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# Walking the tightrope: proteostasis and neurodegenerative disease

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# Walking the tightrope: proteostasis and neurodegenerative disease

## Abstract

A characteristic of many neurodegenerative diseases, including Alzheimer's disease (AD), Parkinson's disease (PD), Huntington's disease (HD), and amyotrophic lateral sclerosis (ALS), is the aggregation of specific proteins into protein inclusions and/or plaques in degenerating brains. While much of the aggregated protein consists of disease specific proteins, such as amyloid- $\beta$ ,  $\alpha$ -synuclein, or superoxide dismutase1 (SOD1), many other proteins are known to aggregate in these disorders. Although the role of protein aggregates in the pathogenesis of neurodegenerative diseases remains unknown, the ubiquitous association of misfolded and aggregated proteins indicates that significant dysfunction in protein homeostasis (proteostasis) occurs in these diseases. Proteostasis is the concept that the integrity of the proteome is in fine balance and requires proteins in a specific conformation, concentration, and location to be functional. In this review, we discuss the role of specific mechanisms, both inside and outside cells, which maintain proteostasis, including molecular chaperones, protein degradation pathways, and the active formation of inclusions, in neurodegenerative diseases associated with protein aggregation. A characteristic of many neurodegenerative diseases is the aggregation of specific proteins, which alone provides strong evidence that protein homeostasis is disrupted in these disease states. Proteostasis is the maintenance of the proteome in the correct conformation, concentration, and location by functional pathways such as molecular chaperones and protein degradation machinery. Here, we discuss the potential roles of quality control pathways, both inside and outside cells, in the loss of proteostasis during aging and disease.

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**Walking the tightrope: Proteostasis and neurodegenerative disease.**

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## **Abstract**

A characteristic of many neurodegenerative diseases, including Alzheimer's disease (AD), Parkinson's disease (PD), Huntington's disease (HD) and Amyotrophic Lateral Sclerosis (ALS), is the aggregation of specific proteins into protein inclusions and/or plaques in degenerating brains. While much of the aggregated protein consists of disease specific proteins, such as amyloid- $\beta$ ,  $\alpha$ -synuclein or SOD1, many other proteins are known to aggregate in these disorders. Although the role of protein aggregates in the pathogenesis of neurodegenerative diseases remains unknown, the ubiquitous association of misfolded and aggregated proteins indicates that significant dysfunction in protein homeostasis (proteostasis) occurs in these diseases. Proteostasis is the concept that the integrity of the proteome is in fine balance and requires proteins in a specific conformation, concentration and location to be functional. In this review we discuss the role of specific mechanisms, both inside and outside cells, which maintain proteostasis, including molecular chaperones, protein degradation pathways and the active formation of inclusion, in neurodegenerative diseases associated with protein aggregation.

**Key words:** Proteostasis, neurodegenerative disease, heat shock proteins, ubiquitin proteasome system, autophagy, extracellular proteostasis, aggregate, amyloid, Alzheimer's, Huntington, ALS, MND, dementia, degradation

## Abbreviations

A $\beta$  – amyloid –  $\beta$  peptide

A2M – alpha-2-macroglobulin

AD – Alzheimer's disease

ALS – Amyotrophic Lateral Sclerosis

CLU - clusterin

CFTR - cystic fibrosis transmembrane conductance regulator

DUB - deubiquitinating enzymes

E3L – E3 ligase

GWAS - genome wide association studies

HD – Huntingtin’s disease

Hp - Haptoglobin

HSP - heat shock protein

HSF1 – heat shock factor1

HSR – Heat shock response

INQ - intranuclear quality control compartment

IPOD – Insoluble protein deposits

iPSC - induced pluripotent stem cells

JUNQ – Juxtannuclear quality control compartment

LTP - long-term potentiation

MND – Motor Neurone disease

MRI – Magnetic resonance imaging

MTOC - microtubule organizing center

PD – Parkinson’s disease

PolyQ – poly glutamine

Proteostasis – protein homeostasis

RISCI – RNA interactor specific compartment/inclusions

sHSP – small heat shock protein

SOD1 – Superoxide dismutase1

Ub - Ubiquitin

UPS - ubiquitin-proteasome system

## **The proteostasis network safeguards cells and organisms from misfolded and damaged proteins**

The term proteome homeostasis or *proteostasis* refers to the maintenance of all proteins in the proteome in a conformation, concentration and location that is required for their correct function (Balch et al. 2008). Proteostasis is essential to maintain normal cellular metabolic function, and is vital for the dynamic changes required for a cell to respond to a given stimulus. An extensive and complex network of signaling pathways are involved in safeguarding cells and organisms against proteotoxic stress. They do so by maintaining the delicate balance between the production and disposal of proteins. Thus, the combined actions of this extended network that maintains proteostasis, the proteostasis network, act as a quality control department in the demanding world of protein production. The proteostasis network comprises pathways that regulate the biogenesis, folding, trafficking and degradation of proteins (Fig. 1). Some of the most significant players in the network are the chaperone proteins, the guardians of the cell that ensure the integrity of the proteome. Other protective processes involve compartmentalizing misfolded proteins into specific regions in the cell (e.g. the aggresome) or removal of proteins by autophagy or the ubiquitin-proteasome system (UPS). The careful regulation of these activities is critical in reducing the toxicity associated with mutant, misfolded and/or damaged proteins. Obviously, the removal of toxic forms of misfolded proteins is important for all cells, but it is especially significant in post-mitotic cells, such as neurons, since these cannot be readily replaced. In neurons, the maintenance of proteostasis is central to healthy ageing; dysregulation of the proteostasis network can lead to neurodegenerative disease. Thus, the successful maintenance of proteostasis is directly related to cellular and organismal longevity.

### **Dysregulation of the proteostasis network in neurodegenerative disease**

A common characteristic of many neurodegenerative disorders is the presence of specific and distinct proteinaceous inclusions in or around the affected neuron in hallmark regions of the brain (Fig. 2). These inclusions are primarily composed of misfolded, aggregated and often toxic forms of one or more specific proteins. As examples, Parkinson's disease is characterized by the deposition of the protein  $\alpha$ -synuclein into Lewy bodies (particularly in the substantia nigra), Alzheimer's disease is associated with amyloid- $\beta$  plaques and tangles of phosphorylated tau, and Huntington's disease is associated with aggregates of huntingtin containing expanded repeats of glutamine in the nucleus and cytoplasm. In contrast, ALS pathology is characterised by a number of different types of inclusions, including Bunina bodies, and ubiquitinated, hyaline and skein-like inclusions (Ciechanover 2005). Thus, the presence of inclusions, the visible products of protein aggregation in a number of neurodegenerative diseases, indicates that a significant disruption to proteostasis has occurred. The specific proteins involved in these diseases form aggregates that can be fibrillar and insoluble, as in the case of amyloid- $\beta$  (Chiti and Dobson 2006), fibrillar and re-soluble as in the case of the hydrogel type aggregates associated with FUS (Han et al. 2012), or amorphous.

Genetic mutations to metastable proteins may increase their propensity to aggregate, causing the proteostasis network to be overloaded. However, there is evidence that expression of aggregation prone proteins can be dealt with by proteostasis networks in early life and that as organisms age the capacity to deal with this added proteotoxic stress is impaired, facilitating aggregation (Ben-Zvi et al. 2009, Wang et al. 2009, David et al. 2010). In the absence of genetic mutations associated with an

increased aggregation propensity of a single protein (i.e. in sporadic cases of these neurodegenerative diseases where there is no genetic cause of disease), the failure of the proteostasis network is likely a requisite for aggregation to occur. How the proteostasis capacity is 'overwhelmed' in these cases is yet to be determined, however, a decline in the levels of proteostasis components during aging is likely to be a key factor. For example, previous work has suggested an age-related attenuation of the ability to activate HSF1 during stress (Shamovsky and Gershon 2004) (see **The role of molecular chaperones in neurodegenerative disease** below). Once aggregation occurs it is probable that a further collapse in proteostasis follows due to the sequestration of chaperones and other proteostasis components (e.g. proteasome subunits) into inclusions (Yu et al. 2014). Taken together, these data suggest that in early life, in the absence of genetic mutation, the proteostasis network has sufficient capacity to deal with aggregating proteins and that a reduction and/or dysfunction in proteostasis capacity, as occurs with age, expedites aggregation and thus the onset and progression of disease.

The most significant universal risk factor for neurodegenerative diseases is age. Neurons are seemingly more susceptible to detrimental age-related metabolic changes than other cell types and several inter-related factors could contribute to this susceptibility. In most regions of the adult brain, damaged neurons are not replaced and central axons regenerate poorly after injury (reviewed in (Liu et al. 2011)). Although neurogenesis can take place in certain areas of the hippocampus and olfactory bulb, this process slows with ageing and the integration of new neurons into functional networks becomes limited (Kuhn et al. 1996, Overstreet-Wadiche et al. 2006). In addition, neurons are highly compartmentalized, with long axons and dendrites that cover large distances and form thousands of connections with other cells. Local protein synthesis at synapses carries a high-energy demand and neuronal ATP requirements increase with ageing (Gabbita et al. 1997). These increased ATP requirements with ageing are possibly due to a reduction in the efficiency of energy utilization by aged neurons, however, the precise reasons for this remain unclear. Moreover, the generation of ATP by oxidative phosphorylation leads to the release of oxidative radicals that damage neuronal DNA, proteins and lipids. In the absence of neuron turnover, oxidative damage accumulates over the life span of the cell/organism. Lastly, chaperones, including the heat shock proteins (HSPs) appear to have a higher threshold for activation and/or lower overall expression in neurons compared to other cells, e.g. induction of HSP70 by heat shock factor 1 (HSF1) is lower in neurons than non-neuronal cells (Marcuccilli et al. 1996, Manzerra et al. 1997). Protein degradation via the Ubiquitin-Proteasome System (UPS) is also highly dependent on ATP (Hershko et al. 1980). Hence, age-related changes in neuronal ATP balance or ATP requirements are likely to have significant effects on the capacity of this system (Huang et al. 2013). Conversely, mitochondrial proteins and components of energy metabolic pathways (glycolysis and oxidative phosphorylation) are substrates of the UPS, indicating the potential for significant crosstalk between neuronal energy metabolism and protein turnover (Heo and Rutter 2011, Livnat-Levanon and Glickman 2011).

Overall it thus appears that neurons are more susceptible to cellular stressors than other cell types. Collectively these factors can lead to substantial overload of proteostasis networks, due to (i) the inability of neurons to dilute aggregates via cell division, (ii) the extreme distances of axons, which



require protein turnover, from the nucleus, and (iii) signaling pathways of the proteostasis network being ATP-dependent. The overload of the proteostasis network can lead to widespread protein misfolding in specific neuronal types in the brain. The inability of neurons to maintain proteostasis does not appear to be random; there are temporal and spatial patterns of inclusion formation during disease progression and the overall 'inclusion load' correlates very well with the advancement and increased severity of pathological changes. It is thus vital to understand the components of the network that govern the proteostasis capacity of the brain.

The following sections of this review detail the central systems in the proteostasis network within the context of neurodegenerative disease, including the molecular chaperones, compartmentalisation of misfolded proteins, the ubiquitin proteasome system, autophagy, and extracellular proteostasis.

### **The role of molecular chaperones in neurodegenerative disease**

Exposure to acute or chronic proteotoxic stress results in the induction of highly conserved and ubiquitous stress response pathways in cells (Voisine et al. 2010, Morimoto 2011). Induction of the heat shock response (HSR) is dependent on the activation of the transcription factor, heat shock factor 1 (HSF1), which involves its transition from an inactive monomer into an active hyperphosphorylated trimer with high affinity for DNA-binding (Akerfelt et al. 2010). DNA-binding of trimeric HSF1 to heat shock elements in promoter regions of target genes leads to the rapid and robust expression of a variety of stress response genes, in particular the HSP molecular chaperones (Anckar and Sistonen 2011, Morimoto 2011, Baird et al. 2014).

Of the proteostasis pathways responsible for combating protein aggregation, molecular chaperones are arguably one of the most important, as they form a cell's first line of defence against protein misfolding and subsequent aggregation (Hartl et al. 2011). Hence, the presence of protein inclusions in neurodegenerative diseases can be interpreted as a failure of chaperones to prevent aggregation in the context of these disorders. Molecular chaperones represent a structurally diverse class of proteins that support correct folding by preventing unproductive interactions between partially folded protein intermediates (Voisine et al. 2010, Hartl et al. 2011, Wyatt et al. 2013, Treweek et al. 2015). A recent comprehensive analysis of the human intracellular "chaperome" (this study did not consider extracellular chaperones which are discussed below) identified 332 chaperone genes (88 of which are functionally classified as chaperones and 244 are classified as co-chaperones) that were placed into nine families: HSP90, HSP70, HSP60, HSP40, Prefoldin, small HSPs (sHSPs), tetratricopeptide repeat (TPR)-domain containing, and chaperones of the endoplasmic reticulum and mitochondria (Brehme et al. 2014). Five of these chaperone families correspond to heat shock proteins (Hsp90, Hsp70, Hsp60, Hsp40 and sHsps), a family of evolutionarily conserved proteins with diverse functions in proteostasis. As a result of their well-characterized molecular chaperone functions, Hsps play a role (directly or indirectly) in most cellular processes. For example, molecular chaperones play important roles in stabilising the cytoskeleton, regulating stress responses, trafficking proteins into and out of cellular compartments, mitigating apoptotic signaling and shuttling damaged proteins for degradation by the proteasome or by autophagy. It is beyond the

scope of this work to provide a comprehensive summary of the role of individual Hsps in proteostasis, however, there have been a number of recent reviews by others in this area, e.g. (Kim et al. 2013, Brandvold and Morimoto 2015, Duncan et al. 2015, Finka et al. 2015, Labbadia and Morimoto 2015, Pratt et al. 2015, Treweek et al. 2015).

One reason that chaperones may fail to prevent protein aggregation associated with neurodegenerative diseases is highlighted by recent work demonstrating that there is, in general, a decrease in chaperone levels (in particular of ATP-dependent chaperones) in the human brain during ageing, and in AD, HD and PD patients; the main exceptions to this being the sHsps and TPRs which increase with age and in the context of these neurodegenerative diseases (Brehme et al. 2014). Changes in the relative balance of the 'chaperome' network may facilitate the cascade of events that manifest as the age- and neurodegenerative disease-associated collapse in proteostasis. Moreover, cellular senescence, as occurs in neurons, results in a decline in proteostasis capacity and could, at least in part, account for the general decrease in chaperone levels seen with age and in neurodegenerative diseases. As such, exogenous application of Hsps, or therapeutic up-regulation of existing proteostatic pathways that regulate their levels, represents a promising avenue for the treatment of neurodegenerative diseases.

There have been a wide range of studies that have examined the protective role (or otherwise) chaperones have on protein aggregation and inclusions formation in cell-based and mouse models of diseases, with varying results. One often overlooked aspect of such work is the interdependence and compensatory mechanisms that exist within the chaperome. For example, the chaperone-mediated degradation of aggregation-prone proteins via autophagy requires the concerted actions of Hsc70, Hsp40 and co-chaperones such as Hip and Hop (Agarraberes and Dice 2001) and there are multiple members (often with overlapping expression and function) of each chaperone class (Brehme et al. 2014). Thus, over-expression or knock-down/out studies of individual Hsps can be an over-simplification and the impact increasing/decreasing the levels of one chaperone isoform has on the levels of others is often not taken into account. Nevertheless, various studies have demonstrated that over-expression of the Hsps can prevent the aggregation and associated toxicity of disease-related proteins, for example amyloid- $\beta$  (Hoshino et al. 2011), polyglutamine-expanded proteins (Wytttenbach et al. 2002, Jiang et al. 2012, Ormsby et al. 2013),  $\alpha$ -synuclein (Auluck et al. 2002, McLean et al. 2002, Tue et al. 2012, Cox et al. 2014) (Auluck et al. 2002, McLean et al. 2002, Tue et al. 2012, Cox et al. 2014) and superoxide dismutase 1 (Koyama et al. 2006, Crippa et al. 2010, Novoselov et al. 2013), proteins implicated in the pathogenesis of AD, HD, PD and MND, respectively. However, others have reported that over-expression of some Hsps do not have any significant effects on disease progression in mouse models of disease, for example (Liu et al. 2005, Krishnan et al. 2008, Shimshek et al. 2010, Xu et al. 2015). Thus, it remains to be determined whether up-regulating chaperone levels is a valid therapeutic approach for the treatment of these neurodegenerative diseases.

In studies that have reported a neuroprotective effect of Hsps it has been primarily attributed to their ability to (i) mitigate the earliest aberrant protein interactions that trigger pathogenic aggregation (and promote subsequent re-folding of the misfolded proteins) or (ii) shuttle proteins for degradation. The co-localization of Hsps with plaques and inclusions in the brains of

neurodegenerative disease patients (e.g. (Wilhelmus et al. 2006, Leverenz et al. 2007) and in mouse models of these diseases (e.g. (Basso et al. 2009, Zetterstrom et al. 2011)) has led to the interpretation that these Hsps are 'overwhelmed' by the increasing levels of protein aggregation, resulting in their subsequent deposition into the inclusion itself (and loss of chaperone function as a result). However, recent work has demonstrated that many chaperones can interact with the aggregated form of proteins and, in doing so, may mediate their packaging into inclusions (Dedmon et al. 2005, Falsone et al. 2009, Waudby et al. 2010, Danzer et al. 2011, Binger et al. 2013). Indeed, it has been recently shown that sequestering proteins into chaperone-enriched aggregates prevents an age-related decline in proteostasis and prolongs lifespan in *C.elegans* (Walther et al. 2015). Thus, Hsps may play an active role in the formation of the inclusions rather than merely being a by-product of their formation. It is likely that this action plays two important roles: (i) inhibiting aggregate fragmentation and secondary nucleation events, both of which can be the source of cytotoxic oligomers associated with protein aggregation (Knowles et al. 2009); and (ii) facilitating the degradation of the aggregated protein via the UPS and chaperone-mediated autophagy (see below).

### **Maintaining proteostasis by aggregation**

Although it is still not clear whether protein aggregation into inclusions is a cause or consequence of neurodegenerative diseases, aggregation alone provides strong evidence that proteostasis has been disrupted in these diseases. Moreover, whilst each neurodegenerative disease is specifically associated with the aggregation of particular proteins into inclusions (e.g.  $\alpha$ -synuclein in PD), there are many other proteins also present in these protein inclusions. Characteristically, these proteins are expressed at levels that exceed their predicted aggregation propensity (i.e. they are super-saturated) (Ciryam et al. 2013). There is still some debate about whether the formation of protein inclusions in cells is a protective mechanism (Saudou et al. 1998, Miller et al. 2011), or toxic to the cells. In any case it is clear that protein aggregation and the formation of inclusions are closely associated with neuronal degeneration (Leigh et al. 1991, Chiti and Dobson 2006, Ticozzi et al. 2010, Ormsby et al. 2013).

Classically, inclusions were thought to be purely the result of the misfolding and random self-assembly of proteins into amorphous and/or fibrillar structures in a process replicating the well-characterized aggregation of proteins *in vitro* (Chiti and Dobson 2006, Knowles et al. 2014). Indeed, it is possible that the chronic misfolding and aggregation of a disease-associated protein, such as SOD1, 'overwhelms' the proteostasis capacity of the cell and may help explain the widespread protein aggregation of metastable proteins (Gidalevitz et al. 2006). Given the observed three dimensional spread of neurodegeneration throughout the nervous system, proteostatic collapse may spread throughout the nervous system in conjunction with the misfolding and aggregation of proteins, such as observed for SOD1 in ALS (Grad et al. 2014).

In contrast, it is now clear, that in an effort to maintain proteostasis, cells are able to actively sequester misfolded and aggregating proteins into subcellular compartments. These compartments are not organelles but spatially distinct regions in the cell that minimize the risk that misfolded proteins pose to cells (e.g. even small aggregates can nucleate further aggregation and be toxic to cells) by clustering proteins so that they can be resolubilized or degraded, as appropriate.

Several mechanisms for forming inclusions in mammalian cells have been described, including those associated with the structures known as aggresomes (Johnston et al. 1998), insoluble protein deposits (IPOD) and juxtannuclear quality control (JUNQ) (Kaganovich et al. 2008), aggresomes (Kopito 2000), aggresome-like structures (ALIS) (Szeto et al. 2006), RNA interactor specific compartments/inclusions (RISCI) (Farrarwell et al. 2015), and ER-associated degradation-associated vesicles (ERADAV) (Kamhi-Nesher et al. 2001) and intranuclear protein quality control compartments (Nollen et al. 2001, Miller et al. 2015). The almost ubiquitous nature of these types of inclusions in neurodegenerative diseases, and the diverse and specific mechanisms that underpin their formation, reveals the importance of inclusions to cellular protein quality control and human pathology.

Originally, cell driven, microtubule-dependent juxtannuclear inclusions of the cystic fibrosis transmembrane conductance regulator (CFTR) that colocalized with the microtubule organizing center (MTOC) were discovered and termed aggresomes (Johnston et al. 1998). Aggresomes were found to organize and sequester aggregated proteins into a specific region of the cell, and to have chaperones and proteasome subunits associated with them (Kopito 2000). Aggresomes are ensheathed by a cage of vimentin, however, it is not clear if this event indicates an attempt to contain the aggregate or if it represents a filament collapse in the cell (Johnston et al. 1998). While there is still little known about the formation of these structures, their formation is dependent on dynein microtubules and HDAC6 (Kawaguchi et al. 2003).

IPOD inclusions have been observed in yeast and mammalian cells and are characterized as dense, immobile compartments consisting of insoluble protein aggregates that (at least initially) are not ubiquitinated (Kaganovich et al. 2008, Hipp et al. 2012). Proteins targeted to IPODs end up as insoluble aggregates or amyloid fibrils. The most common experimental model of IPOD is huntingtin with pathogenic polyQ expansions (Kaganovich et al. 2008, Polling et al. 2014). In yeast, Hsp104 and the autophagy protein Atg8 colocalize with IPODs, consistent with a cellular effort to degrade the aggregated proteins (Kaganovich et al. 2008). In primary neuronal cultures the huntingtin-polyQ IPOD structures are extremely stable with no loss of fluorescently tagged protein over the period of a week (Tsvetkov et al. 2013).

Aggresomes may be related to the compartment referred to as JUNQ (Kaganovich et al. 2008) later observed in yeast and mammalian cells. JUNQ-like inclusions are enriched in ubiquitylated proteins, proteasome subunits, chaperones (such as Hsp70) and proteins are able to freely diffuse in and out of the aggregate in mammalian cells (Kaganovich et al. 2008, Weisberg et al. 2012, Polling et al. 2014). As a result, JUNQ has been proposed to be a cellular quality control center in which soluble misfolded proteins or aggregates from the cytosol accumulate for proteasomal degradation and refolding (Kaganovich et al. 2008, Weisberg et al. 2012). The precise mechanisms that underpin JUNQ formation still remain a mystery, as does the cell's method of containing the aggregated proteins in the inclusion. However, it is clear that in mammalian cells, proteins can be targeted to JUNQ via their ubiquitination, and require transport via microtubules (Kaganovich et al. 2008, Farrarwell et al. 2015). Whilst it was originally thought that JUNQ inclusions possessed the same characteristics in all eukaryotic cells, recently it has been demonstrated that JUNQ-like structures in yeast can be found within the nucleus rather than the cytosol (Miller et al. 2015, Miller et al. 2015).

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It has been proposed that these structures in yeast should be referred to as the intranuclear quality control compartment (INQ). Indeed, additional work demonstrates the intranuclear compartment contains a distinct set of proteins that are ubiquitylated and sumoylated and are a response to genotoxic stress (Gallina et al. 2015). The relationship, if any, these structures have to JUNQ aggregates in the mammalian cytosol, such as those formed by SOD1 remains unclear. In any case, these findings highlight the need to further characterise the processes in cells that act to organize aggregated proteins into specific regions and to identify a set of criteria to properly define and identify various types of inclusions in cells.

Clearly, we are only just beginning to understand the intricate cellular processes that actively promote the formation of inclusions in cellular systems. Further understanding of the molecular properties of these structures, their organization and their involvement in cellular proteostasis may uncover important biological processes critical to the understanding of many neurodegenerative diseases. For example, given that cells actively partition aggregating proteins, under some conditions it may be detrimental to suppress this process with anti-aggregation small molecules.

### **Balancing proteostasis via protein degradation**

#### ***The Ubiquitin Proteasome System (UPS)***

Ubiquitination is one of the most abundant protein modifications in cellular signaling, regulating numerous cellular pathways including transcription, translation, vesicle transport, apoptosis, cell cycle and DNA damage repair. Ubiquitin (Ub) labels substrate proteins via a highly ordered multi-step enzymatic cascade, with specific differences in the length and topology of poly-Ub chains signaling a range of signaling outcomes (e.g. allosteric regulation, intracellular trafficking) or proteolytic degradation via the proteasome.

In the nervous system, Ub contributes to the regulation of neuronal growth and development, excitability, neurotransmission, long-term potentiation (LTP) and synapse formation and elimination (Mabb and Ehlers 2010, Kawabe and Brose 2011). Maintenance of the UPS is central to neuronal health as neurons are very sensitive to prolonged Ub deficiency, which leads to cell death (Tan et al. 2000, Tan et al. 2001). Mounting genetic and functional evidence supports a role for compromised ubiquitin homeostasis in the pathophysiology of neurodegenerative diseases, and the ubiquitination machinery is emerging as a highly promising target for human therapy (Jankowska et al. 2013).

Ubiquitin exists in a dynamic cellular equilibrium, partitioning into four major pools; (i) immobile in the nucleus (primarily bound to histones), (ii) immobile in the cytoplasm (bound to organelles and cytoskeleton), (iii) in soluble polyUb chains and (iv) a small fraction as free monomeric Ub (Dantuma et al. 2006). Ubiquitin homeostasis is tightly regulated at multiple levels. *De novo* replenishment of

Ub is achieved through transcription of four separate mammalian genes (UBB, UBC, UBA52 and UBA80) and Ub is degraded by the 26S proteasome (Ciechanover 2005). However, the key regulator of the balance between free and protein-conjugated ubiquitin pools is the opposing actions of E3 ubiquitin ligases (E3s) and deubiquitinating enzymes (DUBs). Reminiscent of the coordinated action of kinases and phosphatases, there is emerging evidence that E3s and DUBs coordinate to achieve dynamic fine-scale regulation of substrate ubiquitination (e.g. (Diefenbacher et al. 2014)). An example of this dynamic Ub equilibrium is the competition between histones and other Ub substrates for a limited pool of free ubiquitin in an “Ub Cycle” coupled to other cellular process requiring Ub (Dantuma et al. 2006, Groothuis et al. 2006). Kimura et al. (Kimura et al. 2009) used the example of a rapid loss of free Ub following heat shock to propose that free Ub chains act as a cellular reservoir for maintenance of monomeric Ub under normal conditions and provide a capacity for rapid response to stress conditions requiring substrate conjugation (analogous to the glucose/glycogen cycle).

Accumulation of ubiquitylated proteins in insoluble inclusions is another potential mechanism for loss of free Ub, but removal of Ub from the aggregated protein is possible through Ub-specific proteases. Free Ub was recently shown to be increased in cells containing huntingtin aggregates by overexpression of the de-ubiquitylation enzyme USP14 (Hyrskyluoto et al. 2014). Not only did this protect cells from aggregate-induced toxicity, but it also reduced ER stress, which is thought to precede inclusion formation in ALS models (Atkin et al. 2014). For example, proteasome inhibition depletes free Ub levels to as low as 5% of basal in less than 2 h (Mimnaugh et al. 1997, Patnaik et al. 2000). Inhibition of translation also depletes free Ub through reduced production, while toxicity can be rescued by overexpression of Ub (Hanna et al. 2003).

Probably the two most compelling lines of evidence for the role of Ub in neurodegenerative diseases come from the widely observed enrichment of Ub in cytoplasmic inclusion bodies defining many of these diseases, and from the loss of function phenotypes in mouse and human. For example, Ub is a pervasive feature of inclusions in ALS and motor neuron death in all forms of ALS is associated with the formation of aberrant Ub-positive protein inclusions (Giordana et al. 2010). Ub can also accumulate in inclusions without the aggregation of TDP-43 in sporadic ALS (Giordana et al. 2010), suggesting that aggregation of proteins such as TDP-43, FUS and SOD1 may not be necessary for Ub depletion-induced toxicity. Ub accumulation is also linked to impaired function of the cellular proteostasis network in models of Huntington’s disease (Hipp et al. 2012).

Several mouse models of Ub deficiency lead to protein aggregation and neurodegeneration (Hallengren et al. 2013). For example, *Usp14*-null mice display ataxia caused by reduced levels of monomeric Ub, resulting from decreased DUB-mediated enzymatic recycling (Anderson et al. 2005). Mice with loss-of-function mutations in the Parkinson’s-associated gene *Uchl1* (encoding a DUB) also have reduced neuronal monoubiquitin (Osaka et al. 2003). Further, disruption of the *Ubb* poly-ubiquitin gene in mice causes hypothalamic neurodegeneration through decreased total Ub levels (Ryu et al. 2008). Interestingly, compensatory expression from the *Ubc* gene was later shown to be



significantly upregulated in *Ubb*<sup>-/-</sup> mice in other brain regions to maintain free Ub and protect neuronal function (Park et al. 2012). Together, these data suggest that maintenance of Ub homeostasis (particularly the pool of free Ub) is necessary for neuronal protection.

### **Autophagy**

Autophagy involves formation of double-membrane cytosolic vesicles known as autophagosomes, which engulf long-lived proteins or particular organelles (e.g. mitochondria) and transport them to lysosomes for degradation (Ravikumar et al. 2010). Still controversial is the topic of autophagic cell death (Clarke and Puyal 2012), which certainly occurs in dying neurons subjected to oxidative stress (Higgins et al. 2011, Higgins et al. 2012), excitotoxicity and acute ischemic-like injuries (Puyal et al. 2012). Whilst current evidence indicates the contribution of autophagy to neuronal death is caspase-independent, this needs careful scrutiny in the context of brain pathologies since autophagy can recruit compensatory apoptosis and the two processes are intertwined, sharing common mediators such as Beclin 1 (Higgins et al. 2011, Puyal et al. 2012).

Much of our understanding of the mechanistic and genetic regulation of autophagy (and the UPS) comes from work in yeast, *Drosophila* and non-mammalian cells. Indeed, although autophagy was discovered essentially concurrently with lysosomes (in the 1950s), and was initially believed to be a response linked to nutrient and energetic availability and cellular homeostasis, it was not until some 10 years ago that its importance in the brain was recognized. Basal autophagic flux proved hard to detect in healthy neurons because the brain is at least partially protected by tightly controlled mechanisms that regulate its nutrient and energetic supply (Boland and Nixon 2006). However, the essential role of autophagy in brain has been convincingly demonstrated by evidence such as the accumulation of abnormal organelles and ubiquitinated proteins in the autophagy deficient Atg7 (autophagy related protein 7) knockout mouse (Komatsu et al. 2005). Now extensive data have shown autophagy is essential for neuronal health, maintenance of axonal function and morphology, and that compromised autophagy likely contributes to neurodegenerative conditions where toxic aggregates cause the increased abundance of autophagosomes and autolysosomes (Rubinsztein et al. 2005).

Recent genome wide association studies (GWAS) have suggested that compromised autophagic and/or lysosomal mechanisms may underlie (and thus contribute to) the pathology of most neurodegenerative diseases. For example, in frontotemporal degeneration, a clinically heterogeneous syndrome in which the major protein accumulating in dystrophic neurons is tau, two proteins (Rab38 and cathepsin C) involved in lysosomal biology were recently identified in a GWAS (Ferrari et al. 2014), however these are yet to be experimentally confirmed. Nevertheless, these findings do support earlier evidence for decreased function of autophagic processes in frontotemporal dementia (Hu et al. 2010, Brady et al. 2013). Systems biology approaches have also revealed the pivotal role of autophagy in frontotemporal dementia (Caberlotto and Nguyen 2014).

Autophagy also appears to be mechanistically linked to disease progression in Alzheimer's (Moreau et al. 2014) and Parkinson's diseases (Westbroek et al. 2011). Misfolded proteins can be degraded by chaperone-mediated autophagy and autophagy activation appears to protect against  $\alpha$ -synuclein-induced neurodegeneration (Xilouri et al. 2013). This exciting observation represents part of a growing awareness that the autophagy/lysosomal cascade may contain therapeutic targets for the treatment of neurodegenerative diseases (Friedman et al. 2015). However, whilst there is great hope for the clinical management of neurodegenerative diseases via up-regulation of degradative pathways, many unknowns still need to be addressed before these pathways can be therapeutically targeted. These include determining (i) the role(s) of different neuronal populations and glia in degrading aggregated protein, (ii) the cellular "load" (be it damaged organelles or aggregates) and its relationship to total protein degradation mechanisms, and (iii) the timing of potential treatments relative to overall pathology.

Mitochondrial dysfunction with consequent oxidative stress also occurs in most neurodegenerative diseases (Gibson et al. 2010, Higgins et al. 2010). Mitophagy (mitochondrial autophagy) can be negatively impacted upon by the presence of protein inclusions (Ashrafi and Schwarz 2013, Baker et al. 2014). In this context, collapse of the mitochondrial membrane potential initiates recruitment of two proteins, PTEN-induced kinase 1 (PINK1) and Parkin, which orchestrate autophagic degradation of the mitochondria. Mutations in both PINK1 and the ubiquitin ligase Parkin have been associated with familial early-onset Parkinson's disease (Ashrafi and Schwarz 2013). An important component of mitochondrial dynamics is the active transport of mitochondria by microtubules to all morphological compartments of the neuron and, as a result, dysfunction can result in dieback of the neuritic tree during injury or dysregulation of axonal transport (Van Laar and Berman 2013). Components of the UPS have also been implicated in regulating microtubule dynamics (Bheda et al. 2010).

### **Extracellular proteostasis, thinking outside the cell**

Decades of research have led to the current awareness of the importance of the many cellular processes that act to counter inappropriate misfolding and aggregation of intracellular proteins. Like most cells in the body, neurons are bathed in protein-rich extracellular fluids which, relative to the cell cytoplasm, are oxidizing and subject to shear stress as a result of pressure differentials between different body compartments and fluid flows. The extracellular fluid environment is therefore "stressful" to proteins and over time will result in cumulative damage to protein structure leading potentially to protein misfolding and aggregation. Presumably this is one reason why all secreted proteins in the body are "turned-over" with different half-lives (to replace "worn" proteins with new ones before any pathology results) (Wyatt et al. 2013). Given this background, it is obvious how serious pathologies can result from the inappropriate misfolding and aggregation of proteins in body fluids (e.g. in Alzheimer's disease where extracellular aggregating A $\beta$  may be the primary toxic species causing extensive brain cell loss).



Some recent key discoveries have thrown light on processes that have evolved to protect the body from pathological protein species in extracellular fluids. Several proteins abundant in human blood and present at lower levels in cerebrospinal fluid have been shown to have an ATP-independent chaperone action (like the sHsps). These extracellular chaperones include clusterin (CLU) (Humphreys et al. 1999, Poon et al. 2000), haptoglobin (Hp) (Yerbury et al. 2005) and alpha-2-macroglobulin (A2M) (French et al. 2008, Wyatt et al. 2014). The best studied of these is CLU which promiscuously interacts with essentially any misfolding protein to potently inhibit its aggregation. In the case of amorphous aggregation, CLU forms stable, soluble high molecular weight complexes with the misfolded client protein. In a rat model, these complexes are cleared from circulation in the blood on a time scale of a few minutes (Wyatt et al. 2011). *In vitro*, high molecular weight CLU-client complexes are internalised by rat hepatocytes into lysosomes and proteolytically degraded. Both Hp and A2M also form stable complexes with misfolded client proteins that are bound by a variety of cell types. It has also been shown that CLU, Hp and A2M can interact with exposed hydrophobicity on client proteins to neutralise their toxicity (Yerbury et al. 2009). Thus, it appears very likely that ECs are, in a sense, extracellular counterparts to GRP78 in the endoplasmic reticulum or HSP70 in the cytoplasm, binding to exposed regions of hydrophobicity to inhibit aggregation, keep them soluble, and safeguard against toxicity.

The extracellular chaperones form key elements of an integrated model of extracellular proteostasis in which their ability to maintain misfolded proteins in soluble complexes aids their clearance from body fluids via receptor-mediated endocytosis and subsequent lysosomal degradation (Wyatt et al. 2013). In both *in vitro* studies and a rat model, scavenger receptors have been implicated in this clearance although the precise receptor(s) involved have yet to be identified. It appears, therefore, that at least one mechanism to dispose of extracellular misfolded proteins utilizes an intracellular proteolytic system, the lysosome, to carry out end-stage degradation. There are also indications that when extracellular misfolded proteins evade the normal defenses of the extracellular chaperones and form insoluble deposits in the body, extracellular proteolytic mechanisms are triggered. For example, it has been shown that amyloid fibrils formed by A $\beta$  can activate the plasminogen system to generate the very active protease plasmin (Kranenburg et al. 2005). It is also interesting to note that the plasmin- $\alpha_2$ -anti-plasmin (fibrinolytic) system is activated in systemic amyloidosis (Bouma et al. 2007). Furthermore, recent studies indicate that when cells die by acute injury, cross-linked proteins are exposed that can activate plasmin, and that this event is involved in helping clear the proteinaceous cell debris *in vivo* (Samson et al. 2009, Samson et al. 2012). Thus, extracellular proteolytic systems, perhaps in concert with professional phagocytes, may aid in the clearance of large insoluble deposits in the body. The details of the mechanisms that operate in this context however remain to be fully elucidated. From studies relevant to clinical "stroke", it is known that plasmin-mediated degradation of fibrin clots can generate cytotoxic protein fragments (Guo et al. 2009). We do not yet know whether similar pathological protein fragments might be released from extracellularly-degraded misfolded protein deposits, but this knowledge could prove invaluable when, for example, designing a therapy to clear amyloid deposits from the brains of Alzheimer's disease patients.

There are some critical gaps in knowledge remaining that must be addressed before we can be confident of understanding at least the major processes that monitor and control extracellular protein misfolding. The importance of these processes comes from the fact that they are very likely to protect us from neurodegenerative and other serious diseases, and the ageing process itself. Future research is needed to identify: (i) the specific receptor(s) that clear chaperone-misfolded protein complexes from extracellular fluids; (ii) the protease systems that act to help clear extracellular protein deposits, and whether these synergize with extracellular chaperones to safely accomplish this task; (iii) whether it is possible to treat disease pathologies arising from inappropriate extracellular protein misfolding by pharmacologically manipulating the *in vivo* expression levels of extracellular chaperones (or perhaps their activities).

### **Control of proteostasis at the organismal level**

Whilst reductionist approaches that focus on individual cell types have yielded a wealth of information on proteostasis and how it is regulated in the cell, our broader understanding of the interplay between ageing, proteostasis and neurodegeneration has been greatly advanced by studies using more complex cellular models and model organisms, such as *C. elegans*. One of the main strengths of these studies is their ability to elucidate non-cell autonomous mechanisms involved in proteostasis.

There is a strong link between inflammation and neurodegeneration; inflammatory cells, such as microglia, are activated to phagocytose cellular debris and protein aggregates (Roberts et al. 2013) that are generated through neurodegeneration. A new wave of data suggests that inflammation may not only be evoked in order to clear toxic protein aggregates, but also to initiate metabolic changes in cells that directly influence longevity (Riera et al. 2014, Tatum et al. 2015). The coordination of a response to proteotoxic stress in one part of the body can be transmitted via sensory neurons to initiate or upregulate proteostasis pathways in cells of the periphery. For example, the activation of thermosensory neurons enhances serotonin release, which activates the heat shock response by upregulating HSF1 expression (Tatum et al. 2015). Using optogenetics, Tatum et al. (2015) were able to specifically excite serotonergic neurons in *C. elegans* and show that their activation reduces protein misfolding in peripheral tissue. These data provide evidence of a direct link between thermosensory neuron signaling and longevity. Blocking important components in sensory signaling, such as calcitonin gene related peptide or the thermosensing TRPV1 channel, increases metabolic health and prolongs lifespan in *C. elegans* (Riera et al. 2014). Together these data suggest that there is potential for (i) inflammation to directly affect longevity and (ii) for pathogens to activate the proteostasis network and therefore affect longevity even prior to inflammatory signaling. This paradigm-shifting research together highlights the possibility that infections lead to activation of sensory neurons that can directly affect longevity.

Whether manipulation of sensory neuron activity affects longevity in more complex organisms is currently unclear. However investigation of the key players in organismal control of proteostasis in *C. elegans* suggests these processes could be conserved in mammals. Inositol-requiring protein 1 (IRE1)-mediated splicing of the transcription factor X box-binding protein 1 (XBP-1) is a major

pathway for non-cell autonomous proteostasis in *C. elegans* with the ability to upregulate the unfolded protein response in the ER of distal cells (Taylor and Dillin 2013). XBP-1 splicing also controls ER signaling between cell types in mouse models, promoting a proinflammatory phenotype that promotes tumour development (Mahadevan et al. 2011) and controlling immune system homeostasis (Osorio et al. 2014). A number of neurotransmitters that are involved in the coordination of organismal proteostasis in *C. elegans* have counterparts in mammals that may have similar immune consequences. In terms of sensory neuron signaling, the *C. elegans* equivalent of noradrenaline, octopamine, is involved in organismal control of proteostasis (Sun et al. 2011). In mammals noradrenaline is responsible for the Fight or Flight response, conditions of acute stress that depress the immune response. It is likely that similar mechanisms in mammals signal the initiation of proteostasis defence mechanisms, following the signaling of proteotoxic events possibly by neurotransmitters such as serotonin (as described above) and dopamine, which is involved in resistance to infection (Anyanful et al. 2009), whilst GABA and acetylcholine activate and suppress HSF-1-mediated protection against protein aggregation (Garcia et al. 2007). Future studies developing the findings from *C. elegans* into more complex organisms will be a challenge for the next few years in proteostasis research.

#### **Innovations leading to advances in proteostasis research**

In the last few years there have been significant advances in our understanding of how proteostasis collapse is associated with the pathogenesis of neurodegenerative diseases. This progress can be predominately attributed to two major innovations in this research field; (i) advances in information technology that have nurtured and facilitated a systems biology approach to neurodegenerative diseases and proteostasis, and (ii) the use of induced pluripotent stem cells (iPSCs) that have enabled us to model neurodegenerative diseases in a dish (Ooi et al. 2013). These developments signal the birth of a revolution in which ever more complex cell biological networks can be investigated *in silico*, *in vitro* and *in vivo*. For example, we are now in a position to exploit the ability of iPSCs to model disease onset and progression in specific neuronal subtypes and link this with a systems biology approach to investigate how components of the proteostasis network change during the onset of disease-phenotypes in these cells. This information can be used to establish generic changes to the proteostasis network that occur during disease (by comparing across iPSCs from different individuals or across different neuronal subtypes) or specific changes that occur within an individual or within a particular neuronal subtype.

Our ability to monitor pathological events in individual cells in real time and to model multiple cell types in three-dimensions are the logical next steps in the development of the field. In the case of an Alzheimer's disease model, this has included the simultaneous formation of amyloid plaques and deposits of insoluble tau, rarely seen in classical two-dimensional cell models (Choi et al. 2014). The visualisation of cell migration in live animal brains with time-lapse MRI videos is now also providing three-dimensional positional information at the single cell level (Mori et al. 2014). The use of advanced imaging techniques to observe single cell effects in the context of neurodegenerative diseases, such as the propagation of misfolded proteins between individual cells in organisms, would be invaluable. For the field of proteostasis research, advances in these areas will lead to an improved

understanding of the molecular players involved and the cellular events leading to protein aggregation, degradation and clearance and how these pathways mediate degeneration of human neurons. Such techniques will allow us to address the susceptibility of specific neuronal subtypes in distinct diseases, a central question remaining to be answered in many neurodegenerative diseases.

### **Potential proteostasis based therapeutic avenues in neurodegenerative diseases**

If exceeding proteostasis capacity is a fundamental underlying cause of neurodegenerative conditions then it makes sense that either reducing the misfolded protein burden or increasing the proteostasis capacity are valid therapeutic strategies. A new drug development mindset is required. For over a century, pharmacological science has been highly successful in drugging fixed structures with small molecules: an effective strategy for selective targeting of channels, pores and enzyme surface pockets and pits that can induce allosteric change in activity. However, targets for misfolded proteins are often large and “floppy,” with little purchase for small molecules. For effective treatment and diagnosis of protein misfolding diseases, a new paradigm is needed, for example, based on the rational identification of selective antibody targets (epitopes) in the misfolded proteins that are key to the disease process. Selective antibody targeting of misfolded proteins is effective by several mechanisms, including the neutralization of cytotoxicity and inhibition of prion-like propagated misfolding, which has been found to participate in A $\beta$  oligomers/fibrils, tau,  $\alpha$ -synuclein and Cu/Zn superoxide dismutase (SOD1) operant in AD, PD, ALS and the tauopathies (reviewed in (Guest et al. 2011)). Moreover, in some conditions such as infectious prion disease and AD, the specific targeting of misfolded propagating proteins is a “needle in a haystack” scenario in which the misfolded species is present in a thousand to a million fold lower concentration than the natively folded species – a situation dubbed “target distraction”. In the context of the prion-like spread of misfolded protein antibody neutralization of released material may block the cell-to-cell spread and slow the progression of disease (Grad et al. 2014). Finally, specific immunotherapy for misfolded proteins would spare normal isoforms from autoimmune recognition, with attendant risks and narrowed therapeutic index.

An alternative strategy is to target the machinery whose capacity is theoretically exceeded, e.g. the activity of chaperones and the degradative pathways. As the HSR pathway is responsible for a dramatic up-regulation of chaperone expression under conditions of cellular stress it has been shown to be a promising therapeutic target (Akerfelt et al. 2010). For example, inducing the HSR by overexpression of HSF1 can ameliorate disease phenotypes and mitigate neurotoxicity in various models of neurodegenerative diseases (Fujimoto et al. 2005, Lin et al. 2013, Pierce et al. 2013). Moreover, a variety of HSR-inducing compounds that activate HSF1 are currently under investigation (e.g. geranylgeranylacetone, celastrol, arimoclomol, withaferin A and 17-AAG) (Kieran et al. 2004, Niiikura et al. 2006, Hoogstra-Berends et al. 2012, Khan et al. 2012, Kalmar et al. 2014, Sharma et al. 2015). Moreover, the majority of studies using animal models of neurodegenerative diseases have reported a HSR-mediated reduction in the load of toxic protein and enhanced neuroprotection suggesting that this is a viable therapeutic approach. With regards to targeting protein degradation pathways, it may be beneficial to activate the proteasome as overexpression of the proteasome activator subunit PA28 $\gamma$  enhances survival of neurons in a Huntington’s disease cell culture

model (Seo et al. 2007). In addition, small molecule stimulation of autophagy enhances cell survival in neuronal ALS models (TDP-43 aggregation) (Barmada et al. 2014) suggesting that targeting autophagy may be a reasonable therapeutic target (Fleming et al. (2011). It is likely that any therapeutic strategy that increases the proteostasis capacity of organisms will be of benefit to neurodegenerative disease progression.

### **Future perspectives**

While there is a strong association between protein aggregation, inclusion formation and neuronal dysfunction and death, the mechanistic relationship between each of them remains one of the biggest questions in the field. What is clear is that proteostasis collapse is a critical part of this process that can be caused by the burden of pathogenically misfolded proteins or peptides. In contrast, as was the focus of this review, proteostasis imbalance can be caused by dysfunction in pathways that maintain proteostasis such as molecular chaperones and protein degradation and this may contribute to both protein aggregation and neurodegeneration. Regardless, increasing the capacity of the proteostasis network will be an important area of future research.

It remains a central question as to why certain neurons are especially vulnerable to aggregating proteins in distinct neurodegenerative diseases (for example, motor neurons of the motor cortex and spinal cord in ALS; dopaminergic neurons of the substantia nigra in PD; cholinergic neurons of the entorhinal cortex and hippocampus in AD; medium spiny neurons of the striatum in HD). Identifying deficiencies in some cell types, and not others, will be a significant advance in our understanding of the vulnerabilities of neurons in the context of these diseases. Differing expression levels of components of the proteostasis network, as identified in proteomic maps of the brain (Sharma et al. 2015), could underlie neuronal subtype-specific responses in disease. This should also be considered in the context of level of expression of the disease specific proteins such as  $\alpha$ -synuclein, SOD1 and huntingtin. In essence the goal of future neurodegenerative disease research will be to identify deficiencies in cell- or neuron-specific adaptive responses and try to boost them in susceptible cells.

With an ageing population and the corresponding predicted rise in people suffering from neurodegenerative diseases, understanding the dynamics of the proteostasis network in the nervous system is an important task for the research community. Advances in high-throughput single cell analyses will drive our understanding of how and why neurons are different to other cell types, and what makes them so susceptible to defects in the proteostasis network. Unbiased approaches to identify key players in this system will be important for formulating novel therapeutic strategies. Reductionist approaches have identified some elements of proteostasis, but to gain a complete view there is a need to move towards capturing the system as a whole and to consider the impact of different cells and tissue types working together. A more holistic approach to understanding proteostasis in the context of neurodegenerative diseases will therefore be important for future research.

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### Figure Legends

Figure 1. Schematic representation of proteostasis networks. Protein homeostasis networks function to maintain the proteome in a native conformation, in the correct location and concentration. During nascent protein synthesis (cytoplasmic and ER) and folding a significant proportion of the proteome requires attention of molecular chaperones and/or the ubiquitin proteasome system (UPS). Cytosolic misfolded proteins are bound and triaged by molecular chaperones such as the HSPs and ER proteins are sorted by the endoplasmic reticulum associated degradation (ERAD) pathways. Any protein that cannot be degraded may be directed by the cell in to aggresome like structures. Aggregates that form in the cell can be degraded by macroautophagy. Secreted proteins are monitored by extracellular proteostasis pathways. Misfolded proteins in the extracellular space are recognised by extracellular chaperones which bind and direct misfolded proteins to cell surface receptors for degradation in lysosomes. Protein aggregates can also trigger activation of extracellular proteases such as plasminogen activators such as tPA which can result in degradation of aggregates.

Figure 2. Proteostasis imbalance during aging. Proteostasis networks may be reduced in their capacity during aging. For example, HSPs may reduce in number meaning that misfolded proteins generated from synthesis may not be directed to the UPS, but instead may result in an increase in protein aggregation. A reduction in the efficiency of autophagy may allow the accumulation of these aggregates. Similarly, an overloading of the extracellular proteostasis systems may also result in the accumulation of protein aggregates in the extracellular space.



