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The β-secretase BACE1 in Alzheimer's disease

Harald Hampel[a,b*], Robert Vassar[c], Bart De Strooper[d,e,f], John Hardy[g], Michael Willem[h], Neeraj Singh[i], John Zhou[i], Riqiang Yan[i], Eugeen Vanmechelen[j], Ann De Vos[j], Robert Nisticò[k,l], Massimo Corbo[m], Bruno Pietro Imbimbo[n], Johannes Streffer[o,p], Iryna Voytyuk[d,e,q], Maarten Timmers[o,r], Amir Abbas Tahami Monfared[a,s], Michael Irizarry[a], Bruce Albala[a], Akihiko Koyama[a], Naoto Watanabe[u], Teiji Kimura[u], Lisa Yarenis[a], Simone Lista[b,t,v], Lynn Kramer[a], Andrea Vergallo[b,t,v*]

[a] *Eisai Inc., Neurology Business Group, 100 Tice Blvd, Woodcliff Lake, NJ 07677, USA*
[b] *Sorbonne University, GRC n° 21, Alzheimer Precision Medicine (APM), AP-HP, Pitié-Salpêtrière Hospital, Boulevard de l'hôpital, F-75013, Paris, France*
[c] *Department of Neurology, Mesulam Center for Cognitive Neurology and Alzheimer's Disease, Feinberg School of Medicine, Northwestern Univesrity, Chicago, IL, USA*
[d] *KU Leuven Department of Neurosciences, Leuven, Belgium*
[e] *Centre for Brain and Disease Research, VIB (Flanders Institute for Biotechnology), Leuven, Belgium*
[f] *Dementia Research Institute at UCL, ION, University College London, UK*
[g] *Department of Molecular Neuroscience and Reta Lilla Weston Laboratories, UCL Queen Square Institute of Neurology, London, United Kingdom*
[h] *Chair of Metabolic Biochemistry, Biomedical Center (BMC), Faculty of Medicine, Ludwig-Maximilians-University Munich, 81377 Munich, Germany*
[i] *Department of Neuroscience, University of Connecticut Health, Farmington, CT., USA*
[j] *ADx NeuroSciences NV, Technologiepark 4, 9052, Ghent, Belgium.*
[k] *Laboratory of Neuropharmacology, EBRI Rita Levi-Montalcini Foundation, Rome, Italy.*
[l] *School of Pharmacy, Department of Biology, University of Rome Tor Vergata, Rome, Italy.*
[m] *Department of Neurorehabilitation Sciences, Casa Cura Policlinico, Milan, Italy*
[n] *Department of Research and Development, Chiesi Farmaceutici, Parma, Italy*
[o] *Reference Center for Biological Markers of Dementia (BIODEM), Institute Born-Bunge, University of Antwerp, Antwerp, Belgium*
[p] *UCB Biopharma SPRL, Braine-l'Alleud, Belgium*
[q] *ALBORADA Drug Discovery Institute, University of Cambridge, UK*
[r] *Janssen Research and Development, a division of Janssen Pharmaceutica N.V., Beerse, Belgium*
[s] *Department of Epidemiology, Biostatistics and Occupational Health, McGill University, Montreal, QC, Canada*
[t] *Brain & Spine Institute (ICM), INSERM U 1127, CNRS UMR 7225, Boulevard de l'hôpital, F-75013, Paris, France*
[u] *Eisai Co., Ltd, Tokyo, Japan*

[v] *Institute of Memory and Alzheimer's Disease (IM2A), Department of Neurology, Pitié-Salpêtrière Hospital, AP-HP, Boulevard de l'hôpital, F-75013, Paris, France*

*** Correspondence to:**
Andrea Vergallo[1], MD & Harald Hampel[1,2], MD, PhD

[1] Sorbonne University Clinical Research Group (GRC n°21)
"Alzheimer Precision Medicine (APM)"
Établissements Publics à caractère Scientifique et Technologique (E.P.S.T.)

Alzheimer Precision Medicine Initiative (APMI)
https://www.apmiscience.com/

[2] Eisai Inc.
Neurology Business Group
100 Tice Blvd, Woodcliff Lake, NJ 07677, USA
Tel: (+1) 201-746-2060 (o)
harald_hampel@eisai.com

Short title: BACE1 in Alzheimer's disease

ABSTRACT

The β-site amyloid precursor protein cleaving enzyme 1 (BACE1), was initially cloned and characterized in 1999. It is required for the generation of all monomeric forms of Aβ, including Aβ42, which aggregates into bioactive conformational species and likely initiates toxicity in Alzheimer's disease (AD). BACE1 concentrations and rates of activity are increased in AD brains and body fluids, thus supporting the hypothesis that BACE1 may drive AD progression. Therefore, BACE1 is a prime drug target for slowing down Aβ production in early AD. Besides the amyloidgenic pathway, BACE1 has other substrates that may be important for synaptic plasticity and homeostasis. Indeed, germline and adult conditional BACE1-knockout mice display complex neurological phenotypes. All BACE1 inhibitor clinical trials conducted so far were discontinued for futility or safety reasons. Despite these negative results, BACE1 remains a well-validated therapeutic target for AD. A safe and efficacious compound with a high substrate selectivity as well as a more accurate dose regimen, patient population, and disease stage may yet be found. Further research should focus on the role of Aβ and BACE1 in physiological processes and key disease mechanisms of AD. The functions of BACE1 and the homologue BACE2 and the biology of Aβ in neurons and glia deserve further investigation. Cellular and molecular studies of BACE1 and BACE2 knockout mice coupled with biomarker-based human research will help elucidate the biological functions of these important aspartic proteases and identifying their substrates. Such studies will have critical implications for BACE1 inhibition as a therapeutic approach for AD.

Keywords: Alzheimer's disease; BACE1 inhibitors; biomarkers; clinical trials; soluble amyloid; synaptic

β-SITE AMYLOID PRECURSOR PROTEIN CLEAVING ENZYME 1

β-site amyloid precursor protein (APP) cleaving enzyme 1 (BACE1) is an aspartyl protease of the pepsin family and was discovered in 1999. BACE1 is a type I transmembrane protein, which makes it distinct from other peptidases of the same family, like Cathepsin D and E that do not harbor a transmembrane domain(1–4). BACE1 is widely expressed in the brain particularly in neurons, oligodendrocytes and astrocytes, with particular abundance in various neuronal cell types(1–4). At the subcellular level, BACE1 localises on the plasma membrane and in the endosomal compartments and was detected in healthy synaptic terminals and dystrophic neurites surrounding amyloid-β (Aβ) plaques(2,5,6). BACE1 is homologous with another membrane-bound secretase of the pepsin family, BACE2. The two proteases share 59% of their amino acid sequence and are composed of identical structural domain(1–4).

The active site of both secretases consists of two aspartic acid residues in their extracellular domains; they have 21-residue helical transmembrane domains and short cytoplasmic C-terminal domains(1–4). Three disulphide bonds help stabilize their tertiary structure and the secretases are known to be glycosylated on several asparagine residues. Post-translational modifications are known on BACE1 secretase, and are important for lipid raft localization, phosphorylation for cellular trafficking and ubiquitination for degradation (see below).

BACE1 and BACE2 are expressed in the same cell types in the brain, only with BACE2 being much less abundant(7,8). However, BACE2 is thought to be more active in peripheral tissues, with particular functions in melanocytes(9) and pancreatic β cells(10).

BACE1: GENETIC AND EPIGENETIC

Genetic mutations impact BACE1 cleavages

Mutations in BACE1 gene has not yet been linked to AD pathogenesis. However, mutations in APP near β-secretase sites are assumed to be either protective or causing early onset. The most prominent one is the Swedish mutation (K670M671 to N670L671 mutation at the cleavage P^2-P^1 subsite), which increases processing of APP at the β-site by 10-50 fold and causes early onset of AD(11).

Whole-genome sequencing studies identified a genetic variant of APP, significantly more frequent in Icelandic and Scandinavian populations that provides resilience against age-related brain Aβ deposition and AD(12,13).

Intriguingly, an Ala residue at the cleavage $P^{3'}$ subsite mutated to Thr (A673T) in APP confers an intrinsic biochemical resistance to cleavage by BACE1, resulting in both less Aβ production overall but also generation of peptides that are less prone to aggregation(12,13).

In particular, the A673T mutation is associated with a different BACE1 recognition motif at the position P2 (A673T) resulting in 20-30% lower sAPPβ levels compared to controls(12,13). The A673T mutation appears to protect against AD and age-related cognitive decline as a result because of suppressed cleavage of APP at the β-site, and carriers of A673T variant in humans have about 28% lower levels of Aβ40 and Aβ42 in plasma compared to the controls(12,13).

In addition, the E682K mutation in APP, located at the P$^{1'}$ β’site, favouring Aβ production by suppressing the cleavage at the β'-site to favour cleavage at the β-site(12,13).

DNA methylation

Epigenome-wide association studies (EWAS) on neuronal and glial cell sorted from post mortem brains of AD patients and healthy donors have revealed genes specific to neuronal cells including APP which undergo Braak stage-associated methylation changes(14). Interestingly, DNA methylation regulates BACE1 expression, likely due to increased SP1 transcription factor binding to CpG sites on the BACE1 promoter region(15,16). More recently, a large cluster of significantly hypomethylated enhancers in the CpH sites were identified in prefrontal cortex neurons of individuals with severe AD pathology, and hypomethylation of these enhancers in DSCAML1 gene likely upregulate BACE1 transcripts in AD(17). Similar DNA hypomethylation in the promoter region of APP enhances the expression of AD related genes including APP, PSEN1 leading to increased Aβ production(17,18).

DNA Acetylation

Although BACE1 expression and/or its activity have been extensively studied at both transcriptional and post-translational levels, evidence of altered expression of BACE1 due to epigenetic acetylation remains weak. BACE1 mRNA levels are significantly increased in 3xTg mouse brains and in peripheral blood mononuclear cells (PBMCs) from AD patients, but are much less elevated in MCI compared to controls subjects, and this increase is linked to H3 acetylation facilitating the accessibility of the *BACE1* promoter(19). Decreasing acetylated H3 in the BACE1 promoter regions by galangin treatment in SH-SY5Y cells reduces BACE1 mRNA level, likely related to up-regulated endogenous HDAC1-mediated deacetylation(20).

Inhibition of histone acetyltransferase p300 by curcumin can also decrease acetylated H3 to reduce BACE1 transcripts(21). On the other hand, royal jelly peptides appear to regulate BACE1 expression through the control of HDAC1(21). BACE1 mRNA levels are also regulated by diverse factors including different transcription factors, which are summarized elsewhere(22,23).

Regulated BACE1 expression by miRNA

Recently, the role of non-coding RNA, in particular micro-RNA (miRNA) in regulating BACE1 has been gaining traction. Non-coding RNA, often referred to as miRNA, are 19-22 nucleotides long and often regulates gene and protein expression at the post transcriptional level by binding to 3' UTR RNA to form a silencing complex. Over the past two decades, additional non-coding RNA has been shown to negatively regulate BACE1 expression: miR-107, miR29c, miR-339-5p, miR186, miR195, miR-135b, miR-135a, miR124, miR-298/328 (see Table 1 for more details)(24–28).

The emerging field of AD transcriptomic signatures, including non-coding RNA that may be involved in negatively regulating BACE1 expression, can offer a promising platform for developing biomarkers. However, diagnostic and therapeutic applications of miRNAs remain challenging due to multiple reasons, including restricted brain penetration and high-specificity concerns.

Post-translational regulation of BACE1

BACE1 activity is not only regulated at the expression level but also by posttranslational modification. During the course of AD, BACE1 is subjected to numerous posttranslational modifications and plays a role in regulating signalling associated with Aβ production and AD. BACE1 is a typical aspartyl protease with two active aspartate motifs (D_{93}TG and D_{289}SG) located in each lobe. BACE1 is first synthesized in the endoplasmic reticulum (ER) as a 501-aa immature precursor protein (proBACE1). During maturation, BACE1 is N-glycosylated at 4 Asn sites (Asp-153, -172, -223, and -354) in the ER lumen(4) and its prodomain (residue 1-21) is removed by furin-like proprotein convertases in the ER/early Golgi compartment(3,4). Although the presence of prodomain is not sufficient to suppress BACE1 activity(16), unlike most aspartyl proteases, suppressing glycosylation by site-directed mutagenesis of these Asp residues reduces the protease activity of BACE1(29). BACE1 is also reported to undergo sugar modifications by bisecting N-acetylglucosamine (GlcNAc), which is high in brains. In AD patients' brains, higher GlcNAc activity may partially cause increased BACE1 activity and Aβ deposition(30).

The role of SUMOlyation in regulating BACE1 functionality/stability and activity is reported in both in vitro and in vivo AD mouse models.—it was showed that sumoylation of residue K501 on BACE1 enhances its stability and Aβ producing activity(31). By contrast, overexpression of non-SUMOylated BACE1 mutant negated memory decline in WT mice and did not accelerate senile plaque formation(31).

Post-translational modifications of BACE1 have been shown to alter its trafficking and/or localization(32). For example, palmitoylation of BACE1 at 4 cysteine residues (C474, C478, C482, and C485) in the transmembrane and c-terminal domains targets BACE1 to cholesterol rich lipid rafts(32).

BACE1 undergoes phosphorylation at both Ser498 and Thr252, but phosphorylation at ser498 residue appears to regulate intracellular trafficking by shuttling/recycling BACE1 between endosome and plasma membrane(33). This modification at Ser498 has minimal or no effect on Aβ levels(34). Others noted that phosphorylation at Thr252 by p25/Cdk5 was associated with increased BACE1 activity and Aβ production(35).

Similarly, acetylation of BACE1 has also been identified at seven lysine resides(36).

While acetylation imparts BACE1 protein stability(36), ubiquitination of BACE1 promotes its degradation in the lysosome and is impaired in AD(37,38). Overall, as an aspartyl protease, BACE1 requires low acidic environments to reach optimal proteolytic activity, ideally at ~pH 4.5(39,40).

BACE1 PHYSIOLOGICAL FUNCTIONS AND PATHOPHYSIOLOGICAL IMPLICATIONS

Amyloidogenesis

BACE1 is the β-secretase enzyme that cleaves the transmembrane APP and together with γ-secretase and generates Aβ species that, in AD, form increasingly large and conformationally complex soluble regionally deposited brain aggregates (see Figure 1). BACE1 cleavage of APP represents the rate-limiting step for Aβ production.

For this reason, BACE1 has been extensively studied in the context of brain amyloidogenesis and proven to be directly involved in Aβ production based on data from several mouse KO models(41–43). BACE1 has been pharmacologically targeted, with several inhibiting compounds entering clinical development and trials, effectively lowering Aβ concentrations in human individuals.

Cleavage of APP by β-secretase liberates the soluble N-terminus of APP while the C-terminal fragment (CTF-β or C99) remains bound to the membrane. Two mutations at the β-secretase cleavage site (the Swedish mutation KM/NL and an Italian variant A673V) were reported to be linked to familial Alzheimer disease (FAD) and consequently raise the sAPPβ level due to strongly increased affinity of BACE1 for the changed recognition motif in APP(44).

The significant protective effect of the A673T variant against AD has provided a robust proof of principle for the pathophysiological and pharmacological model that reducing the β-cleavage of APP may offer a resilient mechanism against the disease(12). In addition, preliminary evidence suggests that a long-time preventive reduction of BACE1 activity by 20-30% may be sufficient to prevent AD. However, to fully exploit the clinical and pharmacological implications of the A673T mutation, it is essential to understand whether A673T mutation Aβ aggregates display different toxicity rates compared with wild-type scarriers and which molecular pathways underlie the finding that the A673T allele also protects against non-AD cognitive decline(12).

High BACE1 enzymatic activity was found in human AD brain extracts which is consistent with the finding that neurons produce the highest levels of Aβ(3,45). The highest BACE1 protein level was reported in postnatal brain in mouse. Notably, a relatively large accumulation of BACE1 was described in neuritic dystrophies in vicinity of Aβ plaques both in AD amyloidogenic mouse models and in AD brains most likely by a post-translational mechanism(2,5,6). Inducing autophagy in mutant human neurons augments retention of BACE1 in distal axons by autophagy, leading to enhanced β-cleavage of APP(46). To produce Aβ, the fragment CTF-β is cleaved by γ-secretase, which finally releases Aβ into the extracellular space and the APP intracellular domain (AICD) into the cytoplasm(2,5,6).

In a parallel competing non-amyloidogenic pathway, APP is cleaved either by α-secretase or η-secretase to release two additional variants of the APP ectodomain, namely sAPP-α and sAPP-η(47). The η-secretase pathway is used as an alternative when BACE1 is inhibited with the consequence of increased Aη-α activity with an effect on lowering neuronal activity by a so far unknown mechanism(47).

APP is a type I transmembrane protein and is highly expressed in neurons and abundant at the synapse(48–52). Its function remains elusive, although studies implicated it in maintenance of dendritic spines(53), neurotransmission(54), synaptic plasticity(55–58) and maintenance of excitation-inhibition (E/I) balance(58). Soluble APP is a $GABA_B$-ligand that modulates synaptic transmission(50). Rescue experiments in APP KO mice show that sAPPα is sufficient to restore defects in spine density(59), long-term potentiation and spatial learning(60,61). Most of the ectodomain shedding of APP is performed by the α-secretase, which cleaves APP in the Aβ sequence and is therefore believed to protect against AD(47).

Although some evidence suggests that sAPPβ seems much less active in *in vitro* assays of neural activity and plasticity than sAPPα(62), both soluble sAPPα and sAPPβ modulate basal synaptic transmission and short-term synaptic facilitation through binding to $GABA_B$ receptor subunit 1a ($GABA_BR1a$) at the synapse(50). The sushi domains of the $GABA_BR1a$ are also able to bind full-length APP intracellularly(63). Interestingly, this interaction is crucial for axonal trafficking of the complex, and affects presence of the receptor at the presynaptic terminals. Concomitantly, delivery of the complex to axonal cell surface, diminishes the pool of APP available for BACE1 processing in endosomes and lowers Aβ production(63).

Synaptic substrates

Initial evaluation of BACE1 KO mice focused on decreased production of Aβ, shortly after BACE1 deficiency was revealed to be associated with subtle neurological deficits(43,64). Many of the BACE1 KO mouse phenotypes like the peripheral hypomyelination and synaptic deficits are due to loss of function of substrates depending on the activation by BACE1. Lack of BACE1 was also reported to cause sensorimotor impairments, seizures, schizophrenia-like phenotypes and retinal pathology(65–67). In 2012 the neuronal secretome of BACE1 was revealed by two independent studies in primary cultures(68,69), followed by a more complete repertoire of BACE1 substrates identified in mouse CSF (see Table 2). Among BACE1 substrates, neuregulin-1 (NRG1), seizure-related protein 6 (SEZ6) and close homolog of neural cell adhesion molecule L1 (CHL1) are known to have important neuronal functions and merit further discussion given the recent reports that BACE1 blockade in patients causes cognitive worsening.

NRG1 interacts with the EGFR family of receptors to exert signaling cascades crucial for central nervous system (CNS) development(70) and synaptic plasticity(70). BACE1 cleavage of NRG1 is essential for myelination in the CNS and peripheral nerves as well as muscle spindle formation and maintenance(70). SEZ6 is important for dendritic branching, normal synaptic function, and motor coordination(1,71). In the mouse brain, soluble SEZ6 is almost exclusively produced by BACE1(1,71). Its absence, achieved by genetic KO of SEZ6 or pharmacological inhibition of BACE1, synaptic plasticity is impaired. In particular, aberrant BACE1 processing of SEZ6 results in lower spine density and attenuated long-term potentiation (LTP) in the hippocampus(1,71).

One of the most interesting substrate of BACE1 is CHL1. This cell adhesion molecule mediates axonal guidance in response to semaphorin 3A (Sema3A)(72,73). BACE1 cleavage yields an intracellular membrane-bound C-terminal fragment of CHL1 that is able to influence cytoskeleton dynamics leading to growth cone collapse upon presentation of the Sema3A cue. This particular substrate and/or its homologue L1 cell adhesion molecule (L1CAM), both cleaved by BACE1(69,72–74), might be responsible for axonal organisation defects in BACE1 KO mice(69,72–74). Intriguingly, axon guidance abnormalities in the hippocampus persist in the adult conditional knock-out of BACE1 confirming an important role of the secretase in adult circuitry architecture, as well as its established developmental functions(69,72–74).

BACE2 physiological functions: a brief update

Much less is known about the brain relevant substrates and functions of the sister secretase BACE2 that is more prominently expressed in colon, kidney and pancreas(7). In pancreatic β cells, the pro-proliferative plasma membrane protein Tmem27 and islet amyloid polypeptide (IAPP) are proposed BACE2 substrates(75,76). BACE2 also processes the pigment cell-specific melanocyte protein (PMEL) in pigment cells(9). Pharmacological inhibition of BACE2 results in depigmentation, the most consistent side effect seen in pre-clinical studies of BACE1/2 inhibition(9). Thus, BACE1 and BACE2 shedding events seem to be tissue, cell type and context dependent, revealing the intricacy of their functions(7). Inhibition of BACE2 brain substrates might contribute to some of the side effects seen with BACE1 inhibitors.

Human *post-mortem* studies showed high expression levels of BACE2 and strong correlation with BACE1 expression in neurons and astrocytes of AD but not control(77). Huentelman et al. reported that different single nucleotide polymorphism (SNP) variations at the BACE2 locus are associated with AD risk, and altered Aβ processing(78). This was the first genetic evidence of a role for BACE2 in AD pathophysiology. Larger GWAS studies are needed to confirm such important finding that may have significant pharmacological implications.

BACE1 BIOMARKERS: STATE-OF-ART ON THE VALIDATION AND QUALIFICATION FOR DRUG-BIOMARKER CO-DEVELOPMENT PIPELINES

In the last 15 years, a few human in-vivo studies reported good diagnostic performance of CSF BACE1 concentration (supposed to reflect gene expression levels) and activity in discriminating among AD dementia, Mild Cognitive Impairment (MCI) and cognitively healthy individuals(79–85). Some studies also showed association between BACE1 biomarkers and other core CSF and neuroimaging biomarkers of AD as well as presence of

Apolipoprotein E (APOE) e4 allele(79–85). Significant predictive power regarding conversion from MCI to AD dementia has also been reported.

Regarding the blood matrix, BACE1 biomarkers have been investigated in both plasma(82,86,87) and platelets(88,89) displaying good correspondence with CSF and association with brain AD alterations.

A multi-center study reported good correspondence between CSF and plasma BACE1 concentrations(87). In particular, plasma BACE1 activity demonstrated good diagnostic performance discriminating patients with AD dementia, from MCI and cognitively normal individuals(87). A recent study showed association between plasma BACE1 concentrations and amyloid-PET quantitative measures in a cohort of cognitively healthy individuals at risk for AD(86).

By contrast, some studies showed no acceptable diagnostic performance of BACE1 biomarkers(90–92) or no association between them and AD established biomarkers.

Moreover, lower levels of BACE1 were found in advanced dementia stages of AD, potentially due to advanced neuronal and synaptic loss(93–95).

For more details about study populations and outcomes see Supplemental Table 1.

Inter-study results variability may be partially explained by several differences in the study design, confounding factors (disease stage, sex, *APOE* genotype, co-morbidities) and the methodology. Regarding the latter, pre-analytical factors such as the sample collection, processing, and storage protocols as well as analytical factors such as assays used, are likely the most relevant determinants. The above reported conflicting data call for a harmonization and standardization of research protocols.

In summary, there are enough promising data to boost development of BACE1 biomarkers and investigate whether they may enrich the current AD biomarkers panel and potentially support different contexts-of-use in BACE1 clinical trials, including target engagement and proof of mechanism, dose finding, efficacy and safety monitoring.

HUMAN CLINICAL TRIALS WITH BACE INHIBITORS: a schematic overview

All BACE inhibitors, investigated in RCT, were discontinued for either futility or safety reasons.

A Phase 3 trial of verubecestat, conducted in mild-to-moderate AD patients (EPOCH), was terminated due to futility(96).

A Phase 2/3, trial of atabecestat investigated in preclinical AD individuals (EARLY), was discontinued out of liver toxicity(97).

The Phase 3 trials of lanabecestat investigated in prodromal AD and mild AD (AMARANTH and DAYBREAK-ALZ respectively) were stopped due to futility(98).

A Phase 2 trial of LY3202626 involving mild AD patients (NAVIGATE-AD) was discontinued according to the interim futility analysis(99).

The phase 2/3 umibecestat (CNP520) was investigated in asymptomatic at risk for AD, i.e. *APOE ε4* allele carriers (GENERATION trial) was discontinued due to cognitive worsening in the active treatment group(100).

The Phase 2 of elenbecestat (E2609), conducted in MCI-to-moderate AD participants was discontinued after recommendation by Data Safety Monitoring Board (DSMB) due to an unfavourable risk-benefit ratio (https://www.alzforum.org/therapeutics/elenbecestat).

See Supplemental information for more details.

Potential explanation coming from translational data: Selectivity and toxicity of BACE1 inhibitors

To optimise next-generation BACE1 inhibitor clinical trials it is essential to understand all major biological and pharmacological factors that might account for the high attrition rates of the previous trials. For this purpose, three points should be considered: (1) the biological rationale for BACE1 as a pharmacological target, (2) BACE 1/2 selectivity, druggability, inhibition strength by dose adjustment, and the overall benefit/risk ratio, and (3) timing of intervention with BACE1 inhibitors over the course of AD.

Regarding point 1, in consideration of all evidence reported in the sections above, we argue that the target has a good scientific rationale and was properly and extensively validated in experimental models of AD ahead of clinical studies. Regarding point 2, there are more than 40 known BACE1 substrates (see Table 2), and BACE inhibitors may block one or more of them causing functional consequences. Current compounds tested in the clinic had variable amounts of selectivity for BACE1, but all exerted inhibition of BACE2 activity as well. Inhibiting BACE1 lowers Aβ production, but in combination with BACE2 inhibition the processing of a number of other substrates are blocked with potential negative impact, changing the benefit/risk (see also Supplemental Table 2).

Provided these data have not been systematically disclosed during early development of these compounds, it is arguable that all compounds in clinical development have been tested in standard GLP/GCP toxicity studies as requested and reviewed by regulatory authorities.

Therefore, it is conceivable that these pre-clinical tests did not demonstrate systematic biological signatures indicating the observed effects. Dose levels selected for all prior and current ongoing studies may be too high targeting >50% inhibition of BACE1, leading to unwanted side effects, while potentially lower levels of inhibition could have been therapeutically active.

In this regard, it is not possible to rule out that an excessive suppression of BACE1 activity has determined cognitive dysfunction in AD patients by depleting Aβ monomers that have physiological functions and display poor toxicity. Aβ monomers can trigger or sustain intracellular signaling(s) essential for synaptic plasticity and homeostasis(101–103).

Concerning point 3, timing of intervention with BACE1 inhibitors over the course of AD, robust evidence indicates that cerebral Aβ accumulation is one of the earliest mechanistic alterations of the whole pathophysiological dynamic of AD(104–107).

The stronger correlation found between tau biomarkers~~,~~ with neurodegeneration outcome measures and long-term cognitive scores than Aβ markers has raised the question whether Aβ pathophysiology triggers downstream pathways including tau-mediated toxicity and facilitates tau spreading(104–107). However, CSF and PET longitudinal studies support the hypothetical pathophysiological model of AD for which amyloidosis proceeds, either promoting or being permissive to, the spreading of tau pathology that is likely to drive disease clinical evolution(104–107). Such a spatial and temporal dynamics of AD brain proteinopathies implies that Aβ-directed treatments should be initiated at the earliest preclinical stages of the disease and not in dementia stages. If so, BACE1 inhibitors started prior to the spreading of tau pathology may represent the most suitable path to pursue(108).

Some detrimental effects were induced during the initial phase of treatment and were irrespective of disease stage. It is conceivable that these negative effects may be caused by acute synaptic impairment *via* BACE1 inhibition for some substrates other than APP and should be assessed reversibility after treatment-off.

New potential BACE inhibition strategies: drug repositioning programs and modulation of post-translational modification.

A pursuable path for BACE1 inhibition may be represented by drug repurposing (also called drug repositioning or reprofiling) pipelines that aim at identifying new therapeutic avenues for already approved or investigational drugs irrespective of their original medical indication. Two recent animal trials used chronic exposure to lithium chloride – a therapeutic agent approved for major psychiatric disorders, and showed slow-down of cognitive decline and histopathological alterations associated with reduced BACE1 activity(109,110).

In particular, Wilson and colleagues reported that an innovative experimental formulation of lithium microdose release is associated with the lowering of BACE1 gene expression and overall cerebral Aβ accumulation(110), thus confirming previous translational studies pointing at a potential neuroprotective effect of lithium(111).

Modulation of post-translational modification of BACE1 may represent a viable therapeutic avenue. For instance, it was shown that AD mouse models expressing S-palmitoylation–deficient BACE1 had a significantly decrease in Aβ burden and improved memory function, indicating that posttranslational S-palmitoylation of BACE1 influences Aβ pathogenesis(32). In line with this, HEK293 cells treated with KMI-574 specifically caused dissociation of BACE1 from lipid raft to non-raft membranes and BACE1 processing activity was reduced(112). Hence, blocking BACE1 activity in the raft membrane is another venue for reducing Aβ deposition.

OPEN ISSUES

Several genetic data (306 autosomal dominant mutations plus the APP gene duplication and trisomy 21) and multimodal biomarker studies indicate that an imbalance between Aβ production and clearance plays a critical and early role in AD pathogenesis(104–106,113,114). A huge evidence also supports the hypothesis that cerebral Aβ deposition begins decades before AD clinical onset and prior to cortical spreading of tau pathology. However, the full understanding of the molecular dynamics of Aβ species, from loss of proteostasis to synaptic toxicity (either tau-mediated or not) is not achieved yet. In this context, BACE1 is established to play~~s~~ a key role in Aβ homeostasis and may have an important functions in synaptic plasticity.

Incomplete knowledge of the physiological functions of BACE and its downstream pathways may have contributed to the failures of BACE1 inhibitor clinical trials.

Soluble Aβ peptides / oligomers / protofibrils / fibrils / plaques still remain attractive targets (see Figure 2).

The recently discovered human APP Artic(115) and E693Δ (Osaka)(116) mutations show~~s~~ a type of AD with low cerebral deposition of plaques, as indicated by modest Aβ-PET radiotracer binding(117), and higher production of oligomers and protofbrils which are likely to be the initiators of Aβ toxicity(115,116,118,119). These findings indicated that other forms of Aβ, besides fibrils and plaques, may trigger brain toxicity and contribute to AD-synaptic failure(115,116,118,119). Such evidence has fostered the development of novel biomarkers for tracking all Aβ aggregation states and that may be used for novel surrogate endpoints.

Time for biomarkers of synaptic dysfunctions?

From a functional standpoint, “synaptogenic” mechanisms of AD cognitive decline, i.e. network activation and deactivation deficits, abnormal oscillatory rhythmic activity, and network hypersynchrony ~~have all recognized as key synaptic functional alterations that may~~ account for AD-related synaptic failure(120–122).

Clinical trials can benefit from resting-state and task related functional magnetic resonance (fMRI) studies to detect aberrant patterns at the large-scale brain network level, including the default mode network(123–126). Brain networks functional shifts, as well as their association with molecular dynamics, have already been described in aging and AD(127,128). Very recently, it has been shown that genetic risk factors with a pleiotropic biological effect, such as the APOE ε4 allele, impact the trajectories of the DMN cognitively healthy individuals at risk for AD(129,130).

Fluid biomarkers of synaptic dysfunction are currently under development(131–133). Neurogranin (a key regulator calcium-binding protein calmodulin), synaptogamin (a calcium sensor protein), and synaptosome-associated protein 25 (SNAP-25), a component of the SNARE complex, are the strongest candidate for in-vivo tracking synaptic homeostasis(131–133).

CONCLUSIONS

Despite a number of robust discovery stage studies, a number of Phase 3 small-molecule BACE1 inhibitor clinical trials did not reach primary endpoints or showed cognitive worsening or where discontinued due to safety reasons.

The failure of several BACE1 inhibitor clinical trials appears to involve an insufficient understanding of BACE1 biology and physiology, a limited knowledge of the natural history of AD and the optimal stage of disease at which to treat, as well as lack of biomarker-based outcomes and endpoints. In this regard, BACE1 trials failure may benefit from the previous pitfalls of γ-secretase pharmacological investigation(134).

The field needs to fully uncover the physiological functions of BACE1 substrates, including those involved in including synaptic homeostasis, as well as to better understand the physiological role(s) of BACE2.

In the past 20 years, several key genetic, epigenetic and post-translational factors have been established to impact BACE1 gene expression levels and enzymatic activity that may explain~~ing~~ inter-individual heterogeneity in BACE1-related pathophysiological processes and drug response. While the research community continues to debate the most plausible biological and pharmacological explanations for BACE1 clinical trial failure, there is emerging evidence encouraging a new generation compounds with an ultra APP-selectivity BACE inhibitory effect.

Robust evidence indicates that BACE1 concentrations and rate of activity assessed in body fluids, including plasma, may serve for multiple context-of-use (from trial enrolment, to proof of mechanism, response and toxicity dose estimation, drug resistance prediction) in drug-biomarker co-development programs (see Supplemental Figure 1).

Within this conceptual framework, BACE1-oriented therapies continue to represent a rational and central development area for time-sensitive and effective pathway (mechanism)-based preventive strategies for AD.

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CONFLICTS OF INTEREST

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He is co-inventor in the following patents as a scientific expert and has received no royalties:

- *In Vitro* Multiparameter Determination Method for The Diagnosis and Early Diagnosis of Neurodegenerative Disorders Patent Number: 8916388
- *In Vitro* Procedure for Diagnosis and Early Diagnosis of Neurodegenerative Diseases Patent Number: 8298784
- Neurodegenerative Markers for Psychiatric Conditions Publication Number: 20120196300

- *In Vitro* Multiparameter Determination Method for The Diagnosis and Early Diagnosis of Neurodegenerative Disorders Publication Number: 20100062463
- *In Vitro* Method for The Diagnosis and Early Diagnosis of Neurodegenerative Disorders Publication Number: 20100035286
- *In Vitro* Procedure for Diagnosis and Early Diagnosis of Neurodegenerative Diseases Publication Number: 20090263822
- *In Vitro* Method for The Diagnosis of Neurodegenerative Diseases Patent Number: 7547553
- CSF Diagnostic in Vitro Method for Diagnosis of Dementias and Neuroinflammatory Diseases Publication Number: 20080206797
- *In Vitro* Method for The Diagnosis of Neurodegenerative Diseases Publication Number: 20080199966
- Neurodegenerative Markers for Psychiatric Conditions Publication Number: 20080131921

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Table 1: Regulation of BACE1 levels by miRNAs

MiRNA	Mechanism Of Action	Relevance in AD brain	Reference
MiR107	Downregulate BACE1 mRNA levels by binding to its 3' UTR. Other targets downregulated by mir107 include Granulin, Cofilin, CDK5R1, and ADAM10	Decreased miR 107 levels correlated with increased BACE1 levels in Temporal cortex	(135,136)
Mir29c	MiR-29c targets the 3' UTR of BACE1; overexpression of miR-29c in cells reduced BACE1 protein expression and Aβ accumulation.	Decreased miR 29c expression levels correlated with increased BACE1 levels in sporadic AD	(137,138)
MiR186	MiR-186 suppresses BACE1 expression by targeting the 3'UTR of BACE1 mRNA in primary neuronal cells. Inhibition of miR-186 increased BACE1 protein levels and Aβ levels in Neuro-2a cells.	Gradual reduction in miR-186 levels in 13-month-old mouse cortices during aging	(139)
MiR195	miR-195 levels inversely correlated with the protein level of BACE1 in SAMP8 mice. miR-195 overexpression in N2a/WT cells decreased the BACE1 protein and Aβ levels	Downregulated in Human AD CSF samples	(140)
MiR124	Targets BACE1 by binding to 3'UTR. miR-124 mimetic dramatically downregulated BACE1 mRNA and protein while inhibition of miR-124 significantly increased the expression in SH-SY5Y cells	MiR-124 expression significantly reduced in the Hippocampus & anterior temporal cortex in AD brain	(141)
MiR-298/328	Recognize specific binding sites in the 3-UTR of BACE1 mRNA and regulate BACE1 protein expression in N2a neuronal cells		(142)

Abbreviations: miRNA: micro-RNA; mRNA: messenger RNA; AD: Alzheimer's disease; CSF: cerebral spinal fluid

Table 2. BACE1 substrates and their physiological role.

BACE1 substrate	Physiological role
APP	Regulation of neurite outgrowth, synapse formation, and synaptic plasticity. Also regulates metal homeostasis
APLP1	Regulation of neurotransmission and plasticity in CNS synapses
APLP2	Regulation of synaptic function and plasticity in CNS
Contactin-2	Regulates axon guidance, cell adhesion, neurite outgrowth
Jagged-1	Balances astrogenesis and neurogenesis, notch signaling influences neural plasticity, long-term memory, synapse remodeling transmitter release through astrocytes
CHL1	Regulates axon guidance, cell adhesion, neuronal migration, and neurite outgrowth
Neurexin 1α and 3β	Regulates synapse assembly and maintenance
NRG1	Regulates myelination, neuronal migration, and oligodendrocyte differentiation. Regulates synaptic transmission and plasticity via neurotransmitter receptors
SEZ6	Regulates dendritic arborization and affects excitatory synapse development and maintenance and formation of neuronal circuits
SEZ6L	Regulates synapse maturation, tumor suppressor function, and free cholesterol levels
β (β1-4) auxiliary subunits of the VGSC subtype Nav1	Modulates cell surface expression of Nav1 sodium channels and thus controls excitability and propagation of action potentials in the neuronal membrane
VGSC accessory subunits KCNE1 and KCNE2	Regulation of cardiac and brain potassium channel subunit trafficking and maintenance of membrane excitability

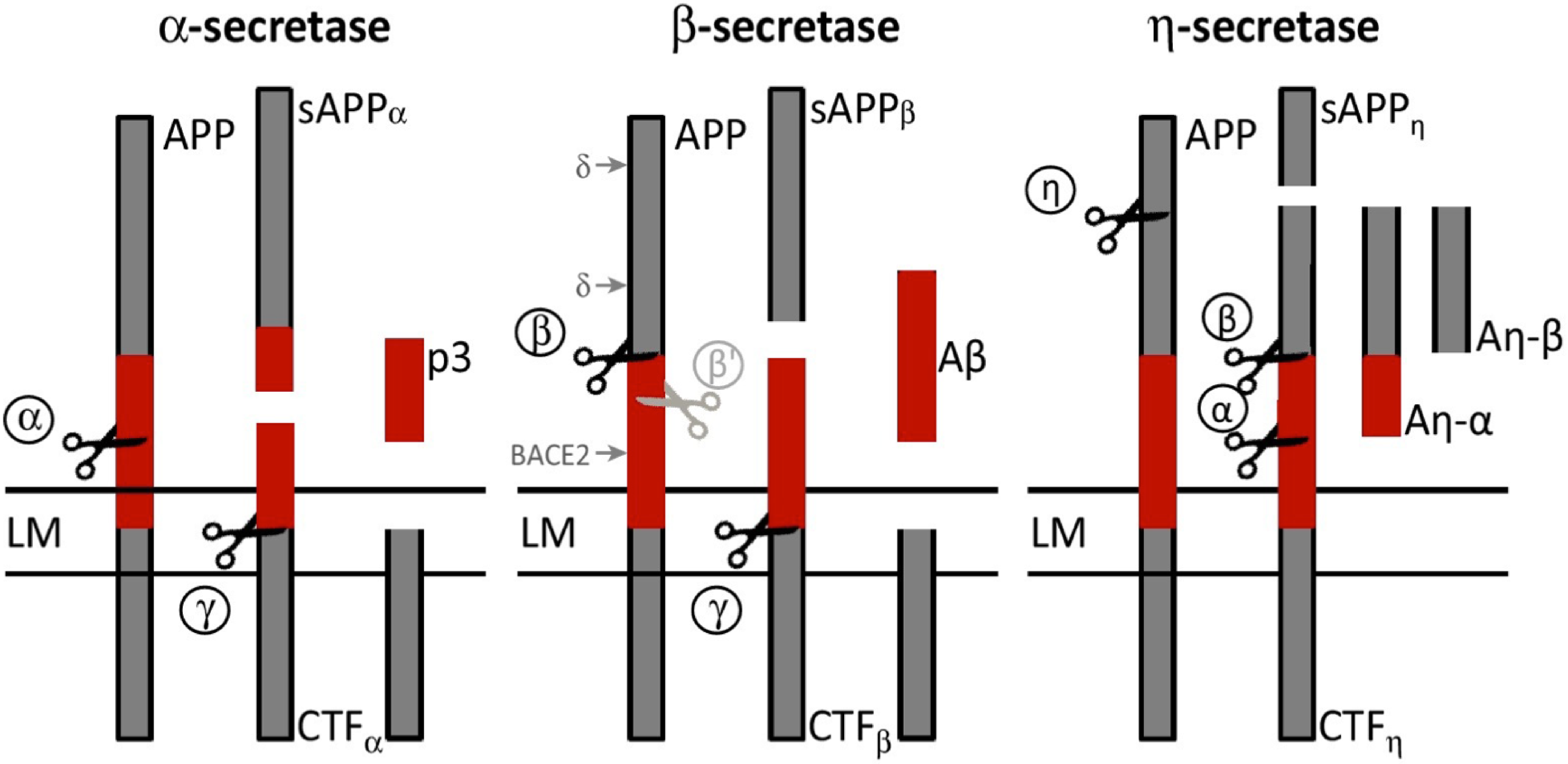
Abbreviations: APP: amyloid precursor protein; APLP1 and 2: Amyloid-like protein 1 and 2; NRG1: neuregulin-1, SEZ6: seizure-related protein 6, SEZ6L: seizure-related protein 6 precursor protein; CHL1: neural cell adhesion molecule L1, VEGFR1: Vascular endothelial growth factor receptor 1, VGSC: Voltage-gated sodium channels. [Adapted from Das B, Yan R. A Close Look at BACE1 Inhibitors for Alzheimer's Disease Treatment. CNS Drugs. 2019 Mar;33(3):251-263]

Figure 1. Schematic Representation of Amyloid Precursor Protein (APP) Processing Pathways

Adapted from Barão S et al. Trends Neurosci. 2016 ;39(3):158-169. doi: 10.1016/j.tins.2016.01.003.

Figure 2. BACE1 and the amyloid-β cycle

Despite the fact that several ~~all~~ clinical trials investigating anti-Aβ compounds did not reach primary endpoints, Aβ peptides / oligomers / protofibrils / plaques still remain an attractive target. Of note, the nature of the toxic Aβ species remains unclear. Evidence suggests that, besides fibrils, dimeric or oligomeric Aβ species but not monomeric Aβ peptides cause neuronal hyperactivity and downstream toxicity in the vicinity of Aβ plaques.


α-secretase
β-secretase
η-secretase
APP
sAPPα
p3
α
γ
LM
CTFα
APP
sAPPβ
δ
δ
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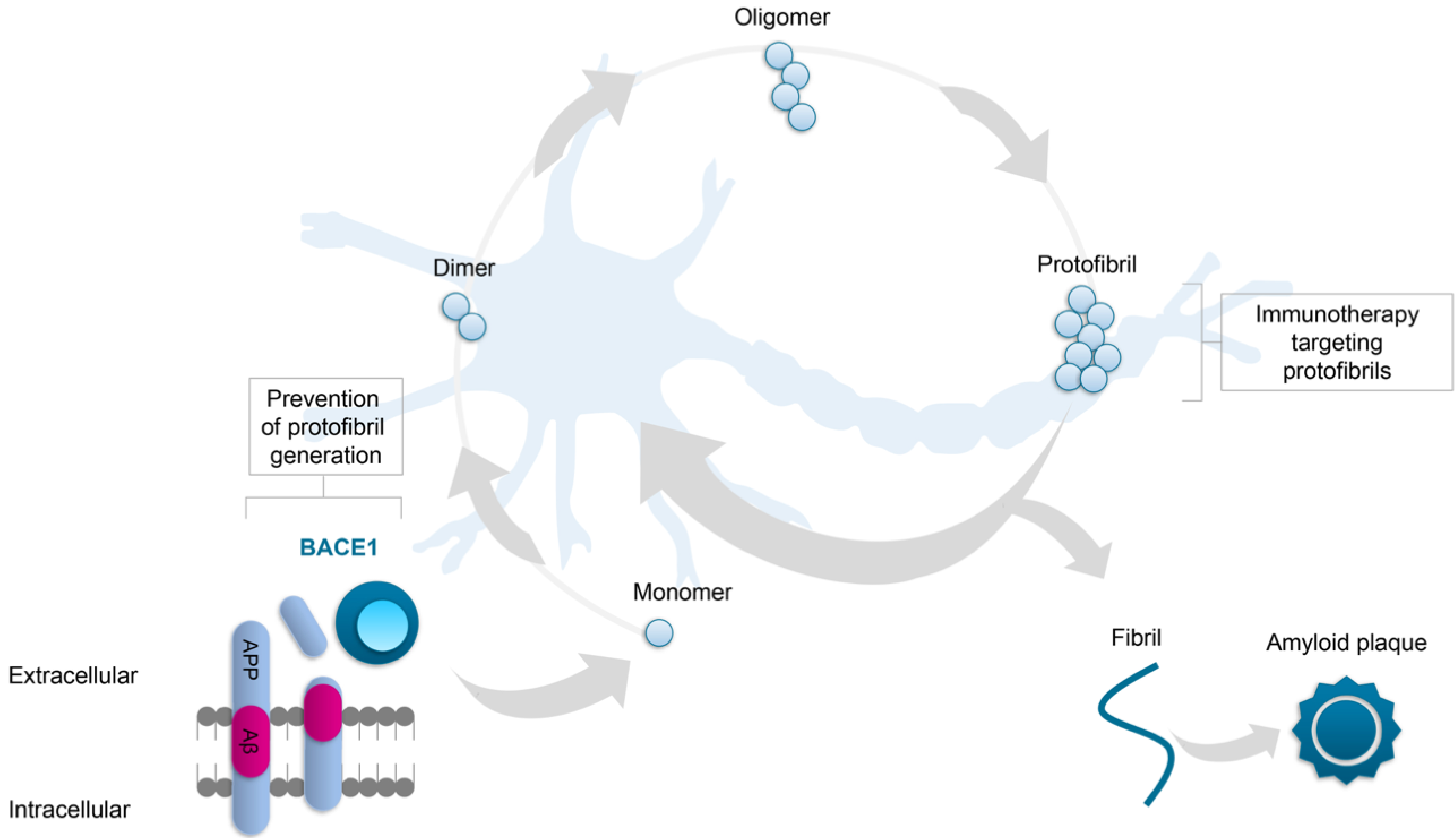
CTFη



Oligomer

Dimer

Protofibril

Immunotherapy targeting protofibrils

Prevention of protofibril generation

BACE1

Monomer

Fibril

Amyloid plaque

Extracellular

Intracellular

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