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Tranilast Binds to A β Monomers and Promotes A β Fibrillation

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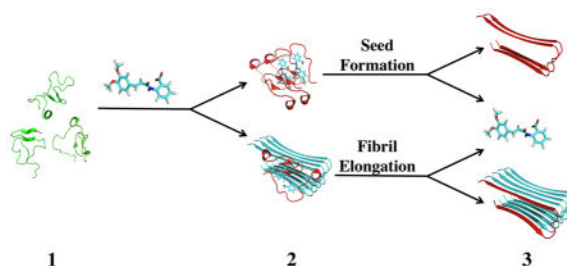
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Abstract



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Supporting Information

The solubility of tranilast under the same buffer conditions used for the CSP titrations was confirmed by measuring a proportional increase in ¹H NMR to increasing tranilast concentration. Overlays of spectra from the CSP titrations are also presented, along with the fit curves for the 10 residues in each peptide that were used to determine *K_d* values. This material is available free of charge via the Internet at <http://pubs.acs.org>.

The antiallergy and potential anticancer drug tranilast has been patented for treating Alzheimer's disease (AD), in which amyloid β -protein ($A\beta$) plays a key pathogenic role. We used solution NMR to determine that tranilast binds to $A\beta$ 40 monomers with $\sim 300 \mu\text{M}$ affinity. Remarkably, tranilast increases $A\beta$ 40 fibrillation more than 20-fold in the thioflavin T assay at a 1:1 molar ratio, as well as significantly reducing the lag time. Tranilast likely promotes fibrillation by shifting $A\beta$ monomer conformations to those capable of seed formation and fibril elongation. Molecular docking results qualitatively agree with NMR chemical shift perturbation, which together indicate that hydrophobic interactions are the major driving force of the $A\beta$ -tranilast interaction. These data suggest that AD may be a potential complication for tranilast usage in elderly patients.

Alzheimer's disease (AD) accounts for 60–80% of all dementia cases, affecting ~ 5.3 million people in the United States alone.¹ AD is pathologically characterized by neurofibrillary tangles and senile plaques. The major component of senile plaques is aggregated, fibrillar, insoluble $A\beta$. $A\beta$ is a cleavage product of the amyloid precursor protein (APP). First, β -secretase cleaves APP at what will be the N-terminus of $A\beta$, followed by γ -secretase cleavage to generate the C-terminus of $A\beta$. The most common forms of $A\beta$ are 40 and 42 amino acid residues in length and are called $A\beta$ 40 and $A\beta$ 42, respectively. $A\beta$ 42 aggregates much faster than $A\beta$ 40 and is more toxic. Though $A\beta$ is considered benign in its monomeric form,^{2–4} $A\beta$ fibrils,^{5–7} protofibrils,⁸ and various oligomers including dimers,⁹ trimers,¹⁰ and 12-mers^{11,12} are toxic, and their presence in the AD brain correlates with the clinical manifestation of dementia.^{13–15}

Tranilast is a small molecule currently marketed in Korea and Japan as an antiallergy drug. It is being investigated for a wide variety of other uses,¹⁶ from reducing the pathological fibrosis associated with myocardial infarctions,¹⁷ to reducing human breast cancer cell migration and colony formation.¹⁸ The drug is particularly promising as a potential anticancer agent¹⁹ due to its antiproliferative effects in prostate,²⁰ breast,²¹ and pancreatic cancers.²² Usage of tranilast and its derivatives in the treatment of neurodegenerative conditions, including AD, has been patented.²³ Oral administration of tranilast inhibited the growth of rat gliomas *in vivo*, suggesting tranilast can cross the blood–brain barrier.²⁴ Tranilast also had an antiapoptotic effect on neurons and increased neurogenesis, both in a dose-dependent manner.²³ Given tranilast's potential use in the treatment for AD, we decided to explore its possible interaction with $A\beta$.

We combined NMR, aggregation assays, and docking simulations to study the tranilast– $A\beta$ interaction in a multidisciplinary approach. First, NMR spectroscopy was used to study tranilast's interaction with monomeric $A\beta$ and to map tranilast's binding site on the $A\beta$ monomer with residue-specific resolution. Second, ThT fluorescence and dot blots with the antioligomer antibody A11 determined tranilast's effect on $A\beta$ self-assembly. Fibril morphology was confirmed using atomic force microscopy (AFM). Finally, molecular docking of tranilast to REMD-simulated structures of $A\beta$ was applied to gain further insight into the interaction between tranilast and $A\beta$.

MATERIALS AND METHODS

NMR Experiments

NMR samples were made from ^{15}N -labeled, HFIP-treated A β 40 or A β 42 (rPeptide, Bogart, GA, USA). Peptide films were resuspended in 1 mL of 10 mM NaOH. Aliquots of 125 μL were then added to 20 mM potassium phosphate, pH 7.3, and 10% D $_2$ O to prepare initial NMR samples for titration. Tranilast was purchased from *Cayman Chemical* and solubilized in either DMSO or DMSO- d_6 to create a stock solution of 20 mg/mL. Chemical shift perturbation (CSP) was monitored using ^{15}N - ^1H -HSQC spectra at increasing molar ratios of tranilast to A β . A control sample of DMSO without tranilast was also titrated into A β samples and CSP due to the addition of DMSO was subtracted from CSP observed during tranilast titrations. CSP was calculated as $\delta = ((10 \delta_{\text{H}})^2 + (\delta_{\text{N}})^2)^{1/2}$. All NMR experiments were performed on an 800 or 600 MHz spectrometer equipped with a cryogenic probe at 277 K, to minimize the aggregation of A β . This protocol of A β sample preparation and NMR setup ensures that NMR signals are from A β monomers.^{25,26} CSP values were fitted to the following equation to determine K_{d} for the A β /tranilast interaction:

$$\Delta\delta_{\text{obs}} = \Delta\delta_{\text{max}} \left\{ ([\text{P}]_{\text{t}} + [\text{L}]_{\text{t}} + K_{\text{d}}) - \sqrt{([\text{P}]_{\text{t}} + [\text{L}]_{\text{t}} + K_{\text{d}})^2 - 4[\text{P}]_{\text{t}}[\text{L}]_{\text{t}}} \right\} / 2[\text{P}]_{\text{t}}$$

where δ_{obs} is observed CSP of A β , δ_{max} is the CSP of A β in the bound state, $[\text{P}]_{\text{t}}$ is total A β peptide concentration, $[\text{L}]_{\text{t}}$ is total ligand concentration, and K_{d} is the disassociation constant.

Thioflavin T (ThT) Assay and Dot Blot

For aggregation experiments, samples of HFIP-treated A β 40 or A β 42 first were resuspended to 1 mg/mL in DMSO, then diluted in PBS to a final concentration of 20 μM and incubated at 37 $^{\circ}\text{C}$. ThT assays were performed in triplicate to measure fibril formation using 50 μL of incubated sample and 350 μL of 10 μM ThT in 50 mM glycine, pH 8.0. Samples were excited at 440 nm and emission at 485 nm was measured using a Hitachi F-4500 fluorescence spectrophotometer (Hitachi High-Technologies Co, Tokyo, Japan). Dot blots were performed using the oligomer-specific antibody A11 (Invitrogen, Carlsbad, CA, USA) and the WesternBreeze Chemiluminescent kit (Invitrogen, Carlsbad, CA, USA). Blots were visualized on a ChemiDoc MP system (Bio-Rad, Hercules, CA, USA).

Atomic Force Microscopy (AFM)

Aggregated samples of A β were prepared in the same manner as for the ThT assay. For each sample, 20 μL was placed on a mica surface for adsorption for 5 min. Nonadsorbed protein was washed away with abundant water. Three-dimensional measurements at the nanometer scale were collected in air using the tapping mode technique with an MFP-3D atomic force microscope (Asylum Research, Santa Barbara, CA, USA) and standard Si cantilevers (AC240TS, Olympus America Inc., Center Valley, PA, USA). Images were then analyzed with IGOR Pro 6 (WaveMetrics, Inc., Lake Oswego, OR, USA).

Molecular Docking

Tranilast was docked onto previously published centroid structures from all-atom REMD simulations of A β 40.²⁷ The structure of tranilast was obtained from the Pub-Chem database (CID: 5282230)²⁸ and subsequently minimized in vacuo with MOE²⁹ by using the MMFF94x force field (a modified version of MMFF94s³⁰), stopping at a gradient of 10⁻³. This ligand structure was blindly docked onto each A β centroid MOE's docking feature²⁹ with the entire centroid as the receptor structure. Placement was done using the triangle matcher algorithm. The top 30 best placements (according to London dG scores) were refined with minimization (stopping at a gradient 10⁻³) using the OPLS-AA force field with Born solvation. The top scoring pose (after rescoring with the London dG algorithm) was then retained. Residue-indexed surface area of contact between A β and tranilast for each of the MOE docks were calculated using LPC software.³¹

RESULTS

Chemical Shift Perturbation

NMR titrations of tranilast into ¹⁵N-labeled A β 40 or A β 42 yielded residue-specific chemical shift perturbation (CSP) (Figure 1). The greatest CSP was observed at the C-terminus of both A β 40 and A β 42. Relatively large CSP was also observed in regions comprising residues 11–21 and 30–37 in A β 40, and to a lesser extent, in similar regions of A β 42. Largest CSP are observed for residues E11, V18, F19, F20, I31, I32, G33, M35, V36, and V40. These residues are largely nonpolar, indicating that hydrophobic interaction may play a key role in tranilast binding to A β . CSP in A β 40 was found to be substantially greater than in A β 42. ¹H and ¹⁵N perturbations for tranilast at 0–8 molar ratio equivalents were then fit to determine the K_d values for the tranilast–A β interaction. Because of the low affinity of binding between A β and tranilast and limitation of tranilast solubility in aqueous solution, titrating A β to near complete saturation was not possible. For the A β 40–tranilast interaction, CSP fittings for residues I31, I32, and V36, where the titration is closer to saturation and there was apparent curvature in the fitted titration curve, were used to calculate an average K_d 0.31 \pm 0.13 mM. For A β 42–tranilast interaction, due to the lower affinity, none of the residues were titrated close to saturation. But for a comparison with A β 40, the average K_d of the three residues in A β 42 with lowest apparent K_d (F4, Y10, and G33) was 2.4 \pm 0.2 mM, still significantly higher than the measured K_d for A β 40.

Aggregation Assays and AFM

To further confirm the A β –tranilast interaction and to probe how tranilast affects A β self-assembly, we carried out ThT assays to study A β β -sheet formation, and dot blots with antibody A11 to study A β oligomer formation. AFM was used to confirm aggregate morphology.

Despite the measured millimolar affinity of tranilast to A β 40 and A β 42, there was a significant effect of tranilast binding on A β fibrillation. ThT assays of A β 40 and A β 42 both showed significant increases in fibril formation with the addition of tranilast (Figure 2). There was nearly no increase in ThT fluorescence for A β 40 in the absence of tranilast, whereas the addition of 1 equiv of tranilast caused more than a 20-fold increase in maximum

ThT signal (Figure 2A). This increase was dose-dependent up to a 5:1 molar ratio, the highest ratio tested. There was also a significant decrease in the lag phase of fibril formation between 1:1 and 3:1, as well as between 3:1 and 5:1 molar ratios of tranilast to A β 40 (Figure 2A). This decrease in the lag phase suggests tranilast not only increased the overall amount of fibrils formed but also promoted formation of fibril seeds. The effect on A β 42 fibril formation was less pronounced (Figure 2B), with only a ~1.7-fold increase in maximum ThT signal at a molar ratio of 5:1, possibly due to the greater affinity of tranilast for A β 40 and the faster aggregation propensity of A β 42 on its own.

To confirm that the increase in ThT signal was due to increased fibril formation, we observed A β samples with AFM. These samples were prepared under the same conditions as the samples for the ThT assay. No fibrillar aggregates were observed in the initial A β samples, both with and without 100 μ M tranilast. Additionally, fibrils were not observed in the A β 40 without tranilast at any time point, consistent with the very small change in ThT signal. After incubation at 37 °C for 12 h, fibrils formed in both A β 42 samples. To a lesser extent, fibrils formed in the A β 40 sample with tranilast. After 72 h, the time where ThT signal plateaued fibrils were seen to form in both A β 42 samples and A β 40 with tranilast, a result consistent with the significant increases in ThT signal observed for these samples.

To determine if tranilast was incorporated into the A β fibrils, we used ^1H NMR on disaggregated fibril samples formed in the presence of tranilast. Fibril samples were first centrifuged. The supernatant was then decanted, leaving only precipitated fibrils, which were washed with PBS two times and then resuspended in disaggregation buffer (8 M urea, 20 mM potassium phosphate, pH 7.3). ^1H NMR spectra were then recorded of the disaggregated samples to determine the presence of tranilast signal. ^1H NMR showed no tranilast signal in the disaggregated fibril samples, while there was clear signal for disaggregated A β monomers (data not shown). Therefore, tranilast was not incorporated into A β fibrils formed in its presence.

A11 dot blots were used to study A β oligomer formation in the absence or presence of tranilast (Figure 4). There was no noticeable difference in oligomer formation between the samples containing tranilast and control samples, suggesting that tranilast binding did not affect A β 40 or A β 42 A11-active oligomerization.

Molecular Docking Studies

To further probe the binding modes of tranilast's interaction with A β , we employed molecular docking with centroid structures of A β 40 derived from replica exchange molecular dynamics (REMD) in explicit water that have been validated by NMR-observed constraints.²⁷ The many structures from these simulations were grouped into clusters comprising structures within a 3 Å RMSD cutoff for A β 40.²⁷ These clusters were then represented by a centroid structure, which had the lowest RMSD to all members within the cluster. Using MOE, we docked tranilast to two centroid structures representing ~30% of all simulated A β 40 structures (Figure 5).

We found qualitative agreement between the binding sites determined by NMR and *in silico* docking. Residues Y10, E11, L17, V18, F19, G29, A30, I31, I32, G33, L34, M35, V36, and

G37 are in direct contact with tranilast, with atoms within 5 Å of tranilast (Figure 5), as calculated by LPC software.³¹ These residues all exhibited amide CSP greater than 0.3 ppm in the presence of 6 mol equiv of tranilast (Figure 1). Among the 12 residues with largest CSP, indicated in Figure 1B, 10 could be explained by their proximity to tranilast in Figure 5. Significant CSP of other two residues, F20 and V40, could not be explained by docking results.

Docking revealed key interactions that drive A β -tranilast binding (Figure 5). The side chain of I32 interacted with the benzoic acid ring of tranilast, while the side chain of I31 showed a similar interaction with the other aromatic ring of tranilast. There was a π -H interaction between the aromatic ring of F19 and the amide group of tranilast. In addition, there was bifurcated hydrogen bonding between the carboxylic acid group of tranilast to its own amide group and to the amide of A30.

DISCUSSION

Implication for Clinical Use of Tranilast in Patients at Risk for AD

The patent for tranilast's use in neuro-degenerative diseases is based on its antiapoptotic and pro-neurogenesis effects regardless of the presence of A β .²³ Given its potential use in the treatment of neurodegenerative diseases and in other diseases commonly affecting elderly patients (e.g., cancer^{18-21,32-44}), the characterization of tranilast's interaction with A β is important. The toxic effect of A β fibrils in AD patients is well documented.⁴⁵ An increase in fibrilization of A β 40 in particular due to tranilast could lead to elevated cerebral amyloid angiopathy and become a devastating side-effect. We showed that there is a ~20-fold increase in A β fibril formation in the presence of an equimolar amount of tranilast, as well as a significant increase in fibril seeding. Thus, in treating elderly patients with tranilast, new signs or the aggravation of dementia need to be carefully monitored. Ideally, a statistical analysis in elderly patient population should be carried out to ascertain whether tranilast indeed affects the onset and progression of AD.

Mechanism of Tranilast Promotion of A β Fibrillation

Although tranilast binds A β monomers with low affinity, it significantly increases A β 40 fibrillation. These ~millimolar binding affinities of tranilast to both A β 40 and 42 monomers are in a range that is traditionally considered too weak for effective drug interaction. However, taking into account that IDPs, such as A β , sample a large number of conformations, drugs like tranilast may only bind certain populations of conformations with relatively high affinity. The observed binding affinities reflect binding to all monomer conformations, including those that do not bind, and thus may be deceptively low. These observed low binding affinities also do not necessarily correlate with the extent of the effect of binding on aggregation, as is the case with tranilast and A β 40. Alternatively, tranilast may bind to most A β monomer conformations with low affinity, although this is unlikely given its significant effects on fibrillation. Because tranilast is not present in the fibrils and does not affect A11-reactive oligomer formation, the effect on fibrillation likely stems from binding of tranilast to A β monomer conformations that favor fibril formation, shifting the thermodynamic equilibrium of sampled conformations.

Presumably, tranilast binds to monomer conformations capable of docking onto growing fibrils, but not to actual fibril conformations, the two of which are thought to be different in the dock-and-lock scheme of A β fibril growth.^{46–49} We propose the mechanisms depicted in Figure 6 for tranilast promotion of A β fibril formation. A β monomers exist in a dynamic equilibrium sampling multiple conformations (step 1). Tranilast binds to A β monomers and stabilizes conformations compatible of binding to pre-existing fibrillar aggregates or creating new fibril seeds. These monomers then dock onto growing fibrils or to each other to create new fibril seeds (step 2). This docking leads to a conformational change that causes the monomer to lock onto the fibril or new seed, releasing tranilast for binding to another A β monomer (step 3). In this model, tranilast acts by promoting fibril elongation or seed formation with one tranilast molecule able to promote the incorporation of many A β monomers into the aggregates. This model can explain how despite having low binding affinity, tranilast has a large effect on A β fibril seeding and elongation.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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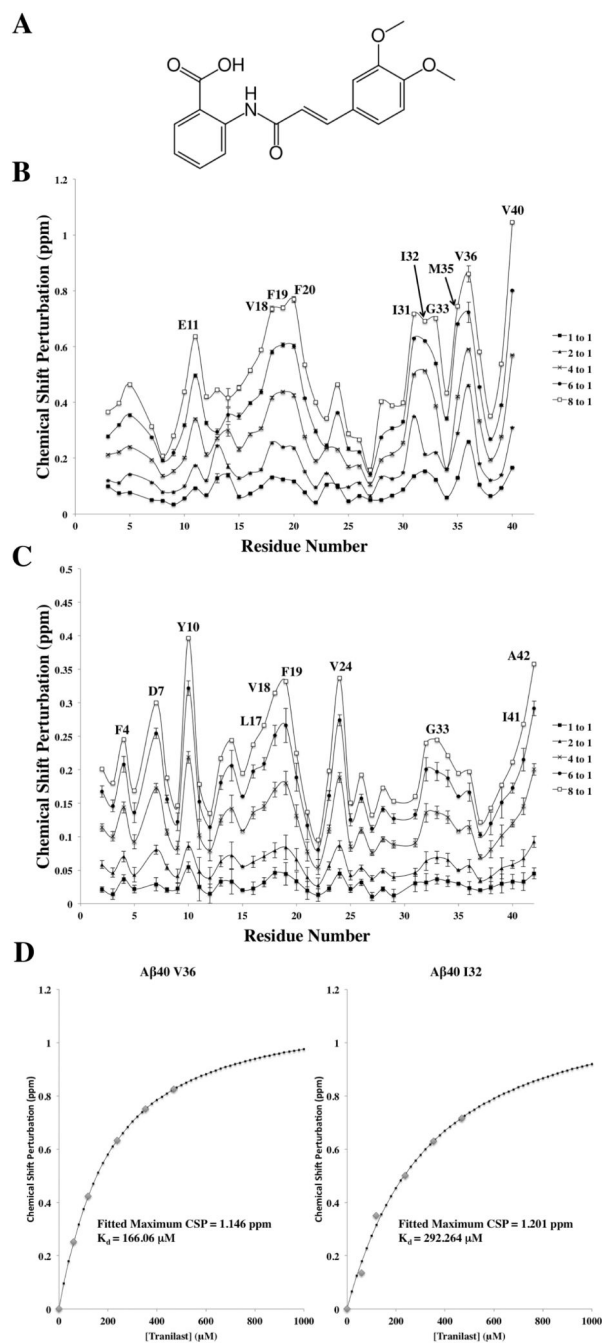


Figure 1.

NMR chemical shift perturbations due to tranilast binding to A β 40 or A β 42. (A) A 2D representation of tranilast, which was titrated from 1 to 8 mol equiv of (B) A β 40 and (C) A β 42. CSP was calculated as $\delta = ((10 \delta_H)^2 + (\delta_N)^2)^{1/2}$, where δ_H and δ_N are CSPs of amide proton and nitrogen, respectively. The 10 residues with the largest CSP in each peptide are labeled. A β 40 CSP due to tranilast was much greater than that of A β 42, suggesting greater affinity for A β 40. (D) Examples of fitted K_d curves calculated using CSP.

Samples of A β monomer were prepared at 60 μ M in 20 mM potassium phosphate (pH 7.3) and 10% D₂O. All NMR experiments were carried out at a temperature of 277 K.

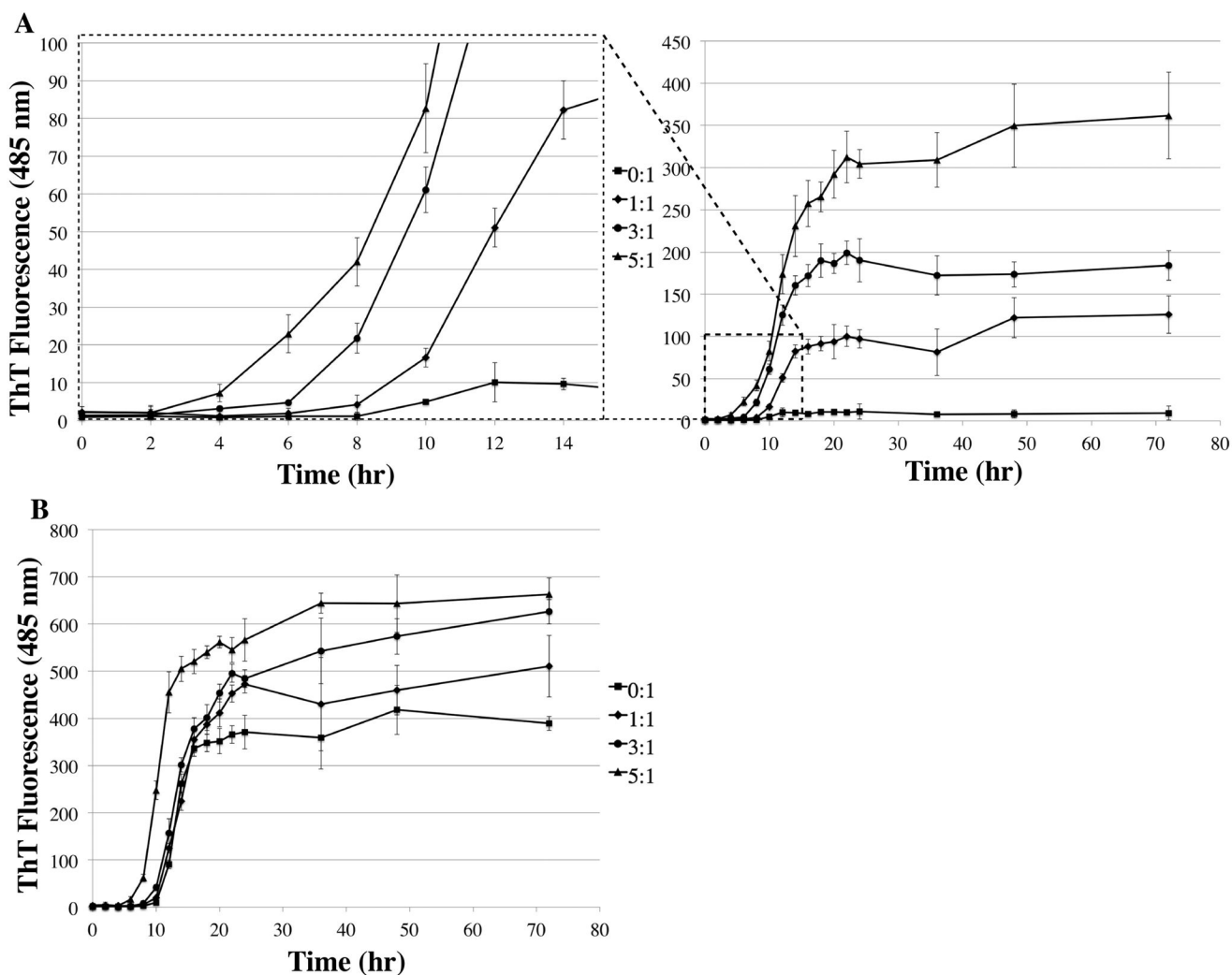


Figure 2. Tranilast promotes $A\beta$ fibrillation. ThT assay measuring the effect of varying molar ratios (0:1, 1:1, 3:1, 5:1) of tranilast to $A\beta$ on fibril formation. (A) Tranilast significantly increased $A\beta_{40}$ maximum fibrillation in a dose-dependent manner. There was also a significant decrease in the lag phase between 1:1 and 3:1, and 3:1 and 5:1 molar ratios of tranilast to $A\beta_{40}$. (B) Tranilast significantly increased $A\beta_{42}$ fibrillation, though the effect was less pronounced. The assay was carried out in triplicate with $20 \mu\text{M}$ $A\beta$ in PBS + 5% DMSO, incubated at 37°C without agitation. Error bars represent ± 1 standard deviation.

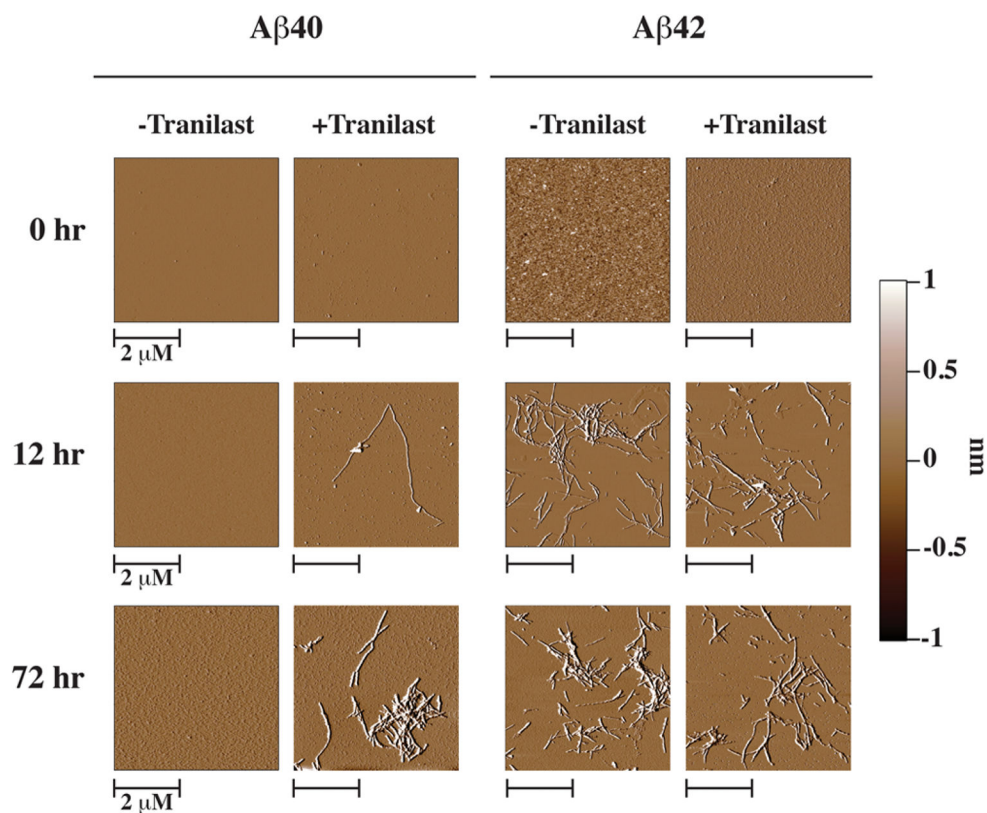


Figure 3.

AFM images of Aβ40 and 42 samples incubated with either 0:1 (-Tranilast) or 5:1 (+Tranilast) molar ratios of tranilast to Aβ. No fibrils were observed at 0 h for any sample. After 12 h, fibrils were observed in both Aβ42 samples, and only a sparse amount of fibrils were observed in the Aβ40 sample with tranilast. After 72 h of incubation at 37 °C, more fibrils were observed in the Aβ40 sample containing tranilast and in both Aβ42 samples. No fibrils were observed in the Aβ40 without tranilast at any point. AFM samples were prepared from 20 μM Aβ in PBS + 5% DMSO, incubated at 310 K without agitation, in either the presence or absence of 100 μM tranilast.

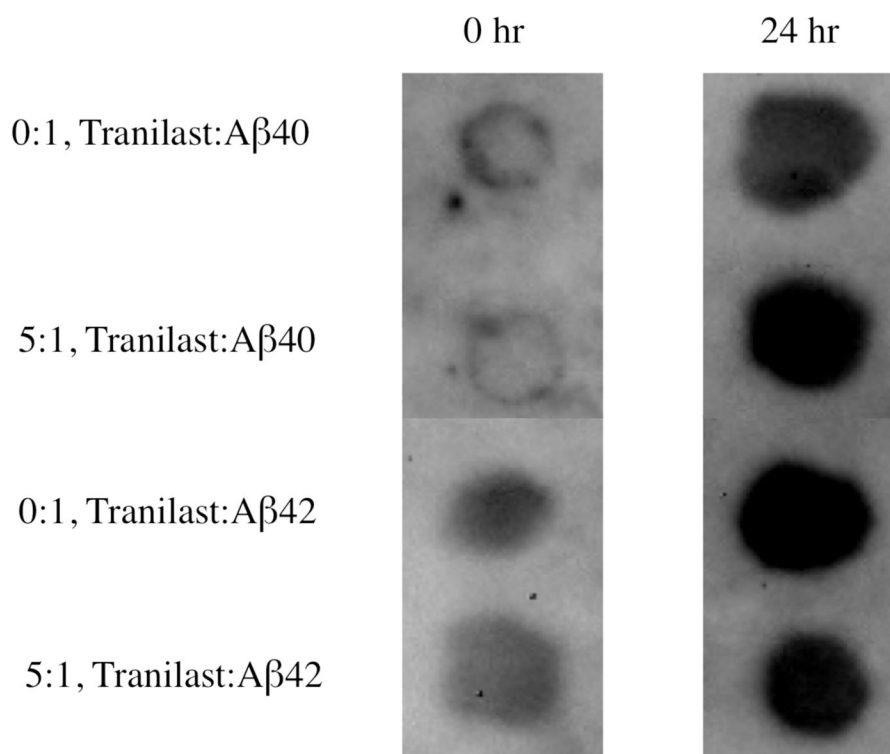


Figure 4.

$A\beta$ dot blots with oligomer-specific antibody A11 in the absence or presence of tranilast. At a 5:1 molar ratio of tranilast to $A\beta$, after 24 h of incubation at room temperature without agitation, there is no significant difference in oligomer formation between samples containing tranilast and control samples. Samples consisted of 20 μ M $A\beta$ in PBS + 5% DMSO.

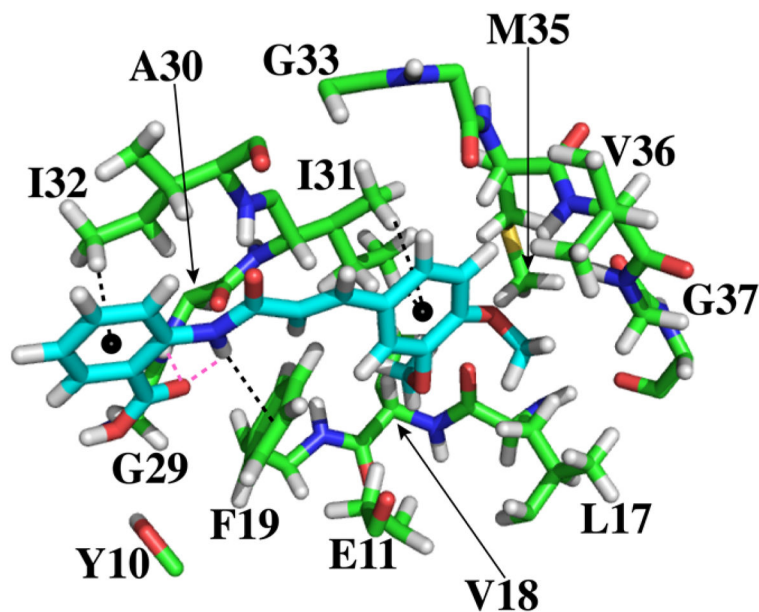


Figure 5. Binding pocket from the top scoring docking simulation produced by MOE between tranilast and the two most representative centroids of A β 40. Only A β atoms (carbon in green, oxygen in red, nitrogen in blue, and hydrogen in white) within 5 Å of tranilast (carbon in cyan, oxygen in red, nitrogen in blue, and hydrogen in white) are depicted. Black dashed lines indicate π -H interactions. Magenta dashed lines indicate hydrogen bonds. This docking pose was the highest scoring dock to tranilast among all of the docks determined for both of the A β centroids used.

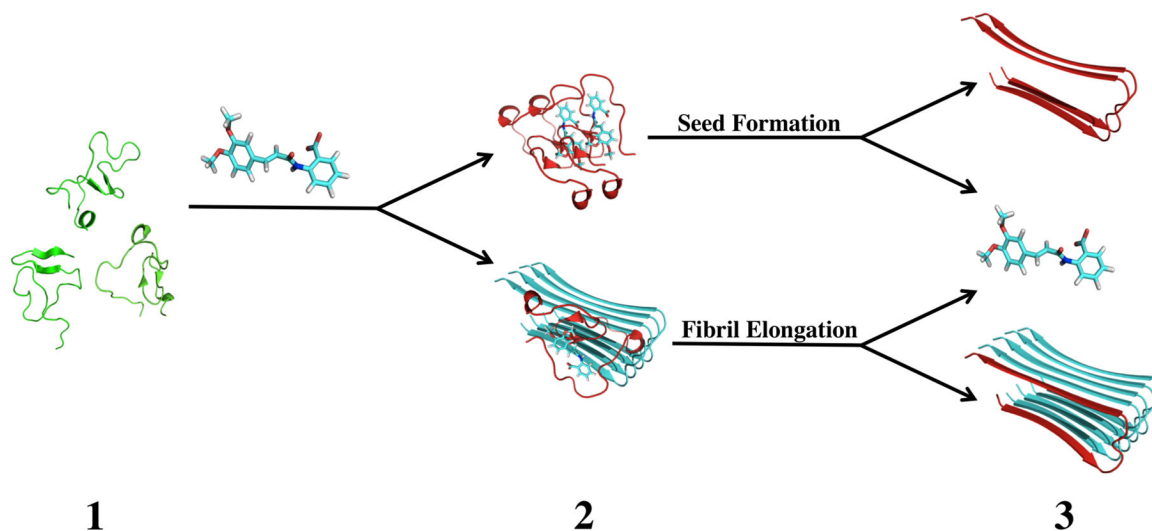


Figure 6.

Proposed mechanism for tranilast binding to Aβ monomers, explaining the increase in fibril formation. (1) Aβ monomers (green) sample many different conformations in solution. (2) Tranilast binds to Aβ monomers and stabilizes conformations (red) capable of docking onto fibrils (cyan) or creating fibril seeds, promoting fibril aggregation. (3) Upon locking onto the fibril or fibril seed, the Aβ monomer adopts a new conformation, releasing tranilast and extending the aggregate.^{27,49}