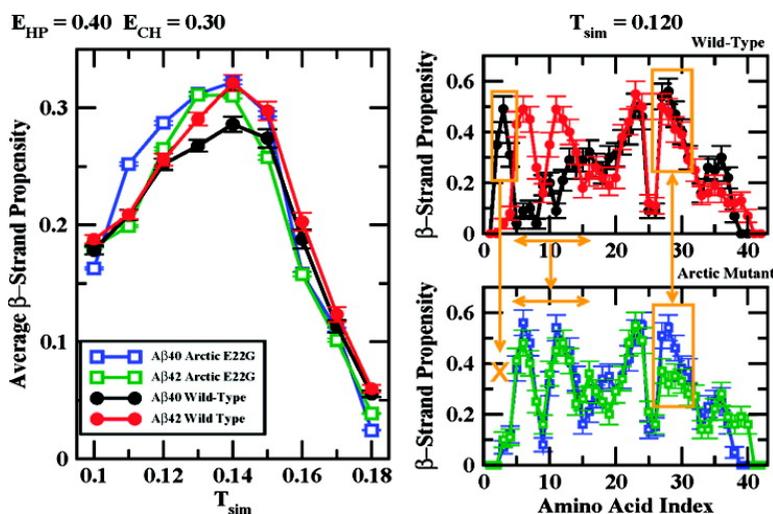


Effects of the Arctic (E#G) Mutation on Amyloid β -Protein Folding: Discrete Molecular Dynamics Study

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Effects of the Arctic (E²²→G) Mutation on Amyloid β -Protein Folding: Discrete Molecular Dynamics Study

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Abstract: The 40–42 residue amyloid β -protein ($A\beta$) plays a central role in the pathogenesis of Alzheimer's disease (AD). Of the two main alloforms, $A\beta_{40}$ and $A\beta_{42}$, the longer $A\beta_{42}$ is linked particularly strongly to AD. Despite the relatively small two amino acid length difference in primary structure, *in vitro* studies demonstrate that $A\beta_{40}$ and $A\beta_{42}$ oligomerize through distinct pathways. Recently, a discrete molecular dynamics (DMD) approach combined with a four-bead protein model recapitulated the differences in $A\beta_{40}$ and $A\beta_{42}$ oligomerization and led to structural predictions amenable to *in vitro* testing. Here, the same DMD approach is applied to elucidate folding of $A\beta_{40}$, $A\beta_{42}$, and two mutants, [G22] $A\beta_{40}$ and [G22] $A\beta_{42}$, which cause a familial ("Arctic") form of AD. The implicit solvent in the DMD approach is modeled by amino acid-specific hydrophobic and electrostatic interactions. The strengths of these effective interactions are chosen to best fit the temperature dependence of the average β -strand content in $A\beta_{42}$ monomer, as determined using circular dichroism (CD) spectroscopy. In agreement with these CD data, we show that at physiological temperatures, the average β -strand content in both alloforms increases with temperature. Our results predict that the average β -strand propensity should decrease in both alloforms at temperatures higher than ~ 370 K. At physiological temperatures, both $A\beta_{40}$ and $A\beta_{42}$ adopt a collapsed-coil conformation with several short β -strands and a small ($< 1\%$) amount of α -helical structure. At slightly above physiological temperature, folded $A\beta_{42}$ monomers display larger amounts of β -strand than do $A\beta_{40}$ monomers. At increased temperatures, more extended conformations with a higher amount of β -strand ($\leq 30\%$) structure are observed. In both alloforms, a β -hairpin at A21–A30 is a central folding region. We observe three additional folded regions: structure **1**, a β -hairpin at V36–A42 that exists in $A\beta_{42}$ but not in $A\beta_{40}$; structure **2**, a β -hairpin at R5–H13 in $A\beta_{42}$ but not in $A\beta_{40}$; and structure **3**, a β -strand A2–F4 in $A\beta_{40}$ but not $A\beta_{42}$. At physiological temperatures, the Arctic mutation, E22G, disrupts contacts in the A21–A30 region of both [G22] $A\beta$ peptides, resulting in a less stable main folding region relative to the wild type peptides. The Arctic mutation induces a significant structural change at the N-terminus of [G22] $A\beta_{40}$ by preventing the formation of structure **3** observed in $A\beta_{40}$ but not $A\beta_{42}$, thereby reducing the structural differences between [G22] $A\beta_{40}$ and [G22] $A\beta_{42}$ at the N-terminus. [G22] $A\beta_{40}$ is characterized by a significantly increased amount of average β -strand relative to the other three peptides due to an induced β -hairpin structure at R5–H13, similar to structure **2**. Consequently, the N-terminal folded structure of the Arctic mutants closely resembles the N-terminal structure of $A\beta_{42}$, suggesting that both Arctic $A\beta$ peptides might assemble into structures similar to toxic $A\beta_{42}$ oligomers.

1. Introduction

Alzheimer's disease (AD) is a progressive neurodegenerative disorder that is characterized pathologically by extensive neuronal loss and the accumulation of extracellular senile plaques and intracellular neurofibrillary tangles. Senile plaques contain fibrillar aggregates of the amyloid β -protein ($A\beta$). $A\beta$ is produced through cleavage of the amyloid precursor protein (APP) and is normally present in the body predominantly in two alloforms, $A\beta_{40}$ and $A\beta_{42}$, that differ structurally by the

absence or presence of two C-terminal amino acids, respectively.^{1,2} An important hypothesis of disease causation, strongly supported by genetic and experimental evidence, posits that $A\beta$ oligomers, rather than fibrils, are the proximate neurotoxic agents in AD.³ In particular, $A\beta_{42}$ oligomers appear to be the most toxic $A\beta$ assemblies.⁴ The linkage of $A\beta$ oligomerization to AD makes imperative the detailed elucidation of the oligomerization process. Unfortunately, the $A\beta$ system is remarkably complex

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in its conformational and assembly dynamics.^{3,5} This has complicated the application of classical structure determination methods such as X-ray crystallography and solution state NMR to the oligomerization question. One approach that has provided information on the initial self-association of A β has been *in situ* chemical cross-linking (for a review, see ref 6). This approach allowed Bitan *et al.*⁷ to determine quantitatively the A β oligomer size frequency distribution, which demonstrated that A β 40 and A β 42 exhibit different oligomerization pathways. A β 42 assembled into pentamer/hexamer units (paranuclei) and multiples of paranuclei, while A β 40 only formed dimers through tetramers in equilibrium with monomers. However, the resolution of the method was insufficient to reveal the interatomic interactions controlling the oligomerization processes.

In vitro studies showed that A β 40 and A β 42 monomers adopted a predominantly α -helical structure in a membrane-mimicking environment,^{8,9} while a collapsed coil structure was reported for A β (10–35) in an aqueous solution.¹⁰ A β folded structure clearly depends on the solvent. Earlier studies of A β 40 using a mixture of trifluoroethanol and water demonstrated a substantial amount of α -helical structure.^{11,12} Initial studies of temperature dependence of the secondary structure of A β 40 in aqueous solution demonstrated that β -strand propensity increased with temperature.¹³ Using CD spectroscopy on both A β 40 and A β 42 monomers in aqueous solution, Lim *et al.* recently demonstrated¹⁴ that the average β -strand structure increased with temperature, in agreement with Gursky and Aleshkov,¹³ with A β 42 monomers having a slightly higher amount of average β -strand structure than A β 40 monomers, suggesting that the two allforms are characterized by differences in folded structures.

Knowledge-based therapeutic drug design requires the definition of target structures at atomic resolution. *In silico* approaches provide a powerful means to achieve this goal. Several *in silico* studies addressed folding of A β 42,^{15,16} A β 39,¹⁷ A β (10–35),^{18,19} A β (25–35),²⁰ A β (1–28),²¹ and A β (21–30) decapeptide.^{22–27} The

latter was hypothesized to nucleate monomer folding.^{28,29} Replica-exchange all-atom molecular dynamics (MD) study of A β 42 monomer in implicit water by Baumketner *et al.* showed three distinct families of folded structures, all dominated by turns and loops with a small amount of α -helical structure at the C-terminus.¹⁶ Using similar all-atom MD approach, Anand *et al.* found that at room temperature, the A β (1–39) monomer did not have a unique structure but rather three distinct families of mostly collapsed coil-like structures existed.¹⁷ Using all-atom MD in explicit water, Massi *et al.* demonstrated that although A β (10–35) is somewhat disordered in water, the central hydrophobic cluster, L17-A21, and the turn region, V24-N27, were particularly stable.^{18,19} Wei *et al.*²⁰ used replica-exchange MD in pure water and HFIP/water cosolvent to demonstrate that A β (25–35) preferentially populated an α -helical structure in apolar organic solvent, while in water, a collapsed coil, and to a lesser extent β -hairpin conformations, were observed. Dong *et al.*²¹ explored the energy landscape of A β (1–28) monomers and concluded that the monomer was predominantly in a collapsed coil conformation with a non-negligible β -strand structure at the N-terminus.

An *ab initio* DMD approach using a four-bead protein model with backbone hydrogen bonding in implicit solvent recently demonstrated that despite relatively small differences in the primary structure, A β 40 and A β 42 not only followed different oligomerization pathways but also folded differently, with A β 42 displaying a turn structure centered at G37-G38 that was not present in A β 40 monomer.³⁰ This structural difference between A β 40 and A β 42 was corroborated by several independent *in vitro* studies.^{28,31,32} In addition, a combined MD/NMR study confirmed that A β 42 monomer was more structured at the C-terminus than A β 40.³³ Using the same DMD approach as the initial study by Urbanc *et al.*,³⁰ Lam *et al.* showed that only selected regions of A β 42 had a well-defined folded structure and that the average amount of β -strand increased with temperature,³⁴ consistent with *in vitro* findings.¹³ Because A β 40 and A β 42 were shown to oligomerize through distinct pathways *in vitro*⁷ and *in silico*,³⁰ the present study is based on a hypothesis that different oligomerization pathways leading to distinct effects *in vivo* are a consequence of folding differences between A β 40 and A β 42. We employ the DMD approach with

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implicit solvent parameters mimicking the *in vitro* aqueous solution¹⁴ to elucidate all structural differences between A β 40 and A β 42 monomers at different temperatures. Because the Arctic mutation, E²²→G, is associated with the familiar form of AD with distinct pathology relative to the sporadic AD, we examine also the effects of the Arctic mutation on folded structures of both isoforms and discuss the implications of our findings for understanding A β isoform-specific folding and its relationship to AD.

2. Methods

2.1. Discrete Molecular Dynamics. Zhou *et al.* proposed the idea of applying discrete molecular dynamics (DMD) combined with a simplified protein model to study protein folding.³⁵ Since then, many groups have implemented this approach to investigate protein folding mechanisms.^{36–40} In DMD, all interparticle interactions are modeled by square-well and step-like potentials. Particles move with constant speeds along straight lines. When two particles reach a distance at which the potential is discontinuous, a collision occurs. The pair of particles with the shortest collision time is chosen as the next collision event and the new positions and velocities of the two particles involved are calculated based on conservation laws for the linear momentum, angular momentum, and total energy. The advantage of DMD is that the numerical integration of Newton's second law equations is avoided, resulting in a substantial decrease in computational burden. This makes the DMD approach much faster than all-atom MD with continuous interparticle potentials.

2.2. Four-Bead Protein Model and Interactions. We use a four-bead protein model,^{41–43} in which up to four beads are used to represent an amino acid. Three beads are used to model the backbone groups N, C α , and C'. The fourth bead represents the side chain centered at the C β group. Only glycine lacks the C β bead and is thus modeled by three beads only. Adjacent beads are connected to each other through covalent or peptide bonds, which are modeled as square well potentials with infinite walls but of finite width corresponding to ~2% variability in covalent/peptide bond lengths. In addition to covalent and peptide bonds, constraints are implemented to ensure the proper geometry of the protein backbone. These constraints are modeled in the same ways as the bonds. All lengths of bonds and constraints are based on statistical properties derived from the protein database of known protein structures.⁴⁴

The backbone hydrogen bond was introduced into the four bead model to account for the α -helical and β -strand secondary structure.⁴³ The bond is introduced between the N $_i$ bead of amino acid *i* and C' $_j$ bead of amino acid *j*. For a hydrogen bond between N $_i$ and C' $_j$ to form, these two beads need to be at a distance <4.2 Å. In addition, auxiliary bonds between the two amino acids involved are introduced to account for the particular backbone geometry allowing hydrogen bond formation. The absolute value of the

potential energy associated with formation of a single hydrogen bond, E_{HB} , represents a unit of energy in our approach. The simulation temperature T_{sim} is expressed in units of E_{HB}/k_B , where k_B is the Boltzmann constant.

The model implements amino acid-specific interactions between two side chain beads due to effective hydrophathy³⁰ and charge.^{34,44} The side chain bead of each amino acid is characterized by an effective hydrophathy following the Kyte and Dolittle scale.⁴⁵ Because the solvent is not explicitly present in the model, effective attractive interactions between two hydrophobic, and repulsive interactions between two hydrophilic, side chain beads are introduced.^{30,44} The strength of the effective hydrophathic interactions as given by the absolute value of the potential energy between two isoleucines E_{HP} (relative to the energy unit E_{HB}) is the first interaction parameter. A double square-well potential is applied to model the effective electrostatic interactions between two charged side chain beads.⁴⁴ The maximal absolute value of the potential energy between two charged side chain beads E_{CH} (relative to the energy unit E_{HB}) is the second interaction parameter. Both interaction parameters E_{HP} and E_{CH} strongly depend on and need to be adjusted to the particular solvent.

2.3. Secondary Structure Analysis. The secondary structure propensities of each amino acid were calculated using the STRIDE program⁴⁶ within the Visual Molecular Dynamics (VMD) software package.⁴⁷ The secondary structure propensities included α -helical, β -strand, turn, and random coil per amino acid. We calculated the average β -strand and α -helix propensities, $\langle\beta\rangle$ and $\langle\alpha\rangle$, by averaging the β -strand/ α -helix propensity over all amino acids at a given temperature and interaction parameters (E_{HP} , E_{CH}).

2.4. Intramolecular Contact Map. We determined the average intramolecular contact frequency for each temperature and interaction parameter set (E_{HP} , E_{CH}). Two amino acids, *i* and *j*, were considered to be in contact when the distance between them $d_{ij} \leq 7.5$ Å. The contact was counted with variable C_{ij} that was defined as the average number of contact pairs between amino acids *i* and *j* from different trajectories. Because each amino acid had up to four beads, the maximum number of contacts C_{ij} (between any two amino acids) was 16. We normalized the contact maps to the same maximum value.

3. Results

The DMD approach employed here has been described in detail by Urbanc *et al.*⁴⁴ In earlier studies, DMD combined with a four-bead amino acid model, and considering backbone hydrogen bonding only, resulted in β -hairpin monomer and planar dimer conformations.⁴⁸ Introducing amino acid-specific interactions due to hydrophathy into the four-bead model enabled the successful *in silico* reproduction of experimentally observed⁷ oligomerization differences between A β 40 and A β 42 and yielded new structural predictions amenable to *in vitro* testing.³⁰ This same study indicated that alloform-specific differences already existed at the stage of monomer folding. In particular, the turn structure centered at G37-G38 was present in a folded A β 42 monomer but not in a folded A β 40 monomer and was associated with the first contacts that formed during monomer folding. Yun *et al.*,⁴⁹ using the same DMD approach, showed that electrostatic interactions promote formation of larger oligomers in both A β 40 and A β 42 while preserving the

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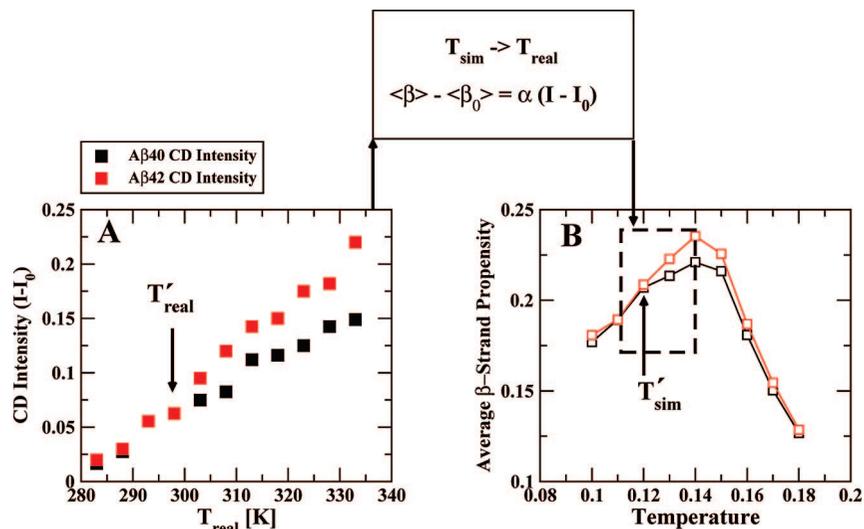


Figure 1. (A) CD data obtained for A β 40 (black squares) and A β 42 (red squares) by Lim *et al.*¹⁴ (B) Average β -strand propensity, $\langle \beta \rangle$, of A β 40 (black squares) and A β 42 (red squares). For all the parameter sets (E_{HP} , E_{CH}), we map the CD data in panel A using the functions defined in the dashed-line box above the plot into the data enclosed in the dashed box in panel B. T_{sim} and T_{real} are related by a conversion factor ($T^* = T_{\text{real}}/T_{\text{sim}}$) that maps all the simulation temperatures onto real temperatures. A similar relationship exists for the CD intensity conversion factor α . $\langle \beta_0 \rangle$ and I_0 are the average β -strand propensity and the CD intensity at 5 °C, respectively.

differences between the two alloforms at both the folding and oligomerization stages of assembly. Lam *et al.* applied this approach in studies of the temperature dependence of A β 42 folding, showing that a collapsed coil conformation at low temperatures converts to a more extended, β -strand-rich conformation at higher temperatures.³⁴ Interestingly, while several regions of A β 42 consistently exhibit a temperature-dependent fold, significant variability of folded structures was found at each temperature. The coexistence of a multitude of monomer conformations is characteristic of naturally unfolded proteins. Here we explore more deeply the differences between the full-length A β 40 and A β 42 peptides. We first describe a technique that allows us to determine the implicit solvent parameters that best match experimental conditions. We then use these parameters to explore not only the folding of wild type A β 40 and A β 42 but also of two clinically relevant mutant alloforms, Arctic [G22]A β 40 and [G22]A β 42.

The primary structure of A β 42 differs from A β 40 by two additional amino acids of A β 42, I and A, at the C-terminus. The sequence of A β 42 is DAEFRHDSGYEVHHQK¹⁶LVFAE²²DVGSNKGK³⁰IIGLMV³⁶GGVV⁴⁰IA. We refer to the segments (L17–A21) and (I31–V36) as the central hydrophobic cluster (CHC) and the mid-hydrophobic region (MHR), respectively. We define the C-terminal region (CTR) as the segment V39–V40 in A β 40 or V39–V42 in A β 42.

The energy unit is set to the absolute value of the hydrogen bond potential energy, $E_{\text{HB}} = 1.0$ and the simulation temperature T_{sim} is expressed in units of E_{HB}/k_B . We explore folding at four different strengths of hydrophobic interactions, $E_{\text{HP}} = 0.1, 0.2, 0.3, 0.4$, and three different strengths of EIs, $E_{\text{CH}} = 0, 0.15, 0.3$. For each set of these effective interaction parameters (E_{HP} , E_{CH}), we first perform DMD simulations of a monomer at a high temperature ($T_{\text{sim}} = 4$) to obtain 100 distinct random coil-like initial conformations to be used in production runs. For given interaction parameters (E_{HP} , E_{CH}), we simulate 100 trajectories spanning a temperature range of [0.10, 0.18].

3.1. Interaction Parameters for Aqueous A β Folding. In an aqueous environment, hydrophobic and hydrophilic effects play key roles in protein folding and assembly. In the DMD approach,

we model hydrophobic effects by a single-well attractive/repulsive potential between two side-chain beads. The strength of the effective hydrophobic interactions, E_{HP} , is by definition equal to the absolute value of the potential energy between two I residues at a distance of <7.5 Å. Similarly, the strength of effective electrostatic interactions, E_{CH} , is defined as the absolute value of the potential energy between two oppositely charged side-chain atoms at a distance of <6 Å.

We examined the temperature dependence of A β 40 and A β 42 folding using 12 different sets of interaction parameters (E_{HP} , E_{CH}). Our goal was to select interaction parameters that would best fit the folded structure of A β in aqueous solution. As an input, we used the *in vitro* data by Lim *et al.*,¹⁴ who applied CD spectroscopy to characterize the secondary structure of A β 40 and A β 42 monomers in a broad temperature range (Fig. 1A). The resulting CD intensities for A β 40 and A β 42 increased linearly with temperature T_{real} and above $T_{\text{real}}' = 298$ K, the CD intensity for A β 42 surpassed the A β 40 intensity, indicating a higher $\langle \beta \rangle$ in A β 42 for $T_{\text{real}} > T_{\text{real}}'$.

At given interaction parameters (E_{HP} , E_{CH}), we calculated the average β -strand propensity, $\langle \beta \rangle$, for each A β 40 and A β 42, which could be compared to the CD intensities. Our *in silico* results for $\langle \beta \rangle$ for both A β 40 and A β 42 were in agreement with the CD data obtained by Lim *et al.* (Fig. 1B). At low temperatures, $\langle \beta \rangle$ in both peptides increased with temperature linearly, and above the temperature T_{sim}' , A β 42 had more β -strand structure than A β 40.

Assuming that $\langle \beta \rangle$ was proportional to the CD intensity, we fitted the calculated temperature dependence of $\langle \beta \rangle$ for A β 42 monomer to the temperature dependence of the CD intensity. For each set of interaction parameters (E_{HP} , E_{CH}), we first determined the simulation temperature T_{sim}' , above which $\langle \beta \rangle$ of A β 42 was larger than $\langle \beta \rangle$ of A β 40. We matched T_{sim}' to T_{real} to obtain the temperature scaling factor T^* (eq 1),

$$T^* = T_{\text{real}}'/T_{\text{sim}}' \quad (1)$$

and used T^* to scale the simulation temperature T_{sim} to the real temperature T_{real} .

CD spectroscopy provides a rapid method for the determination of the population average secondary structure frequency

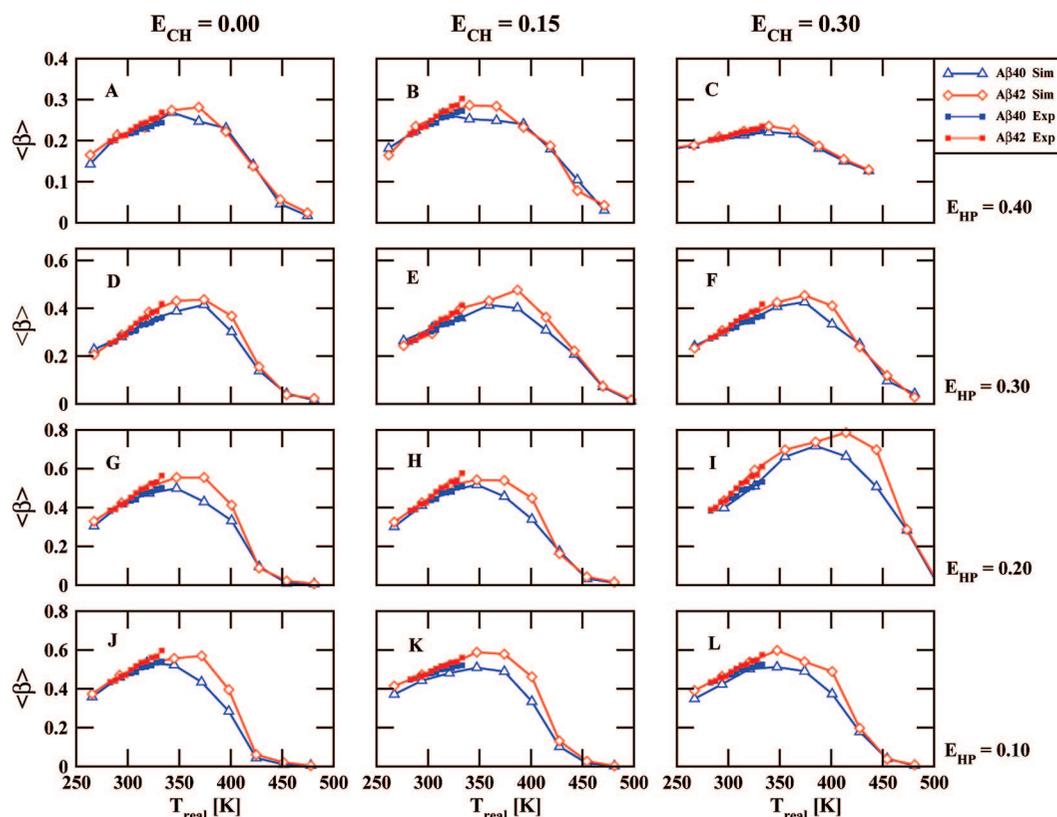


Figure 2. Average β -strand propensity, $\langle\beta\rangle$, versus temperature for all the elements of the parameter matrix (E_{HP} , E_{CH}). The graphs with empty blue triangles and empty red diamonds correspond to the A β 40 and A β 42 simulations, respectively. Similarly for the CD data, blue and red filled squares correspond to A β 40 and A β 42 experimental points, respectively.

distribution. In a recent paper, Greenfield suggested that a linear relationship exists between CD intensity and the sum of the secondary structure elements contributing to it.⁵⁰ To relate the average β -strand propensity $\langle\beta\rangle$ derived from our simulations to CD intensities I_{CD} determined experimentally, we used the data of Lim *et al.*¹⁴ These data were obtained at 222 nm, not at \sim 218 nm, where the minimum in β -strand ellipticity occurs. Nevertheless, because the β -strand is the dominant secondary structure element in our A β monomer conformations and because $\theta_{218} \propto \theta_{222}$, $\langle\beta\rangle$ will be proportional to CD intensity at 222 nm. We thus relate the CD intensity data, $I_{\text{CD}} - I_0$ (the y-axis of Fig. 2C in ref 14), to the calculated $\langle\beta\rangle$ using the following equation:

$$\langle\beta\rangle - \langle\beta_0\rangle = \alpha(I_{\text{CD}} - I_0) \quad (2)$$

where $\langle\beta_0\rangle$ was $\langle\beta\rangle$ at 5 °C (278 K) and I_0 was the corresponding CD intensity at 5 °C. The scaling factor α was obtained by fitting I_{CD} to $\langle\beta\rangle$.

For all sets of interaction parameters (E_{HP} , E_{CH}), the physiological temperature was found to be within the simulation temperature range $T_{\text{sim}} \in [0.11, 0.12]$ (Fig. 2).

We fitted $\langle\beta\rangle$ of the folded A β 42 monomer to the CD intensities for 12 different sets of interaction parameters (E_{HP} , E_{CH}). Once the two fitting parameters, T^* and α , were obtained we used them to calculate $\langle\beta\rangle$ versus temperature not only for A β 42 but also for A β 40. For each interaction parameter set (E_{HP} , E_{CH}), we quantified the quality of the fit, including temperature dependencies of $\langle\beta\rangle$ for both A β 40 and A β 42, by calculating σ :

$$\sigma = \sqrt{\frac{1}{(N-1) \cdot \langle\beta\rangle_{\text{max}}^2} \sum (\langle\beta\rangle_{\text{exp}} - \langle\beta\rangle_{\text{sim}})^2} \quad (3)$$

Table 1. Calculation of σ To Determine the Quality of the Fitting^a

E_{HP}	E_{CH}		
	0.00	0.15	0.30
0.10	0.0459	0.0898	0.0734
0.20	0.0387	0.0490	0.0682
0.30	0.0461	0.0690	0.0478
0.40	0.0596	0.0440	0.024

^a The parameter set (E_{HP} , E_{CH}) that best fit the CD data was (0.40, 0.30) (in italics).

where N is the number of experimental temperatures at which the CD intensity was measured, $\langle\beta\rangle_{\text{max}}$ is the highest value of $\langle\beta\rangle$ in the simulation data set, $\langle\beta\rangle_{\text{exp}}$ is the experimental value of $\langle\beta\rangle$ obtained from fitting the CD intensities to $\langle\beta\rangle$ (eq 2), and $\langle\beta\rangle_{\text{sim}}$ corresponds to the value of $\langle\beta\rangle$ obtained by simulations and interpolated to exactly match the temperatures at which the CD intensities were measured. σ values for each interaction parameter set (E_{HP} , E_{CH}) are listed in Table 1.

Examining the effect of varying the strengths of the two effective interaction parameters, we observed that $\langle\beta\rangle$ decreased with increasing E_{HP} but showed only minor changes with increasing E_{CH} . For $E_{\text{HP}} \in [0.1, 0.2]$, $\langle\beta\rangle$ did not change significantly (Fig. 2G-L). Increasing E_{CH} from 0 to 0.15 at $E_{\text{HP}} = 0.2$ did not change $\langle\beta\rangle$ in either of the two peptides. However, at $E_{\text{CH}} = 0.3$ (Fig. 2I), $\langle\beta\rangle$ amounts in both peptides were higher than the amounts observed at $E_{\text{CH}} \in [0, 0.15]$ but they followed the experimentally observed tendencies: $\langle\beta\rangle_{42} > \langle\beta\rangle_{40}$. $\langle\beta\rangle$ strongly decreased when E_{HP} changed from 0.2 to 0.3 (Fig. 2D-I). Variations in E_{CH} did not significantly affect $\langle\beta\rangle$ at $E_{\text{HP}} = 0.3$. When E_{HP} increased from 0.3 to 0.4 (Fig. 2A-F), we observed a further decrease of $\langle\beta\rangle$ at all temperatures in both peptides while preserving the experimentally observed differ-

(50) Greenfield, N. J. *Nature Protocols* **2007**, *1*, 2876–2890.

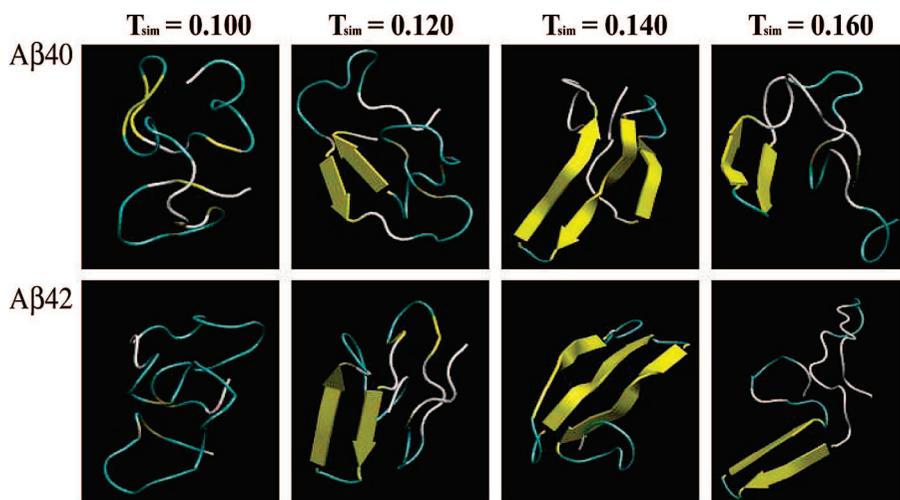


Figure 3. Typical conformations of A β 40 (top) and A β 42 (bottom) at different temperatures.

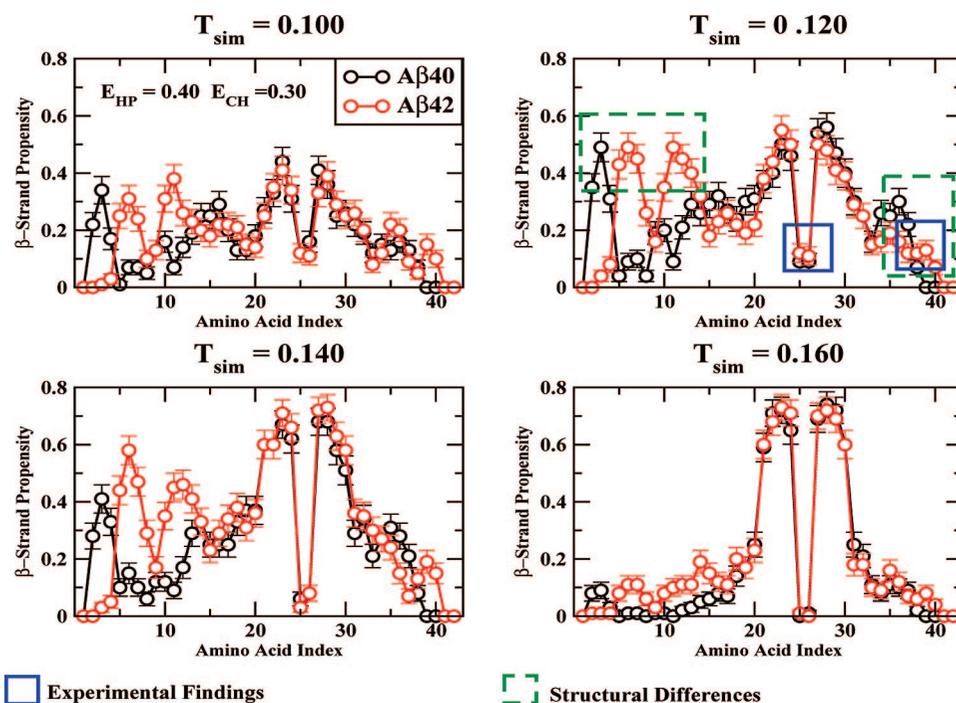


Figure 4. Amino acid-specific β -strand propensities for A β 40 (black) and A β 42 (red) at four different temperatures using the parameter set (0.40, 0.30). Differences in the termini between A β peptides are highlighted by the dashed-line boxes. The solid-line boxes show the turn/loop centered at G25-S26 and G37-G38 observed experimentally.^{28,31,32}

ences in $\langle\beta\rangle$ between the two alloforms. At $E_{\text{HP}} = 0.4$ (Fig. 2A-C), increase in E_{CH} from 0 to 0.3 resulted in a decrease of $\langle\beta\rangle$ at all temperatures in both peptides.

In the following, we used the interaction parameters that best matched the experimental data, $E_{\text{HP}} = 0.4$ and $E_{\text{CH}} = 0.3$, to characterize the structural differences in A β 40 and A β 42 monomer folding at different temperatures. The physiological temperature $T_{\text{real}} = 310$ K was found to correspond to the simulation temperature $T_{\text{sim}} = 0.124$.

3.2. A β 40 and A β 42 Folded Structures Differ. Fig. 3 shows “typical” folded structures of both peptides at four selected temperatures. We define “typical” as a conformation that possesses the average amount of β -strand structure that strongly increases with temperature. At a fixed temperature, a large variability in the conformational space of folded A β monomers has been observed in our own previous study³⁴ and by

others.^{16,33} With increasing temperatures, a larger number of β -strand-rich conformations were observed. At high temperatures, thermal fluctuations destroy any secondary structure and result in random-coil conformations. Similar conformational transitions in a mixture of monomers and dimers in aqueous solution were reported by Gursky and Aleshkov.¹³ To gain more detailed structural information, we calculated amino acid-specific β -strand propensities (Fig. 4) and constructed intramolecular contact maps. These maps show the pairwise amino acid interaction frequencies, thereby allowing identification of peptide regions contributing significantly to folding (Fig. 5).

Fig. 4 shows that all β -strand propensities were below 40% at $T_{\text{sim}} = 0.1$, increased with temperature, reached the highest values of up to 80% at $T_{\text{sim}} = 0.14$, and decreased at yet higher temperatures. At the physiological temperature $T_{\text{sim}} = 0.12$, the regions with the highest β -strand propensities were A2-F4 (A β 40

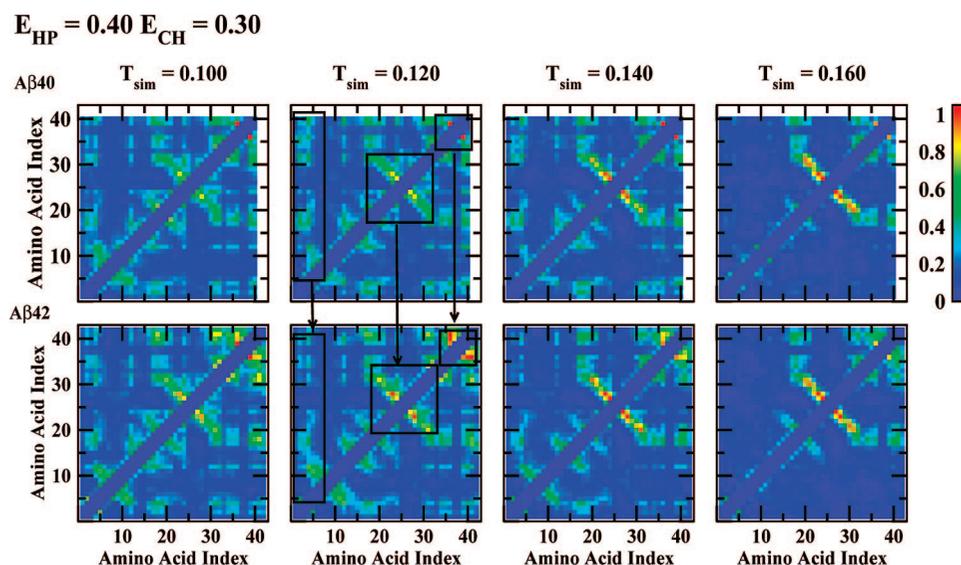


Figure 5. Intramolecular average contact maps of A β 40 (upper) and A β 42 peptides (lower) at different temperatures and $E_{HP} = 0.40$ and $E_{CH} = 0.30$. The axes are numbered according to amino acid position, where 1 is the N-terminus. The pairwise contact frequency is represented by color (see scale at right). The boxes within the maps of A β 40 and A β 42 at $T_{sim} = 0.120$ highlight the differences between these two peptides.

only), R5-D7 and Y10-V12 (A β 42 only), F21-V24, N27-G29, and the MHR (A β 40 and A β 42), and the CTR (A β 42 only). Fig. 5 shows that the largest number of contacts in both alloforms was observed *between* the CHC and MHR. This central folding region which was hypothesized by Lazo *et al.*²⁸ to nucleate the folding, was associated with a turn centered at G25-S26 that was bounded by extended strands at F21-V24 and N27-G29.

The contacts between the MHR and CTR were significantly stronger in A β 42 than in A β 40. In A β 42, the strength of these contacts surpassed that of the central folding region. These contacts were associated with a turn centered at G37-G38 in A β 42, but not in A β 40. The existence of a folded structure at the CTR of A β 42 is supported by a non-zero β -strand propensity ($\approx 10\%$). In contrast, the CTR of A β 40 displays zero β -strand propensity. The existence of this turn structure in A β 42 was observed initially by Urbanc *et al.*³⁰ and confirmed *in vitro* by several experimental groups.^{28,31,32}

The region A2-F4 had a high β -strand propensity in A β 40 but not in A β 42 (40% at $T_{sim} = 0.1$, 50% at $T_{sim} = 0.12$, and $>40\%$ at $T_{sim} = 0.14$). The number of contacts formed between the segment A2-F4 and other parts of the peptide also was larger in A β 40 than in A β 42 (Fig. 5). The segments R5-D7 and Y10-V12 exhibited increased β -strand propensities in A β 42 ($>30\%$ at $T_{sim} = 0.1$, $\approx 50\%$ at $T_{sim} = 0.12$, and $>40\%$ at $T_{sim} = 0.14$). These two segments formed a β -hairpin centered at S8-Y10 in A β 42. This hairpin occurs significantly less frequently in A β 40, in which the entire segment R5-Q15 shows a significantly smaller β -strand propensity ($\leq 20\%$) at all temperatures than does the equivalent segment in A β 42 (Fig. 4). Lim *et al.* reported temperature-induced changes at the N-terminal region of A β 40 and A β 42 that may be important for their amyloidogenic properties.¹⁴ However, the N-terminal (A2-Q15) structural differences between A β 40 and A β 42 were not observed so far.

We next calculated the average α -helix propensity, $\langle\alpha\rangle$, at each simulation temperature T_{sim} . At the physiological temperature, $T_{sim} = 0.12$, $\langle\alpha\rangle$ was 0.1% for A β 40 and 0% for A β 42. At lower temperatures, $\langle\alpha\rangle$ was 0% and 0.3%, respectively. At $T_{sim} = 0.1$, $\langle\alpha\rangle = 0.3\%$ in A β 40 and $\langle\alpha\rangle = 0.1\%$ in A β 42. At

temperatures above the physiological temperature, $\langle\alpha\rangle$ was 0% in both A β 40 and A β 42 (data not shown).

3.3. Effect of the Arctic (E²²→G) Mutation on A β Folding. We explored here the effects of the clinically relevant Arctic mutation⁵¹ on A β folding. *In vitro* studies have determined that [G22]A β 40 has a higher propensity to form protofibrils than does A β but that the overall rate of fibril formation remains constant.⁵¹ A recent study by Grant *et al.*²⁹ showed that the Arctic mutation significantly destabilized the turn structure in the central folding region A21-A30.

We used the optimal interaction parameters $E_{HP} = 0.4$ and $E_{CH} = 0.3$ in our simulations. Fig. 6A shows $\langle\beta\rangle$ over a wide temperature range for A β 40, A β 42, [G22]A β 40, and [G22]A β 42. The temperature dependence of $\langle\beta\rangle$ for Arctic peptides followed the same trend as A β . At low temperatures, $\langle\beta\rangle$ increased gradually until it reached a maximum at $T_{sim} = 0.14$. For $T_{sim} > 0.14$, $\langle\beta\rangle$ decreased.

As described above, $\langle\beta\rangle$ in A β increased with temperature in both alloforms and at $T_{sim} > 0.11$, the average β -strand propensity of A β 42, $\langle\beta\rangle_{42}$ surpassed the average β -strand propensity of A β 40, $\langle\beta\rangle_{40}$. In contrast, in the Arctic mutants in the same temperature range, $\langle\beta\rangle_{[G22]40} > \langle\beta\rangle_{[G22]42}$ (Fig. 6A). As shown in Fig. 6A, at $T_{sim} \in [0.11, 0.15]$, $\langle\beta\rangle$ of [G22]A β 40 (blue line with squares) was larger than that of A β 40 (black line with circles) by 3–5%, while $\langle\beta\rangle$ in [G22]A β 42 was 2–3% larger than in A β 42.

Important structural differences between [G22]A β 40 and [G22]A β 42 were observed in the calculated β -strand propensities per amino acid (Fig. 6B). At a physiological temperature, $T_{sim} = 0.12$, both alloforms showed similar β -strand propensities in the segment F21-V24 (50%), whereas the β -strand propensity of the segment N27-G29 was significantly larger in [G22]A β 40 (50%) than in [G22]A β 42 (35%). Overall, the β -strand propensities in the central folding region of A β 40, A β 42, and [G22]A β 40 were comparable. In the intramolecular contact map

(51) Nilsberth, C.; Westlind-Danielsson, A.; Eckman, C. B.; Condron, M. M.; Axelman, K.; Forsell, C.; Sten, C.; Luthman, J.; Teplow, D. B.; Younkin, S. G.; Naslund, J.; Lannfelt, L. *Nature Neuro.* **2001**, *4* (9), 887–893.

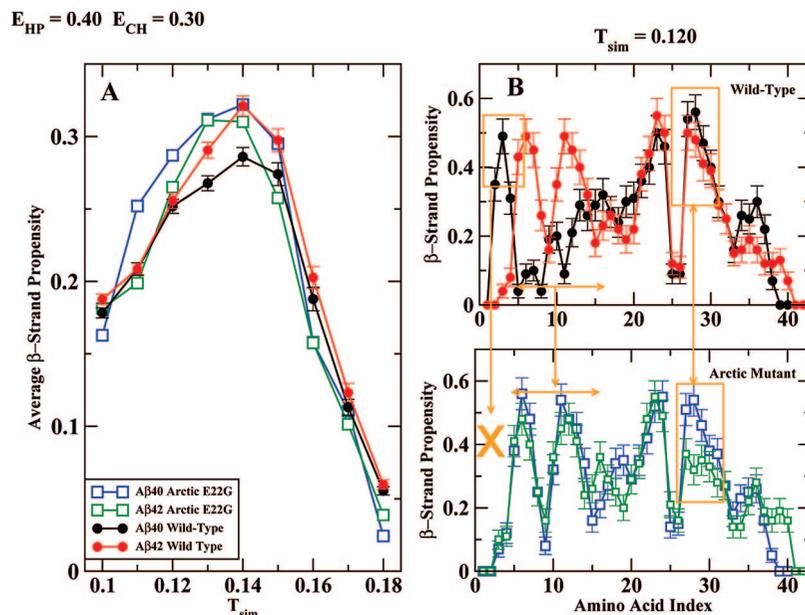


Figure 6. (A) The average β -strand propensity of [G22]A β (solid lines with empty squares; blue for [G22]A β 40 and green for [G22]A β 42) and A β (solid lines with filled circles; black for A β 40 and red for A β 42) at different temperatures. (B) Amino acid-specific β -strand propensity at $T_{sim} = 0.120$ for A β (top) and [G22]A β (bottom) peptides with parameters $E_{HP} = 0.40$ and $E_{CH} = 0.30$. The boxes indicate the structural differences between wild type and Arctic peptides. The yellow X indicates the substantial differences between the N-termini of the two peptides.

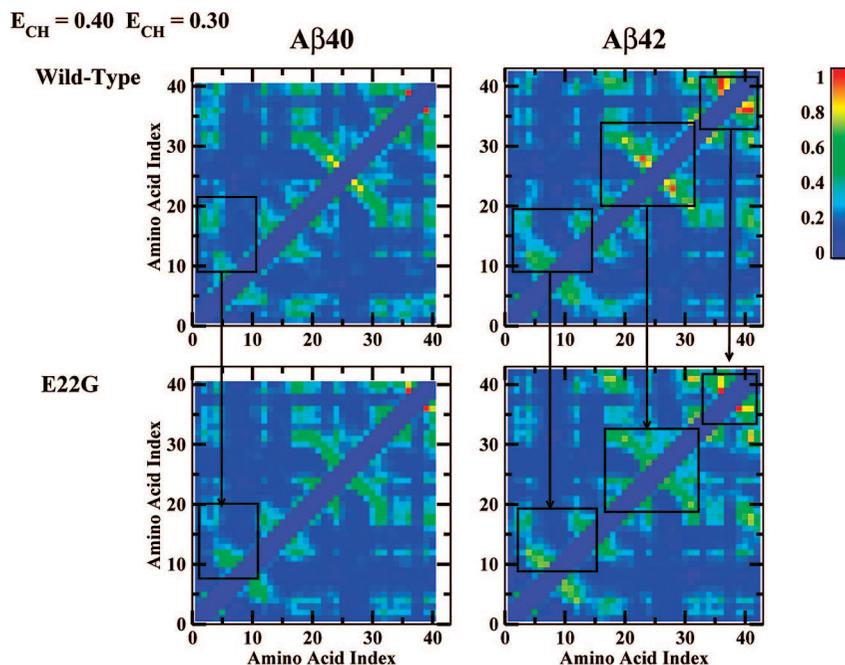


Figure 7. Intramolecular contact maps for A β (top) and [G22]A β (bottom) peptides with parameters $E_{HP} = 0.40$ and $E_{CH} = 0.30$ at $T_{sim} = 0.120$. The black boxes highlight differences in contact frequency between segments of wild type (top) and Arctic mutant (bottom) peptides.

corresponding to the Arctic mutants, decreased numbers of contacts were observed in the central folding region of both [G22]A β 40 and [G22]A β 42 relative to A β 40 and A β 42 (Fig. 7), suggesting that the Arctic mutation destabilizes the central folding region as also observed *in vitro* for the decapeptide A β (21–30) by Grant *et al.*²⁹

At the N-terminus, the β -strand propensity of the segment R5-Q15 (Fig. 6B, top and bottom) was similar in [G22]A β 40, [G22]A β 42, and A β 42, while in A β 40, no significant β -strand propensity was associated with this region. The β -strand

propensity of the segment A2-F4 was small (10%) and similar in both Arctic peptides, similar to A β 42 but in contrast to that same region in A β 40, where the β -strand propensity was 40–50%. The segments R5-D7 and Y10-V12 in [G22]A β 40 had β -strand propensities $>50\%$, compared to only slightly reduced propensity ($\approx 47\%$) in [G22]A β 42. In both Arctic peptides, as well as in A β 42, these two segments form a β -hairpin centered at S8-Y10.

In [G22]A β 42, the β -strand propensity of the CTR was 20% higher than that in A β 42, however, the intramolecular contact map shows a slightly decreased number of contacts in this region, suggesting that the Arctic mutation induced a confor-

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Table 2. Hydrogen Bonds Appearing Most Frequently in $A\beta$ and $[G22]A\beta$ peptides^a

segment	HB pair	$A\beta 40$	$[G22]A\beta 40$	$A\beta 42$	$[G22]A\beta 42$
TR1	F20:D23	5 \pm 0.62	10 \pm 1.27	4 \pm 0.49	7 \pm 0.88
	E22:G29	9 \pm 1.14	3 \pm 0.35	10 \pm 1.27	5 \pm 0.62
	V24:N27	31 \pm 3.69	33 \pm 3.89	31 \pm 3.69	21 \pm 2.60
TR2	V36:V39	11 \pm 1.40	12 \pm 1.52	5 \pm 0.62	6 \pm 0.75
NTR	R5:S8	11 \pm 1.40	3 \pm 0.35	2 \pm 0.22	0
	R5:V12	1 \pm 0.10	4 \pm 0.49	4 \pm 0.49	10 \pm 1.27
	D7:Y10	3 \pm 0.35	20 \pm 2.48	14 \pm 1.77	20 \pm 2.48
	S8:E11	1 \pm 0.10	13 \pm 1.65	19 \pm 2.37	13 \pm 1.65
	H13:K16	14 \pm 1.77	15 \pm 1.89	8 \pm 1.02	8 \pm 1.02

^a The numbers are percent (%) occurrence \pm the standard errors.

mational change in the CTR from a more collapsed into a more extended structure. The turn structure centered at G37-G38 was observed in $[G22]A\beta 42$ but not in $[G22]A\beta 40$ (data not shown). $[G22]A\beta 40$ did not show any β -strand propensity in the CTR region (Fig. 6B, bottom). Consistent with this result, the CTR of $[G22]A\beta 42$ had a larger number of contacts with the MHR (Fig. 7, right column), relative to $A\beta 42$. In the MHR, both Arctic peptides exhibited similar β -strand propensity (>20%). Here, we observed that the MHR of $[G22]A\beta 42$ had higher β -strand propensity than $A\beta 42$. Comparing the intramolecular contact maps of $[G22]A\beta$ and $A\beta$ at a physiological temperature $T_{sim} = 0.120$, we found an increased number of contacts between the MHR and CTR in $[G22]A\beta 42$ relative to $[G22]A\beta 40$. $[G22]A\beta 40$ had less contacts between the N-terminus and the CHC relative to $A\beta 40$ (Fig. 7).

3.4. The Role of Hydrogen Bonding in $A\beta$ Folding. We examined the backbone hydrogen bonds formed in $A\beta$ and $[G22]A\beta$ at the physiological temperature $T_{sim} = 0.120$. We determined the percentage of hydrogen bonds present in three important segments: F20-I31 (central folding region TR1), V36-V39 (C-terminal folding region TR2), and R5-K16 (N-terminal folding region, NTR). The hydrogen bond formation propensity in these segments was lower than suggested by the β -strand propensities per amino acid (Fig. 6B). The most frequent backbone hydrogen bonds are listed in Table 2.

In all four peptides, the central folding region TR1 was associated with the highest hydrogen bond propensity. In $A\beta 40$, the hydrogen bonds F20:D23 and E22:G29 appeared in 5% and 9% conformations, respectively, and the hydrogen bond V24:N27 appeared in 31% conformations. In $[G22]A\beta 40$, the hydrogen bond F20:D23 appeared in 10% of conformations while the propensity of the hydrogen bond E22:G29 decreased to 3%. The hydrogen bond V24:N27 in $[G22]A\beta 40$ had an increased frequency of 33% with respect to the wild type (21%). In $A\beta 42$, the hydrogen bond F20:D23 had low hydrogen bond propensities of 4% while E22:G29 and V24:N27 had propensities of 10% and 31%, respectively. These propensities decreased in $[G22]A\beta 42$ to 7%, 5%, and 21%.

The hydrogen bond in the TR2 region V36:V39 was formed with 11% propensity in $A\beta 40$ and with 5% in $A\beta 42$ conformations. In $[G22]A\beta 40$ and $[G22]A\beta 42$, the TR2 showed an increase 12% and 6%, respectively.

In the N-terminal folding region NTR, there were five relevant hydrogen bonds: R5:S8, R5:V12, D7:Y10, S8:E11, and H13:K16. In $A\beta 40$, the backbone hydrogen bonds R5:S8 and H13:K16 were present with the highest propensities at 11% and 14%, respectively, while R5:V12 (1%), D7:Y10 (3%), and S8:E11

(1%) were present with low propensities. In $A\beta 42$ the hydrogen bonds with the highest propensities D7:Y10 with 14% and S8:E11 with 19%. R5:S8, R5:V12, and H13:K16 had low propensities of 2%, 4%, and 8%, respectively. The Arctic peptide $[G22]A\beta 40$ was characterized by hydrogen bonds D7:Y10 with 20%, S8:E11 with 13%, and H13:K16 with 15%, while R5:S8 and R5:V12 ended with 3% and 4%, respectively. In $[G22]A\beta 42$ only the hydrogen bonds R5:V12, D7:Y10, and S8:E11 were present, with 10%, 20%, and 13% propensities, respectively. Here, R5:S8 was absent and H13:K16 remained with propensity of 8%. These results indicate that the Arctic mutation increased the propensity for backbone hydrogen bond formation with respect to wild type peptides. However, the pattern of the backbone hydrogen bonds in $[G22]A\beta 40$ and $[G22]A\beta 42$ was consistent with a β -hairpin structure at R5:Q15 similar to the one in $A\beta 42$.

4. Conclusions

In this paper we examined folding of full-length $A\beta 40$ and $A\beta 42$, and their Arctic mutants, using DMD combined with a four-bead protein model and implicit solvent interactions. The temperature-induced conformational transitions obtained *in silico* were consistent with *in vitro* experiments that showed conformational transitions from a collapsed coil at low temperatures to a β -strand-rich extended conformations at higher temperatures.¹³ Consistent with the CD measurements by Lim *et al.*,¹⁴ we observed a faster increase of the average amount of β -strand in $A\beta 42$ relative to $A\beta 40$. Our model predicted the central folding region centered at G25-S26 in both $A\beta 40$ and $A\beta 42$, and the C-terminal folded structure centered at G37-G38 in only $A\beta 42$, in agreement with *in vitro* findings of several groups.^{28,31,32}

Existing experimental¹⁰ and all-atom MD^{18,52,53} studies on the fragment $A\beta(10-35)$ are consistent with our observation of the collapsed coil monomer structure dominated by loops, bends, and turns at low temperatures. Our results demonstrate that small changes in the primary structure can have significant impact on folding, suggesting that full-length $A\beta 40$ and $A\beta 42$ and their mutants need to be examined to gain insights into pathological differences between the alloforms. The present study extends our understanding of how the additional amino acids I⁴¹ and A⁴² at the CTR of $A\beta 42$ significantly impact full-length $A\beta$ folding. The more hydrophobic CTR of $A\beta 42$ is known to facilitate structural changes resulting in different oligomerization pathways and pathologies of $A\beta 40$ and $A\beta 42$. Bitan *et al.*⁷ reported that $A\beta 40$ forms smaller oligomers (from dimers to tetramers) while $A\beta 42$ forms larger oligomers (pentamers/hexamers) and their multiples. Our studies demonstrate that structural differences between $A\beta 40$ and $A\beta 42$ that mediate this distinct oligomerization behavior already exist in the isolated peptide monomers. The structural difference between the two alloforms at the C-terminus, a turn centered at G37-G38 in $A\beta 42$ but not in $A\beta 40$, seems to be a direct consequence of two additional hydrophobic amino acids at the C-terminus of $A\beta 42$. However, the folding differences between $A\beta 40$ and $A\beta 42$ at the N-termini, the β -strand at A2-F4 in $A\beta 40$ but not in $A\beta 42$ as well as a β -hairpin centered at S8-Y10 in $A\beta 42$ but not in $A\beta 40$, were surprising. This structural difference at the N-terminus of $A\beta 40$ versus $A\beta 42$ has not been reported experimentally, to our knowledge. Hou *et al.*⁵⁴ studied $A\beta$ with reduced and oxidized M35 and showed that a turn or bend-like structure at D7-E11 in oxidized peptides was less frequent than

(53) Baumketner, A.; Shea, J. E. *J. Mol. Biol.* **2007**, *366* (1), 275–285.

in the redox peptides. As the structure at the N-terminal region was suggested to impact the amyloidogenic properties of A β ,¹⁴ the structural difference between the two alloforms reported here might provide a new clue to understanding oligomerization differences between A β 40 and A β 42.

Examining folding of the two Arctic mutants, [G22]A β 40 and [G22]A β 42, we showed that the presence of Gly²² disrupts contacts close to position 22, and importantly, also at the N-terminus of A β 40, resulting in a [G22]A β 40 conformer that is structurally similar to A β 42 in this region. The average amount of β -strand formed at a physiological temperature in [G22]A β 40 is higher than in [G22]A β 42. Our observation that the substitution E22G increases the propensity for β -strand formation is not surprising. This substitution not only reduces the overall negative charge of the Arctic peptides but also, through the G²² substituent, increases the local backbone flexibility needed for a collective hydrogen bond ordering into a β -strand. In our study, the Arctic mutation did not significantly alter the structure of A β 42. Instead, the major effect appeared to be on the secondary structure of A β 40, which was more "A β 42-like". The increased level of regular secondary structure in A β 40 is likely to affect its oligomerization pathway, as observed *in vitro* and *in vivo*.^{4,55,56}

Several studies have reported that the Arctic mutation significantly increases the protofibril formation rate relative to the wild type.^{51,57} Our simulation result for [G22]A β 40 shows an increase in the average β -strand propensity when compared

to the wild type, which is consistent with these experimental findings. Dahlgren *et al.*⁴ developed two aggregation protocols for the production of stable oligomeric or fibrillar preparations of A β 42 and its Dutch (E²²→Q) and Arctic mutants. In terms of neurotoxicity, the wild type and the mutants were not significantly different, but they observed extensive protofibril and fibril formation by the mutant peptides. Experimental studies by Murakami *et al.* demonstrated that the mutations at positions 22 and 23 played a significant role in A β assembly.⁵⁸ Specifically, the Arctic mutant showed a 50% increase in the average β -strand content in A β oligomers. Whalen *et al.* found that Arctic A β had an increased rate of assembly into oligomers and that these oligomers were more toxic to neurons in culture than were wild type oligomers.⁵⁹ These experimental findings on Arctic peptides are consistent with the increased β -strand propensity in folded Arctic monomers relative to their wild type counterparts. Take together with other data extant, our results suggest that small changes in the primary structure of A β not only may affect peptide monomer folding itself but also the rate of formation, structure, and neurotoxic properties of higher order assemblies.

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