area of ongoing clinical and public debate, largely due to conflicting evidence and concerns regarding potential adverse outcomes (Rocca et al., 2024). While experimental and laboratory studies often suggest neuroprotective or cognitive benefits of hormone therapy, these findings have not been consistently replicated in human populations (Ali et al., 2023; Andy et al., 2024).

Some clinical and epidemiological studies report that MHT may increase the risk of dementia and cognitive decline (Craig et al., 2005; Yuk et al., 2023), and it has been associated with increased Alzheimer's-related tau pathology (Coughlan et al., 2023). However, the overall certainty of this evidence remains limited, as many systematic reviews fail to meet rigorous standards (e.g., GRADE) due to bias, heterogeneity, and inconsistency across studies (Hilton Boon et al., 2021). Early observational studies suggested that MHT might reduce dementia risk, particularly when initiated during midlife and used over extended durations (Henderson et al., 1994; Henderson et al., 2005; Kim et al., 2021; Whitmer et al., 2011; Zandi et al., 2002). However, these findings are highly susceptible to confounding - especially healthy user bias - and have not been consistently reproduced in randomized controlled trials (Rahman et al., 2019).

The Women's Health Initiative Memory Study (WHIMS) reported that combined MHT (conjugated equine estrogens plus medroxyprogesterone acetate) approximately doubled dementia risk, while estrogen-only therapy increased the risk of mild cognitive impairment in women aged 65 years or older (Shumaker et al., 2003; Shumaker et al., 2004). Although these findings are often cited, the late age of therapy initiation limits their generalizability to typical clinical use, where treatment is often initiated earlier in the menopausal transition.

Subsequent observational studies and meta-analyses have yielded inconsistent results. Some large observational cohorts suggest that combined MHT may increase dementia risk, particularly with prolonged use (Pourhadi et al., 2023; Vinogradova et al., 2021), whereas others report a potential reduction in risk - especially with estrogen-only therapy initiated during midlife (Nerattini et al., 2023; Mosconi et al., 2025). However, more stringent umbrella reviews applying risk-of-bias assessments and GRADE criteria have found no reliable evidence supporting a protective "therapeutic window" for MHT and emphasize substantial uncertainty in the literature (Melville et al., 2025). Across randomized and observational evidence, findings remain heterogeneous and frequently limited by methodological constraints, including imprecision, study design variability, and cohort overlap. As such, current evidence does not support the use of MHT solely for dementia prevention, nor does it definitively establish a causal relationship between MHT and increased dementia risk (Livingston et al., 2024).

Notably, the analysis by Melville et al. (2025) did not account for potential modifying effects of genetic factors such as ApoE4 status, which may partially explain heterogeneity across studies. Evidence suggests that responses to estrogen-based therapies are genotype- and age-dependent. In younger postmenopausal women (mean age <65 years), estrogen treatment has been associated with beneficial effects on brain structure and amyloid dynamics, including reduced amyloid deposition and preservation of hippocampal and entorhinal cortex volumes - effects that appear most pronounced in ApoE3/4 carriers (Kantarci et al., 2016). However, outcomes in  $\epsilon 4$  homozygotes remain

uncertain (Saleh et al., 2023; Depypere et al., 2023), and these benefits are not consistently observed in women over the age of 65 (Yaffe et al., 2000; Burkhardt et al., 2004; Kang et al., 2004; Kang & Grodstein, 2012).

Experimental data further support genotype-specific differences in estrogen responsiveness. In female mouse models, acute estradiol administration into the dorsal hippocampus enhanced object recognition and spatial memory consolidation, along with increased dendritic spine density in the CA1 region, in animals carrying ApoE3 or a single ApoE4 allele (E3FAD and E3/4FAD), but not in ApoE4 homozygous mice (E4FAD) (Taxier et al., 2022a; Taxier et al., 2022b). Although the mechanisms underlying this reduced responsiveness remain unclear, ApoE4 homozygous females exhibit elevated ER $\alpha$  expression without corresponding changes in ER $\beta$  levels, suggesting a shift in receptor balance that may influence estrogen signaling outcomes (Taxier et al., 2022a,b).

Importantly, clinical practices such as sequential hormone replacement therapy - where estrogen is administered continuously with intermittent progestin in cycling women - may introduce additional risks. Chronic estrogen exposure in this context has been associated with adverse effects including hyperprolactinemia, hypertension, and metabolic disturbances (Kalenga et al., 2022; MohanKumar et al., 2018), warranting careful consideration when evaluating endocrine interventions.

A limitation of estrogen-based therapies in postmenopausal individuals with AD is their association with increased risk of hormone-sensitive cancers, including breast and endometrial cancer, largely mediated through the proliferative effects of estrogen receptor alpha (ER $\alpha$ ) signaling (Shete et al., 2023). In contrast, activation of ER $\beta$  does not promote cancer cell proliferation (Jia et al., 2015) and has been associated with beneficial effects on cognition (Fleischer et al., 2021). Experimental studies demonstrate that ER $\beta$  activation enhances memory formation in rodent models (Schwabe et al., 2024), and this receptor is highly expressed in brain regions critical for cognition and neuroendocrine regulation, including the hippocampus, medial prefrontal cortex, and hypothalamus (Almey et al., 2014; Shughrue et al., 1998; Milner et al., 2005).

Importantly, ER $\beta$  signaling has been linked to reductions in amyloid- $\beta$  levels and tau phosphorylation within the hippocampus (Tian et al., 2013; Xiong et al., 2015). Consistent with a protective role, constitutive knockout of ER $\beta$  in mice results in increased A $\beta$ 42 deposition and ApoE accumulation in the hippocampus and cortex (Zhang et al., 2004). However, evidence from preclinical models indicates that ER $\beta$ -mediated benefits may be genotype-dependent, with cognitive and neuropathological improvements observed primarily in E3FAD and E3/4FAD mice, but not in ApoE4 homozygous models. Interestingly, a similar pattern of differential responsiveness has been reported in clinical contexts, where ER $\beta$ -targeted approaches appear to confer more consistent benefits in subsets of women experiencing menopausal symptoms (Muhammad, 2025). Together, these findings suggest that while ER $\beta$  signaling may offer a more favorable therapeutic profile than non-selective estrogen approaches, its efficacy is likely influenced by underlying genetic and physiological context. Further studies need to be conducted with human subjects to confirm or deny its clinical utility.

#### *Targeting Metabolic Perturbations in Alzheimer's Disease*

Metabolic perturbations in brain cells represent some of the earliest detectable changes preceding the AD phenotype (Naia et al., 2023). These disturbances are further amplified by FSH-associated signaling dynamics, establishing a metabolic environment that predisposes to downstream dysfunction, including impaired autophagy, microglial activation, disrupted glucose utilization, and the accumulation of pathogenic protein species. In this context, metabolic dysfunction is not merely a consequence of disease progression but a key upstream driver of neurodegenerative vulnerability.

Importantly, metabolic alterations within the hypothalamus may also contribute to dysregulation of FSH signaling itself (Zhang et al., 2013). The menopausal transition is characterized by transient elevations in gonadotropin-releasing hormone GnRH, followed by subsequent declines in postmenopausal stages (Hall et al., 2000). Reduced GnRH signaling has been linked to activation

of NF- $\kappa$ B/IKK- $\beta$ -mediated inflammatory pathways (Zhang et al., 2013), suggesting that hypothalamic metabolic reprogramming may precede and facilitate inflammatory signaling cascades that further disrupt neuroendocrine regulation. These interactions point to a bidirectional relationship in which metabolic dysfunction and endocrine dysregulation reinforce one another across aging.

Among therapeutic strategies targeting metabolic dysfunction in AD, ketogenic diets (KD) have emerged as one of the most promising non-pharmacological approaches. Ketogenic interventions have a well-established role in neurological conditions such as epilepsy and are increasingly being explored as adjunctive therapies in disorders including bipolar disorder, glioblastoma, and neurodegenerative diseases. In AD, a randomized trial demonstrated that a 12-week KD intervention improved quality of life and daily functional performance, although interpretation is limited by small sample size and short duration (Phillips et al., 2021). Additional studies report improvements in cognitive function alongside favorable changes in metabolic and biomarker profiles (Neth et al., 2020), including increased cerebral ketone uptake, enhanced brain perfusion, and improved peripheral lipid and glucose metabolism.

A broader range of trials using varied ketogenic formulations has consistently demonstrated beneficial effects in individuals with mild cognitive impairment (MCI) and AD, with evidence suggesting that efficacy may be greatest during early to moderate stages of disease progression (Oliveira et al., 2023). Although the literature remains heterogeneous with respect to study design, intervention protocols, and outcome measures, the collective evidence supports the therapeutic potential of ketogenic strategies in AD (Grammatikopoulou et al., 2020).

Additional pharmacologic and non-pharmacologic approaches targeting metabolic dysfunction in AD have also been explored, and readers are referred to Stefaniak et al. (2022) and Wang et al. (2023) for further discussion.

## Conclusions

Alzheimer's disease emerges not solely from the accumulation of pathogenic proteins, but from progressive failures in the systems that regulate metabolism, proteostasis, inflammation, and vascular integrity. Reproductive aging represents a critical inflection point in female neurobiology, characterized by coordinated endocrine, immunological, and metabolic shifts that reshape vulnerability to neurodegeneration.

Among these changes, sustained elevations in FSH appear to exert broad and multifaceted effects that extend well beyond reproductive physiology. Evidence synthesized in this review suggests that FSH contributes to AD pathogenesis through convergent mechanisms involving dysregulated glucose metabolism, mitochondrial dysfunction, impaired autophagic clearance, altered apolipoprotein dynamics, and amplification of neuroinflammatory signaling. These effects are further compounded by interactions with genetic risk factors such as ApoE4, as well as age-associated declines in vascular and blood-brain barrier integrity. Importantly, many of the molecular alterations traditionally regarded as defining features of AD - such as amyloid- $\beta$  accumulation and tau pathology - are more accurately understood as downstream consequences of earlier systemic dysregulation. This perspective shifts emphasis toward upstream drivers of disease susceptibility, particularly those emerging during the menopausal transition.

Although therapeutic strategies targeting FSH signaling remain in early stages of development, preclinical evidence suggests that modulation of this axis may attenuate multiple facets of AD pathology. Notably, such modulation need not rely solely on direct FSH blockade; selective targeting of estrogen receptor pathways, particularly ER $\beta$ , may offer an alternative means of mitigating FSH-associated effects while preserving beneficial estrogenic signaling. Future work should aim to clarify the extent to which FSH influences neurodegenerative outcomes in both men and women, as well as how progressive hypothalamic-pituitary alterations in neuroendocrine, metabolic, and immune regulation shape FSH dynamics across aging. Advancing this understanding may enable the development of more precise, biology-informed interventions that address upstream drivers of neurodegeneration rather than its late-stage manifestations.

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