

Small Molecule Microarrays Enable the Discovery of Compounds That Bind the Alzheimer's A β Peptide and Reduce its Cytotoxicity

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Abstract: The amyloid- β (A β) aggregation pathway is a key target in efforts to discover therapeutics that prevent or delay the onset of Alzheimer's disease. Efforts at rational drug design, however, are hampered by uncertainties about the precise nature of the toxic aggregate. In contrast, high-throughput screening of compound libraries does not require a detailed understanding of the structure of the toxic species, and can provide an unbiased method for the discovery of small molecules that may lead to effective therapeutics. Here, we show that small molecule microarrays (SMMs) represent a particularly promising tool for identifying compounds that bind the A β peptide. Microarray slides with thousands of compounds immobilized on their surface were screened for binding to fluorescently labeled A β . Seventy-nine compounds were identified by the SMM screen, and then assayed for their ability to inhibit the A β -induced killing of PC12 cells. Further experiments focused on exploring the mechanism of rescue for one of these compounds: Electron microscopy and Congo red binding showed that the compound *enhances* fibril formation, and suggest that it may rescue cells by accelerating A β aggregation past an early toxic oligomer. These findings demonstrate that the SMM screen for binding to A β is effective at identifying compounds that reduce A β toxicity, and can reveal potential therapeutic leads without the biases inherent in methods that focus on inhibitors of aggregation.

Introduction

Considerable genetic and biochemical evidence indicates that aggregation of the amyloid- β peptide (A β) plays a causative role in the neurodegeneration, memory loss, and dementia associated with Alzheimer's disease (AD).^{1–5} Although the precise structure of the toxic aggregate is still under investigation, the major features of the “amyloid cascade” pathway are understood: Proteolytic processing of the amyloid precursor protein (APP) results in the extracellular release of the 4 kDa A β peptide. Differential cleavage by secretase enzymes leads to the formation of A β variants ranging in size from 39 to 43 amino acids, with the 40-residue A β 40 and 42-residue A β 42 peptides being the most prevalent.^{6–8} Compared to A β 40, A β 42 is more prone to aggregation,⁹ more neurotoxic,¹⁰ and more closely correlated with symptomatic disease.^{2,11}

A β 42 is also the predominant component of the extracellular plaque that has long been viewed as the pathological hallmark of AD.^{12,13} While this insoluble plaque provides posthumous evidence of the disease, numerous findings over the past decade implicate earlier soluble intermediates as the neurotoxic agents. A β -derived diffusible ligands (ADDLs) have been observed to induce neuronal death in cell culture,¹⁴ and soluble A β oligomeric species are more closely associated with cognitive decline in AD patients and synapse loss in transgenic mice than fibril or plaque load.^{15–17} Most recently, a murine model in which ADDLs were endogenously expressed with sequence mutations

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that prevented subsequent plaque formation showed that cognitive deficits depend on soluble A β oligomers rather than end-stage aggregates.¹⁸

With the prevalence of Alzheimer's disease projected to rise dramatically in the coming decades,¹⁹ there is increasing urgency to develop novel therapeutics to prevent and/or treat this debilitating disease. The pharmaceuticals currently used to treat AD include cholinesterase inhibitors and memantine, a modulator of glutamate receptors.^{20,21} These drugs provide symptomatic relief and may slow cognitive decline; however, they do not target the underlying molecular cause of AD. Therefore, currently approved drugs neither halt nor reverse progression of the disease. In contrast to these existing drugs, novel compounds that interfere with A β aggregation, and thereby block the molecular events that cause AD, represent a promising approach to the prevention and/or cure of Alzheimer's disease.

In principle, compounds that interfere with A β aggregation could be discovered by either of two approaches: structure-based rational drug design or high-throughput screening. Since a range of intermediates along the A β aggregation pathway have been implicated as potential toxic species,^{22–25} and none of their precise structures are known, structure-based drug design is not yet possible. For the time being, high-throughput screening remains a more promising approach.

A number of high-throughput methods have been developed to screen for compounds that interfere with A β aggregation. Most screens use synthetic A β peptide and monitor aggregation by following the fluorescence of thioflavin-T or another dye that binds to fibrillar aggregates.^{26–28} Although relatively convenient to perform, these screens have limitations. First, they are hampered by the need for substantial quantities of synthetic peptide, which is expensive and difficult to produce in a form that is free of preaggregated seeds. A second and more significant drawback of dye-binding assays is their reliance on a reporter that detects amyloid fibrils or protofibrils, rather than

the early intermediates that are now thought to be the neurotoxic agent. The limitations of assays that screen for inhibitors of fibrillization are highlighted by recent reports that accelerating fibril formation may, in fact, be advantageous as a way to decrease the presence of toxic soluble A β oligomers.^{29,30}

As an alternative to traditional assays using synthetic A β peptide, our lab previously reported the development of a high-throughput screen using an A β 42-GFP fusion protein expressed in *Escherichia coli*.^{31,32} In that system, aggregation of the A β 42 sequence drags the entire fusion protein into misfolded insoluble aggregates, thereby preventing the folding and fluorescence of GFP. Compounds that inhibit the aggregation of A β 42 enable the GFP part of the fusion to fold into its native structure, and thereby give rise to green fluorescent colonies (or liquid cultures) of *E. coli*. The A β 42-GFP screen overcame two of the limitations of the dye binding assays: (i) synthetic A β peptide was not required, and (ii) the assay reported A β misfolding and aggregation without requiring the formation of amyloid fibrils.

Application of the GFP-based screen enabled the identification of several aggregation inhibitors from a library of triazine derivatives,³² and from other libraries screened subsequently. Some of these compounds look promising and are being evaluated in a *Drosophila* model of AD. Nonetheless, the GFP-based screen also has several limitations. (i) Because the A β 42-GFP fusion protein was expressed in *E. coli*, compounds that fail to cross the cell wall and membrane of *E. coli*, or which were toxic to *E. coli*, may have been missed. (ii) Because the folding and fluorescence of the GFP reporter is based on the solubility of the upstream sequence,³³ the screen may not distinguish between compounds that block all aggregation (by favoring monomeric A β) and those that block fibrillization by favoring the toxic soluble oligomers. Thus, compounds that allow the A β 42-GFP fusion protein to fold and fluoresce by enhancing the stability of soluble oligomers would be mistakenly identified as inhibitors of aggregation (hits) rather than as enhancers of the toxic species. (iii) Most importantly, because the A β 42-GFP screen was designed to identify compounds that inhibit aggregation, it would miss potential therapeutics that remove toxic oligomers by enhancing their aggregation into insoluble fibrils.

These considerations motivated us to develop a novel method to screen compounds based solely on their ability to bind to monomeric A β . Ultimately, whether a small molecule reduces the toxicity of A β by inhibiting aggregation, accelerating it past the toxic species, or redirecting it to an alternate pathway, the compound must first bind the A β peptide.

High-throughput identification of compounds that bind to specific proteins has been accomplished previously through the use of small molecule microarrays (SMMs). SMMs are glass slides on which libraries of small molecules are covalently immobilized in an array of microscopic spots.³⁴ Compounds can be attached to the surface by any of several mild coupling

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reactions. For the current study, SMMs were prepared by installing an isocyanate on the surface of the slides and then attaching the small molecules to this group.^{35–37} Because isocyanate reacts with amines (primary and secondary), thiols, alcohols (primary and secondary), and several other groups, a compound possessing several different functional groups can attach to the surface in a range of orientations with various functional groups available to interact with the probe. To ensure that the small molecules are presented at a distance from the surface sufficient to enable interactions with a soluble probe (A β peptide in the current study), the isocyanate is separated from the surface by a polyethylene glycol spacer.

A single SMM slide typically displays 10800 compounds, allowing for rapid and efficient screening of diverse libraries of small molecules. SMM slides are probed with a fluorophore- or epitope-tagged protein (in this case, fluorescently labeled A β peptide), and compounds that bind the protein are detected by automated fluorescence read-out (a schematic is shown in Figure 2a).^{35–37} SMMs have been used successfully to identify a wide range of protein–ligand interactions, including calmodulin and human immunoglobulin G ligands,^{38,39} transcriptional regulators,^{40,41} and inhibitors of histone deacetylases.⁴²

The SMM technology has several features that make it ideal as a high-throughput screen for compounds that bind A β . First, it does not require knowledge of the protein structure or binding pocket. This unbiased approach is crucial since the structure of the toxic A β aggregate is not known, and a traditional active site pocket is not likely to exist. Second, the high sensitivity of the SMM assay allows the A β peptide to be used at very low concentrations. This is important because A β aggregation occurs via a nucleation-dependent mechanism,⁴³ and keeping the peptide below the critical concentration favors the monomeric form, thereby facilitating the identification of compounds that interact with A β at or before the earliest steps of aggregation. An added benefit is that low concentrations of peptide make the assay relatively inexpensive.

Here we describe the development of SMM technology to screen libraries of small molecules for compounds that bind the Alzheimer's A β peptide. As an initial step toward SMM assay development, we identified conditions that favor the monomeric state of A β . Next, two SMM slide sets, one with natural products and synthetic commercial compounds (NPC) and the other with diversity-oriented synthesis compounds (DIV), were screened with fluorescently labeled A β 40. Compounds in printed features that bound the peptide were identified as hits, as described previously.^{37,44} These compounds were subsequently assayed for their ability to rescue PC12 cells from

A β 42-induced toxicity. Further examination of a commercially available compound revealed dose-dependent rescue of PC12 cells. Finally, we demonstrated that this compound actually *promotes*, rather than inhibits, fibrillogenesis. These results validate the ability of the SMM screen to reveal compounds that interact with the A β peptide, and may provide leads for therapeutics that prevent or cure Alzheimer's disease.

Results and Discussion

Development of an SMM Assay for Binding to A β . Identifying compounds that interact with A β at or before the earliest stages of aggregation required that we develop conditions for the SMM assay wherein the peptide would occur predominantly in its monomeric form. A β , particularly A β 42, is known to aggregate quickly, and aggregation is considerably faster when the sample is agitated,^{45–47} as required for the SMM assays. We assessed the aggregation of A β 40 and A β 42 with N-terminal fluorescent tags under conditions typically used for SMM screening, which include 30 min of gentle agitation (by orbital mixing) at room temperature. Monomeric and oligomeric states were estimated using Tris-Tricine SDS–PAGE. Such gels are used routinely to assess the oligomeric state of A β ,^{48,49} and previous reports indicate that both cell-derived oligomers and those formed *in vitro* resist denaturation by SDS, particularly when gel analysis is performed at room temperature.^{50–52} Nonetheless, the possibility that SDS alters the distribution of oligomeric states cannot be ruled out. With this caveat in mind, we probed the oligomeric states of our samples using the standard Tris-Tricine SDS–PAGE assay.

As shown in Figure 1a, fluorescently labeled A β 42 formed more oligomers and larger oligomers than A β 40. Distinct monomer (4 kDa), dimer (8 kDa), trimer (12 kDa), and tetramer (16 kDa) bands are apparent for A β 42 at 9.35 μ M, with the trimer being the most intense oligomeric band, consistent with previous reports.⁴⁸ Trimer and tetramer bands were also very faintly apparent for A β 42 at 935 nM. In contrast to A β 42, A β 40 produced only monomer and dimer bands at 9.35 μ M, and at concentrations below 1 μ M, A β 40 yielded only monomers.

Because of its reduced propensity to aggregate, we opted to use A β 40 for our SMM screens. Because A β 40 lacks only two residues at its C-terminus and has the same core residues as A β 42, we assumed that most compounds capable of binding A β 40 would also bind A β 42. To assess whether fluorescently labeled A β 40 would remain monomeric under the conditions

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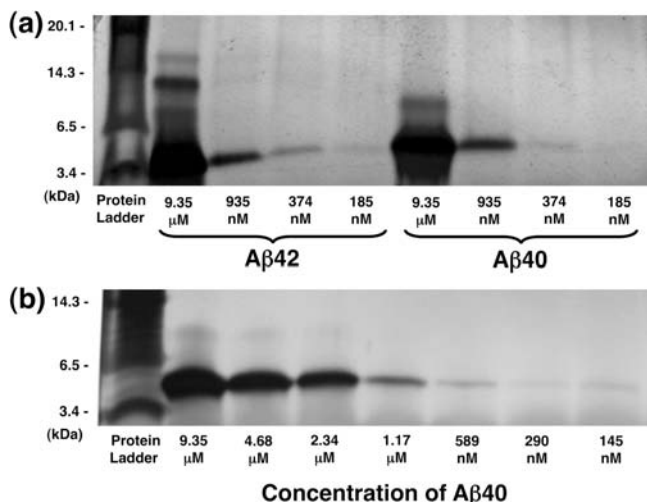


Figure 1. The 10–20% Tris-Tricine SDS–PAGE gels showing the oligomeric state of fluorescently labeled $A\beta$ under SMM agitation conditions. (a) HiLyte Fluor 488-labeled $A\beta_{42}$ (lanes 2–5) and HiLyte Fluor 647-labeled $A\beta_{40}$ (lanes 6–9) after agitation for 30 min. (b) Fluorescently labeled $A\beta_{40}$ after 60 min agitation. Monomeric $A\beta$ appears at ~ 4 kDa. Gels were visualized by silver staining.

of the SMM assay, we incubated the peptide with gentle agitation for 60 min—twice as long as required for typical SMM binding experiments—and probed its oligomeric state by SDS–PAGE. As shown in Figure 1b, at micromolar concentrations, $A\beta_{40}$ forms monomers and dimers, but at concentrations $1.17 \mu\text{M}$ or lower, only monomeric bands are seen. This is consistent with previous reports that the critical concentration of amyloid aggregation occurs in the micromolar or high nanomolar range.^{53,54}

These results suggest that fluorescently tagged $A\beta_{40}$ is largely monomeric in solution at the concentration (185 nM) and incubation conditions used for SMM screening. Therefore, initial encounters between the immobilized small molecule and the peptide are likely to occur with the latter in its monomeric form. After the first peptide binds an immobilized small molecule and becomes attached to the surface, further copies may be recruited to aggregate onto this immobilized complex.

The SMM Screen Identifies Compounds That Bind $A\beta$. The SMM assay was used to screen two collections of compounds. The first collection contained natural product and commercial synthetic compounds (NPC), while the second contained a library of compounds from a diversity-oriented synthesis (DIV). A total of 17905 compounds were screened, and all assays were performed in triplicate. Compounds that bound fluorescently

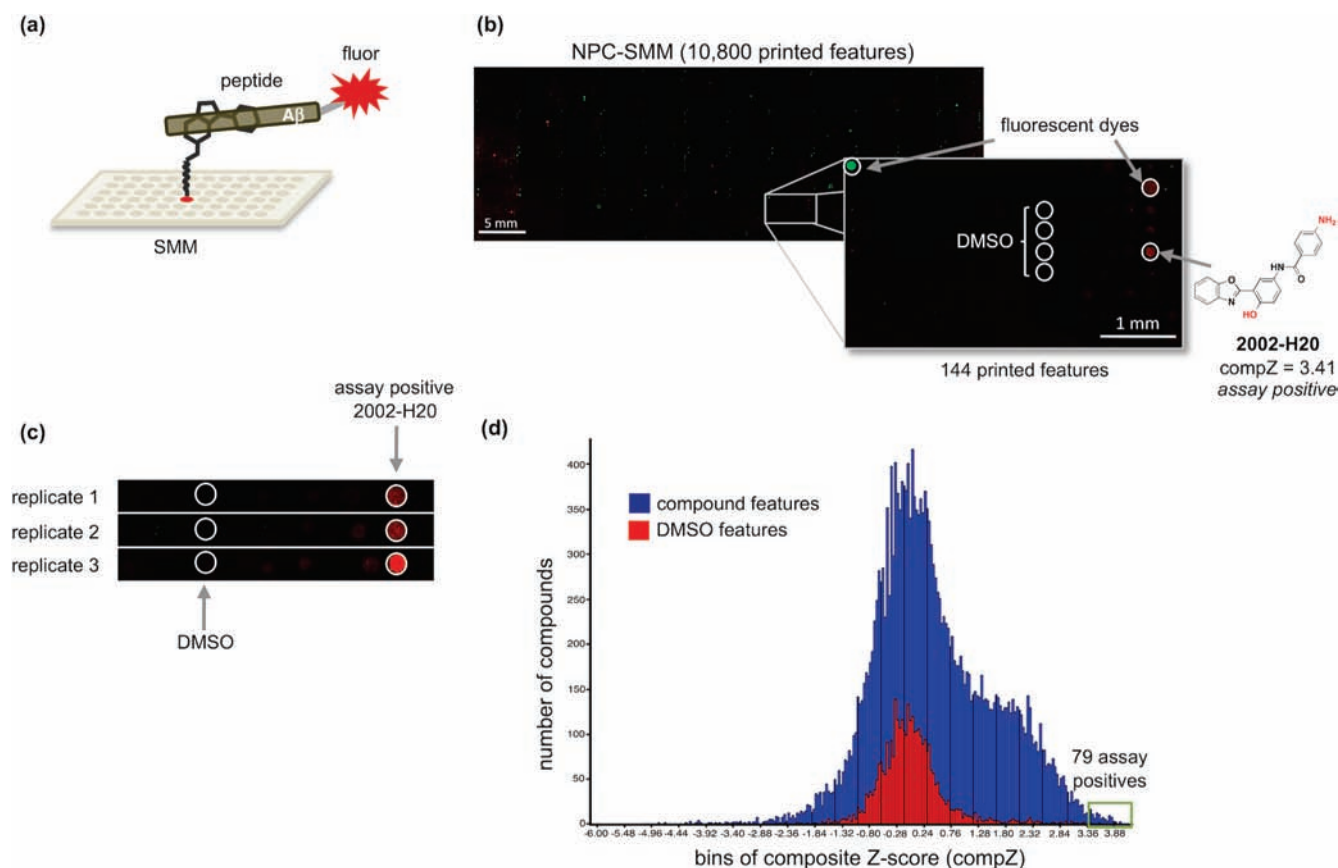


Figure 2. (a) The SMM binding screen. Compounds are covalently attached in an array of spots on the surface of a slide, and probed with fluorescently tagged $A\beta$ peptide. Those compounds that bind $A\beta$ and withstand several washes are revealed as fluorescent spots. (b) Fluorescent read-out of the NPC-SMM slide following incubation with fluorescent $A\beta_{40}$. Enlargement of a grid section shows compound 2002-H20 binding the peptide (false-colored red) as well as fluorescent dyes used in grid alignment (false-colored green and red) and nonfluorescing DMSO control spots. The structure of 2002-H20 is shown with isocyanate-reactive functional groups colored red to indicate the positions available for attachment to the slide. Because two functional groups (an amine and a phenol) are available for cross-linking, the population displayed on the surface is assumed to include molecules displayed in more than one orientation, with some exposing the amine and others exposing the phenol for interaction with $A\beta$. (c) Three replicate SMM screens of the NPC compound set show that compound 2002-H20 binds fluorescently labeled $A\beta_{40}$ reproducibly and consistently. (d) Histogram of the composite Z-scores of SMM fluorescence results from 3 replicates of the DIV and NPC slides. Results are divided into 254 bins with compounds shown in blue and DMSO controls in red. The green box surrounds bins for 79 assay positive compounds with composite Z-scores ≥ 3.4 .

labeled A β 40 yielded spots exhibiting fluorescence at 632 nm (false-colored red). Rhodamine features exhibiting fluorescence at 532 nm (false-colored green) were used for grid alignment. Fluorescence read-out results for the NPC slide screened with the A β 40 probe are shown in Figure 2b. Zooming in on a section of the slide shows the rhodamine grid alignment spots, non-fluorescing DMSO control spots, and the distinct, uniform red fluorescence of a representative compound that bound A β . Figure 2c shows that this compound, hereafter referred to as 2002-H20, bound A β 40 in all three replicates.

Primary SMM assay positives were annotated using fluorescence signal as described previously by Seiler et al.⁴⁴ The fluorescence intensity values from each replica slide were background subtracted and converted to a Z-score, or standard score representing the number of standard deviations that an observation—here, the fluorescence of a grid spot—is above or below the mean value.^{36,37,44} Z-scores from the three replicates performed for each slide set were combined to produce a composite Z-score for each compound. These values, and the composite Z-scores for DMSO control spots, were plotted in a histogram (Figure 2d) with the results divided into 254 bins. The resulting shape of the compound histogram, shown in blue, is normal with a center around zero and a small shoulder on the right side. The DMSO control histogram (red) also exhibits a normal distribution centered on zero. Compounds binding A β with a composite Z-score of 3.4 or greater were identified as “hits” and selected for follow-up testing. From the 17905 compounds assayed from the DIV and NPC libraries, 79 compounds with a composite Z-score above the threshold value were chosen for additional studies.

Inhibition of A β 42-Induced Cytotoxicity. The 79 hits identified in the SMM screens were assayed for their ability to inhibit A β 42-induced killing of PC12 cells. We chose inhibition of cytotoxicity—rather than biophysical studies of A β aggregation—as our initial follow-up assay because it makes no assumptions about the precise mechanism of A β toxicity, and thus allows a less biased search for compounds that may ultimately lead to therapeutics. Because A β 42 is known to be a more important contributor to AD-associated neurotoxicity than A β 40, we used the longer peptide to assay for inhibition of A β -induced cell death. These assays were performed using pure peptide, not linked to the fluorescent probe used in the SMM screen. Therefore, any compounds that were isolated in the SMM screen because of binding to the fluorophore tag would be weeded out at this stage.

PC12 cells were incubated with A β 42 and the SMM assay positive compounds, and cell viability was assessed using the MTT assay, which is based on the reduction of the yellow tetrazolium salt MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) to purple formazan crystals in metabolically active cells. Briefly, PC12 cells were grown to confluence and incubated for 24 h in the presence of 20 μ M A β 42 and 100 μ M of the hit compounds solubilized in DMSO. MTT was added, and after incubation and solubilization, the difference between absorbance at the formazan wavelength (570 nm) and the MTT absorbance (670 nm) was taken as a measure of relative cell viability. At concentrations of 100 μ M, 44 of the 79 SMM hit compounds were found to reduce the toxicity of A β 42 in PC12 cells, with 15 of these compounds increasing

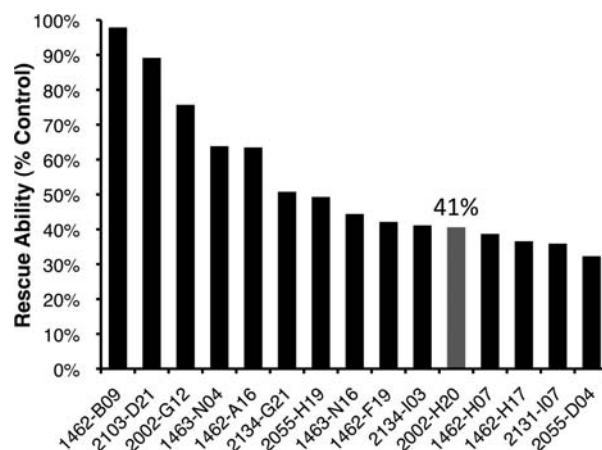


Figure 3. Relative rescue scores for the top 15 compounds, which (at 100 μ M) reduced the toxicity of A β 42 to PC12 cells. Viability of cells in the absence of A β or exogenous compounds was scaled ($A_{570-670} = 0.716$) to 100% and viability of cells exposed to A β 42 alone ($A_{570-670} = 0.496$) was scaled as 0%. As shown in gray, compound 2002-H20 increased viability by 41%. Cell viability was assayed using the MTT assay. Compound identities and toxicity data for all 79 compounds provided in Supporting Information.

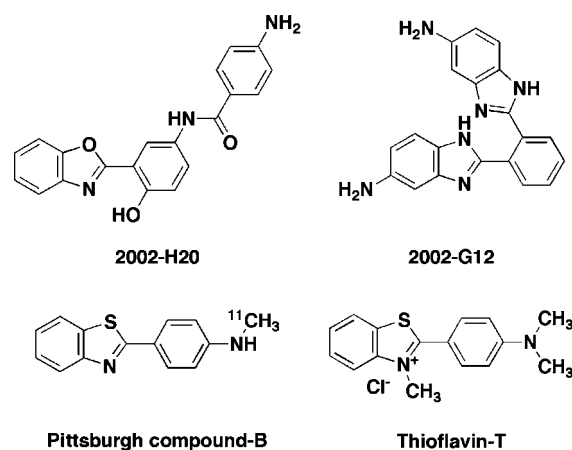


Figure 4. The benzoxazole motif in compound 2002-H20 is similar to the benzothiazole motif in Pittsburgh Compound-B and thioflavin-T, two compounds that bind A β and are used routinely to detect amyloid. Another SMM hit compound, 2002-G12, contains similar benzimidazole motifs and reduced A β 42 toxicity by 76% (Figure 3).

cell viability by >30%. These results for the top 15 rescuers are shown in Figure 3 (toxicity rescue data for all 79 hit compounds can be found in Supporting Information, Table S1). As shown, one compound, 1462-B09, rescued cell viability to nearly 100%, almost eliminating A β -induced toxicity entirely. Another compound, 2002-H20, increases cell survival by 41%. Compound 2002-H20 was chosen for further study as it reproducibly binds A β 40 in the SMM assays (Figure 2c), is readily soluble in DMSO, and is commercially available.

Structural Features of Compound 2002-H20. The structure of compound 2002-H20 is shown in Figure 4. With multiple aromatic groups and several sites for hydrogen bonding, it shares features with compounds identified previously as amyloid aggregation inhibitors.⁵⁵⁻⁵⁷ Its structure also bears some resemblance to thioflavin-T (ThT), a fluorescent dye used to bind and detect amyloid fibrils,⁵⁸ and Pittsburgh Compound-B,⁵⁹ which is used to image amyloid in the brains of AD patients. These compounds all contain a central phenyl ring and an attached benzoxazole or benzothiazole. These similarities to compounds previously known to bind A β support the efficacy

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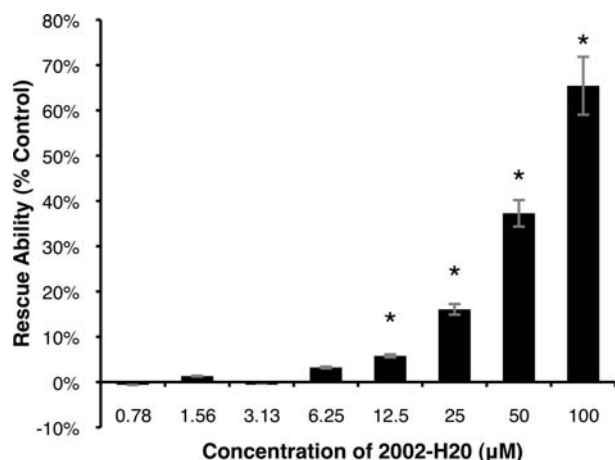


Figure 5. Dose-dependence of compound 2002-H20's ability to rescue PC12 cells from A β 42-induced toxicity. A 100% rescue scaled as the absorbance difference of cells incubated in buffer without peptide ($A_{570-670} = 0.976$) and 0% as absorbance difference of cells with 20 μ M A β 42 and no 2002-H20 ($A_{570-670} = 0.389$). An asterisk (*) indicates statistical significance as determined by the two-tailed Student's *t* test ($p < 0.05$) and error bars reflect standard error from the average of three measurements.

of the SMM method for isolating A β binders. Similar structural features also occur in another SMM hit, compound 2002-G12, which contains a central phenyl ring with two benzimidazole substituents and reduced A β -induced toxicity by 76% (Figure 3). Though this compound was no longer available for purchase from the original commercial supplier, analogues with benzimidazole groups were tested and found to produce statistically significant improvements in the viability of PC12 cells exposed to A β 42 (data not shown).

Compound 2002-H20 Exhibits Dose Dependent Inhibition of A β 42-Induced Cytotoxicity. The MTT assay was used to assess the dose dependence of 2002-H20-mediated rescue of PC12 cells from A β 42-induced toxicity. As shown in Figure 5, concentrations ≤ 3.13 μ M were ineffective. However, beginning at 6.25 μ M, a dose-dependent increase in cell viability was observed with concentrations ≥ 12.5 μ M producing statistically significant rescue of PC12 cells exposed to A β 42. The greatest improvement was at the high dose of 100 μ M 2002-H20, with cell viability increased to 65% of the level of cells that were not incubated with A β 42.

Compound 2002-H20 Does Not Affect Cell Viability. To assess the effect of compound 2002-H20 on cell viability, it was added to PC12 cells in the absence of A β 42. As shown in Figure 6, the compound does not appear to affect viability and there are no concentration-dependent trends. Variations in viability above and below 100% are likely due to the inherent noise of the MTT assay.

Analogues of Compound 2002-H20. To assess whether analogues of compound 2002-H20 inhibit A β 42-induced cytotoxicity, we evaluated 21 related molecules. Compounds were tested at a concentration of 50 μ M for their ability to reduce the toxicity of 20 μ M A β 42 in PC12 cells. Thirteen of these compounds showed statistically significant rescue, but no

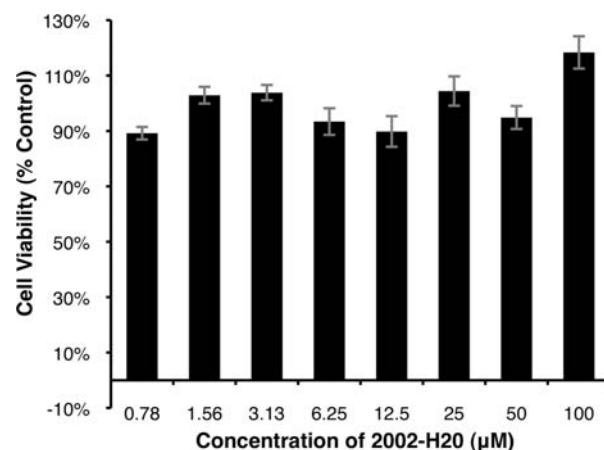


Figure 6. Viability of PC12 cells exposed to compound 2002-H20 at varying concentrations. One-hundred percent is scaled as the measured viability of cells not exposed to exogenous compound or peptide, but incubated in buffer with 1% (v/v) DMSO ($A_{570-670} = 0.976$). Average of three measurements with standard error reported.

significant trends in functional groups were revealed. Only one analogue was more effective than compound 2002-H20 itself (Supporting Information, Table S2 and Figure S1).

Mode of Action for 2002-H20-Mediated Rescue of A β 42-Induced Cytotoxicity. Compound 2002-H20 was identified by the SMM assay for its ability to bind A β 42. Further characterization showed that it enhances the viability of PC12 cells exposed to A β 42. To explore the mechanism by which 2002-H20 binding reduces A β 42 toxicity, we investigated its impact on peptide aggregation *in vitro*. Compound 2002-H20 was incubated at concentrations of either 50 or 100 μ M with synthetic A β 42 at 20 μ M. Amyloid formation was monitored by the Congo red (CR) spectral shift assay, and by transmission electron microscopy (TEM). When CR binds amyloid fibrils, it produces a characteristic spectral shift that enables quantization of amyloid.⁶⁰ As shown in Figure 7a, compound 2002-H20 produces a dose-dependent increase in the CR signal. TEM images (Figure 7b) confirm that fibril formation is enhanced by compound 2002-H20. In the absence of 2002-H20, the predominant aggregates are short fibrils, protofibrils, and oligomeric aggregates. However, in the presence of 50 μ M 2002-H20, A β 42 forms long fibrils. Increasing the 2002-H20 concentration to 100 μ M leads to dense fibrillar networks.

The CR data and TEM images shown in Figure 7 confirm that compound 2002-H20 affects the aggregation pathway of A β 42. However, rather than inhibiting aggregation, 2002-H20 seems to accelerate fibril formation. These results suggest that 2002-H20 inhibits cytotoxicity by driving A β 42 aggregation toward fibrils, thereby reducing the presence of toxic oligomers.

A number of previous studies described compounds that increase A β aggregation. For example, Williams et al. screened a collection of 640 small molecules and isolated a compound that stabilizes protofibrils.⁶¹ Necula et al. examined compounds previously identified as aggregation inhibitors and found that several of these compounds reduced oligomer formation, but promoted fibrillization.⁶² In a related study of the phenothiazine

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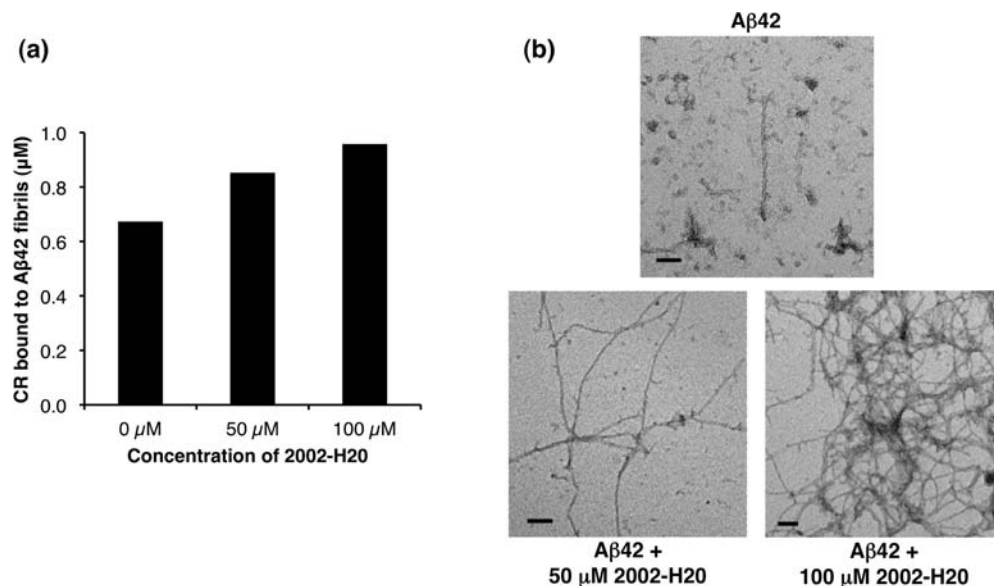


Figure 7. Compound 2002-H20 increases amyloid fibril formation of synthetic A β 42. (a) Congo red spectral shift. (b) Transmission electron microscopy. For both experiments, 20 μ M of synthetic A β 42 was incubated with the indicated concentration of compound 2002-H20. Incubations were at 37 $^{\circ}$ C with gentle agitation for 24 h.

compound, methylene blue, they proposed a causative link between the promotion of fibril formation and reduced oligomerization.³⁰ The potential for the enhancement of fibril formation as a novel therapeutic strategy was suggested by Cheng et al., who found that accelerating fibril formation in transgenic AD mice led to reduced oligomerization and improved behavioral outcomes.²⁹ Our finding that a compound isolated for its ability to bind A β 42 can both increase fibril formation and decrease A β 42-induced toxicity supports the potential efficacy of this strategy.

Compound 2002-H20 Might Have Been Missed by Other High-Throughput Screens. The advantages of the SMM screen are highlighted by the realization that compound 2002-H20 would *not* have been found by previously reported high-throughput screens for inhibitors of A β aggregation.

We found that the most commonly used assay for A β aggregation—ThT fluorescence—was ineffective in the presence of 2002-H20 because the compound and ThT fluoresce at similar wavelengths (data not shown). Indeed, recent studies suggest that ThT assays are often prone to errors in the presence of compounds that absorb or fluoresce in the same region of the spectrum.⁶³ However, even if the fluorescence of 2002-H20 and ThT did not overlap and the compound did not affect ThT fluorescence, a ThT-based assay that screens for inhibition of fibrillization would have missed 2002-H20, which actually *promotes* fibril formation.

Most of the screens described in the literature aim to isolate compounds that alter the aggregation of A β .^{31,32,64} Screens that isolate inhibitors of aggregation would miss compounds like 2002-H20, which favor fibrils. Conversely, screens for enhancers of aggregation would miss compounds that stabilize monomeric A β . In both cases, novel molecules that may ultimately provide leads for Alzheimer's therapeutics would have been missed by screens biased to favor either inhibitors or enhancers of

aggregation. In contrast, the SMM screen described here makes no assumptions about whether aggregation to a particular state is advantageous or detrimental and isolates compounds based solely on their ability to interact with A β .

Conclusions

Our primary aim in this study was to develop the SMM assay as a screen for compounds that may ultimately lead to therapeutics for Alzheimer's disease, and as described above, the assay effectively identified molecules that reduce the cytotoxicity of A β 42. Further examination of one of those compounds revealed dose-dependent rescue of A β -challenged PC12 cells, with a concomitant increase in fibril formation. These findings highlight the benefits of a screen optimized to reveal binding to A β without bias toward a specific type of interaction, and further suggest the potential for the SMM method as a tool for exploring the A β aggregation pathway. For example, future examination of small molecules that bind A β in the SMM assay, but fail to rescue cells from A β -induced toxicity may reveal compounds that stabilize toxic aggregates. With further development, such compounds may prove useful as probes for the intermediates that cause Alzheimer's disease. Additional applications can be envisioned with the SMM assay having potential as an efficient and versatile screen for isolating compounds that interact with intermediates at various stages of the A β aggregation pathway.

Materials and Methods

Materials. Fluorescently tagged amyloid- β peptide was purchased from Anaspec (San Jose, CA), diluted to a stock concentration of 9.35 μ M in 8 mM NaOH, and used without additional purification. A β 40 labeled at the N-terminus with HiLyte-Fluor 647 was reported by Anaspec to have a purity of greater than 90%, and A β 42 labeled at the N-terminus with HiLyte-Fluor 488 had a reported purity of greater than 95%. Nonfluorescently labeled crude amyloid- β peptides, synthesized via Fmoc synthesis, were purchased from the Keck Institute at Yale University (New Haven,

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CT) and purified as described below. SMM slides were prepared as described.⁶⁵

Peptide Purification. Purification of crude peptides was accomplished via reverse phase-HPLC with a C4 column (Grace Vydac 214TP152022; Deerfield, IL). A two-solvent system was run at 60 °C. Solvent A was 95% ultrapure H₂O, 5% acetonitrile, and 0.1% trifluoroacetic acid (TFA); and solvent B was 50% ultrapure H₂O, 50% acetonitrile, and 0.1% TFA. Purified peptides were disaggregated with TFA and 1,1,1,3,3,3-hexafluoro-2-isopropanol, which were applied successively and removed under a gentle argon stream.⁶⁶ Disaggregated peptides were stored as a lyophilized film at -20 °C.

SDS-PAGE Electrophoresis. The 9.35 μM stocks of fluorescently labeled peptides from Anaspec were diluted in 1× PBS to the indicated concentrations, and the pH of all dilutions was checked with pH paper and adjusted to 7–8 with 20% formic acid. The peptides were incubated for 30 or 60 min with gentle orbital shaking, combined with sample buffer, and loaded without boiling onto 10–20% Tris-Tricine gels (precast Ready Gels, Biorad; Hercules, CA). Electrophoresis was performed at 100 V and gels were developed with silver staining.

Small Molecule Microarray Assay. SMM slides were incubated with a slow circular orbit for 30 min at room temperature in 5 mL of 185 nM HiLyte 647-labeled Aβ40 (diluted from the 9.35 μM stock in 1× PBS-T, 0.1% Tween-20). Following incubation, slides were rinsed successively in PBS-T, PBS, and DI H₂O for 2 min each, and then spun dry for 30 s with a slide spinner (Labnet International; Woodbridge, NJ). A GenePix 4200A microarray scanner (Molecular Devices; Sunnyvale, CA) was used to scan the slides with an excitation wavelength of 532 nm (green emission filter, 557–592 nm) and an excitation wavelength of 635 nm (red emission filter, 650–690 nm). All SMM experiments were performed in triplicate, and analyzed using a standard pipeline output for high-throughput screens at the Broad Institute.⁴⁴

Cell Viability. Rat pheochromocytoma (PC12) cells, purchased from ATCC (Rockville, MD), were grown on collagen-coated Petri dishes (Falcon) in complete media (82.5% F12K, 15% horse serum, 2.5% fetal bovine serum; ATCC) in a humidified incubator at 37 °C and 5% CO₂ (HERAcCell, Thermo Scientific). Once they reached confluence, cells were harvested by spraying through an 18.5 gauge needle, resuspended in fresh complete media and plated onto tissue culture-treated flat bottom 96-well plates (Costar) at a density of 10 000 cells per well (100 μL/well). The plates were incubated for an additional 24 h to allow cell attachment. One milligram of synthetic Aβ42, purified as described above, was dissolved in 100 μL of cell culture grade DMSO (ATCC), sonicated briefly to ensure complete solubilization, and then diluted to 200 μM with 1.0 mL of sterile 1× PBS (Invitrogen). Ten microliters of this Aβ42 stock solution was then added to each 100 μL well to give a final peptide concentration of 20 μM. In assaying for their ability to reduce Aβ42-induced toxicity, compounds solubilized in DMSO were added at 1% (v/v) to the wells to reach the final concentrations indicated. One percent (v/v) DMSO without compound was added to wells containing 20 μM Aβ42 for a toxicity control and to wells containing only buffer without peptide for a cell viability control. Plates were then incubated with Aβ42 and compounds for an additional 24 h and cell viability was assessed with the MTT Cell Proliferation kit from Roche, as directed.^{67,68} Following overnight incubation, absorbance was measured at 570 and 670 nm

using a microplate reader (Thermo Varioskan), and $A_{570\text{ nm}} - A_{670\text{ nm}}$ was calculated to evaluate relative formazan dye formation, which is directly correlated to cell viability. The absorbance difference without Aβ42 or exogenous compound was scaled as 100% cell viability in all experiments. In trials assessing the relative rescue ability of compounds, the absorbance difference calculated with Aβ42 only and no compound was scaled as 0% rescue ability. Where indicated, experiments were performed as above without peptide in order to assess the potential cytotoxicity of the compounds alone.

Congo Red Spectral Shift Assay. Samples (0.5 mg) of purified Aβ42 were solubilized in 300 μL of DMSO with sonication. Five milliliters of 8 mM NaOH and 300 μL of concentrated PBS were added (final concentration: 50 mM NaH₂PO₄/100 mM NaCl, pH 7.2–7.4) bringing the final peptide concentration to 20 μM. To remove contaminants and pre-existing aggregates, the samples were filtered with a 0.22 μm low-protein binding syringe filter (Millex-GV; Millipore, Bedford, MA). Compound 2002-H20 (ChemDiv, San Diego, CA) was solubilized in DMSO to 10 and 5 mM concentrations, and added to samples to bring the final compound concentration to 100 and 50 μM. Samples were incubated in 15 mL horizontal polypropylene tubes with shaking (~200 rpm) on a Barnstead/Lab-line titer plate shaker (Dubuque, IA). Samples containing only 2002-H20 without peptide were prepared and incubated in the same fashion in order to evaluate for any effect of the compound alone on the Congo red spectral shift. After 24 h incubation, 400 μL aliquots were removed and mixed with 400 μL of a 34 μM Congo red (CR) solution (0.01 M PBS/10% EtOH, solution syringe filtered and CR concentration measured as described by Klunk et al.⁶⁹). Comparable samples with 0.01 M PBS/10% EtOH lacking Congo red were also prepared to correct for light scattering due to Aβ and 2002-H20. After 30 min of room temperature incubation, samples were mixed by pipetting and absorbance was measured at 403 and 541 nm. The concentration of CR bound to Aβ fibrils (in M) was calculated with background subtraction for light scattering from the absorbance of samples without CR.⁶⁹

$$[\text{CR} - \text{A}\beta] = \frac{A_{541,\text{A}\beta/\text{CR}} - A_{541,\text{A}\beta}}{47800} - \frac{A_{403,\text{A}\beta/\text{CR}} - A_{403,\text{A}\beta}}{38100}$$

Electron Microscopy. The same samples prepared for the Congo red assay were also used for transmission electron microscopy (TEM). Formvar carbon-coated Cu grids were floated on a drop of each sample for 2 min, washed twice for 2 min with DI water, and stained for 2 min with 1% uranyl acetate. Grids were imaged with a Zeiss 912ab electron microscope (Thornwood, NY).

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Supporting Information Available: Complete refs 11 and 59; table of all 79 SMM hit compounds with composite Z and toxicity rescue scores; detailed results from study of structural analogs of compound 2002-H20. This material is available free of charge via the Internet at <http://pubs.acs.org>.

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