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Isoprenoids and Protein Prenylation: Implications in the Pathogenesis and Therapeutic Intervention of Alzheimer's Disease

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Abstract

The mevalonate-isoprenoid-cholesterol biosynthesis pathway plays a key role in human health and disease. The importance of this pathway is underscored by the discovery that two major isoprenoids, farnesyl and geranylgeranyl pyrophosphate, are required to modify an array of proteins through a process known as protein prenylation, catalyzed by prenyltransferases. The lipophilic prenyl group facilitates the anchoring of proteins in cell membranes, mediating protein-protein interactions and signal transduction. Numerous essential intracellular proteins undergo prenylation, including most members of the small GTPase superfamily as well as heterotrimeric G proteins and nuclear lamins, and are involved in regulating a plethora of cellular processes and functions. Dysregulation of isoprenoids and protein prenylation is implicated in various disorders, including cardiovascular and cerebrovascular diseases, cancers, bone diseases, infectious diseases, progeria, and neurodegenerative diseases including Alzheimer's disease. Therefore, isoprenoids and/or prenyltransferases have emerged as attractive targets for developing therapeutic agents. Here, we provide a general overview of isoprenoid synthesis, the process of protein prenylation and the complexity of prenylated proteins, and pharmacological agents that regulate isoprenoids and protein prenylation. Recent findings that connect isoprenoids/protein prenylation with Alzheimer's disease are summarized and potential applications of new prenylomic technologies for uncovering the role of prenylated proteins in the pathogenesis of Alzheimer's disease are discussed.

Keywords

Isoprenoids; protein prenylation; small GTPases; statins; bisphosphonates; prenyltransferase inhibitors; prenylomics; Alzheimer's disease

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Disclosure of interest

The authors report no declarations of interest.

Introduction

In 1964, Konrad Bloch, together with Feodor Lynen, was awarded the Nobel Prize in Physiology or Medicine for discovering the pathway for the biological synthesis of cholesterol. In his Nobel Lecture, Bloch made it clear that the identification of mevalonic acid/mevalonate, produced from 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA), as the precursor of isoprenoids to squalene was one of the major breakthroughs in the elucidation of the cholesterol biosynthesis pathway (Bloch, 1965). Since then, remarkable advances have been achieved in understanding the regulation of isoprenoid and cholesterol metabolism, from basic biology to clinical applications (Goldstein and Brown, 2015). Brown and Goldstein were awarded the Nobel Prize in Physiology or Medicine in 1985 for discovering the LDL receptor and the genetic regulation of cholesterol metabolism (Brown and Goldstein, 1986). These discoveries, together with the discovery of natural fungal products that inhibit the activity of HMG-CoA reductase (Endo, Kuroda, and Tanzawa, 1976), the rate-limiting enzyme in the mevalonate-isoprenoid-cholesterol biosynthesis pathway, eventually led to the development of statins, one of the most widely prescribed medications for the management of plasma cholesterol levels and cardiovascular risks (Goldstein and Brown, 2015). In addition, the discovery of HMG-CoA reductase inhibitors, also facilitated the identification of an important post-translational modification process called protein prenylation, in which mevalonate-derived, short-chain isoprenoids are attached to specific proteins (Schmidt, Schneider, and Glomset, 1984), including oncogenic proteins. This early finding triggered the pursuit of identifying the prenyltransferases and developing prenyltransferase inhibitors as potential therapeutic agents for cancers (Berndt, Hamilton, and Sebti, 2011; Brown and Goldstein, 2012; Winter-Vann and Casey, 2005). In recent years, the interest in isoprenoids and protein prenylation has continued to grow. In addition to cardiovascular disease and cancer, prenylated proteins have been implicated in the development of cerebrovascular diseases (McTaggart, 2006), bone diseases (Luckman et al., 1998), infectious diseases (Charron et al., 2013; Gelb et al., 2003; Hast et al., 2011), progeria (Capell et al., 2008), and neurodegenerative diseases including Alzheimer's disease (AD) (Cheng et al., 2013; Li et al., 2016; Li et al., 2012). This review attempts to provide a general overview of isoprenoid synthesis, the process of protein prenylation and the complexity of prenylated proteins, and pharmacological agents that regulate isoprenoid synthesis and protein prenylation. Further, it aims to summarize recent findings that connect isoprenoids/protein prenylation with AD and explore the potential application of new prenylomic technologies for uncovering the role of prenylated proteins in the pathogenesis of AD.

Isoprenoid Synthesis

Isoprenoids, also known as terpenoids, are a diverse group of lipophilic molecules that are composed of five-carbon isoprene units. These lipids exist ubiquitously in all living organisms, from bacteria, fungi, plants, to mammals, and represent the largest and most diverse family of natural compounds (Sacchettini and Poulter, 1997). Isoprenoids play key structural and functional roles in a wide variety of biological processes, including formation of cell membranes, regulation of gene expression, modification of proteins, regulation of signal transduction pathways, participation in electron transport and photosynthesis,

protection against infections, and biosynthesis of vitamins, cholesterol and related sterols, yeast mating pheromones, and mammalian reproductive hormones (Holstein and Hohl, 2004). Here we mainly focus on the short-chain isoprenoids produced in the mevalonate-isoprenoid-cholesterol biosynthesis pathway in mammalian cells (**Figure 1**).

The synthesis of isoprenoids and ultimately cholesterol starts with “activated acetic acid”, acetyl Co-A, which is condensed with acetoacetyl-CoA (formed by self-condensation of two acetyl-CoA molecules) to produce 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) (Lynen, 1964). The HMG-CoA is converted to mevalonate in the rate-limiting step of the pathway catalyzed by HMG-CoA reductase (Bucher, Overath, and Lynen, 1960; Ferguson, Durr, and Rudney, 1959). Mevalonate is phosphorylated by mevalonate kinase (MK) to form 5-phosphomevalonate (Tchen, 1958). Through additional steps of phosphorylation and decarboxylation, phosphomevalonate is converted into the five-carbon isoprenoid compound, isopentenyl pyrophosphate (IPP) (Tada and Lynen, 1961). At this step, IPP can be converted to its isomer, dimethylallyl pyrophosphate (DMAPP), by the action of isopentenyl pyrophosphate isomerase (Agranoff et al., 1960). DMAPP serves as the isoprene donor in the synthesis of isopentenyl adenine, present in some tRNAs (Faust, Brown, and Goldstein, 1980; Hall, 1971). Continuing on the isoprenoid pathway, IPP and DMAPP are building blocks for all other isoprenoids. These two five-carbon molecules are condensed to produce the 10-carbon compound, geranyl pyrophosphate (GPP), followed by the addition of a second IPP unit to GPP forming the 15-carbon isoprenoid molecule, farnesyl pyrophosphate (FPP). Both of these reactions are catalyzed by FPP synthase (FPPS) (Poulter and Rilling, 1978; Poulter and Satterwhite, 1977). FPP resides at the important branch point between the non-sterol/isoprenoid and sterol/cholesterol synthetic pathways. In the isoprenoid pathway, the addition of a third IPP unit to FPP forms the 20-carbon isoprenoid molecule, geranylgeranyl pyrophosphate (GGPP), catalyzed by GGPP synthase (GGPPS) (Sagami, Ishi, and Ogura, 1981). Elongation via incorporation of additional IPP moieties leads to the formation of longer, biologically important isoprenoid molecules, including dolichols (for N-glycosylation of proteins), heme A, and ubiquinone (Goldstein and Brown, 1990). In the sterol pathway, the condensation of two FPP molecules forms the sterol precursor squalene, catalyzed by squalene synthase (Beytia, Qureshi, and Porter, 1973). Squalene undergoes cyclization to yield lanosterol, the first steroid molecule in the pathway (Bloch, 1965). Subsequently, lanosterol is transformed to cholesterol through two interrelated pathways, the Bloch pathway via desmosterol (Bloch, 1965) or the Kandutsch-Russell pathway via 7-dehydroxycholesterol (Kandutsch and Russell, 1960). The homeostasis of isoprenoids and cholesterol is maintained by multiple feedback regulations on HMG-CoA reductase to ensure normal cell growth and function (Brown and Goldstein, 1980; Brown and Goldstein, 1997; Brown, Radhakrishnan, and Goldstein, 2017). An additional layer of feedback regulation of the pathway has been discovered recently in which FPP binds to the allosteric site of FPPS and locks the enzyme in an inactive state (Park et al., 2017). The interest in isoprenoids and related pathways has been increased substantially in recent years following the discovery that FPP and GGPP could modify the structure and function of unique groups of proteins, which are implicated in cancer and other disorders, through the process of protein prenylation (see detailed discussion below).

Protein Prenylation

Protein prenylation consists of the addition of farnesyl or geranylgeranyl groups on specific cysteine residues located near the C-termini of various proteins. Prenylation was first discovered in 1979 by Kamiya in fungal mating factors (Kamiya et al., 1979), although it was not detected in mammalian cells until 1984 when the incorporation of mevalonate-derived species were discovered in 3T3 cells (Schmidt, Schneider, and Glomset, 1984). This modification is a three step process (**Figure 2**) (Zhang and Casey, 1996) that involves the initial attachment of an isoprenoid group derived from farnesyl (FPP) or geranylgeranyl pyrophosphate (GGPP) to a protein substrate catalyzed by a prenyltransferase. Farnesylated proteins usually undergo subsequent proteolysis to remove residues downstream of the prenylated cysteine, performed by specific proteases, followed by methylation mediated by a SAM-dependent methyl transferase to yield a protein containing a C-terminal farnesylcysteine methyl ester. However, some farnesylated proteins are not further processed post-prenylation including the yeast chaperone Ydj1p (Hildebrandt et al., 2016) and the brain-specific splice variant of Cdc42 (bCdc42) (Nishimura and Linder, 2013). Many geranylgeranylated proteins also undergo this same three-step process while others do not (Leung et al., 2007; Michaelson et al., 2005). Some mature prenylated proteins undergo additional lipid modifications including palmitoylation (Hancock et al., 1989). Ultimately, most prenylated proteins localize to the plasma membrane or internal membranes where they participate in various transduction pathways. The enzymes and biochemistry involved in protein prenylation are described in more detail as follows.

Three prenylating enzymes have been identified from a variety of eukaryotes ranging from yeast to mammals. Farnesyltransferase (FTase) and geranylgeranyltransferase-I (GGTase-I) are $\alpha\beta$ heterodimeric proteins that share a common α -subunit (FNTA) and different β -subunits (FNTB and PGGT1B, respectively) (Casey et al., 1989; Casey, Thissen, and Moomaw, 1991), whereas geranylgeranyltransferase-II (GGTase-II), also a heterodimer, has distinct α and β subunits (RABGGTA and RABGGTB, respectively) along with a third subunit denoted as Rab escort protein (REP) (Seabra et al., 1992). All three of these enzymes are present in the cytosolic fraction of all tissues including the brain. The three-dimensional structures of FTase and GGTase-I are highly similar with active sites that completely envelop the isoprenoid and significant portions of the C-terminus from the substrate protein (**Figure 3**) (Strickland et al., 1998; Taylor et al., 2003). FTase and GGTase-I recognize a tetrapeptide sequence known as a CAAX-box where C is cysteine, A is typically but not exclusively an aliphatic amino acid and X controls whether the sequence is an FTase or GGTase-I substrate. Early work with a limited number of synthetic peptides demonstrated that FTase preferred Cys, Met, Ser, Ala and Gln residues at the X-position whereas GGTase-I showed a preference for Ile, Leu and Phe (Reiss et al., 1991; Yokoyama et al., 1991). However, more recent work with peptide libraries suggests that there are many exceptions to these rules (Hougland et al., 2010; Krzysiak et al., 2007; Wang and Distefano, 2012; Wang et al., 2014). Computational studies have also shown this to be true (London et al., 2011). Very recently, it has been reported that FTase can efficiently prenylate cysteines they are positioned five residues (instead of the usual four) from the C-terminus raising the possibility that the number of prenylated proteins is even larger than originally thought

(Blanden et al., 2017). Interestingly, FTase appears to be more selective than GGTase-I since the latter accepts many FTase substrates while the converse is not generally true, although there are exceptions (Krzysiak et al., 2010). Given that more is known about FTase versus GGTase specificity, additional work is necessary to better define the substrate specificity of the latter enzyme. At this point, it is possible to predict with some certainty whether specific CAAX-box sequences will be prenylated although work remains to be done. GGTase-II recognizes C-terminal sequences including CC, CXC, CCX, CCXX, and CCXXX (Kinsella and Maltese, 1992; Pereira-Leal and Seabra, 2000). However, in contrast to the aforementioned enzymes, GGTase-II cannot prenylate short peptides due to the fact that the active site is somewhat more open; importantly, the escort protein REP serves to recruit substrate proteins and docks with GGTase-II to present them for prenylation (**Figure 3**) (Guo et al., 2008). Additionally, GGTase-II typically transfers geranylgeranyl groups to both Cys residues within the sequences noted above.

Once proteins are prenylated, they typically localize to the endoplasmic reticulum (ER) for further processing although some such as Ydj1p do not (Hildebrandt et al., 2016). The “AAX” residues from the CAAX-box on farnesylated proteins are typically cleaved by one of two proteases that include Ras converting enzyme (Rce1) and Zinc metalloproteinase Ste24 (ZMPSte24) (Boyartchuk, Ashby, and Rine, 1997; Chen, Ma, and Rando, 1996); both of these enzymes have been detected in all tissues including the brain. To date, the human-derived Rce1 enzyme has not been purified to homogeneity in active form although it has been studied in partially purified form (Dolence et al., 2000; Schmidt et al., 1998); that enzyme is believed to be responsible for the processing of Ras proteins. In contrast, ZMPSte24 has been purified and its structure solved by x-ray crystallography (Fujimura-Kamada, Nouvet, and Michaelis, 1997; Quigley et al., 2013). This enzyme is particularly interesting since it appears to cleave two structurally unrelated sequences. In the processing of lamin A, ZMPSte24 cleaves the C-terminal “AAX” residues of the prenylated protein as well as at a site approximately 20 residues upstream of the C-terminus. The structure containing a short bound peptide and an appropriately positioned Zn atom provide a useful model for understanding how cleavage of the “AAX” sequence occurs but does not clarify how the upstream site is proteolyzed.

Following proteolysis of farnesylated CAAX-box sequences, the resulting C-terminal farnesylcysteine is methylated by the SAM-dependent methyl transferase Icmt (Hrycyna et al., 1991), located in the ER and also expressed in all tissues including the brain. While the structure of Icmt has not been determined, a structure of a bacterial homolog has been solved (Yang et al., 2011). To address this paucity of structural data, a variety of biochemical methods have been used to provide insight into the structure and activity of this enzyme (Anderson et al., 2005; Hrycyna and Clarke, 1992).

Complexity of Prenylated Proteins and Their Functions

Hundreds of proteins have been identified or predicted to undergo prenylation (Maurer-Stroh et al., 2007; McTaggart, 2006; Wang and Casey, 2016). They include many important intracellular proteins, ranging from heterotrimeric G protein subunits to nuclear lamins; however, the largest, and most extensively studied group of prenylated proteins is the Ras

superfamily of small GTPases (McTaggart, 2006), which is comprised of over 150 known members. Based on sequence and functional similarities, this superfamily is divided into five subfamilies: Ras, Rho, Rab, Ran and Arf (Colicelli, 2004; Wennerberg, Rossman, and Der, 2005). These proteins serve as molecular switches, cycling between “on” and “off” states during signal transduction, and through interaction with their downstream effectors, they regulate a variety of cellular processes and functions, including cell growth and survival, differentiation and proliferation, cytoskeletal organization, vesicular trafficking, gene expression, and energy metabolism. The biological networks of small GTPases are complex. Each subfamily contains numerous members and each member interacts with multiple downstream effector proteins. Despite that complexity, one essential initiation step for almost all small GTPases to activate downstream signaling pathway is association with membranes, which relies on prenylation (and sometimes other lipid modifications) (Lane and Beese, 2006). Therefore, the prenylation status of small GTPases has a significant impact not only on the structure/function of small GTPases *per se* but also on the functions of their downstream effector proteins. Here we use the Ras subfamily as an example to illustrate the role of prenylation and the complexity of small GTPase biology briefly. For more extended discussions on small GTPases, the interested reader is referred to several excellent reviews (Cherfils and Zeghouf, 2013; Colicelli, 2004; Wennerberg, Rossman, and Der, 2005).

The Ras subfamily contains over 36 members and the best-characterized ones are the three Ras isoforms: H-Ras, K-Ras, and N-Ras, mainly because of their oncogenic roles (Wennerberg, Rossman, and Der, 2005). All three Ras isoforms undergo the three-step modification process, i.e., prenylation, proteolysis and carboxymethylation, at the ER membrane as described above (**Figure 2**). Subsequently, H-Ras and N-Ras undergo additional palmitoylation, trafficking through the Golgi and vesicular transport to the plasma membrane (Prior and Hancock, 2012). For K-Ras (referring to the major splice variant K-Ras4B), the presence of the basic hexalysine patch along with the farnesyl group is sufficient for anchoring into the plasma membrane via a Golgi-independent cytosolic route (Prior and Hancock, 2012) (**Figure 4**). Importantly, all biological functions of Ras occur at the plasma membrane (Simanshu, Nissley, and McCormick, 2017), including interactions with regulatory proteins, downstream effector proteins, and signal transduction.

At the plasma membrane, Ras proteins exist in GDP-bound (inactive) or GTP-bound (active) forms and the switching between GDP/GTP states are highly regulated through sophisticated mechanisms (Cherfils and Zeghouf, 2013). Stimulated by extracellular signals through cell surface receptors, Ras proteins are activated or “turned on” by guanine nucleotide exchange factors (GEFs), which catalyze the release of GDP and the binding of GTP. In contrast, GTPase-activating proteins (GAPs) accelerate the intrinsic GTPase activity of Ras for hydrolysis of GTP and lead to the inactivation or “turning off” of Ras. This GDP/GTP switch is further regulated by guanine dissociation inhibitors (GDIs) and GDI-like proteins. The replacement of GDP for GTP induces a conformational change in Ras proteins that allows them to interact with their downstream effectors and execute their multiple signaling functions (Cherfils and Zeghouf, 2013) (**Figure 4**). Approximately 20 distinct Ras effector proteins have been identified (Prior and Hancock, 2012). Two of the major Ras-driven

signaling pathways are the MAPK (Raf/MEK/ERK) and PI3K/Akt/mTOR pathways, which regulate a plethora of key cellular processes and functions under both physiological and pathological conditions (Nussinov, Tsai, and Jang, 2017; Stephen et al., 2014).

Finally, it is worth noting that, despite the fact that Ras isoforms share a high degree of sequence homology and interact with a common set of regulators/effectors, they are not functionally redundant. It is believed that the specific membrane/compartiment localization for each of the isoforms, where there are different pools and concentrations of regulators and effectors, contribute to the lack of functional redundancy between them (Hancock, 2003; Prior and Hancock, 2012). Supporting this notion, recent work has demonstrated that K-Ras selectively interacts with membrane lipids and forms “nanoclusters” that determine its signaling output; subtle changes to its membrane anchor sequence or prenylation profoundly alter lipid specificity of K-Ras and its signaling output (Zhou et al., 2017). These findings further highlight the importance of prenylation in regulating the functions of Ras and render isoprenoids and prenyltransferases promising therapeutic targets for various disorders.

Pharmacological Agents that Regulate Isoprenoids and Protein Prenylation

Statins – HMG-CoA Reductase Inhibitors

Statins are a class of drugs that selectively inhibit the rate-limiting enzyme, HMG-CoA reductase, in the mevalonate-isoprenoid-cholesterol pathway (**Figure 1**) (Goldstein and Brown, 1990). Thus, these drugs reduce the biosynthesis of isoprenoid intermediates as well as the final product cholesterol. Statins have been successfully used to control plasma cholesterol levels and prevent cardiovascular disease (4S-group, 1994; Goldstein and Brown, 2015; Sacks et al., 1996). The first statin, ML-236B (later known as compactin or mevastatin), was discovered by Akira Endo in 1976 from work with a penicillium mold (Endo, Kuroda, and Tanzawa, 1976). This discovery stimulated the worldwide development of natural and synthetic HMG-CoA reductase inhibitors (Endo, 1992). At present, the US Food and Drug Administration (FDA) have approved the use of seven statins: lovastatin, pravastatin, simvastatin, fluvastatin, atorvastatin, rosuvastatin, and pitavastatin (Li et al., 2012). Each of the statins has a characteristic structure that competes with HMG-CoA binding to HMG-CoA reductase (Istvan and Deisenhofer, 2001) (**Figure 5**). As a result, the enzyme activity of HMG-CoA reductase is inhibited and the biosynthesis of downstream molecules, including isoprenoids and sterols, is blocked. Although all statins share a common mechanism for inhibiting HMG-CoA reductase, other unique structural features render them different in solubility (hydrophilic or lipophilic), potency, and permeability across the blood-brain barrier (BBB) (Li et al., 2012).

While the power of statins to inhibit cholesterol synthesis has been harnessed successfully to manage plasma cholesterol levels and reduce the risk of cardiovascular disease, the clinical significance of statin-induced inhibition on isoprenoid production remains underexplored. Nevertheless, a growing body of evidence indicates that the benefits of statins in curtailing cardiovascular disease extend beyond their cholesterol-lowering property, and their ability to inhibit the synthesis of isoprenoids, in particular FPP and GGPP, and prenylation of small GTPases is responsible for their cholesterol-independent (pleiotropic) effects (Oesterle, Laufs, and Liao, 2017). In addition, owing to these pleiotropic effects, there have been calls

for repurposing statins for disorders other than cardiovascular disease, ranging from cancers, inflammatory diseases, infectious diseases, and neurodegenerative diseases including AD (Hennessy et al., 2016; Iannelli et al., 2017; Moutinho, Nunes, and Rodrigues, 2017; Walton et al., 2016).

However, the pleiotropic effects of statins have been difficult to quantitate because the inhibition of isoprenoids correlate with the inhibition of cholesterol biosynthesis. In addition, technically, it has been challenging to measure FPP and GGPP levels in tissues, including the brain (Wood et al., 2010; Wood, Mupsilonller, and Eckert, 2014). Recently, the development of an HPLC method has advanced the understanding of isoprenoid metabolism *in vivo* (Tong et al., 2008). This method was adapted to determine FPP and GGPP concentrations in the human brain frontal cortex (Hooff et al., 2008). It was found that GGPP levels were higher than FPP levels in both white and gray matter. There was approximately four times as much GGPP as FPP in the human frontal cortex. Consistently, GGPP was in greater abundance than FPP in brain homogenate of mice (Tong et al., 2008). Interestingly, FPP levels were slightly higher than GGPP levels in the kidney, liver, and heart. These findings suggest that regulation of FPP and GGPP may differ in the brain as compared with other organs, although the mechanisms accounting for differences in distribution and levels of FPP and GGPP in brain tissue are not known. As FPP serves as the precursor for other longer chain isoprenoids such as dolichol and ubiquinone in addition to GGPP and cholesterol (**Figure 1**), FPP utilization, turnover, and synthesis may be greater than GGPP. Importantly, with the establishment of a reliable quantitative method for isoprenoids, further studies in animals showed that chronic treatment with peripherally administered simvastatin could indeed significantly reduce the levels of FPP and GGPP in the brain (Eckert et al., 2009). Intriguingly, the effects of simvastatin on FPP and GGPP levels in the brain were not equal in magnitude. Simvastatin treatment had a much greater effect on brain FPP levels (48% reduction) as compared with GGPP (33% reduction) and cholesterol (22% reduction). The significance of such differential effects of statins on FPP and GGPP in the pathway warrants further investigation. It is also noteworthy that squalene synthase, GGPP synthase, and FTase, the three enzymes that use FPP as a substrate, have very different K_m for FPP, in the order of $2 \frac{1}{4}M > 1 \frac{1}{4}M \ggg 5 \text{ nM}$, respectively (Winter-Vann and Casey, 2005). Thus, statin-induced reduction of isoprenoids causes a reduction in sterol/cholesterol production first, followed by a reduction in GGPP synthesis (and therefore protein geranylgeranylation), whereas protein farnesylation is only affected when the level of FPP becomes extremely low. Nevertheless, it has been shown that treatment with simvastatin reduces both farnesylation and geranylgeranylation of specific Ras-related GTPases in mice and extends lifespan in aging flies (Spindler et al., 2012). In support of the brain bioavailability and target engagement of statins, a recent study has shown that treatment with clinically relevant doses of simvastatin decreases the prenylation of small GTPases in the brain of mice and rats (Ostrowski et al., 2016). These studies demonstrate that lipophilic and BBB-permeable statins could modulate isoprenoid metabolism and protein prenylation in the brain, and thus could potentially be used to treat relevant disorders of the central nervous system. The application of statins in AD is discussed in more detail in later sections of this review.

Bisphosphonates – FPP Synthase Inhibitors

Bisphosphonates, specifically the nitrogen-containing bisphosphonates (N-BPs), are another class of drugs that act on the mevalonate-isoprenoid-cholesterol pathway. Different from statins, these drugs inhibit the activity of FPPS, downstream of HMG-CoA reductase in the pathway (Rogers et al., 2011) (**Figure 1**). N-BPs have been widely used to treat bone diseases such as osteoporosis for more than 40 years (Maraka and Kennel, 2015; Russell, 2011). The development of this class of drugs was based on early discoveries that natural pyrophosphate compounds could prevent calcification of soft tissues, regulate bone mineralization, and effectively inhibit bone resorption (Fleisch, Russell, and Francis, 1969; Fleisch et al., 1969; Fleisch, Russell, and Straumann, 1966). Currently, several FDA-approved N-BPs are available, including pamidronate, alendronate, risedronate, zoledronate, and ibandronate (**Figure 6**). The therapeutic application of this group of drugs relies on their backbone P-C-P structure and their ability to chelate calcium ions. Due to these properties, these drugs are targeted rapidly to the bone mineral surface *in vivo*, where they are taken up primarily by osteoclasts (bone-degrading cells) (Roelofs et al., 2010). Thus, the site of action for N-BPs is unique compared with that of statins, which are taken up predominantly by the liver (Sirtori, 2014). The intracellular mechanisms of action for all N-BPs depend on their ability to bind FPPS and inhibit its activity, limiting the synthesis of FPP and GGPP. Thus, similar to statins, N-BPs reduces protein prenylation, in particular the prenylation of small GTPases, disrupting the membrane association and intracellular trafficking of these proteins and consequently, blocking the interactions of GTPases with their effectors and downstream signaling pathways. Concomitantly, inhibition of FPPS by N-BPs also cause the accumulation of the upstream metabolite IPP (**Figure 1**), which leads to the formation of new metabolites such as ApppI (an ATP analog) that induces apoptosis (Monkkonen et al., 2006). Thus, inhibition of protein prenylation and accumulation of ApppI are two main mechanism by which N-BPs exert their anti-resorptive and apoptosis-inducing effects on osteoclasts (Rogers et al., 2011). Through these actions, N-BPs suppress bone degradation, increase bone mass and strength, and reduce the risk of fracture.

One noteworthy aspect for bone metabolism is the relative importance of the two prenylation pathways. It appears that N-BPs work primarily through inhibition of protein geranylgeranylation rather than protein farnesylation, despite the fact that N-BPs depletes both GGPP and FPP. It has been shown that the effects of N-BPs on inhibiting osteoclast formation and bone resorption can be abolished by geranylgeraniol (precursor of GGPP for protein geranylgeranylation), but not by farnesol (precursor of FPP for protein farnesylation) (Fisher et al., 1999). This was further supported by studies where specific prenylation inhibitors were used. Use of a GGTI to suppress protein geranylgeranylation blocked bone resorption in osteoclasts, whereas the use of an FTI to block protein farnesylation had minimal effect (Coxon et al., 2000). Together, these findings suggest that the two prenylation pathways play differential roles in regulating the functions of osteoclasts, in which geranylgeranylated proteins are more crucial than farnesylated proteins.

Since N-BPs are rapidly targeted to the bone, their uses for other conditions are limited. However, the therapeutic potential of N-BPs has been explored for several disorders other than bone diseases *in vitro* and *in vivo*, including cancer, Hutchinson–Gilford progeria

syndrome (HGPS), and AD (Li et al., 2012). In particular, for HGPS, which is caused by mutations in the nuclear lamin A protein and subsequent accumulation of a prenylated form of the mutant lamin A (Dechat et al., 2007; Young et al., 2006), human clinical trials have been conducted recently following the success in animal models with the treatment of N-BPs in combination with statins (Varela et al., 2008). Compared with the monotherapy with an FTI (lonafarnib), the combination therapy of an N-BP (zoledronate) with an FTI and a statin (pravastatin) provided additional bone mineral density benefit as well as attenuating the overall aging symptoms and increased survival (Gordon et al., 2016; Gordon et al., 2012; Gordon et al., 2014). The beneficial effects of N-BPs observed in animal and clinical studies of HGPS raise the possibility that these agents may have broader effects on normal aging processes. A recent study has showed that through its action on protein prenylation, zoledronate attenuates accumulation of DNA damage in stem cells and protects their function by inhibiting the mTOR signaling, a pathway involved in both aging and cancer (Misra et al., 2016). These findings suggest a potential relationship between isoprenoid metabolism/protein prenylation and normal aging processes, thus broadening the spectrum of potential applications of N-BPs.

In addition, a recent study indicates that N-BPs may be used to treat cerebral cavernous malformations (CCMs), common abnormal vascular formations that occur in the brain, spinal cord, and sometimes the retina (Nishimura et al., 2017). Through high-throughput screening, it was found that N-BPs and statins could act synergistically to reverse the phenotype of the disease in cell and fly models. Treatment with zoledronate in combination with fluvastatin effectively attenuated neural and vascular deficits in chronic and acute mouse models of CCMs. The combination treatment significantly reduced lesion burden and extended lifespan in these animals (Nishimura et al., 2017), suggesting inhibition of isoprenoids as a potential therapy for CCM disease.

The prospect of using N-BPs for AD was highlighted by a report that levels of FPP and GGPP are elevated significantly in the brain of Alzheimer's patients (Eckert et al., 2009). Recently, the connection between AD and the isoprenoid pathway was further enhanced by findings that a polymorphic site in the promoter region of the human FPPS gene was significantly associated with the level of phosphorylated tau in the brains of AD patients, and that the mRNA expression of FPPS was markedly elevated in the brains of AD versus control subjects (De Schutter et al., 2014). These findings strongly suggest that inhibition of FPPS may produce beneficial effects against AD. However, minimal systemic exposure and poor BBB permeability of N-BPs limit the clinical use of these drugs in treating neurological disorders such as AD. In this regard, exciting advances have been made recently in developing novel non-BP inhibitors of FPPS that bind to an allosteric site on the enzyme (De Schutter et al., 2014; Gritzalis et al., 2015; Jahnke et al., 2010; Marzinzik et al., 2015). Interestingly, FPP, the natural product of FPPS, can bind to the allosteric site of the enzyme and inhibits its activity (Park et al., 2017). These new inhibitors lack the phosphonate groups of N-BPs and thus are not targeted to bone mineral, offering the hope that this new class of compounds may lead to much broader therapeutic applications of FPPS inhibitors.

Inhibitors for Prenyltransferases and Related enzymes

As discussed above, statins and N-BPs inhibit the biosynthesis of isoprenoids and reduce the availability of isoprenoid substrates for protein prenylation without directly acting on prenyltransferases themselves, and thus have limitations. By inhibiting isoprenoid synthesis, all downstream products are influenced; in contrast, specific inhibition of prenylation itself could potentially be more selective. The discovery that Ras proteins are farnesylated and the fact that farnesylation is required for membrane localization suggested that inhibition of FTase could serve as a strategy for shutting down the effects of constitutively activated mutant Ras proteins in cancer or related pathways that signal via Ras dependent processes. That hypothesis triggered an explosion of research into the development of prenyltransferase inhibitors leading to over 100 clinical trials. A number of excellent reviews on this topic have been previously published (Berndt, Hamilton, and Sebt, 2011; Gibbs, 2000; Leonard, 1997; Ochocki and Distefano, 2013; Wang, Yao, and Huang, 2017).

To date, three broad classes of FTase inhibitors (FTIs) have been developed (**Figure 7, 8**). Compounds such as α -hydroxyfarnesylphosphonate (HFP) (Pompliano et al., 1992) that mimic the substrate FPP and bind within the isoprenoid binding site of FTase (Strickland et al., 1998) have been found to be useful biochemical tools but lack specificity to be used as drugs. Bisubstrate inhibitors that combine elements from the isoprenoid and CAAX-box such as **Schi-872** have also been prepared although none of them has progressed beyond experiments in cell culture (Manne et al., 1995; Patel et al., 1996; Schlitzer and Sattler, 1999). In contrast, peptidomimetic compounds that mimic the CAAX-box have proven to be the most specific and useful. Three general strategies have been employed in their development. Peptidomimetics based on CAAX-box peptides that have been modified by removal of labile amide bonds, exemplified by L-744,832, were among the first compounds studied in detail (Kohl et al., 1995). Rigid peptidomimetic scaffolds have also proved fruitful for the development of FTIs with **FTI-277** being widely used in cell culture models (Lerner et al., 1995). However, the inhibitors Tipifarnib (Venet, End, and Angibaud, 2003) and Lonafarnib (Morgillo and Lee, 2006), obtained via optimization of hits identified from high throughput screening efforts have been the most extensively studied in a range of experiments including human clinical trials along with **BMS-214662** (Rose et al., 2001) and **L-778,123** (Lobell et al., 2002) (**Figure 8**). These compounds produced promising results in cell culture-based experiments and some animal models. Unfortunately, none of these compounds have shown significant efficacy in human trials. A central reason for this lies in the differential enzymology of Ras proteins. As discussed above, mammalian cells typically contain three prenylated isoforms including H-, N- and K-Ras. While H-Ras is only prenylated by FTase, N-Ras and K-Ras are also slow substrates for GGTase-I. In the presence of an FTI, They are alternatively prenylated by GGTase-I to yield proteins that retain signaling activity. This allows tumors driven by N- and K-Ras mutations to circumvent the effects of FTIs. In support of this notion, cancers specifically caused by overactive H-Ras are sensitive to treatment with FTIs (Chen et al., 2014; Kohl et al., 1995). In addition, FTIs may also be useful in some cases that involve prenylated proteins other than Ras but further study is required to determine precisely what proteins are involved in those processes. Highly potent inhibitors of GGTase-I (Kazi et al., 2009) or dual FTase/ GGTase-I inhibitors (Lobell et al., 2002) have also been developed that work well in cell

culture and some animal models but exhibit excessive toxicity in human trials; this is probably related to the fact that geranylgeranylation is more prevalent compared with farnesylation (Berndt, Hamilton, and Sebti, 2011; Reid et al., 2004). Inhibitors of GGTase-II including **3-PEHPC** have also been developed and their use explored in biochemical and cell-based assays (Coxon et al., 2001). However, their use has been limited in the community since none is currently commercially available.

Beyond cancer, prenylation inhibitors are also being explored in other diseases. Positive results with Lonafarnib have recently been obtained in Phase II clinical trials for Hutchinson–Gilford progeria, a debilitating disease that causes premature aging and typically death before age 20 (Gordon et al., 2016; Gordon et al., 2012). In this case, the FTI inhibits prenylation of lamin A that is incorrectly processed due to an upstream mutation. Promising results were also obtained in a Phase II study using Lonafarnib to treat chronic hepatitis infection since farnesylation of the large delta hepatitis antigen is required for viral proliferation (Yurdaydin et al., 2017). More preliminary investigations using prenylation inhibitors for the treatment of other diseases including malaria, leishmania and fungal infections are also in progress (Gelb et al., 2006).

Limited progress has been made on inhibiting the proteases Rce1 and ZMPSte24 that act on prenylated proteins. Compounds that function *in vitro* or in cell-based assays have been developed although those studies have not been extended to animal models this far (Mohammed et al., 2016; Porter et al., 2007). More progress has been made in developing inhibitors of Icmt because genetic knockouts have demonstrated that this enzyme is essential for transformation by oncogenic K-Ras and B-Raf (Bergo et al., 2001; Bergo et al., 2000). A variety of inhibitors based on the structure of N-acetylfarnesylcysteine have been developed (Bergman et al., 2011; Bergman et al., 2012; Donelson et al., 2006). Also, since the development of Cysmethynil (a non-isoprenoid-containing inhibitor), which was shown to induce autophagy-mediated cell death in PC3 prostate cancer cells (Wang et al., 2008), a number of groups have developed Icmt inhibitors with improved pharmacological properties (Yang et al., 2017). However, those studies have not yet progressed into animals.

Connections between Isoprenoids/Protein Prenylation and Alzheimer’s Disease

As discussed above, abnormalities in prenylated proteins, such as Ras and nuclear lamins, cause cancers and premature aging. Recently, there has been an increased interest in understanding the role of isoprenoids and prenylated small GTPase in neurodegenerative diseases. AD is the most prevalent neurodegenerative disorder in the elderly. It destroys memory and other vital cognitive functions, eventually leading to dementia and death. Currently in the United States, over 5 million people live with AD, and the prevalence of this devastating disease is expected to triple by mid-century (Alzheimer’s Association, 2016). The pathological hallmarks of AD include the accumulation of amyloid- β peptide (A β) in neuritic plaques and cerebral vessels, and the formation of neurofibrillary tangles consisting of hyper-phosphorylated tau proteins in the brain (Selkoe, Mandelkow, and Holtzman, 2012). The pathogenic mechanisms that lead to the development of AD, particularly the

sporadic form of AD, remain to be elucidated. Here we summarize multiple lines of evidence that suggest important roles of isoprenoids/protein prenylation in the pathogenesis of AD.

Epidemiological/Clinical Evidence

The link between isoprenoids/prenylation and AD has been suggested from studies with statins. Several cross-sectional, cohort, and case-control studies have found significantly lower incidence and slower progression of AD in statin users (Haag et al., 2009; Jick et al., 2000; Wolozin et al., 2000). However, clinical evidence remains inconclusive due to inconsistent results across randomized clinical trials and cohort studies (Richardson et al., 2013; Shepardson, Shankar, and Selkoe, 2011). A recent longitudinal cohort study that followed 20% of Medicare beneficiaries from 2006 to 2013 found significantly lower risk of AD in individuals who had high exposure to statins than those with low exposure to statins (Zissimopoulos et al., 2017). This suggests that the inconsistencies observed in previous studies may be partly attributable to insufficient doses of statins used in trials. The same study reported that a reduction of AD risk differs across statin types, gender, and ethnic groups suggesting the importance of choosing the right study population for a given statin type. Although the statin-induced cholesterol-lowering effects could contribute to favorable outcomes in individuals with hypercholesterolemia, the beneficial effect of statins has been also reported in AD patients with normal cholesterol levels (Simons et al., 2002). Moreover, other non-statin drugs that lower cholesterol levels do not produce the same benefits in AD patients (Haag et al., 2009). This indicates that mechanisms independent of the inhibition of cholesterol biosynthesis are involved in the neuroprotective effect of statins.

Compelling evidence suggests that the reduction of isoprenoid synthesis and protein prenylation could be a key mechanism mediating statin-induced neuroprotection (Hooff et al., 2010; Li et al., 2016; Ostrowski et al., 2007), although experimental data should be interpreted with caution as statin treatment affects a number of biomolecules and associated pathways/proteins beyond isoprenoids. Eckert *et al.* demonstrated elevated FPP and GGPP, and mRNA expression of their synthases (FPPS and GGPS) in the brain tissues of male AD patients compared with non-AD controls without any changes in brain cholesterol levels (Eckert et al., 2009), suggesting a specific dysregulation of isoprenoid homeostasis in AD. This notion is supported by a recent report that found a significant correlation between the levels of mRNA for FPPS and GGPPS and tau/tangle pathology in the frontal cortex of AD brains, as well as an association between high levels of FPPS and GGPPS mRNA and earlier age of onset in AD (Pelleieux et al., 2018). Consistent with an increase in isoprenoids, abnormal increase in membrane associated (prenylated) Ras and Rho GTPases in post-mortem brain tissues of AD patients were reported in other studies (Gärtner, Holzer, and Arendt, 1999; Zhu et al., 2000). Moreover, Ginsberg *et al.* reported selective upregulation of Rab5 and Rab7 in brain regions that are susceptible to vulnerability in AD such as the basal forebrain, frontal cortex, and hippocampus, but not in relatively spared regions such as the cerebellum and striatum in individuals with diagnosis of mild cognitive impairment (MCI) and AD (Ginsberg, 2011; Ginsberg et al., 2011).

It is also worth noting that dysregulation of isoprenoid synthesis and prenylated proteins are involved in pathological aging and other age-related neurodegenerative disorders. Hutchinson-Gilford progeria syndrome (HGPS), a laminopathy characterized by premature aging, is one of the most well studied diseases involving aberrant prenylation (Gordon et al., 2012; Reddy and Comai, 2012). Most HGPS cases are caused by a point mutation in the LMNA gene, which leads to the production and accumulation of a permanently farnesylated lamin A protein called progerin (Reddy and Comai, 2012). As discussed above, clinical trials have shown that suppression of protein farnesylation by an FTI inhibitor with or without a statin or N-BP drug improves vascular stiffness, bone structure, and audiological status, and significantly increases the survival of children with this fatal disease (Gordon et al., 2016; Gordon et al., 2012; Gordon et al., 2014). Intriguingly, lamin A-dependent nuclear defects also occur during normal aging (Scaffidi and Misteli, 2006). Whether the modulation of protein prenylation modifies the course of normal aging is yet to be investigated. Interestingly, a recent study showed that dysfunction of lamin mediates neurodegeneration in AD and suggested that AD could be an acquired neurodegenerative laminopathy (Frost, 2016). Furthermore, a recent study showed a significant increase in the expression of *PGGT-1B*, which encodes the β subunit of GGTase-I, in motor neurons of individuals with another neurodegenerative disease, amyotrophic lateral sclerosis (ALS), especially in early-onset cases (Li et al., 2016). This suggests that upregulation of protein prenylation may play an important role in the pathogenesis of ALS.

Genetic Evidence

AD is a multifactorial disease with a substantial genetic component. Early onset Alzheimer's disease (EOAD) is inherited in an autosomal-dominant pattern, and accounts for only 1–2% of total AD cases (Rosenthal and Kamboh, 2014). Mutations in three genes, amyloid- β precursor protein (APP), presenilin-1 (PS-1) and presenilin-2 (PS-2) are linked to EOAD (Rosenthal and Kamboh, 2014). On the other hand, late onset Alzheimer's disease (LOAD) accounts for most AD cases, and is much more complex than EOAD. To date, the most important genetic risk factor for LOAD is the *APOE- ϵ 4* allele, which accounts for approximately 25% of heritability. Recent genome-wide association studies (GWASs) and an epigenome-wide association study have identified ~30 putative risk susceptibility genes (Lambert, 2013; Ridge et al., 2017; Rosenthal and Kamboh, 2014; Sims et al., 2017). Yet the functional consequences and individual contributions of these newly identified susceptibility genes are not currently well known.

Although several cholesterol-related genes (e.g., apoE, clusterin (apoJ), and ABCA7) have been identified as top genes associated with AD, genes that are directly involved in isoprenoid synthesis or prenylation have not been identified as AD susceptibility markers in large-scale GWASs. However, small-scale genetic association studies indicate altered dynamics in isoprenoid synthesis and protein prenylation in AD. A recent study, in which five single nucleotide polymorphisms (SNPs) in human FPPS gene loci were examined in the frontal cortex in AD brains and their age-matched controls, found an allele-dose dependent association between one SNP (rs4971072), located in the promoter region of human FPPS gene, and phosphorylated tau (p-tau) levels (De Schutter et al., 2014). The same study further reported an increase in human FPPS mRNA levels in AD cortical brain

samples, consistent with findings from a previous study in which the expression of FPPS is upregulated in AD brains (Eckert et al., 2009). Moreover, microarray correlation analyses in hippocampal samples from AD subjects and control subjects identified upregulation of 6 out of 10 genes involved in isoprenoid metabolism in AD hippocampal samples (Blalock et al., 2004).

Emerging evidence also points toward the importance of the downstream small GTPases in the pathogenesis of AD. An exome sequencing study of neuropathologically defined 170 controls and 185 LOAD patients revealed a significant association between a genetic variant of *RAB11A* (rs117150201) and an increased risk of LOAD (Udayar et al., 2013). In addition, protein-protein interaction network analysis identified that Rab11A and Rab11B, and their effector proteins have significant interactions with bridging integrator 1 (BIN1), a risk gene strongly associated with LOAD that functions in clathrin-mediated endocytosis and endocytic recycling, which regulates β -secretase trafficking and A β production. A more recent study that investigated protective genetic variants in 232 cognitively-intact individuals over age of 75 with at least one *APOE* $\epsilon 4$ allele discovered a significant association of two loss-of-function genetic variants, one variant in *RAB10* (rs142787485; odds ratio (OR) = 0.58), and the other in *SARIA* (secretion associated Ras related GTPase 1A) (rs7653; OR = 0.35), with reduced risk of AD (Ridge et al., 2017). Since prenylation is a pre-requisite for the proper cellular localization and activation of these small GTPases, these genetic studies suggest that uncontrolled upregulation of small GTPase prenylation may play a significant role in the pathogenesis of AD.

Biochemical Evidence

Mounting biochemical evidence from *in vitro* and *in vivo* experiments indicates that isoprenoids and prenylated proteins are implicated in multiple processes pertinent to AD pathology, including APP processing and A β metabolism, tau phosphorylation, neuroinflammation, and synaptic plasticity and cognitive function as described below (Figure 9).

APP processing and A β metabolism: A β is the major component of senile plaques, one of pathological hallmarks of AD, and is generated by sequential cleavages of amyloid- β precursor protein (APP) by β -secretase (BACE1) and γ -secretase. In contrast, α -secretase cleaves within the sequence of A β , thus precluding the formation of intact A β (non-amyloidogenic processing of APP), and produces the neurotrophic soluble fragment, sAPP α (Thinakaran and Koo, 2008). Subsequent cleavage of the C-terminal fragment by γ -secretase yields the small non-amyloidogenic peptide, P3 (Nhan, Chiang, and Koo, 2015). It has been shown that FPP and GGPP significantly elevate A β production by potentially stimulating γ -secretase in H4 neuroglioma cells expressing APP with the Swedish mutation (sweAPP) (Kukar et al., 2005), and in HEK 293 cells expressing sweAPP (Zhou et al., 2008). Interestingly, co-administration of a farnesyltransferase or geranylgeranyl transferase inhibitor with FPP and GGPP did not block the elevation of A β levels (Kukar et al., 2005), indicating that FPP and GGPP may increase A β level through pathways independent of protein prenylation. However, in this study the cells were treated with transferase inhibitors for 6 hours and the level of protein prenylation was not measured (Kukar et al., 2005).

Therefore, it is possible that the short treatment duration did not sufficiently block protein prenylation to observe the effects on A β levels. The notion that statin-induced effects on A β levels are mediated through protein prenylation is supported by other studies described below, where the treatment duration was longer (24 hours) and the level of protein prenylation was measured (Ostrowski et al., 2007; Pedrini et al., 2005). It has also been demonstrated that statins may decrease A β production by reducing dimerization of BACE1, thereby blocking its co-localization with APP through both cholesterol-dependent and cholesterol-independent mechanisms (Parsons et al., 2006). Whereas another group showed that treatment with atorvastatin or simvastatin could stimulate α -secretase activity and shedding of non-amyloidogenic sAPP α by depleting FPP and inhibiting protein farnesylation in a murine neuroblastoma cell line (Pedrini et al., 2005). Furthermore, other *in vitro* studies have reported that treatment with lovastatin or simvastatin promotes intracellular accumulation of APP and A β , while causing a decrease of secreted A β , in a GGPP-dependent manner (Cole et al., 2005; Ostrowski et al., 2007; Zhou et al., 2008). Consistent with the findings from *in vitro* experiments, pharmacological or genetic inhibition of protein prenylation has been shown to reduce A β accumulation *in vivo*. For example, a high-dose simvastatin treatment in guinea pigs led to significant reduction of A β levels in the brain without affecting brain cholesterol levels (Fassbender et al., 2001). Similarly, atorvastatin reduced the brain A β by 38–52% with a minimal decrease in brain cholesterol levels in the APP/PS1 transgenic mouse model of AD (Petanceska et al., 2002). Recently, using genetically modified FTase and GGTase-I haplodeficient mice, we have demonstrated that reduction of protein prenylation (either farnesylation or geranylgeranylation) significantly decreases A β pathology in APP/PS1 transgenic mice (Cheng et al., 2013). We further showed that FTase haplodeficiency enhances non-amyloidogenic processing of APP and degradation of A β . These findings provide direct evidence that modulation of protein prenylation can modify the course of A β metabolism/deposition in the brain.

A growing body of evidence highlights the roles of small GTPase signaling pathways on amyloid pathology. For example, pitavastatin or atorvastatin treatment in APP-expressing rat primary cortical neurons resulted in concentration-dependent inhibition of A β , which was not mitigated by the co-administration of exogenous cholesterol (Hosaka et al., 2013). In the same study, immunoblot analysis of statin-treated primary cortical neurons showed not only a reduction in mature APP, but also a decrease in Thr668-phosphorylated APP. Phosphorylation of APP at Thr668 has been shown to enhance proteolysis by BACE1 in previous studies (Lee et al., 2003). A recent study demonstrated that neuronal exposure to oligomeric A β overactivates the Ras-MEK-ERK pathway which subsequently leads to hyperphosphorylation of APP at Thr668, establishing a vicious feed-forwarding cycle in sweAPP-expressing rat neuroblastoma B103 cells (Kirouac et al., 2017). Notably, both an MEK inhibitor and a farnesyltransferase inhibitor blocked this oligomeric A β -induced APP phosphorylation.

Similarly, the Rho/*Rho*-associated coiled-coil containing kinases (ROCK) pathway has also been shown to play a role in A β production. Constitutive activation of ROCK1 (CA-ROCK1) in murine N2a neuroblastoma cells overexpressing sweAPP was reported to diminish non-amyloidogenic α -secretase-type ectodomain shedding of APP, whereas

treatment on tau pathology and the role of Rho GTPases. Treatment with pitavastatin was found to decrease total and p-tau in primary neurons, and these changes were correlated with decreases in membrane-associated (prenylated) Rho GTPases including RhoA, Rac1 and Cdc42, and inactivation of glycogen synthase kinase-3 β (GSK-3 β) (Hamano et al., 2012). Notably, GSK-3 β is a major kinase driving tau phosphorylation thereby contributing to AD pathogenesis (Hooper, Killick, and Lovestone, 2008). The authors speculate that the hyperactivation of the RhoA/ROCK pathway leads to the overactivation of GSK-3 β which then contributes to tauopathy. The study also pointed out that these statin-associated changes in tau and p-tau levels were dose-dependent. Only a low-to-moderate dose of pitavastatin reduced tau and p-tau levels, whereas a high-dose of pitavastatin activated caspase 3, and increased caspase3-cleaved tau, which could lead to negative effects. This may explain some of the detrimental effects with a high dose of lovastatin observed in an earlier study (Meske et al., 2003). The link between RhoA/ROCK pathway and tauopathy has been further demonstrated in a recent study (Gentry et al., 2016), which showed that ROCK1 and ROCK2 were elevated in the brains of patients with non-AD tauopathies, progressive supranuclear palsy (PSP) and corticobasal degeneration (CBD). The study further showed that inhibition of Rho/ROCK signaling pathway significantly diminished total and p-tau levels in murine cortical neurons and in a *Drosophila* tauopathy model, through enhancing autophagy and reducing tau mRNA. The connection between isoprenoids and tau phosphorylation is supported by a study that reported a significant decrease in p-tau-to-total tau ratio in SH-SY5Y cells after N-BP-induced inhibition of FPPS (De Schutter et al., 2014). Furthermore, a high-throughput cell-based assay identified Ras GTPases as a putative pathway involved in tau phosphorylation (Cavallini et al., 2013). Intriguingly, Kirouac *et al.* reported that exposure to A β oligomers activated GSK-3 β and increased p-tau levels in parallel with the elevation of APP hyperphosphorylation at Thr668 through the activation of Ras-ERK in rat neuroblastoma B103 cells expressing sweAPP (Kirouac et al., 2017). This suggests that the activated small GTPases may serve as an intersection between amyloid and tau metabolisms. However, further investigations are required to unravel the exact molecular link between small GTPase pathways and tau phosphorylation.

Neuroinflammation: In parallel with misfolded aggregates of A β and hyperphosphorylated tau, emerging evidence indicates that microglia-mediated neuroinflammation plays an important role in AD pathogenesis (Akiyama et al., 2000; Heneka et al., 2015). The importance of microglia in AD is further underscored by recent discoveries that rare mutations in the triggering receptor expressed on myeloid cells 2 (TREM2), an innate immune receptor found in brain microglia, are associated with a significantly increased risk of AD (Colonna and Wang, 2016; Guerreiro et al., 2013; Jonsson et al., 2013). While the exact role of TREM2 in AD is being actively investigated (Jay, von Saucken, and Landreth, 2017; Ulrich et al., 2017; Yeh, Hansen, and Sheng, 2017), it is well established that aggregated A β leads to microglial activation by interacting with Toll-like receptors (TLRs) (Landreth and Reed-Geaghan, 2009; Su et al., 2016). In particular, it has been shown that TLR2 and TLR4 are required for fibrillar A β -stimulated microglial activation (Reed-Geaghan et al., 2009), and induce the release of proinflammatory cytokines such as IL-1 β , IL-6, and TNF α upon binding of aggregated A β (Liu et al., 2012; Smith et al., 2012). Under physiological conditions, increases in TLR2/TLR4 activation promote

microglial A β phagocytosis thereby facilitating A β clearance in the brain parenchyma. However, chronic exposure to toxic A β in AD results in the loss of the ability to suppress these immune responses thereby contributing to disease pathology (Wyss-Coray and Rogers, 2012). Emerging evidence suggest that small GTPases play an important role in TLR2 and TLR4 signal cascades. For example, the Rac1-dependent pathway is required for TLR2-mediated inflammatory signaling (Arbibe et al., 2000; Ruse and Knaus, 2006; Zolezzi and Inestrosa, 2017). In support of the role of isoprenoids/protein prenylation in inflammation, numerous studies have reported that statins exert anti-inflammatory activities, and these immunomodulatory properties of statins have been proposed to arise from the regulation of small GTPases (Cordle and Landreth, 2005; Liao and Laufs, 2009; Oesterle, Laufs, and Liao, 2017). Statin-mediated anti-inflammatory effects have been shown in various *in vitro* and *in vivo* models of AD. Treatment with simvastatin or lovastatin inhibited IL-1 β production in primary microglia and THP-1 monocytes after the exposure to fibrillar A β peptides through a cholesterol-independent process that is prevented by GGPP (Cordle and Landreth, 2005). This effect was mimicked by treatment with a GGTase-I inhibitor or direct inactivation of Rho GTPases with *Clostridium difficile* toxin. Simvastatin or lovastatin treatment also prevented fibrillar A β -induced cytokine production and astrocyte death in a human BBB model that consists of a cerebral microvascular endothelial cell monolayer co-cultured with astrocytes (Griffin et al., 2016). In animal studies, long-term treatment (>5 months) with atorvastatin or pitavastatin significantly reduced monocyte chemoattractant protein-1 (MCP-1)-positive neurons, microglial activation, and TNF- α in Tg2576 AD model mice (Kurata et al., 2012). Furthermore, we have shown that direct reduction of protein prenylation by a genetic approach attenuates neuroinflammation in AD mice (Cheng et al., 2013). Heterozygous deletion of FTase or GGTase-I ameliorates A β -induced neuroinflammation in cortical and hippocampal areas in the APP/PS1 double transgenic mouse model of AD, providing direct evidence for the roles of protein prenylation and their downstream pathways in neuroinflammation in AD (Cheng et al., 2013).

Synaptic plasticity and cognitive function: One of the key characteristics of AD brains is synaptic dysfunction demonstrated by a significant reduction of spine densities in neurons, consequently leading to cognitive impairment. It is well known that small GTPases play key roles in regulating synaptic plasticity under physiological conditions, and several lines of evidence suggest that the dysregulation of small GTPase signaling leads to synaptic dysfunction in AD (Hottman and Li, 2014; Stornetta and Zhu, 2010). Ras and Rab GTPases have been shown to regulate neurotransmitter receptor trafficking and recycling undergoing long-term potentiation in multiple studies (Ehlers, 2000; Stornetta and Zhu, 2010). The specific roles of Ras GTPases in neuronal plasticity and memory formation have been demonstrated in a number of studies (Ye and Carew, 2010). Rho GTPases, including Rac1, Cdc42, and RhoA, regulate neurite outgrowth and spine dynamics through their downstream effectors P21-activated kinases and ROCK (Briz et al., 2015; Haditsch et al., 2009; Ohashi et al., 2000). Tight spatiotemporal regulation of Rho GTPase signaling is critical in the neural circuit formation especially during neurodevelopment (Kimberly F. Tolia, 2011). Both hypo- and hyper-activation of these small GTPases and their downstream effectors have been shown to have detrimental effects on synaptic plasticity and cognitive functions, and have been implicated in learning and neurodegenerative disorders (Brambilla et al., 1997;

Haditsch et al., 2009; Zhao et al., 2006). In AD, a recent study showed that differences in dendritic spine morphology distinguish individuals who had or did not have clinical dementia and proposed that dendritic spine plasticity offers cognitive resilience that protects people with AD pathology from developing dementia (Boros et al., 2017). Notably, pharmacologic inhibition of ROCK1 and ROCK2 has been shown to affect dendritic spine morphology in hippocampal neurons (Swanger et al., 2015), suggesting that the Rho/ROCK pathway may play a critical role in dendritic spine remodeling and that ROCK inhibitors could potentially be used to modulate dendritic spine plasticity in AD.

The function of the small GTPases described above depends on proper cellular localization, which is regulated by protein prenylation. Studies using post mortem human brain samples have provided evidence for dysregulation of isoprenoids, and small GTPase pathways in AD brains (De Schutter et al., 2014; Eckert et al., 2009; Gartner et al., 1995; Ginsberg, 2011). Consistently, multiple animal studies reported that statin treatment rescued synaptic plasticity and/or cognitive function in mice with or without AD pathology (Costa et al., 2002; Li et al., 2006; Mans et al., 2010; Mans, McMahon, and Li, 2012; Métais et al., 2014; Ye and Carew, 2010; Zhao et al., 2016). Together, these findings suggest that synaptic dysfunction and memory impairment in AD may be attributable to abnormal upregulation of isoprenoids or protein prenylation.

However, statins inhibit both protein farnesylation and geranylgeranylation by inhibiting upstream mevalonate/isoprenoid biosynthesis. Therefore, it is difficult to dissect the roles of different prenylation pathways in AD pathogenesis. Using a genetic approach, we have demonstrated recently that reduction of FTase, but not GGTase-I, ameliorates spatial learning and memory as well as attenuates A β deposition and neuroinflammation in APP/PS1 mice (Cheng et al., 2013). In a more recent study, we have observed that systemic or forebrain neuron specific deficiency of GGTase-I reduces dendritic spine density and impairs synaptic/cognitive function in wild type mice (Hottman et al., 2018), corroborating the critical role of GGTase-I and protein geranylgeranylation in neuronal structure and function suggested by previous studies (Gao, Yu, and Zhou, 2016; Zhou et al., 2008). These findings suggest that farnesylated and geranylgeranylated proteins play distinctive roles in the pathogenesis of AD. While inhibition of geranylgeranylation might be beneficial under pathological conditions with overactivation or upregulation of GGTase-I, the chronic use of GGTase-I inhibitors could potentially cause adverse effects on synaptic/cognitive function. In contrast, reduction/inhibition of FTase produces cognitive benefits without detectable side effects, which may serve as a novel therapeutic target for AD. Whether these benefits found in animals can be translated to humans awaits further investigation.

Prenylomic Approaches and Their Applications in Alzheimer's Disease Research

Small Molecule Probes Used to Study Protein Prenylation

To improve understanding of protein prenylation, synthetic chemical probes have proven to be quite useful. Beyond the prenylation inhibitors discussed extensively above, a number of small molecule probes have proven useful in studying various aspect of protein prenylation.

Photoactivatable forms of isoprenoid diphosphates such as **DATFPGerOPP** and **BpGerOPP** (**Figure 10**) were developed first and allowed the isoprenoid binding sites on different prenyltransferases to be identified (Bikhtiyarov, Omer, and Allen, 1995; Edelstein and Distefano, 1997; Gaon, Turek, and Distefano, 1996; Gaon et al., 1996; Kuang et al., 1996; Turek-Etienne, Strickland, and Distefano, 2003; Turek, Gaon, and Distefano, 1996; Turek et al., 2001; Yokoyama, McGeedy, and Gelb, 1995). More recently, related probes have been used to study the active site of Icmt (**a-FactorDiazGer**) (Hahne et al., 2012). Photoactivatable probes such as **BiotinCysBpGer** have also been employed to study the interactions between prenylated proteins and their binding proteins (Alexander et al., 2009; Kale and Distefano, 2003; Kale et al., 2001). Examples of this include RhoGDI and PDE δ , two proteins that modulate the activity of prenylated proteins by binding directly to the isoprenoid group itself. These photoactive probes may prove to be useful in understanding the roles of prenylated proteins in Alzheimer's disease since they can be potentially used to reveal specific interactions between prenylated proteins and their binding partners that participate in cellular signaling. Isoprenoid analogues that contain structural modifications comprise a second class of small molecule probes. These compounds include structures with different alkene stereochemistry (**Z,E-FarOPP**) as well as aromatic or bulky substitutions (**BzAnalogOPP**) (Adams et al., 2010; Gibbs et al., 1999; Shao, Eummer, and Gibbs, 1999). They are of particular interest since their incorporation into prenylated proteins can either modulate or eliminate their activity. Fluorescent analogues such as **BdpyGerOPP** have also proved to be useful for monitoring the binding of isoprenoids to prenyltransferases and binding partners of prenylated proteins (Nguyen et al., 2007). Others such as **CouGerOPP** have also proven to be useful for the development of convenient assays to measure prenyltransferase activity (Dozier et al., 2014). In general, these modified isoprenoids should be useful for biochemical analysis of the interactions of various prenylated proteins and other cellular components as they relate to Alzheimer's disease. Small peptides equipped with fluorophores have been tremendously helpful in the development of enzyme assays for prenyltransferase activity as well as for monitoring the proteolytic activity of Ste24 and Rce1 that do not rely on radiolabeled substrates. Prenyltransferase activity is conveniently followed by monitoring the increase in dansyl group fluorescence that occurs upon farnesylation of the synthetic peptide **Dansyl-GCVIA** (Bond, Dolence, and Poulter, 1995; Pompliano, Gomez, and Anthony, 1992). Ste24 and Rce1 activity can be followed by measuring the increase in Abz fluorescence as a Dnp quencher is removed upon proteolysis of peptides such as **Abz-FWDPAC(far)VIK(Dnp)** (Hollander, Frommer, and Mallon, 2000). However, radiochemical methods are the method of choice for monitoring Icmt-catalyzed methylation. Cell penetrating peptides have also been used study localization and processing of prenylated molecules in cells (Ochocki, Wattenberg, and Distefano, 2010; Wollack et al., 2009; Wollack et al., 2010); such peptides are capable of entering astrocytic cell lines making them attractive tools for studying brain-related processes involving prenylated molecules. Prenylated peptides have also been used to prepare full-length forms of Ras for a range of experiments (Chen et al., 2010; Zhang et al., 2017). More recently, isoprenoid analogues functionalized with different "handles" including biotin (Nguyen et al., 2009), antigenic moieties (**AnGerOPP**) (Onono et al., 2010) and biorthogonal groups (**C15AzOPP** and **C15AlkOPP**) (Hosokawa et al., 2007; Rose et al., 2005) have been prepared and employed in pull-down and enrichment experiments designed to identify

prenylated proteins and measure how their levels change. Those containing biorthogonal azides and alkynes have been the most widely used since they can be metabolically incorporated in live cells and then linked to biotin or fluorophores for analysis. This last topic is discussed in more detail below.

Proteomic and Prenylomic Approaches

The growing interest in understanding the roles of prenylated proteins in biology has led to the development of proteomic strategies to characterize the members of the prenylome (prenylomics), the total complement of prenylated proteins. Earlier methods to identify prenylated proteins involved the use of radiolabeled forms of the isoprenoids, [³H]-FPP and [³H]-GGPP (Yalovsky, Loraine, and Gruissem, 1996), or [³H]-mevalonate (Laezza, Wolff, and Bifulco, 1997) and detection through fluorography. However, this approach is limited by its low sensitivity and exacerbated by its cost, arduousness, and the length of time required for the entire process. Gel-based separations were employed to improve sensitivity where protein mixtures are resolved in a gel and digested with trypsin. The peptides are then analyzed on a mass spectrometer to identify the prenylated proteins mapped through their peptide mass fingerprints (Cenedella, 1998).

In the past decade, higher throughput profiling of lipid-modified proteins including the prenylome have emerged as a powerful tool to identify the set of post-translationally lipidated proteins (Tate et al., 2015). This so-called chemical proteomics is a mass spectrometry-based technique that requires an analogue of the lipid functionalized with a bioorthogonal functional group, typically an azide or alkyne. These cell-penetrating probes are introduced into a biological system of interest wherein the cell's machinery metabolically incorporates them into the substrate proteins. The tagged proteins are then ligated via a bioorthogonal reaction (*e.g.* click reaction) with complementary chemical reporters or affinity handles that allow visualization or enrichment of these labeled proteins (**Figure 11A**). For visualization of labeled proteins, labeled lysates are subjected to derivatization with a fluorophore and resolved via SDS-PAGE. In-gel fluorescence is then performed where labeled proteins appear as bands owing to the fluorescence conferred by the conjugated fluorophore. For enrichment of the labeled proteins, biotin is commonly used to derivatize the labeled proteins followed by pulldown using avidin beads. The enriched proteins are then either digested on-bead or eluted, resolved in an SDS-PAGE gel and digested in-gel. The resulting peptides are then subjected to LC-MS/MS methods for proteomic analysis.

Metabolic labeling strategies for chemical proteomic profiling of prenylated proteins have relied on the use of functionalized isoprenoids to identify the prenylome of a given system of interest (**Figure 11B**). The first report using this approach employed an azide-modified farnesol (C15AzOH) into COS-1 cells followed by Staudinger ligation with triphenylphosphine-modified biotin and labeled prenylated proteins were enriched through avidin pulldown (Kho et al., 2004). This resulted in the identification of 17 bona fide prenylated proteins. A subsequent study used azide-functionalized geranylgeraniol (C20AzOH) to metabolically label proteins followed by copper-catalyzed azide-alkyne cycloaddition (click reaction) with an alkyne-modified fluorophore in lysate. Proteins were

then resolved through 2D gel electrophoresis and labeled protein bands were subjected to MS analysis (Chan et al., 2009). A total of 10 geranylgeranylated proteins were identified. However, the use of azide-modified isoprenoids followed by conjugation with an excess of alkyne-modified reporter presents significant background labeling problems (Speers and Cravatt, 2004). For this reason, azide-containing probes have been slowly replaced by alkyne-modified isoprenoids that usually result in lower nonspecific labeling. The first report on the use of alkyne-modified isoprenoids **C10AlkOH**, **C15AlkOH** and their diphosphate analogues, **C10AlkOPP** and **C15AlkOPP**, were evaluated in HeLa cells (DeGraw et al., 2010). Proteomic analysis using **C10AlkOH** has led to the identification of seven prenylated proteins in that study. Metabolic labeling with alkyne-functionalized farnesol (**C15AlkOH**) profiled more than 20 prenylated proteins in macrophages, which included an unannotated zinc-finger antiviral protein that was shown to be indispensable for host defense against viral infection (Charron et al., 2013). A combination of **C15AlkOPP** metabolic labeling and 2D gel electrophoresis identified 19 prenylated proteins that are sensitive to the presence of farnesyltransferase inhibitors (FTIs) (Palsuledesai et al., 2014). Recently, the prenylome of *Plasmodium falciparum*—the causal agent of malaria—was defined in two independent studies using **C15AlkOPP** (Suazo et al., 2016) and **C15AlkOH** (Gisselberg et al., 2017). It was found that this parasite has a limited set of prenylated proteins that are mainly involved in protein trafficking, and thus serves as a good target to develop parasite-specific FTIs. While the incorporation of these functionalized isoprenoids may be of concern in terms of altering protein function, it was recently reported that prenylated peptides using these probes are able to undergo the processes downstream of prenylation and that they retain signaling activity (Diaz-Rodriguez et al., 2017).

A plethora of proteomic studies on actual AD post-mortem tissue have been reported wherein differentially expressed proteins in AD brains compared to healthy controls have been identified (Brinkmalm et al., 2015; Korolainen et al., 2010). In particular, the use of high mass accuracy, label-free quantitative techniques (Andreev et al., 2012) and multiplexing strategies (Musunuri et al., 2014) have been successful. A number of proteins have been identified to be differentially expressed in AD but only a few were found common among the studies conducted (Moya-Alvarado et al., 2016). For example, GAPDH, a protein involved in glycolysis, has been consistently found to have altered levels in AD. Differential expression of some mitochondrial proteins and those that catalyze redox and phosphorylation processes such as peroxiredoxins and kinases, respectively, were also observed. Overall, it has been suggested that proteins associated with the oxidation and phosphorylation of glycolytic intermediates and processes in the mitochondria are drivers of the early progression of AD (Moya-Alvarado *et al.*, 2016). Recently, quantitative label-free proteomics combined with systems biology has allowed networks of proteins to be defined that are associated with the neuropathology of AD with high specificity (Seyfried et al., 2017). Both the proteome and transcriptome analysis converged on networks involved in inflammation and glial dysfunction and thus are implicated in the etiology of AD. These results reflect the significance of non-neuronal drivers in the pathology of AD.

From the proteomic studies conducted, a number of known prenylated proteins were found to have altered expression in AD brain tissues compared to the healthy controls. For

example, decreased levels of 2',3'-cyclic nucleotide-3'-phosphodiesterase (CNP) in the late-myelinating region (frontal cortex) of AD patient brains were determined using 2D gel electrophoresis and MALDI-MS (Vikolinský et al., 2001). It was earlier suggested that the presence of the prenyl group is essential for the interaction of CNP with the hydrophobic components of myelin (De Angelis and Braun, 1996). The same proteomic technique led to the identification of UCHL1 as a major target of oxidative damage in AD (Castegna et al., 2002; Choi et al., 2004). Although it was shown that the farnesylation of UCHL1 is not involved in its association to neuronal membranes (Bishop et al., 2014), inhibition of this process using farnesyltransferase inhibitors (FTIs) reduced the accumulation and neurotoxicity of α -synuclein-transfected cell cultures (Liu et al., 2009). Hence, targeting the UCHL1 farnesylation may be an avenue as a therapeutic strategy for the treatment of Parkinson's disease and other related synucleinopathies such as AD. Label-free quantitative LC-MS proteomic experiments have shown that lamin-B, Rap-2A, Rap-2B and NAP1L1 are increased in AD compared to normally aged human brains (Andreev *et al.*, 2012). The same approach combined with systems biology identified that the levels of RHOB and GNAI1, a G protein subunit that is potentially prenylated (Palsuledesai et al., 2014), were decreased exclusively in the symptomatic stage of AD (Seyfried et al., 2017). Furthermore, a quantitative proteomic study conducted on APP-expressing neuronal-like B103 cells that recapitulate the AD phenotype has found increased levels of the prenylated proteins CNP and Di-Ras (Chaput et al., 2012). Taken together, these studies demonstrate that prenylated proteins indeed have potential implications in AD and that proteomic methods could be an advantageous technique to analyze AD brain samples and models. Thus, proteomic methods such as chemical proteomic profiling may be useful for specifically identifying prenylated proteins involved in AD pathogenesis.

While the above mentioned proteomic analyses have been useful in identifying putative prenylated proteins involved in AD, they do not establish that the prenylated form is relevant nor do they allow changes in the levels of prenylation to be studied since lipid-modified peptides themselves produced upon tryptic digestion of whole proteins are rarely identified in proteomic experiments. In contrast, metabolic labeling studies with probes such as **C15AlkOPP** allow enrichment of the actual prenylated forms of proteins since the enrichment process itself relies on the presence of the modified isoprenoid. A recent report employed the use of **C15AlkOH** to image and quantify levels of prenylated proteins in astrocytes using confocal microscopy and flow cytometry (Palsuledesai et al., 2016), suggesting that metabolic labeling could be used to profile the prenylome in AD cell culture models. It should also be noted that metabolic labeling has been used to incorporate probes containing bioorthogonal functionality in whole animal models raising the possibility that similar experiments could be used to identify and study prenylated proteins involved in AD (Baskin et al., 2007). Overall, further efforts are needed to explore the role of prenylated proteins in AD using prenylomic strategies employing these new probes and tools.

Concluding Remarks/Perspectives

Understanding the biological role of isoprenoids and protein prenylation is of central importance from both a basic scientific and a clinical perspective. Fundamental scientific discoveries often provide critical insights that catalyze progress in the clinic. Remarkable

advances have been achieved in the last century in understanding the regulation of isoprenoid and cholesterol metabolism in the peripheral organs, and successful drugs (e.g., statins and N-BPs) have been developed to treat cardiovascular and bone diseases, respectively. The recognition that isoprenoids can modify the structure and function of many important proteins involved in human diseases has invigorated the prenylation field with the goal of developing effective therapies for a range of disorders, from cancer, premature aging, infectious disease, to neurodegenerative diseases including Alzheimer's disease.

To reach this goal in the context of Alzheimer's disease, advances in several areas must occur. First, while statins that cross the blood brain barrier are available, bisphosphonates and related prodrugs that are able to do this have not yet been developed. More work needs to be done with prenyltransferase inhibitors to increase their brain bioavailability as well. Next, more global and systematic data regarding protein prenylation in the brain must be obtained. This means that the prenylome within the brain must be defined. The new developments in metabolic labeling described herein should be instrumental in accomplishing this goal. In concert with genetically modified animal models, in which prenyltransferase activities can be manipulated in a tissue specific manner coupled with expression of disease-specific genes, these tools should provide unique *in vivo* model systems to identify disease-specific prenylated proteins from the entire prenylome. However, the identification of specific prenylated proteins in the brain must be coupled with methods that allow both changes in prenylation levels and overall protein expression to be measured. For this, new advances in quantitative mass spectrometric methods should be particularly helpful. Ultimately, applying these methods to brain tissue samples from humans with a spectrum of cognition from normal to Alzheimer's dementia should enable a quantitative proteome-wide analysis of prenylated proteins during the progression of the disease. Such data could reveal the underlying roles of prenylated proteins in the pathogenesis of Alzheimer's disease and facilitate the identification of new targets for developing novel therapeutic interventions against Alzheimer's disease. Finally, a better understanding of which prenylated proteins are critical for pathogenesis will catalyze efforts to develop inhibitors that interfere with specific prenylated proteins. Such agents would be inherently more selective than the current generation of prenyltransferase inhibitors that act on a global level. Overall, it is clear that the intersection of research in Alzheimer's disease and protein prenylation is an exciting and accelerating area that holds great promise for therapeutic development.

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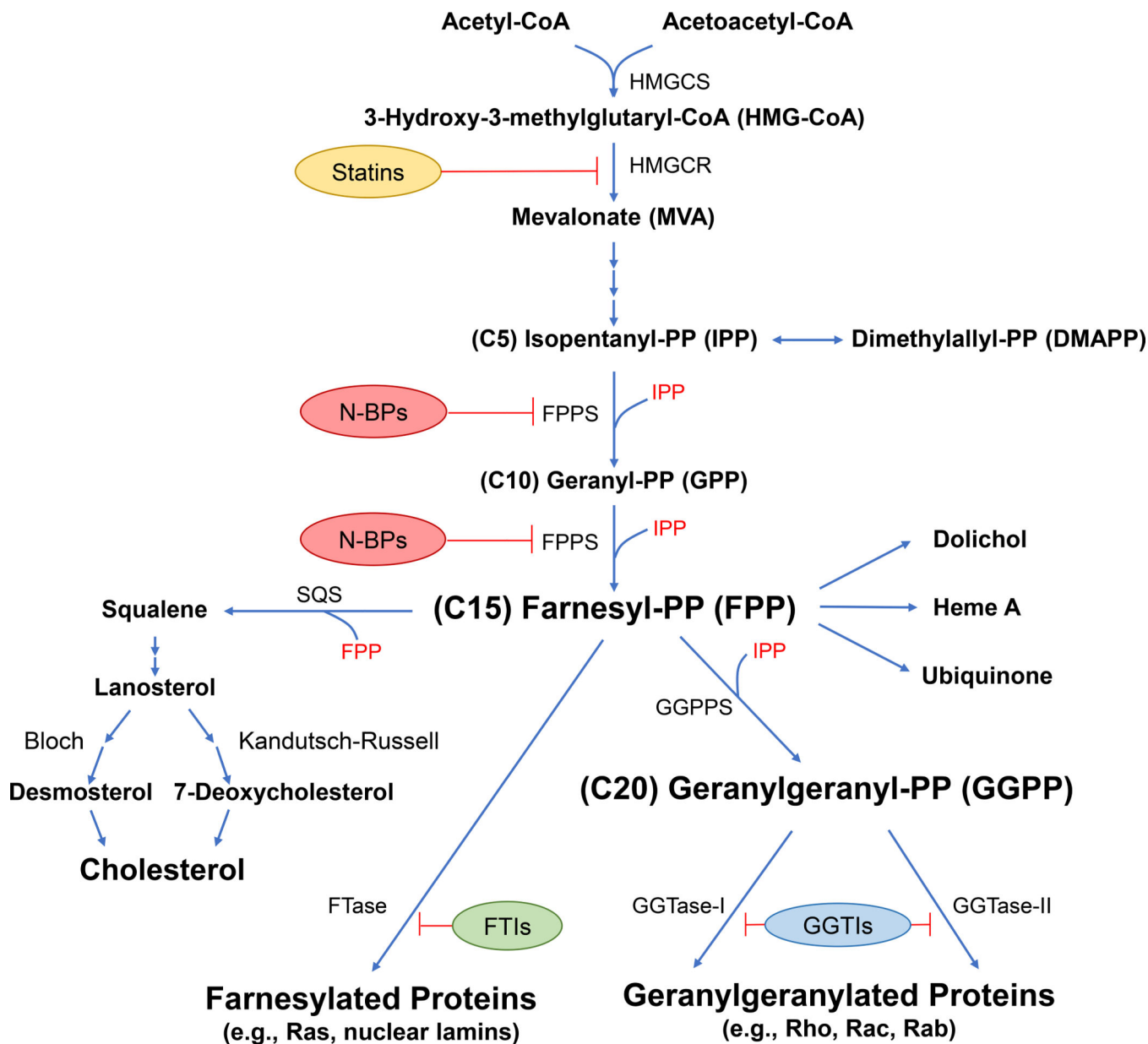


Figure 1. The mevalonate-isoprenoid-cholesterol pathway and pharmacological agents that inhibit the synthesis of key intermediates.

HMGCS: 3-hydroxy-3-methylglutaryl-CoA synthase; HMGCR: 3-hydroxy-3-methylglutaryl-CoA reductase; FPPS: Farnesyl pyrophosphate synthase; N-BPs: Nitrogen-containing bisphosphonates; SQS: Squalene synthase; GGPPS: Geranylgeranyl pyrophosphate synthase; FTase: Farnesyltransferase; GGTase-I/II:

Geranylgeranyltransferase-I/II; FTIs: Farnesyltransferase inhibitors; GGTIs:

Geranylgeranyltransferase inhibitors. A color version of the figure is available online.

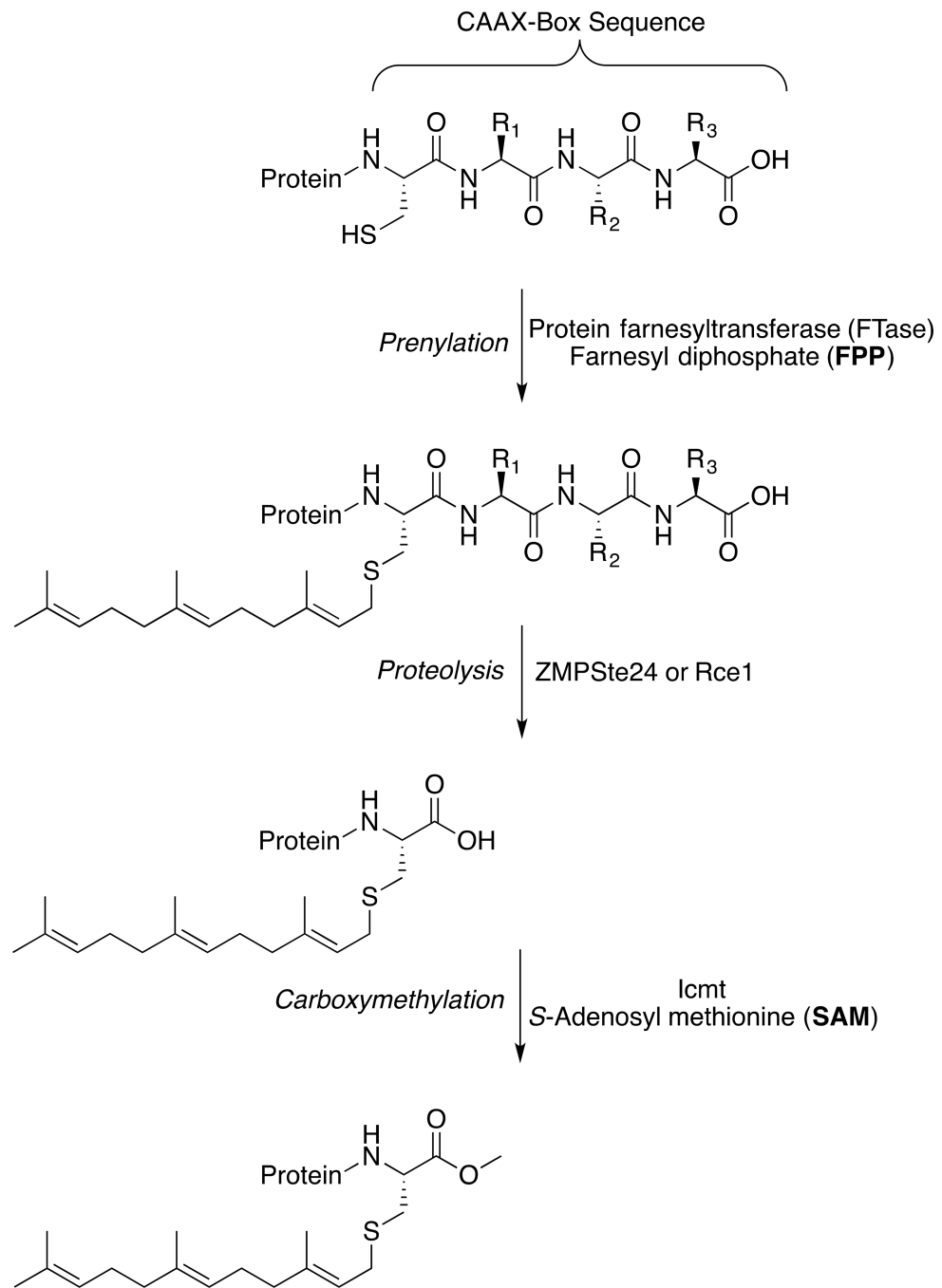


Figure 2. The three-step process of protein prenylation illustrated for farnesylation. As noted in the text, the process is similar for geranylgeranylation of proteins containing CAAX-box sequences prenylated by GGTase-I.

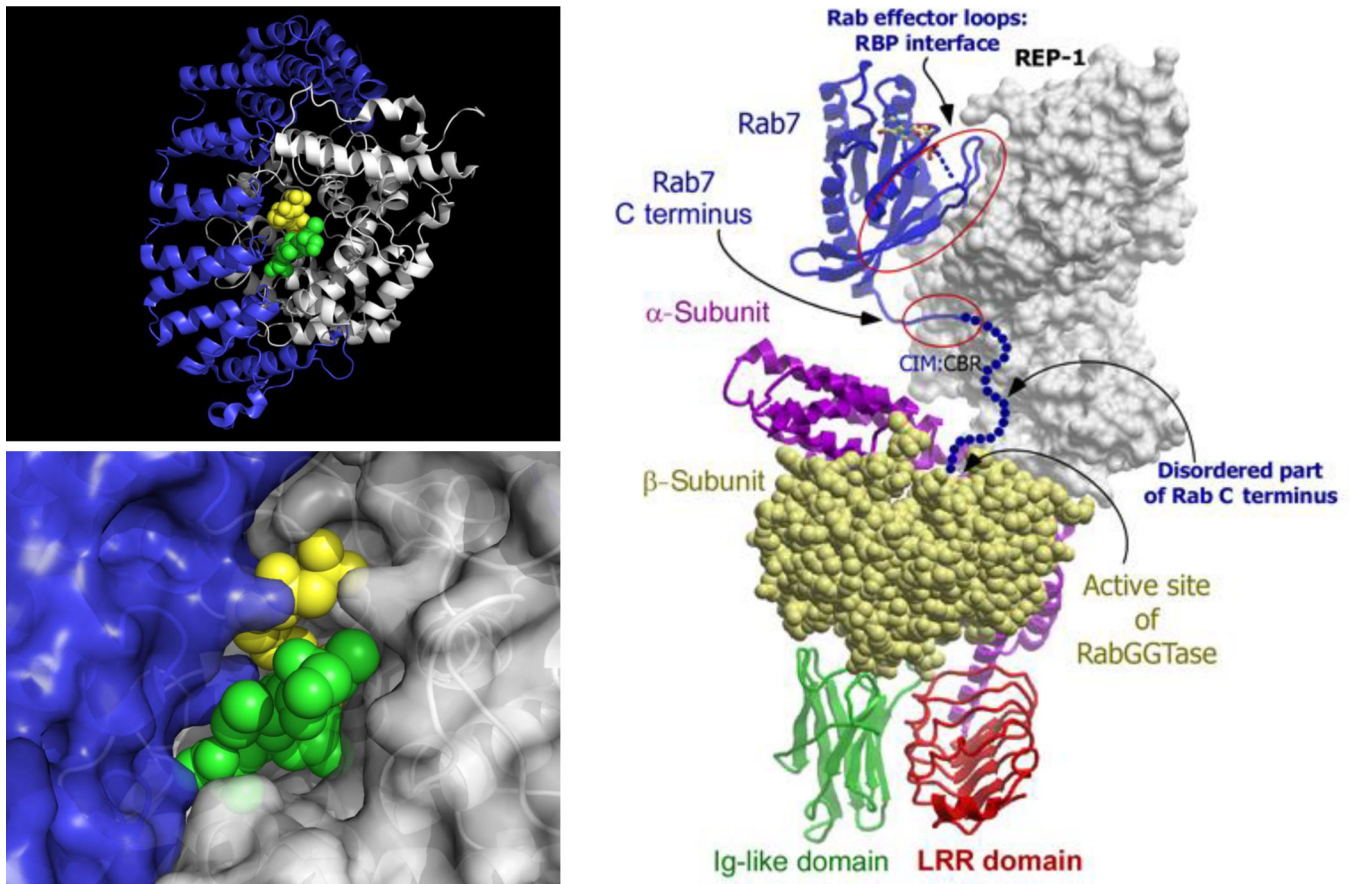


Figure 3. Key structural features of prenyltransferases.

Top Left: Overall $\alpha\beta$ fold for prenyltransferases shown using the structure of FTase (pdb: 1TN8). Bottom Left: Active site structure of FTase showing envelopment of substrates.

Color scheme: α subunit (blue), β subunit (white), FPP (yellow), peptide GCVLS (green).

Right: Model for the structure of GGTase-II showing how Rab7 is presented to the transferase by REP-1. Adapted from Guo et al. (2008) with permission. A color version of the figure is available online.

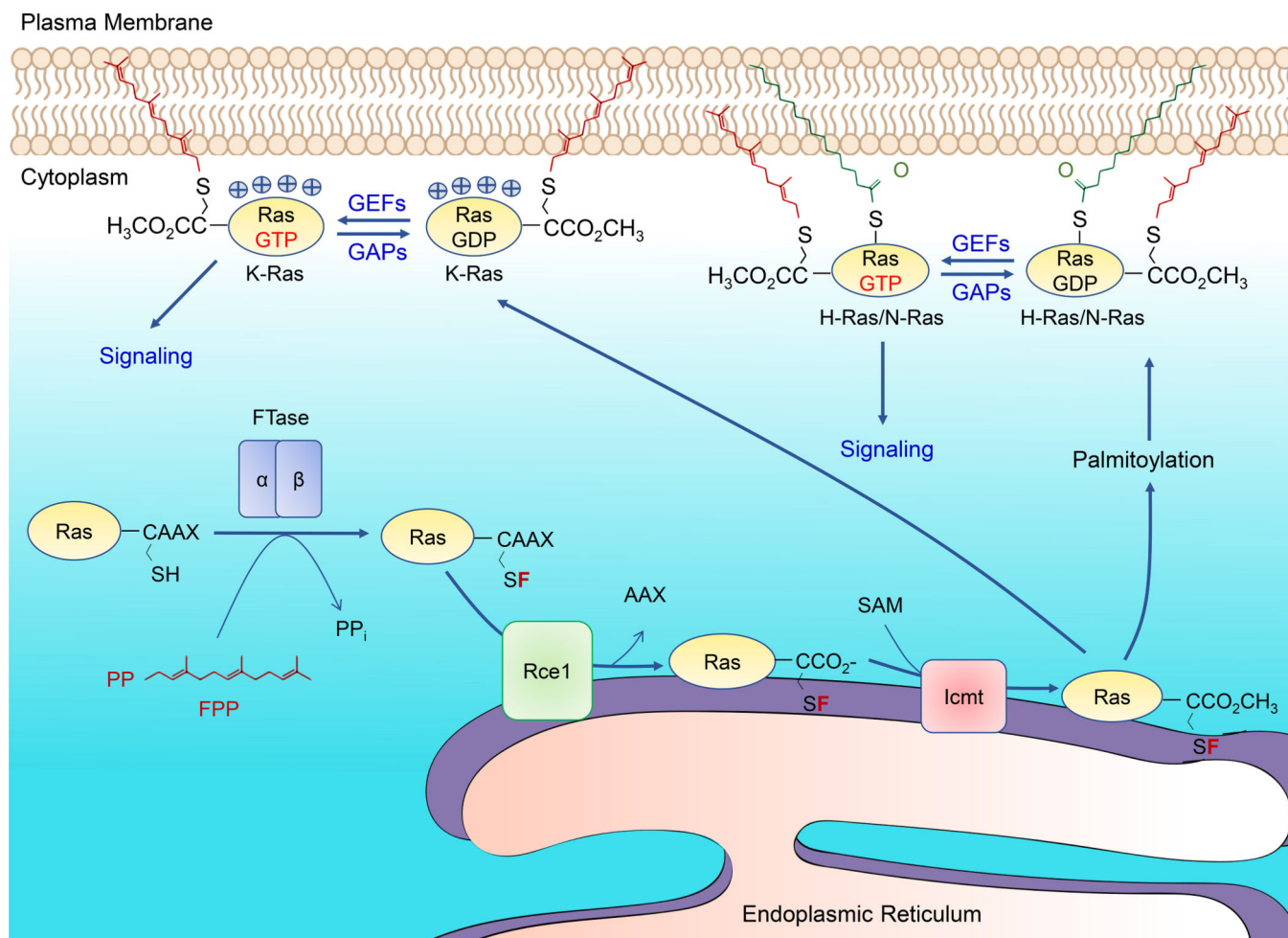


Figure 4. Ras farnesylation and membrane trafficking.

Farnesyltransferase (FTase) adds farnesyl group to the cysteine residue of the CAAX motif of Ras proteins. The following modifications occur on the cytosolic surface of the ER: proteolysis of the terminal three amino acid residues of the CAAX motif by Ras-converting CAAX endopeptidase 1 (Rce1), then methylation by isoprenylcysteine carboxylmethyltransferase (Icmt). The fully processed prenylated Ras proteins are then either directly trafficked to the membrane (e.g. K-Ras) or further undergo palmitoylation at the Golgi complex prior to the membrane trafficking (e.g. N/H-Ras). FPP: farnesyl pyrophosphate; F: farnesyl; SAM: S-adenosyl-homocysteine. A color version of the figure is available online.

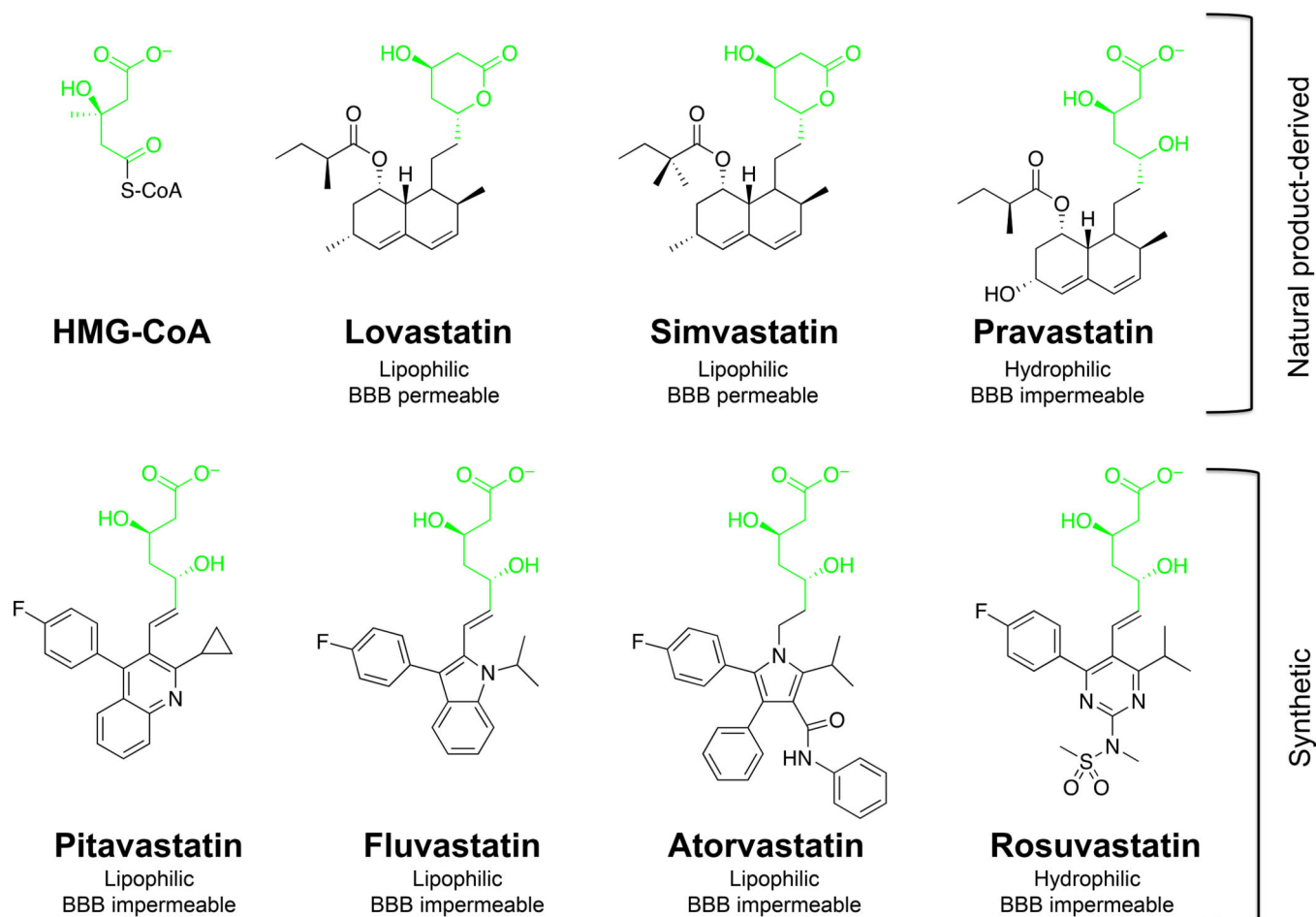


Figure 5. Structure of statins.

The structure in green indicates the HMG-CoA like unit that binds to the enzyme HMG-CoA reductase. A color version of the figure is available online.

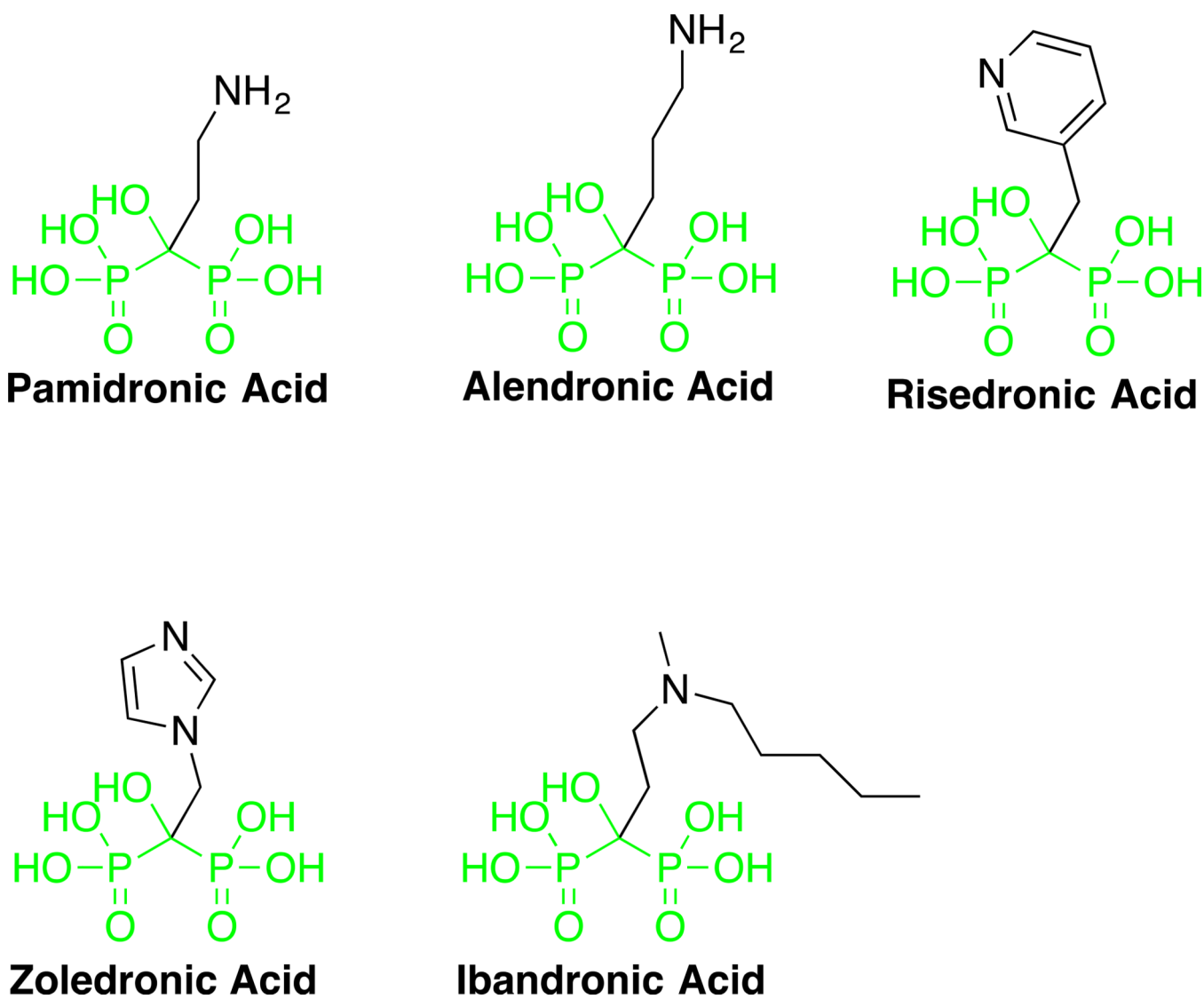


Figure 6. Structure of N-BPs.

Structure of N-BPs. The structure in green shows the conserved bisphosphonate moiety present in all approved drugs. A color version of the figure is available online.

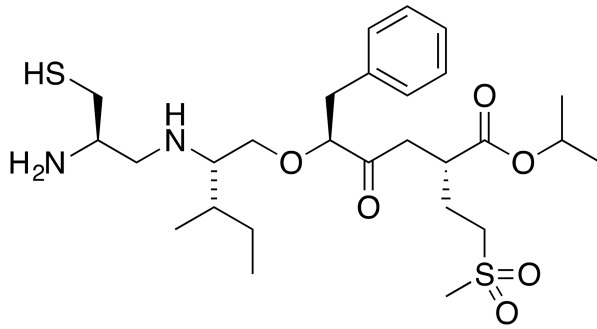
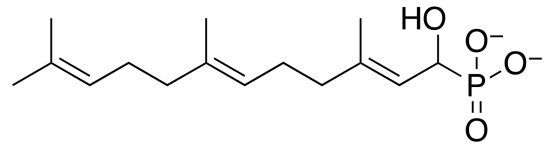
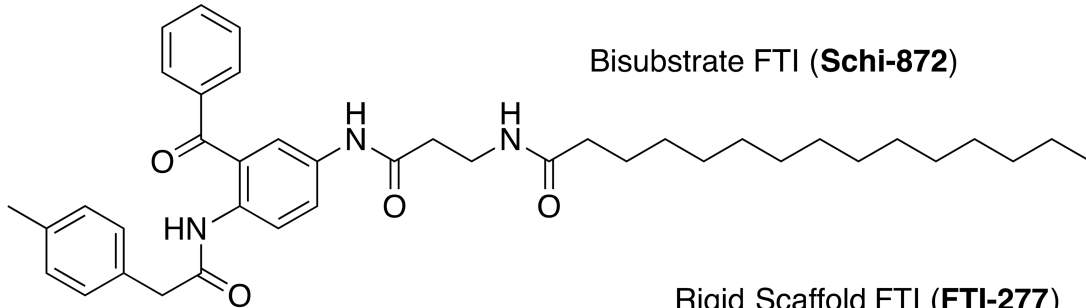
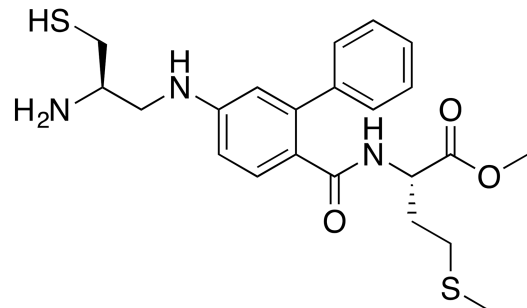
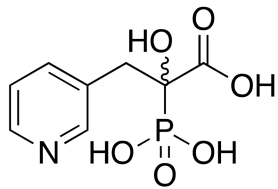
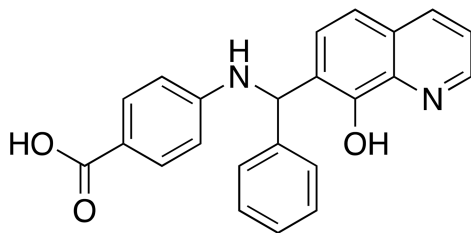
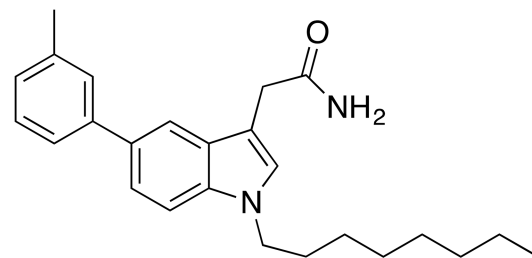
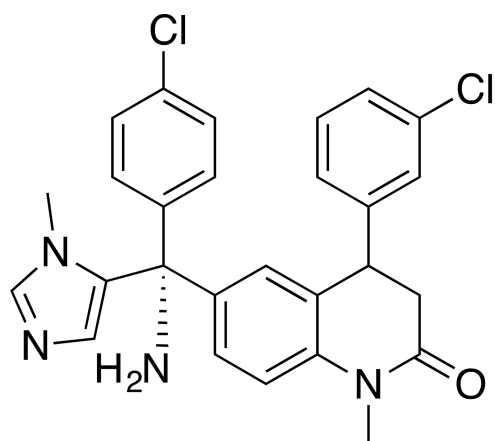
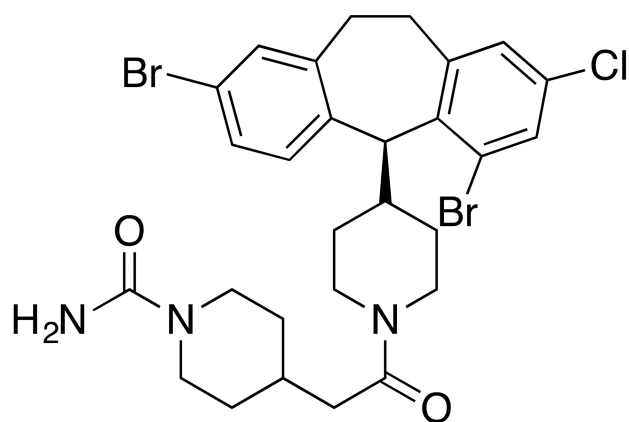
Peptidomimetic FTI (**L-744,832**)Isoprenoid Analogue FTI (**HFP**)Bisubstrate FTI (**Schi-872**)Rigid Scaffold FTI (**FTI-277**)GGTase-II Inhibitor (**3-PEHPC**)Rce1 Inhibitor (**NSC1011**)Icmt Inhibitor (**Cysmethynil**)

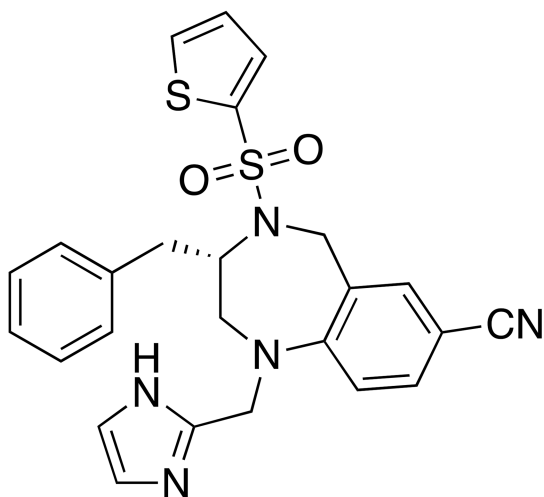
Figure 7.
Inhibitors of enzymes involved in protein prenylation.

**Tipifarnib**IC₅₀: FTase - 0.9 nM

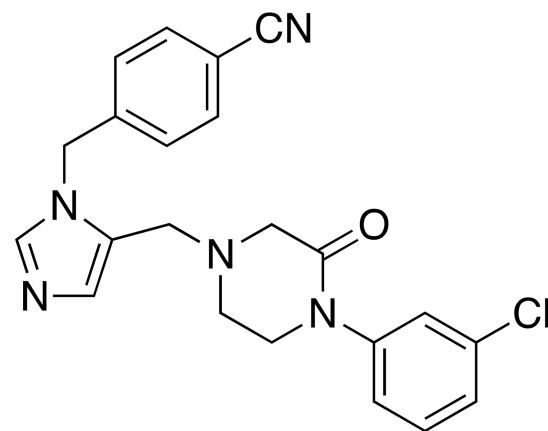
GGTase-I - >50 μM

**Lonafarnib**IC₅₀: FTase - 1.9 nM

GGTase-I - >50 μM

**BMS-214662**IC₅₀: FTase - 1.4 nM

GGTase-I - >1 μM

**L-778,123**IC₅₀: FTase - 2 nM

GGTase-I - 98 nM

Figure 8.

Structures of the four FTIs that have been studied in human clinical trials.

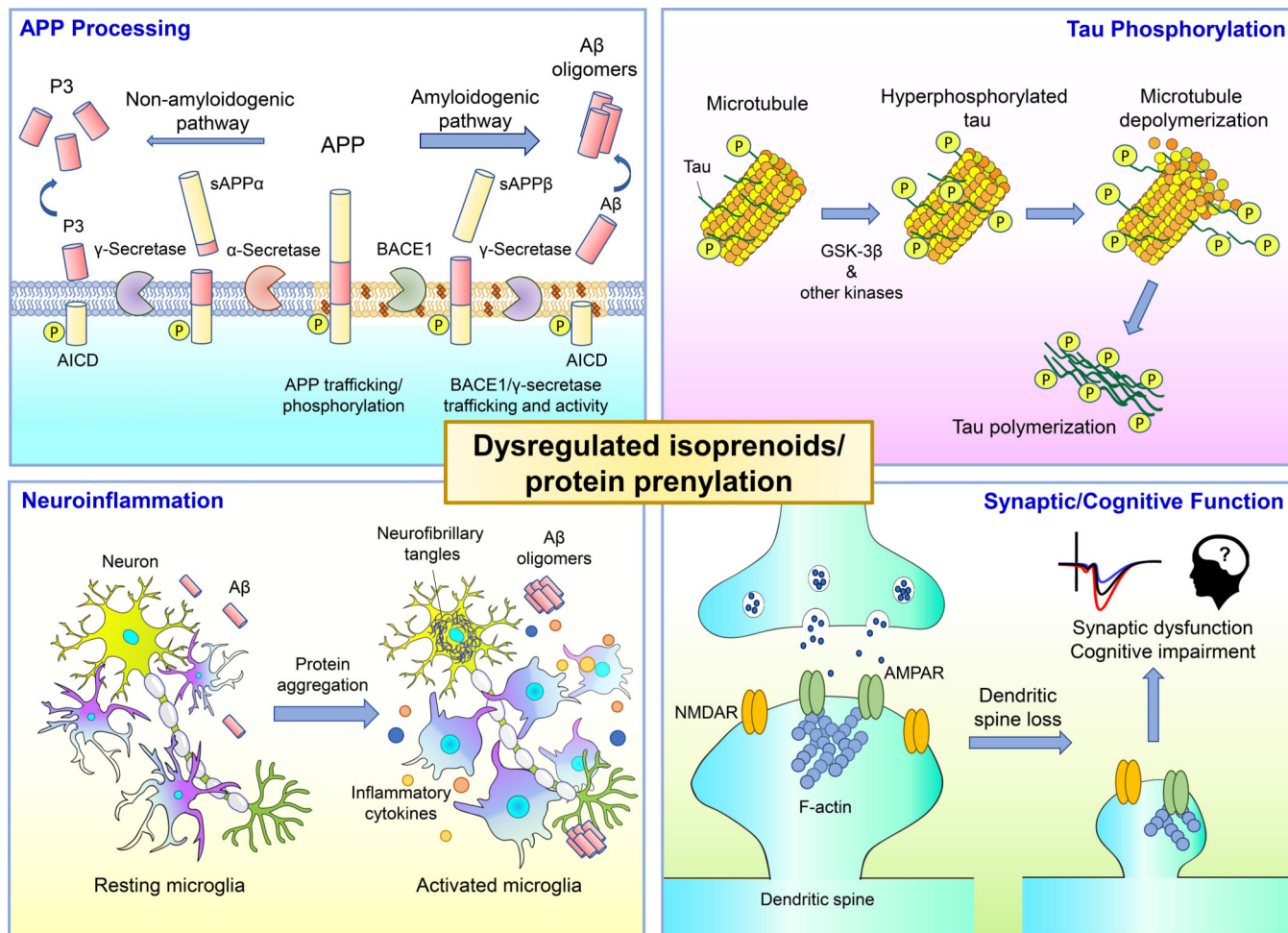


Figure 9. Implications of dysregulated isoprenoid synthesis and protein prenylation in processes pertinent to the pathogenesis of Alzheimer's disease.

Dysregulations in isoprenoid biosynthesis and the prenylation of small GTPases have been linked to (i) alteration of APP trafficking/processing and the activity/localization of the secretases; (ii) increase in tau phosphorylation through the activation of GSK-3 β and other kinases; (iii) microglial activation contributing to enhanced neuroinflammation; (iv) dendritic/synaptic loss leading to cognitive impairment. APP: amyloid- β precursor protein; A β : amyloid- β peptide; BACE1: β -secretase 1; sAPP α : α -secretase-cleaved soluble fragment of APP; sAPP β : β -secretase-cleaved soluble fragment of APP; AICD: APP intracellular domain; P3: non-amyloidogenic peptide (~3 kDa); GSK-3 β : glycogen synthase kinase-3 β ; NMDAR: N-methyl-D-aspartate receptor; AMPAR: α -amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid receptor. A color version of the figure is available online.

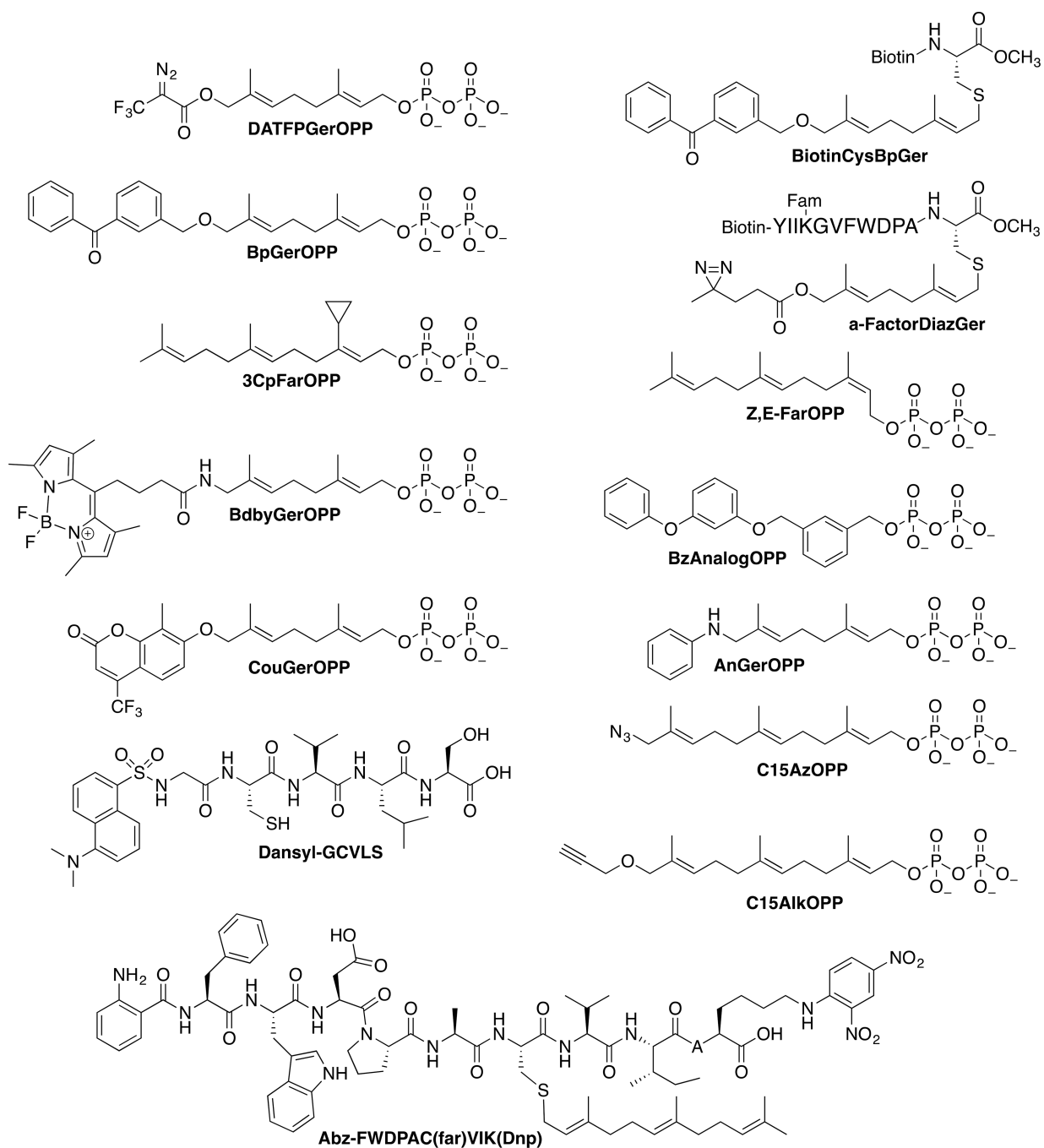


Figure 10.
Small molecule probes used for studying protein prenylation.

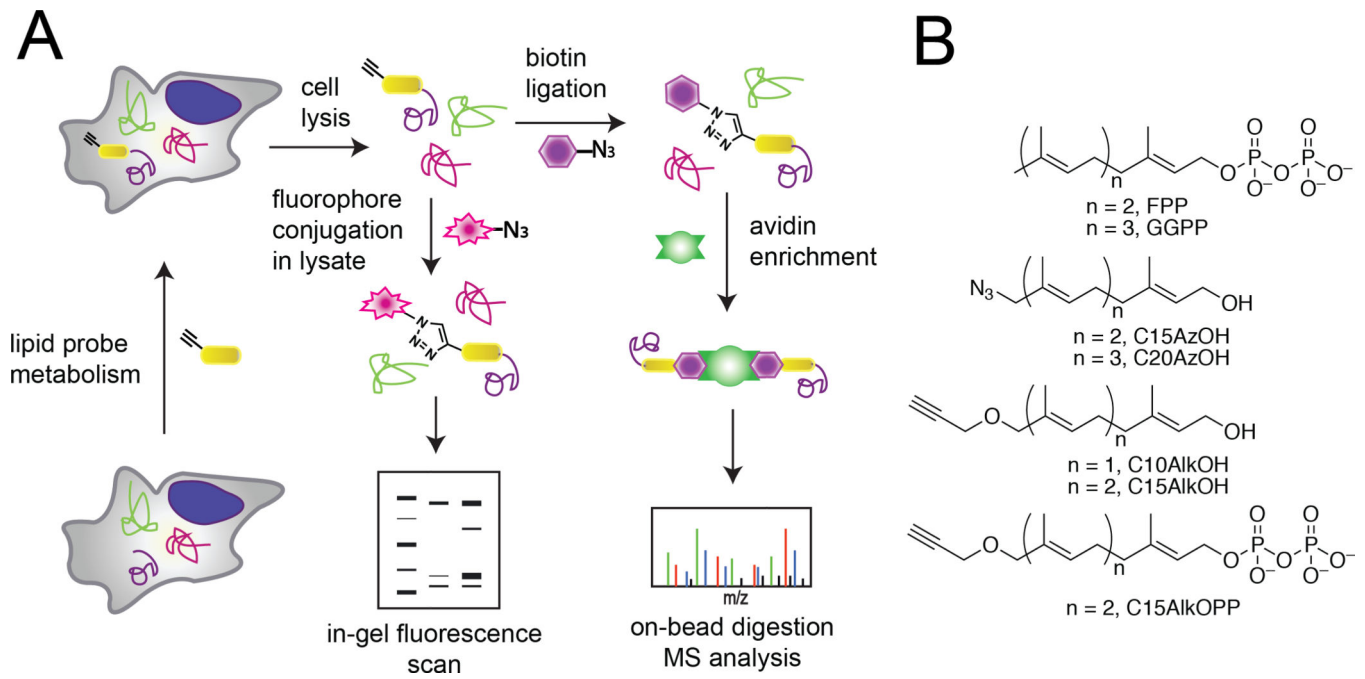


Figure 11. A general chemical proteomic approach to label and enrich proteins of interest via click reaction (A) and the isoprenoid probes used to profile prenylated proteins (B).

A color version of the figure is available online.