Supersaturation is a major driving force for protein aggregation in neurodegenerative diseases

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The solubility of proteins is an essential requirement for their function. Nevertheless, these ubiquitous molecules can undergo aberrant aggregation when the protein homeostasis system becomes impaired. Here we ask: what are the driving forces for protein aggregation in the cellular environment? Emerging evidence suggests that this phenomenon arises at least in part because the native states of many proteins are inherently metastable when their cellular concentrations exceed their critical values. Such 'supersaturated' proteins, which form a 'metastable subproteome', are strongly driven towards aggregation, and are over-represented in specific biochemical pathways associated with neurodegenerative conditions. These observations suggest that effective therapeutic approaches designed to combat neurodegenerative diseases could be aimed at enhancing the ability of the cell to maintain the homeostasis of the metastable subproteome.

Protein aggregation in neurodegenerative disease

Neurodegenerative disorders, including Alzheimer's, Parkinson's, and Huntington's diseases, are on the increase within the aging populations of the modern world, and present great challenges to our healthcare systems as their early diagnosis and effective treatment remain elusive [1–6]. This situation results, at least to some extent, from our limited understanding of the fundamental nature and origins of such diseases. Several contributing factors have been proposed to explain their onset and progression, including oxidative stress, mitochondrial dysfunction, the disruption of the endoplasmic reticulum and of membrane trafficking, the failure of protein folding and clearance mechanisms, and the activation of inflammatory responses [2,3,7,8]. A common upstream feature of these disorders, however, is that specific peptides and proteins, including Aβ and tau in Alzheimer's disease, α-synuclein in Parkinson's disease, and huntingtin in Huntington's disease, misfold and aggregate to form amyloid assemblies with a characteristic cross-β structure [1,4,9,10]. The presence of such aberrant aggregates can generate a cascade of pathological events, leading to the failure of protein homeostasis and the loss of normal biological function [4,9,11–14]. While the causal role of aggregation in these neurodegenerative disorders has not been established conclusively, this phenomenon is strongly associated with pathogenesis in a wide range of cases.

One promising avenue for progress in the development of therapeutic approaches for neurodegenerative disorders is to improve our understanding of the mechanisms by which cellular dysfunction arises from the initial protein aggregation events [1,4,9,11,12,15]. It is increasingly evident that, far from being an unusual property of a few specific proteins, protein aggregation is a common phenomenon and that most, if not all, proteins can form amyloid assemblies under appropriate conditions [1]. It has also been shown that the intrinsic propensity of proteins to aggregate is encoded in their amino acid sequences [16], and a variety of complementary approaches have been developed to predict such aggregation propensities [16–19]. Moreover, misfolded species, particularly the oligomers associated with the formation of larger heterologous assemblies, possess a generic cellular toxicity even under physiological conditions, the degree of which can be rationalized in terms of the physicochemical properties of the proteins involved [20,21].

In this article we discuss the fundamental factors that underlie protein aggregation, and identify supersaturation (Figure 1) as a primary driving force responsible for this phenomenon. We thus suggest that enhancing protein homeostasis mechanisms responsible for maintaining protein solubility may be an effective therapeutic route to prevent and combat neurodegenerative disorders.

Native states of proteins can be metastable towards aggregation

Increasing evidence indicates that many proteins are kinetically, but not thermodynamically, stable in their native states even under physiological conditions [4,22,23]. Despite the high stability of the aggregated state, however, such proteins can remain soluble for long periods of time because of the presence of high kinetic barriers that separate the native and the aggregated states [23,24]. In essence, proteins have evolved to remain soluble, but only to the levels required to meet their functions [25]. It has been recently shown that the concentrations of proteins in the cell are typically close to

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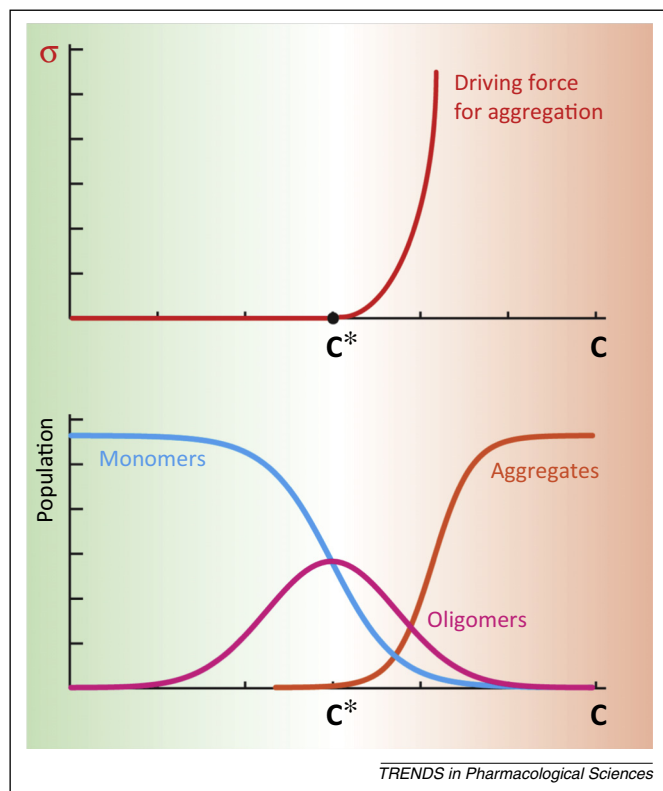
Figure 1. Supersaturation is a major driving force for protein aggregation. The degree of supersaturation, σ, defined as the ratio between the cellular concentration (C) and the critical concentration (C*) of a protein, quantifies such a driving force. Below the critical concentration most protein molecules are in a monomeric form, with a small fraction in oligomeric states. Above the critical concentration, proteins begin to form insoluble aggregates, including amyloid fibrils, with some remaining fractions in soluble monomeric and oligomeric forms. Thermodynamically, supersaturation represents the specific driving force for aggregation associated with the imbalance in the number of molecules in the aggregated and soluble states, and it grows according to $\sigma = e^{(\beta\Delta\mu)}$, where $\Delta\mu$ is the difference of the chemical potentials of the aggregated and soluble states, and $\beta = 1/k_BT$, where T is the temperature and k_B is the Boltzmann constant.

their critical values [25], and a negative correlation between protein aggregation propensity and protein expression has been observed among groups of bacterial, yeast, and human proteins [26,27]. Exceptions to this rule are represented by functional amyloid proteins, such as Pmel17, associated with the production of melanin, whose expression levels are high relative to their aggregation propensities, thus facilitating aggregation under normal conditions *in vivo* [25]. It has also been suggested that the codon usage in highly expressed genes is under pressure to avoid mistranslation-induced protein misfolding [28], and not only amino acid sequences, but also codon choice, may therefore be under selection to avoid aggregation-prone sequences.

Given the metastability of native proteins, it is not surprising that protein aggregation has emerged as a much more widespread phenomenon than previously supposed, and hundreds of different proteins have been shown to aggregate under stress or as a consequence of aging and disease [29–39]. These studies suggest the existence of a metastable subproteome that is inherently in danger of aggregation, and consequently raise the question of why some proteins are more at risk of aggregation than others. This question may be the key to determining how specific misfolding events in the cell evolve into a broad collapse of protein homeostasis [4].

Supersaturated proteins are driven towards aggregation

To understand why some proteins aggregate under specific stress conditions, while others remain soluble, we directed our attention towards proteins that appear to be less soluble than one would expect given their expression levels [40]; we refer to such proteins as being supersaturated [40]. The concept of supersaturation has a long history in the physical and biological sciences; it was for example used over 40 years ago to elucidate the interplay between kinetic and thermodynamic factors determining the aggregation of sickle hemoglobin [41,42], and more recently to characterize protein aggregate formation [23,43–45]. While supersaturation and solubility are thermodynamic concepts, they also have implications for the kinetics of aggregation; when the concentration progressively increases above the critical value, the driving force towards aggregation is likely to become stronger (Figure 1).

We have recently tested the consequences of the metastability of at least a part of the proteome against aggregation, and its implications for the collapse of protein homeostasis, by analyzing the supersaturation levels of thousands of proteins [40]. To obtain these results we estimated the cellular concentrations of proteins from transcriptomic and proteomic data, and the critical concentrations from the prediction of the aggregation propensities from the physicochemical properties of the corresponding amino acid sequences [40]. We found that a substantial fraction of the proteome is intrinsically supersaturated, and thus at risk of aggregation even in the absence of amino acid mutations or increased expression levels. We also found that a wide range of pathological consequences associated with neurodegenerative diseases can be rationalized to a substantial degree on the basis of the supersaturation levels of these metastable proteins [40]. The specific proteins that have been found to co-aggregate with Aβ plaques and tau tangles in Alzheimer's disease, with α-synuclein Lewy bodies in Parkinson's disease, and with artificial amyloid-forming β constructs, are all substantially supersaturated (Figure 2). In addition, we observed that a large majority of proteins which preferentially aggregate during aging in the nematode *Caenorhabditis elegans* are also highly supersaturated [40]. A recent proteomic study in yeast similarly found that arsenite stress results in the aggregation of high-concentration and poorly soluble proteins [46]. We thus propose that supersaturation is a major driving force of aggregation across the proteome, and is a central aspect of understanding the widespread cellular dysfunction evident in many conformational disorders.

Biochemical pathways affected in neurodegenerative diseases are enriched in supersaturated proteins

Neurodegenerative diseases are associated with dysfunction in one or more biochemical pathways [4,9,11,12,15]. In the case of Alzheimer's disease, according to the 'amyloid cascade hypothesis' [9], the aggregation of the Aβ peptide triggers a series of downstream pathological events (Figure 3), ranging from the formation of neurofibrillary tangles, to the disruption of lipid membranes and oxidative stress. The list of these secondary consequences is large because Alzheimer's disease is multifactorial both in terms
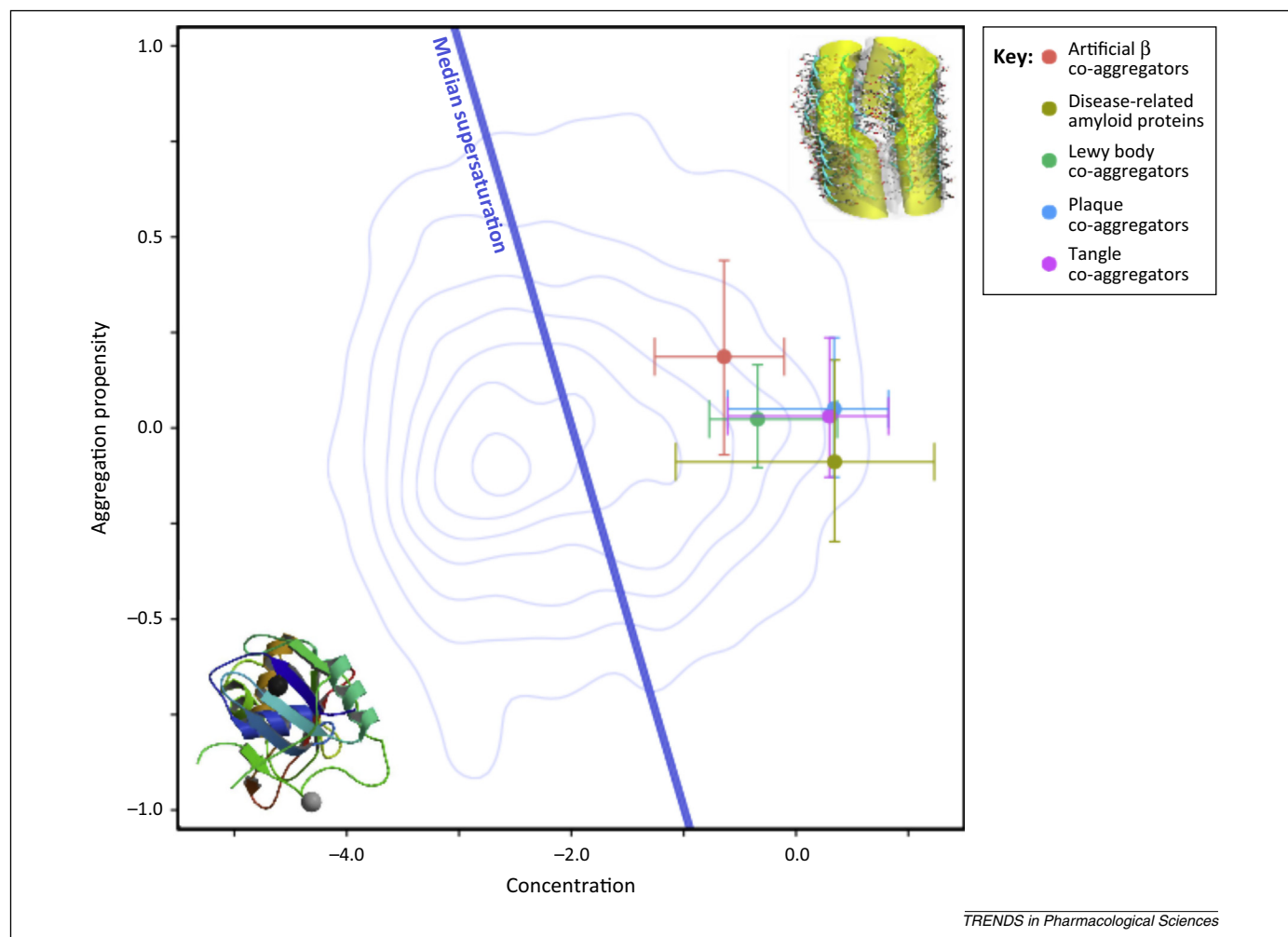
Figure 2. Protein supersaturation underlies widespread protein aggregation. The supersaturation scores for disease-related amyloid proteins and proteins that co-aggregate with several types of protein deposits (colored circles) are above the median supersaturation line (blue line), which divides proteins whose supersaturation is high relative to that of the proteome from those whose supersaturation is low [40]. Error bars represent the 25th and 75th percentiles of concentration and aggregation propensity. Details of the calculation of the supersaturation score and the list of supersaturated proteins have been reported previously [40].

of its genetic risk factors and its physiological effects in the cell [2,3,9]. This bewildering complexity may explain why so many distinct mechanisms have been proposed for disease pathology, including mitochondrial dysfunction, trafficking failure, loss of protein homeostasis, and inflammation [4,9,11,12,15].

Two complementary phenomena could explain this collapse of cellular function. The first is that specific disease-related aggregating peptides and proteins (e.g., Aβ and tau in Alzheimer's disease, α-synuclein in Parkinson's, and huntingtin in Huntington's disease) specifically disrupt numerous cellular processes. The second is that the aggregation of specific proteins saturates the capacity of the protein quality-control system, making it difficult for the cell to maintain the solubility of the proteome as a whole. Our observations regarding supersaturation raise the intriguing possibility that the amyloid cascade may originate at least to some extent from the intrinsic vulnerability to aggregation of a part of the proteome and their consequences on the quality-control machinery. Environmental stressors and accumulated damage may exacerbate these vulnerabilities. Recent investigations of the events that trigger aggregation in supersaturated protein solutions showed that sonication or exposure to trifluoroethanol

(TFE) or hexafluoroisopropanol (HFIP) are all able to perturb the metastable state and induce aggregation [47,48]. These *in vitro* studies suggest that in disease states specific perturbations of protein homeostasis may also potentiate broader disruptions in the maintenance of a fully functional proteome. Because mechanical or chemical stress may reduce *in vitro* the kinetic barrier to aggregation, so can age-related stress *in vivo*. Indeed, it was recently shown that, during aging, a specific subset of molecular chaperones able to prevent protein aggregation is expressed at lower levels [49].

Our investigations of the properties of the pathways populated by proteins predicted to be supersaturated support such an interpretation. We carried out an unbiased search of the hundreds of biochemical pathways assembled in the Kyoto Encyclopedia of Genes and Genomes (KEGG) for those that are enriched in the most supersaturated proteins. We found that the 'KEGG pathways' (i.e., as defined in KEGG) for Alzheimer's, Parkinson's, and Huntington's diseases are highly and specifically populated with supersaturated proteins (Figure 3) [40]. Because the proteins common to these pathways are particularly supersaturated, we referred to them as the core metastable subproteome [40]. We can also speculate that supersaturated
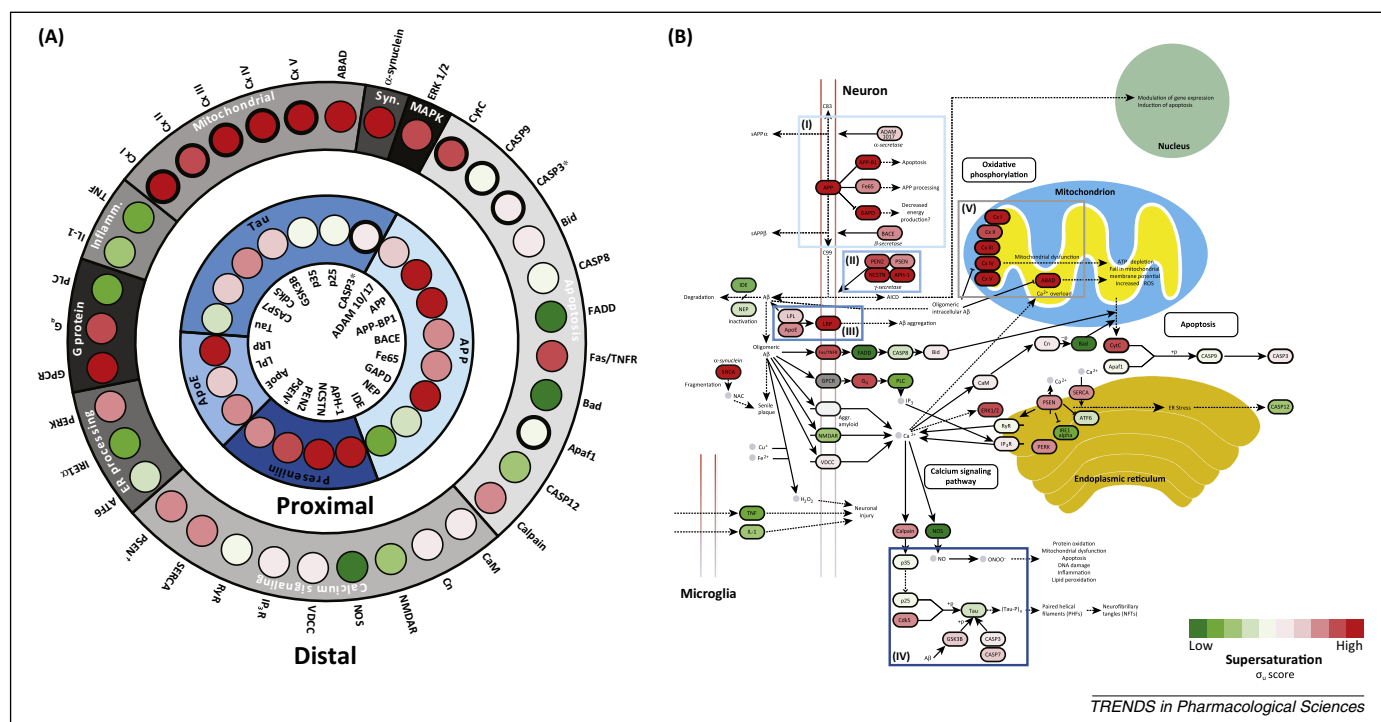
Figure 3. Supersaturated proteins in Alzheimer's disease. **(A)** Organization of the proteins involved in the primary (proximal) and secondary (distal) events in the amyloid cascade hypothesis [9]. According to this hypothesis the initial aggregation of Aβ triggers a series of proximal events (inner ring, blue scale), which is then followed by another series of distal events involving proteins in the same networks (outer ring, gray scale). Supersaturation scores are scaled from green (low scores) to red (high scores). **(B)** Supersaturated proteins (in red) in the KEGG 'Alzheimer's disease pathway'. Some of these pathways (blue boxes), such as the processing of APP (I), the presenilins (II), apolipoprotein E (III), and tau (IV), are known to be linked to genetic perturbations that drive the disease (inner ring in panel A). In addition to these factors, which are proximal to the primary cause of cellular toxicity, other major pathways, such as oxidative phosphorylation (V, gray box) and endoplasmic reticulum function, are distal to the causes. Supersaturated proteins populate both those processes that are tied to the primary aggregation events (I–IV) and those that are likely to be the result of them (V).

proteins cluster in given pathways because they function together, and hence their expression levels are correlated [50,51], because their expression is often controlled by the same transcription factors [52]. While these findings by no means reduce the importance of the toxic events associated with the interactions of specific aggregated species with cellular components, they also suggest that fundamental physicochemical principles contribute strongly to the widespread aggregation and cellular dysfunction that follows the onset of neurodegenerative diseases [40].

The presence of supersaturated proteins in the cell may follow from the requirement for its viability to carry out efficiently specific functions. Protein complexes offer intriguing examples that illustrate this possibility. Many of the pathways that we found to be supersaturated involve large protein complexes, such as the ribosome and components of the electron transport chain. It has been found that the constituent proteins in complexes possess surfaces that tend to be aggregation-prone, a feature necessary for complex assembly [53]. In addition, high concentrations may also increase the probability of assembly. These same properties, which aid in the functional assembly of complexes, could predispose component proteins to aberrant aggregation if their stoichiometries and assembly processes are disrupted, as has been observed for components of the ribosome [33].

Maintaining the homeostasis of the metastable subproteome

The metastability of a substantial part of the proteome with respect to aggregation suggests that diagnostic and therapeutic approaches aimed at limiting this phenomenon could

look beyond individual disease-related proteins. Such an additional perspective is timely given that efforts to target the aggregation of individual proteins have proven less fruitful than anticipated [54]. While one interpretation of these disappointments is to question the amyloid hypothesis itself it has also been pointed out that many of the trials of aggregation-reduction therapies had substantial limitations because of the lack of understanding of the key mechanisms involved in aggregation and of the difference between attempting to reduce pre-existing aggregate levels and preventing aggregation in the first place [55]. Timing is essential because without an effective molecular marker for early diagnoses of sporadic forms of neurodegenerative disorders such as Alzheimer's and Parkinson's diseases, treatments attempted so far may have been initiated too late in the disease progression.

It is therefore of great importance to understand the mechanisms that help to maintain the metastable subproteome in healthy cells and organisms [4]. Although altered transcriptional levels, inherited polymorphisms, and environmental disturbances may push proteins towards supersaturation, the protein homeostasis machinery can still be capable of restoring the balance (Figure 4). For example, it has been proposed that the molecular chaperone Hsp90 can facilitate evolution, permitting a broader search of amino acid sequence space by reducing the cost of destabilizing mutations that might otherwise excessively increase protein supersaturation levels [56]. Indeed, numerous studies have demonstrated that molecular chaperones can suppress pathogenic protein aggregation [57–59], reducing the effective supersaturation level of
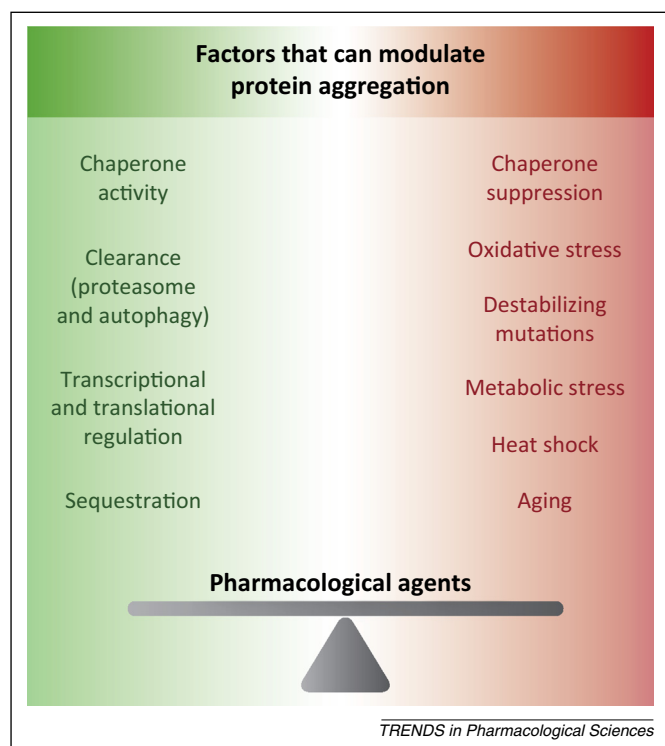
Figure 4. List of representative factors that can modulate protein aggregation. Because the concentrations of proteins in the cellular environment should be maintained below critical levels, a wide range of quality-control mechanisms is in place for this purpose (green side). A variety of events and processes, however, could shift the balance towards more aggregation-prone conditions (red side). A general goal of pharmacological interventions against neurodegenerative diseases should therefore be a reduction of one of the driving forces for protein aggregation by suppressing protein supersaturation.

proteins below that predicted from their intrinsic physico-chemical properties. For example, it was recently shown that Hsp90 helps to regulate protein homeostasis in a cell non-autonomous fashion, revealing another means by which molecular chaperones can act at an organismal level to suppress physicochemical instabilities [60].

Concluding remarks
The presence of proteins near or above their solubility limits is inherently dangerous for living systems because the uncontrolled formation of aggregates can give rise to a variety of pathological events. Such events may then be aggravated by the co-regulation of aggregation-prone proteins, which tend to be clustered in specific biochemical pathways. As we discuss in this article, there have been recent advances in our understanding of the nature and properties of the conformational species populated during the aggregation process as well as of the roles in this context of molecular chaperones and the protein expression and degradation pathways. We believe that the study of protein supersaturation as a major driving force of aggregation will help to bring together these advances and clarify how the inability to maintain proteins in their functional soluble states can give rise to the multifactorial pathology of neurodegenerative conditions. As the failure to control protein solubility is likely to be a major contributor to these complex diseases, chemical interventions that suppress supersaturation levels – by reducing the inherent propensity of proteins to aggregate or enhancing protein

quality control mechanisms – could help not only to treat neurodegenerative diseases, but also to prevent them.

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