



N-Benzyl, *N*-phenethyl and *N*-benzyloxybenzamide derivatives inhibit amyloid-beta (Aβ42) aggregation and mitigate Aβ42-induced neurotoxicity

Yusheng Zhao¹ · Arash Shakeri¹ · Ahmed A. Hefny¹ · Praveen P. N. Rao¹

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Abstract

A library of *N*-benzylbenzamide, *N*-phenethylbenzamide and *N*-benzyloxybenzamide derivatives were designed, synthesized and evaluated as amyloid beta (A β 42) aggregation inhibitors. These compounds were designed by replacing the α , β -unsaturated linker region of chalcone with an amide bioisostere. The A β 42 aggregation inhibition properties of these 27 benzamide derivatives were evaluated by the thioflavin T (ThT)-based fluorescence aggregation kinetics assay, transmission electron microscopy (TEM) studies, A β 42-induced cytotoxicity assay in mouse hippocampal neuronal HT22 cell lines, fluorescence live cell imaging, and computational modelling studies using a pentamer model of A β 42. These studies led to the identification of *N*-benzylbenzamides **3a** and **3f**, *N*-phenethylbenzamide **5a** and *N*-benzyloxybenzamide **7a** as promising compounds that were able to exhibit anti-aggregation properties in the ThT-based fluorescence experiments, TEM studies and more significantly were able to rescue the hippocampal neuronal HT22 cells from A β 42-induced cytotoxicity (91–96% cell viability at 25 μ M). These results demonstrate the usefulness of these benzamide-based templates in the design and development of novel small molecules as chemical tools and therapeutics to study and treat Alzheimer's disease.



Keywords Chalcone · PAINS · Benzamide derivatives · $A\beta 42$ aggregation · TEM · Cytotoxicity · HT22 cell line · Molecular docking

Introduction

Alzheimer's disease (AD) is the most common type of dementia. With an increase in the aging population worldwide, the incidence and prevalence of AD are predicted to rise in the coming years. AD is a neurodegenerative disorder that significantly hampers the function of the central nervous system, especially the brain regions of learning and memory [1–4]. Unfortunately, the diverse, complex, yet unified neurodegenerative pathophysiological pathways, have stalled the discovery of novel drug candidates to treat and cure AD. One of the known factors of AD is the aggregation of amyloid-beta (A β) peptides into neurotoxic forms [4, 5]. Recent evidence have shown that A β aggregation can trigger other AD pathological pathways either directly or indirectly to promote

Praveen P. N. Rao praveen.nekkar@uwaterloo.ca

¹ School of Pharmacy, Health Sciences Campus, University of Waterloo, 200 University Avenue Wes, Waterloo, ON N2L 3G1, Canada

neurodegeneration and cognitive decline [6-9]. The A β peptide formed after the proteolytic degradation of the amyloid precursor protein, undergoes rapid self-assembly and aggregation to form the senile plaques found in AD patient brain [4, 5, 10]. Based on these findings, the inhibition of Aß aggregation would provide therapeutic benefits to AD patients. Recent years saw an uptick in the discovery and development of novel anti-AB therapies as a novel class of disease-modifying agents to treat AD [11, 12]. In this regard, two monoclonal antibodies: aducanumab (Aduhelm[®]) and lecanemab (Legembi[®]) received approval from the US Food and Drug Administration with the later receiving full approval recently. Another monoclonal antibody, donanemab, is poised to receive FDA approval soon [13–16]. These developments in the AD drug discovery field demonstrate that targeting the amyloid cascade holds promise as a strategy to treat AD.

The field is now ripe to discover and develop novel anti-A β therapies based on small molecules since they are less expensive to manufacture, exhibit better stability on storage and can be administered orally which is beneficial to AD patients [17]. In this regard, we are working on designing novel small molecules that can bind to $A\beta$ and prevent its aggregation into toxic forms [18-20]. We focused our attention on the small molecule chalcone (1)considered as privileged structure (Fig. 1) and is known to demonstrate anti-aggregation properties toward AB [21-26]. However, chalcone has been identified as panassay interfering compound (PAINS) [25-30]. They interact with their molecular targets and biological thiols with no specificity, thus providing false positives and interfere with either UV- or fluorescence-based screening assays. The presence of the α,β -unsaturated system in their chemical structure makes them function as Michael acceptors, and the chalcone template can undergo covalent bonding with biological thiols [25, 26, 30]. Therefore, small molecules with these templates are flagged as PAINS

benzamide derivatives based on the known Aß aggregation inhibitor chalcone. The α,β -unsaturated system was replaced by an amide bioisostere. The aromatic rings (yellow, 1st ring; pink, 2nd ring), and the linker regions (red) are color-coded

in drug development. However, these still represent privileged structures in medicinal chemistry that can be optimized to design and develop novel agents. In this regard, previous studies have demonstrated that molecules bearing flat and planar C6-Cn-C6 carbon chain template are favoured to bind and prevent Aß self-assembly (Fig. 1), where C_6 refers to the presence of two aromatic rings and C_n refers to the type of linkage present between two aromatic ring systems [31].

Based on these findings, we adopted the C₆-C_n-C₆ template and replaced the Michael acceptor α,β -unsaturated system with an amide bioisostere to obtain the benzamide template (Fig. 1). This template has the following advantages: i) amide bond is not considered as PAINS [30] and does not undergo Michael addition with biological molecules; ii) the resonance delocalization in amide bond provides double bond characteristic and can act as a bioisostere of the α , β -unsaturated system present in chalcone. Thus, the flexibility of the designed ligands would be comparable to chalcone which fulfils the requirements to bind and prevent A β aggregation; iii) furthermore, from a synthetic chemistry point of view, amide bond eliminates the need to evaluate *cis/trans* or (Z)-/(E) isomers. Based on these hypotheses, we synthesized a library of 27 N-benzyl, N-phenethyl and N-benzyloxybenzamide derivatives, with various aromatic substituents and linkers containing either carbon spacer (3a-i and 5a-i), or oxygen spacer (7a-i). Their bioactivity toward Aβ42 aggregation was investigated by carrying out thioflavin T (ThT) fluorescence-based aggregation kinetic study, transmission electron microscopy (TEM), computational modelling and cell viability studies in mouse hippocampal HT22 neuronal cell lines against Aβ42 induced cytotoxicity. These studies demonstrate that the benzamide derivatives exhibit anti-Aβ42 activity in the thioflavin T (ThT) based fluorescent spectroscopy and electron microscopy experiments. Strikingly, these compounds demonstrate excellent neuroprotection against Aβ42-induced neurotoxicity in HT22 mouse hippocampal neuronal cells.



Aβ Aggregation Inhibitor Template

N-Benzyloxybenzamide (7a-i)

Scheme. 1 Synthetic scheme to prepare 3a–i, 5a–i, and 7a–i. Reagents and conditions: (i) TEA, acid chlorides (RCOCl), THF, room temperature/reflux 6–24 h. (ii) carboxylic acids (R-COOH), TEA, EDC•HCl, HOBt, THF, room temperature overnight

Results and discussion

Chemistry

The synthesis of target benzamide derivatives (27 compounds), was accomplished through direct coupling of primary amines (phenylmethanamine 2, or 2-phenylethan-1amine 4, or O-benzylhydroxylamine 6) with the corresponding acid chlorides (RCOCl) using triethylamine (TEA) either at room temperature or under reflux using known chemistry (Scheme 1). Alternatively, the benzamide derivatives were synthesized by coupling the corresponding acids (RCOOH) with primary amines using standard amide coupling agent EDC•HCl and HOBt in the presence of TEA (Scheme 1) [32, 33]. The target compounds 3a-i, 5a-i and 7a-i were obtained in good-to-excellent yields ranging from 72-93%. Coupling the acids with amines generally provided greater yields. Analytical data of final compounds 3a-i, 5a-i and 7a-i is provided in the Supplementary Material file.

Biological activity studies

Evaluation of the anti-A β 42 aggregation activity of 3a–i, 5a–i and 7a–i in the thioflavin T (ThT) based fluorescence spectroscopy

The structure-activity relationship (SAR) of benzamide derivatives to inhibit A β 42 aggregation was evaluated by ThT-based fluorescence kinetic assay [19]. The benzamide derivatives **3a–i**, **5a–i** and **7a–i** (25 µM) were incubated with A β 42 (10 µM) at 37 °C, pH 7.4 and the ThT fluorescence intensity was measured after 24 h incubation period to determine the anti-aggregation activity. The results are summarized in Fig. 2. In the *N*-benzylbenzamide series (**3a–i**), the presence of an unsubstituted benzene ring in compound **3a** (R=benzene) provided 27.1 ± 2.3% inhibition of A β 42 aggregation (Fig. 2). Replacing the benzene ring with the corresponding pyridine bioisostere in compounds **3b** and **3c**, led to a significant reduction in their anti-aggregation activity (~ 19% and 13% inhibition, Fig. 2). In contrast,



incorporating five-member heterocycles (eg: pyrrole, furan and thiophene) restored the anti-A β 42 activity with compounds 3d, 3e and 3f exhibiting 23.8-27.8% inhibition range (Fig. 2). The SAR was further investigated by incorporating planar, bicyclic aromatic rings (eg: naphthyl, quinoline and indole). These changes led to mixed results with compound 3h (R=quinoline), demonstrating comparable inhibition (~27%, Fig. 2), similar to compound **3a** (R=benzene, 27% inhibition, Fig. 2). Incorporating the planar, bicyclic indole ring led to a significant loss of anti-aggregation activity in compound **3i** (~7% inhibition of A β 42 aggregation, Fig. 2), whereas the presence of a naphthyl ring in compound 3 g, provided moderate inhibition (~16%, Fig. 2). In the *N*-phenethylbenzamide series (5a-i), the addition of an extra carbon spacer did not change their ability to prevent A β 42 aggregation (Fig. 2) and similar pattern was seen. In this series, compound 5a (R = benzene, ~28% inhibition, Fig. 2), was identified as the best with comparable activity as 3a (~27% inhibition). The next best compound was 5 f possessing a five-member thiophene ring (~27%inhibition, Fig. 2). Similar to the N-benzylbenzamide series, the addition of a planar, bicyclic indole ring led to a significant loss in the A β 42 inhibition activity (**5i**, ~7%) inhibition, Fig. 2). In the N-benzyloxybenzamide series (7a-i), the SAR was investigated by adding an oxygen linker next to the amide nitrogen. In this series, compound 7a (R=benzene, 26% inhibition) was identified as the best compound, followed by compounds 7i, 7f, 7d and 7 g with activity ranging from 23–25% (Fig. 2). These studies demonstrate that the *N*-benzyl, *N*-phenethyl and N-benzyloxybenzamide derivatives have the potential to be developed as $A\beta 42$ aggregation inhibitors.

Transmission electron microscopy studies of 3a, 3f, 3h, 5a, 5f and 7a in the presence of $A\beta 42$

Next, we investigated the A β 42 aggregation inhibition properties of representative benzamide derivatives (**3a**, **3f**, **3h**, **5a**, **5f** and **7a**, Fig. 3) by carrying out transmission electron microscopy (TEM) experiments [19]. The morphology of A β 42 (10 μ M) shows a combination of long, twisted, unbranched mature fibrils. In the presence of



Fig. 2 Inhibition activity of benzamide derivatives $(3a-i, 5a-i \text{ and } 7a-i, 25 \,\mu\text{M} \text{ each})$ against Aβ42 aggregation at 24 h time period. The compounds $(25 \,\mu\text{M})$ were incubated with Aβ42 $(10 \,\mu\text{M})$ for 24 h at 37 °C, pH 7.4 and the ThT fluorescence was monitored

(excitation=440 nm, emission=490 nm). The results shown are average±standard deviation of triplicate readings based on three independent experiments



Fig. 3 TEM images of A β 42 (10 μ M) in the presence and absence of benzamide derivatives (25 μ M). Scale: 200 μ m

benzamide derivatives, there was a significant reduction in the formation of A β 42 fibrils which was characterized by the presence of sparse, thinner, and lower-ordered fibrils (Fig. 3). TEM studies further demonstrate the A β 42 aggregation inhibition potential of these benzamides.

Effect of 3a, 3f, 3h, 5a, 5f, and 7a on A β 42-induced cytotoxicity in mouse hippocampal HT22 neuronal cells

In order to determine if the benzamide derivatives were capable of modifying the $A\beta 42$ aggregation pathway in cellular environment, we investigated the ability of

representative benzamide derivatives to prevent Aβ42mediated cytotoxicity in mouse hippocampal HT22 neuronal cell lines. The cytotoxicity of benzamide derivatives (3a, 3f, 3h, 5a, 5f, and 7a) alone, was evaluated in HT22 cells using the cell counting kit 8 (CCK-8)-based colorimetric assay [34]. These studies show that at $25 \,\mu$ M, these benzamide derivatives were not toxic to cells (83-110% viability) compared to untreated cells (UC) as shown in Fig. 4A. Then, HT22 cells were incubated with A β 42 (5 μ M) in the presence and absence of benzamide derivatives $(25 \,\mu\text{M})$ for 48 h. The cell viability reduced dramatically in the presence of Aβ42 (~ 39%, Fig. 4B). In contrast, benzamides 3a, 3f, 3h, 5a, 5f, and 7a demonstrated significant neuroprotection to HT22 cells against Aβ42-induced neurotoxicity, and demonstrated cell viability ranging from 81-97% (Fig. 4B). For example, benzamides 3a (R=benzene), 3f (R=thiophene), 5a (R=benzene), and 7a (R=benzene) exhibited excellent neuroprotection against Aβ42-induced neurotoxicity $(94.9 \pm 5.9\%, 95.9 \pm 13.7\%, 96.7 \pm 14.9\%)$ and $91.5 \pm 8.3\%$ cell viability respectively). These striking neuroprotection observed suggests that benzamide derivatives have the potential to convert toxic A β assemblies into nontoxic forms thereby reducing the cytotoxic effects of A β 42 assemblies [34]. This provides further evidence that N-benzyl, N-phenethyl and N-benzyloxybenzamides are novel templates that can be employed by researchers to design and discover anti-AD agents.





Fig. 4 Neuroprotective effect of benzamides **3a**, **3d**, **3f**, **5a**, **5**, **7a** on HT22 hippocampal cells. Panel **A** (cell viability on y-axis) shows the effect of compounds alone (25 μ M each) on HT22 hippocampal neuronal cells after 48 h incubation and Panel **B** shows the effect of compounds (25 μ M each) on HT22 cells treated with A β 42 (5 μ M) after 48 h incubation. Cell viability was determined by CCK-8 based





Fig. 5 Fluorescence live cell imaging with ProteoStat^{*}. **A** Images of HT22 cells treated with A β 42 (10 μ M) in the presence and absence of compounds **3a**, **5a**, and **7a** at 25 μ M. The images were visualized with the RFP light filter and the binary masks were created to measure the integrated gray value (IGV) of the original fluorescence images.

B Quantitative analysis of ProteoStat^{*} measured by IGV in the presence and absence of compounds **3a**, **5a**, and **7a**. The results shown are averages of three independent experiments from three randomized views. *p < 0.01 compared to the A β 42 control group (One-way ANOVA followed by Bonferroni post hoc test)

ProteoStat[®] based fluorescence imaging studies in mouse hippocampal (HT22) neuronal cells

To further validate the anti-aggregation activities of compounds 3a, 5a, and 7a in the cellular environment, live cell fluorescence imaging studies were carried out. The dye ProteoStat[®] which selectively stains amyloidogenic protein aggregates [35] was used to quantitatively measure and visualize the formation of Aβ42 fibrils in the mouse hippocampal HT22 cell lines in the presence and absence of compounds 3a, 5a, and 7a (25 µM each). When the cells were exposed to Aβ42 alone or the presence of test compounds, the presence of mature β sheet-rich structures was marked by the red ProteoStat[®] stain (Fig. 5A). The stain density was quantified by summing up the pixel values as the integrated gray value (IGV) using the software ImageJ. These studies show that there was a clear decrease in the amount of Aβ42 fibrils formed in the presence of derivatives 3a, 5a, and 7a (Fig. 5B). The highest IGV was observed for the Aβ42 control group, with a value of 3.5×10^7 (Fig. 5B). When the cells were co-incubated with aggregation inhibitors 3a, 5a, and 7a, there was a reduction in the IGV which demonstrates the ability of these compounds to reduce the formation of A β 42 fibrils. For compound **3a**, around 24% decrease in IGV (2.67 × 10⁷) was observed whereas for compounds **5a** and **7a**, around 28% and 29% decreases in A β 42 fibril density was observed which further provides evidence on their ability to inhibit the aggregation of A β 42 in the cellular environment.

LDH release cytotoxicity assay in mouse hippocampal HT22 neuronal cells

One of the mechanisms of A β 42 cytotoxicity is related to its ability to interact with the lipid membrane which leads to the formation of pores and eventual cell lysis [36]. In this regard, the ability of compounds **3a**, **5a**, and **7a** to rescue the HT22 cells from A β 42-induced neurotoxicity was evaluated by the lactate dehydrogenase (LDH) assay. Cell membranes can become damaged and leaky due to A β 42-induced toxicity and consequently, cytosolic LDH can get released which can be measured to determine cytotoxicity [37]. Our studies show that the exposure of A β 42 to HT22 cell lines led to a 1.29fold increase in the LDH release compared to untreated cells (Fig. 6), indicating that A β 42 can cause damage to cell membranes. When the cells were co-incubated with A β 42 and compounds **3a**, **5a**, and **7a** (25 μ M each), the amount of LDH released was reduced significantly (to 0.93, 0.98, and 1.04-fold respectively for compounds **3a**, **5a** and **7a** as shown in Fig. 6). These results further provide evidence that *N*-benzyl, *N*-phenethyl and *N*-benzyloxybenzamides are able to protect HT22 cells from A β 42-induced cytotoxicity.

In silico physicochemical and ADME analysis

The physiochemical properties, blood-brain barrier (BBB) penetration and presence of structural alerts were predicted for representative compounds **3a**, **3f**, **5a** and **7a** using the web tool SwissADME [38]. These results show that benzamide derivatives demonstrate drug-like properties with Log P values ranging from 2.28–2.93, and are predicted to cross into BBB, without the liability of possessing any structural alerts (Table 1).

Molecular docking studies of 3a, 5a and 7a in the $A\beta 42$ pentamer model

The binding interactions of benzamide derivatives from each series (**3a**, **5a**, and **7a**), were investigated in the A β 42



Fig. 6 Percentage LDH release from HT22 cell lines when exposed to A β 42 (10 μ M) in the presence and absence of lead derivatives **3a**, **5a**, and **7a** at 25 μ M. The results shown are averages of quadruplicate readings based on three independent experiments. *p < 0.001 compared to the A β 42 control group; **p < 0.0001 compared to the A β 42 control group; (One-way ANOVA followed by Bonferroni post hoc test)

pentamer assembly by carrying out molecular docking studies [34]. The A β 42 pentamer model was prepared using the solved 3D structure of Aβ42 fibril (PDB: 5KK3) [39]. The two regions of A β 42, the KLVFFA and the C-terminal IGLMVGGVVIA hydrophobic tail region are of great interest due to their role in the self-assembly process. Molecular docking studies show that the benzamide derivatives (3a, 5a and 7a) were able to interact with both the KLVFFA and IGLMVGGVVIA regions (Fig. 7). The ribbon diagram of **3a**, **5a** and **7a** docked to Aβ42 pentamer in Fig. 7A and the 2D interaction maps are shown in Fig. 7B, C. It is interesting to note that all three derivatives exhibited similar binding modes and were in the same binding region between the C- and N-termini (Fig. 7). The aromatic rings at either ends underwent hydrophobic and van der Waal's interactions with Leu17 and Leu34 (distance ~ 5.0 Å) respectively. This study also shows that the aromatic rings were the major contributor to their interactions with the C- and N-termini regions of AB42. Furthermore, the linker regions in 3a, 5a and 7a also underwent van der Waal's interactions with Gln15, Leu17 and Leu34 amino acid residues (distance ~ 5.0 Å). This suggests that the N-benzylbenzamide, N-phenethylbenzamide and N-benzyloxybenzamide templates can undergo hydrophobic and van der Waal's contact with the Leu17 and Leu34 to stabilize the conformation and prevent further aggregation. The CDOCKER energy and the CDOCKER interaction energies for 3a, 5a and 7a are given in (Table 2) which shows that they all form stable complexes with the Aβ42 pentamer.

Conclusion

In summary, we designed a library of 27 small molecules by replacing the α , β -unsaturated system present in the chalcone template with an amide bioisostere to obtain benzamide derivatives and evaluated them as inhibitors of A β 42 aggregation. These derivatives possess either *N*-benzylbenzamide, *N*-phenethylbenzamide or *N*-benzyloxybenzamide templates. The ThT-based anti-aggregation studies show that the compounds **3a**, **3f**, **3h**, **5a**, **6f** and **8a** exhibit ~ 27–28% inhibition of A β 42 aggregation. Their

| Compound | MW | H-Bond Acceptor | H-Bond Donor | TPSA Å ² | BBB Permeability | Consensus LogP | Structural alert |
|----------|--------|--------------------|-----------------|---------------------|---------------------|-------------------|----------------------|
| 3a | 211.26 | 1 | 1 | 29.1 | Yes | 2.6 | 0 |
| 3f | 217.29 | 1 | 1 | 57.3 | Yes | 2.62 | 0 |
| 5a | 225.29 | 1 | 1 | 29.1 | Yes | 2.93 | 0 |
| 7a | 227.26 | 2 | 1 | 38.3 | Yes | 2.28 | 0 |
| Chalcone | 208.26 | 1 | 0 | 17.0 | Yes | 3.25 | 1 (Michael acceptor) |

Table. 1 Predicted physicochemical, BBB permeation, and structural alerts for **3a**, **3f**, **5a**, and **7a** using the web tool SwissADME



Table. 2 Benzamide-A β 42 pentamer complex energy parameters obtained after molecular docking study of **3a**, **5a**, and **7a**

| Cmpd | CDOCKER Energy (kcal/ mol) ^a | CDOCKER Interaction Energy (kcal/mol) ^a |
|------|--|--|
| 3a | - 18.83 | - 23.76 |
| 5a | -21.78 | - 26.50 |
| 7a | - 17.42 | - 23.17 |

^aThe energy terms CDOCKER energy and CDOCKER interaction energy were calculated using the CDOCKER molecular docking algorithm in the Discovery Studio Client – Structure-Based Design software (Dassault Systemes BIOVIA, USA)

anti-aggregation activity was also confirmed by TEM studies which showed a reduction in the formation of A β 42 fibrils. Strikingly, these benzamide derivatives demonstrated excellent neuroprotection against A β 42-induced cytotoxicity in HT22 mouse hippocampal neuronal cells (80–97% cell viability at 25 µM) and were not toxic. Quantification of the A β 42 fibril load in the ProteoStatbased live cell imaging confirmed the ability of compounds **3a**, **5a**, and **7a** to reduce A β 42 fibril load in the cellular environment (27–29% inhibition at 25 µM). In addition, these compounds were also able to offer neuroprotection to HT22 cells exposed to A β 42 in the LDH assay.

These studies suggest that benzamide derivatives can bind to A β 42 assemblies and have the potential to induce changes in their conformation and reduce their cytotoxic effects in the cellular environment. They also exhibit druglike properties and do not possess any structural alerts, unlike the chalcone template that possesses the reactive α , β -unsaturated system which is considered as PAINS [25, 30]. Our studies show that benzamides possessing *N*benzylbenzamide, *N*-phenethylbenzamide or *N*-benzyloxybenzamide templates, hold promise in the design and development of novel small molecules as $A\beta 42$ aggregation inhibitors.

Experimental

General

All chemicals and reagents were purchased from various vendors (Sigma Aldrich USA, Alfa Aesar USA, Bio Basic Canada, AA Blocks USA, Cayman Chemical USA, Thermo Fisher USA, and Corning USA), were >95% pure and used without further purification. The Aβ42 1,1,3,3,3-hexafluoroisopropanol (HFIP) > 95% pure, was purchased from Anaspec USA and rPeptide USA. The chemical reactions were monitored by thin-layer chromatography (TLC), Merck silica gel 60, F254. Column chromatography was carried out using Merck silica gel 230-400 mesh. The spots were visualized with short or long wavelengths (254 nm or 365 nm). The melting points of compounds were determined using a digital melting point apparatus (REACH Devices, USA). The proton NMR (¹H NMR) spectra of compounds were obtained using a 300 MHz Bruker Avance spectrometer. Either $CDCl_3$ or $DMSO-d_6$ were used as the solvents. Coupling constants (J values) were recorded in Hertz (Hz). Abbreviations used to represent ¹H NMR signals were s - singlet, d - doublet, t - triplet, m - multiplet, br s - broad singlet. The mass and purity were confirmed on Agilent 1260 Infinity liquid chromatography (LC) module equipped with 6130 Quadrupole mass spectrometry (Agilent 6100 series LCMS). The column used on LCMS was ZORBAX Eclipse AAA, 4.6 × 75 mm, 3.5 micron (Agilent Technologies, Canada). A mixture of water and acetonitrile 1:1 v/v with 0.1% formic acid (1.0 mL/min flow rate), was used as the solvent system to assess compound purity and mass. The compounds were of $\ge 95\%$ pure as determined by LCMS analysis before testing in various biological screening assays.

General procedure for the synthesis of 3a-h, 5a-h and 7a-h

Phenylmethanamine (2) (1 mmol), or 2-phenylethan-1amine (4) (1 mmol), or O-benzylhydroxylamine (6) (1 mmol) was added into a 50 ml round bottom flask containing 15 ml anhydrous tetrahydrofuran (THF). To this mixture, 1.2 equivalent of triethylamine (TEA) and 1.0 equivalent of corresponding acid chlorides with various R groups were added (Scheme 1). The reaction was kept at either room temperature or under reflux for 6-24 h and monitored by TLC. After the reaction was complete, the solvent was evaporated in vacuo and the resulting reaction mixture was dissolved in 15 mL ethyl acetate (EtOAc), and then washed s with 15 mL brine solution (x 3). The organic layer was collected and dried over anhydrous MgSO4 and filtered. The organic solvent was removed in vacuo and the residue/oil obtained was further purified by silica gel column chromatography using a combination of solvent systems (1:1 n-hexanes: EtOAc or 5:2 n-hexanes: EtOAc or 9:1 dichloromethane (DCM): Methanol (MeOH) or 4:1 DCM: *n*-hexanes) to afford the final compounds **3a-h**, **5a-h** and 7a-h. The yields ranged from 72–93%. The analytical data for these compounds are given in the following section. The ¹H NMR spectra and LCMS chromatograms are provided in the Supplementary Material document.

N-Benzylbenzamide (**3a**): White solid, 92.8% [40, 41]. ¹H NMR (300 MHz, DMSO-d₆) δ 9.00 (t, *J* = 5.6 Hz, 1H), 7.90–7.81 (m, 2H), 7.53–7.39 (m, 3H), 7.29–7.10 (m, 5H), 4.45 (d, *J* = 6.0 Hz, 2H). mp: 105–107 °C. ESI-MS, m/z for C₁₄H₁₄NO [M + H]⁺ 212.1. Purity: 99.9% (LCMS).

N-Benzylisonicotinamide (**3b**): White solid, 72% [41, 42]. ¹H NMR (300 MHz, DMSO-d₆) δ 9.33 (t, J = 5.3 Hz, 1H), 8.79–8.67 (m, 2H), 7.85–7.75 (m, 2H), 7.34–7.27 (m, 5H), 4.51 (d, J = 6.0 Hz, 2H). mp: 95–98 °C. ESI-MS, m/z for C₁₃H₁₃N₂O [M + H]⁺ 213.1. Purity: 99.0% (LCMS).

N-Benzylpicolinamide (**3c**): White solid, 74.3% [42]. ¹H NMR (300 MHz, DMSO-d₆) δ 9.32 (br s, 1H), 8.67–8.65 (m, 1H), 8.10–7.96 (m, 2H), 7.64–7.59 (m,1H), 7.35–7.20 (m, 5H), 4.50 (d, *J* = 6.4 Hz, 2H). mp: 94–97 °C. ESI-MS, m/z for C₁₃H₁₃N₂O [M + H]⁺ 213.1. Purity: 99.6% (LCMS).

N-Benzyl-1*H*-pyrrole-2-carboxamide (**3d**): White solid, 79.6% [43]. ¹H NMR (300 MHz, CDCl₃) δ 9.50 (br s, 1H), 7.51–7.12 (m, 5H), 6.92–6.90 (m, 1H), 6.53–6.51 (m, 1H), 6.23–6.20 (m, 1H), 6.13 (br s, 1H), 4.60 (d, *J* = 5.9 Hz, 2H). mp:122–125 °C. ESI-MS, m/z for C₁₂H₁₃N₂O [M + H]⁺ 201.1. Purity: 96.1% (LCMS). *N*-Benzylfuran-2-carboxamide (**3e**): White solid, 93% [44]. ¹H NMR (300 MHz, DMSO-d₆) δ 9.04 (t, *J* = 5.8 Hz, 1H), 7.84 (d, *J* = 3.7 Hz, 1H), 7.36–7.21 (m, 5H), 7.25 (d, *J* = 6.0 Hz, 1H), 6.62 (d, *J* = 5.0 Hz, 1H), 4.46 (d, *J* = 6.0 Hz, 2H). mp: 120–123 °C. ESI-MS, m/z for C₁₂H₁₂NO₂ [M + H]⁺ 202.1. Purity: 99.6% (LCMS).

N-Benzylthiophene-2-carboxamide (**3 f**): White solid, 78.7% [42]. ¹H NMR (300 MHz, DMSO-d₆) δ 9.04 (t, *J* = 5.7 Hz, 1H), 7.88–7.81 (m, 1H), 7.39–7.19 (m, 5H), 7.15–7.05 (m, 2H), 4.45 (d, *J* = 6.2 Hz, 2H). mp: 115–117 °C. ESI-MS, m/z for C₁₂H₁₂NOS [M + H]⁺ 218.1. Purity: 99.7% (LCMS).

N-Benzyl-1-naphthamide (**3** g): White solid, 87.6% [45]. ¹H NMR (300 MHz, DMSO-d₆) δ 9.09 (t, J = 5.7 Hz, 1H), 8.22–8.19 (m, 1H), 8.06–7.95 (m, 2H), 7.66–7.53 (m, 4H), 7.38–7.26 (m, 5H), 4.55 (d, J = 6.2 Hz, 2H). mp: 127–129 °C. ESI-MS, m/z for C₁₈H₁₆NO [M + H]⁺ 262.1. Purity: 98.3% (LCMS).

N-Benzylquinoline-2-carboxamide (**3 h**): White solid, 93.6% [46]. ¹H NMR (300 MHz, DMSO-d₆) δ 9.47 (t, J = 6.2 Hz, 1H), 8.58 (d, J = 8.5 Hz, 1H), 8.20–8.04 (m, 3H), 7.88 (t, J = 7.6 Hz, 1H), 7.73 (t, J = 7.5 Hz, 1H), 7.40–7.22 (m, 5H), 4.58 (d, J = 6.2 Hz, 2H). mp: 128–130 °C. ESI-MS, m/z for C₁₇H₁₅N₂O [M + H]⁺ 263.1. Purity: 99.5% (LCMS).

N-Phenethylbenzamide (**5a**): White solid, [47]. ¹H NMR (300 MHz, CDCl₃) δ 7.78–7.59 (m, 2H), 7.52–7.28 (m, 5H), 7.24 (q, *J* = 4.9, 4.4 Hz, 3H), 6.10 (s, 1H), 3.71 (q, *J* = 6.9 Hz, 2H), 2.93 (t, *J* = 6.9 Hz, 2H). mp: 122–125 °C. ESI-MS, m/z for C₁₅H₁₆NO [M + H]⁺ 226.1. Purity: 99.9% (LCMS).

N-Phenethylisonicotinamide (**5b**): White solid, 76% [42]. ¹H NMR (300 MHz, CDCl₃) δ 8.71–8.68 (m, 2H), 7.50–7.48 (m, 2H), 7.36–7.20 (m, 5H), 6.15 (br s, 1H), 3.72 (q, *J* = 6.6 Hz, 2H), 2.93 (t, *J* = 6.8 Hz, 2H). mp: 129-130 °C. ESI-MS, m/z for C₁₄H₁₅N₂O [M + H]⁺ 227.1. Purity: 98.7% (LCMS).

N-Phenethylpicolinamide (**5c**): Yellowish oil, 74.5% [48]. ¹H NMR (300 MHz, CDCl₃) δ 8.53 (d, *J* = 4.5 Hz, 1H), 8.22 (d, *J* = 7.8 Hz, 1H), 8.16 (s, 1H), 7.85 (td, *J* = 7.7, 1.6 Hz, 1H), 7.44–7.23 (m, 6H), 3.72 (q, *J* = 7.0 Hz, 2H), 2.97 (t, *J* = 7.3 Hz, 2H). ESI-MS, m/z for C₁₄H₁₅N₂O [M + H]⁺ 227.1. Purity: 99.9% (LCMS).

N-Phenethyl-1*H*-pyrrole-2-carboxamide (**5d**): White solid, 82.8% [**4**9]. ¹H NMR (300 MHz, CDCl₃) δ 9.38 (br s, 1H), 7.37–7.26 (m, 2H), 7.26–7.17 (m, 3H), 6.91–6.88 (m, 1H), 6.41–6.38 (m, 1H), 6.20–6.17 (m, 1H), 5.84 (br s, 1H), 3.66 (q, *J* = 6.7 Hz, 2H), 2.88 (t, *J* = 6.9 Hz, 2H). mp: 134–136 °C. ESI-MS, m/z for C₁₃H₁₅N₂O [M + H]⁺ 215.1. Purity: 98.6% (LCMS).

N-Phenethylfuran-2-carboxamide (**5e**): White solid, 75.5% [47]. ¹H NMR (300 MHz, CDCl₃) δ 7.38–7.20 (m, 5H), 7.08 (d, *J* = 3.5 Hz, 1H), 6.46–6.36 (m, 2H), 3.67 (q,

J = 7.0 Hz, 2H), 2.90 (t, J = 7.0 Hz, 2H). mp: 115–117 °C. ESI-MS, m/z for C₁₃H₁₄NO₂ [M + H]⁺ 216.1. Purity: 99.7% (LCMS).

N-Phenethylthiophene-2-carboxamide (**5 f**): White solid, 73.2% [50]. ¹H NMR (300 MHz, CDCl₃) δ 7.41–7.18 (m, 7H), 7.08–7.01 (m, 1H), 6.00 (br s, 1H), 3.67 (q, J = 7.0 Hz, 2H), 2.90 (t, J = 7.0 Hz, 2H). mp: 116–119 °C. ESI-MS, m/z for C₁₃H₁₄NOS [M + H]⁺ 232.1. Purity: 99.8% (LCMS).

N-Phenethyl-1-naphthamide (**5** g): White solid, 72.8% [47]. ¹H NMR (300 MHz, CDCl₃) δ 8.20–8.16 (m, 1H), 7.81–7.75 (m, 2H), 7.50–7.44 (m, 3H), 7.40–7.23 (m, 6H), 5.96 (br s, 1H), 3.82 (q, *J* = 6.6 Hz, 2H), 2.99 (t, *J* = 6.8 Hz, 2H). mp: 125–128 °C. ESI-MS, m/z for C₁₉H₁₈NO [M + H]⁺ 276.1. Purity: 99.2% (LCMS).

N-Phenethylquinoline-2-carboxamide (**5** h): White solid, 79.9% [51]. ¹H NMR (300 MHz, CDCl₃) δ 8.36–8.27 (m, 1H), 8.30 (s, 2H), 8.04 (d, *J* = 8.5 Hz, 1H), 7.86 (dd, *J* = 8.1, 1.5 Hz, 1H), 7.74 (ddd, *J* = 8.5, 6.9, 1.5 Hz, 1H), 7.60 (dd, *J* = 8.2, 6.8 Hz, 1H), 7.36–7.19 (m, 5H), 3.78 (q, *J* = 7.6 Hz, 2H), 2.99 (t, *J* = 7.3 Hz, 2H). mp: 81–84 °C. ESI-MS, m/z for C₁₈H₁₇N₂O [M + H]⁺ 277.1. Purity: 99.56% (LCMS).

N-(Benzyloxy)benzamide (**7a**): White solid, 77.9% [**33**]. ¹H NMR (300 MHz, DMSO-d₆) δ 11.76 (s, 1H), 7.75 (d, *J* = 7.6 Hz, 2H), 7.55–7.32 (m, 8H), 4.93 (s, 2H). mp: 104–106 °C. ESI-MS, m/z for C₁₄H₁₄NO₂ [M + H]⁺ 228.1. Purity: 99.6% (LCMS).

N-(Benzyloxy)isonicotinamide (**7b**): White solid, 86.1%. ¹H NMR (300 MHz, DMSO-d₆) δ 12.07 (br s, 1H), 8.72 (d, *J* = 4.9 Hz, 2H), 7.65 (d, *J* = 5.3 Hz, 2H), 7.43 (dd, *J* = 19.5, 6.8 Hz, 5H), 4.96 (s, 2H). mp: 117–120 °C. ESI-HRMS, m/z for C₁₃H₁₄N₂O₂ [M + H]⁺ 229.0977, found 229.0966. Purity: 99.4% (LCMS).

N-(Benzyloxy)picolinamide (**7c**): Yellowish oil, 77.0% [52]. ¹H NMR (300 MHz, DMSO-d₆) δ 12.04 (s, 1H), 8.61 (d, *J* = 4.7 Hz, 1H), 8.00 (d, *J* = 4.0 Hz, 2H), 7.62–7.37 (m, 6H), 4.95 (s, 2H). ESI-MS, m/z for C₁₃H₁₃N₂O₂ [M + H]⁺ 229.1. Purity: 99.7% (LCMS).

N-(Benzyloxy)-1*H*-pyrrole-2-carboxamide (**7d**): White solid, [53]. ¹H NMR (300 MHz, CDCl₃) δ 9.51 (br s, 1H), 7.39–7.24 (m, 5H), 6.91 (td, *J* = 2.7, 1.3 Hz, 1H), 6.52 (dd, *J* = 3.8, 2.5 Hz, 1H), 6.21 (dt, *J* = 3.7, 2.6 Hz, 1H), 6.13 (br s, 1H), 4.60 (d, *J* = 5.9 Hz, 2H). mp: 77–80 °C. ESI-MS, m/z for C₁₂H₁₃N₂O₂ [M + H]⁺ 217.1. Purity: 96.5% (LCMS).

N-(Benzyloxy)furan-2-carboxamide (**7e**): White solid, 77.9% [54]. ¹H NMR (300 MHz, DMSO-d₆) δ 11.74 (s, 1H), 7.86 (s, 1H), 7.46–7.36 (m, 5H), 7.10 (d, *J* = 4.3 Hz, 1H), 6.63 (s, 1H), 4.90 (s, 2H). mp: 82–85 °C. ESI-MS, m/z for C₁₂H₁₂NO₃ [M + H]⁺ 218.1. Purity: 99.9% (LCMS).

N-(Benzyloxy)thiophene-2-carboxamide (**7 f**): White solid, 92.9% [55]. ¹H NMR (300 MHz, DMSO-d₆) δ 11.79 (s, 1H), 7.83–7.81 (m, 1H), 7.65–7.62 (m, 1H), 7.46–7.34

(m, 5H), 7.15 (d, J = 4.3 Hz, 1H), 4.92 (s, 2H). mp: 103–106 °C. ESI-MS, m/z for $C_{12}H_{12}NO_2S$ [M + H]⁺ 234.1. Purity: 98.7% (LCMS).

N-(Benzyloxy)-1-naphthamide (**7** g): White solid, 72.1% [56]. ¹H NMR (300 MHz, CDCl₃) δ 8.30–8.21 (m, 2H), 7.90 (d, *J* = 8.2 Hz, 1H), 7.87–7.79 (m, 1H), 7.58–7.32 (m, 8H), 5.13 (s, 2H). mp: 132–135 °C. ESI-MS, m/z for C₁₈H₁₆NO₂ [M + H]⁺ 278.1. Purity: 98.9% (LCMS).

N-(Benzyloxy)quinoline-2-carboxamide (**7 h**): White solid, 80.1% [57]. ¹H NMR (300 MHz, CDCl₃) δ 10.35 (s, 1H), 8.26 (dd, *J* = 8.5 1.5 Hz, 2H), 8.02 (d, *J* = 8.5 Hz, 1H), 7.9 (dd, *J* = 8.2, 1.4 Hz, 1H), 7.74 (dd, *J* = 8.5, 6.9 Hz, 1H), 7.61 (dd, *J* = 8.1, 6.8 Hz, 1H), 7.52–7.49 (m, 2H), 7.41–7.38 (m, 2H), 5.11 (s, 2H). ESI-MS, m/z for C₁₇H₁₈N₂O₂ [M + H]⁺ 279.1. Purity: 99.7% (LCMS).

General procedure for the synthesis of 3i, 5i, 7i

Phenylmethanamine (2) (1 mmol), or 2-phenylethylamine (4) (1 mmol), or O-benzyloxyamine (6) (1 mmol) was added into a 50 mL round bottom flask containing 15 mL anhydrous THF. Next, 1.0 equivalent 1H-indole-2-carboxylic acid, 1.2 equivalent EDC hydrochloride, 1.5 equiv 1-hydroxybenzotriazole (HOBt), and 2.2 equivalent TEA were added in sequence. The reaction was kept at room temperature overnight. The solvent was evaporated in vacuo and the resulting reaction mixture was dissolved in 15 ml EtOAc and washed with 15 ml brine solution (x 3). The organic layer was collected, dried over anhydrous MgSO₄ and filtered. The organic solvent was then removed in vacuo to obtain a residue/oil which was further purified by silica gel column chromatography using either 1:1 *n*-hexanes: EtOAc or 5:2 *n*-hexanes: EtOAc as eluents to afford 3i, 5i and 7i in yields ranging from 80-92%. Their analytical data is given below. The ¹H NMR spectra and LCMS chromatograms are provided in the Supporting Information.

N-Benzyl-1*H*-indole-2-carboxamide (**3i**): White solid, 90.6% [45]. ¹H NMR (300 MHz, DMSO-d₆) δ 11.56 (s, 1H), 9.00 (t, *J* = 6.1 Hz, 1H), 7.57 (d, *J* = 8.0 Hz, 1H), 7.41 (d, *J* = 8.2 Hz, 1H), 7.38–7.27 (m, 4H), 7.17–7.12 (m, 3H), 7.03–6.98 (m, 1H), 4.49 (d, *J* = 6.0 Hz, 2H). mp: 229–232 °C. ESI-MS, m/z for C₁₆H₁₅N₂O [M + H]⁺ 251.1.Purity: 95.4% (LCMS).

N-(Phenethyl)-1*H*-indole-2-carboxamide (**5**i): White solid, 87.5% [**5**8]. ¹H NMR (300 MHz, DMSO-d₆) δ 11.51 (br s, 1H), 8.57 (t, *J* = 5.6 Hz, 1H), 7.60 (d, *J* = 7.9 Hz, 1H), 7.43 (d, *J* = 8.2 Hz, 1H), 7.34–7.01 (m, 6H), 3.49–3.55 (m, 2H), 2.87 (t, *J* = 7.4 Hz, 2H). mp: 191–194 °C. ESI-MS, m/z for C₁₇H₁₇N₂O [M + H]⁺ 265.1. Purity: 97.6% (LCMS).

N-(Benzyloxy)-1*H*-indole-2-carboxamide (**7i**): White solid, 82.7% [**59**]. ¹H NMR (300 MHz, DMSO-d₆) δ 11.81 (s, 1H), 11.66 (s, 1H), 7.60 (d, *J* = 7.9 Hz, 1H), 7.42 (dq, *J* = 14.0, 7.0, 6.4 Hz, 6H), 7.20 (t, *J* = 7.5 Hz, 1H),

7.09–6.96 (m, 2H), 4.96 (s, 2H). mp: 152–155 °C. ESI-MS, m/z for $C_{16}H_{15}N_2O_2 \ [M+H]^+$ 267.1. Purity: 95.6% (LCMS).

Biological activity assay

ThT-based Aβ42 aggregation inhibition assay

The ability of benzamide derivatives 3a-i, 5a-i and 7a-i to inhibit the AB42 aggregation was evaluated using the thioflavin T (ThT) based fluorescence kinetic assay [34]. A 15 µM ThT solution was prepared in ultra-pure-water (UPW) in 50 mM glycine buffer. The pH of the solution was adjusted to 7.4 with 50 mM sodium hydroxide solution. The aggregation assay was carried out using 215 mM sodium phosphate dibasic heptahydrate buffer prepared in UPW and the pH was adjusted to 7.4 by using 50 mM hydrochloric acid solution. The A β 42•HFIP>95% pure (Anaspec, USA) was treated with 1% ammonium hydroxide solution to afford 1 mg/mL stock solution. The stock solution was then vortexed and sonicated for 5 min before diluted to 50 µM working solution using the assay buffer. The stock solutions of test compounds 3a-i, 5a-i, 7a-i and resveratrol (RVT), were prepared in assay buffer with DMSO as the solubilizing agent (final concentration per well was less than 2%). The 24 h aggregation kinetics assay was carried out using 384-well plates (Costar, black, clearbottom), by adding 44 µL of ThT, 12 µL of assay buffer, $16 \,\mu\text{L}$ of A β 42 solution (10 μ M final well concentration), and $8 \,\mu L$ of test compound dilution (25 μM) into each well. The Aβ42 control wells contained ThT, Aβ42 solution and the assay buffer without any test compound. The plates were covered with a transparent plate cover and were incubated at 37 °C for 24 h with shaking at 300 cpm between readings for 30 s. The readings were taken every 10 min (bottom reading), with an excitation wavelength of 440 nm and an emission wavelength of 490 nm using the BioTek Synergy H1 microplate reader. Each sample was measured in triplicate readings and the results were obtained based on three independent experiments.

TEM studies to determine Aβ42 morphology

The TEM assay was carried out by first running the A β 42 aggregation assay (as described above in the ThT assay) [34] by incubating test compounds **3a**, **3f**, **3h**, **5a**, **5f** and **7a** (25 μ M each) with A β 42 (10 μ M) for 24 h at 37 °C. The TEM grids were prepared by aliquoting 20 μ L each sample from the 384-well plate after the 24 h incubation period. These samples were loaded onto 400-mesh formvar-coated copper grid (Electron Microscopy Sciences, USA). The grids were air-dried overnight before washing with 40 μ L of

UPW for three times. After washing, the grids were further air-dried for another 4 h. Then, grids were stained with $20 \,\mu\text{L} 2\%$ phosphotungstic acid solution for 30 s. The imaging studies were carried out using a Philips CM 10 TEM (Dept. of Biology, University of Waterloo) at 60 kV and the micrographs were obtained through 14-megapixel AMT camera at 60,000X magnification.

Aβ42-induced cytotoxicity assay in mouse hippocampal HT22 neuronal cell line

The cytotoxicity and neuroprotective effects of benzamide derivatives 3a, 3f, 3h, 5a, 5f and 7a toward HT22 cells was carried out by using the UV-based cell metabolism assay kit (cell counting kit 8, CCK-8, TargetMol, USA). The HT22 cells were cultured in DMEM/F12 1:1 with the addition of glutamate supplemented with 10% FBS and 1% penicillin and streptomycin at 37 °C in 5% CO2. The cells were seeded at a density of 50,000 cells per 1 mL. After 24 h, the cells were treated with various compounds (25 µM) prepared in phosphate buffer pH 7.4 and DMSO (less than 2%) and incubated for 48 h. After that, the CCK-8 reagent was added to each well, and incubated for another 2 h, before measuring the UV absorbance at 450 nm as per the manufacturer's protocol. The neuroprotective effects of test compounds (25 µM) toward Aβ42-induced cytotoxicity was determined by treating the HT22 cells with 5 µM of A β 42•HFIP (>95%, rPeptide USA), and then incubating for 48 h at 37 °C [34]. The cell viability assay was determined by adding the CCK-8 reagent and incubating for another 2 h to measure the absorbance at 450 nm. The cell viability was calculated as average percent cell viability based on quadruplicate readings and based on three independent experiments.

Fluorescence live cell imaging in mouse hippocampal HT22 cell line

The A β 42 used in the assay was purchased from Bachem Americas Inc, Torrance, CA, USA. The HT22 cells were cultured and treated as per A β 42-induced cytotoxicity assay. After treatment, the cells were washed with PBS and then stained with ProteoStat[®] working solution (prepared according to the vendor's manual, ENZO Life Sciences, USA) for 20 min under dark at 37 °C [35]. Then the cells were washed with PBS three times with 5 min incubation at 37 °C to rinse out the excessive amount of dye. The cells were then visualized with an EVOS[®] FL Auto imaging system with an RFP light cube at fixed light intensity. The binary masks were generated by thresholding the original fluorescence images using the Huang algorithm in ImageJ software and used to measure the integrated gray value (IGV) of ProteoStat[®]-positive stains. The results presented are averages of three independent experiments with three randomized views.

LDH release cytotoxicity assay in mouse hippocampal HT22 cell line

The CytoScan^{*} LDH assay kit was used to determine the LDH release (G-Biosciences, St. Louis, MO, USA) [37]. The reagents and solutions were prepared according to vendor's manual. The HT22 cells were cultured and treated with 10 μ M A β 42 (Bachem, USA) as per A β 42-induced cytotoxicity assay protocol. After treatment, 50 μ L of the cell medium was transferred to a new well plate followed by the addition of 50 μ L reaction mixture and further incubated for 20 min at 37 °C. This was followed by the addition of 50 μ L stop solution before taking the readings at 490 nm and 680 nm. The percentage LDH release was calculated by subtracting the absorbance reading at 680 nm from that of 490 nm, and compared to A β 42 control group. The results shown are averages of quadruplicate readings based on three independent experiments.

Molecular docking studies of compounds in Aβ42

The binding interactions 3a (N-benzylbenzamide), 5a (*N*-phenethylbenzamide) and **7a** (*N*-benzyloxybenzamide) Aβ42 were investigated by carrying out molecular docking studies conducted on Discovery Studio software program v20.1.0.19295, Structure-Based-Design program (BIOIA Inc. San Diego, USA). The A β 42 pentamer model was prepared by extracting the coordinates from the solved 3D structure of Aβ42 fibril (PDB id: 5KK3) [34, 39]. A binding sphere of 20 Å radius was selected and defined as the ligand binding site which covers the KLVFFA and the C-terminal IGLMVGGVVIA hydrophobic region of the A β 42. Compounds **3a**, **5a** and **7a** were built in 3D using the Small Molecules module in the software and were subjected to energy minimization protocol (1000 and 2000 steps of steepest descent followed by conjugate gradient method) using CHARMm force field. The CDOCKER algorithm was used to carry out the docking studies. The Receptor-Ligand Interactions module in the software was used to perform CDOCKER simulations. The docking simulation included 2000 heating steps, a heating target temperature of 700 K and 5000 cooling steps and a cooling target temperature of 300 K. The top ligand binding modes of **3a**, **5a** and **7a** with A β 42 pentamer assembly was analyzed by evaluating the CDOCKER energy and CDOCKER interaction energies (in kcal/mol). Further analysis was carried out by determining the polar and nonpolar contacts of test compounds in the A β 42 pentamer assembly.

In silico physicochemical and ADME analysis

The physicochemical properties including H-bond acceptors, H-bond donors, topological polar surface area (TPSA), blood-brain barrier permeability (BBB), lipophilicity parameter Log P, and structural alert flags were calculated for representative compounds (**3a**, **3f**, **5a**, **7a** and chalcone) using the SwissADME web tool [38].

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Author contributions PPNR and YZ conceived the project and designed experiments. YZ, AS and AAF performed experiments. PPNR, YZ, AS and AAF analyzed and interpreted results. PPNR and YZ wrote the manuscript. PPNR, YZ, AS and AAF revised the manuscript.

Compliance with ethical standards

Conflict of interest The authors declare no competing interests.

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