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Redox Proteomics and Amyloid β -Peptide: Insights into Alzheimer Disease

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Abstract

Alzheimer disease (AD) is a progressive neurodegenerative disorder associated with aging and characterized pathologically by the presence of senile plaques, neurofibrillary tangles, and neurite and synapse loss. Amyloid beta-peptide (1–42) [$A\beta(1-42)$], a major component of senile plaques, is neurotoxic and induces oxidative stress *in vitro* and *in vivo*. Redox proteomics has been used to identify proteins oxidatively modified by $A\beta(1-42)$ *in vitro* and *in vivo*. In this review, we discuss these proteins in the context of those identified to be oxidatively modified in animal models of AD, and human studies including Familial AD (FAD), Preclinical AD (PCAD), Mild Cognitive Impairment (MCI), Early AD (EAD), Late AD (LAD), Down syndrome (DS) and DS with AD (DS/AD). These redox proteomics studies indicate that $A\beta(1-42)$ -mediated oxidative stress occurs early in AD pathogenesis and results in altered antioxidant and cellular detoxification defenses, decreased energy yielding metabolism and mitochondrial dysfunction, excitotoxicity, loss of synaptic plasticity and cell structure, neuroinflammation, impaired protein folding and degradation, and altered signal transduction. Improved access to biomarker imaging and the identification of lifestyle interventions or treatments to reduce $A\beta$ production could be beneficial in preventing or delaying the progression of AD.

Graphical Abstract

In this review we discuss how redox proteomics provided insights into how $A\beta(1-42)$ -mediated cell death in Alzheimer disease (AD) and its earlier stage, amnesic mild cognitive impairment (MCI), and in *in vitro* and *in vivo* models thereof, is initiated by lipid peroxidation. Oligomeric $A\beta(1-42)$ embeds in the lipid bilayer inducing lipid peroxidation, leading to reactive 4-hydroxy-2-nonenal (HNE). HNE covalently binds Cys, His, and Lys residues on proteins by Michael addition, changing the proteins' conformation and decreasing their function. Key processes in brain that are damaged and dysfunctional as a result of $A\beta(1-42)$ -mediated HNE modification identified by redox proteomics are glucose metabolism, synaptic plasticity, synaptic glutamate clearance, and proteostasis, ultimately leading to neuronal death.

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CONFLICT OF INTEREST STATEMENT

The authors have no conflicts of interest to declare.

Keywords

Redox proteomics; Alzheimer disease; amyloid β -peptide; oxidative stress

Alzheimer Disease (AD) is a neurodegenerative disorder characterized by changes in brain chemistry associated with cognitive decline and aging. AD is the most common cause of dementia (Wilson *et al.* 2012; Barker *et al.* 2002) and is currently the 6th leading cause of death in the United States (US). It is estimated that there are over 5.7 million Americans currently living with AD and of those 5.5 million are age 65 or older; however, with the aging baby boomer population, it is projected that the number of Americans age 65 or older living with AD will increase to 7.1 million by 2025 and to 13.8 million by 2050. Additionally, due to medical advances, it is also expected that the population of Americans living beyond age 85 will increase subsequently increasing the population most at risk of developing AD. Given that no definitive cause, treatment, preventative, or cure exists for AD, the US is facing a growing public health crisis as national costs associated with AD are projected to increase from \$277 billion to \$1.1 trillion by 2050 (Alzheimer's Association 2018).

One percent or fewer of AD cases are familial, due to inherited genetic mutations (Bekris *et al.* 2010), meaning that the overwhelming majority of cases are sporadic and likely due to a concert of multiple factors. The greatest risk factors for developing AD include age, family history, and apolipoprotein E (ApoE) genotype. Three allelic forms of *ApoE* exist: *e2*, *e3*, and *e4*. *e3* is the most common form followed by *e4*, and finally *e2* (Mahley and Rall 2000). *e4* is associated with an increased risk of developing AD with heterozygotes having a three times greater risk and homozygotes having an eight to twelve times greater risk than those homozygous in *e3* (Loy *et al.* 2014; Holtzman *et al.* 2012). While the *ApoE e4* is associated with an increased risk of developing AD, it does not guarantee that one will develop AD (Chouraki *et al.* 2014). Those with the *e2* form have a decreased risk compared to those with the *e3* form (Loy *et al.* 2014; Holtzman *et al.* 2012). Collectively, age, family history, and genetics are factors beyond our control; however, there are also a number of risk factors that can be influenced by lifestyle modifications over which we do have control. Obesity (Rönnekaa *et al.* 2011; Loef *et al.* 2013; Anstey *et al.* 2011; Gottesman *et al.* 2017a), diabetes (Wu *et al.* 2008; Gudala *et al.* 2013; Vagelatos *et al.* 2013; Reitz *et al.* 2011), impaired glucose metabolism (Rönnekaa *et al.* 2011; Crane *et al.* 2013), hyperlipidemia (Solomon *et al.* 2009; Meng *et al.* 2014), and hypertension (Launer *et al.* 2000; Ninomiya *et al.* 2011; Debette *et al.* 2011; Livingston *et al.* 2017; Gottesman *et al.* 2017b) are all associated with increased risk of developing AD. Increased physical activity (Willis *et al.* 2012; Tan *et al.* 2017; Wiley *et al.* 2016; Stephen *et al.* 2017; Blondell *et al.* 2014; Koscak 2017) and consuming a heart-healthy diet are associated with a decreased risk of developing AD (Barberger-Gateau *et al.* 2007; Hardman *et al.* 2016; Lourida *et al.* 2013; Morris *et al.* 2015a; Morris *et al.* 2015b; Féart *et al.* 2010; Solfrizzi *et al.* 2011). Recent studies indicate that brain changes associated with AD may begin 20 or more years before the onset of cognitive symptoms (Villemagne *et al.* 2013; Reiman *et al.* 2012; Jack *et al.* 2009; Bateman *et al.* 2012) suggesting that lifestyle interventions that decrease midlife obesity, diabetes, hypertension, and high cholesterol could potentially reduce the prevalence, or delay the

onset, of Alzheimer's disease. Delay of onset by 5 years is estimated to reduce costs by 33 (Alzheimer's Association 2015) to 39 percent (Zissimopoulos *et al.* 2014).

Extraneuronal deposition of amyloid beta-peptide (A β), measured by positron emission tomography (PET), precedes (Aizenstein *et al.* 2008; Mintun *et al.* 2006; Rowe *et al.* 2010) and positively correlates with cognitive decline and cerebral atrophy (Villemagne *et al.* 2013). A β is a 40- to 42-amino acid peptide derived from amyloid precursor protein (APP) by the concerted proteolytic action of β -secretase at the amino-terminus and γ -secretase at the carboxy-terminus. A β (1–42), which comprises the majority of A β found in senile plaques in AD brain (Selkoe 2001), is the more toxic of these species (Butterfield 1997; Butterfield *et al.* 2002; Copani *et al.* 1991; Walsh and Teplow 2012) with several studies indicating that, rather than fibrils, small soluble oligomers are the toxic form of A β (Drake *et al.* 2003; Lambert *et al.* 2001; Oda *et al.* 1995; Walsh *et al.* 1999). Genetic mutations that lead to familial AD (FAD) involve the genes encoding *presenilin-1* or *presenilin-2*, which comprise the catalytic element of γ -secretase, or *APP* and all subsequently increase the production of A β (1–42) (Selkoe 2001; Goate and Hardy 2012; Jarrett *et al.* 1993; Scheuner *et al.* 1996). Down Syndrome (DS) lends further genetic evidence as to the importance of APP and the consequential role of A β in AD pathogenesis. DS patients have three copies of chromosome 21 which contains the gene encoding APP resulting in increased production of A β (Beyreuther *et al.* 1993) which initially accumulates intracellularly, but then decreases intracellularly as extracellular A β deposits form (Gyure *et al.* 2001; Mori *et al.* 2002). If DS patients live long enough, they develop brain pathology and cognitive symptoms indistinguishable from AD (Wisniewski *et al.* 1985; Lott and Head 2005; Lott and Dierssen 2010).

Progression of AD can be viewed as a continuous spectrum consisting of four stages: preclinical AD (PCAD), mild cognitive impairment (MCI), early AD (EAD), and late-stage AD (LAD). IN PCAD, the patient is fully functional, but brain pathology changes – which can be divided into three stages – have begun to develop unbeknownst to the patient (Dubois *et al.* 2016; Vos *et al.* 2013; Pietrzak *et al.* 2015; Small *et al.* 2001; Sperling *et al.* 2011; Vlassenko *et al.* 2012). Stage 1 is classified by the presence of abnormal A β biomarkers, stage 2 is classified by the presence of abnormal A β biomarkers and neuronal injury, and stage 3 is an extension of stage 2 in which subtle cognitive changes are present (Sperling *et al.* 2011). MCI represents the transition between PCAD and EAD in which cognitive decline is noticeable but does not interfere with activities of daily living. MCI is further subdivided into amnesic MCI (aMCI) and non-amnesic MCI with aMCI having a higher conversion rate to AD (Kelley and Petersen 2007; Petersen 2000, 2004). EAD and LAD are marked by noticeable and progressive cognitive decline and behavioral changes that significantly impact the ability of the patient to carry out everyday functions. Imaging studies document progressive neuropathology and neurodegeneration as the disease advances from EAD into LAD (Drayer *et al.* 1985; Farrow *et al.* 2007; Jack *et al.* 1999, 2018; Rowe *et al.* 2010; Villemagne *et al.* 2013).

Elevated oxidative stress is implicated in the pathogenesis of AD (Butterfield *et al.* 2013; Swomley and Butterfield 2015) and is also detected in DS brain (Cenini *et al.* 2012; Jovanovic *et al.* 1998; Perluigi and Butterfield 2011, 2012). A β (1–42) induces oxidative

stress *in vitro* and *in vivo* (Hensley *et al.* 1994; Butterfield *et al.* 1999; Butterfield and Boyd-Kimball 2004, 2018; Sultana *et al.* 2009) and, in AD brain. There are many hypotheses regarding the mechanism by which A β (1–42)-mediated oxidative stress plays a causative role in the progression of AD (Cheignon *et al.* 2018); however, our laboratory proposed that oligomers of A β (1–42) insert into the bilayer initiating lipid peroxidation (Butterfield and Lauderback 2002; Butterfield *et al.* 2001; Mark *et al.* 1997; Markesbery 1997; Mattson 1997) and the increased protein, lipid, DNA, and RNA oxidation observed in AD brain (Butterfield and Lauderback 2002; Butterfield and Stadtman 1997; Smith *et al.* 1997; Hensley *et al.* 1995; Markesbery and Lovell 1998; Zhang *et al.* 1994; Mecocci *et al.* 1994; Gabbita *et al.* 1998; Shan and Lin 2006; Ding *et al.* 2006; Butterfield and Boyd-Kimball, 2018). Redox proteomics studies have allowed insight into the specific proteins susceptible to oxidation. Biomarkers of oxidative modification include protein carbonyls and the lipid peroxidation by-product, 4-hydroxy-2-*trans*-nonenal (HNE), and a marker of nitration, 3-nitrotyrosine (3-NT), which have been the foci of most redox proteomics analyses relevant to AD to date (Subramaniam *et al.* 1997; Butterfield and Perluigi 2017; Swomley *et al.* 2014; Sultana and Butterfield 2009, 2011; Sultana *et al.* 2009). Such irreversible oxidative protein modifications induced by A β (1–42) initiate conformation changes resulting in altered or lost function with consequences toward disease progression (Butterfield *et al.* 2007; Butterfield and Boyd-Kimball 2018). Reversible oxidative modifications, including S-nitrosylation (Nakamura *et al.* 2013) and cysteine oxidation (Gu and Robinson 2016), may also provide insights into pathogenesis; however, the focus of this review is irreversible oxidative modifications associated with A β (1–42) indexed by protein carbonyls, HNE and 3-NT as we summarize our current knowledge of A β (1–42)-induced protein oxidation *in vitro* and *in vivo* as evidenced by redox proteomics. Here, we first highlight the proteins identified by redox proteomics as oxidatively modified in these models, relate these same proteins that also are oxidized in aMCI and AD brain, and then discuss the implications of such modifications in the context of our current knowledge of AD.

***In vitro* A β (1–42)-induced protein oxidation**

Currently, redox proteomics studies of the *in vitro* effects of A β (1–42) have focused solely on protein carbonylation (Table 1). In cortical synaptosomes incubated with A β (1–42), β -actin, glial fibrillary acid protein (GFAP), and dihydropyrimidinase-related protein-2 (DRP-2 also called collapsin response mediated protein-2, CRMP-2) were found to be significantly carbonylated (Boyd-Kimball *et al.* 2005a); however, in primary neuronal culture incubated with A β (1–42) 14-3-3 ζ , glyceraldehyde-3-phosphate dehydrogenase (GAPDH), pyruvate kinase (PK), and malate dehydrogenase (MDH) were found to be increasing carbonylated (Boyd-Kimball *et al.* 2005b; Sultana *et al.* 2006d). Proteins identified as oxidized by A β (1–42) *in vitro* are consistent with proteins identified to be oxidized in AD and aMCI brain (Castegna *et al.* 2002a,b, 2003; Aksenov *et al.* 2001; Sultana *et al.* 2006a,c, 2007; Butterfield *et al.* 2006a; Reed *et al.* 2008).

***In vivo* A β (1–42)-induced protein oxidation: Models of Alzheimer's Disease**

Various models of the *in vivo* effects of A β (1–42) have been studied using redox proteomics (Table 2). One such model includes the intracerebral ventricular (ICV) injection of A β (1–

42) into the nucleus basalis magnocellularis (NBM) of 3-month-old male Wistar rats. Seven days post-injection, 14-3-3 ζ and chaperonin 60 (HSP60) were found to be significantly carbonylated in the NBM. Notably, this modeled also showed that the oxidative damage induced by A β (1–42) could spread beyond the site of injection resulting in the significant carbonylation of α - and β -tubulin and glutamine synthetase (GS) in the cortex, and 14-3-3 ζ , β -synuclein, pyruvate dehydrogenase (PDH), GAPDH, and phosphoglycerate mutase 1 (PGM1) in the hippocampus (Boyd-Kimball *et al.* 2005c).

C. elegans expressing human A β (1–42) were previously reported to cause elevated protein carbonyls correlated with aggregated A β (1–42) (Yatin *et al.* 1999). Subsequent studies used a mRNA surveillance system to degrade foreign mRNA at permissive (regular) growth temperatures. The non-permissive elevated growth temperature caused the surveillance system to be inactive, resulting in expression of A β (1–42) for any given time chosen by the experimenter. Return to permissive temperature stopped A β (1–42) expression. Expression of A β (1–42) for 24 h led to elevated oxidative damage (protein carbonyls) in the worm that was correlated with paralysis, since a muscle wall promoter was used to express A β (1–42), and there was absence of A β fibril formation, consistent with the notion that oligomers of A β (1–42) inserted into the muscle cell membranes led to oxidative stress (Drake *et al.* 2003). Redox proteomics analysis of this *C. elegans* strain identified both short and medium chain acyl-CoA dehydrogenase (acyl CoA DH), elongation factor 1 γ (Ef-1 γ), MDH, arginine kinase (AK), RACK1 ortholog, myosin regulatory light chain (MRLC), actin, adenosine kinase (ADK), lipid binding protein (LBP), transketolase (TK), proteasome α - and β -subunit, and glutathione-S-transferase (GST) to be significantly carbonylated (Boyd-Kimball *et al.* 2006).

The canine model of the aged beagle deposits A β (1–42) identical to the human amino acid sequence as a function of age (Miligram *et al.* 2004; Head 2013). Long-term administration of an antioxidant-rich diet and behavioral enrichment resulted in the significantly decreased carbonylation of glutamate dehydrogenase (GDH), GAPDH, α -enolase, neurofilament triplet L, GST P, and fascin actin bundling protein compared to age-matched control (Opii *et al.* 2008). These findings support a role for lifestyle intervention as a therapeutic approach to prevent or delay A β (1–42) induced oxidative stress.

Redox proteomics has also been utilized to analyze several transgenic or knock-in rodent models of AD including the APP/PS-1 double human mutant knock-in mouse (the APP/PS-1 mouse), the triple transgenic AD mouse (3 \times Tg-AD), the senescence accelerated mouse P8 (SAMP8), and the J20 mouse (Table 3). The APP/PS1 double human knock-in mouse is the APP^{NLh/NLh} \times PS-1^{P264L/P264L} strain which expresses normal levels of human APP, but significantly increased levels of A β (1–42) prior to two months of age. A β deposition occurs by 6 months of age and increases linearly as a function of age (Flood *et al.* 2002) similar to A β solubility and deposition exhibited in human brain during the progression of AD (Murphy *et al.* 2007). This age-dependent increase in A β (1–42) production correlates with cognitive impairment (Bruce-Keller *et al.* 2011; Webster *et al.* 2013), oxidative stress (Abdul *et al.* 2008; Huang *et al.* 2010), decreased manganese superoxide dismutase (MnSOD or SOD2) activity and mitochondrial respiration (Anantharaman *et al.* 2006; Sompol *et al.* 2008), and loss of phospholipid asymmetry (Bader Lange *et al.* 2010). Redox proteomics

was used to analyze the oxidative modification of proteins, as indexed by protein carbonyls, in the brain of APP^{NLh/NLh} × PS-1^{P264L/P264L} mice as a function of age compared to age-matched wild-type control. Proteins identified to be significantly oxidized can be broadly classified as structural, regulatory, synaptic, and involved in glucose metabolism. The structural protein β -actin was found to be significantly oxidized at 1 month and 15 months of age while the synaptic protein β -synuclein was found to be significantly oxidized at 12 months of age. The regulatory proteins identified were 14-3-3 $\zeta/\delta/\gamma$ and peptidylprolyl cis-trans isomerase-1 (Pin1). 14-3-3 $\zeta/\delta/\gamma$ was found to be significantly oxidized at 1, 9, 12, and 15 months, while Pin-1 was found to be significantly oxidized at 9, 12 and 15 months of age. α -enolase, pyruvate dehydrogenase E1 (PDH), and ATP synthase α -subunit – all proteins involved in generating cellular energy – were determined to be significantly oxidized. α -enolase was found to be significantly oxidized at 6, 9, 12, and 15 months and ATP synthase was found to be significantly oxidized at 12 and 15 months while PDH was found to be significantly oxidized only at 6 months of age (Sultana *et al.* 2011a).

The 3 \times Tg-AD mouse model develops age related progressive neuropathology including senile plaques, neurofibrillary tangles, and synaptic dysfunction (Oddo *et al.* 2003a). Increased intracellular A β is detected by 3 months of age with cognitive impairment observed at 4 months of age (Billings *et al.* 2005) and extracellular deposition occurs by 6 months of age (Oddo *et al.* 2003a,b). Redox proteomics analysis of carbonylated proteins in the hippocampus of 3 month-old 3 \times Tg-AD mice identified 14-3-3 ζ/γ , mitochondrial aconitase, GS, GAPDH, α -enolase, phosphoglycerate kinase 1 (PGK1), heat shock protein 90- β , mitochondrial MDH, neurofilament light polypeptide, protein disulfide-isomerase A3, T-complex protein 1 subunit ϵ , and tubulin β -2A chain to be significantly oxidized compared to age-matched non-transgenic controls (Shen *et al.* 2015).

SAMP8 mice are a model for gerontological and age-related dementia research that exhibit learning and memory deficits with age (Flood and Morley 1993, 1998). These changes correlate with increased oxidative stress (Butterfield *et al.* 1997; Farr *et al.* 2003; Poon *et al.*, 2005; Butterfield and Poon 2005) starting as early as 4 months. SAMP8 mice exhibit an age-related increase in APP (Morley *et al.* 2000; Nomura *et al.* 1996) and hippocampal A β peptide (Kumar *et al.* 2000; Takeda 2009) depositing as granules in the hippocampus by 6 months of age (Takemura *et al.* 1993; Del Valle *et al.* 2010;) with plaque formation late in life at 20 months (Morley *et al.* 2000). Cognitive deficits occur prior to plaque formation supporting the role for small, soluble oligomers of A β inducing oxidative damage resulting in learning and memory impairments. Consequently, the SAMP8 mouse is considered a model of oxidative stress and AD (Morley *et al.* 2012). Redox proteomics analysis of the brain of 12 month old SAMP8 mice identified lactate dehydrogenase 2 (LDH-2), creatine kinase (CK), DRP-2 (CRMP-2), and α -spectrin 2 to be significantly oxidized as indexed by protein carbonyls compared to 4 month old SAMP8 mice (Poon *et al.* 2004a). Antisense oligonucleotide (AO) directed against the A β region of *APP* gene in aged SAMP8 mice significantly decreased APP protein levels, reversed learning and memory deficits (Kumar *et al.* 2000) and significantly decreased brain A β levels and oxidative stress biomarkers compared to age-matched SAMP8 mice that received a random AO (Poon *et al.* 2004b). In this model, carbonylation of aldolase 3 (Aldo 3), coronin 1a (Coro 1a), and peroxiredoxin 2 (Prx2) was found to be significantly decreased in the 12-month-old SAMP8 mice that

received the AO directed against the A β region of *APP* gene (Poon *et al.* 2005). Another study determined that the age-related increase in APP and A β may be due to an age-related increase in PS-1 protein level in the hippocampus of SAMP8 mice (Kumar *et al.* 2009). AO directed against the *PS-1* gene in 12 month old SAMP8 mice resulted in significantly decreased PS-1 protein levels, oxidative stress parameters, and reversed learning and memory deficits in the hippocampus. In this model, nitration of LDH, DRP-1 (CRMP-1), dynamin-1 (Dyn-1), GFAP, vesicle-fusing ATPase (NSF), α -enolase, isocitrate dehydrogenase (IDH), actin-related protein 2 (Actr2), and septin-11 (SEP11) was significantly decreased in SAMP8 mice receiving AO directed against the *PS-1* gene while nitration of DRP-2 (CRMP-2) and peptidase α (DPL2) was significantly increased (Fiorini *et al.* 2013).

The J20 mouse model expresses human APP with the Swedish (670/671_{KM->NL}) and Indiana (717_{V->F}) FAD mutations generating increased A β (1–42) by 2 months of age with plaques forming by 5 months of age (Mucke *et al.* 2000). This increase in soluble A β (1–42) correlates with a decrease in presynaptic terminals (Mucke *et al.* 2000) and an increase in oxidative stress (Butterfield *et al.* 2010) and learning and memory deficits (Mucke *et al.* 2000; Galvan *et al.* 2006; Harris *et al.* 2010) that again supports the role of soluble A β (1–42)-induced oxidative stress in synaptic toxicity in AD. Redox proteomics analysis has shown decreased nitration of phosphatidylethanolamine-binding protein 1 (PEBP-1) and Pin1 in brain of 9-month-old J20 mice compared to the age-matched non-transgenic control (Robinson *et al.* 2011).

Collectively, redox proteomics analyses of *in vivo* models of A β (1–42)-induced oxidative stress can be categorized as involved in cellular redox homeostasis and detoxification defense, glucose metabolism, synaptic plasticity, vesicle-mediated transport and cell structure, neuroinflammation, protein folding and degradation, and signal transduction and are consistent with reports of such functional proteins being oxidatively modified and usually dysfunctional in aMCI and AD brains (Sultana *et al.* 2006a,c, 2007; Reed *et al.* 2008; Aluise *et al.* 2011; Castegna *et al.* 2002a,b, 2003; Aksenov *et al.* 2001; Butterfield *et al.* 2006a).

***In vivo* A β (1–42)-induced protein oxidation: PCAD, MCI, AD, and DS Human Studies**

Redox proteomics analyses were conducted to identify oxidatively modified proteins in brain representing all stages of the AD continuum and DS (Table 4). In PCAD inferior parietal lobule (IPL), a significant increase in insoluble monomeric A β (1–42) is observed compared to control, but no difference in oligomeric A β or oxidative stress biomarkers were detected (Aluise *et al.* 2010). MCI IPL, however, exhibits increased protein carbonyls compared to PCAD IPL. Redox proteomics analysis showed α -enolase and heat shock protein 90 (HSP90) to be significantly carbonylated in MCI IPL compared to PCAD IPL (Aluise *et al.* 2011). Carbonic anhydrase II (CA II), heat shock protein 70 (HSP70), mitogen-activated protein kinase I (MAPKI), and syntaxin binding protein I (SBP1) are also significantly carbonylated in MCI IPL compared to age-matched control (Sultana *et al.*

2010). In MCI hippocampus, α -enolase, GS, pyruvate kinase M2 (PKM2), and Pin1 were identified to be significantly carbonylated compared to age-matched control (Butterfield *et al.* 2006a). HNE-bound protein modifications have also been assessed in MCI hippocampus and IPL. In the hippocampus, α -enolase, LDH, PGK, HSP70, carbonyl reductase, and neuropolypeptide h3 (PEBP1) had significantly increased levels of protein-bound HNE while β -actin, PK, initiation factor α (eIF- α), and elongation factor Tu (EF-Tu) were identified in MCI IPL. ATP synthase was found to have increased levels of protein-bound HNE in both MCI hippocampus and IPL (Reed *et al.* 2008). Protein nitration in MCI IPL and hippocampus has also been assessed by redox proteomics. α -enolase was found to be significantly nitrated in both MCI IPL and hippocampus while glucose related protein precursor, aldolase, GST mu (GSTM3), multidrug resistant protein (MRP3), and 14-3-3 γ were significantly nitrated in MCI IPL and peroxiredoxin 6 (Prx6), DRP-2 (CRMP-2), fascin 1, and HSP70 isoform A8 were significantly nitrated in MCI hippocampus (Sultana *et al.* 2007).

In EAD IPL, phosphoglycerate mutase 1 (PGM1), GFAP, and fructose bisphosphate aldolase C (FBA-C) are significantly carbonylated (Sultana *et al.* 2010), while MnSOD, α -enolase, ATP synthase, DRP-2 (CRMP-2), MDH, and triose phosphate isomerase (TPI) have significant increases in protein-bound HNE compared to age-matched control (Reed *et al.* 2009). Assessment of HNE-bound proteins in LAD have identified increased levels modifying MnSOD, ATP synthase, DRP-2 (CRMP-2), and GS in IPL and aldolase, aconitase, α -enolase, Prx6, and α -tubulin in hippocampus compared to respective age-matched controls (Perluigi *et al.* 2009). Also in LAD brain, ubiquitin carboxy-terminal hydrolase L-1 (UCH-L1), DRP-2 (CRMP-2) and α -enolase were found to be significantly carbonylated in both IPL and hippocampus compared to respective age-matched controls (Castegna *et al.* 2002a,b; Sultana *et al.* 2006c). Creatine kinase BB (CK BB), GS, and heat shock cognate 71 (HSC71) also were significantly carbonylated in IPL (Castegna *et al.* 2002a,b), and Pin1, PGM1, CA II, TP1, and γ -synaptosomal protein like soluble N-ethylmaleimide-sensitive factor (γ -SNAP) were significantly carbonylated in hippocampus (Sultana *et al.* 2006c). CAII, GAPDH, ATP synthase, and voltage-dependent anion-channel protein-1 (VDAC1) are significantly nitrated in LAD hippocampus, and TPI and neuropeptide h3 are increasingly nitrated in LAD IPL. α -enolase was found to be significantly nitrated in LAD IPL and hippocampus (Castegna *et al.* 2003; Sultana *et al.* 2006a). Frontal cortex of two FAD patients each with a mutation in PS1 have been analyzed using redox proteomics. Because of the limited sample size only proteins with elevated carbonylation compared to age-matched controls were reported. These proteins included γ -enolase, dimethylarginine dimethylaminohydrolase 1 (DMDMAH-1), UCH-L1, and actin (Butterfield *et al.* 2006b), consistent with the notion that glucose metabolism, nitric oxide metabolism, synaptic remodeling, and protein quality control are detrimentally affected in inherited AD.

As discussed previously, redox proteomics analyses of DS brain can provide insights into the *in vivo* effects of A β (1–42). In DS frontal cortex, GDH, Prx2, complex III Rieske protein (cyt b-c₁), fructose bisphosphate aldolase-A, FBA-C, DRP-2, GFAP, UCH-L1, α -internexin, and myelin binding protein (MBP) have significantly elevated levels of protein-bound HNE (Di Domenico *et al.* 2014), while succinyl CoA-3-ketoacid-CoA transferase 1 (SCOT-1),

cathepsin D (CatD), 78kDa glucose-regulated protein (GRP78), UCH L-1, and V_o-type proton ATPase (V_o-ATPase) were significantly carbonylated (Di Domenico *et al.* 2013) compared to age-matched control. Protein-bound HNE levels of Cu,ZnSOD, cyt b-c₁, α -enolase, GAPDH, MDH, GFAP, HSC71, T-complex protein 1 subunit β (TCPB), and neurofilament medium polypeptide (NMP) were significantly increased in frontal cortex from DS with AD (DS/AD) compared to age-matched control while GDH, DRP-1, DRP-2, SBP1, GRP78, aconitase, HSP90B1 and MBP were significantly increased in DS/AD frontal cortex compared to DS (Di Domenico *et al.* 2014).

Redox proteomics analyses of MCI, AD, and DS brain provides insight into the proteins of the proteome that are particularly sensitive to oxidative modification. Notably, GS is oxidatively modified in MCI (Butterfield *et al.* 2006a) and LAD brain (Castegna *et al.* 2002a; Perluigi *et al.* 2009), and ATP synthase, α -enolase, and DRP-2 (CRMP-2) are oxidatively modified in MCI (Butterfield *et al.* 2006a; Sultana *et al.* 2007; Reed *et al.* 2008; Aluise *et al.* 2011), EAD (Reed *et al.* 2009) and LAD (Castegna *et al.* 2002b, 2003; Sultana *et al.* 2006a,c; Perluigi *et al.* 2009). α -enolase also was oxidatively modified in DS/AD brain, while DRP-2 was also oxidized in both DS and DS/AD brain (Di Domenico *et al.* 2014). Likewise, redox proteomics analyses provide a snapshot of the oxidative modification of the proteome at a given point in time. Interestingly, HSP 70 and HSP90 are only oxidized in MCI brain (Sultana *et al.* 2007, 2010; Reed *et al.* 2008; Aluise *et al.* 2011), suggesting that oxidative modification of these molecular chaperones and maintenance of proper protein folding may be affected early in the progression of AD. Similarly, PK which catalyzes the final step in aerobic glycolysis is oxidatively modified only in MCI (Butterfield *et al.* 2006a; Reed *et al.* 2008) and DS brain (Di Domenico *et al.* 2014). A β (1–42) induces oxidative modification of DRP-2 (Boyd-Kimball *et al.* 2005a) and PK (Sultana *et al.* 2006d) *in vitro* and GS *in vivo* (Boyd-Kimball *et al.* 2005c) strongly support the idea that A β (1–42) plays a significant role in the oxidative modification of these proteins in AD or DS brain.

Serum, CSF, and Peripheral Lymphocyte Mitochondria

Adaptation of redox proteomics methods to analyze plasma, serum, and cerebrospinal fluid (CSF) (Di Domenico *et al.* 2016a) and circulating biomarkers of protein oxidation in Alzheimer's disease have been previously reviewed (Aluise *et al.* 2008; Di Domenico *et al.* 2011; Lista *et al.* 2013). In cerebrospinal fluid, decreased A β (1–42) and increased tau phosphorylated at threonine 181 (p-tau181) correlate with disease progression from MCI to AD (Mattsson *et al.* 2009; Di Domenico *et al.* 2016b). Just like changes in brain pathology, CSF levels of A β (1–42) and tau begin to change about two decades prior to the onset of symptoms, with changes in A β (1–42) preceding changes in tau (Wildsmith *et al.* 2014; Bateman *et al.* 2012; Buchhave *et al.* 2012). Redox proteomics analysis of CSF identified α -1 β -glycoprotein, vitamin D-binding protein (DBP), ApoE, prostaglandin-H2 D-isomerase (PGDS), and α -1-anti-trypsin (A1AT) to be significantly carbonylated in both aMCI and AD compared to age-matched control. Gelsolin was the only protein identified to be significantly carbonylated in CSF of AD compared to aMCI (Di Domenico *et al.* 2016b). λ chain precursor has also been identified as significantly carbonylated in AD CSF compared to control (Korolainen *et al.* 2007). Redox proteomics analysis of plasma has identified A1AT, fibrinogen γ -chain precursor protein, transferrin, and hemopexin to be significantly

carbonylated in AD compared to age-matched control (Choi *et al.* 2002; Yu *et al.* 2003). More recently, increased carbonylation of α 2-macroglobulin has been identified in AD plasma compared to control, while increased carbonylation of haptoglobin has also been identified in AD plasma and aMCI plasma compared to control. Increased carbonylation of haptoglobin was also detected between AD and aMCI plasma (Cocciolo *et al.* 2012). Moreover, plasma levels of heme oxygenase –1/biliverdin reductase-A, that normally produce the antioxidant bilirubin, are found at different levels in plasma in AD (Di Domenico *et al.* 2012). More redox proteomics studies of serum and CSF are necessary to expand our understanding of the progression of AD and potentially identify additional biomarkers.

Peripheral lymphocyte mitochondria showed elevated oxidative stress in both aMCI and AD that correlated with decreased levels of small molecule antioxidants, with elevated levels of A β (1–42), and with decreased performance on tests of cognition (Sultana *et al.* 2011b, 2013b).

Redox Proteomics and A β (1–42)-mediated oxidative stress in the progression of AD

A β (1–42) induces oxidative stress by forming small soluble oligomers that insert into the lipid bilayer and initiate lipid peroxidation, forming free radicals that further propagate lipid peroxidation events by abstracting allylic hydrogen atoms from acyl chains of lipids in the lipid bilayer (Figure 1). This process leads to a chain reaction eventually resulting in lipid peroxidation products, such as HNE that further contribute to protein oxidation by reacting with proteins via Schiff base chemistry or with Cys, Lys, and His residues of proteins by Michael Addition (Butterfield *et al.* 2001, 2007, 2013; Butterfield and Lauderback 2002; Halliwell 2006; Di Domenico *et al.* 2017; Luczaj *et al.* 2017) (Figure 2). Such protein modifications result in conformational changes and often loss of function (Table 5) leading to necrotic or apoptotic cell death (Subramaniam *et al.* 1997; Butterfield and Stadtman 1997).

Imaging studies indicate that increase in brain A β (1–42) may begin up to 20 years prior to the onset of cognitive symptoms (Villemagne *et al.* 2013; Reiman *et al.* 2012; Jack *et al.* 2009; Bateman *et al.* 2012). Early detection of A β (1–42) pathology may allow a timeframe for interventions that may prevent or delay the onset of cognitive symptoms; however, a greater understanding of the brain chemistry changes resulting from the increase in A β (1–42) is necessary to elucidate the progression of AD. Redox proteomics is a high-throughput method that has provided insight into the proteins that are particularly susceptible to oxidative damage as AD neuropathology accumulates from PCAD through LAD (Swomley and Butterfield 2015; Sultana *et al.* 2013a; Sultana and Butterfield 2013; Reed *et al.* 2010; Butterfield and Sultana 2007). Here we will focus our discussion to proteins found to be oxidatively modified in two or more of the models previously described (Figure 3). These proteins that have been identified to be oxidatively modified can be broadly classified into the following categories: antioxidants and cellular detoxification defenses, energy yielding

metabolism and mitochondrial dysfunction, excitotoxicity, synaptic plasticity and cell structure, neuroinflammation, protein folding and degradation, and signal transduction.

Antioxidants and cellular detoxification defenses

GSTs catalyze the conjugation of HNE to the cysteinyl residue of glutathione (GSH) forming GS-HNE adducts to be cleared from the cell by the multidrug resistant protein, MRP-1 (Sharma *et al.* 2004; Balogh and Atkins 2011). GST is carbonylated *in vivo* in *C. elegans* expressing A β (1–42) (Boyd-Kimball *et al.* 2006) and in the canine model of aging (Opii *et al.* 2008). Additionally, GST is excessively nitrated in MCI IPL (Sultana *et al.* 2007) and has significantly elevated levels of protein-bound HNE in AD hippocampus resulting in significantly decreased activity (Sultana and Butterfield 2004; Lovell *et al.* 1998). Decreased GST activity significantly impacts the activity of this detoxification process preventing the clearance of HNE, allowing for increased accumulation of HNE (Singhal *et al.* 2015; Luczaj *et al.* 2017; Siems and Grune 2003) and the subsequent HNE-modification of other proteins.

Peroxiredoxins (Prxs) are a family of thiol-dependent peroxidases that rapidly reduce H₂O₂ (Wood *et al.* 2003). Prxs are subcategorized into 2-Cys-Prx or 1-Cys-Prx enzymes. 2-Cys-Prx isoforms function as dimers each containing a conserved Cys residue in the amino-terminal region that reacts with peroxides and is oxidized to sulfenic acid. The sulfenic acid moiety then oxidizes an additional conserved Cys residue in the carboxy-terminal region of the other subunit to form an intrasubunit disulfide bond that is resolved by thioredoxin in an NADPH-dependent reduction. 1-Cys-Prx isoforms react with peroxides in the same manner as 2-Cys-Prx, but function catalytically as a monomer and lack the sacrificial carboxy-terminal Cys residue (McBean *et al.* 2015). Oxidized 1-Cys-Prx isoforms form a disulfide linkage with GST that is resolved by successive reaction with GSH (Rhee and Kil 2017) (Figure 4). Prx2 is a 2-Cys-Prx that is expressed primarily in the cytosol of neurons (Hattori and Oikawa 2007) and is oxidized in DS brain (Di Domenico *et al.* 2014). Oxidation of Prx2 was significantly decreased in brain of SAMP8 mice treated with an antisense oligonucleotide (AO) directed against the A β region of APP indicating that oxidative modification of Prx2 is A β (1–42) dependent (Poon *et al.* 2005). Prx6 is a 1-Cys-Prx isoform that is expressed in the cytosol and nucleus of astrocytes and oligodendrocytes (Hattori and Oikawa 2007) and is oxidatively modified in MCI (Sultana *et al.* 2007) and LAD brain (Perluigi *et al.* 2009). Expression of Prx2 is increased in AD and DS brain (Kim *et al.* 2001; Krapfenbauer *et al.* 2003), but this may be a compensatory mechanism. Oxidative modification of Prx2 and Prx6 not only contribute to impairment of the antioxidant response in the central nervous system in AD, but also may impact the signaling properties of Prxs and their ability repair peroxidized cell membranes (Fisher 2017) and to prevent, or delay, apoptotic cell death (Hampton and O'Connor 2016). In addition to their antioxidant function, Prxs also exhibit thiol redox-regulated chaperone activity (Kumsta and Jakob 2009; Conway and Lee 2015). Irreversible oxidative modifications of Prxs including carbonylation, nitration, and protein-bound HNE may inhibit the thiol redox-regulated activation of Prx chaperone activity contributing to increased protein misfolding and aggregation in AD brain (Kundra *et al.* 2017).

Energy Yielding Metabolism and Mitochondrial Dysfunction

Glycolytic enzymes including aldolase, TPI, GAPDH, PGK, PGM, enolase, and PK are significantly oxidatively modified in AD brain (Sultana *et al.* 2006a,c, 2007, 2010; Perluigi *et al.* 2009; Reed *et al.* 2008, 2009; Castegna *et al.* 2003; Butterfield *et al.* 2006a). Of these, GAPDH was found to be oxidatively modified in primary neuronal culture treated with A β (1–42) (Boyd-Kimball *et al.* 2005b; Sultana *et al.* 2006d), in hippocampus of rats following ICV injection of A β (1–42) (Boyd-Kimball *et al.* 2006), in aged canine (Opii *et al.* 2008), in 3 \times Tg-AD mice (Shen *et al.* 2015), in LAD (Sultana *et al.* 2006a), and DS/AD brain (Di Domenico *et al.* 2014), while oxidation of PK was observed in MCI and DS and was induced by A β (1–42) in primary neuronal culture (Sultana *et al.* 2006d). α -enolase is extensively oxidized in multiple AD mouse models (Sultana *et al.* 2011a; Shen *et al.* 2015; Fiorini *et al.* 2013) and in MCI (Butterfield *et al.* 2006a; Sultana *et al.* 2007; Reed *et al.* 2008; Aluise *et al.* 2011), EAD (Reed *et al.* 2009), LAD (Castegna *et al.* 2002b, 2003; Sultana *et al.* 2006a,c; Perluigi *et al.* 2009), and DS/AD brain (Di Domenico *et al.* 2014). Decreased glucose catabolism in the progression of AD has been well documented with the use of PET imaging studies (Yamaguchi *et al.* 1997; Marcus *et al.* 1997; Kato *et al.* 2016). The brain preferentially utilizes glucose (Sokoloff *et al.* 1977), but can also utilize ketone bodies in times of need (Hertz and Rothman 2016), to meet its cellular energy needs; however, beyond the production of ATP, glucose is also needed as a precursor for neurotransmitter biosynthesis, and plays a role in regulation of cell death and autophagy (Hertz and Chen 2017; Mergenthaler *et al.* 2013). Oxidative modification of glycolytic enzymes could result in glucose hypometabolism in AD.

Mitochondrial dysfunction also plays a role in AD pathogenesis (Reddy and Reddy 2011; Tu *et al.* 2014). In an APP/PS1 transgenic mouse model of AD, greater mitochondrial dysfunction is evident in the hippocampus and cortex that corresponded with increased A β mitochondrial levels and cognitive deficits (Dragicevic *et al.* 2010). In female 3 \times Tg-AD mice, mitochondrial dysfunction corresponded with the onset of oxidative stress, but precedes the development of plaque and tangle neuropathology (Yao *et al.* 2009), suggesting the mitochondrial dysfunction is an early event in AD pathogenesis. MDH, an important enzyme in the tricarboxylic acid (TCA) cycle, has been identified by redox proteomics as oxidized by A β (1–42) *in vitro* (Sultana *et al.* 2006d) and *in vivo* (Boyd-Kimball *et al.* 2006) and in 3 \times Tg-AD mice (Shen *et al.* 2015), EAD (Reed *et al.* 2009), and DS/AD brain (Di Domenico *et al.* 2014). Beyond the TCA cycle, MDH is important in the malate-aspartate shuttle that regenerates cytosolic NAD⁺ for GAPDH and glycolytic activity. Aconitase, another TCA cycle enzyme, is oxidized in 3 \times Tg-AD mice (Shen *et al.* 2015) and in LAD (Perluigi *et al.* 2009) and DS/AD brain (Di Domenico *et al.* 2014). ATP synthase (complex V) is also oxidized in APP/PS1 double human mutant knock-in mice (Sultana *et al.* 2011a) and in MCI (Reed *et al.* 2008), EAD (Reed *et al.* 2009), and LAD brain (Sultana *et al.* 2006a; Perluigi *et al.* 2009). Oxidation and altered function of mitochondrial enzymes critical for maintaining cellular energy needs could contribute to synaptic dysfunction, neurite loss and cell death evident in AD brain (Figure 5). See further discussion of glucose dysmetabolism in the progression of AD below in the Conclusion and Future Directions section.

Excitotoxicity

Glutamate is an excitatory neurotransmitter that is cleared from the synapse by the glial glutamate transporter (GLT-1), also known as the excitatory amino acid transporter-2 (EAAT2), where it is converted to glutamine by glutamine synthetase (GS). GLT-1 activity is decreased in AD brain (Masliah *et al.* 1996), which is likely due to the elevated levels of HNE bound to GLT-1 in AD brain (Lauderback *et al.* 2001). Redox proteomics has identified GS as oxidatively modified *in vivo* in *C. elegans* expressing A β (1–42) (Boyd-Kimball *et al.* 2006), and in MCI (Sultana *et al.* 2010) and LAD brain (Castegna *et al.* 2002a; Perluigi *et al.* 2009). GS activity is significantly decreased in AD brain (Smith *et al.* 1991; Hensley *et al.* 1995) and is likely explained by the increased protein-bound HNE and carbonylation present in AD brain (Perluigi *et al.* 2009; Castegna *et al.* 2002a). Taken together, oxidation of GLT-1 and GS could result in decreased clearance of synaptic glutamate inducing excitotoxicity and neuronal death.

Synaptic plasticity and cell structure

Dihydropyrimidinase-related protein-2 (DRP-2), also known as collapsin response mediator protein-2 (CRMP-2), was first characterized as functioning in neurite outgrowth by guiding the axonal growth cone (Goshima *et al.* 1995; Inagaki *et al.* 2001). More recently, DRP-2 has been identified as a microtubule associated protein that functions as an adaptor in several additional processes including establishing neuronal polarity, kinesin-dependent transport, neurotransmitter release, and Ca²⁺ channel regulation (Hensley *et al.* 2011; Hensley and Kursula 2016). DRP-2 is oxidatively modified by A β (1–42) *in vitro* (Boyd-Kimball *et al.* 2005a) and *in vivo* in SAMP8 mice (Poon *et al.* 2004; Fiorini *et al.* 2013) and in MCI (Sultana *et al.* 2007), EAD (Reed *et al.* 2009), LAD (Castegna *et al.* 2002b; Sultana *et al.* 2006c; Perluigi *et al.* 2009), DS, and DS/AD brain (Di Domenico *et al.* 2014). Cytoskeletal proteins β -actin and α -tubulin also are susceptible to oxidative modification by A β (1–42). β -Actin is oxidized *in vitro* and *in vivo* by A β (1–42)-related processes (Boyd-Kimball *et al.* 2005a, 2006), in APP/PS1 double human mutant knock-in mice (Sultana *et al.* 2011a), and in MCI and FAD brain (Reed *et al.* 2008; Butterfield *et al.* 2006b), while α -tubulin is oxidized *in vivo* by A β (1–42) (Boyd-Kimball *et al.* 2005c), in 3 \times Tg-AD (Shen *et al.* 2015), and in LAD brain (Perluigi *et al.* 2009). DRP-2 has been shown to mediate axonal growth by interacting with and stabilizing tubulin (Rogemond *et al.* 2008; Chae *et al.* 2009) and indirectly stabilizing actin microfilaments (Hensley and Kursula 2016). Oxidative modification and conformation changes of DRP-2, α -tubulin, and β -actin likely impacts this interaction in addition to vesicle-mediated transport and thereby contribute to the loss of cognition in AD.

The cholinergic system is significantly disrupted in AD brain (Ferreira-Vieira *et al.* 2016). Cholinergic neurons are lost in the progression of AD (Whitehouse *et al.* 1981; Whitehouse *et al.* 1982), and choline acetyl transferase (ChAT), which catalyzes the synthesis of acetylcholine (ACh), exhibits decreased activity in AD brain (Wilcock *et al.* 1982). Levels of HNE-bound ChAT are significantly increased by A β (1–42) *in vitro* (Butterfield and Lauderback 2002) suggesting that A β (1–42)-induced oxidative modification may contribute to the decreased ChAT activity observed in AD brain. Redox proteomics has identified neuropeptide h3 to be oxidatively modified *in vivo* in the J20 mouse (Robinson *et al.*

2011), and in MCI (Reed *et al.* 2008) and LAD brain (Castegna *et al.* 2003). Neuropolypeptide h3 is also known as phosphatidylethanolamine binding protein-1 (PEBP-1), which is a pleiotropic protein that binds ATP in addition to phosphatidylethanolamine (Sato *et al.* 2017). PEBP-1 is also known as hippocampal cholinergic neurostimulating peptide precursor protein (HCNPPp) and Raf kinase inhibitor protein (RKIP). Reduced *HCNPPp* gene expression has been shown in AD hippocampus (Maki *et al.* 2002) and HCNPPp has been shown to co-localize with DRP-2 at presynaptic terminals in hippocampal neurons (Kato *et al.* 2012). HCNP, an 11 amino acid peptide, is cleaved from within the amino-terminus of HCNPPp and increases ACh synthesis by increasing ChAT levels (Ojika *et al.* 2000). Oxidative modification of HCNPPp may further disrupt presynaptic function in AD brain by impacting its interaction with DRP-2 and may potentially alter its recognition and cleavage to yield HCNP further impacting cholinergic neurotransmission.

Neuroinflammation

GFAP is the main constituent of the intermediate filament system in adult astrocytes and is considered a marker of reactive gliosis (Pekny and Pekna 2004). Reactive astrocytes can provide some neuroprotective and repair functions in mild to moderate astrogliosis; however, extreme astrogliosis can result in glial scar formation that is reported to inhibit axon regeneration (Sofroniew 2009; Silver and Miller 2004). Reactive astrogliosis is evident in MCI, suggesting it occurs early in the progression of AD (Carter *et al.* 2012). Reactive astrocytes are co-localized with senile plaques (Nagele *et al.* 2003) and produce proinflammatory signals (Li *et al.* 2011) that enhance A β (1–42) production in astrocytes (Blasko *et al.* 2000; Frost and Li 2017) and impair microglial phagocytosis (Koenigsknecht-Talboo and Landreth 2005). A β (1–42) has been shown to play a role in initiating inflammation in the CNS (Minter *et al.* 2016). GFAP is oxidized *in vitro* (Boyd-Kimball *et al.* 2005a) by A β (1–42), and *in vivo* in SAMP8 mice brain (Fiorini *et al.* 2013) and EAD (Sultana *et al.* 2010), DS, and DS/AD brain (Di Domenico *et al.* 2014). Oxidation of GFAP could indicate damage to astrocytes consistent with astrocytic dysfunction (Acosta *et al.* 2017; Garwood *et al.* 2017) and neuroinflammation (Latta *et al.* 2015) evidenced in AD brain and exacerbate glutamate excitotoxicity as previously described.

Protein folding and degradation

Protein homeostasis, or proteostasis, is the maintenance of the proteome such that all proteins are in the correct conformation, location, and concentration for their function. Structure dictates function; consequently, chaperones are required to prevent misfolding while sorting and trafficking functions are required to target proteins to the appropriate cellular location, and, in addition, the concentration of each protein is controlled by regulating protein synthesis and degradation (Klaips *et al.* 2018). The Unfolded Protein Response (UPR) is a protective mechanism in which the endoplasmic reticulum (ER) responds to increased levels of unfolded or misfolded proteins in the ER lumen. UPR works in concert with endoplasmic reticulum associated degradation (ERAD) that directs unfolded proteins for destruction by the ubiquitin proteasome system (UPS) (Penke *et al.* 2018). Failure of the UPR to keep up this screening mechanism leads to the buildup of misfolded proteins in the ER which accumulate in mitochondria-associated ER membranes and cause

mitochondrial dysfunction (Volgyi *et al.* 2015; Schon and Area-Gomez 2013) resulting in aberrant APP processing, decreased energy production, and triggering apoptotic cell death consistent with AD (Area-Gomez and Schon 2016; Hiramatsu *et al.* 2015; Safra *et al.* 2013). Several molecular chaperones have been identified by redox proteomics to be oxidatively modified AD brain and models thereof. HSP60 is increasingly carbonylated by A β (1–42) *in vivo* (Boyd-Kimball *et al.* 2006), while HSC71 exhibited increased carbonylation in LAD brain (Castegna *et al.* 2002b) and increased protein-bound HNE in DS/AD brain (Di Domenico *et al.* 2014). HSP70 is oxidized and nitrated in MCI brain (Reed *et al.* 2008; Sultana *et al.* 2007, 2010), and HSP90 is oxidatively modified in 3 \times Tg-AD mice (Shen *et al.* 2015) and in MCI (Aluise *et al.* 2011) and DS/AD brain (Di Domenico *et al.* 2014). Oxidation of HSPs may prevent appropriate interactions with target proteins, resulting in increased protein misfolding and impaired repair mechanisms consistent with the increased protein aggregation evident in AD brain (Ashraf *et al.* 2014; Ross and Poirier 2004). Additionally, molecular chaperones including HSC71, HSP70, and HSP90 have been found in the synaptic compartment and play an important role in maintaining synaptic proteostasis (Gorenberg and Chandra 2017). Oxidation and altered function of these chaperones could further contribute to loss of synaptic plasticity and decreased cognition.

Proteasomal activity is decreased in AD brain (Keller *et al.* 2000) with a reduction in trypsin and chymotrypsin-like activities being reported (Lopez-Salon *et al.* 2003; Mishto *et al.* 2006). A similar decrease in proteasomal activity also exists in DS brain (Di Domenico *et al.* 2013). Inhibition of proteasomal activity impairs synaptic plasticity in animals (Lopez-Salon *et al.* 2001; Fonseca *et al.* 2006), which may indicate that decreased proteasomal activity in AD brain may play a role in loss of synaptic plasticity. Oligomeric A β (1–42) inhibits proteasomal activity *in vitro*, and proteasomal function decreases in 3 \times Tg-AD mice at ages consistent with oligomeric A β (1–42) production suggesting that A β (1–42) may also inhibit proteasomal function *in vivo* (Tseng *et al.* 2008). Redox proteomics analysis of *C. elegans* expressing A β (1–42) identified both α - and β -proteasomal subunits to be oxidatively modified (Boyd-Kimball *et al.* 2006) suggesting a likely mechanism by which proteasome function is decreased in AD brain.

A β (1–42) induces inhibition of long-term potentiation (LTP), a form of synaptic plasticity associated with learning and memory, in hippocampal slices from wild type mice (Cullen *et al.* 1997; Walsh *et al.* 2002) and an APP/PS1 transgenic mouse model that overexpresses A β (1–42) also shows loss of LTP as early as 3 months of age (Trinchese *et al.* 2004). UCH-L1 ameliorates A β (1–42)-induced LTP loss *in vitro* and *in vivo*. This APP/PS1 transgenic mouse model of AD also shows no difference in the protein level of UCH-L1 in the hippocampus, but rather a shift in UCH-L1 from soluble to insoluble with a significant decrease in UCH-L1 specific activity in the insoluble fraction compared to the soluble fraction (Gong *et al.* 2006). UCH-L1 is an abundant protein localized to neurons that is a deubiquitinating enzyme (Wilkinson *et al.* 1989; Nijman *et al.* 2005), but also has been reported to stabilize monoubiquitinated proteins *in vivo* (Osaka *et al.* 2003) and is itself regulated by ubiquitinylation (Setsuie and Wada 2007; Bishop *et al.* 2016). In dimeric form, UCH-L1 has ATP-independent ligase activity (Liu *et al.* 2002). Redox proteomics identified that brain-resident UCH-L1 is oxidatively modified in FAD (Butterfield *et al.* 2006b), LAD (Castegna *et al.* 2002a; Choi *et al.* 2004; Sultana *et al.* 2006c), and DS (Di Domenico *et al.*

2013, 2014). Additionally, UCH-L1 activity is significantly decreased in AD brain compared to age-matched control, suggesting that the increased carbonylation of the protein impairs its function (Sultana *et al.* 2006c). Likewise, oxidative modification of UCH-L1 by HNE significantly decreases its hydrolase activity (Nishikawa *et al.* 2003) while significantly increasing its insolubility and protein aggregation, likely due to structural alterations (Kabuta *et al.* 2008). Taken together, these studies suggest that oxidative modification of UCH-L1 causes conformational change resulting in loss of deubiquitylation activity, resulting in increased protein aggregation and impaired UPS function and loss of synaptic plasticity consistent with what is known in AD.

Signal transduction

14-3-3 proteins are highly expressed in neuronal cytosol but are also detected in other cellular compartments. 14-3-3 proteins consist of 7 isoforms that have been found to interact with up to 200 different proteins to regulate metabolism, cell cycle, differentiation, autophagy, and apoptosis (Umahara *et al.* 2012; Steinacker *et al.* 2011; Heverin *et al.* 2012). 14-3-3 proteins function by inducing conformational change in a target, by using their hydrophobic domain to occlude structural features of a target, or by scaffolding (Heverin *et al.* 2012). Decreased expression of 14-3-3 ζ induces an ER stress response and exacerbates excitotoxicity *in vitro* (Murphy *et al.* 2008) and overexpression of 14-3-3 ζ ameliorates these alterations *in vivo* (Brennan *et al.* 2013). 14-3-3 ζ also is reported to regulate neurite outgrowth (Ramser *et al.* 2010), differentially regulate protein kinase C (Acs *et al.* 1995) and may act to sequester misfolded proteins (Kaneko and Hachiya 2006). 14-3-3 proteins co-localize with neurofibrillary tangles (NFTs) in AD brain (Layfield *et al.* 1996) and 14-3-3 ζ co-immunoprecipitates with microtubule associated tau (Hashiguchi *et al.* 2000). 14-3-3 ζ facilitates glycogen synthase kinase 3 β (GSK3 β)-dependent phosphorylation of tau in culture (Agarwal-Mawal *et al.* 2003; Yuan *et al.* 2003) suggesting a role for 14-3-3 ζ in formation of neurofibrillary tangles (Sluchanko and Gusev 2011; Li and Paudel 2016). 14-3-3 ζ was identified to be oxidatively modified by A β (1–42) *in vitro* (Boyd-Kimball *et al.* 2005b; Sultana *et al.* 2006) and *in vivo* (Boyd-Kimball *et al.* 2005c) and in APP/PS1 double human mutant knock-in (Sultana *et al.* 2011a) and 3 \times Tg-AD mice (Shen *et al.* 2015). It should be noted that oxidized 14-3-3 ζ was detected at an early age in both transgenic mouse models. Thus, oxidative modification of 14-3-3 ζ occurred prior to A β deposition in the APP/PS1 double human mutant knock-in mice and prior to both A β deposition and tau pathology in the 3 \times Tg-AD mice. 14-3-3 γ protein levels are increased in AD brain (Fountoulakis *et al.* 1999) and 14-3-3 γ is oxidatively modified in MCI brain (Sultana *et al.* 2007) indicating that oxidative modification of 14-3-3 occurs early in the pathogenesis of AD and could have impacts on axonal guidance and transport, protein aggregation, autophagy, and apoptosis, all functions affected in AD.

Pin1 is a peptidyl prolyl cis/trans isomerase that induces a conformational change in phosphoproteins possessing phosphorylated Ser/Thr-Pro motifs (Lu *et al.* 1996; Lu *et al.* 1999a; Zhou *et al.* 1999; Liou *et al.* 2011). Notably, Pin1 activity is decreased by phosphorylation post-translational modification (Lu and Zhou 2007). In the CNS, Pin1 is expressed primarily in neurons and is mainly localized to the nuclei in normal brain; however, in AD brain, the Pin1 is colocalized in the cytoplasm with neurofibrillary tangles

and purifies with paired helical filaments of hyperphosphorylated tau from AD brain (Lu *et al.* 1999b; Ramakrishnan *et al.* 2003). p-Thr231 tau has been shown to promote further phosphorylation of tau (Lin *et al.* 2007) leading to hyperphosphorylation (Hamdane *et al.* 2003). p-Thr231 tau is a target for Pin1 binding, and conformational change of the peptidyl proline bond in tau from cis to trans facilitates phosphoprotein phosphatase A2 (PPA2) mediated dephosphorylation of tau (Lu *et al.* 1999b; Ranganathan *et al.* 1997; Zhou *et al.* 2000). Pin1 knockout mice develop tau hyperphosphorylation and filament formation with age (Liou *et al.* 2003) and, when Pin1 knockout mice were crossed with Tg2576 mice that overexpress APP with the Swedish mutations K670N and M671L, knockout of Pin1 was found to increase amyloidogenic processing of APP resulting in increased intracellular A β (1–42) accumulation (Pastorino *et al.* 2006). Redox proteomics has identified Pin1 to be oxidatively modified in J20 (Robinson *et al.* 2011) and APP/PS1 double human mutant knock-in mice (Sultana *et al.* 2011a) and in MCI (Butterfield *et al.* 2006a) and LAD brain (Sultana *et al.* 2006b,c). Pin1 activity is significantly decreased in both MCI (Butterfield *et al.* 2006a) and LAD brain (Sultana *et al.* 2006b). Further study has shown that Cys113 of Pin1 is oxidatively modified *in vivo* in AD brain and in AD mouse models. *In vitro* oxidation of Cys113 results in loss of function, but not substrate recognition indicating that oxidized Pin1 can bind and trap substrates but be unable to complete the catalytic cycle. Mutation of this residue to alanine resulted in loss of catalytic function confirming that Cys113 is critical for Pin1 activity (Chen *et al.* 2015). Taken together, as Pin1 activity is proposed to promote nonamyloidogenic processing of APP, decreased Pin1 activity could shift APP processing further toward the amyloidogenic pathway resulting in increased production of A β (1–42) (Pastorino *et al.* 2006). Likewise, as Pin1 plays a role in regulating the phosphorylation state of tau, impaired Pin1 activity could lead to tau hyperphosphorylation and neurofibrillary tangles present in AD brain (Wang *et al.* 2007; Zhou *et al.* 2000). Impaired Pin1 activity in AD brain could also affect cell cycle regulation (Lin *et al.* 2015), UPS protein degradation (Liou *et al.* 2011) and synaptic plasticity (Xu *et al.* 2017).

Conclusion and Future Directions

Redox proteomics has been invaluable in identifying proteins that are particularly sensitive to oxidative modification pinpointing molecular targets in cellular processes or signaling pathways that are damaged and may be dysfunctional. In PCAD brain total A β (1–42) is significantly increased, but no significant difference in oxidative stress biomarkers were detected compared to control brain (Aluise *et al.* 2010); However, in MCI only small differences in AD neuropathology are observed compared to PCAD, but protein carbonyls are significantly increased in MCI brain compared to PCAD brain (Aluise *et al.* 2011). Some protein expression changes exist in PCAD brain compared to control brain (Aluise *et al.* 2010), but in our hands no oxidatively modified proteins were detected until MCI (Aluise *et al.* 2011) providing further evidence that a window of opportunity for treatment or lifestyle interventions may exist if AD can be detected in its earliest stages. Redox proteomics has the potential to screen for oxidized proteins in peripheral tissues; however, more studies of peripheral tissues along the progression of PCAD to LAD are needed to identify possible peripheral biomarkers that correlate with the changes observed in brain. Such studies have

the potential to lead to the development of tools that could aid in diagnosis and staging the of disease beyond our current methods.

Overproduction and accumulation of A β (1–42) is known to induce oxidative stress and is key to the neuropathogenesis of AD. Redox proteomics has provided insight into the molecular targets susceptible to A β (1–42)-induced oxidative modification. In this review, we surveyed the proteins identified by redox proteomics to be oxidized by A β (1–42) *in vitro* and *in vivo* and discussed these in the context of oxidatively modified proteins identified by redox proteomics analyses of animal models of AD, human FAD, PCAD, MCI, EAD, LAD, DS and DS/AD brain. These commonalities indicate that A β (1–42)-induced oxidative modifications involve proteins that largely contribute to decreased energy yielding metabolism, synaptic dysfunction and excitotoxicity, and loss of proteostasis due to impaired molecular chaperones and degradation contributing to protein misfolding and aggregation, altered APP processing yielding increased production of A β (1–42) and, ultimately, resulting in cell death (Figure 6). Taken together, these redox proteomics studies indicate that A β (1–42)-mediated oxidative stress occurs early in AD progression. Consequently, improved access to biomarker imaging and the identification of treatments to reduce A β production or the oxidative damage induced by A β could be beneficial in preventing or delaying the progression of AD.

Indeed, a recent study demonstrates the value of imaging modalities in determining the order of pathological alterations in the progression of AD (Gordon *et al.* 2018). Consistent with our findings using redox proteomics and our overall A β (1–42)-centered hypothesis for oxidative stress, glucose dysmetabolism, and neuronal death in AD (Butterfield 2014; Butterfield and Boyd-Kimball 2018; Butterfield and Lauderback 2002; Butterfield *et al.* 2001, 2002, 2007, 2013), Gordon *et al.* (2018) demonstrated using PET imaging on thousands of individuals who are known to have dominantly inherited AD over a period of 22 years prior to expected onset of symptoms to 3 years following symptoms (the DIAN Network) that A β (1–42) deposition was the first pathological alteration observed, followed later by glucose dysmetabolism. In the current review, A β (1–42) oligomers were shown to oxidatively modify glycolytic and TCA enzymes and portions of ATP synthase, thereby decreasing glucose metabolism resulting in lower levels of ATP. This, in turn, leads to loss of neuronal membrane potential, opening voltage-gated Ca²⁺ channels with consequent influx of detrimental Ca²⁺, and eventual neuronal death. Gordon *et al.* (2018) showed by MRI that the third temperol alteration in AD pathology was thinning of the hippocampus and frontal cortex, consistent with neuronal death, in agreement with our redox proteomics findings and overall hypothesis.

Redox proteomics has identified potential promising therapeutic targets and pathways for eventually slowing if not halting progression of this devastating dementing disorder that is AD. Continued use of redox proteomics in the stages of AD likely will provide additional insights and new targets and pathways that may be beneficial in treating this disease.

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Abbreviations:

3-NT	3-nitrotyrosine
3×Tg-AD	triple transgenic AD mouse
A1AT	α-1-anti-trypsin
Actr2	actin-related protein 2
Acyl CoA DH	acyl-CoA dehydrogenase
ADK	adenosine kinase
AK	arginine kinase
Aldo 3	aldolase 3
aMCI	Amnesic Mild Cognitive Impairment
AO	antisense oligonucleotide
ApoE	Apolipoprotein E
APP	Amyloid Precursor Protein
Aβ	Amyloid beta-peptide
CA II	carbonic anhydrase II
CatD	cathepsin D
ChAT	choline acetyltransferase
CK BB	creatine kinase BB
CK	creatine kinase
Coro 1a	coronin 1a
CRMP-1	collapsing response mediated protein-1
CRMP-2	collapsing response mediated protein-2
cyt b-c₁	complex III Rieske protein
DBP	vitamin D-binding protein
DMDMAH-1	dimethylarginine dimethylaminohydrolase 1
DPL2	peptidase α

DRP-1	dihydropyrimidinase-related protein-1
DRP-2	dihydropyrimidinase-related protein-2
DS	Down syndrome
DS/AD	Down syndrome with Alzheimer's disease
Dyn-1	dynamamin-1
EAAT2	excitatory amino acid transporter-2
EAD	Early Alzheimer's disease
EF-1γ	elongation factor 1 γ
EF-Tu	elongation factor Tu
eIF-α	initiation factor α
ERAD	endoplasmic reticulum associated degradation
FAD	Familial Alzheimer's disease
FBA-C	fructose bisphosphate aldolase C
GAPDH	glyceraldehyde-3-phosphate dehydrogenase
GDH	glutamate dehydrogenase
GFAP	glial fibrillary acid protein
GLT-1	glial glutamate transporter
GRP78	78kDa glucose-regulated protein
GS	glutamine synthetase
GSH	glutathione
GST	glutathione-S-transferase
GSTM3	GST mu
HCNP	hippocampal cholinergic neurostimulating peptide
HCNPpp	hippocampal cholinergic neurostimulating peptide precursor protein
HNE	4-hydroxy-2- <i>trans</i> -nonenal
HSC71	heat shock cognate 71
HSP60	chaperonin 60
HSP70	heat shock protein 70

HSP90	heat shock protein 90
ICV	intracerebral ventricular
IPL	inferior parietal lobule
LAD	Late Alzheimer's disease
LBP	lipid binding protein
LDH-2	lactate dehydrogenase 2
MAPKI	mitogen-activated protein kinase I
MBP	myelin binding protein
MCI	Mild Cognitive Impairment
MDH	malate dehydrogenase
MnSOD or SOD2	manganese superoxide dismutase
MRLC	myosin regulatory light chain
MRP1	multidrug resistant protein 1
MRP	multidrug resistant protein
NBM	nucleus basalis magnocellularis
NMP	neurofilament medium polypeptide
NSF	vesicle-fusing ATPase
PCAD	Preclinical Alzheimer's disease
PDH	pyruvate dehydrogenase
PEBP-1	phosphatidylethanolamine-binding protein 1 or neuropolypeptide h3
PET	Positron Emission Tomography
PGDS	prostaglandin-H2 D-isomerase
PGK1	phosphoglycerate kinase 1
PGM1	phosphoglycerate mutase 1
Pin1	peptidylprolyl cis-trans isomerase-1
PK	pyruvate kinase
PKM2	pyruvate kinase M2
Prx2	peroxiredoxin 2

Prx6	peroxiredoxin 6
Prxs	peroxiredoxins
PS-1	presenilin 1
SAMP8	senescence accelerated mouse
SBP1	syntaxin binding protein I
SCOT-1	succinyl CoA-3-ketoacid-CoA transferase 1
SEP11	septin-11
TCA	tricarboxylic acid cycle
TCPB	T-complex protein 1 subunit β
TK	transketolase
UCH-L1	ubiquitin carboxy-terminal hydrolase L-1
UPR	Unfolded Protein Response
UPS	ubiquitin proteasome system
VDAC1	voltage-dependent anion-channel protein-1
V_o-ATPase	V _o -type proton ATPase
γ-SNAP	soluble N-ethylmaleimide-sensitive factor

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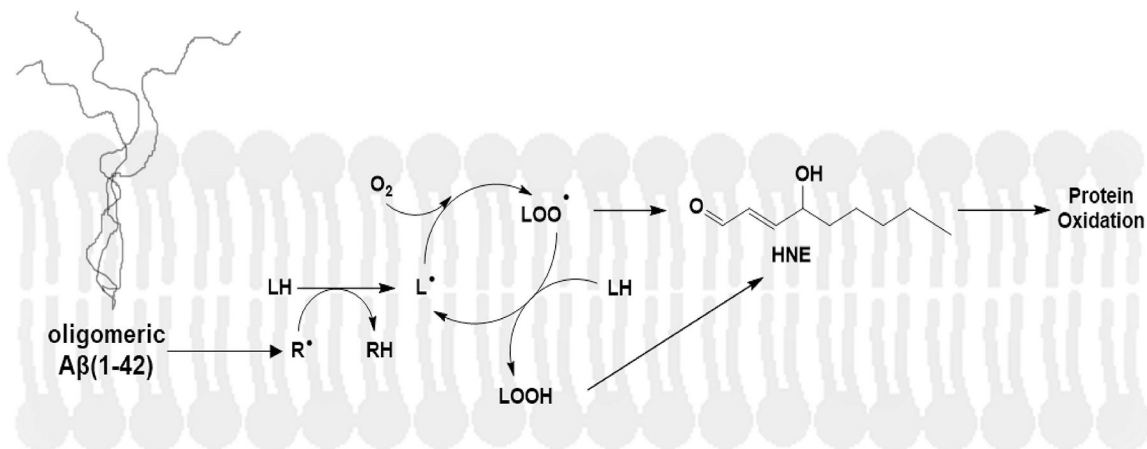
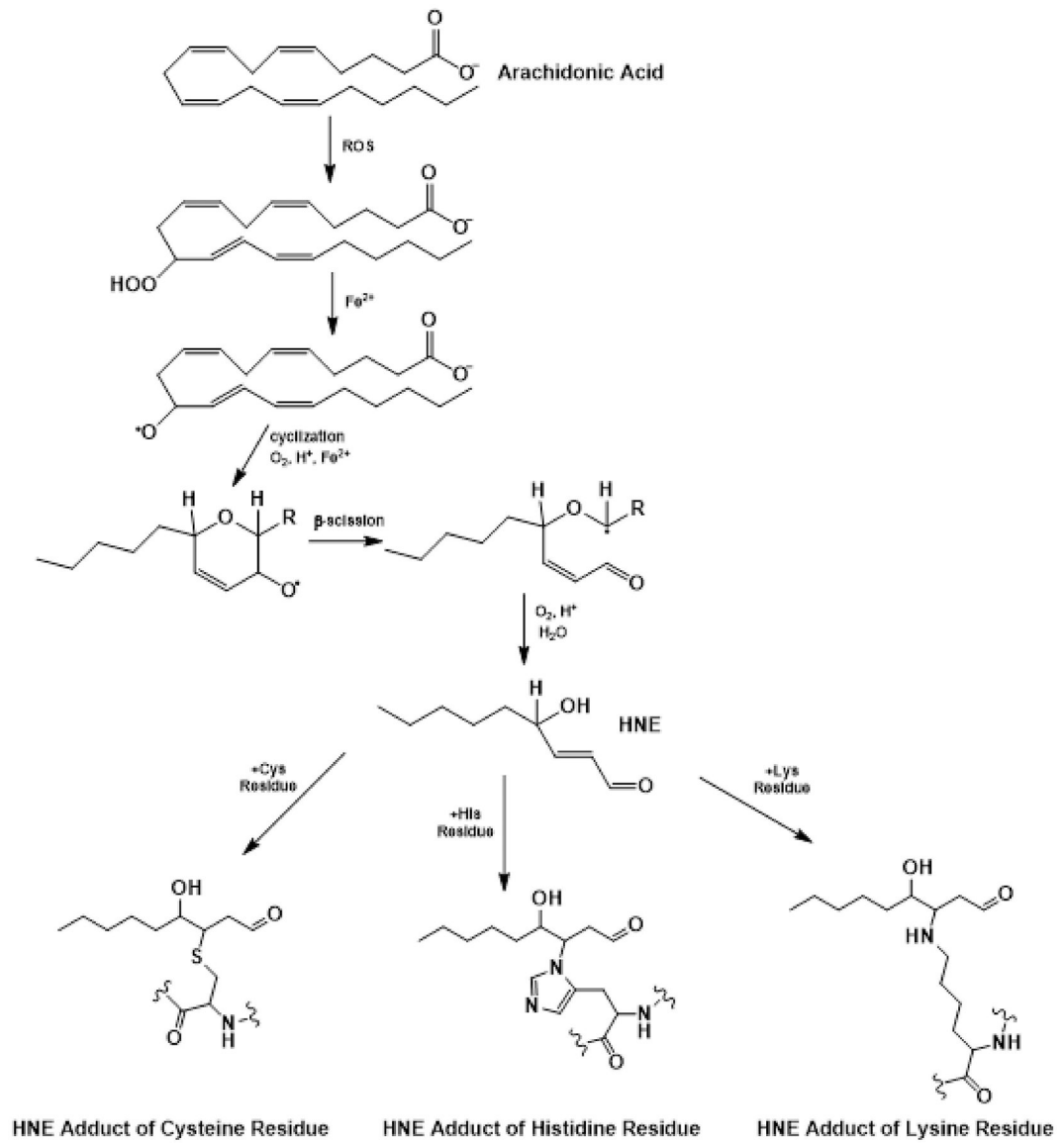


Figure 1:

Oligomeric Aβ(1–42)-induces lipid peroxidation. Oligomeric Aβ(1–42) embedded in the lipid bilayer initiates free radical formation (R•) mediated by Met 35 which leads to abstraction of a labile, allylic hydrogen atom from unsaturated fatty acids forming lipid radicals (L•) that rapidly combine with oxygen to form lipid peroxy radicals (LOO•). Lipid peroxy radicals propagate lipid peroxidation by abstracting allylic hydrogen atoms from other unsaturated fatty acids in the membrane forming lipid hydroperoxides (LOOH) and lipid radicals (L•), thereby propagating the chain reaction. The reactive lipid peroxidation product, 4-hydroxy-2-*trans*-nonenal (HNE) can be formed from lipid hydroperoxides of arachidonic acid, linoleic acid, and linolenic acid. This process of lipid peroxidation, coupled to HNE formation and subsequent reaction with and dysfunction of cellular proteins, amplifies greatly the effects of a small amount of free radical formation on Aβ(1–42).

**Figure 2:**

HNE is formed from arachidonic acid and leads to oxidative protein modifications by reacting with Cys, His, and Lys residues via Michael addition.

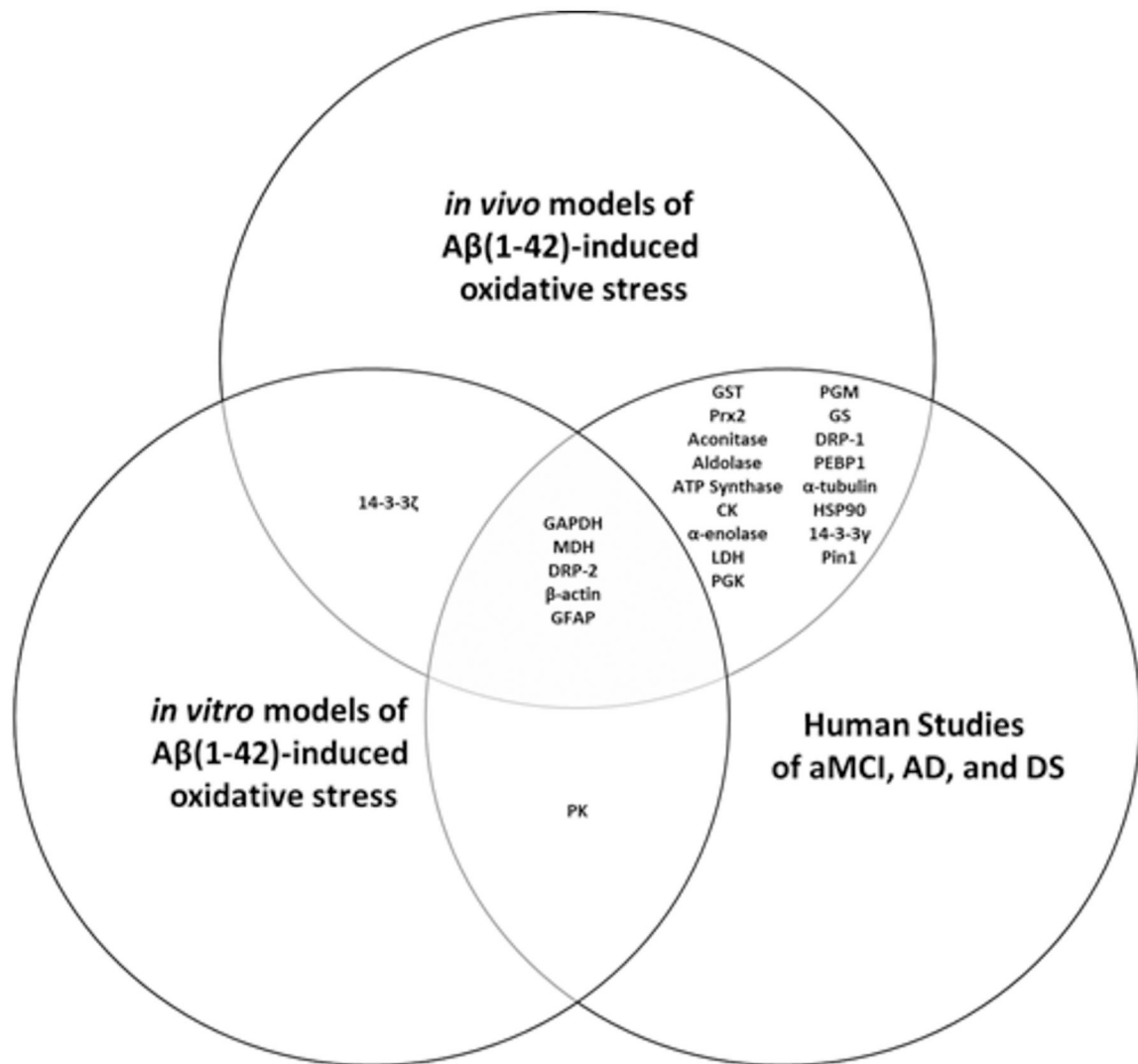


Figure 3:

Venn diagram of proteins commonly oxidized *in vitro* and *in vivo* by Aβ(1–42) and in human studies of aMCI, AD, and DS brain.

Abbreviations: CK creatine kinase, DRP-1 dihydropyrimidinase-related protein-1 or collapsin response mediated protein-1 (CRMP-1), DRP-2 dihydropyrimidinase-related protein-2 or collapsin response mediated protein-2 (CRMP-2), GAPDH glyceraldehyde-3-phosphate dehydrogenase, GFAP glial fibrillary acidic protein, GS glutamine synthase, GST glutathione S-transferase, HSP90 heat shock protein 90, MDH malate dehydrogenase, LDH lactate dehydrogenase, PEBP1 neuropolypeptide h3 or hippocampal cholinergic neurostimulating peptide precursor protein (HCNPpp), PGK phosphoglycerate kinase, PGM phosphoglycerate mutase, Pin1 peptidyl cis-trans isomerase-1, PK, pyruvate kinase, Prx2 peroxiredoxin 2.

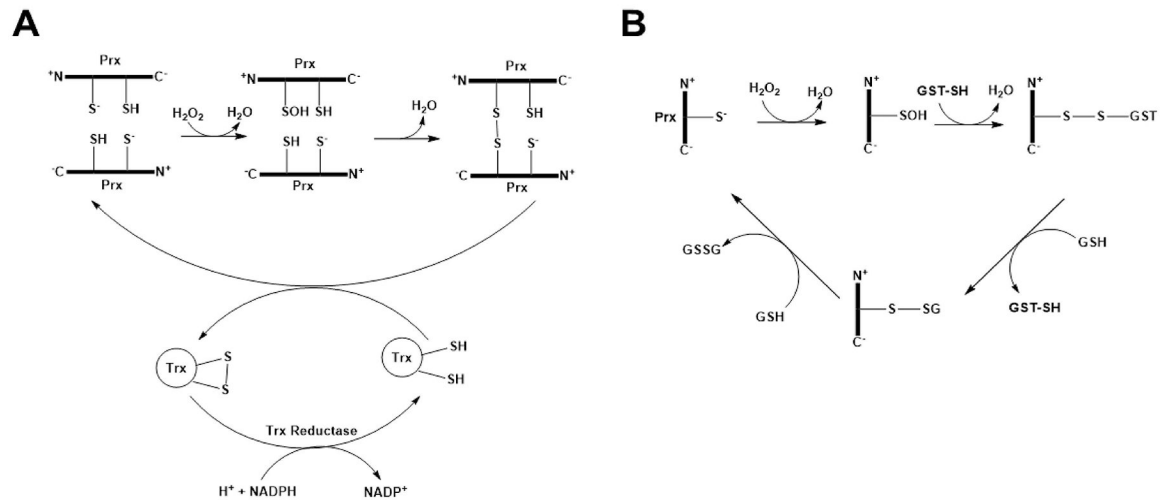


Figure 4:
Mechanisms of reduction of H_2O_2 by 2-Cys-Prx and 1-Cys-Prx by peroxiredoxin are shown in A and B, respectively. The reader is referred to the text for further details.

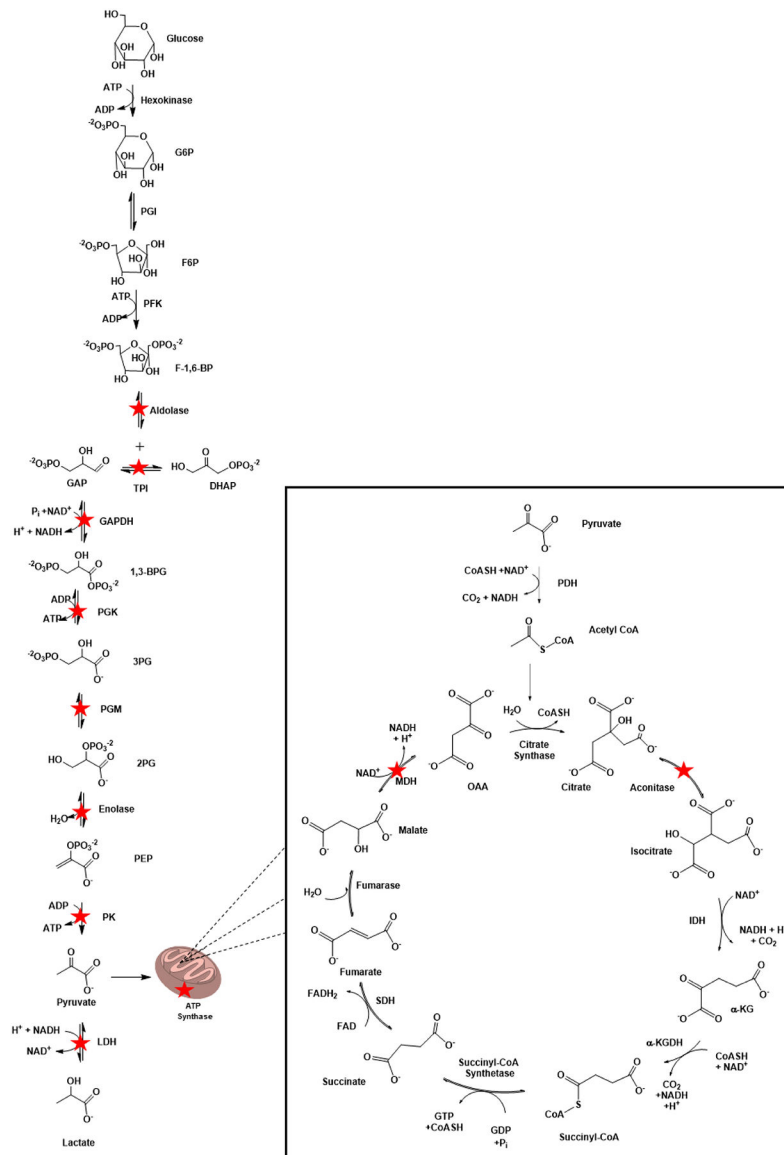


Figure 5:

A summary of the cytosolic and mitochondrial enzymes critical for energy yielding metabolism and mitochondrial function are shown. Enzymes that are oxidatively modified by HNE in the progression of AD are starred for emphasis. Note that a stoichiometry of two exists for all reactions shown following the production of GAP.

Abbreviations: G6P: Glucose-6-Phosphate; PGI: Phosphoglucose isomerase; F6P: Fructose 6 Phosphate; PFK: Phosphofructokinase; F-1,6-BP: Fructose-1,6-Bisphosphate; TPI: Triose Phosphate Isomerase; GAP: Glyceraldehyde-3-Phosphate; DHAP: Dihydroxyacetone Phosphate; GAPDH: Glyceraldehyde-3-Phosphate Dehydrogenase; 1,3-BPG: 1,3-Bisphosphoglycerate; PGK: Phosphoglycerate Kinase; 3PG: 3-Phosphoglycerate; PGM: Phosphoglycerate Mutase; 2PG: 2-Phosphoglycerate; PEP: Phosphoenolpyruvate; PK: Pyruvate Kinase; LDH: Lactate Dehydrogenase; PDH: Pyruvate Dehydrogenase; OAA: Oxaloacetate; IDH: Isocitrate Dehydrogenase; α-KG: α-Ketoglutarate; α-KGDH: α-

Ketoglutarate Dehydrogenase; SDH: Succinate Dehydrogenase; MDH: Malate Dehydrogenase.

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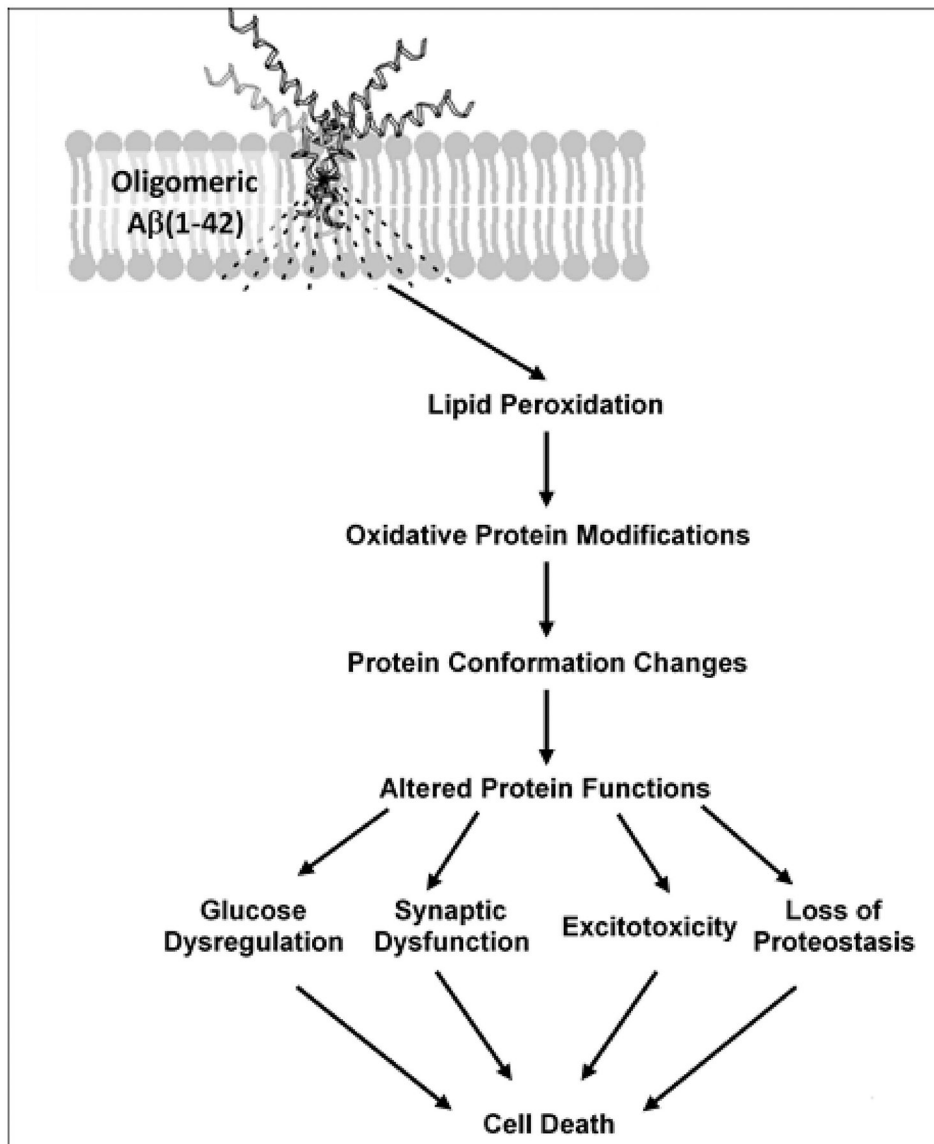


Figure 6: Aβ(1-42)-mediated cell death is initiated by lipid peroxidation. Oligomeric Aβ(1-42)-embeds in the lipid bilayer inducing lipid peroxidation and propagating free radical reactions that oxidatively modify proteins resulting in conformational change and altered function impairing glucose metabolism, synaptic plasticity, synaptic glutamate clearance, and proteostasis, ultimately leading to cell death.

Table 1:**A β (1–42)-Induced Carbonylated Proteins *in vitro***

Function	Protein	Model	References
Energy Metabolism	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	primary neuronal culture	Boyd-Kimball <i>et al.</i> 2005b; Sultana <i>et al.</i> 2006d
	Malate dehydrogenase (MDH)	primary neuronal culture	Sultana <i>et al.</i> 2006d
	Pyruvate kinase (PK)	primary neuronal culture	Sultana <i>et al.</i> 2006d
Synaptic plasticity, vesicle-mediated transport, and cell structure	Dihydropyrimidinase-related protein 2 (DRP-2)	cortical synaptosomes	Boyd-Kimball <i>et al.</i> 2005a
	β -actin	cortical synaptosomes	Boyd-Kimball <i>et al.</i> 2005a
Neuroinflammation	Glial fibrillary acidic protein (GFAP)	cortical synaptosomes	Boyd-Kimball <i>et al.</i> 2005a
Signal transduction	14-3-3 ζ	primary neuronal culture	Boyd-Kimball <i>et al.</i> 2005b; Sultana <i>et al.</i> 2006d

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Table 2:**A β (1–42)-Induced Carbonylated Proteins *in vivo***

Function	Protein	Model	Tissue	References
Antioxidants and Cellular Detoxification Defenses	Glutathione S-Transferase	Canine ^b	--	Opii <i>et al.</i> 2008
		<i>C. elegans</i> ^b	--	Boyd-Kimball <i>et al.</i> 2006
	Adenosine kinase	<i>C. elegans</i> ^b	--	Boyd-Kimball <i>et al.</i> 2006
	Arginine kinase	<i>C. elegans</i> ^b	--	Boyd-Kimball <i>et al.</i> 2006
	Glutamate dehydrogenase	Canine ^b	--	Opii <i>et al.</i> 2008
	Lipid binding protein	<i>C. elegans</i> ^b	--	Boyd-Kimball <i>et al.</i> 2006
Energy Metabolism	acyl-CoA DH (medium chain)	<i>C. elegans</i> ^b	--	Boyd-Kimball <i>et al.</i> 2006
	acyl-CoA DH (short-chain)	<i>C. elegans</i> ^b	--	Boyd-Kimball <i>et al.</i> 2006
	α -enolase	Canine ^b	--	Opii <i>et al.</i> 2008
	Glyceraldehyde-3-phosphate dehydrogenase	Canine ^b	--	Opii <i>et al.</i> 2008
		Wistar Rat ^a	HP	Boyd-Kimball <i>et al.</i> 2005c
	Malate dehydrogenase	<i>C. elegans</i> ^b	--	Boyd-Kimball <i>et al.</i> 2006
	Phosphoglycerate mutase 1	Wistar Rat ^a	HP	Boyd-Kimball <i>et al.</i> 2005c
	Pyruvate dehydrogenase (PDH) (lipoamide)	Wistar Rat ^a	HP	Boyd-Kimball <i>et al.</i> 2005c
Transketolase	<i>C. elegans</i> ^b	--	Boyd-Kimball <i>et al.</i> 2006	
Excitotoxicity	Glutamine Synthetase	Wistar Rat ^a	Cortex	Boyd-Kimball <i>et al.</i> 2005c
Synaptic plasticity, vesicle-mediated transport, and cell structure	actin	<i>C. elegans</i> ^b	--	Boyd-Kimball <i>et al.</i> 2006
	β -synuclein	Wistar Rat ^a	HP	Boyd-Kimball <i>et al.</i> 2005c
	Fascin actin bundling protein	Canine ^b	--	Opii <i>et al.</i> 2008
	Myosin regulatory light chain	<i>C. elegans</i>	--	Boyd-Kimball <i>et al.</i> 2006
	Neurofilament triplet L	Canine ^b	--	Opii <i>et al.</i> 2008
	α -/ β -tubulin	Wistar Rat ^a	Cortex	Boyd-Kimball <i>et al.</i> 2005c
Protein Synthesis	Elongation factor 1 γ	<i>C. elegans</i> ^b	--	Boyd-Kimball <i>et al.</i> 2006
Protein Folding and Degradation	HSP60	Wistar Rat ^a	NBM	Boyd-Kimball <i>et al.</i> 2005c
	Proteasome α -subunit	<i>C. elegans</i> ^b	--	Boyd-Kimball <i>et al.</i> 2006
	Proteasome β -subunit	<i>C. elegans</i> ^b	--	Boyd-Kimball <i>et al.</i> 2006
Signal Transduction	14-3-3 ζ	Wistar Rat ^a	HP, NBM	Boyd-Kimball <i>et al.</i> 2005c

Note: HP, hippocampus; NBM, nucleus basalis magnocellularis

^aICV injection of A β (1–42) into the NBM with analysis 7 days post injection;

b expresses A β (1–42) with human amino acid sequence.

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Table 3:

Oxidatively Modified Proteins Identified in AD mouse models

Function	Protein	Transgenic Mouse Model	Age (months)	Oxidative Modification	References
Cellular Redox Homeostasis and Detoxification Defense	Peroxiredoxin 2 (Prx2)	SAMP8 ^a	12	C [↓]	Poon <i>et al.</i> 2005
Energy Metabolism	Aconitase	3×Tg-AD	3	C [↑]	Shen <i>et al.</i> 2015
	Aldolase	SAMP8 ^a	12	C [↓]	Poon <i>et al.</i> 2005
	ATP Synthase	APP/PS1 KI	12,15	C [↑]	Sultana <i>et al.</i> 2011a
	Creatine Kinase (CK)	SAMP8	12	C [↑]	Poon <i>et al.</i> 2004
	α-enolase	APP/PS1 KI	6,9,12,15	C [↑]	Sultana <i>et al.</i> 2011a
		3×Tg-AD	3	C [↑]	Shen <i>et al.</i> 2015
		SAMP8 ^b	12	N [↑]	Fiorini <i>et al.</i> 2013
	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	3×Tg-AD	3	C [↑]	Shen <i>et al.</i> 2015
	Isocitrate dehydrogenase (IDH)	SAMP8 ^b	12	N [↑]	Fiorini <i>et al.</i> 2013
	Lactate dehydrogenase (LDH)	SAMP8 ^b	12	N [↑]	Fiorini <i>et al.</i> 2013
		SAMP8	12	C [↑]	Poon <i>et al.</i> 2004
	Malate dehydrogenase (MDH)	3×Tg-AD	3	C [↑]	Shen <i>et al.</i> 2015
	Phosphoglycerate kinase (PGK)	3×Tg-AD	3	C [↑]	Shen <i>et al.</i> 2015
	Pyruvate dehydrogenase (PDH) (E1)	APP/PS1 KI	6	C [↑]	Sultana <i>et al.</i> 2011a
Synaptic plasticity, vesicle-mediated transport and cell structure	β-synuclein	APP/PS1 KI	12	C [↑]	Sultana <i>et al.</i> 2011a
	Dihydropyrimidinase-related protein 1 (DRP-1)	SAMP8 ^b	12	N [↑]	Fiorini <i>et al.</i> 2013
	Dihydropyrimidinase-related protein 2 (DRP-2)	SAMP8	12	C [↑]	Poon <i>et al.</i> 2004
		SAMP8 ^b	12	N [↓]	Fiorini <i>et al.</i> 2013
	Dynamin-1	SAMP8 ^b	12	N [↑]	Fiorini <i>et al.</i> 2013
	Vesicle-fusing ATPase	SAMP8 ^b	12	N [↑]	Fiorini <i>et al.</i> 2013
	Septin 11	SAMP8 ^b	12	N [↑]	Fiorini <i>et al.</i> 2013
	Neuropolypeptide h3 (PEBP1)	J20	9	N [↓]	Robinson <i>et al.</i> 2011
	β-Actin	APP/PS1 KI	1,15	C [↑]	Sultana <i>et al.</i> 2011a
	Actin related protein 2	SAMP8 ^b	12	N [↑]	Fiorini <i>et al.</i> 2013
Coronin1A	SAMP8 ^a	12	C [↓]	Poon <i>et al.</i> 2005	

Function	Protein	Transgenic Mouse Model	Age (months)	Oxidative Modification	References
	Neurofilament light polypeptide	3×Tg-AD	3	C [↑]	Shen <i>et al.</i> 2015
	α-Spectrin 2	SAMP8	12	C [↑]	Poon <i>et al.</i> 2004
	Tubulin β-2A chain	3×Tg-AD	3	C [↑]	Shen <i>et al.</i> 2015
Neuroinflammation	GFAP	SAMP8 ^b	12	N [↑]	Fiorini <i>et al.</i> 2013
Protein Folding and Degradation	HSP90AB1	3×Tg-AD	3	C [↑]	Shen <i>et al.</i> 2015
	Protein disulfide-isomerase A3	3×Tg-AD	3	C [↑]	Shen <i>et al.</i> 2015
	T-complex protein 1 subunit e	3×Tg-AD	3	C [↑]	Shen <i>et al.</i> 2015
Signal Transduction	14-3-3ζ/δ/γ	APP/PS1 KI	1,9,12,15	C [↑]	Sultana <i>et al.</i> 2011a
	14-3-3ζ/δ	3×Tg-AD	3	C [↑]	Shen <i>et al.</i> 2015
	Pin1	J20	9	N [↓]	Robinson <i>et al.</i> 2011
		APP/PS1 KI	9,12,15	C [↑]	Sultana <i>et al.</i> 2011a

Note: C, carbonylation; N, nitration;

↑ oxidative modification was significantly increased;

↓ oxidative modification was significantly decreased;

^a Antisense Oligonucleotide directed against Aβ region of *APP* gene;

^b Antisense Oligonucleotide directed against *PS-1* gene;

Table 4:

Oxidatively Modified Proteins Identified in aMCI, EAD, LAD, DS, and DS/AD Brain

Protein	Disease State	Brain Region	Oxidative Modification	References
Cellular Redox Homeostasis and Detoxification Defense				
Carbonyl reductase	MCI ^a	HP	H	Reed <i>et al.</i> 2008
Glutamate dehydrogenase (GDH)	DS ^a	FC	H	Di Domenico <i>et al.</i> 2014
	DS/AD ^{a,b}	FC	H	Di Domenico <i>et al.</i> 2014
Glutathione S-Transferase (GST) Mu	MCI ^a	IPL	N	Sultana <i>et al.</i> 2007
Multidrug resistance protein 3 (MRP3)	MCI ^a	IPL	N	Sultana <i>et al.</i> 2007
Peroxiredoxin 2 (Prx2)	DS ^a	FC	H	Di Domenico <i>et al.</i> 2014
Peroxiredoxin 6 (Prx6)	MCI ^a	HP	N	Sultana <i>et al.</i> 2007
	LAD ^a	HP	H	Perluigi <i>et al.</i> 2009
Cu,Zn Superoxide dismutase (SOD)	DS/AD ^a	FC	H	Di Domenico <i>et al.</i> 2014
Mn Superoxide dismutase (SOD)	EAD ^a	IPL	H	Reed <i>et al.</i> 2009
	LAD ^a	IPL	H	Perluigi <i>et al.</i> 2009
Energy Metabolism				
Aconitase	LAD ^a	HP	H	Perluigi <i>et al.</i> 2009
	DS/AD ^b	FC	H	Di Domenico <i>et al.</i> 2014
Aldolase	MCI ^a	IPL	N	Sultana <i>et al.</i> 2007
	EAD ^a	IPL	C	Sultana <i>et al.</i> 2010
	LAD ^a	HP	H	Perluigi <i>et al.</i> 2009
	DS ^a	FC	H	Di Domenico <i>et al.</i> 2014
ATP Synthase	MCI ^a	HP	H	Reed <i>et al.</i> 2008
	MCI ^a	IPL	H	Reed <i>et al.</i> 2008
	EAD ^a	IPL	H	Reed <i>et al.</i> 2009
	LAD ^a	HP	N	Sultana <i>et al.</i> 2006a
	LAD ^a	IPL	H	Perluigi <i>et al.</i> 2009
Creatine Kinase BB (CK)	LAD ^a	IPL	C	Castegna <i>et al.</i> 2002a
Cyt b-c ₁ R1eske Protein	DS ^a	FC	H	Di Domenico <i>et al.</i> 2014
	DS/AD ^a	FC	H	Di Domenico <i>et al.</i> 2014
α -enolase	MCI ^a	HP	C	Butterfield <i>et al.</i> 2006a

Protein	Disease State	Brain Region	Oxidative Modification	References
	MCI ^a	HP	N	Sultana <i>et al.</i> 2007
	MCI ^a	HP	H	Reed <i>et al.</i> 2008
	MCI ^a	IPL	N	Sultana <i>et al.</i> 2007
	MCI ^a	IPL	C	Aluise <i>et al.</i> 2011
	EAD ^a	IPL	H	Reed <i>et al.</i> 2009
	LAD ^a	HP	C	Sultana <i>et al.</i> 2006c
	LAD ^a	HP	N	Sultana <i>et al.</i> 2006a
	LAD ^a	HP	H	Perluigi <i>et al.</i> 2009
	LAD ^a	IPL	C	Categna <i>et al.</i> 2002b
	LAD ^a	IPL	N	Categna <i>et al.</i> 2003
	DS/AD ^a	FC	H	Di Domenico <i>et al.</i> 2014
Glucose Regulated Protein Precursor	MCI ^a	IPL	N	Sultana <i>et al.</i> 2007
Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	LAD ^a	HP	N	Sultana <i>et al.</i> 2006a
	DS/AD ^a	FC	H	Di Domenico <i>et al.</i> 2014
Lactate dehydrogenase (LDH)	MCI ^a	HP	H	Reed <i>et al.</i> 2008
Malate dehydrogenase (MDH)	DS/AD ^a	FC	H	Di Domenico <i>et al.</i> 2014
	EAD ^a	IPL	H	Reed <i>et al.</i> 2009
Phosphoglycerate kinase (PGK)	MCI ^a	HP	H	Reed <i>et al.</i> 2008
Phosphoglycerate mutase 1 (PGM1)	EAD ^a	IPL	C	Sultana <i>et al.</i> 2010
	LAD ^a	HP	C	Sultana <i>et al.</i> 2006c
Pyruvate kinase (PK)	MCI ^a	IPL	H	Reed <i>et al.</i> 2008
	DS ^a	FC	H	Di Domenico <i>et al.</i> 2014
	MCI ^a	HP	C	Butterfield <i>et al.</i> 2006a
Succinyl CoA-3-ketoacid-CoA transferase-1 (SCOT-1)	DS ^a	FC	C	Di Domentico <i>et al.</i> 2013
Triose phosphate isomerase (TPI)	EAD ^a	IPL	H	Reed <i>et al.</i> 2009
	LAD ^a	HP	C	Sultana <i>et al.</i> 2006c
	LAD ^a	IPL	N	Castegna <i>et al.</i> 2003
Excitotoxicity				
Glutamine Synthetase (GS)	MCI ^a	HP	C	Butterfield <i>et al.</i> 2006a
	LAD ^a	IPL	C	Castegna <i>et al.</i> 2002a

Protein	Disease State	Brain Region	Oxidative Modification	References
	LAD ^a	IPL	H	Perluigi <i>et al.</i> 2009
Synaptic plasticity, vesicle-mediated transport and cell structure				
Carbonic anhydrase II (CA II)	MCI ^a	IPL	C	Sultana <i>et al.</i> 2010
	LAD ^a	HP	C	Sultana <i>et al.</i> 2006c
	LAD ^a	HP	N	Sultana <i>et al.</i> 2006a
Dihydropyrimidinase-related protein 1 (DRP-1)	DS/AD ^{a,b}	FC	H	Di Domenico <i>et al.</i> 2014
Dihydropyrimidinase-related protein 2 (DRP-2)	MCI ^a	HP	N	Sultana <i>et al.</i> 2007
	EAD ^a	IPL	H	Reed <i>et al.</i> 2009
	LAD ^a	HP	C	Sultana <i>et al.</i> 2006c
	LAD ^a	IPL	C	Castegna <i>et al.</i> 2002b
	LAD ^a	IPL	H	Perluigi <i>et al.</i> 2009
	DS ^a	FC	H	Di Domenico <i>et al.</i> 2014
	DS/AD ^{a,b}	FC	H	Di Domenico <i>et al.</i> 2014
Fascin 1	MCI ^a	HP	N	Sultana <i>et al.</i> 2007
Neuropolypeptide h3 (PEBP1)	MCI ^a	HP	H	Reed <i>et al.</i> 2008
	LAD ^a	IPL	N	Castegna <i>et al.</i> 2003
Syntaxin binding protein I (SBP1)	MCI ^a	IPL	C	Sultana <i>et al.</i> 2010
	DS/AD ^{a,b}	FC	H	Di Domenico <i>et al.</i> 2014
γ -synaptosomal protein like soluble N-ethylmaleimide-sensitive factor (γ -SNAP)	LAD ^a	HP	C	Sultana <i>et al.</i> 2006c
Voltage-dependent anion-channel protein-1 (VDAC-1)	LAD ^a	HP	N	Sultana <i>et al.</i> 2006a
β -actin	MCI ^a	IPL	H	Reed <i>et al.</i> 2008
α -internexin	DS ^a	FC	H	Di Domenico <i>et al.</i> 2014
Myelin binding protein (MBP)	DS ^a	FC	H	Di Domenico <i>et al.</i> 2014
	DS/AD ^b	FC	H	Di Domenico <i>et al.</i> 2014
Neurofilament medium polypeptide (NMP)	DS/AD ^a	FC	H	Di Domenico <i>et al.</i> 2014
α -tubulin	LAD ^a	HP	H	Perluigi <i>et al.</i> 2009
Neuroinflammation				
Glial fibrillary acidic protein (GFAP)	EAD ^a	IPL	C	Sultana <i>et al.</i> 2010
	DS ^a	FC	H	Di Domenico <i>et al.</i> 2014
	DS/AD ^a	FC	H	Di Domenico <i>et al.</i> 2014

Protein	Disease State	Brain Region	Oxidative Modification	References
Protein Synthesis				
Elongation factor-Tu (EF-Tu)	MCI ^a	IPL	H	Reed <i>et al.</i> 2008
Initiation factor α (eIF- α)	MCI ^a	IPL	H	Reed <i>et al.</i> 2008
Protein Folding and Degradation				
Cathepsin D (CatD)	DS ^a	FC	C	Di Domenico <i>et al.</i> 2013
78kDa glucose-regulated protein (GRP78)	DS ^a	FC	C	Di Domenico <i>et al.</i> 2013
	DS/AD ^{a,b}	FC	H	Di Domenico <i>et al.</i> 2014
Heat shock cognate 71 (HSC71)	LAD ^a	IPL	C	Castegna <i>et al.</i> 2002b
	DS/AD ^a	FC	H	Di Domenico <i>et al.</i> 2014
Heat shock protein (HSP70)	MCI ^a	HP	H	Reed <i>et al.</i> 2008
	MCI ^a	HP	N	Sultana <i>et al.</i> 2007
	MCI ^a	IPL	C	Sultana <i>et al.</i> 2010
Heat shock protein (HSP90)	MCI ^c	IPL	C	Aluise <i>et al.</i> 2011
	DS/AD ^b	FC	H	Di Domenico <i>et al.</i> 2014
T-complex protein 1 subunit β (TCPB)	DS/AD ^a	FC	H	Di Domenico <i>et al.</i> 2014
Ubiquitin carboxy-terminal hydrolase L-1 (UCH-L1)	LAD ^a	FC	C	Choi <i>et al.</i> 2004
	LAD ^a	HP	C	Sultana <i>et al.</i> 2006c
	LAD ^a	IPL	C	Castegna <i>et al.</i> 2002a
	DS ^a	FC	C	Di Domenico <i>et al.</i> 2013
	DS ^a	FC	H	Di Domenico <i>et al.</i> 2014
V _o -ATPase	DS ^a	FC	C	Di Domenico <i>et al.</i> 2013
Signal Transduction				
14-3-3 γ	MCI ^a	IPL	N	Sultana <i>et al.</i> 2007
Mitogen-activated protein kinase I (MAPKI)	MCI ^a	IPL	C	Sultana <i>et al.</i> 2010
Peptidylprolyl cis-trans isomerase-1 (Pin1)	MCI ^a	HP	C	Butterfield <i>et al.</i> 2006a
	LAD ^a	HP	C	Sultana <i>et al.</i> 2006b; Sultana <i>et al.</i> 2006c

Note: FC, frontal cortex; HP, hippocampus; IPL, inferior parietal lobule; C, carbonylation; N, nitration; H, HNE bound

^a compared to age-matched control

^b compared to DS brain

^c compared to PCAD

Table 5:

Summary of Oxidatively Modified Proteins Identified by Redox Proteomics and Enzymatic Activity in aMCI, AD, and DS Brain

Protein	Disease State	Brain Region	Oxidative Modification	Enzyme Activity	References
Cellular Redox Homeostasis and Detoxification Defense					
Mn Superoxide dismutase (SOD)	EAD ^a	IPL	H	↓	Reed <i>et al.</i> 2009
Energy Metabolism					
Aconitase	LAD ^a	HP	H	↓	Perluigi <i>et al.</i> 2009
ATP Synthase	MCI ^a	HP	H	↓	Reed <i>et al.</i> 2008
	MCI ^a	IPL	H	↓	Reed <i>et al.</i> 2008
	LAD ^a	IPL	H	↓	Perluigi <i>et al.</i> 2009
α-enolase	MCI ^a	HP	C	↓	Butterfield <i>et al.</i> 2006a
	EAD ^a	IPL	H	↓	Reed <i>et al.</i> 2009
Lactate dehydrogenase (LDH)	MCI ^a	HP	H	↓	Reed <i>et al.</i> 2008
Malate dehydrogenase (MDH)	EAD ^a	IPL	H	↑	Reed <i>et al.</i> 2009
Pyruvate kinase (PK)	MCI ^a	IPL	H	↓	Reed <i>et al.</i> 2008
	MCI ^a	HP	C	↓	Butterfield <i>et al.</i> 2006a
Synaptic plasticity, vesicle-mediated transport and cell structure					
Carbonic anhydrase II (CA II)	LAD ^a	HP	C	↓	Sultana <i>et al.</i> 2006c
Protein Folding and Degradation					
Ubiquitin carboxy-terminal hydrolase L-1 (UCH-L1)	LAD ^a	HP	C	↓	Sultana <i>et al.</i> 2006c
	DS ^a	FC	C	↓	Di Domenico <i>et al.</i> 2013
Signal Transduction					
Peptidylprolyl cis-trans isomerase-1 (Pin1)	MCI ^a	HP	C	↓	Butterfield <i>et al.</i> 2006a
	LAD ^a	HP	C	↓	Sultana <i>et al.</i> 2006b

Note: FC, frontal cortex; HP, hippocampus; IPL, inferior parietal lobule; C, carbonylation; N, nitration; H, HNE bound

^a compared to age-matched control