ATP Impedes the Inhibitory Effect of Hsp90 on Aβ40 Fibrillation

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https://doi.org/10.1016/j.jmb.2020.11.016
Edited by J. Buchner

Abstract

Heat shock protein 90 (Hsp90) is a molecular chaperone that assists protein folding in an Adenosine triphosphate (ATP)-dependent way. Hsp90 has been reported to interact with Alzheimer’s disease associated amyloid-β (Aβ) peptides and to suppress toxic oligomer- and fibril formation. However, the mechanism remains largely unclear. Here we use a combination of atomic force microscopy (AFM) imaging, circular dichroism (CD) spectroscopy and biochemical analysis to quantify this interaction and put forward a microscopic picture including rate constants for the different transitions towards fibrillation. We show that Hsp90 binds to Aβ40 monomers weakly but inhibits Aβ40 from growing into fibrils at substoichiometric concentrations. ATP impedes this interaction, presumably by modulating Hsp90’s conformational dynamics and reducing its hydrophobic surface. Altogether, these results might indicate alternative ways to prevent Aβ40 fibrillation by manipulating chaperones that are already abundant in the brain.

Introduction

Heat shock protein 90 (Hsp90) is a ubiquitously expressed, evolutionarily conserved, and highly dynamic molecular chaperone, which mainly consists of three structural domains: an N-terminal ATP-binding domain, a middle domain for client protein binding, and a C-terminal dimerization domain. Hsp90, including yeast Hsp90 (Hsp82) used in this study (Table S1), usually locate intracellularly, but can also be secreted into extracellular space. It participates in a variety of cellular processes including cell survival, hormone signaling, cell cycle control and response to cellular (heat) stress, as well as in assisting folding, maturation and degradation of more than 200 ‘client proteins’ in eukaryotes. These functions of Hsp90 are achieved in concert with different co-chaperones and adaptor proteins and often with the help of ATP.

Amyloid-β (Aβ) peptide fibrillation and accumulation are usually triggered by a conformational transition from random coil to β-sheet secondary structures and progresses via the classical lag-, elongation-, and plateau-phases, in which hydrophobic interactions are involved. These processes usually take place extracellularly and play central roles in the progression of Alzheimer’s disease according to the amyloid cascade hypothesis. However, Aβ can be
produced intracellularly or taken up from extracellular space to the cytoplasm through receptor binding and subsequent internalization and accumulates intracellularly including in mitochondria. Intracellular Aβ accumulation influences a variety of physiological activities like autophagy, degradation and apoptosis, indicative of the crucial role of intracellular Aβ in Alzheimer’s disease. Recent evidence suggests that lipid raft and lipid membranes play crucial roles in Alzheimer’s disease by promoting the production and oligomer formation of Aβ peptides, while Aβ oligomers can bind to lipid membranes and induce the aberrant clustering of lipid raft and membranes. As the disease progresses, intracellular Aβ oligomers may interact with lipid membranes, induce neuronal dysfunction, or pass into the extracellular space as a source of fibril deposits. Changes in the raft-lipid composition or membranes of the cells can induce the release of heat shock proteins, like Hsp90, from cytoplasm to modulate intercellular signalling. In vivo studies indicate that intracellular chaperones can play a role in modulating intracellular Aβ metabolism and toxicity. Thus interactions between Hsp90 and Aβ can possibly take place both extracellularly and intracellularly, while Aβ aggregation mainly occur extracellularly. The in vivo interaction between Hsp90 and Aβ and the physiological relevance of this interaction remain to be explored. Molecular chaperones such as Hsp90 are in the first line of the cellular defense system against protein aggregation. A growing body of evidence indicates that Hsp90 inhibits amyloid protein aggregation, cellular toxicity, or clearance of Alzheimer’s Aβ, but the molecular mechanism of Hsp90 modulating Aβ remains unknown. For instance, does Hsp90 interfere with Aβ fibrillation in an ATP-dependent and/or specific way? How do different Hsp90 conformations influence Aβ fibrillation? In which phase does Hsp90 interfere with Aβ fibrillation?

To answer these questions, we investigated how Aβ40 fibrillation is affected by dimeric wild type Hsp90 (WT), Hsp90 tetramer, and the ATPase defective mutant E33A also lacking the charged linker region between the N-terminal and middle domains. We assumed that each one has a different dynamics in equilibrium, therefore exposing varied time-dependent hydrophobic surfaces as possible client binding sites. The fibrillation of Aβ was observed with atomic force microscopy (AFM) imaging under various environmental conditions, by Thioflavin T (ThT) fluorescence, circular dichroism (CD) spectroscopy and SDS-PAGE. AFM imaging has already revealed a variety of structural information about Aβ40 aggregation and its interaction with small molecules. Furthermore, AFM imaging was also previously used to support that the chaperones Hsp60, GroEL, and HspB1 inhibit Aβ40 aggregation. However, to the best of our knowledge neither the role of Hsp90 on the Aβ40 aggregation, nor the effect of ATP on this system have been studied by AFM experiments yet. In addition, our specific modulation of Hsp90 allows us to put forward a mechanism for the inhibition of fibril growth. We observed that all three Hsp90 forms inhibit Aβ40 fibrillation to different degrees and this effect of Hsp90 can be impeded by the addition of ATP, which can induce a change in the conformation dynamics and hydrophobicity of Hsp90. We therefore suggest that Hsp90 inhibits Aβ40 fibrillation through the modulation of conformational dynamics and hydrophobic surfaces. Our results provide a new perspective for the mechanism of inhibition of amyloid fibrillation by Hsp90 and other chaperones.

Results

Hsp90 inhibits Aβ40 fibrillation

We used AFM in air to investigate the morphology changes of the Aβ40 peptides in the absence or presence of Hsp90 dimers (wild type), tetramers, and an ATPase-deficient E33A mutant. Figure 1 shows the AFM images recorded after an incubation of 10 μM Aβ40 alone or with 0.5 μM Hsp90 variants at 37 °C for 24 h. The Aβ40 sample alone forms fibrils in an unbranched, twisted helical morphology while the Aβ40 samples in the presence of three Hsp90 forms display other distinct morphologies. In the presence of Hsp90 proteins, the Aβ40 peptides aggregated into irregular small amorphous aggregates. Likely, the larger Aβ40 aggregates observed in the presence of the Hsp90 tetramer may result from the co-aggregation with the Aβ40 peptides and the aggregation-prone tetramer. This result indicates that Hsp90 proteins suppress the formation of Aβ40 fibrils, but to different degrees depending on their forms, WT induced the formation of smaller amorphous aggregates compared with tetramer and E33A, suggesting that WT is probably the most efficient one to inhibit the Aβ40 fibrillation.

Hsp90 inhibits Aβ40 peptide secondary structure transitions during fibrillation

To investigate the influence of Hsp90 proteins on Aβ peptide secondary structure, we carried out CD spectroscopy measurements. CD spectra were recorded over time to quantify the secondary structure transition of the Aβ40 peptides with or without the different Hsp90 forms. The aggregation of 10 μM Aβ40 in the presence or absence of 0.04 μM Hsp90 was monitored in the far-UV region from 190 to 260 nm after 0, 0.5, 1, 1.5, 2, 3, 4, 5, 6, 7, 8, and 22 h incubation at 37°C. Figure 1 and Figure S1 illustrate that the CD spectrum of Aβ40 at time zero is characterized by a typical random coil conformation, with a characteristic minimum at ~198 nm. As the incubation time increases, the random coil conformation of Aβ40 converts gradually into the
typical β-sheet structure showing the characteristic curve with a minimum at ~220 nm and a maximum at ~195 nm via an isodichroic point at ~210 nm, similar to the result in our previous study. However, in the presence of Hsp90 proteins, no signal corresponding to a β-sheet secondary structure conformation is observed and the signal of the initial Aβ40 random coil secondary structure conformation decreases step by step as the incubation carries on and finally disappears. The latter might, to a large extent, be caused by some large aggregates formed by Hsp90 and Aβ40. Three Hsp90 forms at a low concentration of 0.04 μM are similarly efficient in inhibiting the secondary structure transition of the Aβ40 peptides.

Based on our AFM and CD spectroscopy results, we suggest that Hsp90 structurally modulates the transition pathway of Aβ40 aggregation and morphologically impedes the formation of Aβ40 fibrils.

**Hsp90 impedes the secondary pathways of Aβ40 fibrillation**

By using a ThT kinetics assay, we investigated how Aβ40 amyloid fibrillation kinetics is modulated by Hsp90 proteins. ThT is a commonly used fluorescence dye to monitor the formation of amyloid fibrils, as its fluorescence intensity sharply increases when bound to amyloid fibrils. Figure 3 and Figure S2(A) show the results of the ThT kinetic fluorescence assays. In non-agitating condition, all Hsp90 proteins inhibit Aβ40 fibrillation in a concentration-dependent manner, with WT being the most efficient, probably because it is more dynamic than the other forms. The general aggregation course of amyloid protein aggregation is shown in Figure 3(A). Calculated from sigmoidal curve fitting, the phenomenological parameters tlag and t1/2 of the fibrillation of 10 μM Aβ40 alone were estimated to tlag = 8.6 ± 1.56 h and t1/2 = 10.8 ± 0.95 h and Hsp90 significantly prolongs the tlag and t1/2 of the fibrillation, as the concentration of Hsp90 increases (Figure 3(B) and (C)).

To get further insight into the microscopic mechanisms of Aβ40 fibrillation in the presence of Hsp90, global fit analysis of the kinetic data was performed with an integrated rate law by using the AmyloFit online software server. It has been reported that amyloid proteins usually aggregate through either primary or secondary dominated pathways and Aβ40 undergoes fibrillation mainly via secondary nucleation processes. Therefore, we selected the secondary nucleation dominated model and first fitted the ThT data of Aβ40 alone, obtaining a set of parameters including the primary nucleation rate constant (kn) = 0.00174 in concentration nc+1 time−1 (nc is the reaction order of primary nucleation that simply interpretes...
Figure 3. Aβ40 aggregation kinetics. (A) General aggregation course of amyloid protein fibrillation. Typically, this process goes through the lag-, elongation-, and plateau- phases, in which primary nucleation (rate constant, $k_n$), secondary nucleation (rate constant, $k_2$), and/or elongation (rate constant, $k_+\$) processes are involved. (B) and (C) The $t_{lag}$ and $t_{1/2}$ of the fibrillation of 10 μM Aβ40 in the absence or presence of different Hsp90 forms (WT, tetramer, and E33A) at concentrations of 0.02, 0.04, 0.08, and 0.1 μM, were derived from sigmoidal fitting of ThT data of each repeat. Error bars represent standard deviation of at least three replicates (D) Secondary processes of Aβ40 fibrillation are influenced by Hsp90. Aggregation kinetics of 10 μM Aβ40 in the absence or presence of different Hsp90 forms were monitored by ThT fluorescence over time (the raw data can be found in Figure S2(A)) and then globally fitted by using the AmyloFit online software server.47 For the fitting procedure, the data of Aβ40 alone were first fitted (the result is shown in Figure S3) with a secondary nucleation dominated model, from which a set of parameters including $k_n = 0.00174$ in concentration $C_0^{-1}$ time $C_0^{-1}$, $k_2 = 7.11e+7$ in concentration $C_0^{-1}$ time $C_0^{-1}$, and $k_+ = 9.22e+6$ in concentration $C_0^{-1}$ time $C_0^{-1}$ of Aβ40 fibrillation were obtained and used as the initial guess values for the following global fit. Each one of the rate constants $k_n$, $k_2$, or $k_+$ was fitted freely, while the other two were set as initial guess values, by choosing the secondary nucleation dominated model. When $k_2$ and $k_+$, but not $k_n$, were freely fitted then the data was well described (see main text for details). The mean square error (MSE) values for each set of Aβ40/Hsp90 samples were normalized against the one with the best fit (lowest MSE value). (E) Relative rate constants (relative to the rate constants of Aβ40 alone) derived from global fitting for different concentrations of Hsp90.
a nucleus size), the secondary nucleation rate constant \(k_2 = 7.11 \times 10^{-17}\) in concentration \(^{-1}\) time \(^{-1}\) (\(n_2\) is the reaction order of secondary nucleation that simply interprets a nucleus size), and the elongation rate constant \(k_\epsilon = 9.22 \times 10^3\) in concentration \(^{-1}\) time \(^{-1}\) of \(\alpha\beta_{40}\) fibrillation process, which were used as the initial guess values for the following fit. Each one of the three rate constants \((k_m, k_2, k_\epsilon)\) was fitted freely, while the other two were kept as initial guess values. The result of the global fit analysis is shown in Figure 3(D) and the relative rate constants derived from the global fit are presented in Figure 3(E). The global fit analysis depicts that if the rate constants \(k_2\) and \(k_\epsilon\), rather than the \(k_m\), were freely fitted, the results can describe the Hsp90-dependent aggregation data, suggesting that the secondary pathways (the secondary nucleation and/or elongation processes) of \(\alpha\beta_{40}\) aggregation are the ones mostly affected by Hsp90 proteins.

**Hsp90 modulates the hydrophobic surface of \(\alpha\beta_{40}\) peptides**

To determine which microscopic rate constant, \(k_2\) or \(k_\epsilon\), of \(\alpha\beta_{40}\) is most influenced by Hsp90, we performed seeding experiments of \(\alpha\beta_{40}\) peptide fibrillation kinetics in the presence and absence of Hsp90 proteins. Pre-formed \(\alpha\beta_{40}\) seeds were added at time zero to the samples with \(\alpha\beta_{40}\) monomers and Hsp90 proteins. In the presence of seeds, the primary nucleation processes are nearly negligible compared to the secondary processes. At a high seed concentration, with a concave ThT aggregation kinetic curve, the growth of fibrillar aggregates mainly originates from elongation processes. The results of the seeding assays in Figure 4(A) and Figure S2(B) show the absolute and normalized signal corresponding to the aggregation concentration, respectively. It illustrates that the addition of \(\alpha\beta_{40}\) seeds to \(\alpha\beta_{40}\) monomers (the \(\alpha\beta_{40}\) + seeds curve) significantly speeds up the \(\alpha\beta_{40}\) fibrillation, reaching the plateau phase within the time the unseeded \(\alpha\beta_{40}\) sample remains in the lag phase. Notably, the seeded kinetic curve shows a concave shape in opposite to the sigmoidal curve for unseeded \(\alpha\beta_{40}\). The unseeded samples with \(\alpha\beta_{40}\) supplemented with Hsp90 proteins dramatically slow down the process with slower aggregation kinetics with sigmoidal curves. This is consistent with the results of ThT assay in Figure 3 that all variants inhibit \(\alpha\beta_{40}\) fibrillation, with WT being the most efficiently. In both Figures 3(D) and 4(A), the mutant E33A without ATPase activity inhibits \(\alpha\beta_{40}\) fibrillation, suggesting that \(\alpha\beta_{40}\) may not only bind to one specific site on Hsp90, and that the ATPase activity is also not the only determinant in the effect of Hsp90 on \(\alpha\beta_{40}\) fibrillation. In the presence of both \(\alpha\beta_{40}\) seeds and Hsp90, the fibrillation process of \(\alpha\beta_{40}\) is prolonged as compared to \(\alpha\beta_{40}\) alone without seeds. This indicates that the elongation process of \(\alpha\beta_{40}\) fibrillation with seeds is significantly inhibited by Hsp90.

As both hydrophobic and electrostatic interactions play an important role in the aggregation process of amyloid proteins, we performed ANS (8-anilino-1-naphthalenesulfonic acid) fluorescence studies (see methods) to understand the effect of Hsp90 protein on the surface hydrophobic reorganization of \(\alpha\beta_{40}\) peptides. The ANS assay was conducted for 10 \(\mu\)M \(\alpha\beta_{40}\) in the presence or absence of 0.1 \(\mu\)M Hsp90 protein forms, to check how Hsp90 influence the hydrophobic surface and the fibrillation behavior of \(\alpha\beta_{40}\) (Figure 4(B)). The decrease of the fluorescence signal after the addition of Hsp90 WT, tetramer or mutant (E33A) compared to that of \(\alpha\beta_{40}\) alone, suggests that the hydrophobic surface of \(\alpha\beta_{40}\) to interact with ANS is decreased. Among these Hsp90 proteins, Hsp90 WT is the most effective one to reduce the hydrophobic surface of \(\alpha\beta_{40}\), which is in line with our ThT data, with Hsp90 WT as the most effective inhibitor against the fibrillation. This suggests that the accessible hydrophobic surfaces of \(\alpha\beta\) have a crucial role in \(\alpha\beta\) fibrillation. But if this was the only effect, a red-shift of the emission peak would have been expected. Therefore, some electrostatic interaction will also be involved.

To further investigate the aggregation behavior, a photo-induced crosslinking experiments was carried out to stabilize 90 \(\mu\)M \(\alpha\beta_{40}\), in the absence or presence of 2 \(\mu\)M Hsp90. The data in Figure 4(C) and (D) suggest that \(\alpha\beta_{40}\) alone aggregates into a series of different oligomer sizes, but that Hsp90 significantly retains \(\alpha\beta_{40}\) as monomers on the SDS-PAGE gel, with the wild type Hsp90 being the most efficient.

Therefore, we can propose that the Hsp90 slows down the elongation process of \(\alpha\beta_{40}\) fibrillation presumably by decreasing the accessible hydrophobic surfaces of \(\alpha\beta_{40}\) and thus keeping the peptides as monomers or small oligomers.

To further confirm this observation, we continued with a photo-induced cross-linking assay to stabilize \(\alpha\beta_{40}\) samples but this time at the end point of the ThT assay (Figure 4(E)). Results of reference experiments conducted with samples at 0 h are shown in Figure S4(B), indicating that Hsp99s almost show no effect on \(\alpha\beta_{40}\) fibrillation at time zero of ThT experiment). In the presence of Hsp90, \(\alpha\beta_{40}\) monomers were observed, while almost no \(\alpha\beta_{40}\) monomers were found in the absence of Hsp90 on the SDS-PAGE gel after the cross-linking assay, which might be caused by the formation of the fibrils that are too large to go through the SDS-PAGE gel.

**Hsp90 modulates the hydrophobic surface of \(\alpha\beta_{40}\) peptides**

Figure 4(C) also shows some higher-molecular-weight proteins, which probably are Hsp90 aggregates after the cross-linking at a high concentration (2 \(\mu\)M), which is less present at a low concentration (0.5 \(\mu\)M) (Figure 4(E)). In Figure 4(E), the bands above 170 kDa can be
SDS-resistant wild-type or E33A Hsp90 tetramers and Aβ40 fibrils do not run into the page because of the insolubility. 10 μM Aβ40 peptides in the presence of 0.1 μM Hsp90 protein WT (blue), tetramer (cyan) or mutant E33A (light green), monitored by ThT fluorescence at 37 °C without agitation. As controls, 10 μM Aβ40 fibrillation kinetic assays were conducted without the seeds in the absence (purple) or presence of 0.1 μM Hsp90 protein WT (green), tetramer (yellow) or mutant E33A (orange). (B) ANS fluorescence assay performed with 10 μM Aβ40 in the presence or absence of 0.1 μM Hsp90 protein variants at 37 °C. (C) SDS-PAGE of the photo-induced cross-linking samples of 90 μM Aβ40 in the presence or absence of 2 μM Hsp90 after 15 min incubation at room temperature. (D) Quantitative comparison of oligomers from the cross-linking experiment. (E) SDS-PAGE of the photo-induced cross-linking samples of 10 μM Aβ40 with or without 0.5 μM Hsp90 after the ThT assay shown in Figure S4(A).

Figure 4. Hsp90 inhibits the elongation process of Aβ40 fibrillation by attenuating hydrophobic interactions among the Aβ40 peptides. (A) The seeding experiments of 10 μM Aβ40 in the presence of 1 μM Aβ40 seeds without (gray) or with 0.1 μM Hsp90 protein WT (blue), tetramer (cyan) or mutant E33A (light green), monitored by ThT fluorescence at 37 °C without agitation. As controls, 10 μM Aβ40 fibrillation kinetic assays were conducted without the seeds in the absence (gray) or presence of 0.1 μM Hsp90 protein WT (green), tetramer (yellow) or mutant E33A (orange). (B) ANS fluorescence assay performed with 10 μM Aβ40 in the presence or absence of 0.1 μM Hsp90 protein variants at 37 °C. (C) SDS-PAGE of the photo-induced cross-linking samples of 90 μM Aβ40 in the presence or absence of 2 μM Hsp90 after 15 min incubation at room temperature. (D) Quantitative comparison of oligomers from the cross-linking experiment. (E) SDS-PAGE of the photo-induced cross-linking samples of 10 μM Aβ40 with or without 0.5 μM Hsp90 after the ThT assay shown in Figure S4(A).

SDS-resistant wild-type or E33A Hsp90 tetramers and Aβ40 fibrils do not run into the page because of the insolubility. 10 μM Aβ40 peptides in the presence of 0.5 μM Hsp90 likely remain as monomers before (Figure S4(B)) or after (Figure 4(E)) the ThT assay, supporting that 0.5 μM Hsp90 completely suppresses Aβ40 fibrillation in Figure S4(A). These results also show that Hsp90 retains Aβ40 as mainly monomeric species and slows down the fibril formation in vitro.

ATP modulates the hydrophobic surface of Hsp90 and thereby Aβ40 fibrillation

To investigate the potential mechanism by which ATP affects the protective activity of Hsp90 protein against Aβ40 fibrillation, we conducted kinetic aggregation studies with 10 μM Aβ40 and 0.1 μM Hsp90 (WT) in the absence or presence of 2 mM ATP or AMP-PNP. It is well known that ATP slightly shifts Hsp90 towards a closed conformation and AMP-PNP mainly locks Hsp90 in the closed conformation.143 The aggregation kinetics observed in Figure 5(A) and Figure S2(C) indicate that ATP or AMP-PNP on its own (i.e. in the absence of Hsp90) does not significantly influence Aβ40 fibrillation, but that both negatively regulate the effect of Hsp90 on Aβ40 fibrillation.

Again, we used the ANS fluorescence assay to test for hydrophobic surfaces, this time of 6 μM Hsp90 (WT) on its own, in the absence or presence of 2 mM ATP or AMP-PNP. Figure 5(B) shows the reduction of the hydrophobic surface of...
Hsp90 upon the addition of the nucleotides, which likely has the negative regulatory inhibition efficiency of Hsp90 against Aβ40 fibrillation. Our hydrophobicity assay agrees with the observed fibrillation kinetics: the accessible hydrophobic surface decreases from apo Hsp90 to ATP/Hsp90.

Figure 5. (A and B) ATP negatively regulates the inhibitory efficiency of Hsp90 against Aβ40 fibrillation by modulating the conformation dynamics and reducing hydrophobic surfaces of Hsp90. (A) Aggregation kinetics of Aβ40 fibrillation monitored by ThT fluorescence. The experiment was conducted with 10 μM Aβ40 and 0.1 μM Hsp90, in the presence or absence of 2 mM ATP or AMP-PNP at 37 °C without agitation, and the averaged data were normalized with AmyloFit. The normalized data of individual curves were shown in Figure S5. (B) ANS fluorescence experiment performed with 6 μM WT Hsp90 in the presence or absence of 2 mM ATP or AMP-PNP at 37 °C. (C–H) Results of AFM imaging in liquid. (C) Aβ40 peptides only. (D) Aβ40 peptides with Hsp90 (10:1). (E) Aβ40 peptides with Hsp90 (10:1) and ATP (5.0 mM). All samples (Aβ40 concentration: 75 μM) were incubated for 92 h at 300 rpm at 30 °C. The respective sample was deposited on a flat mica surface and measured in HEPES pH 7.0 with 10 mM MgCl2 with a scan size of 3 μm × 3 μm and a scan rate of 2.44 Hz. In total, about 5 images of each sample were taken and the experiments were performed twice. (F) Height histograms of Aβ40 structures, showing height values of 5 (±1) nm in all cases. (G) Contour length histogram (bin width 28 nm) of the Aβ40 structures, showing values of (546 ± 464) nm (Aβ40 incubation only), (37 ± 23) nm (Aβ40 peptides incubated with Hsp90), (72 ± 106) nm (Aβ40 peptides incubated with Hsp90 and ATP). The large error for the latter is due to the bimodal distribution (monomers and oligomers). (H) Zoom into the first part of (G) with a bin width of 10 nm. Please note that longer structures (>100 nm) are only visible in the absence of Hsp90 (red) or if Hsp90 + ATP are present (blue).
to AMP-PNP/Hsp90, similar to the inhibitory effects of Hsp90 on Aβ40 fibrillation in Figure 5(A). The decrease of Hsp90 inhibition by AMP-PNP is not as strong as for ATP, indicating that the hydrophobicity is not the only determinant, but that conformational dynamics likely also plays a significant role.

We then further confirm the inhibitory effect of Hsp90 on Aβ40 fibrillation and the influence of ATP on this effect by using AFM imaging in aqueous environment under various conditions. First Aβ40 was incubated for 92 h at 300 rpm and 30 °C at a concentration of 75 μM to form mature fibrils (Figure 5(C)). The same experiment was repeated in the presence of Hsp90 (Aβ40: Hsp90 ratio of 10:1). Figure 5(D) shows that no fibrils were formed, i.e. that Hsp90 efficiently inhibited Aβ40 fibrillation at substoichiometric concentrations, consistent with previously reported experiments.28 Finally, the same experiment was repeated with Hsp90 in the presence of 5 mM ATP. In this case, some fibrils could be observed, but to a much lower extent as with Aβ40 alone (Figure 5(E)). Figure 5(F)–(H) show the heights and contour lengths of Aβ40 aggregates under the various conditions. The AFM images show straight and spiral fibrils, with contour lengths around 500 nm, which were formed in the absence of Hsp90 and ATP. The height of the fibrils is around 5 nm in agreement with previous reports.32,34 In the presence of Hsp90 and absence of ATP, mainly monomers and oligomers with contour lengths below 50 nm were observed representing most likely monomers or small co-aggregates of Aβ40 and Hsp90. In the presence of Hsp90 and ATP, monomers, oligomers as well as fibrils were observed, indicating a suppressing effect of ATP on the capability of Hsp90 to inhibit the fibrillation process.

**Binding mode between Hsp90 and the Aβ40 peptides**

To investigate the binding affinity between Hsp90 and Aβ peptides, fluorescence polarization (FP) experiment was carried out. The result shown in Figure 6(A) indicates that Hsp90 does not display any strong affinity (Kd is estimated to be lower than 100 μM) for the Aβ40 peptides (monomers) in the absence or presence of AMP-PNP. Both closed and open Hsp90 proteins presumably protect the Aβ40 peptides from the fibrillation via surface hydrophobic solubilization rather than a specific interaction, in agreement with our ANS assays where Hsp90 stabilizes Aβ with changed hydrophobic surface. As shown in Figure S6, Hsp90 with open conformation offers more hydrophobic surfaces than that in closed state, supporting Figure 5(A) and (B) where Hsp90 without AMP-PNP has more hydrophobic surfaces and better inhibition efficiency than the one with AMP-PNP.

![Figure 6](image-url)
AMP-PNP (closed state). The weak/unspecific interaction between Hsp90 and Aβ40 can be converted to covalent connection through PICUP. To further investigate if Hsp90 offers the surfaces for Aβ solubilization, the PICUP experiments were conducted (Figure 6(B), followed by the LC/MS analysis in Figure S7(A) and (B)). Hsp90 forms more higher-molecular-weight bands in the presence of Aβ40 on the SDS-page gel than these without Aβ40 in Figure 6(B), suggesting that Hsp90 forms several complexes with different numbers of Aβ40 monomers. Followed by liquid chromatography, ESI–time-of-flight (TOF) mass spectrometry enables to determine the spectrum m/z of the Hsp90 complexes from the PICUP assay. As shown in Figure S7(A), PICUP products eluted from the column with different elution times indicate the formation of Hsp90 complexes with different polarities. Hsp90 without PICUP gives a single peak in the m/z spectra in Figure S7(B). After PICUP, Hsp90 with the Aβ40 peptides (in green and red curve, Figure S7(B)) seems to form more complexes in comparison to the one without the peptides (in purple curve, Figure S7(B)). Altogether this data indicates that Hsp90 solubilizes Aβ peptides to large degree through hydrophobic surfaces as suggested by the ANS assay, although the binding to monomers is weak, which we conclude from our fluorescence polarization assay. This is consistent with the interaction of Hsp90 with several disordered proteins like tau via a transient and weak binding on the extended substrate binding surfaces that crosses the domain boundaries.

**Discussion**

Here we report how wild type Hsp90 and Hsp90 variants slow down Aβ40 peptide fibril formation at substoichiometric ratios in vitro. Our AFM and CD experiments further show that Hsp90 proteins alter the conversion of secondary structure conformations of Aβ40 during fibrillation and induce formation of amorphous Aβ40 aggregates. Our global fit analysis of the kinetic data suggests that Hsp90 proteins influence both the secondary nucleation and elongation processes. The seeding assay confirms the finding that the elongation process of Aβ40 is significantly modulated by Hsp90. The cross-linking assay further shows that, in the presence of Hsp90, Aβ40 even remains predominantly in its monomeric state compared to in the absence of Hsp90 proteins. In order to elucidate the molecular mechanisms behind the interaction between Hsp90 and Aβ40, an ANS fluorescence assay was conducted, from which we conclude that Hsp90 decreases the accessible hydrophobic surfaces of the Aβ40 peptides. The Hsp90 protein is intrinsically flexible with a number of accessible hydrophobic surfaces and coexists in various conformations. Furthermore, the conformational transition of Hsp90 can be modulated upon the binding of diverse substrates, chaperones, adaptor proteins, or nucleotides. Here we investigated the effect of nucleotides by repeating the experiments in the presence of ATP or the non-hydrolysable AMP-PNP. In particular, our ThT kinetics experiments show that ATP alone hardly inhibits the aggregation of Aβ40, which is consistent with a previous study. On the contrary, the inhibitory effect of Hsp90 on Aβ40 fibrillation is significantly attenuated by the addition of ATP, while AMP-PNP reduces this effect of Hsp90 to a lower extent, confirming that our observations are related to the conformational dynamics of Hsp90 proteins. To study the influence of ATP on the hydrophobicity and electrostatic interactions of Hsp90, an ANS fluorescence assay was conducted, which shows that ATP or AMP-PNP decreases the total hydrophobic surface of Hsp90. Thus, ATP diminishes the inhibitory effect of Hsp90 on Aβ40 fibrillation also by decreasing the hydrophobic surface of Hsp90. Nevertheless, this is likely not the only effect, as ATP reduces the inhibitory effect of Hsp90 more than AMP-PNP; despite AMP-PNP having a larger effect on the hydrophobic surface (Figure 5(A) and (B)). Therefore, we speculate that also the large conformational dynamics of Hsp90s plays a crucial role. In addition, ATP hydrolysis might displace Aβ40 monomers from Hsp90, further reducing the inhibitory potency of Hsp90.

We briefly summarize in a schematic model in Figure 7 how Aβ40 fibrillation can be influenced by Hsp90 as well as ATP at the microscopic and molecular levels: (1) Hsp90 inhibits the fibrillation (mostly the elongation process) of Aβ40 monomers by interfering with the hydrophobic interactions between Aβ40 monomers and/or oligomers; (2) ATP suppresses the inhibitory effect of Hsp90 on Aβ40 fibrillation. Conceivably, ATP triggers a conformational conversion of Hsp90’s quaternary structure even in the presence of Aβ40 and thus reduces the global hydrophobic surfaces of Hsp90, leading to the release of the Hsp90-bound Aβ40 peptides and/or less binding of free Aβ40. In other words, ATP hydrolysis would lead to something considered as a ’clean cycle’ to leave the relatively bare Hsp90 and more unbound Aβ40 available for fibrillation. AMP-PNP on the other hand is known to close the Hsp90 dimer and therefore stably reduce the accessible hydrophobic surface of Hsp90. This is consistent with the concept that Hsp90 usually interacts with its clients via a large number of low energy contacts in a dynamic and transient way. Similar to the hydrophobic surfaces of Hsp90 for Aβ40, the binding site of Tau on the Hsp90 mainly consists of hydrophobic residues. The binding surface of Aβ40 or Tau on Hsp90 are generally in accordance with how Hsp90 interacts with the other amyloid proteins, like the misfolded transthyretin monomer, the GR-LBD (glucocorticoid receptor-ligand binding domain), or the unfolded kinase.
Since Aβ40 is 10 times size smaller than Tau, Hsp90 may stoichiometrically bind to more Aβ40 compared to Tau or other amyloid protein. Tau takes 106-Aβ-long binding patch of Hsp90 for the low-affinity interaction, while Hsp90 forms several complexes with different numbers of Aβ40 monomers as observed by the PICUP in Figure 6 (B) and the following LC-MS assay (Figure S7 (A) and (B)) with low binding affinity (Figure 6(A)).

We still do not fully understand the molecular action of the tetramer and E33A mutant, as shown in Figure 4(A) and (B), because the tetramer and E33A show similar effects regarding the reduction of Aβ40 hydrophobicity but a different effect of Aβ40 fibrillation. Nevertheless, the tetramer and E33A helped us to delineate factors that determine the interaction between Hsp90 and Aβ40. It became clear, that the ATPase activity is very important, but not the only determinant. One other determinant is a reduction of Hsp90 hydrophobicity. Besides, we are convinced that a third determinant is the conformational dynamics/flexibility of Hsp90, but this is a point of further investigation.

Taken together, the different behaviors of Aβ40 fibrillation in the presence of wild type Hsp90 and the variants are presumably caused by Hsp90 conformation dynamics, ATPase activity, hydrophobicity, and the heterogeneity of Aβ40 aggregation process. This can also explain the differences in the behavior of Aβ40 aggregation kinetics in the presence of different Hsp90 isoforms in Figures 3(D) and 4(A). Like other oligomeric proteins, tetrameric Hsp90 may equilibrate to dimer or monomer. The equilibria might cause the interface change of tetrameric Hsp90, therefore changing the different hydrophobic surfaces for Aβ40 and leading to the similar effect with that of E33A mutant. The tetrameric equilibria and Aβ40 aggregation can be further explored but are not an aim of our study. Oligomer equilibria can be dependent of sample preparation conditions, like temperature. The different equilibrium of Hsp90 tetramer may explain the slight different effects of the tetramer on Aβ40 fibrillation shown in Figures 3(D) and 4(A).

On the physiological relevance, we can only speculate. In Alzheimer’s disease, mitochondrial electron transport chain is severely affected by Aβ aggregation, leading to a decrease of ATP production. With less ATP, there might be less Hsp90-client complexes. Instead, there could be more accessible hydrophobic surfaces on client-free Hsp90 available for binding Aβ, inhibiting the aggregation, and further restoring the function of ATP production. Although the direct physiological relevance of Hsp90 and ATP for modulating Aβ fibrillation remain to be explored, increasing evidence indicates that Aβ can be produced and can aggregate inside cells and that there is a communication between the extracellular and intracellular Aβ pools. Furthermore, our study provides a
potential mechanism how Hsp90 and variants may regulate Aβ fibrillation. These shed light on the multiple facets of the chaperone Hsp90 interaction with amyloid proteins.

Materials and Methods

Purification of recombinant Hsp90 from E. Coli

Gene expression and subsequent protein purification was performed following established protocols with minor modification.24 The construct used in this study were yeast Hsp90 WT carrying an N-terminal His6-tag and yeast Hsp90 E33A with a substituted charged linker region and a cleavable His6-SUMO-tag.1 In short, pET28 derived expression constructs were transformed with BL21 Star (DE3) cells. Gene expression was induced at OD600 = 0.7 with 1 mM IPTG in cells grown in (DE3) cells. Gene expression and subsequent protein purification was performed following established protocols with minor modification.71 The construct used in this study were yeast Hsp90 WT carrying an N-terminal His6-tag and yeast Hsp90 E33A with a substituted charged linker region and a cleavable His6-SUMO-tag.1 In short, pET28 derived expression constructs were transformed with BL21 Star (DE3) cells. Gene expression was induced at OD600 = 0.7 with 1 mM IPTG in cells grown in lyso- geny broth media at 37 °C. The cells were harvested 4 h after induction.

Cells were resuspended in HEPES buffer ‘pH7.5’ containing 150 mM NaCl and 20 mM Imidazole and lysed with a Cell Disrupter (Constant Systems) at 1.6 kbar. Cleared lysate was then applied to HisTrap HP column followed by anion exchange chromatography with HiTrap Q and gel filtration on S200 (all columns GE Healthcare). Fractions corresponding to the dimer and to a higher oligomer were pooled separately. The protein was flash frozen in liquid nitrogen in concentrations of 130–315 μM and stored at −80 °C. Cleavage of the SUMO-tag was done by dialysis of the HisTrap eluate in the presence of 1/100 mol SENP protease against imidazole free buffer and removal of free SUMO and uncleaved fusion-protein by a second HisTrap.

The oligomeric state of the higher oligomer was examined with right angle light scattering and refractive index analysis (Viscottek TDA 305) after separation on a S200 10/300 GL increase column (GE Healthcare) confirming a predominantly tetrameric composition.

Other materials and sample preparation

Concentrated Hsp90 protein stock solutions were diluted to working concentration in 40 mM Heps buffer supplemented with 150 mM KCl, pH 7.5. Aβ40 was purchased from (Alexo Tech) and Adenosine 5'-triphosphate disodium salt hydrate (ATP, CAS: 34369-07-8); Adenyllyimidodiphosphate (AMP-PNP, CAS: 25612-73-1), 8-Anilino-1-naphthalenesulfonic acid (ANS, CAS: 82-76-8); Thioflavin T (ThT, CAS: 2390-54-7), Tris (2,2'-bipyridyl) dichlororuthenium(II) hexahydrate (Ru(Bpy), CAS: 50525-27-4), and Ammonium persulfate (APS, CAS: 7727-54-0) were purchased from Sigma-Aldrich. Aβ40 stock solutions were prepared by dissolving the lyophilized powder in 10 mM NaOH to a concentration of 2 mg/mL and then sonicated in an ice-water bath for 1 min, as described previously in our publications.5,76 ATP and AMP-PNP stock solutions were prepared at a concentration of 100 mM in 50 mM Tris-HCL, pH 7.5. ThT and ANS stocks were prepared to 3 and 10 mM in 50 mM Tris buffer pH 7.4 and DMSO, respectively. The concentrations of Ru(Bpy) and APS were 1 and 20 mM in 10 mM sodium phosphate buffer, pH 7.4, respectively. All of the buffers, 10 mM NaOH, ThT and ANS stocks were filtered with 0.2 μm (micrometer) syringe-driven filters.

ThT fluorescence assays

To study the effect of Hsp90 (WT, tetramer, and E33A mutant) on the fibrillation kinetics of the Aβ40 peptides, Hsp90 solutions at the different concentrations (0, 0.02, 0.04, 0.08, and 0.1 μM) were prepared with 40 μM ThT and 10 μM Aβ40 in the assay buffer (20 mM sodium phosphate buffer, pH 7.4, 0.2 mM EDTA, 0.02% NaN3) on ice. 40 μL of each sample was then transferred into a 384-well black plate with transparent bottom (NUNC) and sealed with a piece of foil film. The plate was incubated in a microplate reader (PHERAstar FSX, BMG LABTECH, Germany) and the fluorescence kinetics of Aβ40 was monitored at 37 °C without agitation every 5 min, using wavelengths of 430 nm and 480 nm for excitation and emission, respectively.

To investigate how ATP and AMP-PNP affect the activity of Hsp90 on Aβ40 fibril formation, we conducted another ThT assay with 40 μM ThT, 10 μM Aβ40, 0.1 μM Hsp90 (WT, tetramer, or E33A mutant), in the presence or absence of 2 mM ATP and AMP-PNP. The samples were prepared and the kinetics was monitored in the same way as mentioned above. As a control, the effect of ATP and AMP-PNP on Aβ40 fibrillation kinetics was studied as well.

In a seeding assay, 10 μM Aβ40 seeds were freshly prepared from a monomeric solution allowed to incubate for ~15 h at 37 °C in a 384-well black plate (NUNC) without agitation. The seeds were then sonicated in ice-water bath for 2 min. The samples were prepared as described above in the presence of 1 μM Aβ40 seeds. These ThT assays were conducted with at least three replicates.

All of the original ThT data were plotted with Prism7.0 (GraphPad Software). The averaged ThT data were normalized with equation (1) and globally fitted in AmyloFit.67 the sigmoidal fitting were performed with data of individual curves by using equation (2). The averaged data of seeding assays and the data of individual curves obtained from ThT assays with ATP or AMP-PNP were normalized with equation (1) in AmyloFit.

\[
y_{\text{norm},i} = \left(1 - M_{0,\text{trac}}\right) \frac{y_i - y_{\text{baseline}}}{y_{\text{plateau}} - y_{\text{baseline}}} + M_{0,\text{trac}} \tag{1}
\]
\[ y = \frac{Y_{\text{baseline}} - Y_{\text{plateau}}}{1 + e^{\frac{t - t_0}{dt}}} + Y_{\text{plateau}} \]  

where \( y_{\text{baseline}} \) and \( y_{\text{plateau}} \) are the values of the data at the baseline and the plateau, \( M_{0,\text{frac}} \) is the relative initial concentration of aggregates (i.e., a value between 0 and 1), \( t \) is the time of amyloid aggregation course and \( t_0 \) is the time when the fluorescence intensity reaches half of the plateau value, while \( dt \) is the time constant. \( y_{\text{norm, i}} \) is the normalized value of \( y_i \), the original value of the \( i \)th data point, and \( y \) was the fitted value of the data at time \( t \). The lag time \( t_{\text{lag}} \) and aggregation half time \( t_{1/2} \) were given as follows.

\[ t_{1/2} = t_0 \]  

\[ t_{\text{lag}} = t_{1/2} - 2dt \]

The normalized data, \( t_{\text{lag}} \) and \( t_{1/2} \) were plotted with Prism7.0 (GraphPad software).

**Global fitting**

To identify which microscopic rate processes of Aβ40 aggregation are the ones most influenced by Hsp90, the ThT data of Aβ40/Hsp90 (0, 0.02, 0.04, 0.08, and 0.1 μM) were fitted globally with an integrated rate law \(^{43,44} \) in AmyloFit online software server. \(^{47} \) The secondary nucleation dominated model was selected, the data of Aβ40 alone was first fitted, obtaining a set of parameters, which were used as the initial guess values for the following fits. Among these obtained parameters, the primary nucleation rate constant \( (k_n, \text{units of } \text{time}^{-1} \text{concentration}^{-n_c+1}) \), where \( n_c \) is the reaction order of primary nucleation that simply interprets a nucleus size), the secondary nucleation rate constant \( (k_2, \text{units of } \text{time}^{-1} \text{concentration}^{-n_2}) \), where \( n_2 \) is the reaction order of secondary nucleation that simply interprets a nucleus size), or the elongation rate constant \( (k_e, \text{units of } \text{time}^{-1} \text{concentration}^{-n_e}) \) was fitted freely while the other two rate constants were set as fixed initial values. For detailed definitions of these parameters and fitting procedure, please refer to the nature protocol.\(^{47} \)

**Atomic force microscopy (AFM) imaging in air**

For AFM measurement in air, 10 μM Aβ40, with or without 0.5 μM Hsp90 (WT, tetramer, or E33A mutant) were incubated at 37 °C in 1.5 mL microcentrifuge tubes for 24 h at 300 rpm. 15 μL of each sample was then added onto the freshly cleaved muscovite mica (Electron Microscopy Sciences) and incubated for 5 min at room temperature. The excess sample was removed with filter paper and the mica plate with the sample was rinsed once with 150 μL of Milli-Q water. The excess water was removed with filter paper and the mica plate with the sample was dried under nitrogen gas. The images were obtained with the Bruker Dimension Icon Scanning Station (Bruker, USA) in intermittent contact mode in air and processed with the WSxM 4.0 software.\(^{72} \)

**Atomic force microscopy imaging in liquid**

For AFM imaging, Aβ40 peptides were diluted with PBS buffer (Dulbecco’s Phosphate Buffered Saline, pH 7.2, 500 mL, Sigma-Aldrich, USA) to a final concentration of 75 μM with 7.5 μM Hsp90 (WT), 5.0 mM ATP or 7.5 μM BSA. The peptides were incubated at 30 °C for 92 h at 300 rpm (Eppendorf Thermotop, Germany). A flat mice surface (muscovite, diameter 10–12 mm, Plano, Germany) was cleaved, immobilized on an AFM specimen (diameter: 15 mm) using UV curable glue (NOA 63, Norland Products, USA) and washed with ultrapure water (30 μL, 18.2 MΩ cm, Purelab Chorus 1, Elga LabWater, Germany) and the Aβ40 solution was incubated on the mica surface at 60 °C for 30 min. Finally, the surface was washed with ultrapure water (30 μL).

AFM imaging was performed on a Cypher ES (Asylum Research, an Oxford Instruments Company, USA) using a heating/cooling sample stage set to 25 °C and AC mode based on the blueDrive (photothermal excitation). The measurements were performed in HEPES buffer (pH 7.0) with 10 mM MgCl₂. The images were obtained with the BioLever-AC40TS cantilevers (Olympus, Japan) with a resonance frequency of about 20–25 kHz in liquid. The following parameters were chosen for the measurements: a scan size of 5 μm, a scan rate of 2.44 Hz, a setpoint of 300–400 mV and a scan angle of 0°.

The images were processed with the Gwyddion Free SPM analysis software (Petr Klapetek, version 2.53).\(^{73} \) To correct the recorded height image (using the trace image), the data was levelled by mean plane subtraction, the rows were aligned to the median value and the minimum data value was shifted to 0.

Grain analysis using Gwyddion Free SPM analysis software was performed to obtain height values of the imaged structures. First, the threshold of grain-like features was marked. Then, the generated grain data was exported and the height values of the grains were taken to provide histograms, mean and error values using Origin (Version 2019, OriginLab, USA).

**Circular dichroism (CD) spectroscopy**

In CD spectroscopy, the sample was performed with 10 μM Aβ40 supplemented with or without 0.04 μM Hsp90 proteins (WT, tetramer, or E33A
conformation dynamics will influence this interaction, Liquid chromatography-mass spectrometry (LC-MS) experiments were performed with 10 μM Hsp90 in native state, 2 μM Hsp90/2 mM AMP-PNP (cross-linked), 2 μM Hsp90/90 μM Aβ40 (cross-linked), and 2 μM Hsp90/2 mM AMP-PNP /90 μM Aβ40 (cross-linked). LC/MS analysis was performed on a LCT Premier mass spectrometer and HPLC Waters 2795 (Waters, US). Samples were chromatographed on a Reprosil-PUR 2000 C18-AQ column (3 μm, 100mmX2mm) heated to 50 °C using the following condition (see Table 1):

Fluorescence polarization (FP) assay

To investigate the binding affinity of Hsp90 with Aβ40, FP assays were performed with Hsp90 (WT, two-fold serial dilution, with a highest concentration of 100 μM, the results are shown in Figure 6(A)) and 30 nM HL488-Aβ40 in the absence or presence of 2 mM AMP-PNP with 480 nm and 520 nm as the excitation and emission wavelengths, respectively. The measurements were performed with a microplate reader (PHERAsar FSX, BMG LABTECH, Germany) at 37 °C. The data were plotted with Prism7.0 (GraphPad software). To confirm these results, we performed the experiments once more with WT at the highest concentration of 160 μM with the same method, and obtained similar results (data not shown).

ANS experiments

To study the effect of ATP and AMP-PNP on the hydrophobic surface of the Hsp90 proteins, the samples were prepared in the presence or absence of 6 μM WT Hsp90 with 2 mM ATP or AMP-PNP and then incubated for 1 h at room temperature. ANS fluorescence dye was added to the prepared samples at a final concentration of 30 μM. ANS is believed to binding to (buried) hydrophobic sites of proteins. The observed features of ANS, a blue shift of fluorescence emission maxima and the increase of fluorescence intensity and lifetime, are generally attributed to the hydrophobicity of a binding site and the restricted mobility of ANS. 40 μL of each mixed sample was then transferred into a 384-well white plate (PerkinElmer, USA). The samples were measured using a multi-mode microplate reader from BioTek at 37 °C, with an excitation wavelength of 400 nm and an emission

Table 1 HPLC Method description

| Time (min) | Solvent A (acetonitrile with 0.1% formic acid) | Solvent B (water with 0.1 % formic acid) | Flow (mL/min) |
|------------|-----------------------------------------------|-----------------------------------------|---------------|
| 0          | 2%                                            | 98%                                     | 0.5           |
| 2          | 25%                                           | 75%                                     | 0.5           |
| 25         | 50%                                           | 50%                                     | 0.5           |
| 30         | 80%                                           | 20%                                     | 0.5           |

The result of MS experiment was given as the spectrum m/z.
wavelength region of 440–580 nm. The obtained values were averaged, plotted and smoothed with Origin (Version 2018, OriginLab).

We also conducted the ANS experiment to investigate whether Hsp90 (WT, tetramer, and E33A) influence the hydrophobic surface of Aβ40. Samples containing 10 μM Aβ40 in the presence of 0.1 μM Hsp90 (WT, tetramer, or E33A) were prepared, incubated, and measured in the same way as mentioned above.

**CRediT authorship contribution statement**

Hongzhi Wang: Conceptualization, Investigation, Validation, Project administration. Max Lallemang: Investigation, Validation. Bianca Hermann: Investigation. Cecilia Wallin: Validation. Rolf Loch: Validation. Alain Blanc: Investigation. Bizan N. Balzer: Conceptualization, Validation. Thorsten Hugel: Conceptualization, Validation. Jinghui Luo: Conceptualization, Validation, Project administration.

**Acknowledgment**

We appreciate Natacha Olieric for her kind help with the CD experiment and acknowledge the use of the PSI SPM Userlab at PSI.

**Funding**

M.L., B.N.B. and T.H. were funded by the Deutsche Forschungsgemeinschaft (DFG, German Research Foundation) under Germany’s Excellence Strategy – EXC-2193/1 – 390951807. H.W. was sponsored by the State Scholarship Fund (China Scholarship Council (CSC): 201806200097) and J.L. was supported by the Fund (China Scholarship Council (CSC): 201806200097) and J.L. was supported by the Deutsche Forschungsgemeinschaft (DFG, German Research Foundation) under Germany’s Excellence Strategy – EXC-2193/1 – 390951807.

**Declaration of Competing Interest**

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

**Appendix A. Supplementary material**

Supplementary data to this article can be found online at https://doi.org/10.1016/j.jmb.2020.11.016.

Received 7 June 2020;
Accepted 11 November 2020;
Available online 19 November 2020

**Keywords:**
Hsp90; Aβ40; fibrillation; conformation; hydrophobic interaction

**Abbreviations:**
Hsp90, heat shock protein 90; ATP, adenosine triphosphate; AFM, atomic force microscopy; CD, circular dichroism; ThT, Thioflavin T; ANS, 8-anilino-1-naphthalenesulfonic acid; Aβ, amyloid-β; WT, wild type Hsp90; GR-LBD, glucocorticoid receptor-ligand binding domain; ETC, mitochondrial electron transport chain; UPR, unfolded protein response; PICUP, photo-induced cross-linking of unmodified proteins; ER, endoplasmic reticulum; AMP-PNP, Adenylyl-imidodiphosphate; APS, Ammonium persulfate

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