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Development and Mechanism of γ -Secretase Modulators for Alzheimer Disease

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Abstract

γ -Secretase is an aspartyl intramembranal protease composed of presenilin, Nicastrin, Aph1 and Pen2 with 19 transmembrane domains. γ -Secretase cleaves the amyloid precursor proteins (APP) to release A β peptides that likely play a causative role in the pathogenesis of Alzheimer disease (AD). In addition, γ -secretase cleaves Notch and other type I membrane proteins. γ -Secretase inhibitors (GSIs) have been developed and used for clinical studies. However, clinical trials have shown adverse effects of GSIs that are potentially linked with non-discriminatory inhibition of Notch signaling, overall APP processing and other substrate cleavages. Therefore, these findings call for the development of disease modifying agents that target γ -secretase activity to lower A β 42 production without blocking the overall processing of γ -secretase substrates. γ -Secretase modulators (GSMs) originally derived from non-steroidal anti-inflammatory drugs (NSAIDs) display such characteristics and are the focus of this review. However, first generation GSMs have limited potential due to low potency and undesired neuropharmacokinetic properties. This generation of GSMs has been suggested to interact with the APP substrate, γ -secretase or both. To improve the potency and brain availability, second generation GSMs including NSAID-derived carboxylic acid and non-NSAID-derived heterocyclic chemotypes as well as natural product-derived GSMs have been developed. Animal studies of this generation of GSMs have shown encouraging preclinical profiles. Moreover, using potent GSM photoaffinity probes, multiple studies unambiguously have showed that both carboxylic acid and heterocyclic GSMs specifically target presenilin, the catalytic subunit of γ -secretase. In addition, two types of GSMs have distinct binding sites within the γ -secretase complex and exhibit different A β profiles. GSMs induce a conformational change of γ -secretase to achieve modulation. Various models are proposed and discussed. Despite the progress of GSM research, many outstanding issues remain to be investigated to achieve the ultimate goal of developing GSMs as effective AD therapies.

γ -Secretase and A β peptides

γ -Secretase modulators (GSMs) have emerged to the forefront of Alzheimer disease (AD) research due to their potential as disease modifying agents and despite an unclear mechanism of action. GSMs are a class of compounds that selectively reduce the formation of pathogenic A β 42 species and yet do not affect the total amount of A β produced.⁽¹⁾ Moreover, they have little effect on γ -secretase-dependent Notch processing since the

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generation of Notch intracellular domain (NICD) is not inhibited.⁽¹⁾ Several reviews^(2–7) have highlighted the progress made in developing the next generation of GSMs. This review focuses on recent progress in molecular probe development and studies toward elucidating the mechanism of action of GSMs.

Although the precise pathological mechanism of AD remains elusive, it is widely believed that A β peptides, the major constituents of amyloid plaques,^(8, 9) play a central role in AD through a process named the “amyloid cascade hypothesis”.⁽¹⁰⁾ In this hypothesis, A β peptides form a neurotoxic species that triggers a pathological cascade and ultimately leads to neurodegeneration and dementia. A β peptides are excised from the amyloid precursor protein (APP) through two proteases: β - and γ -secretases (Fig. 1A). This process also generates sAPP β and APP intracellular C-terminal domain (AICD), which could have different biological roles.⁽¹¹⁾ Alternatively, APP can be processed by α - and γ -secretases to generate α CTF, sAPP α , P3 and AICD with varying biological activities.⁽¹¹⁾ Recent studies suggest that α -secretase cleavage can function as a negative feedback regulator to modulate γ -secretase for A β production,^(12, 13) in addition to competing with β -secretase for APP substrates.^(14–17)

γ -Secretase cleaves APP at multiple sites including γ -, ζ - and ϵ -cleavages^(18, 19) (Fig. 1B) to generate A β species with heterogeneous C-termini, which are 37–46 amino acids long.^(20, 21) Compelling evidence indicates that these A β peptides can be generated through a processive mechanism that travels from the ϵ -site to the γ -site and removes three to four amino acids at each step.⁽²²⁾ It has also been proposed that there are two γ -secretase product lines; one from A β 49 to A β 46, A β 43, A β 40 and A β 37; and the other from A β 48 to A β 45, A β 42 and A β 38. However, recent studies showed that A β 38 can be generated from A β 42 and A β 43⁽²³⁾, suggesting that both product lines can be crossed with various combinations. Furthermore, multiple studies have shown that the γ - and ϵ -cleavages are not always correlated^(12, 24–30). Mutations in APP and PS1 lead to different effects on γ - and ϵ -cleavages, and even within γ -sites (such as A β 42 and A β 38)^(12, 24, 27–29). In addition, interaction of γ -secretase with other proteins and/or different assay conditions can dissociate these events.^(25, 26, 30) Whether these findings reflect that γ - and ϵ -cleavages are differentially regulated during sequential processing or just indicate that they represent independent events merits further investigation.

Among the different forms of A β species, the role of A β 40 and A β 42 in AD has been intensively investigated. While both A β 40 and A β 42 have been implicated in AD,⁽¹⁰⁾ A β 42 is more prone to aggregation and is believed to play a critical role in the initiation of AD pathogenesis.^(31, 32) However, recent studies suggest that the ratio of A β 42/A β 40, rather than the total amount of A β , exhibits a better correlation with the age of onset of FAD.⁽³³⁾ Moreover, *in vitro* and animal studies showed that A β 40 can play a role in preventing A β 42 aggregation and therefore reduction of A β 40 that alters the ratio of A β 42/A β 40 may lead to enhanced amyloidogenesis.^(34–39) Direct evidence demonstrating that A β 40 inhibits amyloid deposition came from the studies of bitransgenic (BRL-A β 40/Tg2576) mice in which the over-expression of A β 40 peptide significantly reduced the amyloid deposition.⁽³⁵⁾

Non-selective inhibition of γ -secretase drastically affects the processing and metabolism of APP proteins, which have been shown to regulate various neuronal and synaptic functions conferred by distinct APP domains.^(11, 40) Furthermore, the accumulation of APP β CTF that results from γ -secretase inhibition has been implicated in neurotoxicity.⁽⁴¹⁾ Also, it has been shown that γ -secretase inhibitors (GSIs) can cause A β elevation when administered at low concentrations and withdrawing of GSIs leads to a rebound increase in A β plasma levels.⁽⁴²⁾ In addition, it has been found that an increased concentration of β CTF can

augment the A β 42/A β 40 ratio⁽⁴³⁾. Together these data suggest that total inhibition of APP processing could actually aggravate AD pathology.

Autosomal dominant inheritance of mutations in three genes—the amyloid precursor protein (APP), Presenilin-1 (PS1) and Presenilin-2 (PS2)—causes early-onset and familial AD (FAD).^(44–46) Although how these FAD mutations cause the disease is controversial,⁽⁴⁷⁾ it appears that the overwhelming majority of mutations lead to an increase in the ratio of A β 42/A β 40,⁽⁴⁸⁾ further supporting the A β hypothesis. It is noteworthy to mention a recent discovery showing that an APP mutation, which reduces A β production, protects against AD and age-related cognitive decline,⁽⁴⁹⁾ providing another line of support for the amyloid cascade hypothesis.

Notch1 was the second γ -secretase substrate identified after APP, and functional γ -secretase knockouts result in a notch phenotype.^(50–52) The Notch signaling pathway plays an essential role in cell fate decisions during development.⁽⁵³⁾ Notch signaling also plays an important role in the adult brain, which includes the maintenance and differentiation of neuronal stem cells, structure and synaptic plasticity as well as neuron survival.^(54, 55) In addition, Notch can act as a proto-oncogene or tumor suppressor in some cancers.⁽⁵⁶⁾ Notch1 is processed at least three times (S1–S3 cleavages) for its signaling. First, Notch is cleaved by a furin-like protease (S1 site) in the Golgi that converts a single chain into a heterodimer.⁽⁵⁷⁾ Next, ligand binding to Notch triggers two sequential proteolytic events (S2 and S3): Notch is cut by ADAM metalloproteases at site 2 (S2) and then by γ -secretase at site 3 (S3), which is within the transmembrane domain⁽⁵⁸⁾ and analogous to the ϵ -site of APP (Fig. 2).⁽¹⁹⁾ Following the S3 cleavage, the Notch intracellular domain (NICD) is released from the membrane tether and translocates to the nucleus, where it activates transcription of target genes. NICD binds the CSL (*CBF-1/Su(H)/Lag-1*) transcription factor, thereby dissociating co-repressors and recruiting co-activators such as mastermind (MamL), ultimately leading to the activation of effector genes.^(53, 57) There are five Notch ligands (Dll-1, -3, -4, Jagged-1, -2) and four mammalian Notch receptors (N1-4). All four receptors have been shown to be cleaved by γ -secretase.⁽⁵⁹⁾

The wide spectrum of γ -secretase substrates has made it even more challenging to develop target-based therapy. More than 90 putative γ -secretase substrates have been reported,⁽⁶⁰⁾ reflecting the diverse functions of this protease. However, it is worth considering that many of the experimental studies have only demonstrated that γ -secretase can cleave these protein substrates. Deeper investigation is required in order to determine how many of these proteins are *bone fide* physiological substrates of γ -secretase, and which ones are most likely to cause detrimental side effects when γ -secretase is inhibited. The Phase III clinical trial of semagacestat, a non-selective γ -secretase inhibitor, was terminated due to slightly worse cognition scores and an increase in the risk of skin cancer compared to placebo.⁽⁶¹⁾ Although the precise mechanism that caused these adverse effects is unknown, increased incidents in skin cancer are likely associated with γ -secretase dependent Notch1 signaling that functions as a tumor suppressor.^(62, 63) In addition, semagacestat treatment also led to a lightening in hair color,⁽⁶⁴⁾ which could be associated with tyrosinase, a substrate of γ -secretase.⁽⁶⁵⁾ Therefore, it's critical to know how many substrates are affected by *in vivo* inhibition of γ -secretase, and what the consequences of these events are.

γ -Secretase is an intramembranal complex which relies on the assembly of an active enzyme complex that is composed of a quartet of proteins: Nicastrin (NCT), Presenilin (PS), Pen-2, and Aph-1 with 19 putative transmembrane domains (Fig. 3).⁽⁶⁶⁾ All four proteins are obligatory for cellular γ -secretase activity.⁽⁶⁷⁾ PS is the catalytic subunit of γ -secretase,^(68–70) and belongs to a unique family of GxGD type aspartyl proteases.^(71, 72) Recently, the crystal structure of a PS/signal peptide peptidase (SPP) homologue (PSH)

from the archaeon *Methanoculleus marisnigri* has offered insights into how the transmembrane domains and catalytic dyad are organized in PS1.⁽⁷³⁾ Both the PS1 and PS2 polypeptides undergo endoproteolysis, whereby the N- and C-terminal cleavage products (NTF and CTF) remain associated as heterodimeric integral membrane proteins.⁽⁷⁴⁾ There are two isoforms of presenilin: PS1 and PS2, and three isoforms of Aph-1: Aph-1aS, Aph-1aL and Aph-1b. At least six active γ -secretase complexes have been reported (2 presenilins \times 3 Aph-1s).^(76, 77) Remarkably, PS1 and PS2 are not engaged in the same complex albeit both of them co-exist in the same cells,⁽⁷⁵⁾ indicating a tight and precise control of the assembly of the γ -secretase complex. Aph-1 and NCT play critical roles in the assembly, trafficking, and stability of γ -secretase as well as substrate recognition.^(66, 78, 79) Lastly, Pen-2 facilitates the endoproteolysis of PS into its N-terminal (NTF) and C-terminal (CTF) fragments thereby yielding a catalytically competent enzyme.^(66, 78, 80–82) Although a γ -secretase complex of ~200 kDa, which contains only one of each subunit, is catalytically active,⁽⁸³⁾ the endogenous γ -secretase complex appears to possess a higher molecular weight ranging from 500–2,000 kDa.^(83–87) Taken together, these studies suggest that the quaternary protein complex⁽⁸³⁾ may be the basic functional γ -secretase unit in cells, and additional cofactors and/or varying stoichiometry of subunits exist in the high molecular weight γ -secretase complexes for modulating γ -secretase activity and specificity. Nonessential factors, such as CD147, TMP21, γ -secretase activating protein (GSAP), β -arrestin-1 β -arrestin-2, Erin-2, syntexin-1, voltage-dependent anion channel 1 (VDAC1), contactin-associated protein 1 (CNTNAP1), TPPP and NDUFS7 have been found to be associated with the γ -secretase complex and modulate γ -secretase activity and specificity,^(26, 88–94) however, the functional significance of some of these interactions has been contended.^(95, 96)⁽⁹⁷⁾ Moreover, γ -secretase has been shown to interact with tetraspanin-enriched microdomains, or lipid rafts.⁽⁹⁸⁾ It has been suggested that different γ -secretase complexes can contribute to substrate specificity,^(99, 100) which is exemplified by genetic knockout of Aph-1b in a mouse AD model that improved the disease-relevant phenotypic features without Notch-related side effects.⁽¹⁰⁰⁾

Another unique feature of γ -secretase is that only a small fraction of the four protein complex is catalytically active^(85, 101) and the total amount of PS protein is not always correlated with γ -secretase activity.^(75, 101, 102) Lai et al found that less than 14% of PS1 is engaged in active γ -secretase complexes.⁽⁷⁵⁾ Activity-based probes designed from transition state GSIs have been used broadly to study the active γ -secretase complex because they do not bind to the inactive complex.^(68, 75, 99, 102–104)

Discovery and Development of GSMs

1) First Generation NSAID GSMs

The concept of γ -secretase modulation was discovered when a subset of NSAIDs, such as ibuprofen, indomethacin and sulindac sulfide, were found to selectively lower the formation of A β 42 in favor of A β 38 without inhibiting Notch1 cleavage.⁽¹⁾ Furthermore, the effect of these NSAIDs on A β modulation was dissociated from their COX activity.⁽¹⁾ GSMs have many unique characteristics, which include: 1) reducing A β 42 production; 2) promoting shorter forms of A β species (A β 38 or A β 37); 3) having no significant effect on the total amount of A β produced nor accumulation of β CTF; and 4) lacking inhibitory effect on Notch cleavage and other substrates. Not surprisingly, these ideal properties have inspired the development of GSMs as potential disease modifying agents for AD treatment. Of note, although the role of A β 37 or A β 38 in AD is unknown, it is believed that the short forms are less pathogenic than A β 42.

The NSAID GSMs selectively lower the formation of A β 42 with a concomitant increase in the generation of A β 38, without inhibiting the proteolysis of Notch1. The first generation

GSMs include the NSAIDs: ibuprofen, indomethacin, sulindac sulfide, flurbiprofen and the close analog CHF5074 (Fig. 4). These compounds provided the first evidence that γ -secretase could be specifically modulated to reduce the more pathogenic A β 42 species. However, their weak *in vitro* potencies (A β 42 IC₅₀ > 10 μ M) and poor brain penetration has limited their development. Despite its weak potency (A β 42 IC₅₀ ~ 200–300 μ M),⁽¹⁰⁵⁾ R-flurbiprofen (tarenflurbil) was advanced into clinical studies and a hint of efficacy was seen in a Phase II trial in a subgroup of patients with mild AD.⁽¹⁰⁶⁾ However, the Phase III clinical trial of R-flurbiprofen did not achieve statistically significant improvement compared to placebo.⁽¹⁰⁷⁾ R-flurbiprofen is a weak GSM and whether it crossed the blood brain barrier and significantly lowered A β 42 levels in the clinical studies is unknown. Chiesi has prepared flurbiprofen analogs with improved A β 42 inhibitory potency leading to CHF5074 (A β 42 IC₅₀ = 41 μ M).⁽¹⁰⁸⁾ This compound has been advanced into clinical trials and was found to lower the levels of the soluble CD40 ligand, a marker of microglia activation, but not A β 42 in both plasma and CSF so it is now being referred to as a microglial modulator.⁽¹⁰⁹⁾

2) Second Generation GSMs

A key goal in the development of second generation GSMs has been to improve the potency and brain availability, and advances toward this end have resulted in GSMs with encouraging preclinical profiles in recent years.^(2, 3) Structurally, second generation GSMs can be generally divided into three categories: NSAID-derived carboxylic acid GSMs, non-NSAID-derived heterocyclic GSMs and natural product-derived GSMs.

NSAID-derived carboxylic acid GSMs—Next-generation NSAID-derived GSMs, including GSM-1, GSM-2, GSM-10h, EVP-0015962, JNJ-40418677, and BIIB042, with improved *in vitro* potency and brain penetration have been reported (Fig. 5A). Merck and GSK have substituted the core aryl ring with a piperidine ring and optimized the substituent on the piperidine nitrogen to generate a potent series of piperidine acetic acid GSMs. This series is exemplified by GSM-1 and close analogs GSM-2 and GSM-10h, which have become the prototypical 2nd generation acid GSMs and have been extensively investigated from cellular to animal studies (see Table 1). Overall, this class of GSMs reduces the production of A β 42 and promotes the generation of A β 38 and has little effect on A β 40 production, total A β levels, AICD and Notch1 processing.

The first *in vitro* characterization of GSM-1 appeared in 2008 where it was shown to significantly decrease A β 42 and increase A β 38 in cells expressing either WT PS1 or WT PS2.⁽²⁸⁾ In contrast, cells expressing PS1 L166P or PS2 N141I FAD mutants showed no change in A β 42 with GSM-1 treatment, but a robust increase in A β 38 was still observed.⁽²⁸⁾ This observation translated to an *in vivo* setting since administration of GSM-1 to Tg2576 mice resulted in a dose-dependent reduction in brain A β 42 and an increase in A β 38, whereas administration to APP-Swe/PS2N141I double transgenic mice showed no significant change in brain A β 42 despite robust increases in A β 38. Furthermore, the levels of A β 40 and total A β were unchanged, which is consistent with the profile of the NSAID GSMs discussed above. Therefore, one must be careful when transgenic PS FAD models are chosen for GSM studies because certain mutants could give rise to false-negative results for the effect of GSMs on A β 42. However, a study by Kretner et al that looked at over 20 different PS1 FAD mutations found that the majority of the mutations responded well to GSM-1, with the exception of L166P.⁽¹¹⁰⁾ This finding suggests that GSMs could be considered as a candidate therapy for prevention trials in asymptomatic Alzheimer's disease patients with PS1 FAD mutations.^(111, 112) The A β profile in response to GSM-1 has also been characterized for a number of FAD-associated APP mutations in both cell-free and cell-based assays.⁽¹¹³⁾ GSM-1 lowered A β 42 robustly for each APP mutant, but the reciprocal

increase in A β 38 was attenuated in several cases (i.e. T43F, V44F, and I45F); and for certain mutants A β 39 (i.e., V46I and V46F) and A β 41 (i.e., V44F) were lowered by GSM-1 treatment. Therefore, it appears that the relationship between A β 42 and A β 38 is not always interdependent, and the effect of GSMs on each FAD mutant should be considered independently.

GSM-10h, a pyridyl analog of GSM-1 with lower lipophilicity, has also demonstrated excellent bioavailability and good CNS penetration.⁽¹¹⁴⁾ Additionally, acute and sub-chronic administration of GSM-10h to rats decreased A β 42 in plasma, CSF and brain.⁽¹¹⁵⁾ Furthermore, GSM-10h did not cause A β -rebound in rat plasma nor accumulation of β -CTF.⁽¹¹⁶⁾

Recently, a study was conducted comparing the efficacy of two GSIs (LY450139 and BMS-708,163) and GSM-2, a piperidine acetic acid (Fig. 5A).⁽⁴¹⁾ These compounds were administered to wild-type and 5.5 month-old Tg2576 mice for 8 days and Y-maze tests were conducted to evaluate spatial working memory. Only GSM-2 ameliorated the cognitive deficit in Tg2576 mice. While all three drugs reduced hippocampal A β 42 levels, β -CTF levels increased with the two GSIs, but were unchanged with GSM-2. Subchronic treatment with LY450139 actually impaired normal cognitive function in WT mice, while treatment with GSM-2 had no effect. This data suggests that the cognitive impairment associated with GSI treatment could be due, at least in part, to β -CTF elevation.⁽⁴¹⁾

EnVivo and Janssen have returned to the phenyl acetic acid core of flurbiprofen and added additional substituents on the core aryl ring to generate potent compounds such as EVP-0015962⁽¹¹⁷⁾ and JNJ-40418677.⁽¹¹⁸⁾ Chronic treatment with EVP-0015962 in Tg2576 mice reduced soluble (Tris buffered saline extractable), insoluble (formic acid extractable), and aggregated A β 42; amyloid plaque load in the hippocampus; and cognitive deficits in the contextual fear-conditioning test.⁽¹¹⁷⁾ The major concern with this compound is its high lipophilicity with a clogP of 6.8 (measured logD = 3.88) and it remains to be seen if the promising preclinical profile can be matched by an acceptable safety profile. Acute treatment with JNJ-40418677 reduced brain A β 42 levels in wild-type mice with a concomitant increase in A β 38, while total A β levels in brain were not affected. In contrast, chronic administration in Tg2576 mice from 6 to 13 months of age resulted in dose-dependent reductions of all A β species in soluble and deposited fractions. As with the other 2nd generation acids, the increase in potency of JNJ-40418677 came at the expense of increased lipophilicity. No data was reported on the safety profile other than 7 months of dosing was tolerated with no weight loss.⁽¹¹⁸⁾ Biogen has disclosed a phenyl acetic acid GSM (BIIB042) which appears to be a hybrid of flurbiprofen and GSM-1.⁽¹¹⁹⁾ High drug concentrations in the brain appear to be necessary to achieve robust lowering of A β 42 and this may be due in part to the high protein binding of BIIB042 (>99.9% protein-bound in all species tested).

The carboxylic acid moiety is critical for both first and second generation NSAID and NSAID-derived GSMs. Multiple studies have shown that if a carboxylic acid GSM is converted to the corresponding ester or amide (Fig. 5B), the compound behaves as an inverse GSM (iGSM) and actually increases A β 42 production (Fig. 5C).^(120–123)

non-NSAID-derived heterocyclic GSMs—The first examples of non-NSAID-derived heterocyclic GSMs were reported in the patent literature by Neurogenetics in 2004 and by Eisai in 2005 and are characterized by the presence of an arylimidazole moiety.⁽³⁾ Since then several additional members from this class have been disclosed (Fig. 6).

In contrast to the NSAID-like GSMs, the imidazole GSMs alter the cleavage site preference of γ -secretase such that both A β 42 and A β 40 decrease, while A β 37 and A β 38 increase albeit to different degrees depending on the compound (Table 2).^(127–129) The prototypical imidazole GSM is exemplified by E2012 and has been used as a standard by many labs. E2012 lowers A β 42, A β 40 and A β 39 and raises A β 37 and, to a lesser extent, A β 38 (Table 2)^(128–130). E2012 entered phase I trials in 2006, and it represents the first non-NSAID GSM to enter clinical development. Following the observation of lenticular opacity in a 13-week rat safety study, clinical development of E2012 was temporarily halted. Subsequent safety studies in rats and monkeys, however, did not show ocular toxicity, and the clinical trial was allowed to proceed in April of 2008. Dose-dependent reductions of A β 40/42 were observed in plasma in the Phase I clinical trial⁽¹³¹⁾. Eisai recently reported that E2012 was not developed further in favor of an improved compound, E2212. E2212 was reported to be more potent both *in vitro* and *in vivo* than E2012 and to have a wider safety margin. The first human study began in January 2010 (doses ranging from 10 mg to 250 mg, ClinicalTrials.gov identifier: NCT01221259), however the present status of development is not known.

Neurogenetics has recently disclosed a detailed *in vitro* and *in vivo* characterization of imidazole GSM compound 4,⁽¹²⁷⁾ which was identified as NGP-555⁽¹³²⁾. This compound reduced A β 42 and A β 40 levels while concomitantly elevating levels of A β 38 and A β 37 without inhibiting NICD or AICD formation (Table 2). Administration of NGP-555 to 8-month old Tg2576 mice for 7 months showed significant reduction in plaque density and amyloid deposition. The compound appeared to be well tolerated with no change in body weights and intestinal goblet cell densities. However, in contrast to results from acute dosing and cell-based assays where an increase in A β 38 levels was observed, all brain A β peptides (A β 42, A β 40 and A β 38) were lowered in the soluble-DEA-extractable, denaturing-SDS-extractable and formic acid-extractable brain fractions from Tg2576 mice dosed chronically with NGP-555 from 8- to 15 months of age. The reasons for the A β 38 lowering, most surprisingly in the soluble fraction from DEA brain extracts, are not known. Nonetheless, this is a significant study since it was the first demonstration that a non-NSAID GSM could lower plaque density and amyloid load in a transgenic mouse model of AD.

The identification of the heterocyclic imidazole-containing GSM class by Neurogenetics and Eisai has spurred intense research activity throughout the industry as is evident by the large number of publications and patent applications related to this chemotype that have been published over the past several years (Fig. 6). For example, Merck/Schering Plough has reported analogs of E2012, exemplified by GSM-53, that incorporate a conformational constrained fused oxadiazine as an amide replacement.^(133, 134) Merck, Hoffman LaRoche, AstraZeneca and Janssen have each disclosed variations of the arylimidazole series that incorporate an aminoheterocycle. For example, Merck replaced the methylenepiperidinone of E2012 with an aminopyridone to give GSM-35.⁽¹³⁵⁾ Hoffman LaRoche used a similar strategy, but replaced the pyridone with a pyrimidine to give the aminopyrimidine GSM RO-02.⁽¹³⁶⁾ AstraZeneca has also explored this chemical space and disclosed the A β profiles and binding characteristics of several aminopyrimidine GSMs, exemplified by AZ4800.⁽¹²⁹⁾ AZ4800 reduced A β 42, A β 40, and A β 39 in HEK-APPs cells and cell membranes, whereas A β 38 and A β 37 were increased by 750% and 300%, respectively. Interestingly, the close analog AZ3303 increased A β 37 more than A β 38, and another analog, AZ1136, actually decreased A β 38 and increased A β 39 (Table 2). Taken together with the A β profiles of E2012 and NGP-555, it is apparent that small structural changes can greatly influence the relative amounts of A β 37 and A β 38 that are generated, although the mechanistic basis for this is not clear.

Despite the improvement in potency for the 2nd generation GSMs, many are still very lipophilic which puts them at a higher risk of having off-target toxicity. As a result, it is clear from the recent patent literature that an important goal within industry is to lower the lipophilicity of candidate GSMs to improve the drug-like properties while maintaining the improved potency (improved lipophilic efficiency). For example, Janssen has removed the linker altogether and attached a triazolo-oxazine heterocycle directly to the arylimidazole to give JNJ-16.⁽¹⁴⁰⁾ This compound has a good pharmacokinetic profile in dog and lowered CSF A β 42 by 30–40% (20 mg/kg). The reduced lipophilicity of JNJ-16 (clogP = 3.1) relative to earlier GSMs translated into an improved safety profile compared to JNJ-42601572. Another example can be seen in a patent application from Pfizer where the aryl core has been replaced with a bicyclic pyrido-pyrazinedione core as in PF-118. This compound is reported to lower A β 42 in CHO-APP cells with an IC₅₀ < 10 nM, while possessing improved lipophilicity (clogP = 3.1).⁽¹⁴⁵⁾

Additional GSMs with distinct chemotypes—All of the non-NSAID derived heterocyclic GSMs discussed so far contain an aryl imidazole (or similar heterocycle such as triazole or pyridine), but alternative cores are starting to emerge (Figure 7). For example, Merck has disclosed a series of GSMs where the aryl imidazole has been replaced with a 4-methoxyphenylpiperazine as in Merck-8.^(141, 142) Furthermore, a recent patent from Hoffmann-La Roche highlighted a series of bridged amino-piperidines represented by RO-18⁽¹⁴⁶⁾ in which a large portion of the exemplified compounds contain a thiadiazole left hand ring. Additionally, BMS has disclosed GSMs where the ubiquitous left-hand heterocycle (imidazole, triazole, pyridine) has been replaced with a nitrile.⁽¹⁴⁷⁾ For example, BMS-3 is reported to have an A β 42 IC₅₀ < 10 nM. Despite this structural diversity, the basic pharmacophore is maintained where two H-bond acceptors are separated by a conformationally constrained cyclic core with the presence of a lipophilic aryl group on the right hand side.

A truly structurally distinct chemotype has been introduced by Satori Pharmaceuticals (Figure 7). They have disclosed a new series of GSMs that were isolated from the black cohosh plant with the triterpene glycoside Satori-1 as the initial hit.⁽¹⁴³⁾ Subsequent optimization to improve metabolic stability and CNS disposition led to SPI-1810.⁽¹⁴⁴⁾ These GSMs have a distinct A β profile in that they lower both A β 42 and A β 38, but maintain total A β levels by raising A β 39 and A β 37.

Mechanism of action of GSMs

To determine the mechanism of action of GSMs, the following critical questions have to be addressed: 1) What are the targets of GSMs? 2) Do different classes occupy the same or overlapping binding sites of the target(s)? 3) What is the molecular basis for cleavage shifting and substrate specificity? 4) Do different classes of GSMs have similar mechanisms?

1) Notable chemical biology and biochemical techniques

Due to the lack of high resolution structural information and intrinsic complexity of the γ -secretase complex, investigators have had to use creative methods to study the mechanism of action of the diverse and myriad small molecules that target γ -secretase activity. Photoaffinity labeling (PAL) has widely been used for target identification of small molecules.⁽¹⁴⁸⁾ PAL has been instrumental in not only the identification of presenilin as the catalytic component of γ -secretase,⁽⁶⁸⁾ but also for determining the target of many γ -secretase inhibitors.^(12, 149–151) Common cross-linking moieties include the photoreactive benzophenone, diazirine, and phenylazide motifs.⁽¹⁵²⁾ Many GSM photoprobes contain a biotin tag for affinity purification of the labeled enzyme (Fig. 8A). However, incorporation

of a bulky biotin group could reduce the potency of parental compounds. Therefore, employing PAL with a smaller alkyne tag can be beneficial; moreover, the alkyne is more versatile because either a biotin or fluorescent tag can be “clicked” on using a copper catalyzed azide-alkyne cycloaddition (CuAAC) reaction^(153, 154) (Fig. 8B).

Another challenge is to detect small molecule induced conformational changes in γ -secretase within the lipid bilayer. Currently, three select approaches that have been used for such studies are Fluorescence Lifetime Imaging (FLIM), photophore walking, and the Surface Cysteine Accessibility Method (SCAM). By using FLIM, which measures the decay rate of a fluorophore rather than the intensity, one can measure the distance, or more importantly, changes in the distance between two Fluorescence Resonance Energy Transfer (FRET) pairs. Studies have looked at both the distance between the substrate and enzyme (APP-C-terminus and PS1-loop),⁽¹⁵⁵⁾ and distances from the CTF to NTF domains within PS1 itself.^(155, 156) The conformational changes within presenilin have been studied by 2 methods: one used a pair of FITC and CY3 labeled antibodies which bind two different epitopes on presenilin-1⁽¹⁵⁵⁾, while the other used a G-PS1-R fusion protein that has a GFP tag on the N-terminus and an RFP tag within the C-terminal loop of presenilin.^(123, 156) Through these studies, it appears that γ -secretase adopts an “open” conformation when GSMs bind, resulting in an increased distance between the N and C termini of PS1 as measured by a longer fluorescence lifetime of the donor fluorophore.

The “photophore walking” approach⁽¹⁵⁷⁾ has been developed to detect conformational changes in the γ -secretase active site. Requirements of photophore walking probes include: 1) that they directly interact with the active site, and 2) that photoactivatable groups are incorporated into different side chains along the probe, and therefore crosslink to different subpockets within the active site. Since the efficiency of photolabeling depends on the contact region and proximity to residues within the active site, conformational changes induced by GSMs that alter the orientation or distance between a subpocket and the photophore can lead to different cross-linking efficiencies. By exploiting the complementarity of more than one probe, one can examine changes within the active site of γ -secretase by comparing differences in labeling efficiency of each probe in the presence or absence of a modifier. This approach has been used to characterize different inhibitors and GSMs,^(12, 154, 158, 159) as well as to investigate the conformational changes caused by PS1 FAD mutants.⁽¹⁵⁷⁾ Importantly, the structure activity relationship (SAR) of the active-site directed photoprobes^(68, 160–162) indicates that the subpockets within γ -secretase have enough plasticity for interacting with different sized side chains since substitution of Phe with BPA (benzoylphenyl alanine) at different positions did not alter the potency of these probes.^(68, 160–162) This method allows investigation of endogenous γ -secretase in any cell type or tissue. The Surface Cysteine Accessibility Method (SCAM) is another interesting and unique methodology that has been used to characterize γ -secretase modulators. This method allows for identification of which amino acid residues are membrane embedded and what environmental changes, such as GSM binding, can alter the water accessibility of certain amino acids on presenilin.⁽¹²³⁾

2) Mechanism of action

First generation NSAID GSMs—Initially it was reported that NSAIDs bound to the γ -secretase complex at some undefined allosteric site due to their non-competitive inhibition of γ -secretase⁽¹⁶³⁾ and non-competitive displacement of radiolabeled GSIs.^(164, 165) Furthermore, it was shown that sulindac sulfide could also non-competitively displace [³H]L-685,458 from SPP, an aspartyl intramembrane protease, thus suggesting that NSAID GSMs also had a binding site for SPP.⁽¹⁶⁶⁾ Using FLIM-based FRET imaging, Lleó et al showed that the presence of NSAID GSMs resulted in an increase in the distance between

APP-C-terminus and the loop region of PS-1 as determined by a measured increase in the lifetime of the donor fluorophore, the FITC labeled C-terminus of APP⁽¹⁵⁵⁾. Through similar methods they were also able to show an increase in the distance between PS1-NTF and PS1-CTF fragments upon GSM binding, suggesting a conformational change to PS1 upon NSAID binding⁽¹⁵⁵⁾ (Table 3).

However, in 2008 Kukar et al published a paradigm-shifting paper suggesting that GSMs bound to the substrate APP rather than to the γ -secretase complex.⁽¹²⁰⁾ Using benzophenone and biotin containing molecular probes derived from fenofibrate and flurbiprofen (Flurbi-BpB, Fig. 8), they found probe incorporation in APP-CTF83 (α CTF), but not APP-CTF99 (β CTF), from CHAPSO solubilized H4-APP-alkaline phosphatase cells. Moreover, they were unable to find any labeling of γ -secretase complex subunits purified from CHO cells.⁽¹²⁰⁾ Both probes showed a dose-dependent (10–150 μ M) increase in binding to a recombinant APP-C100-Flag substrate, which is essentially the β CTF substrate of γ -secretase required for A β production. Furthermore, they show that labeling of C100-Flag by the fenofibrate probe can be partially competed with 100 μ M of multiple NSAID GSMs, and fenofibrate prefers binding to APP(C100)-Flag compared to Notch(C100)-Flag substrate. Using a series of truncated A β peptides, they mapped the binding site of the GSMs to A β 28–36 (see Fig. 1), which includes the beginning of the transmembrane domain of APP.⁽¹²⁰⁾ This finding not only offers a straightforward explanation of substrate selectivity, but also provides an interesting mechanism for modulation of γ -secretase through targeting substrate, rather than the enzyme. Similarly, Espeseth et al had previously reported on a series of APP binding compounds that also inhibited A β 42 production.⁽¹⁷²⁾

Munter et al demonstrated that the GxxxG motif that corresponds to residues 29–33 within A β , was not only important for dimerization of the APP transmembrane domain, but that an increase in dimerization strength within the TM region is correlated with an increase in A β 42 production relative to other A β species.⁽¹⁷³⁾ Conversely, if the GxxxG motif is mutated and/or disrupted so that dimerization is lost, then γ -secretase cleavage is altered so that there is an increase in A β 38 production but a decrease in A β 42.⁽¹⁷³⁾ This led to the hypothesis that GSMs may bind to the GxxxG motif in β CTF and alter the transmembrane dimerization of APP, resulting in modulation of cleavage from A β 42 to A β 38 production. Support for this hypothesis emerged from Richter et al's work which suggests that sulindac sulfide, and to a lesser degree indomethacin, could inhibit dimerization of the APP TM domain in a β -galactose based dimerization assay using a ToxR fusion protein with residues 29–42 of the APP membrane.⁽¹⁶⁹⁾ They also showed that sulindac sulfide could directly bind to immobilized A β 42 as measured by Surface Plasmon Resonance (SPR) and that incubation of 100 μ M A β 42 with 300 μ M sulindac sulfide yielded NMR chemical shifts at several residues including a few within the purported binding domain of GSMs.⁽¹⁶⁹⁾ Further studies using SPR showed that sulindac sulfide prefers binding a C100 mutant that has an increased propensity for dimerization compared to wild type C100.⁽¹⁶⁸⁾ Similarly, sulindac sulfide prefers binding wild type with respect to a G33I mutant that disrupts the GxxxG motif and does not readily form dimers.⁽¹⁶⁸⁾ However, this work has not been repeated with more potent 2nd generation GSMs so the functional significance awaits further studies.

Beel et al studied the biochemical nature of the interaction between β CTF and GSMs by using recombinant purified [U-15N]C99 in LMPG micelles monitored by ¹H-¹⁵N TROSY protein NMR; but they found no specific binding between C99 and R-flurbiprofen, fenofibrate, indomethacin or sulindac sulfide.⁽¹⁷⁰⁾ Instead, they only found a few chemical shifts that were non-specific in nature and did not correspond to the purported A β 28–33 binding region of GSMs.⁽¹⁷⁰⁾ Interestingly, they found that GSMs did in fact bind to aggregated C99, and that the aggregated protein seems to promote the formation of GSM aggregates.⁽¹⁷⁰⁾ Similarly, in response to findings that GSMs bind directly to A β ,^(168, 169)

Barrett et al performed additional SPR and protein NMR experiments with the A β 42 peptide.⁽¹⁷¹⁾ They again found that GSMs only non-specifically bind to A β and this binding can be eliminated with micelle formation.⁽¹⁷¹⁾ Importantly, they also show using dynamic light scattering (DLS) that sulindac sulfide forms aggregates at concentrations above 50 μ M.⁽¹⁷¹⁾ Furthermore, Page et al examined the effect of GSMs on multiple APP FAD mutations together with systemic phenylalanine scanning mutagenesis near the γ -secretase cleavage site (including the GxxxG domain) and found that the overwhelming majority of mutants responded well to the second generation NSAID-derived GSM-1, and that the iGSM fenofibrate was also responsive to G33I and K28E mutations, thus further creating uncertainty about the binding of GSMs to the GxxxG domain.⁽¹¹³⁾ Recently, NMR structural studies revealed that β CTF exists as a monomer and the GxxxG motif plays an important role in cholesterol binding.⁽¹⁷⁴⁾

If the first hypothesis is that GSMs bind γ -secretase, and the second is that GSMs bind directly to the APP substrate, then the third is that the compounds bind both. The latter theory is supported by several FRET based FLIM assays with fluorescently tagged PS1 in APP/APLP2 knock out cells.⁽¹⁶⁷⁾ Uemura et al., show that the conformational changes induced by NSAID GSMs in PS1 first require substrate docking by either C99, Notch Δ EC or a helical peptide.⁽¹⁶⁷⁾ It is interesting to note however that neither Notch Δ EC nor the helical peptide contain the GxxxG motif, suggesting that substrate dimerization is not necessary for NSAID induced PS1 conformation changes.

If NSAIDs do indeed bind solely to APP, and this is how selectivity is achieved, then one would expect NSAIDs to be selective for APP and not bind other γ -secretase substrates. There is controversy over whether NSAID GSMs affect any substrates other than APP. Several groups have claimed that NSAIDs have an effect on Notch, by either reducing N β ⁽¹⁷⁵⁾ or by binding to N100-Flag⁽¹²⁰⁾—but in both of these studies higher concentrations of NSAIDs were required for Notch than for APP. However, other groups have found that NSAIDs have no effect on N β ^(176, 177) nor CD44- β or an APP-Notch TMD chimera.⁽¹⁷⁷⁾ Furthermore, NSAIDs have been shown to non-competitively compete for binding of SPP⁽¹⁶⁶⁾ and to also alter the cleavage site of the SPP substrate Prl.⁽¹⁷⁸⁾ These data suggest that NSAID GSM binding is unlikely to be entirely on the substrate, but could be on the interface between substrate and enzyme.

There is likely a complicated binding mechanism for GSMs, perhaps on the interface between the enzyme and the substrate or perhaps multiple binding sites are present, and unfortunately the high concentrations required due to low efficacy of first generation compounds complicates the interpretation of findings.

Second Generation GSMs—Despite the large structural variation among second generation GSMs, all work done to date on the more potent (IC₅₀ < 300 nM) GSMs shows invariably that γ -secretase is indeed the target of these molecules. By immobilizing an imidazole based 2nd generation GSM, Kounnas et al first showed that this GSM could pull down components of the γ -secretase complex such as Pen-2, PS1-NTF and PS1-CTF, but not APP.⁽¹²⁷⁾ Soon to follow, several independent labs simultaneously designed photo-crosslinking probes based on multiple 2nd generation GSMs and indisputably show specific labeling of PS1-NTF but not APP^(123, 136, 154, 179, 180) (Table 4).

The NSAID-derived piperidine acetic acid GSM-1 directly binds to PS1-NTF using photoaffinity probes GSM-1-BpB, GSM-1-BPyne and GSM-5 (see Fig. 8).^(123, 154) Furthermore, GSM-1-BpB was suggested to bind to residues 78–100 of TMD1 of PS1-NTF.⁽¹²³⁾ It appears that upon binding to this region of PS1, GSM-1 is able to induce an overall conformational change in γ -secretase as visualized by a FLIM study⁽¹²³⁾ as well as a

conformational change within the active site of γ -secretase.⁽¹⁵⁴⁾ Interestingly, GSM-1-BpB was found to also bind full-length PS1,⁽¹²³⁾ the zymogen of γ -secretase.^(68, 70) Importantly, GSM-1-BPyne and GSM-5 bind to a reconstituted PS1 mutant, PS1 Δ E9, in liposomes without any substrates present.⁽¹⁵⁴⁾ Together, these data paint a very different picture than what has previously been hypothesized for NSAID GSMs: GSM-1 can bind PS1 independent of any substrates and can presumably bind an inactive enzyme. Interestingly, the GSM-1 probes were also able to specifically label SPP,^(123, 154) a structurally related intramembrane aspartyl protease, which was also reported for the NSAID sulindac sulfide.⁽¹⁶⁶⁾

The Roche imidazole based GSMs were also found to directly label PS1-NTF and PS2-NTF.⁽¹³⁶⁾ Competition studies with labeling of RO-57-BpB probe showed good competition with E2012, but not NGP-555 like GSMs—all of which belong to the imidazole class of 2nd generation GSMs. Moreover, sulindac sulfide (100 μ M) could compete for RO-57-BpB binding but neither GSM-1 nor fenofibrate had any effect on RO-57-BpB labeling of PS1, although GSM-1 was found to partially block RO-57-BpB labeling of PS2, suggesting there could be partial overlap in binding sites.⁽¹³⁶⁾ This also raises a critical issue for cross-talk studies regarding concentrations and solubility of competing compounds. It can be addressed by conducting the competition in a dose responsive fashion in which compounds maintain solubility under assay conditions, further elucidating the nature of the competition.

Recently, using a series of reciprocal labeling experiments with GSM-1- and E2012-based photoaffinity probes, our groups have shown that the two compounds have distinct binding sites on PS1-NTF.⁽¹⁸⁰⁾ Moreover, unlike GSM-1-BPyne, E2012-BPyne labeling to PS1-NTF is significantly potentiated in the presence of L458, showing direct cross-talk between the E2012 binding site and the active site of the enzyme.⁽¹⁸⁰⁾ Surprisingly, binding of L458 has no effect on the RO-57-BPyne labeling,⁽¹⁸⁰⁾ suggesting that E2012 and RO-57 could have distinct effects even though both are from the same imidazole class of GSMs. In contrast to GSM-1-BpB, E2012-BPyne specifically labels PS1-NTF (active γ -secretase) but not full-length PS1 (inactive γ -secretase). Furthermore, the GSI BMS-708,163 binds to PS1-NTF, and the binding site does not overlap with the sites that interact with GSM-1 or E2012 (Fig. 9).^(159, 180)

Taken together, although both piperidine acetic acid GSMs and E2012-like GSMs target PS1, it appears they occupy different sites within the γ -secretase complex (Fig. 9). Consequently, they lead to varying pharmacological effects on A β species (Tables 1 and 2), such that acid GSMs reduce A β 42 production and enhance A β 38, whereas imidazole GSMs differentially decrease A β 42 and A β 40, and concurrently increase A β 38 and/or A β 37 levels. It is noteworthy to point out there is great diversity within the imidazole GSMs, which are exemplified by NGP-555, E2012 and RO-57 (Fig. 6),^(136, 180). Therefore, the interplay between different subtypes of imidazole GSMs and other classes of GSMs should be carefully examined.

The next key question is how the binding of second generation GSMs to γ -secretase induces a conformational change that has been detected by FLIM⁽¹⁵⁶⁾, SCAM⁽¹²³⁾ or photophore walking⁽¹⁵⁴⁾ (Fig. 10A). We propose two alternative models of how GSM-induced conformation, such as the S1 subpocket alteration⁽¹⁵⁴⁾, leads to γ -secretase modulation (Fig. 10). (1) Acid GSMs mainly affect the sequential processing cycle of A β 42 to A β 38⁽¹⁸¹⁾, which has been suggested to be due to slower dissociation of the A β 42 substrate from the γ -secretase complex allowing further processing to A β 38 (Fig. 10B).⁽²³⁾ The overall result is A β 42 reduction and A β 38 elevation. However, E2012 and many imidazole GSMs are known to preferentially increase A β 37 (Table 2), which presumably represents a fifth γ -secretase cleavage from the A β 49 product line. Therefore, imidazole GSMs could bind to γ -secretase

in a way that alters the sequential cycles of A β 42 to A β 38 and A β 40 to A β 37 to achieve γ -secretase modulation. (2) Alternatively, the GSM-induced conformational change could specifically block A β 42 or A β 40 production and potentiate the A β 38 or A β 37 generation based on the independent cleavage model in which all sites of cleavage are parallel (Fig. 10C). However, the newly discovered natural product GSMs (Fig. 7) inhibit both A β 38 and A β 42 while increasing A β 37 and A β 39, suggesting a different mechanism than imidazole and acid GSMs. These Satori compounds could be operating by a mechanism similar to model (1) where both the A β 40 and A β 42 peptide substrates have a slower dissociation rate, resulting in further processing to A β 37 and A β 39 peptides, or alternatively by model (2) in which A β 38 and A β 42 cleavage is specifically and independently blocked while A β 37 and A β 39 cleavage is enhanced. However, more information is clearly needed to determine how these natural product compounds compare with imidazole and acid GSMs.

Summary and future perspective

APP is processed into three major species, sAPP, A β and AICD. GSMs cause a shift from A β 42 to shorter less toxic A β species and have little effect on the generation of AICD and NICD, thus allowing their signaling roles to remain intact. As a result, GSI-mediated adverse effects should not be a concern, offering the hope that GSMs will become promising disease modifying agents. Indeed, comparative studies of GSIs and GSMs in mice have supported such a notion.⁽⁴¹⁾ Moreover, γ -secretase contains distinct sites that interact with different GSMs, which highlights that γ -secretase can be modulated in multiple ways.⁽¹⁸⁰⁾ Although modulation of γ -secretase holds much promise, significant questions remain to be answered. First, although it is clear that GSMs differentiate from GSIs, it is not known if other safety issues will emerge with chronic treatment of GSMs. Second, while much progress has been made in understanding the target of GSMs, more work is needed to determine their precise binding sites and the molecular basis for their mechanism of action. The mechanism that regulates when γ -secretase cleavage of APP ends and A β is released is not well understood and it will be important to understand the influence GSMs have on that process. In addition, since different GSMs have distinct A β profiles, it may be difficult to determine the mechanism without considering the full A β profile including shorter A β peptides such as A β 37. It will be important to find efficient ways to quantitatively measure all A β species. Furthermore, it has been shown recently that mutation of Lysine 624 of APP (K28A of A β) shifts the final γ -secretase cleavage site to favor shorter A β species such as A β 1–33 and 1–34, suggesting a pivotal role for this charged residue in preventing the continuation of APP cleavage by γ -secretase.⁽¹⁸²⁾ Further studies that help elucidate the precise mechanism of action of GSMs are highly anticipated. Third, it would be interesting to consider if different classes of GSMs could be used as a combination therapy or in combination with a BACE inhibitor. Finally, it is unknown whether successful GSM clinical trials could be conducted without the availability of effective biomarkers for early diagnosis of AD. It has been suggested that the pathological process of AD starts more than 10 years before clinical symptoms manifest.⁽¹⁸³⁾ Since some 2nd generation GSMs have been found to be responsive to several PS1 and APP mutations,⁽¹¹⁰⁾⁽¹¹³⁾ perhaps a prevention trial in asymptomatic patients with FAD mutations could be considered similar to the DIAN trial that is being planned.^(111, 112) Clearly, development of GSMs for the treatment AD not only relies on discovery of effective drug candidates, but also is dependent on the progress of AD research in molecular pathogenesis, biomarkers, diagnosis and other therapeutic developments. Undoubtedly, with the recognition that AD is the fastest growing threat to human health, an interdisciplinary approach and significant effort are required to drive these critical issues toward resolution for the development of effective AD therapies.

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LIST OF ABBREVIATIONS

αCTF	α -secretase cleaved C terminal fragment of APP
βCTF	β -secretase cleaved C terminal fragment of APP
AD	Alzheimer's disease
ADAM	A disintegrin and metalloproteinase domain-containing protein
AICD	APP intracellular domain
APH-1	Anterior pharynx defective-1
APLP2	Amyloid beta precursor-like protein 2
APP	Amyloid precursor protein
Aβ	β -Amyloid peptide
CHAPSO	3-[(3-Cholamidopropyl)dimethylammonio]-2-hydroxy-1-propanesulfonate
COX	cyclooxygenase
CSF	Cerebral spinal fluid
CSL	CBF1/Su(H)/Lag-1, also known as RBP-J κ family
CuAAC	Copper(I)-catalyzed Azide-Alkyne Cycloaddition
FAD	Familial Alzheimer's disease
FITC	Fluorescein isothiocyanate
FLIM	Fluorescence-lifetime imaging microscopy
FRET	Förster (Fluorescence) resonance energy transfer
GSAP	γ -secretase activating protein
GSI	γ -secretase inhibitor
GSK	GlaxoSmithKline
GSM	γ -secretase modulator
HES1	Hairy and enhancer of split-1
HEY	Hairy/enhancer-of-split related with YRPW motif protein
iGSM	inverse γ -secretase modulator
LMPG	lyso-myristoylphosphatidylglycerol
MamL	Mastermind-like
NCT	Nicastrin
NICD	Notch intracellular domain

NMR	Nuclear magnetic resonance
NotchΔEC	Notch with extracellular domain removed
NSAIDs	Non-steroidal anti-inflammatory drugs
PAL	Photoaffinity labeling
PEN2	Presenilin enhancer 2
PS	Presenilin
PS1-CTF	Presenilin1 C-terminal fragment
PS1-NTF	Presenilin1 N-terminal fragment
PS1ΔE9	Presenilin1 Exon9 removed
sAPPα	Soluble APP, α -secretase cleaved
sAPPβ	Soluble APP, β -secretase cleaved
SPP	Signal peptide peptidase
TM	Transmembrane
TMD	Transmembrane domain
TROSY	Transverse relaxation optimized spectroscopy
TSA	Transition state analog

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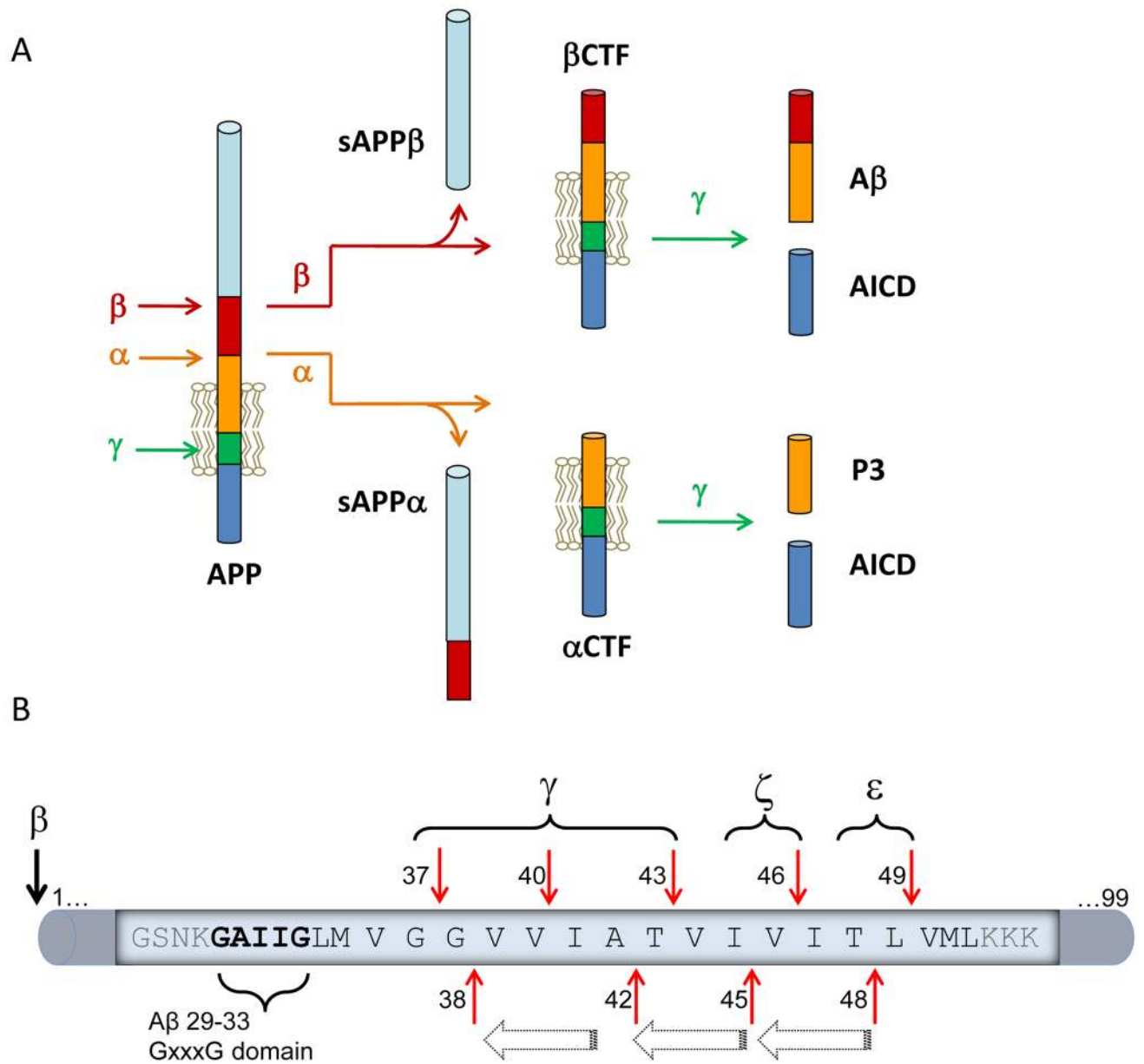


Figure 1.
 (A) Illustration of APP processing by α -, β -, and γ -secretases and the corresponding products. (B) Sequence of the membrane and nearby regions of the β -CTF substrate and relevant cleavages. Thick horizontal arrows represent the hypothesized processive cleavage by γ -secretase. Vertical red arrows show locations of γ , ζ , and ϵ cleavages.

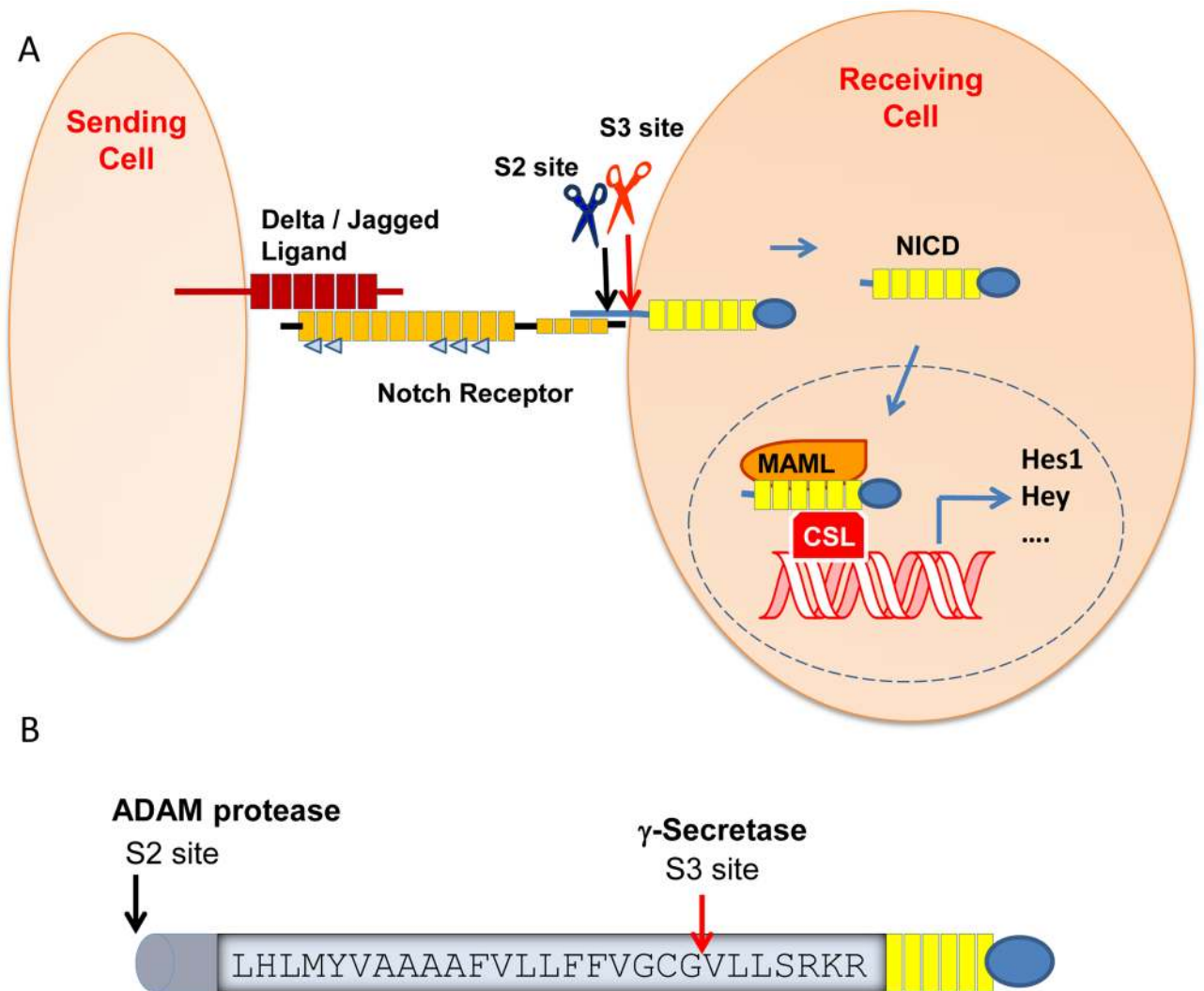


Figure 2. Illustration of the notch signaling cascade (A) depicting activation by a sending cell, which induces S2 cleavage by an ADAM protease, followed by S3 cleavage by γ -secretase within the membrane domain. Subsequently, notch intracellular domain (NICD) is released from the membrane and translocates to the nucleus where it can turn on target genes. (B) Sequence of the membrane domain and S3 site cleavage of the Notch-1 receptor.

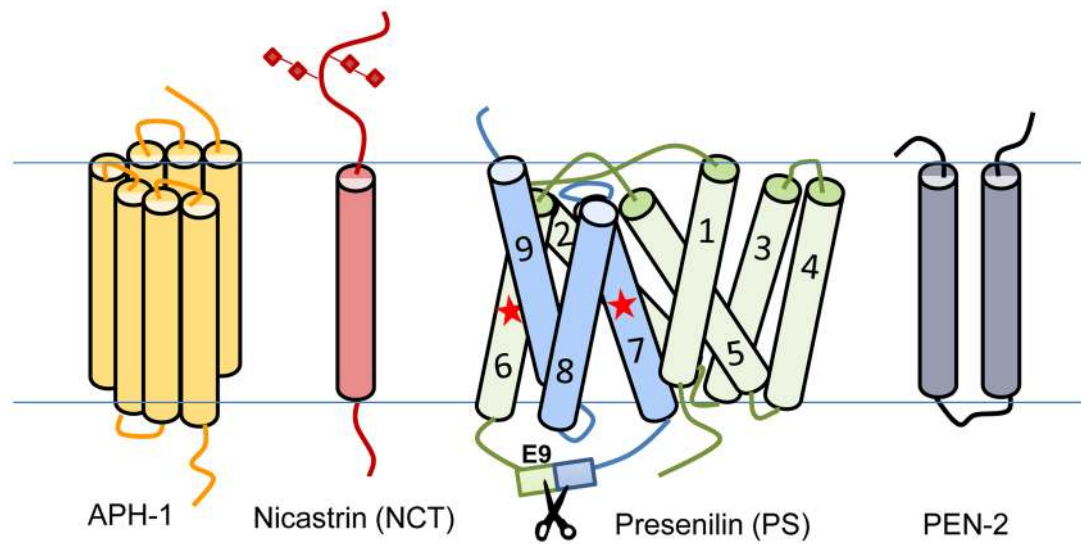


Figure 3. The four essential components of γ -secretase. Presenilin, the catalytic center, is depicted in zymogen form before endoproteolysis of Exon 9 and according to the predicted structure by Li et al ⁽⁷³⁾. Stars represent the relative location of the two aspartic acid residues required for catalysis.

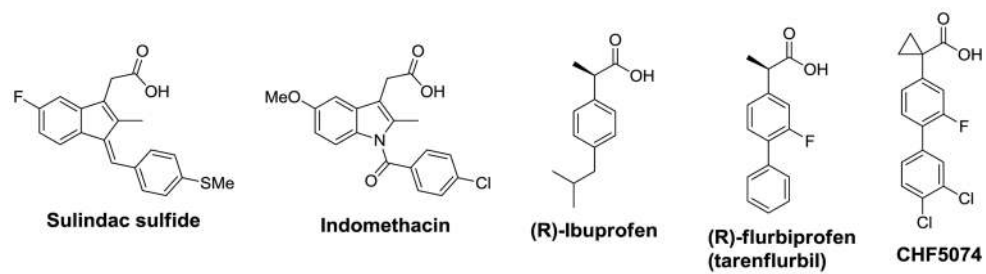


Figure 4.
Structures of NSAID-based GSMs.

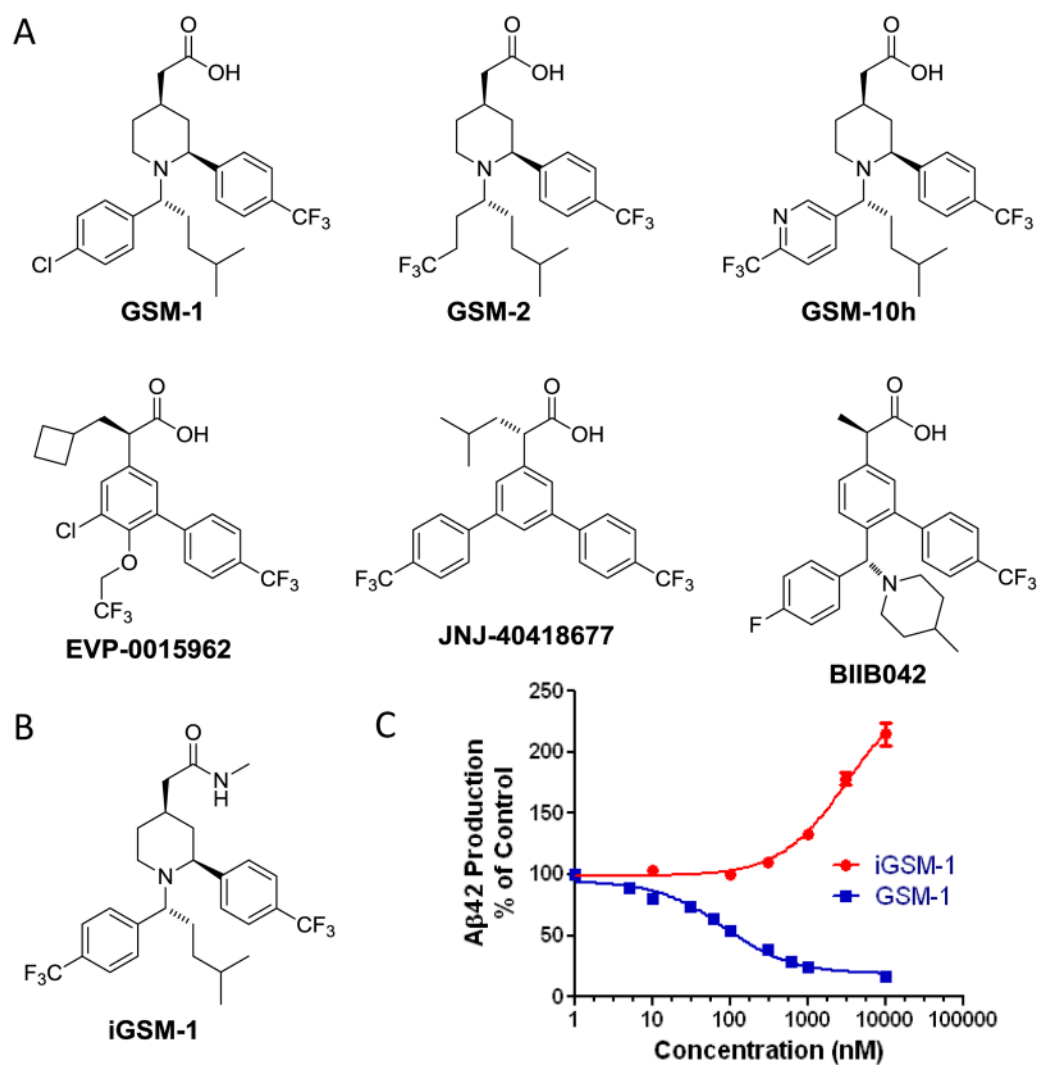


Figure 5.
Structures of 2nd generation NSAID-derived GSMs with acetic acid chemotype.

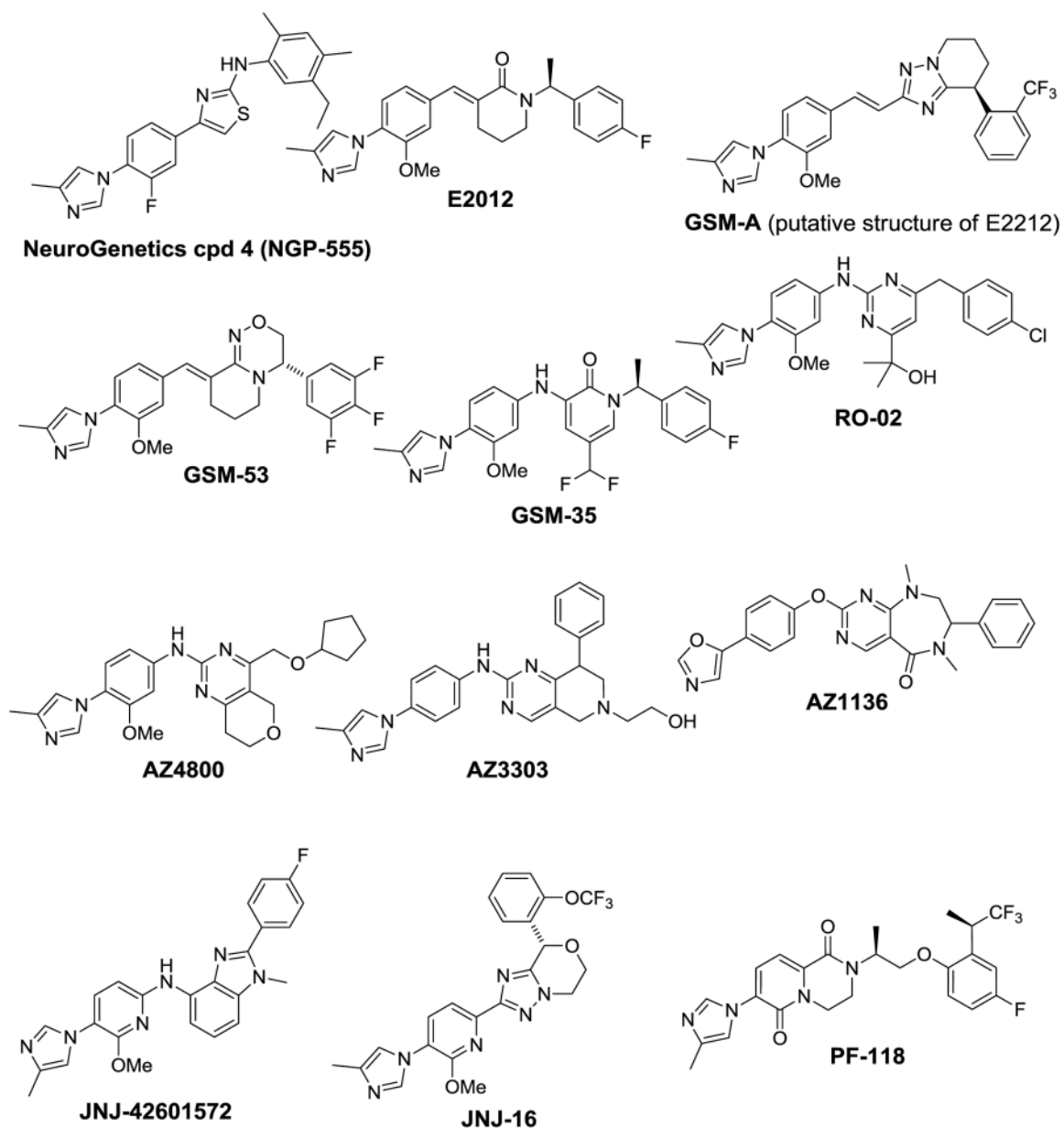


Figure 6. Structures of non-NSAID-derived heterocyclic GSMs containing the aryl imidazole chemotype.

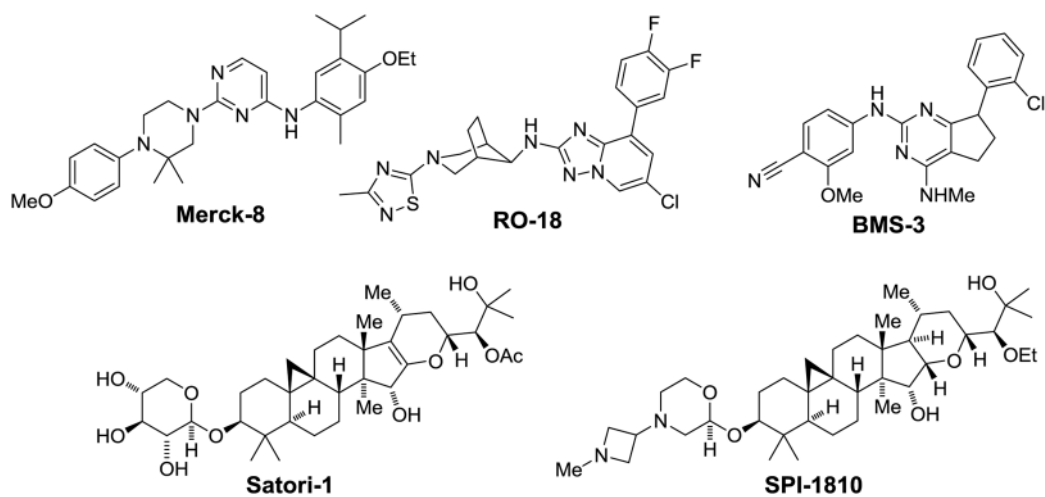


Figure 7.
Additional GRMs with distinct chemotypes.

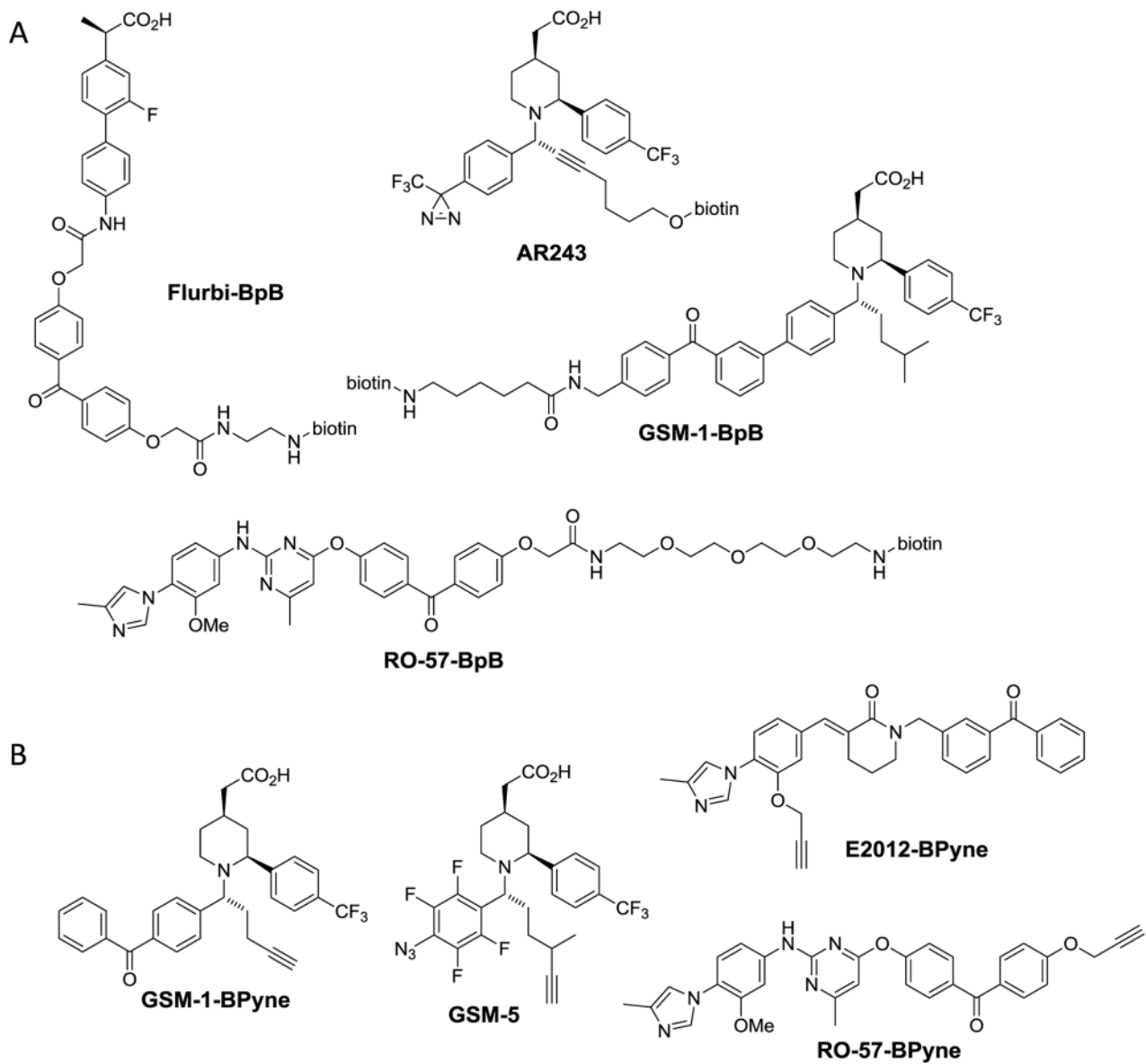


Figure 8.
Structures of GSM derived photoaffinity probes containing (A) biotin or (B) clickable alkyne handle.

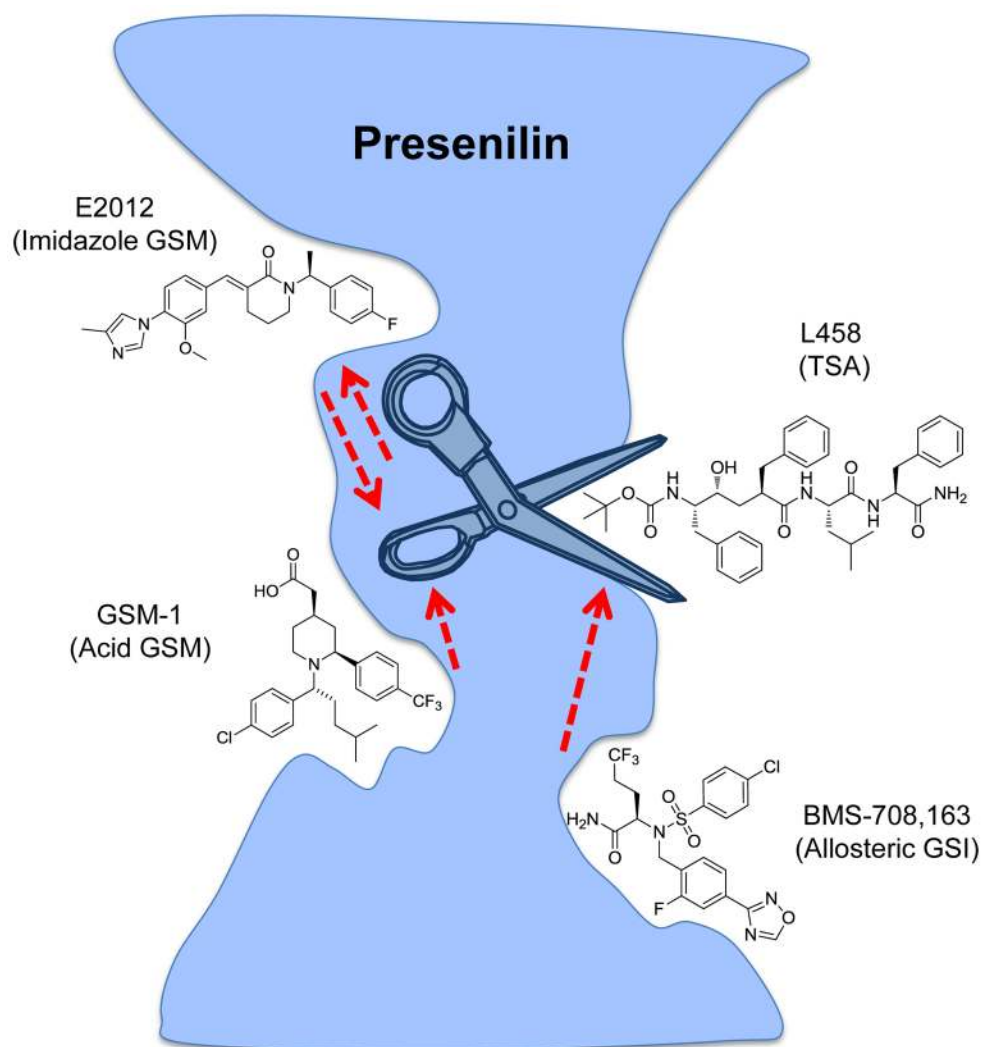


Figure 9. Model for different binding sites of GSMs and GSIs. The active site of γ -secretase is represented by a pair of scissors. GSMs alter the “handle” of the scissors, thereby manipulating the way the enzyme cuts and/or the location of the cleavage sites. In contrast, an allosteric GSI will shut the blades, whereas a transition state analog (TSA) will block the blades of the scissors, preventing substrate binding and cleavage of the substrate.

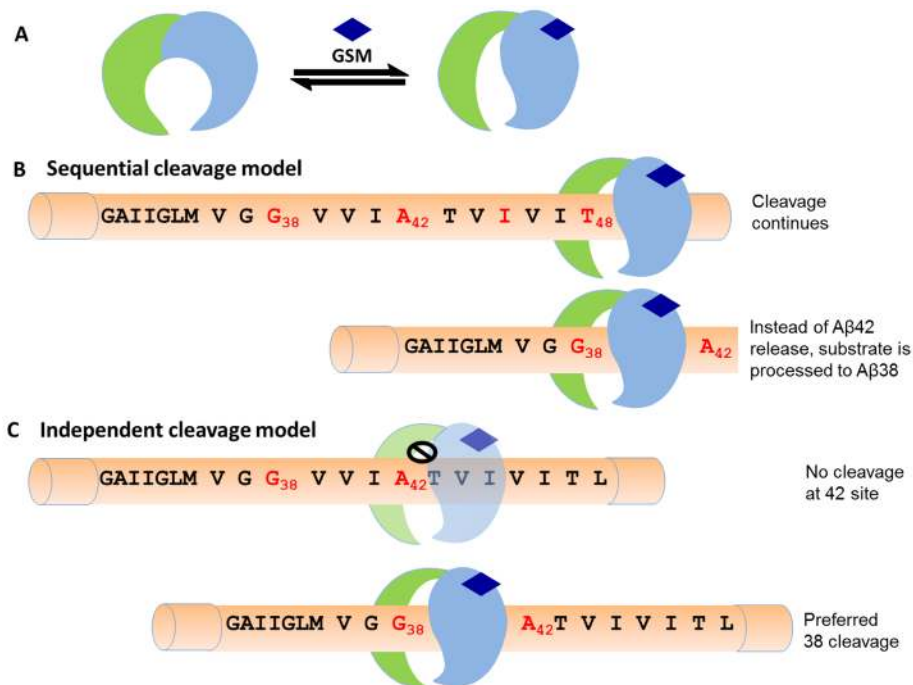


Figure 10.

Proposed models for the mechanism of GSMs. A) GSM binding leads to a conformational change in the active site, such as the S1 subpocket. B) Sequential cleavage model: GSM binding has little effect on processivity of γ -secretase at 48 and 45 sites; however, a tighter association of γ -secretase with A β ₄₂ results in reduced release of A β ₄₂ and an increase in the generation of A β ₃₈.

C) Independent cleavage model: all cleavage sites are parallel; GSM binding inhibits A β ₄₂ cleavage site, but enhances A β ₃₈ cleavage and has little effect on other cleavages including AICD production.

Table 1

Effect of 2nd generation acid GSMs on the production of A β peptides

Acid GSM	Cell-based A β 42 IC ₅₀	In vivo studies	A β profile		
			38	40	42
GSM-1	348 nM ⁽¹²³⁾	guinea pig ⁽¹²⁴⁾	↑	-	↓
GSM-10h	300 nM ⁽¹¹⁴⁾	rat ⁽¹¹⁵⁾ , mouse ⁽¹²⁵⁾			↓
GSM-2	65 nM ⁽⁴¹⁾	mouse ⁽⁴¹⁾ , (126)			↓
EXP-0015962	67 nM ⁽¹¹⁷⁾	mouse ⁽¹¹⁷⁾	↑	-	↓
JNJ-40418677	200 nM ⁽¹¹⁸⁾	mouse ⁽¹¹⁸⁾	↑	-	↓
BIIB042	170 nM ⁽¹¹⁹⁾	mouse, rat, monkey ⁽¹¹⁹⁾			↓

Table 2

Effect of 2nd generation non-acid GSMs on the production of A β peptides

Non-Acid GSM	Cell-based A β 42 IC ₅₀	In vivo data	A β profile				
			37	38	39	40	42
E2012	92 nM ⁽¹³⁰⁾ , 143 nM ⁽¹³⁷⁾	rat ⁽¹³⁰⁾ , dog ⁽¹²⁸⁾ , guinea pig ⁽¹³⁷⁾	↑	↑	↓	↓	↓
GSM-A	8–33 nM ⁽¹²⁴⁾	guinea pig ⁽¹²⁴⁾		↑		↓	↓
NGP-555	10–29 nM ⁽¹²⁷⁾	mouse ⁽¹²⁷⁾	↑	↑		↓	↓
GSM-53	33 nM ⁽¹³³⁾	rat, dog, monkey ⁽¹³⁴⁾	↑	↑	↓	↓	↓
GSM-35	44 nM ⁽¹³⁵⁾	rat ⁽¹³⁵⁾					
RO-02	~14 nM ⁽¹³⁶⁾		↑	↑		↓	↓
AZ4800	26 nM ⁽¹²⁹⁾	mouse ⁽¹²⁹⁾	↑	↑	↓	↓	↓
AZ3303	74 nM ⁽¹²⁹⁾	mouse ⁽¹²⁹⁾	↑	↑	↓	↓	↓
AZ1136	990 nM ⁽¹²⁹⁾		↑	↓	↑	↓	↓
INJ-42601572	16 nM ⁽¹³⁸⁾	rat & mouse ⁽¹³⁸⁾ , dog ⁽¹³⁹⁾	↑	↑		↓	↓
INJ-16	56 nM ⁽¹⁴⁰⁾	dog ⁽¹⁴⁰⁾					↓
PF-118	<10 nM						
Merck-8	36–77 nM ^(141, 142)						
RO-18	158 nM						
BMS-3	< 10 nM						
Satori-1	100 nM ⁽¹⁴³⁾		↑	↓	↑	-	↓
SPL-1810	100 nM ⁽¹⁴⁴⁾	mouse ⁽¹⁴⁴⁾	↑	↓	↑	-	↓

Table 3

Summary of Evidence for Target of NSAID GSMs

GSM used in study	Method	Target	Ref.
Fenofibrate R-flurbiprofen	Biotinylated probes label recombinant C100 and APP-CTF83 from cells	APP	(120)
Ibuprofen Flurbiprofen Indomethacin Fenofibrate	Conformational changes induced by GSMs and/or C99, Notch Δ EC, or helical peptide substrates were monitored using a FRET based FLIM assay.	APP/PS-1 border, PS-1 with docking	(155) (167)
Sulindac Sulfide	Circular dichroism and electron spin resonance with SDS solubilized C100 and C100 mutant substrates	C100 and C100 dimer	(168)
Sulindac Sulfide Indomethacin	Surface Plasmon Resonance (SPR) and solution state NMR	A β 42	(169)
Sulindac sulfide Sulindac sulfone R-flurbiprofen	Noncompetitive displacement of [3 H] GSIs	γ -secretase	(164) (165)
Sulindac Sulfide	<i>In vitro</i> assay shows non-competitive inhibition of γ -secretase	γ -secretase Not APP	(163)
Sulindac sulfide	Noncompetitive displacement of [3 H]L-685,458	SPP	(166)
R-flurbiprofen Indomethacin Fenofibrate Sulindac sulfide	Monitored binding with TROSY-NMR of GSMs with [U- 15 N]C99; or titration of C99 while measuring 19 F GSMs	Not APP	(170)
Sulindac Sulfide Flurbiprofen Sulindac Sulfone	Measure binding with 15 N HSQC and Surface Plasmon Resonance (SPR).	Not A β	(171)

Table 4Summary of Evidence for Target of 2nd Generation GSMs

GSM used in study	Method	Target	Ref
GSM-1 (acid GSM)	Biotinylated or clickable photoprobes label PS1-NTF in cell membranes or with recombinant PS proteins.	PS1-NTF PS1-FL PS1-ΔE9 without APP	(123) (154)
BB25 AR80 (acid GSM)	Biotinylated photoprobes label PS1-NTF in cell membranes and live cells	PS1-NTF	(179)
GSM-97555 (imidazole GSM)	Pull-down with GSM immobilized Affigel matrix	Pen-2 ≫ PS1-NTF > PS1-CTF	(127)
RO-57 (imidazole GSM)	Biotinylated photoprobes label PS-NTF in cell membranes	PS1-NTF PS2-NTF	(136)
E2012 (imidazole GSM)	Clickable photoprobes label PS1-NTF in cell membranes, recombinant PS proteins, and live cells and neurons	PS1-NTF PS1-ΔE9 without APP	(180)