

Synthesis of Monomeric Derivatives To Probe Memoquin's Bivalent Interactions

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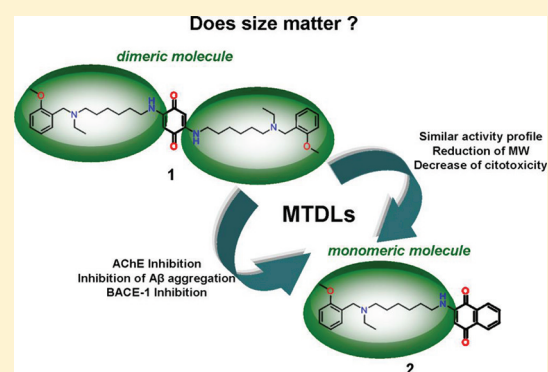
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S Supporting Information

ABSTRACT: Eight monomeric congeners, related to the multitarget lead candidate memoquin, were prepared and evaluated at multiple targets to determine their profile against Alzheimer's disease. 2–4 bind to AChE with similar low nanomolar affinities and function as effective inhibitors of amyloid aggregation. The most potent monovalent ligand 2 also inhibits BACE-1 in vitro and APP metabolism in primary chicken telencephalic neurons.



■ INTRODUCTION

Memoquin (**1**) was rationally designed to create a new chemical entity (NCE) with a polypharmacological profile against Alzheimer's disease (AD).^{1,2} An in vitro and in vivo characterization revealed its multifunctional mechanism of action and its interaction with three molecular targets involved in AD pathology, namely, acetylcholinesterase (AChE), β -amyloid ($A\beta$), and β -secretase (BACE-1).³ **1** is thus the successful product of one of the first AD multitarget drug discovery efforts. This strategy is emerging as an alternative way to develop effective anti-AD drugs.^{4–7} Although the single-target approach remains the main strategy in big pharmaceutical companies, the ongoing failure of current candidates is convincing the pharmaceutical community that the desired outcome may be provided more effectively by a drug that modulates multiple targets.⁸ From a medicinal chemistry point of view, **1** is a bivalent ligand, with a symmetrical structure composed of two 2-methoxybenzylidiamino moieties connected by a benzoquinone spacer. Several examples of linking two pharmacophoric units via spacers of different length and flexibility were reported by Portoghese in the field of opioids.⁹ In AD too, the bivalent ligand strategy has received attention over the past decade.^{10–12} This was mostly motivated by the peculiar topology of a classical AD target, the enzyme AChE, which has two recognition sites sharing common molecular features.¹³ Consequently, improved potency is shown by drugs

that simultaneously bind the catalytic and the peripheral anionic (PAS) sites of AChE.^{14–18}

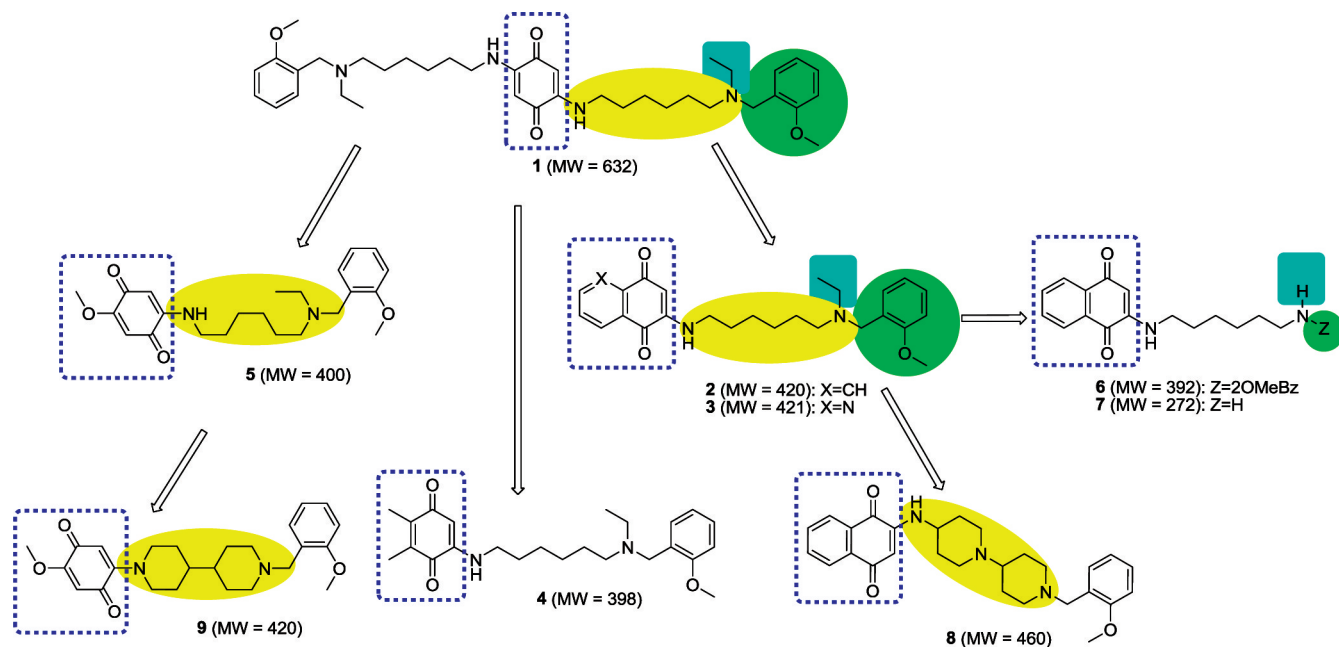
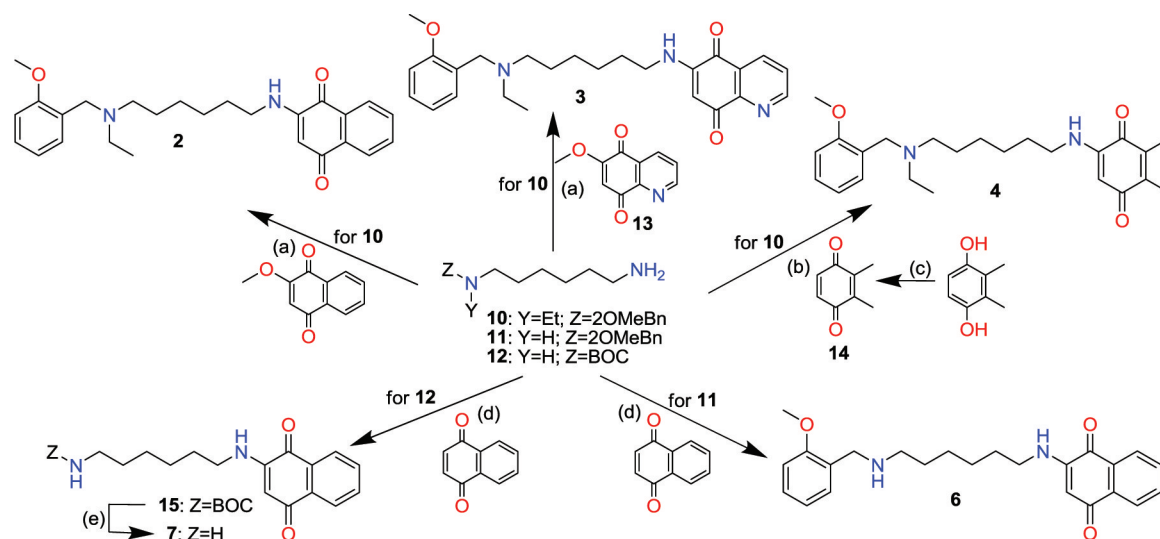
The multitarget approach could be considered an evolution of the bivalent ligands concept. This is because combining structural elements from two ligands into a single molecule.¹⁹ The rationale for using the bivalent ligand approach in AD also stems from the possibility that dimeric structures may be capable of bridging independent recognition sites on other validated targets (such as $A\beta$ and BACE-1), resulting in a binding interaction that is thermodynamically more favorable than the monovalent binding of two molecules. In principle, this would be particularly advantageous in view of the complexity of the recognition mechanism of protein–protein interactions in amyloidosis.²⁰ As a matter of fact, several amyloid binding compounds share a common bivalent structure and bivalent “molecular tweezers” have been envisaged as the next generation of ligands.²¹ Another positive feature of anti-AD bivalent ligands is that because of their high hindrance, they can efficiently fit the extended substrate binding site of BACE-1.²² However, their high molecular weight (MW) has negative consequences for the pharmacokinetic profile.

For **1**, we could verify absorption through oral administration and access to the central nervous system.²³ Nevertheless, if we

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Chart 1. Design Strategy for Monovalent Ligands 2–9

Scheme 1^a

^aReagents and conditions: (a) EtOH, 4 h, reflux; (b) CH₂Cl₂, 3 h, air, room temp; (c) MnO₂, dry Et₂O, 4 h, room temp; (d) MeOH, 4 h, air, room temp; (e) TFA, CHCl₃, 5 h, room temp.

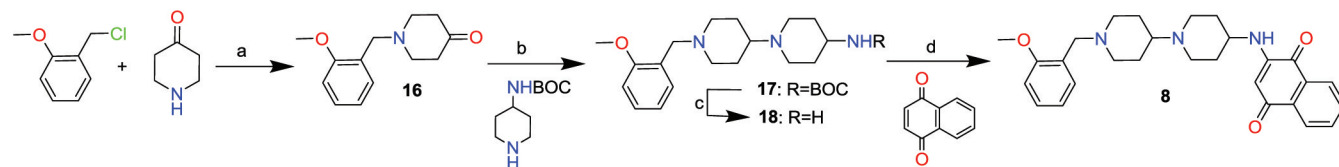
strictly reason in terms of Lipinski's rule,²⁴ **1** violates the MW parameter, being out of range (632 vs 500). On this basis, we sought to generate analogues of **1** with a reduced MW, yet maintaining its promising multitarget profile.

RESULTS AND DISCUSSION

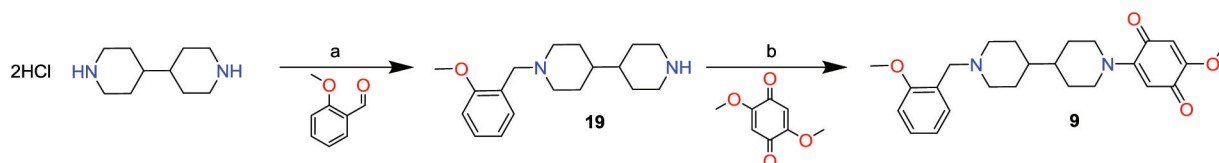
To this end, we prepared and then evaluated at multiple targets (AChE, $\alpha\beta$, BACE-1) eight congeners (**2–9**), which we formally obtained by cutting the dimeric structure of **1** in two halves. In the resulting monomeric compounds **2–5**, one of the two 2-methoxybenzyl-diamino chains of **1** is always preserved, with the ending fragments being a quinone, as a privileged motif for modulating protein–protein interactions.^{25–27} The selected quinones were a naphthoquinone (**2**), a quinolinoquinone (**3**), a 2,3-dimethylbenzoquinone (**4**), and a 2-

methoxybenzoquinone (**5**). Conversely, in **6** and **7** a structural simplification has been performed to investigate the role of the ethyl- and 2-methoxybenzyl substituents on the basic nitrogen of **2**. Moreover, we reduced the flexibility at the polymethylene chain of **2** and **5** because conformationally restricted analogues **8** and **9** might show improved potency. Notably, all compounds displayed a MW below the 500 Da cutoff (see Chart 1 for design strategy).

In previous studies, we verified that 1,4-Michael addition or substitution reactions would allow us to effectively incorporate a diamine chain into the 2-position of a quinone.^{1,2,28} In the cases of **2** and **3**, we used a substitution reaction, which also led to the unambiguous synthesis of **3**. Thus, treating 2-methoxynaphthalene-1,4-dione or 6-methoxyquinoline-5,8-dione (**13**)²⁹ with diamine **10**^{1,2} gave target compounds in

Scheme 2^a

^aReagents and conditions: (a) K_2CO_3 , KI, DMF, 4 h, reflux; (b) dry THF, $(CH_3COO)_3BHNa$, CH_3COOH , N_2 , overnight, room temp; (c) TFA, dry CH_2Cl_2 , 5 h, room temp; (d) MeOH, 5 h, air, room temp.

Scheme 3^a

^aReagents and conditions: (a) $NaBH_3CN$, KOH, MeOH, 3 h, room temp; (b) $CHCl_3$, 72 h, reflux.

Table 1. Inhibitory Activity on Human AChE and BuChE, BACE-1, and Amyloid Aggregation by 2–9 and Reference Compound 1

compd	IC_{50} (nM) ^a		inhibition of BACE-1 (%) ^b	inhibition of $A\beta$ aggregation (%)	
	hAChE	hBuChE		AChE-induced ^c	self-induced ^d
1	1.55 ± 0.11	144 ± 100	>80	87.1 ± 1.7	66.8 ± 4.4
2	9.73 ± 0.44	1490 ± 100	60.2 ± 1.6	69.1 ± 3.2	27.3 ± 4.3
3	27.9 ± 1.6	2560 ± 170	na	41.3 ± 0.7	15.4 ± 6.7
4	29.0 ± 4.0	314 ± 21	12.8 ± 2.0	60.6 ± 0.2	30.2 ± 1.4
5	65.3 ± 2.2	22800 ± 1600	32.8 ± 2.4	nt	45.7 ± 3.4
6	1850 ± 30	3320 ± 260	na	nt	29.5 ± 0.9
7	64500 ± 2700	294000 ± 25000	na	nt	13.8 ± 4.1
8	17200 ± 1000	3160 ± 130	na	nt	21.4 ± 1.3
9	24400 ± 1400	3580 ± 150	32.9 ± 1.0	nt	20.5 ± 1.0

^aHuman recombinant AChE and BuChE from human serum were used. $IC_{50} \pm SEM$ values represent the concentration of inhibitor required to decrease enzyme activity by 50% and are the mean of two independent measurements, each performed in duplicate. ^bInhibition of BACE-1. The concentration of the tested inhibitor was $3 \mu M$. Experimental conditions are as in ref 22. For 2 $IC_{50} = 2.8 \pm 0.1 \mu M$. IC_{50} represents the concentration of inhibitor required to decrease enzyme activity by 50% and is the mean of three independent measurements, each performed in duplicate; na = not active. ^cInhibition of AChE-induced $A\beta_{40}$ aggregation. The concentration of the tested inhibitor and $A\beta_{40}$ was 100 and $230 \mu M$, respectively, whereas the $A\beta_{40}/AChE$ ratio was equal to 100:1. Values are the mean of two independent experiments each performed in duplicate; nt = not tested. ^dInhibition of $50 \mu M A\beta_{42}$ self-aggregation when $[I] = 10 \mu M$ was used. The $A\beta_{42}/inhibitor$ ratio was equal to 5:1. Values are the mean of two independent experiments each performed in duplicate.

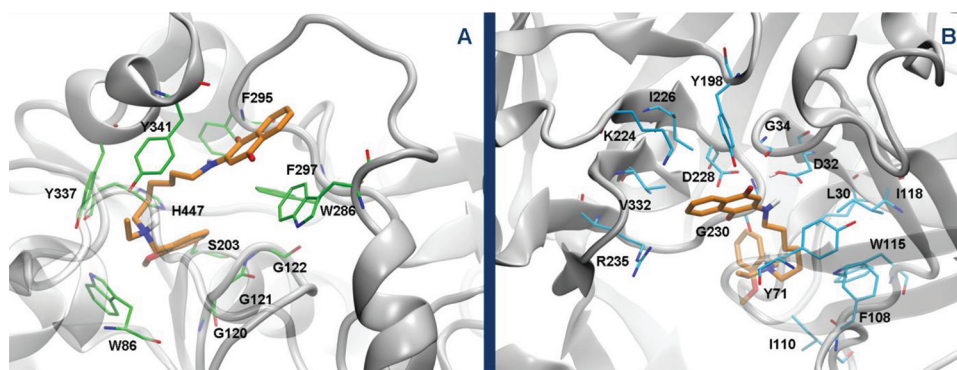


Figure 1. Low energy docking model of 2 (orange) into the active sites of AChE (A, residues displayed in light green) and BACE-1 (B, residues displayed in light cyan).

good yields. Conversely, 4 was synthesized by reacting 10 with quinone 14, obtained, in turn, by oxidation of 2,3-dimethylbenzene-1,4-diol. Similarly, Michael addition of amines

11² and 12 afforded 6 and 15, respectively. Subsequent deprotection of BOC protecting group of 15 led to final compound 7 (Scheme 1). Michael addition was also used to

synthesize **8**, starting from naphthoquinone and **18** (Scheme 2). The amine **18** was derived by reductive amination between the commercially available *tert*-butyl piperidin-4-ylcarbamate and **16**, obtained by a nucleophilic substitution reaction, followed by BOC removal. Finally, to obtain **9**, monosubstitution of 2,5-dimethoxy-1,4-benzoquinone with diamine **19**, synthesized through an efficient reductive amination protocol, was carried out as reported for **5**³⁰ (Scheme 3).

To characterize the multitarget profiles of **2–9**, their inhibitory activity at human AChE and butyrylcholinesterase (BuChE) (Table 1) was tested. Kinetic and molecular modeling evidence has demonstrated that **1** is a dual binding cholinesterases inhibitor, which accounts for its remarkable nanomolar activity.^{1,2} Interestingly, all compounds, except **6–9** were effective inhibitors of AChE, with **2** being just 6 times less potent than **1**. This suggests that even the monovalent structures of **2–5** could establish interactions with both sites of the enzyme. However, the low activity displayed by **6** and **7** confirms the importance of an ethyl and a 2-methoxybenzyl group as substituents on the terminal protonable nitrogen, as verified for **1** derivatives.^{2,27} It is also plausible that the constrained structures of **8** and **9** did not allow an optimal docking into the AChE gorge. Figure 1A reports the bound conformation of **2**, resulting from docking simulations carried out at the active site of hAChE (PDB code 1B41; see Supporting Information). Here, we see that **2** was able to interact with the catalytic region and at the same time to protrude toward the solvent-exposed gorge entrance. The following interactions between **2** and hAChE were observed: (i) the ligand protonated nitrogen established a cation– π interaction with the indole ring of W86 and the phenol ring of Y337; (ii) the oxygen in position 1 of the quinone moiety established an H-bond interaction with the backbone of F295; (iii) the naphthalenedione moiety established a favorable π – π stacking with the indole ring of W286 of the PAS. This last finding was relevant in the context of previous reports that linked inhibition of AChE-induced $A\beta$ aggregation with a binder's ability to interact with the PAS of the enzyme.^{31,32}

Indeed, the AChE-induced $A\beta$ aggregation experiments,^{31,32} performed on the three most active AChEs **2–4**, are in agreement with the proposed binding mode at AChE. Activities in the AChE-induced aggregation and AChE inhibition were highly correlated for **2**, which was the most potent in both assays. The IC_{50} for the inhibition of the AChE-induced $A\beta$ aggregation by **2** was also calculated, being $45 \pm 6 \mu\text{M}$. A different pattern was found for **4**, which is the less potent against AChE, while showing an intermediate antiaggregation activity. Concerning the physiological relevance of these *in vitro* studies, it must be taken into account that the AChE concentration in the induced $A\beta$ aggregation assay is roughly 1000–3000 times higher than that in the cerebrospinal fluid of AD patients.³³ Consequently, inhibitory activity reported in Table 1 refers to a normalized inhibitor concentration of 35–100 nM, a concentration that is closely correlated with those needed to exert the other activities.

In light of the remarkable antiaggregating properties of **1**³⁴ and several other bivalent ligands,^{22,35} the ability of **2–9** to reduce $A\beta_{42}$ spontaneous aggregation was then investigated. Data in Table 1 show that **2–9** at $10 \mu\text{M}$ inhibited $A\beta$ self-aggregation in a range from 14% to 46%. At the same concentration, **1** displayed 68%, which is less than 2 times higher than that of the most potent compound **5**. Interestingly, two protonable diamino chains of **1** do not appear to be

necessary for $A\beta$ binding. Conversely, these data pinpoint to the quinone core as an essential feature for potent aggregation inhibition, in agreement with the well-documented inhibitory capability of quinones toward $A\beta$ assembly.^{25–27,36–38} Spacer flexibility also seems to be important, with **9** showing halved percent inhibition with respect to **5**. When rigid **8** is compared to flexible **2**, the relatively lower reduction in potency (29% vs 22%, respectively) might be attributed to the concomitant presence in **8** of an additional protonable nitrogen atom, which could establish additional positive interactions.

As part of its multitarget profile, **1** inhibits BACE-1 quite effectively.¹ Therefore, preliminary studies were carried out to assess whether the monomeric derivatives retained the ability to inhibit BACE-1 *in vitro*. **2–9** were tested at $3 \mu\text{M}$, and their inhibition percentages are reported in Table 1 in comparison to **1** (80%). The most potent compounds were **2**, **5**, and **9**, which inhibited enzyme activity at 32–60%, whereas **3** and **6–8** showed no activity. For **2** we also determined an IC_{50} of $2.8 \mu\text{M}$. To check for nonspecific effects, additional experiments were performed on **1** and **2** with a different source of enzyme and type of substrate and in the presence of a detergent (see Supporting Information). In this second assay, **2** showed a similar potency ($IC_{50} = 3.0 \mu\text{M}$) while **1** was less active ($IC_{50} = 4.6 \mu\text{M}$). The discrepancy of results between the two assays for **1** is likely to be a consequence of differences in the substrate, protein, and assay buffer. Docking simulations were performed in an attempt to provide a plausible binding mode compatible with the BACE-1 inhibitory profile of **2**. Figure 1B reports the binding mode of **2** at BACE-1 protease site (PDB code 2QZL). The leading interactions that characterized the bound complex were the following: (i) the proximal nitrogen of the spacer established two H-bond interactions with the side chain of catalytic D32 and with the carbonyl oxygen of G34 backbone; (ii) the oxygen in position 4 of naphthalenedione moiety interacted via H-bond with the side chain of Y198; (iii) the protonated nitrogen established an H-bond interaction with the carbonyl oxygen of G230 backbone; (iv) the aliphatic chain of the spacer was lodged in a hydrophobic subpocket described by Y71, F108, I110, L30, I118, and W115; (v) the quinone formed hydrophobic contacts with I226 and V332. In summary, in the reported bound conformation, **2** contacted directly the catalytic dyad and several subsites that have been previously exploited to achieve inhibitory potency.³⁹

To further substantiate the secretase inhibitory activity of **2**, **5**, and **9**, we also tested whether they affect APP processing in a cellular context. This study was carried out in primary chicken telencephalon neurons to assess the effect on secretion of $A\beta_{38}$, $A\beta_{40}$, and $A\beta_{42}$.⁴⁰ Thus, intrinsic cell toxicity of **2**, **5**, and **9** was first evaluated, using **1** as reference compound. Treating primary neurons for 24 h with **2** ($0.01–50 \mu\text{M}$) did not lead to modified viability, whereas treatment with high concentrations of **5** ($50 \mu\text{M}$), **1** ($25 \mu\text{M}$), and **9** ($25 \mu\text{M}$) significantly abolished neuronal viability (see Supporting Information). Notably, **1** exhibited a similar toxicity in the SH-SY5Y cell line.²⁷ These data are encouraging because they point to a molecule-based toxicity rather than to a potential mechanism of toxicity related to the quinone moiety. Concerning studies on amyloid peptides production, **2** inhibited $A\beta_{38}$, $A\beta_{40}$, and $A\beta_{42}$ secretion, with IC_{50} values of 19, 21, and $46 \mu\text{M}$, respectively. These values were corrected with mean neurons viability, obtained in the MTT reduction assay. Conversely, because of their toxicity, a clear concentration-dependent decrease in $A\beta$

secretion could not be observed for **1**, **5**, and **9** (see Supporting Information).

There is a growing body of evidence that multitarget-directed ligands (MTDLs)⁴ provide a viable area for AD drug discovery. One limitation to this approach is that most of the hits discovered so far tend to have high MW, resulting in new NCEs that are eventually associated with poor oral bioavailability.⁴¹ The low ligand efficiency of MTDLs is a critical issue. This is because affinity at the different targets usually parallels the increase in MW, whereas pharmacokinetic properties are improved by reducing the MW.⁴¹ However, small molecule MTDLs (MW \approx 500) have been reported.⁴² Interestingly, in the present series of **1** derivatives, the reduction of MW did not necessarily correspond to a reduction in the multiple activities. In fact, for the most active compound **2**, the MTDL activity profile remains almost unchanged with respect to **1**, with the toxicity profile actually being improved.

In conclusion, if the decrease in MW translates into the expected superior bioavailability, **2** could be a promising starting point in the search for new MTDLs against AD.

EXPERIMENTAL SECTION

Chemistry. All starting reagents were of the best grade available from Aldrich and TCI. Melting points were taken in glass capillary tubes on Buchi SMP-20 apparatus and are uncorrected. Direct infusion ESI-MS spectra were recorded on Waters ZQ 4000 apparatus. ¹H NMR and ¹³C NMR spectra were recorded either at 200 MHz (¹H) and 50.3 MHz (¹³C) or at 400 MHz (¹H) and 100 MHz (¹³C). Chemical shifts are reported in parts per million (ppm) relative to tetramethylsilane (TMS), and spin multiplicities are given as s (singlet), brs (broad singlet), d (doublet), t (triplet), or m (multiplet). Elemental analysis was used to confirm $\geq 95\%$ sample purity, and the elemental compositions of the compounds agreed to within $\pm 0.4\%$ of the calculated value. Chromatographic separations were performed on silica gel columns by flash chromatography (Kieselgel 40, 0.040–0.063 mm; Merck). Reactions were followed by thin-layer chromatography (TLC) on Merck (0.25 mm) glass-packed precoated silica gel plates (60 F254), then visualized in an iodine chamber or with a UV lamp. Compounds were named following IUPAC rules as applied by Beilstein-Institute AutoNom (version 2.1), a PC integrated software package for systematic names in organic chemistry.

Synthesis of 2. The 2-methoxynaphthalene-1,4-dione (0.15 g, 0.83 mmol) was dissolved in EtOH (6 mL) at reflux temperature. To this suspension, a solution of **10**¹² (0.2 g, 0.76 mmol) in EtOH (6 mL) was added. The resulting reaction mixture was stirred at reflux temperature for 4 h. The solvent was evaporated under vacuo, and the final red crude product was purified by gravity chromatography (CH₂Cl₂/EtOH/aqueous 33% ammonia = 9/1/0.03). Compound **2** (0.11 g) was obtained as a red solid. Yield 34%; mp = 72 °C. ESI-MS (*m/z*): 421 (*M* + *H*⁺). ¹H NMR (CDCl₃, 400 MHz): δ 8.08 (d, *J* = 8.4, 1H), 8.02 (d, *J* = 8.4, 1H), 7.71 (t, *J* = 7.2, 1H), 7.59 (t, *J* = 7.2, 1H), 7.41–7.39 (m, 1H), 7.19 (t, *J* = 7.2, 1H), 6.92 (t, *J* = 6.8, 1H), 6.83 (d, *J* = 8.0, 1H), 5.85 (br s exch, 1H), 5.70 (s, 1H), 3.80 (s, 3H), 3.59 (br s, 2H), 3.12 (q, *J* = 6.4, 2H), 2.53–2.50 (m, 2H), 2.49–2.46 (m, 2H), 1.67–1.62 (m, 2H), 1.54–1.46 (m, 2H), 1.38–1.30 (m, 4H), 1.13–0.95 (m, 3H). ¹³C NMR (CDCl₃, 100 MHz): δ 182.9, 181.9, 157.7, 147.9, 134.7, 133.7, 131.9, 130.5, 130.1, 126.2, 126.1, 120.3, 110.2, 100.7, 100.6, 55.3, 53.2, 51.3, 47.7, 42.5, 28.2, 27.1, 26.9, 15.2, 11.7. Anal. Calcd for C₂₆H₃₂N₂O₃ (420.54): C, 74.26; H, 7.67; N, 6.66. Found: C, 74.60; H, 7.29; N, 6.31.

ASSOCIATED CONTENT

Supporting Information

Experimental details of the synthesis of **2–9** and computational and biological methods. This material is available free of charge via the Internet at <http://pubs.acs.org>.

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ABBREVIATIONS USED

A β , β -amyloid; AChE, acetylcholinesterase; AD, Alzheimer's disease; APP, amyloid precursor protein; BACE-1, β -secretase; BuChE, butyrylcholinesterase; MTDL, multitarget-directed ligand; MW, molecular weight; NCE, new chemical entity; PAS, peripheral anionic site

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