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## Roles of Amyloid $\beta$ -Peptide-Associated Oxidative Stress and Brain Protein Modifications in the Pathogenesis of Alzheimer's Disease and Mild Cognitive Impairment

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### Abstract

Oxidative stress has been implicated to play a crucial role in the pathogenesis of a number of diseases, including neurodegenerative disorders, cancer, and ischemia just to name a few. Alzheimer's disease (AD) is an age-related neurodegenerative disorder that is recognized as the most common form of dementia. AD is histopathologically characterized by the presence of extracellular amyloid plaques, intracellular neurofibrillary tangles, the presence of oligomers of amyloid  $\beta$ -peptide ( $A\beta$ ), and synapse loss. In this review we discuss the role of  $A\beta$ -peptide in the pathogenesis of AD and also the use of redox proteomics to identify oxidatively modified brain proteins in AD and mild cognitive impairment (MCI). In addition, redox proteomics studies in *in vivo* models of AD centered around human  $A\beta(1-42)$  are discussed.

### Keywords

Alzheimer's disease; mild cognitive impairment; oxidative stress; amyloid  $\beta$ -peptide; redox proteomics

### Introduction

Oxidative stress has been implicated to play a crucial role in the pathogenesis of a number of diseases including neurodegenerative disorders, cancer, ischemia [1]. Among all the body organs, brain is particularly vulnerable to oxidative damage because of its high utilization of oxygen, increased levels of polyunsaturated fatty acid (that are readily attacked by free radicals), and relatively high levels of redox transition metal ions; in addition, brain has relatively low levels of antioxidants [2-5]. The presence of iron ion in an oxygen-rich environment can further lead to enhanced production of hydroxyl free radicals and ultimately lead to a cascade of oxidative events.

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Oxidative stress occurs due to an imbalance in the pro-oxidants and anti-oxidant levels. Reactive oxygen species (ROS) and reactive nitrogen species (RNS) are highly reactive with biomolecules including proteins, lipids, carbohydrate, DNA and RNA [6]. Oxidative damage to these moieties lead to cellular dysfunctions [1,2,5,7-9]. The markers of oxidative stress that are commonly used in biological samples include: protein carbonyls and 3-nitrotyrosine for protein oxidation; thiobarbituric acid reactive substance (TBARS), free fatty acid release, iso- and neuroprostane formation, 2-propen-1-al (acrolein) and 4-hydroxy-2-trans-nonenal (HNE) for lipid peroxidation; advanced glycation end products for carbohydrates; and 8-OH-2'-deoxyguanosine and 8-OH-guanosine and other oxidized bases, and altered DNA repair mechanisms for DNA and RNA oxidation. Among the earliest of these changes following an oxidative insult are increased levels of toxic carbonyls, 3-nitrotyrosine (3-NT), and HNE [2, 4,7,10-13].

Protein carbonyl groups are generated by direct oxidation of certain amino acid side chains (i.e., Lys, Arg, Pro, Thr, and His), peptide backbone scission, Michael addition reactions of His, Lys, and Cys residues with products of lipid peroxidation, or glycol-oxidation of Lys amino groups [6,14-17]. Protein carbonyls are stable and hence are widely used as markers to assess the extent of oxidation of proteins both in *in vivo* and *in vitro* conditions [14,15,17,18]. The levels of protein carbonyls can be determined experimentally by derivatization of the carbonyl groups with 2,4-dinitrophenylhydrazine (DNPH), followed by spectroscopic or immunochemical detection of the resulting hydrazone product [6,15,19].

In addition to direct effects, oxidative stress could also stimulate additional damage in brain via the overexpression of inducible nitric oxide synthase (NOS: iNOS) and the action of constitutive neuronal NOS (nNOS) that increase the production of nitric oxide (NO $\cdot$ ) via the catalytic conversion of arginine to citrulline. Nitric oxide reacts with superoxide anion (O $_2^{\cdot-}$ ) at a diffusion controlled rate to produce peroxynitrite (ONOO $^-$ ). Peroxynitrite is highly reactive with a half-life of less than a second, and can undergo a variety of chemical reactions depending upon its cellular environment, the presence of CO $_2$ , and the availability of reactive targets forming modifications such as 3-NT (Figure 1) [20,21]. 3-Nitrotyrosine is a covalent protein modification that has been used as a marker of nitrosative stress under in a variety of disease conditions [22,23]. Peroxynitrite can also react with sulfhydryl compounds intracellularly due to the high concentration of free thiols within the cell [24]. Sulfhydryls can also react via S-nitrosylation with NO to form a nitrosothiol (RSNO). Cysteine residues are preferentially nitrosylated due to favorable reaction kinetics [25,26].

Protein oxidation could lead to aggregation or dimerization of proteins; in addition, protein oxidation can also lead to unfolding or conformational changes in the protein thereby exposing more hydrophobic residues to an aqueous environment. This exposure may lead to loss of structural or functional activity and protein aggregation and subsequent accumulation of the oxidized proteins as cytoplasmic inclusions, such as tau aggregation in the form of tangles and amyloid- $\beta$  aggregation as senile plaques, as observed in Alzheimer's disease (AD) [27,28]. The accumulation of oxidatively modified proteins may disrupt cellular functions by alterations in protein expression and gene regulation, protein turnover, modulation of cell signaling, induction of apoptosis and necrosis, etc., which suggest that protein oxidation could have both physiological and pathological significance [6,29-31]. In our laboratory, we used redox proteomics analyses to identify specific oxidatively modified brain proteins carbonylated proteins in neurodegenerative diseases and models thereof [10,12,13,32-41].

Mild cognitive impairment is considered an intermediate phase between normal aging and Alzheimer's disease. Some researchers believe that MCI is in fact the earliest form of AD [42]. Persons with MCI have cognitive complaint, decline in cognition compared to previous years, and most notably no signs of dementia. Additionally, activities of daily living are not

affected. These characteristics require informant confirmation for diagnosis of MCI. Accurate diagnosis can only be confirmed by medical examination to establish a level of cognitive decline [43-45]. Pathologically, MCI has also been characterized using magnetic resonance imaging technology to show measurable atrophy in the hippocampus and entorhinal cortex [46,47]. Alzheimer's disease patients have considerable neurodegeneration in these aforementioned areas. Since the hippocampus is the region of the brain primarily responsible for processing of memory, atrophy in this brain region is consistent with memory loss in AD and MCI.

An age-related neurodegenerative disorder, AD is recognized as the most common form of dementia. AD is clinically associated with cognitive impairment, loss of language and motor skills, and changes in the behavior. AD is pathologically characterized by the presence of extracellular senile plaques, which consist of a core of A $\beta$ , and intracellular neurofibrillary tangles (NFT), and loss of synaptic connections within entorhinal cortex and progressing into the hippocampus and cortex. NFTs are composed of paired helical filaments (PHF) that consist of aggregates of the hyperphosphorylated microtubule associated protein tau [48], while senile plaques (SP) are rich in A $\beta$  [49].

In this paper, we review the involvement of A $\beta$  and other sources of oxidative stress in AD brain and the use of redox proteomics to identify oxidatively modified brain proteins in AD and MCI. New insights into potential oxidative mechanisms underlying molecular processes in these disorders and progression from MCI to AD have emerged.

## Amyloid $\beta$ -peptide

A $\beta$ , a 40-42 amino acid peptide, is derived by proteolytic cleavage of an integral membrane protein known as amyloid precursor protein (APP) by the action of beta- and gamma-secretases. A $\beta$ (1-40) and A $\beta$ (1-42) constitute the majority of the A $\beta$  peptide found in human brain and has been considered to play a role in the development and progression of AD [49]. A $\beta$ (1-42) is the more toxic of these species both *in vitro* and *in vivo*. Further, a number of studies suggest that the small oligomers of A $\beta$  are the actual toxic species of this peptide rather than A $\beta$  fibrils [50-53]. In addition, genetic mutations in genes for APP or presenilin-1 or presenilin-2, which lead to familial AD, have been reported to increase the production of A $\beta$ (1-42) and, consequently, to early onset of AD [49]. Presenilin-1 and presenilin-2 comprise the catalytic element of gamma-secretase [54]. Another critical component of gamma-secretase is presenilin enhancer 2 (Pen-2). Pen-2 binds to presenilins and subsequently enhances gamma-secretase activity, thereby accumulating high levels of toxic A $\beta$  (1-42) [55,56].

A $\beta$  (1-42) has a critical methionine residue at position 35, which is believed to be associated with the toxicity of A $\beta$  peptide [57-61]. Oxidation of the Met<sup>35</sup> produces methionine sulfoxide (MetO) or through further irreversible oxidation, methionine sulfone (Figure 2) [62]. Methionine sulfoxide can be reduced back to methionine by the enzyme, methionine sulfoxide reductase. This stereospecific reaction is facilitated by thioredoxin and is NADPH-driven [63]. Methionine sulfoxide modulates oxidative stress and neurotoxic properties of A $\beta$  (1-42), and studies have shown the activity of methionine sulfoxide reductase is reduced in AD brain [64,65].

This Met35 residue has been shown to be critical for A $\beta$ (1-42) toxicity and oxidative stress [57]. The secondary structure of A $\beta$ (1-42), which is helical as a small oligomer in membrane lipid bilayers, contributes to the oxidative stress and neurotoxicity of this peptide [66]. When Ile31 of A $\beta$ (1-42) is substituted by the helix-breaking amino acid, proline, in the "i + 4"  $\alpha$ -helix conformation, no protein oxidation occurs [66]. A sulfuranyl radical (MetS<sup>•+</sup>) results as the lone pair of electrons on the S atom undergo a one-electron oxidation (Figure 3) [57,67, 68]. The sulfuranyl radical can initiate free radical chain reactions with allylic H-atoms on

unsaturated acyl chains of lipids until a termination step is reached. Sulfuranyl radicals can react with molecular oxygen to produce sulfoxide and superoxide [69]. Similarly,  $\text{MetS}^+$  can react with oxygen to form  $\text{MetO}$  [70], making various proteins inactive [71].  $\text{A}\beta$  (1-40) is a shorter peptide fragment produced from APP, which is also neurotoxic [72]. There is an abundance of  $\text{A}\beta$ (1-40)  $\text{MetO}$  in senile plaques [73]. The oxidation of this methionine is reported to prevent  $\text{A}\beta$ (1-40) from forming beta sheets during fibril formation [74]; therefore,  $\text{A}\beta$ (1-42) could be more toxic by this mechanism. With the I31P substitution of  $\text{A}\beta$ (1-42), the interaction of the carboxyl oxygen of Pro31 with the S-atom of Met35 is disrupted, yielding no neurotoxicity or protein oxidation in neurons [66]. The sulfuranyl radical can react with the methylene moieties of Met to form the  $\alpha$ -(alkylthio)alkyl radical of methionine ( $-\text{CH}_2-\text{CH}_2-\text{S}-\text{CH}_2$ ). Others showed, using computer modeling, that the  $\beta$ -sheet conformation of this toxic peptide contains the sulfur-centered radical cation of Met35, which bolsters the creation of an  $\alpha$ -carbon centered radical on the Gly33 residue. This gives rise to a hydrophobic environment that is ideal for lipid peroxidation in the lipid bilayer [75,76]. The sulfuranyl radical (a positively charged radical) on the Met35 can in principle be stabilized by the helix-associated dipole of the C-terminal end of  $\text{A}\beta$ (1-42). Since the dipole of  $\text{A}\beta$ (1-42) would be greater than that of  $\text{A}\beta$ (1-40), the differential toxicity of  $\text{A}\beta$ (1-42) and  $\text{A}\beta$ (1-40) may be related to this characteristic. The importance of the hydrophobic environment of the Met35 residue was evaluated. By substituting aspartic acid for Gly37, the critical methionine residue no longer remained in a hydrophobic environment, and  $\text{A}\beta$ (1-42) oxidative stress and neurotoxicity was abrogated [76]. This result suggests that  $\text{A}\beta$ (1-42)-mediated lipid peroxidation is an early and crucial step in the toxicity of this peptide.

If Gly33 residue is substituted by the hydrophobic amino acid, valine, neurotoxicity is minimal and protein oxidation is significantly reduced in comparison to the wildtype  $\text{A}\beta$ (1-42) peptide [77]. Several groups [58,59,61] have confirmed our findings that substitution of the S-atom of Met35 by  $\text{CH}_2$  (to make the R-group, norleucine, Nle) abrogates the oxidative stress and neurotoxicity of the resulting peptide [68]. Other researchers point to the role of Tyr10 as a source of free radicals of  $\text{A}\beta$ (1-42). This free radical is proposed to reduce  $\text{Cu}^{2+}$  bound to His6, His13, and His14, leading to  $\text{Cu}^+$ -mediated chemistry to produce  $\text{OH}\cdot$  [78,79]. These researchers point out that rat  $\text{A}\beta$ (1-42) lacks Tyr10 and is not toxic. However, substitution of Tyr10 by Phe (to keep aromaticity present but to prevent any possible electron flow in contrast to this possibility with Tyr), as well as substitution of three His residues by Asn (which binds  $\text{Cu}^{2+}$  at least 100-fold less than His) led to a toxic peptide similar to native human  $\text{A}\beta$ (1-42) [57]. Also rat  $\text{A}\beta$ (1-42) was shown to be toxic upon longer incubation with neurons [80]. The p3 fragment of human  $\text{A}\beta$ (1-42),  $\text{A}\beta$ (17-42), which does not contain Tyr10 or His6, His13, and His14, was reported to be toxic [60]. This Met-containing peptide, which is present in AD brain, was no longer toxic if the Met35 was substituted by Nle [60]. The dissociation constant of  $\text{Cu}^{2+}$  binding to  $\text{A}\beta$ (1-42) was resigned to be attomolar [79]. While some of these researchers propose an AD therapy based on  $\text{Cu}^{2+}$  chelation using clioquinol, which has a  $K_d$  of nanomolar [81], the nine orders of magnitude difference in affinity of  $\text{Cu}^{2+}$  between  $\text{A}\beta$ (1-42) and clioquinol make it unlikely that the effectiveness of this agent is correctly ascribed to its chelating ability. However, we propose that clioquinol could chelate relevant weakly bound  $\text{Cu}^{2+}$ , for example if  $\text{Cu}^{2+}$  were loosely bound to Met35 of  $\text{A}\beta$ (1-42). This scenario would account for the oxidation of Met to a sulfuranyl radical while  $\text{Cu}^{2+}$  would be reduced to  $\text{Cu}^+$ , from whence further oxidative chemistry conceivably could ensue. Further investigation will be required to test this notion. Thus, while a role for  $\text{Cu}^{2+}/\text{Cu}^+$  in the oxidative stress and neurotoxicity of  $\text{A}\beta$ (1-42) can not be excluded, it appears that there is a paramount role of Met35 in these properties.

Finally, several researchers employ the 11-mer,  $\text{A}\beta$ (25-35), as a model for the AD-relevant (but more costly)  $\text{A}\beta$ (1-42). Even in the case of the 11-mer, substitution of the C-terminal Met by Nle abrogated the free radical oxidative stress induced by this shorter peptide as did use of

the 10-mer A $\beta$ (25-34) [68]. Moreover, because Met is C-terminal in A $\beta$ (25-35), while Met is intrachain in A $\beta$  (1-42), the mechanism by which the sulfuranyl free radical on Met35 is generated is different in these two peptides [68]. This fact, coupled with the absence of evidence for A $\beta$ (25-35) in AD brain, suggests to us that use of A $\beta$ (25-35), though of possible academic interest, is of no relevance for gaining insight into AD.

## Oxidative Stress in AD Brain

Oxidative stress is observed in the AD brain [1-5]. This increase has been well documented with markers for protein, DNA, and RNA oxidation as well as lipid peroxidation [4,6,11,82, 83].

### Protein Oxidation

Protein oxidation is indexed in the AD brain by an increase in carbonylated [82], HNE- [84], and 3-NT- [11] modified proteins. The initial origin of AD pathogenesis has not been determined though it has become evident that oxidative stress is implicated in the development of this disease [1,5,85]. Studies have shown an increase in protein carbonyls in the hippocampus and parietal cortex, but not in the cerebellum where there is less significant AD pathology [82].

### Protein Nitration

Another common marker of protein oxidation is the addition of a nitro group to tyrosine residues forming 3-NT. Increased protein nitration in the AD brain supports the notion that nitrosative stress also contributes to neurodegeneration in AD [10,11,13,16,86]. Protein nitration also increases the susceptibility of brain proteins to proteosomal degradation [26]. The overexpression of iNOS and nNOS could be responsible for increased levels of RNS. Previous studies have reported mitochondrial abnormalities in the AD brain [87], which could lead to superoxide (O<sub>2</sub><sup>-</sup>) leakage. As shown in Figure 1, superoxide then reacts with nitric oxide (NO $\cdot$ ) to form peroxynitrite (ONOO<sup>-</sup>).

Tyrosine is particularly susceptible to nitration but tryptophane and phenylalanine can also be nitrated, albeit at lower rates. Tyrosine residues are important to redox cell signaling and are often the site of phosphorylation, a prominent regulation function [88]. The nitration of tyrosine at the 3-position sterically hinders the phosphorylation and also may change the structure of proteins, thereby rendering a protein dysfunctional, and could lead to cell death [6,89].

Increased levels of nitrated proteins have been reported to be present in AD brain and cerebrospinal fluid CSF implying a role for RNS in AD pathology [10,11,13,90]. An increase in 3-NT immunoreactivity in neurons from AD brain was observed [11], as well as elevated dityrosine and 3-NT levels in hippocampus, inferior parietal lobule (IPL), and neocortical regions of the AD brain and in ventricular cerebrospinal fluid (VF) when compared with aged matched controls. [11,86]. The demonstration of nitrated tau in pretangles, tangles, and tau inclusions in AD brain, suggests that tau nitration may be an early event in AD [91]. This notion is strengthened by our finding of elevated 3-NT in brain of subjects with MCI (see below).

### Lipid Peroxidation

Amplified lipid peroxidation has been described in several neurodegenerative diseases including AD [7,83,84,92]. Analysis of AD brains demonstrates an increase in free HNE in amygdala, hippocampus, and parahippocampal gyrus of the AD brain when compared with age-matched controls [83]. This increased alkenal concentration corresponds with the regions showing the most striking histopathologic alterations in AD. A significant elevation of free HNE in ventricular cerebrospinal fluid (CSF) and serum provides a potential biomarker for

AD [93,94]. Protein-bound HNE, which is indication of Michael addition of HNE to proteins, is elevated in AD [2,4,84,95]. HNE is elevated in neurons treated with A $\beta$  (1-42) [8,84,96]. Protein-bound HNE alters conformation and function of proteins [84,97]. In AD brain protein-bound HNE is found on the glutamate transporter (Glt-1 or EAAT), glutathione-S-transferase (GST), and multi-drug resistant protein (MRP-1) [84,98]. Thus processes related to excitotoxicity may be facilitated, while processes related to removal of HNE from neurons (via GST and MRP1) may be compromised.

### DNA Oxidation

More than four decades ago, it was suggested that DNA is the primary target of ROS leading to cellular aging [99]. Due to the high oxygen consumption rate by the brain, ROS may contribute to neuronal damage in aging and neurological disorders [5]. Oxidative damage to DNA by ROS results in strand breaks, DNA-DNA and DNA-protein cross-linking, and sister chromatid exchange and translocation [100,101]. DNA bases are also attacked by lipid peroxidation products HNE and acrolein, which lead to formation of bulky exocyclic adducts. This modification can cause inappropriate base pairing that alters protein synthesis. DNA oxidation by ROS also produces oxidized base adducts, such as 8-hydroxy-2-deoxyguanine (8-OHdG) [102,103]. Guanine, because it has the lowest oxidation potential of the four DNA bases, is the most readily oxidized base and therefore the mostly commonly used analysis of DNA oxidation.

Previous studies have demonstrated a two-fold increase in DNA strand breaks in AD brain that consequently results in depletion of energy stores and cell death [104]. DNA oxidation has been shown to escalate with age, shown by an increase in 8-OHdG in the cerebral cortex and cerebellum brain regions [105]. Similarly both mitochondrial DNA (mtDNA) and nuclear DNA (nDNA) have increased 8-hydroxyguanine (8-OHG), 8-hydroxyadenine (8-OHA), and 5-hydroxyuracil (5-OHU) in temporal, parietal, and frontal lobes in AD [105,106]. Overall, mtDNA shows an approximately 10-fold higher intensity of oxidized bases than nDNA. This result demonstrates that nDNA and mtDNA undergo extensive oxidative damage in AD, which may contribute to the neurodegenerative pathology of this disorder.

### RNA Oxidation

Studies have shown that 30–70% oxidation of the mRNAs in the frontal cortex of the AD brain in comparison to only 2% oxidation age-matched controls [107]. A specific increase in rRNA oxidation has also been shown in the AD IPL when compared to age-matched controls [108]. Increased levels of 8-hydroxyguanine (8-OHG) have also been reported in the hippocampus and cerebral neocortex of the AD brain, while the 8-OHG level in the cerebellum was not significantly altered when compared with controls [108-110]. An increase in 8-OHdG has been identified not only in brain tissue but also in CSF from AD patients [111]. RNA oxidation in the AD brain could render the cell incapable of initiating protein synthesis, hindering the cell's defense against further oxidative damage an effect observed in AD [108].

### Mitochondrial Dysfunction

Mitochondrial dysfunction in AD is central to the development of oxidative stress since it is primary source of cellular oxidants [112,113]. *In vivo* positron emission tomography (PET) has provided specific evidence of brain metabolism abnormalities associated with AD [114], which precede neuropsychological impairment and visual atrophy [115,116]. Frontal cortex and middle temporal gyrus show a significant decrease in metabolism as well as synaptic dysfunction [117-121]. Studies of autopsied AD brain tissue also revealed decreased pyruvate dehydrogenase activity in the parietal, temporal, and frontal cortex [122-124]. Cytochrome c oxidase (COX), Complex IV in the electron transport chain (ETC), consistently shows decreased activity in AD brain [125]. Decreased  $\alpha$ -ketoglutarate dehydrogenase activity in the

parietal and temporal cortex of AD patients has also been reported that could be related to the HNE binding to  $\alpha$ -KG [126-130], though this could be affected by longer postmortem intervals [131]. All the above-mentioned mitochondrial changes would limit ATP production and increase ROS production and suggest possible abnormalities in mitochondrial functions in AD. ROS production is directly related to mitochondrial membrane potential ( $\Delta\psi$ ) such that hyperpolarization (high  $\Delta\psi$ ) promotes ROS production [132-134]. In addition, several *in vitro* studies of A $\beta$  and mitochondrial function have reported that A $\beta$  affects mitochondrial DNA and proteins, leading to impairments of the electronic transport chain (ETC) and ultimately mitochondrial dysfunction [135,136]. Dysfunction of mitochondria is reported to alter APP metabolism, enhancing intraneuronal accumulation of amyloid beta-peptide and enhancing neuronal vulnerability [137]. Consistent with the importance of A $\beta$ (1-42) in AD pathogenesis, recent research has suggested the presence of intracellular A $\beta$  (1-42) in mitochondria from brains of transgenic mice and AD patients [138,139], and showed increased expression of mitochondrial genes before A $\beta$  deposition in APP transgenic mice, and suggested that the up regulation of mitochondrial genes may be a compensatory response because of mitochondrial oxidative damage caused by the over-expression of mutant APP and/or A $\beta$  [139]. Further, the accumulation of A $\beta$  in the mitochondria may be associated with diminished enzymatic activity of mitochondria [140], where the peptide is proposed to disrupt energy production while promoting mitochondrially derived apoptotic processes via the intrinsic pathway. This claim of mitochondrial A $\beta$  needs replication but is a provocative hypothesis that provides potential insight into metabolic alterations and oxidative stress in AD brain.

### Vascular Factors in the Conversion from MCI to AD

Oxidative stress is also associated with vascular factors [141-144] that reportedly play a role in the conversion of MCI to AD [145]. Vascular factors include, but are not limited to, APOE4 allele, diabetes, smoking, hypertension and heart disease [146]. ApoE4 isoform is associated with increased peripheral lipid levels, glial cell activation, and decreased peripheral lipid metabolism, and cerebral glucose metabolism, that may eventually lead to inflammation, oxidative stress, and dementia. A recent study by Wolozin and Bednar (147) suggests that ApoE does not directly contribute to AD by increasing serum cholesterol, but rather ApoE might act via a mechanism involving A $\beta$  [147]. From our laboratory we showed that increased oxidative stress in APP/PS-1 mice is independent of dietary cholesterol, which further supports the role of A $\beta$  in the induction of oxidative stress rather than the direct effect of cholesterol [148]. In addition to ApoE other risk factors for AD are coronary artery bypass surgery, congestive heart failure, cerebrovascular-carotid atherosclerosis, atrial hypotension, and transient ischemia attacks [149]. In all these conditions, one common factor is the production of oxidative stress that often occurs by ischemic reperfusion injury. Patients with cardiovascular disease and MCI are reported to have increased short-term memory loss and decreased ability to learn and retain new material, and decreased recall and short-term memory compared to MCI patients without vascular risk factors [150]. Another risk factor for AD is diabetes mellitus in which increased levels of glucose and insulin may increase the levels of free radicals such as superoxide and hydrogen peroxide [151]. Monomeric A $\beta$  is known to compete with insulin for insulin degrading enzyme, so diabetes may lead to elevated levels of A $\beta$ , thereby posing a risk factor for development of AD [49]. Prevention or treatment of vascular risk factors can reduce oxidative stress [152]. Vascular factors are also associated with AD [153-156]. Therefore, it is possible that vascular factors contribute to the conversion of MCI to AD [157,158].

### Oxidative stress in MCI Brain

As described above, MCI is characterized by mild current memory loss without dementia or significant impairment of other cognitive functions or activities of daily living [159,160]. As

also noted above, a number of MCI subjects show neuropathological hallmarks similar to AD, including temporal lobe atrophy and low CSF A $\beta$  levels [161].

Plasma of MCI patients is reported to have decreased levels of non-enzymatic antioxidants and decreased activity of antioxidant enzymes compared to those of controls, while there were no alterations of protein levels [162]. This diminution of antioxidants could possibly increase the production of free radicals during the progression of the disease. Previous studies reported increased oxidative damage in nuclear and mitochondrial DNA in MCI, as indexed by increased levels of 8-OHdG, 2,6-diamino-4-hydroxy-5-formamidopyrimidine (fapyguanine), 8-hydroxyadenine, 4,6-diamino-5-formamidopyrimidine (fapyadenine) and 5-hydroxycytosine [163,164]. Markesbery and co-workers showed that subjects with MCI have higher levels of isoprostanes (F<sub>2</sub>isoP) in the plasma, urine and cerebrospinal fluid compared to that of the healthy subjects [165]. Lipid peroxidation markers such as free HNE, protein-bound HNE, TBARS, and MDA were reported to be elevated in MCI brain [166-168]. Our laboratory showed that protein-bound HNE levels and 3-NT are elevated in the MCI brain compared to control IPL and hippocampus [166,169]. Protein carbonyls are also elevated in MCI brain [36,167]. These results suggest the accumulation of oxidative stress [36,108,166,167] in MCI brain and are consistent with the notion that oxidative stress could be an early event in the progression of MCI to AD.

## Redox Proteomics identification of oxidatively modified brain proteins in AD

### Redox Proteomics

Redox proteomics used in our laboratory to identify specifically oxidized proteins in Alzheimer's disease brain involves coupling two-dimensional-polyacrylamide gel electrophoresis-mediated separation of proteins to mass spectroscopic analysis (Figure 4). Two-dimensional (2D) gel electrophoresis allows the analyses of complex protein mixtures based on two important physicochemical properties, i.e., isoelectric focusing (IEF) and relative mobility (Mr) [170]. The 2-D gel and blot maps obtained from proteomics provide information about the pI, molecular weight, expression, and post-and co-translational modifications of a protein of interest. Usually a single spot on the 2-D gel corresponds to a single protein [171]. 2D-PAGE for separation of proteins has some important limitations, such as solubilization of membrane proteins [172], highly basic proteins, and inability to detect low-abundance proteins.

To use the 2D for maximum optimization, chaotropic agents, such as urea and thiourea, coupled with nonionic or zwitterionic detergents, are used to solubilize proteins and avoid protein precipitation during the IEF and the SDS gel electrophoresis. To avoid cathodic drift, immobilized pH IEF strips are used instead of tube gels, which improve protein map reproducibility between samples. Further, the use of narrow range IEF strips can expand the area of interest in a map of a proteome to give high-resolution separation.

In addition to the often-used method of 2D-PAGE, other separation methods, including 2D-HPLC and isotopically coded affinity tags (ICAT), are also used for protein separation. The ICAT method is used to analyze protein expression in two different sets of samples together by labeling the samples with different isotopes that bind to cysteine residues [173].

In our laboratory we used redox proteomics techniques to identify oxidatively modified proteins in oxidative stress-related diseases and their models. In this method we use a parallel analysis that couples 2D-PAGE with 2D-immunochemical detection of protein carbonyls derivatized by DNPH, nitrated proteins indexed by 3-NT, or protein adducts of HNE, on 2D Western blots, followed by MS analysis of the corresponding gel spot, as shown in Fig. 4. Proteins containing reactive carbonyl groups/3-NT/HNE in AD and control brain samples are detected by 2D Western blot analysis using specific antibodies. The 2D Western blots and 2D



gel images are matched by computer-assisted image analysis, and the anti-DNP/nitrotyrosine/HNE immunoreactivity of individual proteins are normalized to their content, obtained by measuring the intensity of colloidal Coomassie Blue or SYPRO ruby stained spots. Such analysis allows comparison of levels of oxidatively modified brain proteins in AD versus control subjects.

### Mass Spectrometry and Database Searching

Once a protein spot is identified as significantly involved in AD or MCI, it is digested with trypsin in the gel, and the resulting tryptic peptides undergo mass spectrometry analysis [10, 12,13,36-38,174]. The peptide mass fingerprints obtained are characteristic of a specific protein, which allows correct identification of a particular protein using a suitable database that compares the experimental masses with theoretical masses of trypsin-generated protein sequences.

The mass spectrometric methods that are mostly used include MALDI (matrix assisted laser desorption/ionization) and ESI (electrospray ionization). In MALDI analysis the peptide sample is mixed with a matrix (usually  $\alpha$ -cyano-4-hydroxycinnamic acid or 2,5-dihydroxybenzoic acid) and deposited on to a plate that is subjected to laser radiation, which allows the matrix to absorb the energy and then transfer the proton to the peptides in the gas phase. In ESI, MS/MS analysis of peptides leads to sequence information of these tryptic peptides. The exact mechanism for the ionization process in ESI is not well understood; however, a number of hypotheses were put forward to explain the ionization process in ESI. One of such hypothesis resulted from the use of HPLC-coupled to ESI, which suggests that as the liquid leaves the nozzle, the electric field induces a net charge on the small droplets. As the solvent evaporates, the droplet shrinks and the charge density at the surface of the droplet increases. This will eventually lead to the explosion of the droplet producing multiply charge analyte ions.

Surface-enhanced laser desorption /ionization time-of-flight (SELDI-TOF) is another proteomics tool that couples the classical methods of chromatographic sample preparation with mass spectrometry analysis. This method is important for applications in biomarker analysis, but is optimal for proteins below a relatively low molecular weight (<30kDa) [175].

The correct identity of the protein is determined by analysis using peptide mass data to interrogate on-line protein databases. The protein sequence database SwissProt is the most commonly used database for protein identification that is based on computer algorithms [176], and is available gratis through the internet. Most of the various protein search databases that are available online are listed in Table I.

The information obtained from proteomics has significant potential to provide insight into AD pathogenesis, to develop disease markers, and to identify potential targets for drug therapy in AD.

### Oxidative Modification of Brain Proteins in AD: Carbonylation and Nitration

Any type of oxidative modification (i.e., nitration, carbonylation, etc.) generally causes the protein to lose of functionality and lower enzyme activity [12]. Oxidatively modified proteins have been identified in AD hippocampus and AD IPL [10,13,37,38,177,178]. Previous reports of an increased total protein carbonyls in AD brain [82]initiated studies to determine if specific proteins were more vulnerable or targeted for protein oxidation. Using redox proteomics, we identified specific carbonylated proteins in the hippocampus and inferior parietal lobe (IPL) of the AD brain. . In the IPL region, we reported dihydropyrimidinase-related protein 2 (DRP2),  $\alpha$ -enolase, heat shock cognate 71(HSC 71), creatine kinase BB (CK BB), glutamine synthase

(GS), and ubiquitin carboxyl terminal hydrolase L-1 (UCHL-1) showing a specific increase in protein carbonyls in the AD brain as compared to age-matched control [37,38]. In a separate study of the AD hippocampus,  $\alpha$ -enolase, UCHL-1, DRP2, HSC 71, CK BB, peptidyl prolyl-*cis,trans*isomerase 1 (Pin1), triosephosphate isomerase (TPI), and carbonic anhydrase 2 (CA II) were identified showing an increase in protein carbonyls in the AD brain as compared to age-matched control brain [12]. These data support the notion that protein carbonylation affects energy metabolism, pH regulation, and mitochondrial functions.

Protein nitration has detrimental effects as seen in key proteins such as glutamine synthase [179], ubiquitin [180], tyrosine hydroxylase [181,182] and Mn superoxide dismutase [183-186], which lose activity upon protein nitration. As noted above, previous research has shown that protein nitration is associated with AD [10,11,13,90,187]. Our laboratory [10,13] identified several proteins significantly nitrated in AD hippocampus and IPL compared to control brain. These proteins include: glyceraldehyde-3-phosphate dehydrogenase, ATP synthase  $\alpha$ - chain, carbonic anhydrase-II, voltage-dependent anion channel-protein,  $\alpha$ -enolase,  $\gamma$ -enolase,  $\beta$ - actin, L-lactate dehydrogenase (LDH), neuropolypeptide h3, and triosephosphate isomerase (TPI) (Table II).

### Functional Classification of Redox Proteomics-Identified Oxidatively Modified Brain Proteins in AD

**Energy-related enzymes**— $\alpha$ - and  $\gamma$ -enolase, TPI, GAPDH, LDH, PGM1, and CK are seven proteins that were identified to be oxidatively modified in AD brain that affect energy production and use in the cell.  $\alpha$ - and  $\gamma$ -enolase are two subunits in the enolase enzyme. This enzyme converts 2-phosphoglycerate to phosphoenolpyruvate in glycolysis. Alpha enolase levels are increased AD brain, but activity is reduced, causing impairment in glucose metabolism [12,188]. TPI catalyzes the conversion of dihydroxyacetone phosphate (DHAP) to glyceraldehyde-3-phosphate (G3P) in glycolysis. In the previous step, fructose 1,6-bisphosphate is cleaved into DHAP and G3P. Dihydroxyacetone phosphate is not directly involved in glycolysis. The enzyme TPI catalyzes this reaction converting DHAP into G3P (the aldose isomer), and causes an additional molecule of glyceraldehyde 3-phosphate to continue along the glycolytic pathway. TPI has been shown to be oxidatively modified in the AD brain [12]. Another glycolytic protein, PGM1 has been shown to be oxidized in the AD brain, specifically in the hippocampus. PGM 1 converts 3-phosphoglycerate to 2-phosphoglycerate. Glycolysis is especially important to the energy production in the brain, since glucose is the main source of energy. Impaired glycolytic function directly relates to less ATP available to the cells and various cellular processes that require ATP may be impaired, which is consistent with findings of altered glucose metabolism and tolerance in AD patients [189-192].

Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) is the enzyme responsible for the converting glyceraldehyde-3-phosphate to 1,3-bisphosphoglycerate, a high-energy phosphate product.  $\text{NAD}^+$  and inorganic phosphate are needed to drive the reaction, consequently producing NADH as a byproduct of the reaction. Studies of the AD brain have shown GAPDH to be oxidatively modified with decreased enzyme activity [193,194]. L- Lactate dehydrogenase (LDH) reduces pyruvate to lactate using NADH as a cofactor. A benefit of this reaction is to generate  $\text{NAD}^+$ , which is used as a co-factor for GAPDH in glycolysis. The oxidation and consequential dysfunction of LDH in AD also leads to reduced GAPDH activity. A reduction in GAPDH activity hinders glycolysis, lowering energy production in the cell. GAPDH also serves as a NO trap, which utilizes a large number of Cys residues [195]. Hence, oxidative modification of GAPDH would lead to a decreased protection of neurons and increased 3-NT formation. CK BB catalyzes the phosphorylation of creatine to creatine phosphate, which is an important high energy storage molecule [196]. The phosphate group is

then used in the production of ATP providing immediate energy to the cell [197]. ATP is in constant demand by various ATPases to maintain ion pumps, lipid asymmetry, and cell-cell-communication. The oxidative dysfunction of these enzymes identified by redox proteomics could interrupt glycolysis and disrupt energy metabolism in brain, consistent with reduced energy utilization observed in AD brain [190,191].

**Proteasome-related proteins**—The ubiquitin – proteasome pathway has been shown to be dysfunctional in the AD brain [198]. Ubiquitin carboxy terminal hydrolase-1 (UCHL-1) is crucial to the degradation of damaged or misfolded proteins through proteasomal pathway. UCHL-1 has been found to be oxidized in the hippocampus and IPL regions of the AD brain [12,37,199], which is consistent with AD pathology [200]. The dysfunction of UCHL-1 would be consistent with the dysfunction of the proteasome, accumulation of damaged and aggregated proteins, and excess protein ubiquitinylation observed in AD [198]. Also, recent studies show that UCHL-1 can recover synaptic function and contextual memory formation from A $\beta$ -induced oxidation [201]. Hence, oxidatively dysfunctional UCHL-1 may contribute to altered synaptic function and memory of AD.

The cooperation of proteasome and molecular chaperones are required to control protein-protein interaction and the development of aggregates [202]. The identification of the oxidatively – modified heat shock cognate 71 (HSC 71) is consistent with impairment of the proteasomal pathway in AD, as HSC 71 is involved with the proteasome and protein degradation [38,203]. HSC 71 also directly binds to the cytoplasmic domain of APP, which conceivably could contribute to alterations in APP processing and A $\beta$  production observed in the AD brain [204].

**Structural proteins:  $\beta$ - actin and DRP-2** Maintaining cytoskeletal integrity is important, because shortened dendritic length can be associated with or AD pathology [205]. Actin is a major component of thin microfilaments.  $\beta$ -actin plays a role in preserving cytoskeletal structure. Since  $\beta$ -actin is carbonylated [206] and nitrated in AD brain [10], structural integrity could be compromised and these changes may contribute to neuronal death [22].

DRP-2 is a neuronal repair protein identified as oxidized in AD brain [12,38]. DRP-2 modulates collapsin activity, which is essential to elongating and directing dendrites to adjacent neurons. Collapsin is also critical in axonal outgrowth. Oxidative modification of DRP-2 may lead to the observed shortened dendrite length in AD [207], with consequent impairment of neuronal communication.

DRP-2 is downregulated in Down's syndrome and AD patients [208]. Shortened dendritic length observed in AD [207] conceivably could be a result of loss of function of oxidatively modified DRP-2. The protein DRP-2 was also identified as oxidized in the inferior parietal lobule of AD patients and in A $\beta$ -treated synaptosomes [38,209]. Neuronal miscommunication is a likely contributory factor in the memory loss and cognitive decline in seen in AD patients as demonstrated in those with the ApoE4 allele, a risk factor for AD [210]. These redox proteomics results are consistent with the memory and synapse loss attributed to AD as a consequence of the decreased function of these two structural proteins.

**Cholinergic function and lipid asymmetry**—Neuropeptide h3, also known as RAF kinase inhibitor (RKIP), phosphatidylethanolamine binding protein (PEBP), and hippocampal cholinergic neurostimulating protein (HCNP), is critical to the production of choline acetyltransferase, which is vital in signal transduction. The loss of choline acetyltransferase leads to reduced levels of the neurotransmitter, acetylcholine, causing poor neurotransmission [211]. More specifically, there is decreased expression of HCNP in AD hippocampus [212]. N-methyl-D-aspartic acid (NMDA) receptors activate the production of this enzyme, and

alteration of the NMDA receptor mediates cholinergic deficits [213]. Alzheimer's disease is associated with cholinergic neuronal loss [214-216]. Since neuropolypeptide h3 is also PEPP, it is possible that lipid asymmetry is also affected by oxidized PEPP. We showed that lipid asymmetry is lost in synaptic membranes treated with A $\beta$ (1-42) or HNE [217,218].

**Neurotransmitter-related proteins**—An excess of glutamate causes toxicity to neurons by over-stimulation of neurons by this excitatory neurotransmitter, e.g., excitotoxicity. A high concentration of glutamate over-activates ionotropic glutamate receptors, which leads to an increase of intracellular Ca<sup>2+</sup>, resulting in cell death. Synaptic depletion is one of the characteristics of AD brain that could be secondary to glutamate excitotoxicity. Glutamine synthetase (GS) is an enzyme identified by redox proteomics as being oxidatively modified in AD brain [37]. GS catalyzes the reaction of glutamate with ammonia to form glutamine, a non-toxic amino acid. Previous studies have shown GS to be oxidatively modified in the AD brain [37]. Further studies have also revealed reduced GS activity in the AD brain [6,82]. These results are consistent with those of others, who showed that excessive extracellular glutamate leads to intracellular ROS [219]. Decreased GS activity and excitotoxicity leads to neurodegeneration, consistent with synaptic loss in AD.

**Synaptic abnormalities and LTP**—Soluble N-ethylmaleimide-sensitive factor (NSF) attachment proteins are highly conserved and are involved in intracellular membrane fusion and vesicular trafficking, which is critical to the function of the synapse. These proteins are involved in neurotransmitter release, hormone secretion, mitochondrial organization, and vesicular transport.  $\gamma$ -Soluble NSF attachment protein ( $\gamma$ -SNAP), is one of three isoforms and is involved in long-term potentiation, a key process for learning and memory [220].  $\gamma$ -SNAP was identified as oxidatively modified in the AD brain [12], which has clear implications in AD pathology through impaired neurotransmission [221]. This finding also has implications with respect to LTP learning and memory, the diminution of which is a hallmark of AD.

**pH regulation protein**—Carbonic anhydrase II (CA II) catalyzes the hydration of CO<sub>2</sub> to HCO<sub>3</sub><sup>-</sup>, regulates pH in the cell, and aids in transporting HCO<sub>3</sub><sup>-</sup> and CO<sub>2</sub>. The main function of CA II is maintaining electrolyte and water balance [222,223]. The activity of CA II is diminished in AD hippocampus [178,188]. Nitration of CA II can deregulate pH in the cell. Since so many reactions and enzymes, as well as the mitochondrial proton gradient for ATP synthesis, are pH-dependent, malfunction of this enzyme carbonic anhydrase II may be involved in AD.

**Cell cycle, tau phosphorylation, Abeta production**—Pin-1 is one of the peptidyl-prolyl isomerases (PPIase) that regulates biological functions of proteins including protein assembly, folding, intracellular transport, intracellular signaling, transcription, cell cycle progression and apoptosis. Of particular relevance to AD, Pin1 regulates enzymes associated with both phosphorylation and dephosphorylation of the critical cytoskeletal protein, tau [224]. Also, Pin1 binding to APP regulates the production of A $\beta$  [225]. Finally, Pin1 is related to neurons in the cell cycle [224]. Since we showed that Pin1 was oxidatively dysfunctional in both MCI and AD brain [12,36,177], three major pathological hall marks of this dementing disorder (NFT, SP, and synapse loss due to neurons trapped in the cell cycle) may be related to damaged Pin1. In MCI brain elevation of cell cycle proteins was found [226], consistent with this notion. In addition, previous studies reported down regulation of Pin1 levels and activity in AD brain [36,178]. Pin1 was reported to co-localize with phosphorylated tau in AD brain, and showed an inverse relationship to the levels of tau. In addition, an *in vitro* study reported that Pin1 protects neurons against age-related neurodegeneration [227]. Pin1 can also restore the ability of phosphorylated tau to bind microtubules and promote their assembly *in vitro*, a process that

might represent a potential therapeutic use for Pin1 [228]. Studies to test the hypothesis of the critical importance of Pin1 in AD pathogenesis are ongoing in our laboratory.

**Mitochondrial-related proteins**—Voltage-dependent anion channel-protein (VDAC) is the outer component of the mitochondrial permeability transition pore (MPTP). VDAC is critical to importing and exporting various metabolites (i.e., ATP) into the mitochondria. This protein, in its role as a part of the MPTP, plays a part in the release of cytochrome c [229], caspases [230], and apoptosis inducing factor [231] from the mitochondria, essential for apoptosis. Nitration of VDAC alters MPTP function and can induce apoptosis by preventing Bcl-2/VDAC interaction in favor of increasing the proapoptotic factor, Bax and cytochrome c release [232]. Thus neuronal death could ensue. Recent research suggests that VDAC plays a role in A $\beta$ -mediated neurotoxicity [233].

ATP synthase,  $\alpha$ -subunit, is an ATP synthesizing enzyme composed of a coupling factor 1 (F<sub>1</sub>) head and the hydrophobic F<sub>0</sub> component. The F<sub>1</sub> head is composed of three catalytic sites for ATP production. Once ADP and inorganic phosphate (P<sub>i</sub>) bind to the catalytic site of this enzyme, one ATP is created. This binding of ADP to P<sub>i</sub> must be in a precise “tight” conformation for ATP to be produced. If the ADP and P<sub>i</sub> are in the “loose” or “open” conformations, their affinity is not high enough for ATP production. Therefore, ATP production through ATP synthase occurs in a “rotary catalysis and proton electrochemical gradient” [234]. The rotation occurs by protons inducing a conformational shift. Loss of function of this protein can be detrimental to ATP production and in energy metabolism, consistent with PET studies of AD.

## Redox proteomics Identification of oxidatively modified brain proteins in mci

Recent redox proteomics study from our laboratory identified alpha-enolase, glutamine synthetase, pyruvate kinase M2 and Pin1 in MCI hippocampus as being oxidatively modified [36]. In AD brain, three of these proteins, i.e., Pin1, glutamine synthetase, and enolase, were reported as oxidatively modified [37,38,177]. These proteins are crucial for energy metabolism, and neurotransmission. The identification of Pin1 as a common target of oxidation between AD and MCI suggests that Pin1 oxidation might be one of the driving forces for the initiation or progression of AD pathogenesis that may ultimately lead to cell death and neurodegeneration. Research to test this notion is ongoing in our laboratory.

## Redox proteomics analysis of In-vivo models of AD centered around human A $\beta$ (1-42)

### Human A $\beta$ (1-42) Injected into Rat Cholinergic-Rich Basal Forebrain

A cholinergic animal model of AD was prepared by injecting A $\beta$ (1-42) into the nucleus basalis magnocellularis (NBM) of rat brain to replicate the cholinergic dysfunction reported in AD brain [235,236]. Degeneration of the basal forebrain cholinergic neurons is pronounced in AD and is associated with cognitive deficits [237,238]. In this animal model oxidative stress was observed in hippocampus, cortex and nucleus basalis; however, an extensive protein oxidation was observed in hippocampus compared to that of other regions [35,237].

Using regional redox proteomics, a large number of oxidized proteins were identified in this animal model that include: 14-3-3 zeta,  $\beta$ -synuclein, pyruvate dehydrogenase, GAPDH, and PGM1, GS and tubulin ( $\beta$ -chain 15/ $\alpha$ ) and chaperonin 60 (HSP60) [35]. These proteins play a crucial role in signal transduction, cellular structure, energy metabolism, and stress response. As discussed above, a number of proteins that were identified in this animal model were already reported to be oxidatively modified in AD brain, including PGM1, GAPDH, GS

and tubulin [10,12,13]. The expression of 14-3-3 proteins were reported to be increased in AD brain and CSF [239,240] and these proteins also were found to be associated with NFT [241].

Recently, it has been shown that 14-3-3 zeta acts as a scaffolding protein simultaneously binding to tau and glycogen synthase kinase 3  $\beta$  (GSK3 $\beta$ ) in a multiprotein tau phosphorylation complex [242]. The hyperphosphorylation of tau could be associated with the oxidation of 14-3-3 zeta in this rat model following A $\beta$ (1-42) injection into NBM that could unite both the importance of A $\beta$ (1-42), and the hyperphosphorylation of tau. Heat shock proteins 60 is a mitochondrial chaperone protein that is involved in mediating the proper folding and assembly of mitochondrial proteins, especially in response to oxidative stress [243]. Expression of HSP60 is significantly decreased in AD and A $\beta$ (25-35) has been shown to induce oxidation of HSP60 in fibroblasts derived from AD patients compared to age matched controls [203,244]. The proteomics identification of the oxidation of HSP60 by A $\beta$ (1-42) *in vivo* [35] could presumably lead to loss of function of HSP60 that may lead to increased protein misfolding and aggregation, as well as an increased vulnerability to oxidative stress. Moreover, as noted above, in AD there is evidence that A $\beta$ (1-42) migrates to mitochondria, where HSP 60 conceivably could be affected.

### Human A $\beta$ 1-42-Expressing *Caenorhabditis elegans* (*C. elegans*)

Transgenic *C. elegans* is a worm model in which human A $\beta$  (1-42) is expressed through a body-wall muscle myosin promoter and an A $\beta$  minigene [245]. This model has been used to study A $\beta$  toxicity, fibril formation and oxidative stress *in vivo* [50,246,247]. Increased protein oxidation that preceded fibrillar deposition of human A $\beta$ (1-42) was observed, consistent with the notion that small, soluble oligomers of the peptide are the toxic species [50]. We also showed that *C. elegans* expressing human A $\beta$ (1-42) exhibited an increased oxidative stress and also suggested association of methionine 35 of A $\beta$ (1-42) in the mechanism of oxidative damage [247]. A redox proteomics study in this animal model identified sixteen proteins that were oxidatively modified [34]. The oxidatively modified proteins in this model of A $\beta$  include: ATP synthase  $\alpha$  chain, glutamate dehydrogenase, proteasome  $\alpha$ - and  $\beta$ -subunit, glutathione S-transferase ( $\epsilon$ -class), medium and short-chain acyl-CoA dehydrogenase, arginine kinase, myosin regulatory light chain, actin, adenosine kinase, malate dehydrogenase, transketolase, translation elongation factor EF-1  $\gamma$ , lipid binding protein, and RACK1 ortholog. These identified proteins were involved in a variety of cellular functions including energy metabolism, protein degradation, cytoskeletal integrity, antioxidant system, signal transduction, and lipid metabolism. Many of these classes of oxidized proteins are also represented in AD brain as noted above.

### Canine Model

Beagle dogs are a good model to study the role of A $\beta$ , since these animals have the same A $\beta$  sequence as humans. In addition, aged beagles deposit A $\beta$  and have cognitive dysfunctions similar to humans [248,249]. Histopathologically, aged beagle canines show reduced cerebral volume, cortical atrophy, ventricular widening as assessed by *in vivo* magnetic resonance imaging [250-252]. Beagle dogs absorb dietary nutrients in similar ways as humans. Previous studies in aged canines showed that long-term antioxidants reduce cognitive decline [253-255] and lead to rapid improvements in complex learning ability in aging dogs [256, 257]. These characteristics make the beagle dog a highly relevant for studying human AD considering the similarities in A $\beta$  deposition, histopathology, and nutrition. The histopathological results in aged beagle dog imitate human AD brain pathology before any occurrence of amyloid deposition [258-260].

Using redox proteomics, our group identified six brain proteins that showed decreased oxidation in aged beagles that had received behavioral enrichment and an antioxidant-

supplemented diet relative to control aged animals. These proteins that were protected from oxidative modification in aged beagles include: glutamate dehydrogenase (GDH), GAPDH,  $\alpha$ -enolase, neurofilament triplet L protein, GST and fascin actin bundling protein [174]. In addition, our group also reported increased activity of key antioxidant enzymes such as glutathione-S-transferase (GST) and superoxide dismutase (SOD) in this co-treated animal model of A $\beta$  [174]. These protected proteins play an important role in energy metabolism, maintenance and stabilization of cell structure, and cellular defense. We suggest that these proteins identified by redox proteomics may play key roles in learning and memory in normal physiology, since protection of these proteins from oxidation in aged beagles was correlated with improved learning and memory. Among the brain proteins identified by proteomics as oxidized in aged beagles, enolase, GAPDH and GST were found to be commonly oxidized between AD and aged beagle dogs.

The *in vivo* models of A $\beta$  support a critical role of A $\beta$ -induced oxidative stress and consequently the role of A $\beta$  in AD pathology. The beagle studies suggest a possible therapeutic approach to lowering risk of developing AD that combines behavioral enrichment with an antioxidant-rich diet that, similar to the aged beagles with A $\beta$ (1-42) of the same sequence as humans, could delay or significantly modulate AD pathology while improving memory.

## Future Research

The increased oxidative stress parameters in MCI brain regions [36,166,167,169] suggest that oxidative stress may be an early event in the progression from normal brain to AD pathology. These results further support the hypothesis that oxidative stress is a mediator of synaptic loss and a presumed factor for the formation of neurofibrillary tangles and senile plaques [10,12,13,37,38,98,199]. A better understanding of MCI could help in delineating the mechanism of AD and in developing effective therapeutics to slow or prevent conversion of MCI to AD and to treat AD. Recent AD clinical research has emphasized early detection of AD with the hope that early treatment will slow or prevent the progression of AD pathogenesis. On-going efforts in our laboratory include testing of promising therapeutic approaches to inhibit oxidative damage in MCI, AD, and models thereof [29,60,261-268]. Given the expected 14-16 million Americans and more than 22 million persons worldwide expected to develop AD in the relatively near future in the absence of effective intervention, increased national funding for AD-related research is imperative.

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## Abbreviations

3-NT, 3-nitrotyrosine; 5-OHU, 5-hydroxyuracil; 8-OHA, 8-hydroxyadenine; 8-OHdG, 8-hydroxy-2-deoxyguanine; 8-OHG, 8-hydroxyguanine; A $\beta$ , amyloid  $\beta$ -peptide; AD, Alzheimer's disease; APP, Amyloid precursor protein; C. elegans, *Caenorhabditis elegans*; CAII, Carbonic anhydrase 2; CK BB, Creatine kinase BB isoform; CSF, cerebrospinal fluid; DHAP, Dihydroxyacetone phosphate; DNPH, 2,4-dinitrophenylhydrazine; DRP2, Dihydropyrimidinase-related protein 2; ESI, Electrospray ionization; G3P, Glyceraldehyde-3-phosphate; GAPDH, Glyceraldehyde-3-phosphate dehydrogenase; GDH, Glutamate dehydrogenase; GS, Glutamine synthase; GSK3 $\beta$ , Glycogen synthase kinase 3  $\beta$ ; GST, Glutathione-S-transferase; HNCP, Hippocampal cholinergic neurostimulating protein; HNE, 4-hydroxy-2-*trans*-nonenal; HSC 71, Heat shock cognate 71; HSP60, Chaperonin 60; ICAT, Isotopically coded affinity tags; IEF, isoelectric focusing; iNOS, Inducible nitric oxide synthase; IPL, Inferior parietal lobe; LDH, L-lactate dehydrogenase; MALDI, Matrix assisted laser desorption/ionization; MCI, Mild cognitive impairment; mtDNA, Mitochondrial DNA;

MetO, Methionine sulfoxide; MetS<sup>+</sup>, Sulfuranyl radical; MPTP, mitochondrial permeability transition pore; MRP-1, Multi-drug resistant protein; NBM, nucleus basalis magnocellularis; nDNA, Nuclear DNA; NFT, Neurofibrillary tangles; NMDA, N-methyl-D-aspartic acid; nNOS, Neuronal NOS; NO<sup>•</sup>, Nitric oxide; NSF, N-ethylmaleimide-sensitive factor; O<sub>2</sub><sup>•-</sup>, Superoxide radical anion; ONOO<sup>-</sup>, Peroxynitrite; PEBP, Phosphatidylethanolamine binding protein; PGM1, Phosphoglycerate mutase 1; PHF, Paired helical filaments; Pin1, Peptidyl prolyl-*cis,trans* isomerase 1; RKIP, RAF kinase inhibitor; RNS, Reactive nitrogen species; ROS, Reactive oxygen species; RSNO, Nitrosothiol; SELDI-TOF, Surface-enhanced laser desorption/ionization time-of-flight;  $\gamma$ -SNAP,  $\gamma$ -Soluble N-ethylmaleimide-sensitive attachment protein; SOD, Superoxide dismutase; SP, Senile plaques; TBARS, Thiobarbituric acid reactive substance; TPI, Triosephosphate isomerase; UCHL-1, Ubiquitin carboxy-terminal hydrolase L-1; VDAC, Voltage-dependant anion channel protein; VF, Ventricular cerebrospinal fluid.

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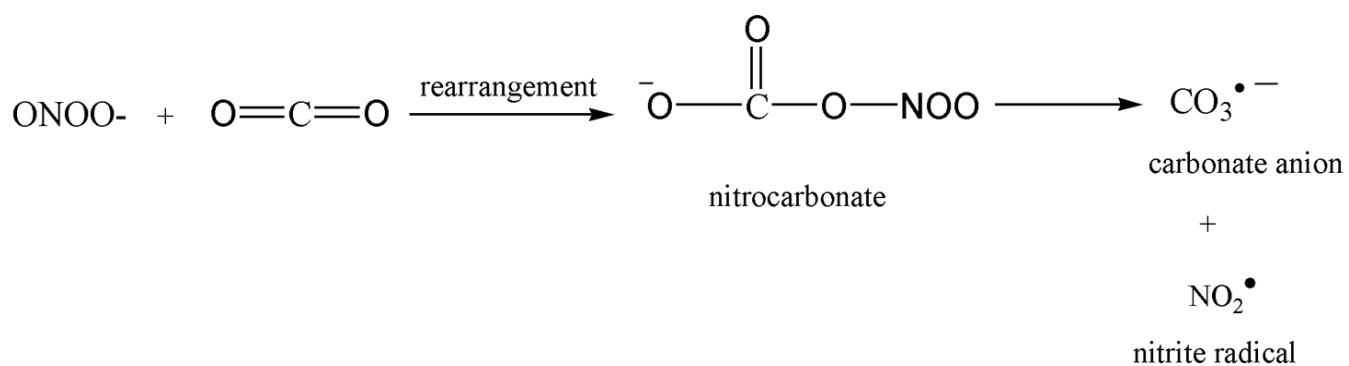
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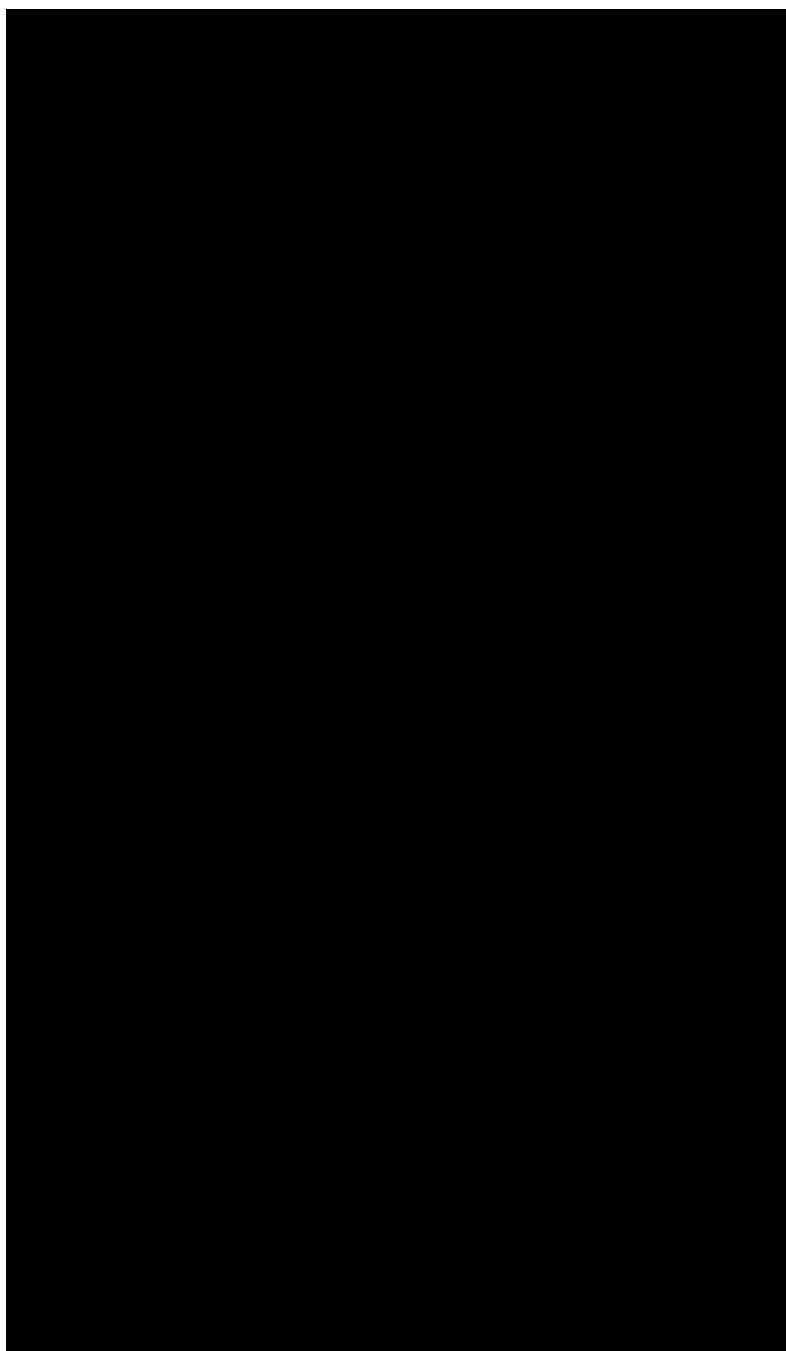
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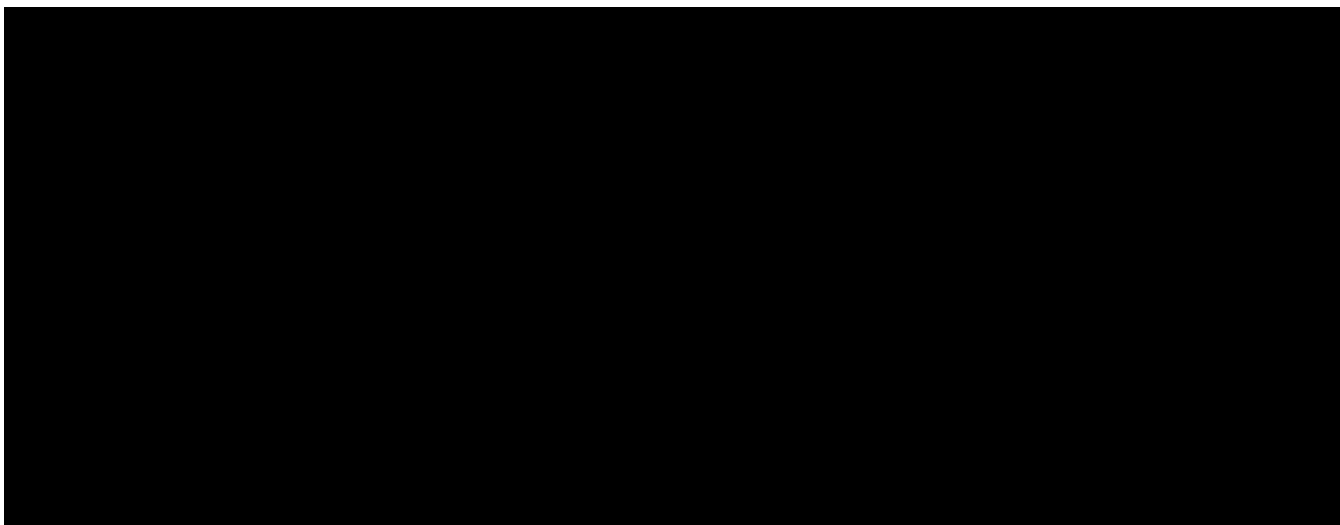
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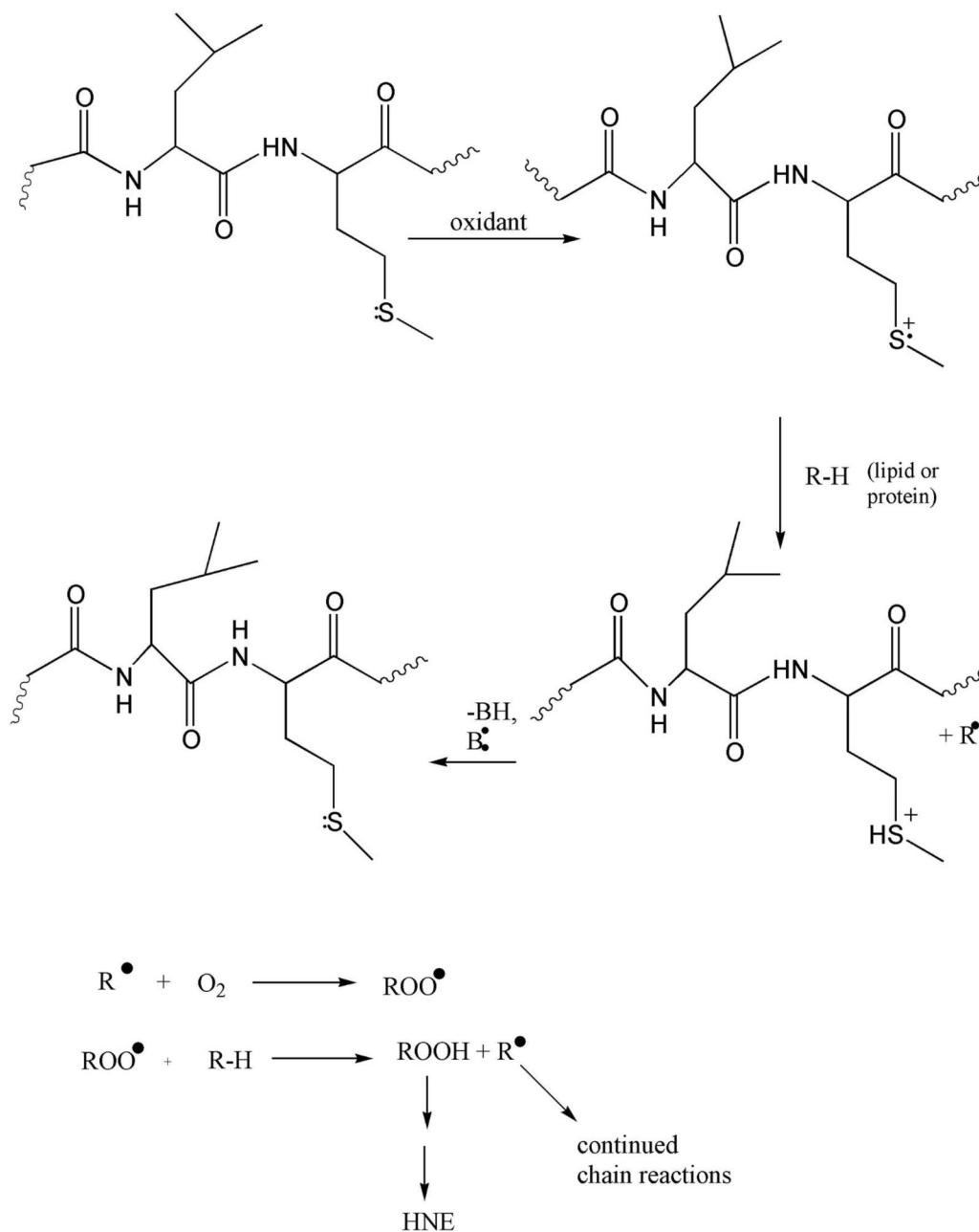


**Figure 1.** Tyrosine nitration. 'A' represents reaction of peroxynitrite and carbon dioxide. 'B' represents formation of 3-nitrotyrosine.



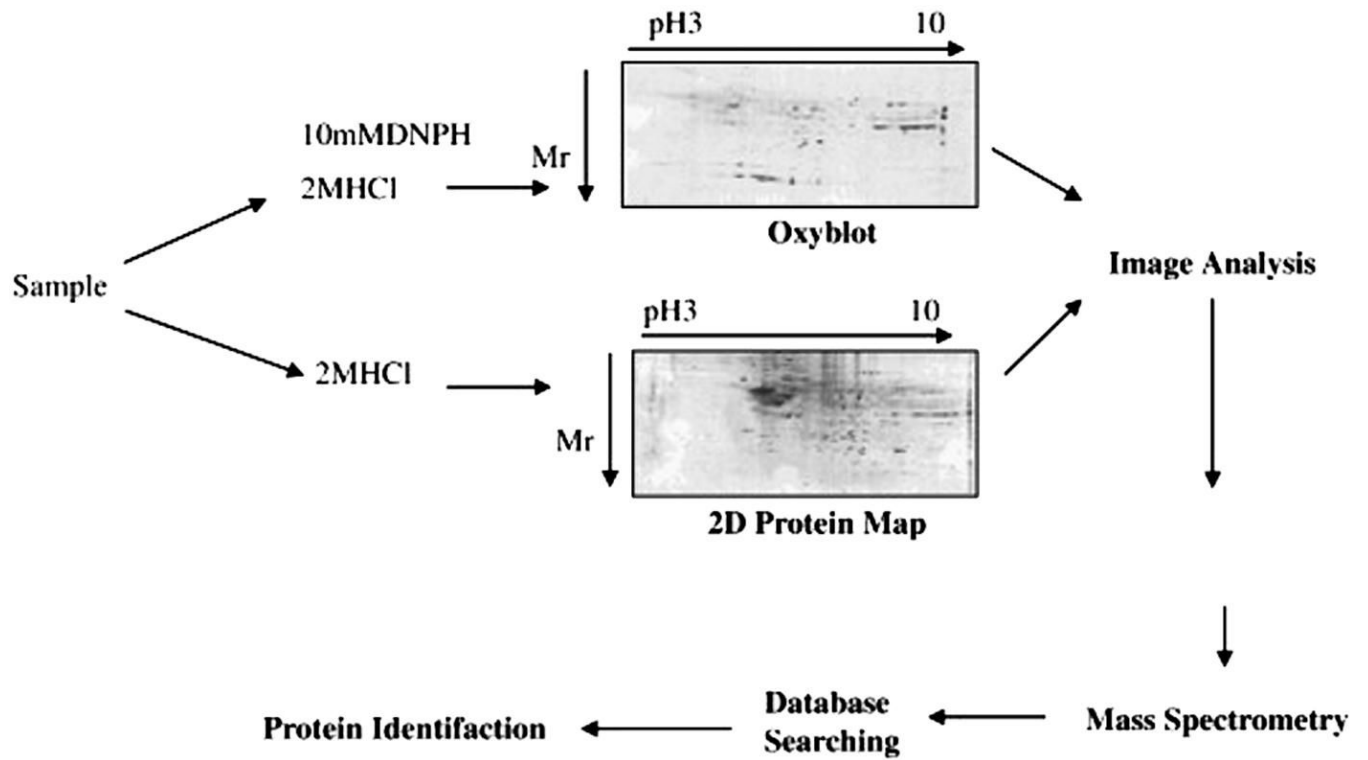


**Figure 2.**  
Methionine chemistry. Formation of methionine sulfoxide and methionine sulfone.

**Figure 3.**

$\text{A}\beta(1-42)$  as a small oligomer is postulated to reside in the lipid bilayer. One-electron oxidation of the S-atom on Met-35, facilitated by the  $\alpha$ -helical  $i + 4$  interaction of the backbone carbonyl of Ile-31 with the S-atom of Met-35, forms a positively charged sulfuranyl radical that is stabilized in part by the helical dipole of  $\text{A}\beta(1-42)$  located in the lipid bilayer. This radical can abstract a lipid acyl allylic H-atom, forming a lipid carbon radical that immediately binds paramagnetic  $\text{O}_2$ . This peroxy radical can abstract an allylic H-atom making the lipid hydroperoxide and propagating the chain reaction. The lipid hydroperoxide on arachidonic acid can decompose to HNE, which can subsequently bind to proteins by Michael addition, resulting in oxidative damage to the protein. The  $\text{SH}^+$  acid on Met has a  $\text{pK}_a$  of minus 5, so

loses the  $H^+$  easily to reform Met. That is, the reaction is catalytic. This mechanism is consistent with an amplification of damage by a relatively minor degree of conversion of Met to the sulfuranyl free radical of  $A\beta(1-42)$ .



**Figure 4.**  
Diagrammatic representation of redox proteomics.

**Table I**  
Mass spectrometry search engines for peptide mass fingerprinting

Search engine	URL
Mascot	<a href="http://www.matrixscience.com">http://www.matrixscience.com</a>
MOWSE	<a href="http://www.hgmp.mrc.ac.uk/Bioinformatics/Webapp/mowse">http://www.hgmp.mrc.ac.uk/Bioinformatics/Webapp/mowse</a>
Profound	<a href="http://prowl.rockefeller.edu/profound_bin/WebProFound.exe">http://prowl.rockefeller.edu/profound_bin/WebProFound.exe</a>
MS-fit	<a href="http://prospector.ucsf.edu/ucshtml4.0/msfit.htm">http://prospector.ucsf.edu/ucshtml4.0/msfit.htm</a>
Peptident	<a href="http://ca.expasy.org/tools/peptident.html">http://ca.expasy.org/tools/peptident.html</a>

**Table II**

Oxidatively modified proteins identified in AD hippocampus and IPL brain regions

Protein function	Hippocampus	Inferior parietal lobule	Oxidative modification	Reference
Energy-related enzymes	$\alpha$ -enolase <sup>*</sup> , TPI, PGM1, GAPDH	$\alpha$ -enolase, TPI <sup>*</sup> , CK, $\gamma$ -enolase <sup>*</sup> , LDH	Carbonylation and nitration	10,12,13,37,38
Proteasome-related proteins	UCHL-1, HSC-71	UCHL-1, HSC-71	Carbonylation	12,37,38
Structural proteins	DRP-2	DRP-2, $\beta$ -actin <sup>*</sup>	Carbonylation and nitration	10,12,13,37
Neurotransmitter-related proteins		GS	Carbonylation	37
Cholinergic function and lipid asymmetry		Neuropolypeptide h3 <sup>*</sup>	Nitration	10
pH regulation protein	CAII <sup>*</sup>		Carbonylation and nitration	12,13
Cell cycle; tau phosphorylation; Abeta production	Pin-1		Carbonylation	12
Synaptic abnormalities and LTP	$\gamma$ -SNAP		Carbonylation	12
Mitochondrial related protein	VDAC <sup>*</sup> , ATP synthase ( $\alpha$ -chain) <sup>*</sup>		Nitration	13

\* indicates this protein was found to be significantly nitrated