A Rapid *in vivo* Pipeline to Identify Small Molecule Inhibitors of Amyloid

Aggregation

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Abstract

Amyloids are associated with over 50 human diseases and have inspired significant

effort to identify small molecule remedies. Here, we present a novel *in vivo* platform

that efficiently yields small molecule disruptors of amyloid formation. We previously

identified small molecules that kill the nematode *C. elegans* by forming membrane-

piercing crystals in the pharynx cuticle, which is rich in amyloid-like material. We show

here that many of these molecules are known amyloid-binders whose crystal-formation

in the pharynx can be blocked by amyloid-binding dyes. Furthermore, we found that

amyloid fibrils can seed small molecule crystal formation *in vitro*. These observations

suggest that small molecule crystals are seeded by the cuticle's amyloid-like material.

We asked whether this phenomenon could be exploited to identify additional molecules

that interfere with the ability of amyloids to seed higher-order structures. We screened

2560 compounds and identified 85 crystal suppressors, which we found to be 10-fold

enriched in known amyloid disruptors relative to a random set. Of the uncharacterized

suppressors, we found 25% to inhibit Ab42 fibril nucleation and/or extension *in vitro*,

which is a hit rate that far exceeds other screening methodologies. Hence, screens for

suppressors of crystal formation can efficiently reveal small molecules with amyloid-

disrupting potential.

Introduction

Previous small molecule screens with the free-living nematode *C. elegans* serendipitously revealed compounds that visibly accumulate within the heads of worms [1-4]. This accumulation can be observed using a low magnification dissection light microscope [5]. We demonstrated that the accumulated small molecules form either birefringent irregular objects, globular non-birefringent spheres, or a mixture of the two, depending on the structure of the compound [5]. Birefringence is an optical property that reveals the subject to harbour repeating units that uniformly alter the angle of incidence of polarized transmitted light. We showed that these birefringent objects: i) are observable within minutes of exposure of the worms to the small molecule; ii) contain the exogenous small molecule; iii) grow over time; iv) are formed exclusively in association with the pharynx cuticle; and v) are not due to the consumption of precipitate in the media by the worm [5,6]. Given their birefringent nature and growth over time, we refer to the birefringent objects as crystals for simplicity's sake, although their exact biophysical nature remains to be determined (Figure 1A-C). The crystals kill younger animals likely because they perforate the plasma membrane of surrounding cells and rapidly grow to occlude the pharynx lumen [5].

More recently, we described how the crystals form in tight association with the non-luminal face of the *C. elegans* pharyngeal cuticle [6]. This cuticle is a flexible non-collagenous chitin-rich matrix that is repeatedly shed and rebuilt at each larval stage [7,8]. We also constructed a spatiotemporal map for the development of the pharyngeal cuticle of *C. elegans* [9]. That study revealed the pharynx cuticle to be highly enriched with

intrinsically disordered proteins (IDPs) and proteins with intrinsically disordered regions

(IDRs) [9]. Many of these IDP and IDR-rich proteins have amyloidogenic features that

include an enrichment in π-bonding and hydrogen-bonding capabilities, and have

protofilament formation propensity [9]. Furthermore, we and others showed that

amyloid-binding dyes specifically stain the pharyngeal cuticle [9,10]. Despite these findings,

neither transmission electron microscopy (TEM) nor diagnostic tests provide evidence

for extended amyloid fibrils within the pharyngeal cuticle [9,11-13], which is consistent with

the flexible nature of the cuticle [14,15]. Taken together, these observations indicated that

the cuticle is rich in amyloid-like material that lacks the highly ordered nature of amyloid

fibrils.

Here, we show that molecules that form crystals *in vivo* can indeed form a crystalline

lattice *in vitro* through π-bond interactions. We go on to show that over 50% of the 29

distinct structural scaffolds that form crystals *in vivo* are reported amyloid binders.

Consistent with these observations, we find that, i) nascent crystals distort the amyloid-

like material within the cuticle without a concomitant effect on the chitin matrix; ii)

Aβ42 fibrils can seed the formation of objects *in vitro* from a small molecule that forms

crystals *in vivo*; and iii) worms incubated with the amyloid-binders Congo Red and

Thioflavin S can block crystal formation. Collectively, these results suggest that the

amyloid-like material in the pharynx cuticle can seed the formation of small molecule

crystals.

Given that well-characterized amyloid binders can block the seeding of crystals in the

pharynx, we wondered whether the crystallization phenomenon could be exploited to

identify other small molecules that block the ability of amyloids to seed higher order

structures such as amyloid fibrils. We therefore screened 2560 drugs and natural

products for those that could suppress crystal formation in the *C. elegans* pharynx. The

screen yielded 85 reproducible suppressors, several of which are fluorescent and

specifically localize to the cuticle, which is consistent with their expected site of action.

The 85 crystal suppressors can be grouped into 45 distinct small molecule scaffolds.

Of these 45, one third are previously characterized disruptors of amyloid fibril

formation. We tested 44 of the suppressors that have not been previously implicated in

amyloid disruption and found that 11 (25%) inhibit Aβ42 aggregation. In total, 40 of the

85 suppressors (47%) were shown to disrupt amyloid formation of one type or another,

which is a hit rate higher than most previously reported screening methodologies [16-18].

We conclude that screens for suppressors of crystal formation within the *C. elegans*

pharynx cuticle can enrich for small molecules with amyloid-disrupting potential.

Results

Crystallizing Molecules are Aromatic, Compact, and Crystalize via π Bond Interactions

We previously identified 38 compounds that form crystals in association with the *C.*

elegans pharynx cuticle by surveying 238 compounds from our custom library of <u>worm-</u>

<u>act</u>ive (wactive or wact) small molecules [2,5]. We have since identified additional

crystalizing molecules from a targeted survey of the wactive library molecules to yield a

total of 48 crystallizing compounds (Supplemental Figure 1).

To better understand how these 48 crystallizing molecules differ from the 149 true

negatives that fail to crystalize, we extended our previous physicochemical analysis to

analyze a total of 72 features (Supplemental Table 1). We found no major differences in

molecular weight (*p*=0.75) or hydrophobicity (i.e., cLogP) (*p*=0.05), and as previously

reported [5], the crystallizing molecules have fewer rotatable bonds (*p*=4.3E-05) and

fewer hydrogen-bond donors (*p*=2.4E-06) than non-crystalizing wactives (Figure 1D).

Our more in-depth analysis shows that the crystallizing wactives are highly aromatic

(*p*=2.6E-10) and more compact (i.e., smaller van der Waals volume, *p*=7.3E-04). A

measure that combines these features, called fraction Csp3, reports the ratio of sp3

hybridized carbon atoms over the total carbon atom count of the small molecule [19] and

reveals the compactness of the crystallizing molecules (*p*=5.5E-09).

To test whether these features are specific to crystallizing molecules from the wactive

library, we screened two other libraries for crystallizing molecules. The first library was a

custom collection of 1178 small molecules called RLL1200 (Supplementary Datafile 1).

The second was the Spectrum library of 2560 drugs and natural products (Microsource

Inc). To identify crystalizing molecules from these libraries, we first screened them for

those that kill L1 larvae in our standard 6-day viability assay [2], reasoning that crystalizing

molecules invariably kill larvae [5] and would be among the hits. We identified 70 lethal

molecules from the RLL1200 library and 78 from the Spectrum library. To find

crystallizing molecules among these hits, we exploited our previous finding that the *sms-*

5(0) null mutant resists crystal-induced death by blocking crystal formation [5]. Re-

screening the lethal hits against the *sms-5(0)* mutant revealed 16 molecules from

RLL1200 and 1 molecule from Spectrum that: i) kill wild type; ii) fail to kill *sms-5(0)*

mutants; and iii) form crystals in association with the pharynx (Supplementary Datafile

1). The physicochemical features of the RLL1200 crystallizing molecules are not

significantly different from those of the wactive crystallizing molecules ($p>0.001$) (Figure

1D; Supplemental Table 1; Supplementary Datafile 1). Statistical analysis was not

conducted with the one Spectrum hit, but its properties are similar to the means of the

other crystalizing molecules. Hence, compact aromatic properties are common to most

crystallizing molecules.

Given that aromatic structures are rich in π bonds, we asked whether π bond

interactions might play a role in the crystallization of the small molecules *in vitro*. To

investigate, we used crystal powder-X-ray diffraction (PXRD) with two exemplar

molecules wact-190 and wact-416. Wact-190 crystallized in the triclinic crystal system

with the space group P-1, whereas wact-416 crystallized in the orthorhombic crystal

system with the space group Pna2$_1$ (Figure 2A-C, 2F-H; Supplemental Table 2;

Supplemental Figure 2). The centroids of the aromatic rings for the respective

crystalized molecules had distances of 5.0 Å or less, indicating that π-π interactions play

a key role in their assembly into higher ordered structures [20] (Figure 2D and I). We

compared the crystallization results with their simulated data to validate the bulk phase

purity of the crystals. In comparison to the computer-simulated data, the small molecule

crystals displayed a similar crystalline nature, peak-pattern matching and single-phase

identification, confirming the individual structural purity of the samples (Figure 2E and J;

Supplemental Figure 2).

Molecules that Induce Crystal Formation in *C. elegans* are Enriched with Amyloid-

Binding Substructures

To investigate the structural diversity among crystal-forming compounds, we created a

structural-similarity network by first reducing each molecule to its core scaffold. We

then linked the scaffolds that had a Tanimoto similarity coefficient of 0.8 or more (see

methods). This produced a network of 6 clusters that are unconnected with one another

and 15 singletons (Figure 3A). Visual inspection of the molecules within the network

reveals 30 structurally distinct families (Figure 3A; Supplemental Figure 1).

A search of the patent and academic literature using the SciFinder search tool [21]

revealed that 15 of the 30 scaffolds (50%) are found in molecules that bind amyloids

(pink-outlined nodes in Figure 3A, Supplemental Figure 1, and Supplemental Table 3).

For example, scaffolds (a), (k) and close analogs of wact-102 have been shown to bind

Aβ42 amyloid aggregates with low nanomolar affinity [22-24]. Scaffold (i) and close analogs

of wact-128 and wact-415 were shown to bind prion amyloid aggregates with low

nanomolar affinity [25]. In another example, wact-498 is a flavonoid, which is an

intensively studied class of molecules that have therapeutic potential for treating

amyloid-related neurodegeneration (reviewed [26]). In particular, isoflavone analogs of

wact-498 can disrupt Aβ42 plaque formation in a *C. elegans* model of the human disease

[27] and were shown to directly bind Aβ42 *in vitro* [28]. The same analysis was performed on

62 randomly chosen scaffolds from molecules that do not form crystals [5]. We found only

6 scaffolds (10%) that were previously described to bind amyloids (Supplemental Table

4). These data suggest that the collection of crystal-forming molecules is enriched with

amyloid-associating substructures.

Crystals Disrupt the Amyloid-Like Material of the Pharyngeal Cuticle

We sought to better understand how crystal growth perturbs the materials of the

cuticle. To investigate, we used cuticle-binding dyes and fluorescent reporters. We

previously found that the red-fluorescent Congo red (CR) and blue fluorescent Thioflavin

S (ThS), both of which are well-established amyloid-binding dyes [29-32], specifically bind

the pharyngeal cuticle [9]. Similarly, the blue-fluorescent Calcofluor white (CFW) and the

yellow-red-fluorescent Eosin Y (EY), which bind chitin [33] and its deacetylated derivative

chitosan [34] respectively, specifically bind the pharyngeal cuticle [9].

We incubated worms in wact-190 and wact-390 (a second crystalizing molecule) for 3

hours followed by 2 hours of incubation of the dyes. We found that the amyloid dye

patterns are often disrupted by the nascent objects (Figure 4). We also observe a similar

pattern in the background where a single IDR-rich protein (ABU-14) is tagged with GFP [10]

(Supplemental Figure 3). By contrast, the chitin and chitosan dyes are relatively

unperturbed (Figure 4; Supplemental Figure 3). In some instances, the birefringent

crystals overlap with amyloid stain (blue arrows, Figure 4). In other cases, there is little

overlap between the birefringent signal and the amyloid stain (orange arrows, Figure 4).

To control for the possibility that the dyes bind the crystals, we asked whether the

dyes bind to *in vitro* precipitated small molecules. None of the dyes fluoresced brightly

in association with the *in vitro* precipitated small molecules (Figure 4G). We also

examined the dye-staining patterns in the presence of much larger 24-hour old *in vivo*

crystals. We found many obvious examples where the larger birefringent signals do not

overlap with the CR signal (orange arrows, Supplemental Figure 4). These results suggest

that nascent crystals can displace the CR-stained material, which often appears to

surround the small crystals. This is consistent with the matrix-like material that

surrounds the objects in the TEM images (see Figure 2h for example in [6]. As the crystals

grow, their larger mass becomes more distinct from the cuticle and their intimate

association with the amyloid-staining material is often lost.

Amyloids Likely Seed the Formation of Small Molecule Crystals

As shown above, crystal-forming small molecules are rich in amyloid-binding

substructures and that crystals can perturb the amyloid-like material in the pharynx

cuticle as they grow. These observations raised the possibility that the amyloid-like

material in the pharynx cuticle [9] might seed the formation of the small molecule crystals.

If true, then coating the amyloid-like material with well-characterized amyloid-binding

dyes might block crystal formation. We tested this idea by first asking whether wact-

190-associated lethality of *C. elegans* is suppressed by co-incubating the worms with the

amyloid-binding dyes CR and ThS in our standard 6-day viability assay [5]. Indeed, we

found that CR and ThS robustly suppress wact-190 lethality whereas the chitin/chitosan-

binding dyes do not (Figure 5A). Second, we asked whether the canonical amyloid-

binding dyes can suppress wact-190 crystal formation. We incubated CR and ThS, along

with CFW and EY with the animals either for 3 hours before incubating the worms with

wact-190 for another 3 hours (i.e. a pre-incubation) or at the same time as a 3-hour

incubation with wact-190 (i.e. a co-incubation). We found that both CR and ThS

suppress crystal formation in both incubation schemes, but that the CFW and EY dyes do

not (Figure 5B and 5C). These data suggest that the crystals formed from the exogenous

compounds may be seeded by the amyloid-like material in the pharynx cuticle, which

can be blocked by other amyloid-interacting compounds.

We further investigated the idea that amyloids might seed the small molecule crystals

by asking whether Aβ42 fibrils could seed the formation of wact-190 objects *in vitro*.

We prepared solutions of Aβ42 at 25 μM and wact-190 at 25, 0.5 and 0.1 μM in PBS and

incubated them overnight either alone or in combination with each other at different

ratios. The next day, we examined the self-assembled structures by TEM (see Methods).

We found objects associated with the Aβ42 fibrils were present in solutions with wact-

190 present in either 10-fold more (Figure 6D), 2-fold more (Figure 6C), or 50-fold less

than the concentration of Aβ42 (Figures 6G-H), but not 250-fold less (Figures 6K-L) or

without wact-190 present (Figures 6A, E, and I). We infer that the objects are self-

assemblies of wact-190. Together with the *in vivo* data presented above, these data

suggest that amyloids are capable of seeding wact-190 self-assembly into higher order

structures.

Amyloid Disruptors are Revealed in a Screen for Small Molecule Suppressors of Crystal

Formation

Above, we show that amyloid-binding probes can block crystal formation. This raised the

possibility that screens for small molecules that disrupt crystal formation might yield

new amyloid-interacting and/or disrupting molecules. To investigate, we screened

Microsource's Spectrum library of 2560 drugs and natural products for those that might

suppress crystal formation.

We screened the Spectrum library in our standard six-day liquid viability assay

whereby multi-well plates are seeded with first larval stage animals (see methods and [2]).

We previously established that wact-190's lethality in young larvae is dependent on

crystal formation [5]. Control (solvent-only) wells are overgrown with worms after six days

(Supplemental Table 5). By contrast, wells with wact-190 (3.75 μM) contain either

arrested or dead L1s at the assay endpoint (Supplemental Table 5 and [5]).

Screening the Spectrum library molecules at 60 μM yielded 85 hits that: i) suppress

wact-190-induced lethality; ii) suppress wact-190 crystal formation ($p<0.05$); and iii) fail

to suppress lethality induced by a counter-screen control that does not form crystals

(the succinate dehydrogenase inhibitor wact-11 [2]) (Supplemental Table 5). To assess the

structural diversity of the suppressors, we built a structural similarity network of the

molecules (Figure 7A). A Tanimoto coefficient cut-off of 0.8 and manual inspection

revealed 45 distinct core scaffolds, 17 of which are represented by multiple molecules

(Figure 7A-B).

Informatic analyses of the 85 suppressors revealed that 15 of the 45 scaffold groups

(33%) contained at least one molecule known to play a direct role in disrupting amyloid

fibril formation (bold outline in Figure 7A; Supplemental Table 5). Most of these

scaffolds are enriched among the suppressors relative to the entire Spectrum library

(see Figure 7B for p values). Of note, a benzaldehyde substructure is significantly

enriched among the suppressors (2.8-fold enrichment, p=2.3E-14; blue highlight in

Figure 7B). Importantly, we found that several of the suppressors are fluorescent and of

these, all specifically stain the pharyngeal cuticle (Figure 7C and Supplemental Figure 5).

We investigated whether the set of 85 wact-190 suppressors is enriched for amyloid

disruptors relative to the molecules within the Spectrum library. The lack of a

comprehensive database of previously characterized small molecule amyloid disruptors

precluded a systematic analysis. We therefore randomly selected 100 molecules from

the remaining Spectrum molecules to further investigate. We used the same analytical

approach that we employed for the 85 Spectrum suppressors. We first assembled the

random molecules into a structural similarity network, revealing 75 structurally-distinct

scaffolds (11 clusters plus 64 singletons) (Supplemental Figure 6A). We then investigated

the literature for evidence of the ability to disrupt amyloid fibril formation for each of

the 100 random molecules (see methods). Two of the 75 core scaffolds (3%) had one

molecule shown to be a disruptor of amyloid fibril formation (Supplemental Figure 6B).

From this limited analysis, we found that the 85 Spectrum suppressors are over 10-fold

enriched in amyloid disruptors relative to the randomly selected set.

Small Molecule Suppressors of Crystal Formation Inhibit Aβ42 Fibril Formation

The above results suggest that the mechanism by which molecules suppress crystal

formation is intimately related to amyloid disruption. We therefore asked whether any

of the molecules for which we could not find literature-based evidence for amyloid

disruption have such capability. While different suppressors have been shown to disrupt

different types of amyloids (Supplemental Table 5), we focused on Aβ42 for reasons of

convenience [35,36]. We measured the incubation time by which Aβ42 fibril formation

reaches saturation and asked which molecules are capable of significantly ($p<0.05$)

extending the half-time of saturation by at least 50% in a standard assay [35]. Of the eight

molecules previously shown to disrupt amyloids, 3 inhibited Aβ42 fibril formation in our

assay (Figure 7A, Supplemental Table 5), indicating that not all published results

translate to this specific assay. Of the 44 unknowns tested, 11 (25%) inhibited Aβ42 fibril

formation (Figures 7A, D-H, Supplemental Table 5). Follow up analyses on the hits

shown in Figure 7E-H shows that Candesartan is a specific nucleation inhibitor while the

other molecules inhibit either nucleation and/or elongation. Importantly, all of these

inhibitory mechanisms require fibril binding (Supplemental Figure 7). Hence, the ability

of a small molecule to suppress crystal formation *in vivo* is predictive of its ability to

inhibit amyloid fibril growth *in vitro*.

A Scaffold's Ability to Crystalize or Suppress Crystallization is Interchangeable

A comparison of the structures of crystallizers and suppressors revealed that the former

have fewer hydrogen-bond donors than the latter and completely lacked hydroxyl

groups (p<1E-10) (Figure 8A-B). The crystallizers are also more halogenated than the

suppressors (Figure 8C). We also found that some crystallizers share the identical

scaffold as some suppressors. For example, the scaffolds of the wact-128 and wact-498

crystallizers are identical to that of oxyclozanide and koparin crystal suppressors,

respectively (Figure 8D). In addition, the scaffold of the wact-415 crystallizer is similar to

that of ThS, which also suppresses crystal formation (Figure 8D). These observations

raised the possibility that both classes of molecules (crystallizers and suppressors)

compete for the same environment within the cuticle.

   We tested whether we could convert a crystalizing molecule into a suppressor, and a

suppressor into a crystallizer, by altering the abundance of hydroxyl and halogen

decorations on the respective core structures. To do this, we searched the ZINC

database of the world's commercially available molecules [37] for close structural analogs

of the 85 suppressors that lacked hydroxyl groups and are halogenated. We screened 33

available analogs of 6 different suppressors. We found that 11 (33%) of these molecules

induced object formation within the pharynx in at least 25% of the population

(Supplemental Table 6; Figure 8E). This percentage is comparable to the 36% of

molecules that induce object formation from our heavily biased collection of worm

bioactive small molecules [5]. Second, we tested 25 hydroxylated analogs of 10 different

crystalizing small molecules for their ability to suppress the lethality associated with

crystal-forming wact-190. Five of the 25 hydroxylated crystallizers (20%) suppress wact-

190 lethality, and all of these suppress wact-190 crystal formation ($p<0.05$)

(Supplemental Table 7; Figure 8F). We conclude that select core small molecule

structures can be pushed towards crystal formation or its suppression by changing the

relative abundance of halogens and hydroxyls that decorate the molecule. These data

further supports the model that crystallizers and suppressors likely compete for the

same niche.

Finally, we tested the five converted suppressor molecules in the Aβ42 fibril

formation assay and found that the most robust suppressor (OC-17) robustly inhibited

Aβ42 fibril formation (Figure 8G; Supplemental Table 7; Supplemental Figure 7E).

Hence, converting crystallizers into suppressors is another route with which to identify

amyloid disruptors.

Discussion

Insights into Crystal Formation within the *C. elegans* Pharynx Cuticle

Here, we have described our investigation into why some small molecules crystalize

within the cuticle of the *C. elegans* pharynx. We found that: i) many crystal-forming

molecules have a core scaffold known to bind amyloid; ii) crystals can displace amyloid-

like material within the pharyngeal cuticle; iii) other molecules that are known to bind

amyloids can block crystal formation; iv) molecules that block crystal formation

specifically localize to the tissue where crystals form; and v) Aβ42 fibrils can seed the

formation of wact-190 objects *in vitro*. Together with our previous work that shows the

pharynx cuticle to be rich in amyloid-like material [9], these observations suggest that the

amyloid-like material within the pharynx cuticle seed the formation of crystals.

We can speculate in general terms as to how the amyloid-like material in the pharynx

cuticle might seed small molecule crystals. Our physicochemical analyses of crystalizing

compounds show that they are rich with π bonding capability, hydrogen bond acceptors,

and polar surface areas (this work and [5]). Indeed, our *in vitro* analysis also shows that π

bond interactions likely play a key role in the ability of these molecules to crystalize

within the pharynx. Concomitant with its amyloid-like nature [38,39], pharynx cuticle

proteins are highly enriched in π-bonding capability relative to other tissue proteomes in

C. elegans and is only surpassed by the collagens [9]. Furthermore, the pharynx secretome

is uniquely rich with polar uncharged residues with hydrogen bond donor capability (i.e.,

Ns, Qs, Ss, Ts, and Ys) (($p<$1E-11) [9]). Hence, the unique complementarity between the

proteins within the pharyngeal cuticle and the crystal-forming compounds likely

facilitates the seeding of small molecule crystals.

Small molecule crystallization is restricted to the pharyngeal cuticle [5], yet the

collagens (which are highly abundant within the body cuticle) are also rich in π-bonding

capability [9]. Hence, there are likely additional properties of the pharynx cuticle beyond

its amyloid-like nature that creates the unique niche that facilitates crystal formation.

Indeed, our recent work shows that polar lipids within the pharynx cuticle likely act as a

sink to concentrate the hydrophobic molecules that go on to crystallize [6].

A model of crystal formation emerges upon considering these and other

observations. First, polar lipids within the pharynx cuticle likely act as a sink to

concentrate hydrophobic small molecules, including those that go on to crystallize [6].

Once concentrated, the amyloid-like material within the pharynx cuticle seeds the

crystallization of small molecules that are capable of interacting with the amyloid-like

material. Many of the molecules that suppress crystal formation have similar properties

to the crystallizing molecules except that they are rich in hydroxyl groups and therefore

cannot crystalize themselves. Instead, they mask the niche to prevent the seeding of

crystals from small molecules that would otherwise do so.

Crystal Formation can be Exploited to Identify Candidate Amyloid Inhibitors

Through this investigation, we discovered that the phenomenon of small molecule

crystal formation can be readily exploited to identify candidate inhibitors of amyloid

growth. Our screen of just over 2500 small molecules for those that can suppress crystal

formation yielded 85 reproducible hits. One third of these were previously known

inhibitors of amyloid formation. For example, the heme and chlorophyl precursor

protoporphyrin IX, its synthetic derivative haematoporphyrin, and chlorophyllide-Cu are

the only porphyrins contained within the Spectrum library, and all three were found to

suppress crystal formation. Multiple studies have shown that porphyrins suppress

amyloid formation both *in vivo* and *in vitro* and act through direct interaction with

amyloidogenic proteins [40-42]. The porphyrin ring is thought to disrupt the intrapeptide π-

π interactions of the amyloidogenic peptide that is necessary to achieve superstructure

[42]. The porphyrins may suppress crystal formation by disrupting the ability of the

amyloid-like material to seed crystals or may disrupt the small molecule crystallization

itself.

A second common suppressor class are the flavonoids, which are a large class of

polyphenolic secondary metabolites synthesized by plants [43]. Many flavonoid structures

have been shown to antagonize amyloid formation *in vitro* [44-46], in culture [47], and *in vivo*

[48-50]. Poor bioavailability may contribute to a lack of flavonoid-based therapies in the

clinic, although converting anti-amyloid flavonoids into prodrugs may circumvent

absorption barriers [51]. Flavonoid interaction with Aβ42 is driven by hydrophobic and

hydrogen bond interactions that antagonize the ability of Aβ42 to adopt a β-sheet

secondary structure [52]. Whether the flavonoids interact with amyloidogenic proteins

within the cuticle in a similar way to suppress crystallization remains to be determined.

Upon testing 44 small molecules not known to us at the time to disrupt amyloid

formation, we found that 25% disrupt Aβ42 aggregation. This hit rate is far higher than

that previously reported for Aβ42 (0.4%) [16] or α-synuclein (<0.01%) [18]. Notably, *C.*

elegans screens for suppressors of crystal-induced death are inexpensive and high-

throughput. Furthermore, the *in vivo* environment in which suppressors must act is

complex and, relative to other *in vitro* assays, may better approximate the environment

in which anti-amyloid compounds must act. Hence, screens for molecules that suppress

crystal-induced lethality in *C. elegans* represent a novel and efficient approach to enrich

for molecules that might have utility against human amyloid formation.

Methods

***C. elegans* Culture, Strains and Microscopy**

C. elegans strains were cultured and synchronized as previously described [5]. Six day

viability assays were conducted as previously described [2]. The wild type N2 Bristol strain

was used (obtained from the *C. elegans* genetic Centre); NQ824 qnEx443[Pabu-14:abu-

14:sfGFP; rol-6(d); unc-119(+)], which was a kind gift from David Raizen [10], was

integrated into the genome in our lab as *trIs113*. For all imaging, a Leica DMRA

compound microscope with a Qimaging Retiga 1300 monochrome camera was used.

Before mounting worms on a 3% agarose pad for imaging, worms are washed 3X with

M9 buffer and paralyzed with 50 mM levamisole or 30 mM NaN$_3$. Dye staining

experiments were performed as previously described [9].

Identification of Crystallizing Small Molecules and Crystal Counts

The RLL1200 library of 1178 commercially available analogs of *C. elegans*-lethal

molecules was assembled and purchased from ChemBridge (Supplemental Data File 1).

This library was screened at 30 µM in liquid NGM media against synchronized *C. elegans*

L1 larvae and *Rhabditophanes diutinus* [53] as previously described [2], with approximately

20 L1s plated per well of a 96-well plate. The final volume in each well was 100 µL and

the DMSO concentration was 0.3% v/v. After 6 days of incubation at 25°C the number of

living worms in each well was quantified. Molecules that killed *C. elegans* N2 and

Rhabditophanes were tested for resistance in *C. elegans sms-5(ok2498)* mutants at 1.9,

7.5, and 30 µM. Crystal counts were performed as previously described [5].

Characterization of the Structure of wact-190 and wact-416 *in vitro* Crystals

Both wact-190 and wact-416 crystal powder samples were deposited on a quartz zero-

background sample holder. The sample was loaded in a 0.7 mm diameter capillary, to

avoid preferment orientation. The powder X-ray diffraction (PXRD) pattern was

collected using a Bruker D8 Discover diffractometer (Bruker, Germany) equipped with

Goebel's mirrors to create a θ:θ parallel beam geometry with a sealed X-ray tube source

with a copper anode (40 Kv, 40 mA) and a LYNXEYE XE linear detector. The diffraction

patterns were collected between 5 and 60° 2θ with step 0.02° 2θ for 4 seconds per step

[54]. The cell indexing was performed by TOPAS 5.0 software, using the LSI-Index

algorithm [55]. The structure resolution was obtained by using the simulated annealing

method in EXPO2014 [56]. The founded structure was refined by the Rietveld Method

using GSAS-IIin order to precisely refine the atomic positions [57]. The CIF files obtained

from the above method and structures were solved using Mercury software.

Transmission Electron Microscopy (TEM) of Aβ42 and wact-190 *in vitro* Crystals

5 mM of each of Aβ42 and wact-190 were dissolved in pure DMSO and heated at 55 °C

for 2 minutes for complete dissolution. Thereafter, all molecules were further diluted in

1X PBS to prepare a final concentration of 25 μM. This solution mixture was further

heated at 90 °C for 3 hours, followed by a vortex and the mixture was then allowed to

gradually cool down overnight that resulted in self-assembled structures in some cases.

The combinations used for Aβ42 plus wact-190 were 1:1, 1:2, 1:5, and 1:10 ratios.

Uncombined Aβ42 and wact-190 were used as controls (25 μM in 1X PBS). The self-

assembled samples of all three (5 μL, 25 μM in 1X PBS) were drop cast on a 400-mesh

carbon-stabilized Formvar-coated Cu grid (Ted Pella, California, USA). The sample was

allowed to bind the surface for 2 minutes and then the excess sample was removed

using a lint-free tissue, dried at room temperature, and imaged. Sample morphology

was visualized using a JEM-1400 TEM (JEOL, Tokyo, Japan) accelerating at 80 kV [54].

Identification of Chemical Suppressors of Crystal-Induced Death and Crystal Formation

To identify chemical suppressors of crystal-induced death, the Spectrum Collection

(MicroSource Discovery Systems Inc.) of 2560 approved drugs and natural products was

screened at a concentration of 60 μM in the background of 3.75 μM wact-190. This

concentration of wact-190 results in crystal formation in the pharynx causing *C. elegans*

N2 to arrest at the L1 stage. This screen was performed in liquid NGM media as

previously described [2], with approximately 20 N2 L1s plated per well of a 96-well plate.

The final volume in each well was 50 μL and the DMSO concentration was 0.8% v/v.

After 6 days of incubation at 20°C the number adult and larval worms that have

progressed from arrested L1 stage was quantified. Hits that suppressed the wact-190

crystal-induced L1 arrest were retested against solvent control, wact-190, and the non-

crystal forming lethal molecule wact-11 at 10 μM (see [2]) using the same method

described above. Hits were further investigated for their ability to suppress crystal

formation by co-incubating 3.75 μM of wact-190 and 60 μM of the suppressor with wild

type animals in 96-well plate format. The fraction of animals with birefringent crystals

was then counted at 100X magnification 48 hours later, counting 20 animals per sample

per trial on average.

Chemoinformatic Network Analysis, Network Display, Small Molecule Art, and

Informatic Analyses

Structural similarity networks were constructed based on pairwise similarity scores

calculated as the Tanimoto coefficient of shared FP2 fingerprints. Pairwise similarity

scores were calculated using OpenBabel (http://openbabel.org) and the networks were

visualized using Cytoscape [58] as previously described [2]. For each network generated, a

range of Tanimoto coefficient cut-offs were tested to determine which cut-off yielded a

network that clustered obvious structural analogs together as determined by manual

inspection. Suppressors were analysed for the presence of substructures (Figure 4b)

using Filter-it version 1.0.2 from Silicos-it. Structures were drawn using ChemDraw

(PerkinElmer Informatics). A random Spectrum network (Supplemental Figure 5) was

generated by assigning all molecules within the Spectrum library a random number

using excel, then sorting the molecules in order of the random number, then choosing

the top 100 molecules that did not include any of the 85 Spectrum suppressors.

We investigated whether the crystalizing molecules and a randomly selected set of

true negatives (that fail to robustly form crystals [5]) were previously characterized to

interact with amyloids using the SciFinder Scholar tool [21]. To do this, we first assembled

the crystalizing molecules into 29 groups based on distinct scaffolds and ensured that

our set of 62 true negatives represented 62 distinct core scaffolds (within the set of true

negatives). We then reduced each group (or single molecule if it was not part of a group)

to its core scaffold structure by removing hydroxyl groups, halogens, or substructures

that were not in common to all members of the group. With the resulting core scaffold

structures, we first searched SciFinder for any molecule that contained that core

scaffold. With these resulting molecules, we then searched the associated biological

literature abstracts within SciFinder for the term 'amyloid'. Because of the simplicity of

some core scaffolds, the number of respective analogs and associated abstracts

numbered in the tens of thousands. In these cases, we instead first chose one molecule

from the group (or the single molecule if it was not part of a group) and searched

SciFinder for analogs with >80% identity. This reduced the number of relevant structures

and associated literature to search and kept the focus on closely related structures.

Which of the two tactics was employed is indicated in the relevant Supplementary Table

and Supplementary Data File for each scaffold group (or single molecule). Abstracts

containing the term 'amyloid' were read (and where unclear, the associated literature

was read) to ensure that evidence of either direct amyloid interaction *in vitro* was being

measured or that if *in vivo* samples were being analyzed, staining that was coincident

with amyloid structures was being measured. Evidence relying solely on the reduction of

amyloids *in vivo* were not considered 'hits' because of potential indirect mechanisms.

The PubMed IDentification numbers (PMIDs) and/or patent numbers of the 'hits' are

reported in the associated Supplementary Tables and Supplementary Data File.

We analyzed both the list of 85 Spectrum suppressors of crystal formation and the

100 randomly chosen molecules by searching that compound and the word 'amyloid' in

both a PubMed search and a Google search. We inspected the search results for

evidence that the molecule of interest had a demonstratable inhibitory effect on

amyloid formation *in vitro*, with or without supporting *in vivo* evidence. *In vivo* or *in*

silico evidence of a decrease in fibril abundance without evidence of a direct effect was

excluded from consideration. Molecules that lacked evidence for a direct effect, but had

close structural analogs that have a demonstratable inhibitory effect on fibral formation

were also excluded from further consideration.

To identify hydroxylated analogs of the crystallizing molecules and reduced analogs of

the suppressors, Open Babel [59] was used for the analog searches. Using SmiLib v2.0 [60], a

virtual library of approximately 55,000 variably hydroxylated analogs of 161 distinct

crystallizing molecules was generated, as well as a virtual library of approximately

950,000 de-hydroxylated and variably halogenated analogs of 12 distinct crystal

suppressor molecules. The 55K and 950K virtual libraries were de-duplicated and

independently combined with de-duplicated and de-salted versions of MolPort's All

Stock Compounds Database and the ZINC In-Stock Database [37]. A duplicate search of

these combined datasets revealed 34 crystallizer analogs and 88 crystal suppressor

analogs that were available for purchase from MolPort. These analogs were further

filtered by price, real availability, redundancy among parent Spectrum suppressors, and

aqueous solubility, leaving 26 crystallizer analogs and 33 crystal suppressor analogs to

be assayed.

Dye Suppression Assays

To test for the ability of dyes to suppress wact-190-induced worm lethality, 80 μL of

NGM containing HB101 bacteria (OD_{600} = 1.8-2.2) and 3.75 μM wact-190 was added to

each well of a 96-well plate, to which each dye was pinned (pinner model VP381N, V & P

Scientific, Inc) to a final concentration of 0, 0.94, 1.88, 3.75, 7.5, 15, 30, 60, 120, 240,

480 and 960 μM, in quadruplicates. 20 μL of M9 containing synchronized wildtype L1s

were then added to each well at ~50 L1/well. Three sets of controls were simultaneously

set up: wact-190 + DMSO (or 70% ethanol) (no dye), DMSO + dye (no wact-190) and

DMSO + DMSO (or 70% ethanol) (no wact-190, no dye). All samples were set up in

quadruplets (Day 0) and incubated at 20°C in a shaker at 200 rpm. Worm viability was

scored on Day 6.

To test for the ability of dyes to suppress wact-190-induced crystal formation,

synchronized wildtype young adults were added (~ 1,000 worms in 50 μL) to a 1.5 mL

Eppendorf tube containing 500 μL NGM buffer and bacteria. Adult worms were either (i)

pre-incubated for 3 hours with 60 μM or 1200 μM of each dye or solvent (DMSO) only,

rinsed 3X with M9 buffer then incubated with 60 μM wact-190 in a fresh Eppendorf

tube, or (ii) co-incubated for 3 hours with 60 μM or 1200 μM of each dye (or solvent)

and 60 μM wact-190. Crystal formation was recorded by observing the birefringence of

the wact-190 crystals both in the presence and absence of the dye. wact-190 crystal

formation was compared with a negative control (no wact-190), that yielded no such

birefringence. All observations and imaging were carried out using 40X objective lens of

Leica DMRA2 compound microscope. The amount of birefringence was quantified using

Fiji/ImageJ software. 10-20 worms per sample were analyzed in 3 biological trials.

***In vitro* Crystal Signal Emission Controls with and without Dye Staining**

To test for signal emission of wact-190 or wact-390 crystals, as detected with our

fluorescent microscopy filter sets, 3 μL of a 10 mM wactive stock was first added to 7 μL

of water and mixed in a microcentrifuge tube, then directly added to a microscope glass

slide and coverslip applied. The appearance and birefringence of the formed crystals

were observed under differential interference contrast (DIC), birefringence, and

fluorescence filter sets.

To test for whether the dyes specifically bind the *in vitro* precipitated crystals, the

same procedure was followed as above, but each dye was added at a final concentration

that was used in the dye staining experiments after the wactive precipitated in water.

Correlation between crystal birefringence (bright white dots in a dark background) and

dye fluorescence in their respective fluorescence channels was examined. All

observations were made using the 10X objective lens of the Leica DMRA2 compound

microscope.

Aβ42 Aggregation Assay

Recombinant Aβ42 expression - The recombinant peptide MDAEFRHDSGY EVHHQKLVFF

AEDVGSNKGA IIGLMVGGVV IA, here called Aβ42, was expressed in the *E. coli* BL21 Gold

(DE3) strain (Stratagene, CA, U.S.A.) and purified as described previously [35]. Briefly, the

purification procedure involved sonication of *E. coli* cells, dissolution of inclusion bodies

in 8 M urea, and ion exchange in batch mode on diethylaminoethyl cellulose resin

followed by lyophilisation. The lyophilised fractions were further purified using Superdex

75 HR 26/60 column (GE Healthcare, Buckinghamshire, U.K.) and eluates were analysed

using SDS-PAGE for the presence of the desired peptide product. The fractions

containing the recombinant peptide were combined, frozen using liquid nitrogen, and

lyophilised again.

Aβ42 aggregation kinetics and fibril preparation - Solutions of monomeric Aβ42 were

prepared by dissolving the lyophilized Aβ42 peptide in 6 M guanidinium hydrocholoride

(GuHCl). Monomeric forms were purified from potential oligomeric species and salt

using a Superdex 75 10/300 GL column (GE Healthcare) at a flowrate of 0.5 mL/min, and

were eluted in 20 mM sodium phosphate buffer, pH 8 supplemented with 200 μM EDTA

and 0.02% NaN_3. The centre of the peak was collected and the peptide concentration

was determined from the absorbance of the integrated peak area using extinction

coefficient ε_{280} = 1490 l Mol^{-1} cm^{-1}. The obtained monomer was diluted with buffer to

the desired concentration and supplemented with 20 μM Thioflavin T (ThT) from a 2

mM stock. Each sample was then pipetted into multiple wells of a 96- well half-area,

low-binding, clear bottom and PEG-coated plate (Corning 3881), 80 μL per well, in the

absence and the presence of different molar-equivalents of small molecules (1% DMSO).

Assays were initiated by placing the 96-well plate at 37 ºC under quiescent conditions in

a plate reader (Fluostar Omega, Fluostar Optima or Fluostar Galaxy, BMGLabtech,

Offenburg, Germany). The ThT fluorescence was measured through the bottom of the

plate using a 440 nm excitation filter and a 480 nm emission filter.

Statistics and Graphs

Except where indicated, statistical differences were measured using a two-tailed

Students T-test. Dot plots were generated using Prism 8 graphing software.

Animal Ethics Statement

We (the authors) affirm that we have complied with all relevant ethical regulations for

animal testing and research. Given that our experiments focused exclusively on the

invertebrate nematode worm *C. elegans*, no ethical approval was required for any of the

presented work.

Data Availability Statement

Any primary data generated or analyzed during this study that are not included in this

published article and its supplementary information files are available upon request.

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Author Contributions

PJR and MK found that crystals form in the pharyngeal cuticle. MK performed the

microscopy and associated quantification. JK performed additional small molecule

screens that revealed new crystal-forming compounds, performed the screen of the

Spectrum library for suppressors of crystal-induced death and follow-up work, and

performed the network analyses. ARB designed the novel 1,178-compound custom

library and identified the crystallizer and suppressor analogs. RIH under the guidance

and funding of MV, performed the Ab42 fibril inhibition assay. OST, under the guidance

and funding of DLB-Y and EG, determined the structure of wact-190 and wact-416 *in*

vitro crystals and showed that Aβ42 fibrils can nucleate wact-190 objects. DH

determined whether the fluorescent Spectrum suppressors specifically stain the

pharyngeal cuticle. PJR supervised, coordinated and secured funding for the project,

composed the display items and wrote the manuscript with the help of co-authors.

647 **Competing Interests**

648 RIH is a consultant of WaveBreak Therapeutics (formerly Wren Therapeutics). MV is a

649 founder of WaveBreak Therapeutics.

Literature Cited

1   Kwok, T. C. *et al.* A small-molecule screen in C. elegans yields a new calcium
channel antagonist. *Nature* **441**, 91-95 (2006).
2   Burns, A. R. *et al.* Caenorhabditis elegans is a useful model for anthelmintic
discovery. *Nat Commun* **6**, 7485, doi:ncomms8485 [pii]
10.1038/ncomms8485 (2015).
3   Risi, G. *et al.* Caenorhabditis elegans Infrared-Based Motility Assay Identified
New Hits for Nematicide Drug Development. *Vet Sci* **6**,
doi:10.3390/vetsci6010029 (2019).
4   Galford, K. F. & Jose, A. M. The FDA-approved drugs ticlopidine, sertaconazole,
and dexlansoprazole can cause morphological changes in C. elegans.
Chemosphere **261**, 127756, doi:10.1016/j.chemosphere.2020.127756 (2020).
5   Kamal, M. *et al.* The marginal cells of the Caenorhabditis elegans pharynx
scavenge cholesterol and other hydrophobic small molecules. *Nat Commun* **10**,
3938, doi:10.1038/s41467-019-11908-0 (2019).
6   Kamal, M. *et al.* PGP-14 Establishes a Polar Lipid Permeability Barrier within the
C. elegans Pharyngeal Cuticle. *PLoS Genet* **19(11):e1011008**,
doi:10.1371/journal.pgen.1011008 (2023).
7   Cox, G. N., Kusch, M. & Edgar, R. S. Cuticle of Caenorhabditis elegans: its isolation
and partial characterization. *J Cell Biol* **90**, 7-17 (1981).
8   Altun, Z. F. & Hall, D. H. in *WormAtlas*   (2020).
9   Kamal, M. *et al.* A spatiotemporal reconstruction of the C. elegans pharyngeal
cuticle reveals a structure rich in phase-separating proteins. *Elife* **11**,
doi:10.7554/eLife.79396 (2022).
10   George-Raizen, J. B., Shockley, K. R., Trojanowski, N. F., Lamb, A. L. & Raizen, D.
M. Dynamically-expressed prion-like proteins form a cuticle in the pharynx of
Caenorhabditis elegans. *Biol Open* **3**, 1139-1149, doi:10.1242/bio.20147500
(2014).
11   Wright, K. A. & Thomson, J. N. The buccal capsule of Caenorhabditis elegans
(Nematodea:Rhabditoidea): an ultrastructural study. *Canadian Journal of
Zoology* **59**, 1952-1961 (1981).
12   White, J. G., Southgate, E., Thomson, J. N. & Brenner, S. The structure of the
nervous system of the nematode Caenorhabditis elegans. *Philos Trans R Soc Lond
B Biol Sci* **314**, 1-340, doi:10.1098/rstb.1986.0056 (1986).
13   Sparacio, A. P., Trojanowski, N. F., Snetselaar, K., Nelson, M. D. & Raizen, D. M.
Teething during sleep: Ultrastructural analysis of pharyngeal muscle and
cuticular grinder during the molt in Caenorhabditis elegans. *PLoS One* **15**,
e0233059, doi:10.1371/journal.pone.0233059 (2020).
14   Huang, K. M., Cosman, P. & Schafer, W. R. Automated detection and analysis of
foraging behavior in Caenorhabditis elegans. *J Neurosci Methods* **171**, 153-164,
doi:10.1016/j.jneumeth.2008.01.027 (2008).
15   Avery, L. Motor neuron M3 controls pharyngeal muscle relaxation timing in
Caenorhabditis elegans. *J Exp Biol* **175**, 283-297 (1993).

16 McKoy, A. F., Chen, J., Schupbach, T. & Hecht, M. H. A novel inhibitor of amyloid
beta (Abeta) peptide aggregation: from high throughput screening to efficacy in
an animal model of Alzheimer disease. *J Biol Chem* **287**, 38992-39000,
doi:10.1074/jbc.M112.348037 (2012).
17 Pujols, J. *et al.* High-Throughput Screening Methodology to Identify Alpha-
Synuclein Aggregation Inhibitors. *Int J Mol Sci* **18**, doi:10.3390/ijms18030478
(2017).
18 Kurnik, M. *et al.* Potent alpha-Synuclein Aggregation Inhibitors, Identified by
High-Throughput Screening, Mainly Target the Monomeric State. *Cell Chem Biol*
25, 1389-1402 e1389, doi:10.1016/j.chembiol.2018.08.005 (2018).
19 Daina, A., Michielin, O. & Zoete, V. SwissADME: a free web tool to evaluate
pharmacokinetics, drug-likeness and medicinal chemistry friendliness of small
molecules. *Sci Rep* **7**, 42717, doi:10.1038/srep42717 (2017).
20 Burley, S. K. & Petsko, G. A. Aromatic-aromatic interaction: a mechanism of
protein structure stabilization. *Science* **229**, 23-28, doi:10.1126/science.3892686
(1985).
21 Somerville, A. N. SciFinder Scholar. *Journal of Chemical Education* **75**, 959-960,
doi:doi.org/10.1021/ed075p959 (1998).
22 Ono, M., Haratake, M., Saji, H. & Nakayama, M. Development of novel beta-
amyloid probes based on 3,5-diphenyl-1,2,4-oxadiazole. *Bioorg Med Chem* **16**,
6867-6872, doi:10.1016/j.bmc.2008.05.054 (2008).
23 Watanabe, H. *et al.* Synthesis and biological evaluation of radioiodinated 2,5-
diphenyl-1,3,4-oxadiazoles for detecting beta-amyloid plaques in the brain.
Bioorg Med Chem **17**, 6402-6406, doi:10.1016/j.bmc.2009.07.020 (2009).
24 Yang, Y. *et al.* Radioiodinated benzyloxybenzene derivatives: a class of flexible
ligands target to beta-amyloid plaques in Alzheimer's brains. *J Med Chem* **57**,
6030-6042, doi:10.1021/jm5004396 (2014).
25 Geissen, M. *et al.* From high-throughput cell culture screening to mouse model:
identification of new inhibitor classes against prion disease. *ChemMedChem* **6**,
1928-1937, doi:10.1002/cmdc.201100119 (2011).
26 Ayaz, M. *et al.* Flavonoids as Prospective Neuroprotectants and Their
Therapeutic Propensity in Aging Associated Neurological Disorders. *Front Aging*
Neurosci **11**, 155, doi:10.3389/fnagi.2019.00155 (2019).
27 Gutierrez-Zepeda, A. *et al.* Soy isoflavone glycitein protects against beta amyloid-
induced toxicity and oxidative stress in transgenic Caenorhabditis elegans. *BMC*
Neurosci **6**, 54, doi:10.1186/1471-2202-6-54 (2005).
28 Hirohata, M. *et al.* Anti-amyloidogenic effects of soybean isoflavones in vitro:
Fluorescence spectroscopy demonstrating direct binding to Abeta monomers,
oligomers and fibrils. *Biochim Biophys Acta* **1822**, 1316-1324,
doi:10.1016/j.bbadis.2012.05.006 (2012).
29 Bennhold, H. Specific staining of amyloid by Congo red. *Muenchen. Med.*
Wochenschr **69**, 1537-1538 (1922).
30 Divry, P. F., M. Sur les propriétées optiques de l'amyloide. *C. R. Soc. Biol.* **97**,
1808-1810 (1927).

31   Vassar, P. S. & Culling, C. F. Fluorescent stains, with special reference to amyloid
738   and connective tissues. *Arch Pathol* **68**, 487-498 (1959).
739   32   Larbig, G., Pickhardt, M., Lloyd, D. G., Schmidt, B. & Mandelkow, E. Screening for
740   Inhibitors of Tau Protein Aggregation into Alzheimer Paired
741   Helical Filaments: A Ligand Based Approach Results in Successful Scaffold
742   Hopping. *Current Alzheimer Research* **4**, 315-323 (2007).
743   33   Harrington, B. J. & Raper, K. B. Use of a fluorescent brightener to demonstrate
744   cellulose in the cellular slime molds. *Appl Microbiol* **16**, 106-113 (1968).
745   34   Baker, L. G., Specht, C. A., Donlin, M. J. & Lodge, J. K. Chitosan, the deacetylated
746   form of chitin, is necessary for cell wall integrity in Cryptococcus neoformans.
747   *Eukaryot Cell* **6**, 855-867, doi:10.1128/EC.00399-06 (2007).
748   35   Cohen, S. I. *et al.* Proliferation of amyloid-beta42 aggregates occurs through a
749   secondary nucleation mechanism. *Proc Natl Acad Sci U S A* **110**, 9758-9763,
750   doi:10.1073/pnas.1218402110 (2013).
751   36   Knowles, T. P. *et al.* An analytical solution to the kinetics of breakable filament
752   assembly. *Science* **326**, 1533-1537, doi:10.1126/science.1178250 (2009).
753   37   Sterling, T. & Irwin, J. J. ZINC 15--Ligand Discovery for Everyone. *J Chem Inf Model*
754   **55**, 2324-2337, doi:10.1021/acs.jcim.5b00559 (2015).
755   38   Gazit, E. A possible role for pi-stacking in the self-assembly of amyloid fibrils.
756   *FASEB J* **16**, 77-83, doi:10.1096/fj.01-0442hyp (2002).
757   39   McGaughey, G. B., Gagne, M. & Rappe, A. K. pi-Stacking interactions. Alive and
758   well in proteins. *J Biol Chem* **273**, 15458-15463, doi:10.1074/jbc.273.25.15458
759   (1998).
760   40   Caughey, W. S., Raymond, L. D., Horiuchi, M. & Caughey, B. Inhibition of
761   protease-resistant prion protein formation by porphyrins and phthalocyanines.
762   *Proc Natl Acad Sci U S A* **95**, 12117-12122, doi:10.1073/pnas.95.21.12117 (1998).
763   41   Lee, B. I. *et al.* Photoexcited Porphyrins as a Strong Suppressor of beta-Amyloid
764   Aggregation and Synaptic Toxicity. *Angew Chem Int Ed Engl* **54**, 11472-11476,
765   doi:10.1002/anie.201504310 (2015).
766   42   Yuan, C. & Gao, Z. Abeta interacts with both the iron center and the porphyrin
767   ring of heme: mechanism of heme's action on Abeta aggregation and
768   disaggregation. *Chem Res Toxicol* **26**, 262-269, doi:10.1021/tx300441e (2013).
769   43   Panche, A. N., Diwan, A. D. & Chandra, S. R. Flavonoids: an overview. *J Nutr Sci* **5**,
770   e47, doi:10.1017/jns.2016.41 (2016).
771   44   Akaishi, T. *et al.* Structural requirements for the flavonoid fisetin in inhibiting
772   fibril formation of amyloid beta protein. *Neurosci Lett* **444**, 280-285,
773   doi:10.1016/j.neulet.2008.08.052 (2008).
774   45   Yin, F. *et al.* Silibinin: a novel inhibitor of Abeta aggregation. *Neurochem Int* **58**,
775   399-403, doi:10.1016/j.neuint.2010.12.017 (2011).
776   46   Choi, E. Y., Kang, S. S., Lee, S. K. & Han, B. H. Polyphenolic Biflavonoids Inhibit
777   Amyloid-Beta Fibrillation and Disaggregate Preformed Amyloid-Beta Fibrils.
778   *Biomol Ther (Seoul)* **28**, 145-151, doi:10.4062/biomolther.2019.113 (2020).

47   Kimura, J. *et al.* Nobiletin Reduces Intracellular and Extracellular beta-Amyloid in
iPS Cell-Derived Alzheimer's Disease Model Neurons. *Biol Pharm Bull* **41**, 451-
457, doi:10.1248/bpb.b17-00364 (2018).
48   Ahmad, A. *et al.* Neuroprotective Effect of Fisetin Against Amyloid-Beta-Induced
Cognitive/Synaptic Dysfunction, Neuroinflammation, and Neurodegeneration in
Adult Mice. *Mol Neurobiol* **54**, 2269-2285, doi:10.1007/s12035-016-9795-4
(2017).
49   Kim, J. K. *et al.* Protective effects of kaempferol (3,4',5,7-tetrahydroxyflavone)
against amyloid beta peptide (Abeta)-induced neurotoxicity in ICR mice. *Biosci*
Biotechnol Biochem **74**, 397-401, doi:10.1271/bbb.90585 (2010).
50   Wei, D., Tang, J., Bai, W., Wang, Y. & Zhang, Z. Ameliorative effects of baicalein
on an amyloid-beta induced Alzheimer's disease rat model: a proteomics study.
Curr Alzheimer Res **11**, 869-881 (2014).
51   Chen, C. *et al.* The prodrug of 7,8-dihydroxyflavone development and
therapeutic efficacy for treating Alzheimer's disease. *Proc Natl Acad Sci U S A*
115, 578-583, doi:10.1073/pnas.1718683115 (2018).
52   Wang, L., Zeng, R., Pang, X., Gu, Q. & Tan, W. The mechanisms of flavonoids
inhibiting conformational transition of amyloid-b42 monomer: a comparative
molecular dynamics simulation study. *RSC Advances* **5**, 66391-66402, doi:DOI:
10.1039/c5ra12328c (2015).
53   Dulovic, A. *et al.* Rhabditophanes diutinus a parthenogenetic clade IV nematode
with dauer larvae. *PLoS Pathog* **16**, e1009113, doi:10.1371/journal.ppat.1009113
(2020).
54   Tiwari, O. S. *et al.* Entropically-Driven Co-assembly of l-Histidine and l-
Phenylalanine to Form Supramolecular Materials. *ACS Nano* **17**, 3506-3517,
doi:10.1021/acsnano.2c09872 (2023).
55   Coelho, A. A. Indexing of powder diffraction patterns by iterative use of singular
value decomposition. *J Appl. Cryst.* **36**, 86-95,
doi:https://doi.org/10.1107/S0021889802019878 (2003).
56   Altomare, A. *et al.* EXPO2013: a kit of tools for phasing crystal structures from
powder data. *J. Appl. Cryst.* **46**, 1231-1235,
doi:https://doi.org/10.1107/S0021889813013113 (2013).
57   Toby, B. H. & Von Dreele, R. B. GSAS-II: the genesis of a modern open-source all
purpose crystallography software package. *J. Appl. Cryst.* **46**, 544-549,
doi:https://doi.org/10.1107/S0021889813003531 (2013).
58   Cline, M. S. *et al.* Integration of biological networks and gene expression data
using Cytoscape. *Nat Protoc* **2**, 2366-2382, doi:10.1038/nprot.2007.324 (2007).
59   O'Boyle, N. M. *et al.* Open Babel: An open chemical toolbox. *J Cheminform* **3**, 33,
doi:10.1186/1758-2946-3-33 (2011).
60   Schüller, A., Hähnke, V. & Schneider, G. SmiLib v2.0: A Java-Based Tool for Rapid
Combinatorial Library Enumeration. *QSAR & Combinatorial Science* **3**, 407-410
(2007).

61   Habchi, J. *et al.* Systematic development of small molecules to inhibit specific
microscopic steps of Abeta42 aggregation in Alzheimer's disease. *Proc Natl Acad*
Sci U S A **114**, E200-E208, doi:10.1073/pnas.1615613114 (2017).
824

Figure 1. Crystal-Forming Small Molecules are Compact and Aromatic. A. A schematic

of *C. elegans* anatomy (from WormAtlas; used with permission). The pharynx is green.

B & C. Anterior-most region of a worm expressing the IDPC-1::GFP cuticle marker [9]

treated with either 1% DMSO solvent control (B) or 30 μM wact-190 (C) for six hours.

Orange arrows indicate the buccal cavity cuticle, the green arrows highlight the buccal

collar, the white arrows indicate the cuticle that lines the channels, and the blue

arrowheads highlight the birefringent crystals. Differential interference contrast (DIC),

birefringent (BIRE), and the IDPC-1::GFP (cuticle) images are shown. The scale bar in B

applies to all images in the upper right-hand side. **D.** Crystalizing molecules have

significantly fewer rotatable bonds and hydrogen-bond donors, but greater aromaticity,

and compactness (as measured by van der Waals volume and fraction Csp3) compared

to non-crystalizing molecules from the same library. The mean and standard error is

shown.

Figure 2. Biophysical Analyses of *in vitro* Small Molecule Crystals. A. The chemical

structure of wact-190. **B.** The unit cell with wact-190 molecules whose centroid lies

within the unit cell with the three coordinates shown with white letters and black

corresponding arrows. The wact-190 crystal unit cell shows two molecules per

asymmetric unit cell in a triclinic and anti-parallel packing arrangement. **C.** The 3D

crystal packing arrangement along the b-axis (see Supplemental Figure 2a-2c for other

aspects). **D.** The calculated distance between the indicated centroid (pink sphere) of two

adjacent molecules stacked along crystallographic b-axis within the wact-190 crystal is

approximately 5.0 Å. **E.** The experimental and simulated PXRD patterns of wact-190

molecule (see Supplemental Figure 2d for more details). **F.** The chemical structure of

wact-416. **G.** The unit cell with wact-416 molecules whose centroid lies within the

crystal unit cell. The wact-416 crystal unit cell shows four molecules per asymmetric unit

cell in an orthorhombic and parallel packing arrangement. **H.** The 3D crystal packing

(view along crystallographic b-axis) shows parallel packing for wac-416 crystals (see

Supplemental Figure 2e-2g for other aspects). **I.** The calculated distance between the

indicated centroid (pink sphere) of the 6-membered rings of two adjacent molecules

stacked along crystallographic b-axis within the wact-416 crystal is approximately 4.9 Å.

J. The experimental and simulated PXRD patterns of wact-416 molecule (see

Supplemental Figure 2h for more details).

857 **Figure 3. A Structural Similarity Network of 65 Crystal-Forming Compounds. A.** An

858 unsupervised structural similarity network of the 65 crystalizing molecules. Each node

859 represents a small molecule, labelled with a wactive number or DHV (dehydrovariabilin).

860 The link represents a Tanimoto score of structural similarity of the core scaffold of 0.8 or

861 higher. The lower-case labels indicate groups of molecules with the same core scaffolds

862 as indicated in B. Nodes highlighted in pink indicate a core scaffold known to interact

863 with amyloids (see Supplemental Table 3 and Supplemental Data File 1 for details). The

864 asterisks on the wact-128 node highlights that visual inspection reveals that it is a

865 distinct scaffold despite its connection to wact-381 and represents the 30th unique

866 family. **B.** Markush representations of the core scaffolds of structural analogs able to

867 crystalize in the worm. R, X, and Y groups are shown in Supplemental Figure 1.

Figure 4. Crystals Preferentially Disrupt Amyloid Dye-Staining Material of the

Pharyngeal Cuticle. A-F. Images of the anterior-most end of the worm**.** The imaging

channel is indicated (lower left) as is the wactive treatment (left-hand side of

micrograph series). DIC, differential interference contrast; bire, birefringence; CFW,

calcofluor white; ThS, thioflavin S; EY, eosin Y. Merge 1 is the merge of the two dye

signals. Merge 2 is the merge of the signals from the amyloid-binding dye and

birefringence. Blue arrows indicate overlapping signals of the amyloid-binding dye and

birefringence; orange arrows show a lack of amyloid-binding dye signal associated with

birefringence signal. The scale in A applies to A-F. **G.** Control for the ability of dyes to

bind wactive crystals. Precipitate of wact-190 or wact-390 was formed in solution (or

DMSO solvent control) and was subsequently stained with the dye indicated on the right

of each set. The dyes were used at the same concentration as the *in vivo* staining

experiments as described in the methods. Each condition was imaged using DIC,

birefringence (bire.) or the appropriate fluorescent (floures.) channel, as indicated on

the left of each panel. The dyes were not rinsed from the slide, which accounts for the

non-specific signal in the EY fluorescent channel. The scale in the upper left micrograph

applies to all images in G. **H-I.** Controls for the fluorescence of crystals in the different

channels. D, differential interference contrast (DIC); B, birefringence; C, CFP; G, GFP; Y,

YFP; R, RFP channels. The scale bar in H also applies to I. 60 μM of wact-190 and wact-

390 was used in all experiments relevant to panels A-I.

Figure 5. Amyloid-Binding Dyes Suppress Crystal Formation. A. Six-day viability assay

results illustrating that amyloid binding dyes (CR and ThS) can suppress wact-190-

induced lethality, but that chitin/chitosan-binding dyes (CFW and EY) cannot. Each cell

shows the summary of 3 trials each done in quadruplicate. **B-C.** Amyloid-binding dyes,

but not chitin/chitosan-binding dyes, can suppress crystal formation. On the top row,

animals were pre-incubated in the indicated dye or solvent control for 3 hours. Then,

the right-most five samples were incubated in 60 μM wact-190 for three hours without

the initial dyes present. On the bottom row of (B), animals were incubated in the

indicated dye or solvent control, and for the five right-most five samples, simultaneously

incubated with wact-190 (60 μM) for 3 hours. Representative birefringence images are

shown in (B) and the corresponding signal quantification is reported in (C). The scale bar

in the upper left of B applies to all images in the series. Samples labelled with an asterisk

indicates a significant difference relative to control ($p<0.01$). Standard error of the mean

is shown.

Figure 6. Aβ42 Fibrils can Seed wact-190 Objects. Transmission electron microscopy

(TEM) images of solutions allowed to self-assemble overnight. **A-D.** Mixing solutions of

25 μM Aβ42 and 25 μM wact-190 in PBS. Unmixed 25 μM Aβ42 (A) and 25 μM wact-190

(B); 1-fold Aβ42 diluted with 2-fold wact-190 (to a final concentration of 8.33 μM Aβ42

and 16.66 μM wact-190) (C); 1-fold Aβ42 and 10-fold wact-190 (to a final concentration

of 2.27 μM Aβ42 and 22.72 μM wact-190) (D). **E-H.** Mixing solutions of 25 μM Aβ42 and

0.5 μM wact-190 in PBS. Unmixed 25 μM Aβ42 (E) and 0.5 μM wact-190 (F); 1-fold Aβ42

diluted with 1-fold wact-190 (to a final concentration of 12.5 μM Aβ42 and 0.25 μM

wact-190)(G and H). **I-L.** Mixing solutions of 25 μM Aβ42 and 0.1 μM wact-190 in PBS.

Unmixed 25 μM Aβ-42 (I) and 0.1 μM wact-190 (J); 1-fold Aβ42 diluted with 1-fold wact-

190 (to a final concentration of 12.5 μM Aβ42 and 0.05 μM wact-190) (K and L).

Examples of Aβ42 amyloid fibrils are indicated with a blue arrow and examples of

presumptive wact-190 objects that are associated with Aβ42 fibrils are indicated with a

red arrow.

Figure 7. A Screen for wact-190 Suppressors Reveals Amyloid-Disrupting Molecules. A.

A structural similarity network of the 85 Spectrum library hits that suppress wact-190

lethality and crystal formation. The nodes (circles) represent a drug or natural product.

The links (straight lines) represent a Tanimoto score of structural similarity of 0.8 or

more (see Methods). A bold red outline indicates known disruptors of amyloid fibril

formation. See Supplementary Table 3 for details and names of the compounds. **B.** Core

scaffolds among the drug suppressors of crystal formation. The small case letter

preceding the scaffold name corresponds to the nodes indicated in (A). The number (n)

of individual molecules within the network is indicated, as is the enrichment of that

scaffold within the network relative to that expected by random chance based on the

prevalence of that scaffold within the entire library (the hypergeometric p value is

shown). The benzaldehyde substructure is highlighted in blue. **C.** Examples of the

localization of crystal suppressors (60 μM) that are fluorescent. Calcofluor white (CFW)

is used as a counter-stain control; curcu., curcumin; harmal., harmaline; erythro.,

erythrosine. See Supplemental Figure 5 for additional examples and controls. The scale

in panel C applies to all images in the series. **D-H.** *In vitro* assays to characterize the

ability of the indicated molecule to inhibit Aβ42 fibril formation in secondary nucleation

assays (see methods, Supplementary Table 5 and Supplementary Figure 8 for additional

details). Adapalene is a known standard inhibitor of Aβ42 fibril formation [61].

Figure 8. Crystallizers and Suppressors can Share Identical Core Structures. A-C.

Physicochemical features of crystallizers and suppressors. A single and double asterisk

indicate *p*<0.001 and *p*<1.0E-10, respectively. The standard error of the mean is shown.

D. Crystallizers and suppressors sharing an identical or similar core structure. **E.** Core

scaffolds of suppressing molecules that can be turned into crystallizers (see

Supplemental Table 6 for additional details). **F.** Core scaffolds of crystallizing molecules

that can be turned into suppressors (see Supplemental Table 7 for additional details). **G.**

In vitro assays to characterize the ability of the indicated suppressor molecule to inhibit

Aβ42 fibril formation in secondary nucleation assays (see methods and Supplementary

Figure 8 for additional details).

A

B

C

D ~5.0 Å

E

F

G

H

I ~4.9 Å ~4.9 Å

J

A

dye	wact-190 [µM]	dye concentration (µM) 0	1.9	3.8	7.5	15	30	60	120	240	480	960
CFW	0											
CFW	3.75											
CR	0											
CR	3.75											
EY	0											
EY	3.75											
ThS	0											
ThS	3.75											

Legend: green = culture overgrown; light purple = 11-50 animals; purple = fewer than 11 animals

B

wact-190-treated

control | control | congo red | ThS | CFW | EY

dye pre-treatment, then wact-190 treatment (birefringent signal shown)

co-incubation of dye and wact-190 (birefringent signal shown)

5 µm

C

birefringence (normalized)

dye pre-incubation

*DMSO>DMSO, ETOH>w190, DMSO>w190, *60 uM CR>w190, *1.2 mM CR>w190, 60 uM ThS>w190, 1.2 mM ThS>w190, 60 uM CFW>w190, 1.2 mM CFW>w190, 60 uM EY>w190, 1.2 mM EY>w190

dye co-incubation

*DMSO+DMSO, ETOH+w190, DMSO+w190, *60 uM CR+w190, *1.2 mM CR+w190, 60 uM ThS+w190, 1.2 mM ThS+w190, 60 uM CFW+w190, 1.2 mM CFW+w190, 60 uM EY+w190, 1.2 mM EY+w190

	source	wactive crystal (avg)	wactive no-crystal (avg)	wactive ttest	RLL1200 crystal (avg)	RLL1200 no-crystal (avg)	RLL1200 ttest	wact v RLL crystallizer ttest	Spectrum dehydrovariabili	Spectrum no-crystal (avg)
Size Features										
molecular weight	Open Babel	307.16	304.30	7.5E-01	288.09	324.67	2.3E-03	1.6E-01	282.29	328.75
molar refractivity	Open Babel	82.05	84.59	3.2E-01	73.28	87.32	5.8E-06	2.9E-02	79.17	88.36
van der Walls volume	Open Babel	315.72	356.40	7.3E-04	280.14	356.26	2.6E-07	5.4E-02	320.08	424.60
Hydrogen Bonding Features										
hydrogen bond acceptors (method 1)	Open Babel	2.96	2.53	3.3E-02	2.44	3.79	6.8E-05	4.9E-02	3.00	5.13
hydrogen bond acceptors (method 2)	Open Babel	3.73	2.82	4.6E-05	3.06	4.62	2.8E-04	5.5E-02	4.00	5.40
hydrogen bond donors	Open Babel	0.35	0.95	2.4E-06	0.38	0.41	8.0E-01	9.0E-01	0.00	1.93
number of OH at pH 7.4	Open Babel	0.02	0.04	5.3E-01	0.00	0.00	8.4E-01	5.7E-01	0.00	1.03
Bond (non-aromatic) Features										
bonds	Open Babel	22.90	21.85	1.2E-01	20.44	24.18	2.0E-05	2.2E-02	24.00	24.50
aromatic bonds	Open Babel	16.54	12.26	2.6E-10	15.44	16.08	4.1E-01	2.8E-01	16.00	7.66
single bonds	Open Babel	5.73	8.83	4.3E-06	4.25	7.49	7.7E-07	7.7E-02	8.00	14.89
double bonds	Open Babel	0.63	0.74	4.0E-01	0.75	0.53	2.1E-01	6.3E-01	0.00	1.92
triple bonds	Open Babel	0.00	0.02	3.2E-01	0.00	0.08	2.6E-01	n/a	0.00	0.03
rotatable bonds	Open Babel	3.38	4.54	4.3E-05	2.81	4.50	6.6E-05	9.7E-02	2.00	4.70
Atom Features										
number of heavy atoms	Open Babel	20.79	20.30	4.0E-01	18.75	22.20	1.1E-05	3.0E-02	21.00	22.89
number of H	Open Babel	12.06	16.32	9.1E-07	9.81	14.65	1.1E-06	5.9E-02	14.00	21.18
number of C	Open Babel	15.75	15.64	8.2E-01	14.38	16.69	2.7E-04	1.0E-01	17.00	16.88
number of N	Open Babel	2.27	1.94	3.9E-02	2.00	2.51	1.4E-02	2.8E-01	0.00	1.50
number of O	Open Babel	1.65	1.36	7.0E-02	1.06	1.78	5.2E-03	1.4E-02	4.00	3.97
number of S	Open Babel	0.21	0.27	4.4E-01	0.00	0.40	3.7E-03	7.6E-02	0.00	0.20
number of P	Open Babel	0.00	0.00	na	0.00	0.00	na	na	0.00	0.02
number of F	Open Babel	0.33	0.37	8.1E-01	0.50	0.24	1.0E-01	3.8E-01	0.00	0.10
number of Cl	Open Babel	0.31	0.55	4.8E-02	0.31	0.42	5.3E-01	1.0E+00	0.00	0.15
number of Br	Open Babel	0.23	0.11	4.7E-02	0.50	0.17	4.1E-04	4.1E-02	0.00	0.01
number of I	Open Babel	0.04	0.05	7.4E-01	0.00	0.01	7.8E-01	4.1E-01	0.00	0.03
number of B	Open Babel	0.00	0.00		0.00	0.00	na	na	0.00	0.00
number of As	Open Babel	0.00	0.00		0.00	0.00	na	na	0.00	0.00
number of Si	Open Babel	0.00	0.00		0.00	0.00	na	na	0.00	0.00
number of Se	Open Babel	0.00	0.00		0.00	0.00	na	na	0.00	0.00
number of Te	Open Babel	0.00	0.00		0.00	0.00	na	na	0.00	0.00
number of halogens	Open Babel	0.92	1.09	3.6E-01	1.31	0.82	3.2E-02	1.3E-01	0.00	0.29
halides as a percentage of MW	Open Babel	0.13	0.13	9.5E-01	0.20	0.10	8.0E-05	5.2E-02	0.00	0.03
Aromaticity Features										
number of rings	Open Babel	3.10	2.56	2.1E-05	2.69	2.98	4.9E-02	2.9E-02	4.00	2.61
aromatic rings	Open Babel	2.94	2.15	1.1E-09	2.69	2.84	3.2E-01	2.0E-01	3.00	1.35
non-aromatic rings	Open Babel	0.17	0.41	1.1E-02	0.00	0.14	1.2E-01	1.3E-01	1.00	1.26
fraction of atoms in aromatic rings	Open Babel	0.79	0.60	1.3E-09	0.82	0.72	1.1E-03	5.4E-01	0.71	0.35
fraction of aromatic rings over total rings	Open Babel	0.95	0.86	3.0E-03	1.00	0.96	1.2E-01	1.2E-01	0.75	0.56
number of aromatic heavy atoms	SwissADME	16.33	12.05	4.3E-11	15.38	15.97	4.3E-01	3.4E-01	15.00	7.39
fraction Csp3	SwissADME	0.08	0.24	5.5E-09	0.01	0.16	3.4E-09	1.7E-02	0.18	0.44
Charge Features										
number of (+) charges at pH 7.4	Open Babel	0.15	0.52	1.8E-04	0.00	0.06	3.0E-01	1.1E-01	0.00	0.41
number of (-) charges at pH 7.4	Open Babel	0.10	0.09	7.3E-01	0.00	0.00	na	1.8E-01	1.00	0.35
net charge at pH 7.4	Open Babel	0.04	0.44	1.7E-05	0.00	0.06	3.0E-01	4.1E-01	-1.00	0.06
number of aliphatic primary amines	Open Babel	0.00	0.01	5.7E-01	0.00	0.00	na	na	0.00	0.09
number of aliphatic secondary amines	Open Babel	0.00	0.15	4.6E-03	0.00	0.00	na	na	0.00	0.06
number of aliphatic tertiary amines	Open Babel	0.02	0.25	1.0E-03	0.00	0.06	3.3E-01	5.7E-01	0.00	0.16
number of aliphatic amines	Open Babel	0.02	0.40	2.3E-05	0.00	0.06	3.3E-01	5.7E-01	0.00	0.32
number of COOH/COO-	Open Babel	0.00	0.00	na	0.00	0.00	na	na	0.00	0.23
Solubility Features										
LogP	Open Babel	4.04	3.76	5.0E-02	3.99	4.14	3.2E-01	7.8E-01	4.01	2.55
iLogP	SwissADME	2.99	3.05	4.7E-01	2.96	3.22	2.3E-02	7.4E-01	3.29	2.22
XLogP3	SwissADME	3.77	3.72	6.9E-01	3.94	3.93	9.5E-01	4.1E-01	3.47	2.08
WLogP	SwissADME	3.95	3.58	1.7E-02	4.10	4.01	6.0E-01	5.2E-01	3.86	2.16
MLogP	SwissADME	2.75	2.95	1.3E-01	3.04	2.68	6.9E-02	2.0E-01	1.95	1.31
LogP (Silicos-IT)	SwissADME	3.77	3.71	7.3E-01	3.93	4.12	2.4E-01	6.1E-01	4.01	2.21
Consensus LogP	SwissADME	3.45	3.40	6.8E-01	3.59	3.59	9.9E-01	4.4E-01	3.32	1.99
LogS	Open Babel	-5.13	-5.01	4.2E-01	-5.05	-5.61	5.1E-03	7.8E-01	-5.16	-3.24
LogS (Ali)	SwissADME	-4.62	-4.38	6.0E-02	-4.49	-4.99	1.3E-02	7.7E-01	-4.01	-3.46
LogS (Silicos-IT)	SwissADME	-6.37	-5.82	5.0E-03	-6.31	-6.72	7.1E-02	8.7E-01	-6.07	-3.71
LogS (ESOL)	SwissADME	-4.48	-4.22	8.9E-03	-4.53	-4.57	8.1E-01	3.7E-01	-4.17	-3.10
Drug-Like Features										
leadlikeness (# of violations)	SwissADME	1.02	1.02	9.9E-01	0.69	1.05	5.3E-01	7.1E-02	0.00	1.12
Lipinski Drug Prediction (# of violations)	SwissADME	0.06	0.07	9.1E-01	0.06	0.03	4.7E-01	1.0E+00	0.00	0.29
Ghose Drug Prediction (# of violations)	SwissADME	0.02	0.03	8.2E-01	0.00	0.02	5.9E-01	5.7E-01	0.00	0.79
Veber Drug Prediction (# of violations)	SwissADME	0.00	0.00	na	0.00	0.01	7.0E-01	na	0.00	0.19
Egan Drug Prediction (# of violations)	SwissADME	0.00	0.01	4.2E-01	0.00	0.03	4.9E-01	na	0.00	0.19
Muegge Drug Prediction (# of violations)	SwissADME	0.04	0.03	7.9E-01	0.00	0.08	2.6E-01	4.1E-01	0.00	0.75
bioavailability score	SwissADME	0.55	0.55	1.6E-14	0.55	0.55	9.1E-01	2.8E-06	0.55	0.53
PAINS (# of alerts)	SwissADME	0.10	0.12	7.7E-01	0.00	0.01	7.7E-01	1.8E-01	0.00	0.09
Brenk (# of alerts)	SwissADME	0.42	0.58	3.2E-01	0.38	0.11	1.4E-02	8.6E-01	0.00	0.62
log Kp (cm/s) (skin permeation)	SwissADME	-5.50	-5.51	8.7E-01	-5.26	-5.49	7.8E-02	6.9E-02	-5.56	-6.78
synthetic accessibility	SwissADME	2.74	2.48	1.7E-03	2.56	2.89	1.1E-03	9.2E-02	3.42	3.46
Miscellaneous Features										
melting point	Open Babel	148.97	135.06	3.6E-02	138.46	152.54	1.1E-01	3.1E-01	131.56	169.94
topological polar surface area	Open Babel	55.14	46.89	1.8E-02	40.65	64.70	6.2E-04	6.4E-03	40.83	85.95
BBB permeant (1=yes; 0=no)	SwissADME	0.83	0.87	5.0E-01	1.00	0.66	4.3E-03	8.3E-02	1.00	0.45
MDR1 substrate	SwissADME	0.08	0.15	2.2E-01	0.00	0.05	3.5E-01	2.4E-01	1.00	0.31

Compound	Wact-190	Wact-416
CCDC number	2281946	2282440
Crystal description	White crystalline powder	White crystalline powder
Diffractometer	Bruker D8 DISCOVER	Bruker D8 DISCOVER
Temperature (K)	298	298
Chemical Formula	$C_{20}H_{15}N_3O_2$	$C_{15}H_{12}BrNO$
Formula weight (g/mol)	329.35	302.16
Wavelength	1.54050	1.54050
z	2	4
Crystal System	Triclinic	Orthorhombic
Space group	P-1	$Pna2_1$
a(Å)	5.004(2)	7.58957(25)
b(Å)	10.662(5)	5.77111(20)
c(Å)	16.651(18)	29.4038(15)
α(°)	91.89(5)	90
β(°)	104.029(18)	90
γ(°)	107.259(3)	90
Volume(Å³)	817.9(3)	1287.89(6)
P(g/cm³)	1.337	1.558
μ(mm⁻¹)	0.718	4.234
F(000)	344.0	608.0
2θ range(°)	5-70	5-70
Index max	h=3,k=7,l=12	5,4,21
N. reflections	712	285
n. parameters	98	33
R_{wp}, GOF on the pattern	4.65%, 1.6	4.74%, 1.4
R_F, R_{F^2}	9.69, 9.62	4.90, 7.14

Supplemental Table 2. Crystallographic data collection and refinement statistics data for the crystal of wact-190 and wact-416.

#	scaffold[a]	trivial name	Chembridge ID[b]	%	sd	N	Structure[d]	Common Substructure[d] (aka Core Scaffold)	SciFinder Scholar Substructure[e]	PMID/Patent (2022-04)[f]
1	a	wact-13-3	5690016	52	9	2	n1c(noc1c1cc(OC)ccc1)c1ccccc1	c1(c2ccccc2)noc(c3ccccc3)n1	*2250 analogs, 127 refs	18550375, 23766818; US20110081297;
2	a	wact-13-6	5910375	100	0	2	n1c(noc1c1ccc(cc1)Br)c1ccccc1			
3	a	wact-13-7	6141272	100	0	2	n1c(noc1c1ccc(cc1)Br)c1ccc(cc1)F			
4	a	wact-13-21	7530844	100	0	2	n1c(c2c(F)cccc2)onc1c1ccc(cc1)Cl			
5	a	wact-135	7986793	47	40	8	n1c(noc1c1ccccc1)c1cc(OC)ccc1			
6	a	wact-158	9017109	99	2	4	n1c(noc1c1ccc1)F)c1cc(Br)ccc1			
7	a	wact-184	9034543	100	1	4	n1c(noc1c1ccccc1)c1ccc(cc1)Br			
8	a	wact-589	5229759	88	5	3	n1c(noc1c1ccccc1)c1ccc(cc1)Cl			
9	b	wact-10-2	6033348	98	3	2	n1c(noc1c1ccc(cc1)Br)c1cnccc1	c1(c2cccnc2)noc(c3ccccc3)n1	2431 analogs, 353 refs	US20110081297
10	b	wact-154	9013615	34	12	4	n1c(noc1c1ccc(OCc2ccccc2)cc1)c1cnccc1			
11	b	wact-558	9008591	29	15	4	n1c(noc1c1ccc(OCC(C)C)cc1)c1cnccc1			
12	c	wact-8-3	5905759	100	0	2	n1c(noc1c1ccc(cc1)Br)c1ccnnc1	c1(c2ccnnc2)noc(c3ccccc3)n1	1309 analogs, 101 refs, 0 amy.ints	
13	c	wact-8-4	6715898	49	10	2	n1c(c2c(c(c(cc1)C)Cl)c1ccnccc1			
14	c	wact-106	7783279	81	22	5	n1c(c2c(ccc(c2)Br)Cl)onc1c1ccnnc1			
15	c	wact-156	9016428	71	20	6	n1c(c2c(cc(c(c2)F)F)Cl)onc1c1ccnccc1			
16	c	wact-711	6945665	43	17	2	n1c(noc1c2c(cc1)cccc2)c1ccnnc1			
17	d	wact-174	9026631	99	1	3	n1c(noc1c1ccncc1)c1ccc(NC(=O)c2c(F)cccc2)cc1	c1(c2ccccc2)noc(c3ccncc3)n1	2089 analogs, 117 refs	US20120263646
18	d	wact-190	9036812	98	3	6	n1c(noc1c1ccncc1)c1ccc(OCc2ccccc2)cc1			
19	d	wact-195	9040512	80	9	3	n1c(onc1c1ccc(OCc2ccccc2)cc1)c1ccncc1			
20	d	wact-713	7990228	51	5	2	n1c(noc1c1ccncc1)c1ccc(cc1)Cl			
21	e	wact-113	7834045	84	14	5	n1c(noc1c1ccc(cc1)Br)c1occc1	c1(c2ccco2)onc(c3ccccc3)n1	1493 analogs, 71 refs, 0 amy.ints	
22	e	wact-165	9020086	85	14	4	n1c(noc1c1ccc(cc1)F)c1occc1			
23	f	wact-58	6039582	62	34	4	n1c(noc1c1ccc(cc1)Cl)c1ncccc1	c1(c2ccccc2)onc(c3ccccn3)n1	2986 analogs, 183 refs, 0 amy.ints	
24	f	wact-153	9013537	59	38	5	n1c(noc1c1ccc(OCc2ccccc2)cc1)c1ncccc1			
25	f	wact-507	7629983	23	6	4	n1c(c2c(ccc(c2)Cl)Cl)onc1c1ncccc1			
26	g	wact-2	5185411	80	23	4	n1c(noc1c1ccc(cc1)Br)c1sccc1	c1(c2cccs2)onc(c3ccccc3)n1	4224 analogs, 429 refs, 0 amy.ints	
27	g	wact-136	7989399	48	31	4	n1c(onc1c1ccc(OC)ccc1)c1sccc1			
28	g	wact-169	9024879	69	35	4	n1c1c(cc(cc1)Cl)Cl)c1sccc1			
29	g	wact-570	9028223	85	8	3	n1c(noc1c1ccc(NC(=O)c2c(F)cccc2)cc1)c1sccc1			
30	h	wact-391	5307255	100	0	3	[N+](=O)(c1ccc(N/C=C/C(=O)c2ccccc2)cc1)[O-]	O=C(c1ccccc1)/C=C/Nc2ccccc2	*1273 analogs, 110 refs	21755599, US9095596, US20120237446
31	h	wact-416	5404872	100	0	3	C(=C\Nc1ccc(Br)cc1)/C(=O)c1ccccc1			
32	h	wact-709-2	6088831	39	4	2	C(=C\Nc1c(F)cccc1)/C(=O)c1ccccc1			
33	h	wact-709-4	6642644	100	0	2	c1(cc(ccc1N/C=C/C(=O)c1ccccc1)Br)F			
34	h	wact-709-5	6669323	100	0	2	c1(cc(ccc1N/C=C/C(=O)c1ccccc1)F)Br			
35	h	wact-709-6	6872372	100	0	2	C(=C\Nc1ccc(Cl)cc1)/C(=O)c1ccccc1			
36	h	wact-709-8	7313533	99	2	2	c1(cc(N/C=C/C(=O)c2ccc(cc2)Br)ccc1F)F			
37	h	wact-709-9	6370432	100	0	2	C(=C\Nc1ccc(F)cc1)/C(=O)c1ccccc1)Br			
38	i	wact-49	5459938	88	15	3	N1(c2ccc(cc2)F)CCN(C2CCC(CC2)c2ccccc2)CC1	c1(N2CCN(CC2)C3CCCCC3)ccccc1	5265 analogs, 387 refs	DOI:10.1007/s11094-019-02000
39	i	wact-50	5556756	99	2	8	[N+](=O)(c1ccc(N2CCN(C(=O)C(c3ccccc3)CC2)CC2)cc1)[O-]	O=C(c1ccccc1)N2CCN(CC2)C(C(=O)cc1	9419 analogs, 407 refs	29394041, US20140187556
40	i	wact-364	5269853	69	22	3	[N+](=O)(c1ccc(N2CCN(C(=O)c3sccc3CC2)cc1)[O-]	O=[N+]([O-])c1ccc(N2CCN(CC2)C(C(=O)cc1		
41	i	wact-381	5221072	100	1	4	[N+](=O)(c1ccc(N2CCN(C(=O)c3ccc(cc3)Br)CC2)cc1)[O-]	O=[N+]([O-])c1ccc(N2CCN(CC2)C(C(=O)cc1		
42	j	wact-51	5631017	51	28	4	lc1cccc(c1)c1nnc(o1)c1ccccc1	c1(c2oc(c3ccccc3)nn2)ccccc1	*824 analogs, 118 refs	19651517, 23766818, 24936678, DOI: 10.1039/c3md00189j;
43	j	wact-425	5570574	47	16	5	Brc1ccc(cc1)c1nnc(o1)c1ccccc1			
44	k	wact-81	7634492	94	5	4	n1c(noc1/C=C/c1(Cl)cccc1)c1ccncc1	c1(c2ccccc2)noc(/C=C/c3ccccc3)n1	6678 analogs, 16 refs	US8183276
45	k	wact-609	7750501	97	5	3	n1c(noc1/C=C/c1ccccc1)c1ccc(NC(=O)c2occc2)cc1			
46	l	wact-86	7640928	62	24	5	c1(c2c(c1)cccc2)C(=O)Nc1cc(c(NC(=O)c2c(Cl)cccc2)cc1)O	O=C(c(c1)oc2c1cccc2)Nc3ccccc3	29324 structures, 811 refs, 0 amy.ints	
47	l	wact-134	7985302	46	40	6	c1(oc2c(c1)cccc2)C(=O)Nc1cc(c(N2CCN(C(=O)CC2)cc1)Cl			
48		wact-15	7687977	86	38	7	n1c(sc2c1cccc2)COc1ccc(F)cc1	c1(COc2ccccc2)sc3ccccc3n1	3345 analogs, 258 refs, 0 amy.ints	
49		wact-24	5162985	70	13	4	n1c(cnc2c1cccc2)c1ccc(cc1)OCC	COc1ccc(c2cnc3ccccc3n2)cc1	9419 analogs, 407 refs	23047223, 33475377, US20020155172
50		wact-37	1	14	27	4	c1(=O)n(ncc(c1Cl)OC)c1cc(C(F)(F)F)ccc1	O=c1cc(OC)cnn1c2ccccc2	43522 analogs, 262 refs, 0 amy.ints	
51		wact-40	5360297	12	6	4	c1(nc2c(o1)cccc2)c1nc2c(cc1)cccc2	c1(c2ccc3ccccc3n2)oc4ccccc4n1	328 analogs, 25 refs, 0 amy.ints	
52		wact-102	7747740	45	31	5	O(c1ccc(cc1)OC)Cc1ccc(Cl)cc1	COc1ccc(OCc2ccccc2)cc1	*330 analogs, 474 refs	24936678, 26170205, WO2015090122
53		wact-105	7782912	99	2	5	c1(C(=O)O/N=C/c2ccncc2)\N)c(ccc(c1)Br)Cl	O=C/O/N=C(N)/c1ccncc1)c2ccccc2	79 analogs, 11 refs, 0 amy.ints	
54		wact-120	7889289	92	9	9	C(=O)(Nc1ccc(c2ccccc2)cc1)OC	C(=O)(Nc1ccc(c2ccccc2)cc1)OC	8518 analogs, 658 refs, 0 amy.ints	
55		wact-128	7971816	41	27	8	c1(C(=O)Nc2ccc(Br)cc2)c(cc(cc1)F)F	O=C(Nc1ccccc1)c2ccccc2	*10324 analogs, 127 refs	19191553, 21755599, 25515893, 26007606,
56		wact-220	5784085	99	2	4	Clc1ccc(cc1)N1CCN(CC1/N=C\c1ccccn1	c1(N2CCN(/N=C\c3ncccc3)CC2)ccccc1	42 analogs, 8 refs, 0 amy.ints	
57		wact-390	5307019	88	2	3	n1c(noc1CCC)c1ccc(c2ccc(cc2)F)cc1	c1(c(ccc3ccccc3)ccc1)nocn1	2994 analogs, 585 refs, 0 amy.ints	
58		wact-393	5308491	54	21	4	n1c(scc1c1ccc(c1)I)Nc1ccc(Cl)cc1.Br	c1(Nc2ccccc2)scc(c3ccccc3)n1	19794 analogs, 828 refs, 0 amy.ints	
59		wact-415	5403320	100	0	4	c1(nc2c(s1)cccc2)c1ccc(NC(=O)c2c(F)cccc2)cc1	O=C(c1ccccc1)Nc2ccc(c3sc4ccccc4n3)cc	1640 analogs, 83 refs	21755599,24297602, US20140105820
60		wact-446	5962739	80	28	3	c1(n[nH]c(c1)c1ccc(F)ccc1)c1c(cc(cc1)C)O	c1(c2ccccc2)cc(c3ccccc3)[nH]n1	*5667 analogs, 2487 refs	US10435373
61		wact-469	6433196	98	4	6	n12c(nc3c1cccc3)SC(CC2=O)c1sccc1	n12c(nc3c1cccc3)SC(CC2=O)c1sccc1	2 analogs, 3 refs, 0 amy.ints	
62		wact-498	7426700	99	1	3	c1(c(=O)c2c(oc1ccc2)OC)c1ccc(cc1)Br	O=c1ccc(OCC)ccc2occc1c3ccccc3	16848 analogs, 8384 refs	22587837, 23766818, 29191087, 32616652
63		wact-587	5175165	99	1	3	[N+](=O)(c1cc2c(nc1)cc(cc2)OC)[O-]	[N+](=O)(c1cc2c(nc1)cc(cc2)OC)[O-]	*101 analogs, 12 refs	30956012
64		wact-712-1	7972897	79	1	2	n1c(onc1c1ccc(Cl)c1cccc1	c1(c2ccccc2)onc(c3ccccn3)n1	5088 analogs, 178 refs	US20110081297
65		dehydrovar		85	25	3	c12c(c3c(o1)ccc3c)MD)COc1c2ccc(c1)OC	c12oc3ccccc3c1COc4ccccc42	70 analogs, 384 refs, 0 amy.ints	

Supplemental Table 3. A Literature-Based Search for Evidence of Amyloid Interaction Among 65 Crystalizing Molecules.
[a]The substructure that is in common to a group of molecules (aka the core scaffold) is depicted in Figure 2A.
[b]The Chembridge identification number for reordering at Chembridge Inc.
[c]The percentage of animals within the population, grown in 30 μM of compound, is shown, along with the standard of deviation (sd) and the number of independent biological repeats (N).
[d]The SMILES codes for the small molecule structure or the core scaffold used in SciFinder searches
[e]The number of analogs found in SciFinder searches using the core scaffold in substructure searches. The number of academic or patent-based publications (refs) associated with the analogs is also shown. In cases where searches with the core scaffold yielded >20,000 references, we instead used the primary structure to perform SciFinder searches and used a cutoff of 80% structural similarity or more to perform the searches. Searches performed this way are marked with an asterisks. The cell is colored pink if no evidence was found for amyloid interaction (0 amy.ints). The date of the searches is shown in brackets.
[f]The pubmed ID (PMID) and/or patent number is shown that provides evidence for a primary role in amyloid interaction. The date of the searches is shown in brackets.

	wactive	Chembridge ID[a]	Structure[b]	Common Substructure (aka Core Scaffold)[b]	SciFinder Scholar Substructure Search (2022-04)[c]	PMID/Patent (2022-04)[d]
1	wact-204	9063096	C1(CC1)NCc2ccc(OCc2ccc(Cl)cc2)cc1.Cl	C1(NCc2ccc(OCc3ccccc3)cc2)CC1	778 structtures- 54 refs- 0 amy.ints	
2	wact-35	5344384	n1(c2c(c3c1cccc3)cc(cc2)Cl)CO	c12ccccc1c3ccccc3n2	*595 analogs, 144 refs	34498871, WO2010092111, DOI:10.1021/acs.jpcb.1c06161
3	wact-614	9039813	c1(c2c(cc2)Cl)Cl)oc(cc1)CNC1CC1.Cl	c1(c2ccccc2)ccc(CNC3CC3)o1	754 structtures- 26 refs- 0 amy.ints	
4	wact-1	5121613	c12nc(cn1ccs2)c1ccc(cc1)Cl	c12sccn1cc(c3ccccc3)n2	*358 analogs, 185 refs, 0 amy.ints	
5	wact-4	5352487	c1(oc(nn1)SCC)c1c(cc(cc1)Cl)Cl	CCSc1nnc(c2ccccc2)o1	*280 analogs, 65 refs, 0 amy.ints	
6	wact-7	5652963	o1nc(nc1c1ccccs1)c1ccccc1	o1nc(nc1c1cccs1)c1ccccc1	4224 structures, 429 refs, 0 amy.ints	
7	wact-19	5104063	c12c(SCCc3ccncc3)cccc1cccc2	c12c(SCCc3ccncc3)cccc1cccc2	24 strctres, 2 papers, 0 amy.ints	
8	wact-139	9000631	n1c(onc1c1cc(Br)ccc1)c1occc1	c1(c2ccco2)onc(c3ccccc3)n1	1493 structures, 71 refs, 0 amy.ints	
9	wact-423	5547023	COc1ccc(CNc2ccc(Br)cc2)cc1	COc1ccc(CNc2ccccc2)cc1	*656 analogs, 51 refs, 0 amy.ints	
10	wact-596	5649594	Fc1ccccc1Nc1nc(cs1)c1ccccc1	c1(Nc2scc(c3ccccc3)n2)ccccc1	19794 structures, 828 refs, 0 amy.ints	
11	wact-23	5156707	c1(ncc(o1)c1ccc(cc1)C)c1ccnc1	c1(c2ccnc2)oc(c3ccccc3)cn1	550 structures, 240 refs, 0 amy.ints	
12	wact-29	5264250	s1c(ccc1CN1CCN(c2ccc(cc2)F)CC1)Br	c1(CN2CCN(CC2)c3ccccc3)sccc1	6636 analogs, 249 refs	WO2017159484; US8420640
13	wact-30	5267230	N1(c2ccc(cc2)F)CCN(Cc2cc(Br)ccc2)CC1	N1(CCN(CC1)Cc2ccccc2)c3ccccc3	*784 analogs, 34 refs, 0 amy.ints	
14	wact-481	6631407	n1c(scc1c1ccc(cc1)Cl)CC(=O)OCC	O=C(OCC)Cc1scc(c2ccccc2)n1	1246 structures, 43 refs, 0 amy.ints	
15	wact-521	7688376	c1(C(=O)NC(c2ccccc2)C)c(ccc(c1)Br)OCC	O=C(Nc1ccccc1)c2ccccc2	*2103 analogs, 79 refs, 0 amy.ints	
16	wact-54	5686969	n1c(noc1COc1ccc(Cl)cc1)c1cnccc1	c1(c2ccccnc2)noc(COc3ccccc3)n1	186 structures, 25 refs, 0 amy.ints	
17	wact-560	9010683	C(=O)(Nc1c(Cl)cccc1)c1ccc(cc1)CC	O=C(c1ccccc1)Nc2ccccc2	*3616 analogs, 146 refs, 0 amy.ints	
18	wact-65	6858658	c1(C(=O)N2CCN(c3cc(C(F)(F)F)ccc3)CC2)c(ccc(c1)Cl)Cl	O=C(N1CCN(CC1)c2ccccc2)c3ccccc3	56127 structures, 1713 refs, 0 amy.ints	
19	wact-74	7597064	c1(ncccn1)SCc1ccc(Cl)cc1	c1(SCc2ccccc2)ncccn1	41555 structures, 928 refs, 0 amy.ints	
20	wact-11	6222549	C(c1c(C(=O)NCCc2ccc(Cl)ccc1)cccc1)(F)(F)F	O=C(NCCc1ccc1)c2ccccc2	*626 analogs, 53 refs, 0 amy.ints	
21	wact-103	7756678	C(=O)(c1sccc1)Nc1cc(c(N2CCN(CC2)CC)cc1)Cl	O=C(Nc1ccc(N2CCNCC2)cc1)c3sccc3	832 analogs, 39 refs, 0 amy.ints	
22	wact-121	7889470	c1(nccn1)SCC#CCOc1ccc(Cl)cc1	c1(SCC#CCOc2ccccc2)nccn1	*644 analogs, 15 refs, 0 amy.ints	
23	wact-132	7983837	S(=O)(=O)(c1cc(c1cl)OCC)Cl)NCc1ccncc1	O=S(c1ccccc1)(NCc2ccncc2)=O	*15086 analogs, 428 refs, 0 amy.ints	
24	wact-141	9003606	C(=O)(Nc1ccc(Cl)cc1)Cc1cc(F)ccc1	O=C(c1ccccc1)Nc2ccccc2	*3663 analogs, 78 refs, 0 amy.ints	
25	wact-150	9012025	N1(c2c(cc(NC(=O)c3ccc(C3)CC)cc2)Cl)CCN(CC1)C	O=C(c1ccccc1)Nc2ccc(N3CCNCC3)cc2	14917 analgos, 283 refs	US20110250135, 23008501 (the core is a small part of the molecule)
26	wact-160	9017218	C(=O)(C1CCN(CC1)CCOc1c(cc(cc1)Cl)Cl)OCC.Cl	O=C(OC)C1CCN(CCOc2ccccc2)CC1	2007 analogs, 99 refs, 0 amy.ints	
27	wact-161	9017369	n1c(nc(nc1Nc1ccc(Cl)cc1)N)C(F)(F)F	c1(Nc2ccccc2)ncncn1	*1117 analogs, 159 refs, 0 amy.ints	
28	wact-164	9020008	O(c1ccc(cc1)CNC)Cc1ccc(Cl)cc1.Cl	c1(OCc2ccccc2)ccccc2	*382 analogs, 16 refs	
29	wact-200	9053402	C(=O)(N1CCN(CC1)CCC)Nc1ccc(cc1)Cl)Cl	O=C(Nc1ccccc1)N2CCNCC2	*1067 analogs, 22 refs, 0 amy.ints	
30	wact-380	5218876	C(=O)(c1sccc1)Nc1ccc(Cl)cc1	O=C(Nc1ccccc1)c2cccs2	*5859 analogs, 214 refs, 0 amy.ints	
31	wact-93	7695043	n1(c(nc2c1ccccc2)c1scnc1)Cc1c(F)cccc1	n1(Cc2ccccc2)c3ccccc3nc1c4cncs4	32 analogs, 9 refs, 0 amy.ints	
32	wact-99	7747049	C(=O)(c1occc1)Nc1cc(c(N2CCN(CC2)CC)cc1)Cl	O=C(Nc1ccc(N2CCNCC2)cc1)c3ccco3	1386 analogs, 73 refs, 0 amy.ints	
33	wact-100	7747140	N(=C(\c1ccncc1)/N)/OC(=O)c1c(cc(cc1)C)C	O=C(c1ccccc1)O/N=C/c2ccncc2	320 analogs, 31 refs, 0 amy.ints	
34	wact-101	7747622	N1(C(=O)c2ccc(cc2)c2ccccc2)CC(CC1)c1ccccc1	N1(C(=O)c2ccc(cc2)c2ccccc2)CC(CC1)c1ccccc1	121 analogs, 8 refs, 0 amy.ints	
35	wact-104	7780917	C(=O)(O/N=C(/c1ccncc1\)N)C(Oc1ccc(Br)cc1)C	O=C(Oc1ccccc1)O/N=C/c2ccncc2	99 analogs, 9 refs, 0 amy.ints	
36	wact-107	7785818	C(=S)(Nc1cc(c(cc1)Cl)Cl)NC1CCN(Cc2ccccc2)CC1	S=C(N1CCN(CC1)Cc2ccccc2)Nc3ccccc3	505 analogs, 38 refs, 0 amy.ints	
37	wact-108	7788232	C(=S)(NC1CCN(Cc2ccccc2)CC1)NCc1ccc(Cl)cc1	S=C(NCc1ccccc1)NC2CCN(CC2)Cc3ccccc3	154 analogs, 6 refs, 0 amy.ints	
38	wact-109	7795345	[N+](=O)(c1ccc(NC(=S)NCc2cc(c(cc2)Cl)Cl)cc1)[O-]	O=[N+]([O-])c1ccc(NC(NCc2ccccc2)=S)cc1	1444 analogs, 108 refs, 0 amy.ints	
39	wact-111	7805914	C(=S)(N1CCN(c2cc(c(cc2)Cl)Cl)CC1)NCC1OCCC1	S=C(NCC1OCCC1)N2CCN(CC2)c3ccccc3	30 analogs, 0 refs, 0 amy.ints	
40	wact-112	7831354	C(c1cc(NC(=O)Nc2ccc(OC(F)F)cc2)ccc1)(F)(F)F	O=C(Nc1ccccc1)Nc2ccccc2	*250 analogs, 49 refs, 0 amy.ints	
41	wact-114	7837303	n1(ncc(c1)NC(=S)NCc1ccc(F)cc1)Cc1ccc(Br)cc1	S=C(Nc1ccccc1)Nc2ccc(Bc3ccccc3)nc2	235 analogs, 9 refs, 0 amy.ints	
42	wact-115	7839427	[N+](=O)(c1ccc(N2CCN(C(=S)NCc3ccc(Cl)cc3)CC2)cc1)[O-]	O=[N+]([O-])c1ccc(N2CCN(CC2)C(NCc3ccccc3)=S)cc1	287 analogs, 5 refs, 0 amy.ints	
43	wact-117	7854576	[N+](=O)(c1cc(C(F)(F)F)ccc1NCCCNC(=O)c1ccc1)F)[O-]	O=C(c1ccccc1)NCCCNc2ccccc2	132 analogs, 6 refs, 0 amy.ints	
44	wact-118	7862504	s1c(ccc1)CNCc1cc(OCc2ccccc2)ccc1.Cl	c1(CNCc2ccccc(OCc3ccccc3)c2)ccs1	274 analogs, 16 refs, 0 amy.ints	
45	wact-12	7003409	c1(C(=O)NCCOc2ccc(cc2)CC)c(I)cccc1	O=C(NCCOc1ccccc1)c2ccccc2	*1582 analogs, 22 refs, 0 amy.ints	
46	wact-122	7930372	c1([N+](=O)[O-])c(cc(N2Cc3c(CC2)cccc3)c(c1)F)N1CCN(C(=O)C)CC1	c1(N2CCNCC2)cc(N3Cc4ccccc4CC3)ccc1	78 analogs, 10 refs	US20160283652, CA2735158
47	wact-125	7949759	c1(C(=O)NCCSC2CCCCC2)c(SC)cccc1	O=C(NCCSC1CCCCC1)c2ccccc2	1739 analogs, 27 refs, 0 amy.ints	
48	wact-127	7962412	CCCCCNC(=O)C1=CC=CC=C1SC	CCCCCNC(=O)C1=CC=CC=C1SC	23545 analogs, 409 refs, 0 amy.ints	
49	wact-13	7632721	n1c(noc1c1cc(ccc1)C)c1ccc(cc1)OC	c1(c2ccccc2)noc(c3ccccc3)n1	*2949 analogs, 121 refs	US20110081297, JP2009203166
50	wact-130	7974202	n1c(oc2c1cc(N)cc2)c1ccc(cc1)C(C)C	c1(c2ccccc2)oc3ccccc3n1	*1191 analogs, 168 refs, 0 amy.ints	
51	wact-137	7996054	n1c(oc2c1nccc2)c1ccc(c(NC(=O)c2cc(Cl)ccc2)cc1)C	O=C(c1ccccc1)Nc2ccc(c3oc4cccnc4n3)cc2	449 structures, 19 refs, 0 amy.ints	
52	wact-143	9008780	c1(c(c(ce(c1)Cl)Cl)C)OCCCN1CCN(CC1)C)Br.Cl	c1(OCCCN2CCNCC2)ccccc1	*632 analogs, 4 refs, 0 amy.ints	
53	wact-144	9009342	c1(c(ccc(c1)I)OCCCN(C)C.Cl	CN(C)CCCOc1ccccc1	**75%, 1858 analogs, 31 refs, 0 amy.ints	
54	wact-146	9010643	N1(CCCCOc2ccc(c3ccccc3)cc2)CCOCC1.Cl	N1(CCOOC1)CCCCOc2ccc(c3ccccc3)cc2	33 structures, 33 refs, 0 amy.ints	
55	wact-147	9011168	c1(c2ccccc2)ccc(cc1)OCCNCC=C.Cl	C=CCNCOc1ccc(c2ccccc2)cc1	18497 structures, 460 refs, 0 amy.ints	
56	wact-148	9011314	c1(c2c(ccc1OCCCn1nccc1)cccc2)Cl.Cl	c12ccccc1OCCCn3ccnc3)c2	557 structures, 28 refs, 0 amy.ints	
57	wact-151	9012797	N1(CCCOc2ccc(c3ccccc3)cc2)CCOCC1.Cl	N1(CCOOC1)CCCOc2ccc(c3ccccc3)cc2	247 structures, 83 refs, 0 amy.ints	
58	wact-155	9014681	C(c1cc(OCCCCn2cnnc2)ccc1)(F)(F)F.Cl	c1(OCCCCn2ccnc2)ccccc1	*28 analogs, 5 refs, 0 amy.ints	
59	wact-162	9018123	N(C(=O)c1ccncc1)(C(=O)c1occc1)c1ncc(cc1)I	O=C(c1ccncc1)N(c2ccccc2)C(c3ccco3)=O	16 structures, 4 refs, 0 amy.ints	
60	wact-166	9023097	S(=O)(=O)(NCc1ccncc1)c1ccc(cc1)C1CCCCC1	S(=O)(=O)(NCc1ccnc1)c1ccc(cc1)C1CCCCC1	11 structures, 3 refs, 0 amy.ints	
61	wact-163	9018909	c12c(c(ccc1Cl)OCCNCc)cccc2.Cl	Clc1c2ccccc2c(OCCNCc)cc1	*262 structures, 23 refs, 0 amy.ints	
62	wact-365	5318059	C(=O)(c1cc(Cl)ccc1)N/N=C/c1ccc(SC)cc1	O=C(N/N=C/c1ccc(SC)cc1)c2ccccc2	*824 analogs, 118 refs	19651517, JP2009203166, DOI:10.1039/C3MD00189J

Supplemental Table 4. A Literature-Based Search for Evidence of Amyloid Interaction Among 62 Molecules that Fail to Form Crystals.
[a]The Chembridge identification number for reordering at Chembridge Inc.
[b]The SMILES codes for the small molecule structure or the core scaffold used in SciFinder searches.
[c]The number of analogs found in SciFinder searches using the core scaffold in substructure searches. The number of academic or patent-based publications (refs) associated with the analogs is also shown. In cases where searches with the core scaffold yielded >20,000 references, we instead used the primary structure to perform SciFinder searches and used a cutoff of 80% structural similarity or more to perform the searches. Searches performed this way are marked with an asterisk. The cell is colored pink if no evidence was found for amyloid interaction (0 amy.ints). The date of the searches is shown in brackets.
[d]The pubmed ID (PMID) and/or patent number is shown that provides evidence for a primary role in amyloid interaction. The date of the searches is shown in brackets.

Node ID[a]	cluster[b]	Name of Molecule	viability assay[c] DMSO n=2	w190 3.8 uM n=5	w11 10 uM n=3	Crystal Formation Assay[d] wact-190 + suppressor % crystals	n	SD	p value	Evidence for anti-amyloid activity (PubMed ID or Patent Number)[e]	Targeted Amyloid in Study	Aβ42 Secondary Fibril Inhibition Assay[f] Hit?	T-half mean	n	SD	p value
		solvent control										no	1.00	4	0	1
		solvent control	OG	0	0					none found	na	no	1.00	4	0	1
		positive control (Adapalene)										yes	4.12	4	1.2	1.2E-03
		positive control (Adapalene)										yes	4.17	4	2.3	1.8E-02
s1	a	RHAMNETIN	OG	OG	0	0	2	0	0.0E+00	16248550	Abeta42	no	0.93	4	0.1	6.5E-02
s2	a	BAICALEIN	OG	OG	0	42	3	25	1.6E-02	25043951, 23686791, 25043951, 25274114	Abeta42, IAPP					
s3	a	NOBILETIN	OG	OG	0	7	2	10	5.4E-03	none found	na					
s4	a	MORIN	OG	OG	0	27	4	40	1.0E-02	22762350, 16248550	Abeta42					
s5	a	FISETIN	OG	OG	0	29	2	11	1.2E-02	16248550, 18761054, 26944285	Abeta42	no	1.17	3	0.2	3.8E-02
s6	a	6,7-DIHYDROXYFLAVONE	OG	OG	0	0	2	0	0.0E+00	none found	na					
s7	a	KAEMPFEROL	OG	OG	0	4	2	5	1.5E-03	24468532, 16248550	Amylodosis, Abeta42, IAPP					
s8	a	HESPERETIN	OG	OG	0	20	4	15	4.6E-05	28672874, 22383310	Abeta42					
s9	a	SILIBININ	OG	OG	0	18	2	3	6.9E-04	21185897, 19552690	Abeta42					
s10	a	ISOGINKGETIN	OG	OG	0	3	2	4	8.6E-04	31697876	Abeta42					
s11	b	DICHLOROPHEN	sick	sick	0	19	4	26	7.6E-04	none found	na	yes	5.43	4	1.6	7.3E-04
s12	b	2,3,4-TRIHYDROXY-4'-ETHOXYBENZOPHENONE	OG	OG	0	14	3	12	2.3E-04	none found	na	no	0.86	3	0	1.7E-05
s13	b	3,4-DIDESMETHYL-5-DESHYDROXY-3'-ETHOXYSCLEROIN	OG	OG	0	20	4	13	1.7E-05	none found	na		0.90	3	0	4.2E-04
s14	b	CLOFOCTOL	OG	OG	0	0	2	0	0.0E+00	none found	na	yes	1.94	4	0.2	1.0E-05
s15	b	ROSOLIC ACID	OG	OG	0	70	2	1	1.6E-04	none found	na	no	1.32	3	0.1	3.2E-04
s16	c	PYROGALLIN	OG	OG	0	15	4	20	1.4E-04	US9463195B2	β-2 microglobulin fibril					
s17	c	PURPUROGALLIN-4-CARBOXYLIC ACID	OG	OG	0	74	2	0	1.6E-04	none found	na					
s18	c	METHYL 7-DESHYDROXYPYROGALLIN-4-CARBOXYLATE	OG	OG	0	0	2	0	0.0E+00	US9463195B2	β-2 microglobulin fibril					
s19	c	PURPUROGALLIN	OG	OG	0	0	2	0	0.0E+00	15611092, US9463195B2	Tau, β-2 microglobulin fibril	no	0.41	4	0.1	1.1E-04
s20	d	2,4-DINITROPHENOL	OG	OG	0	9	3	16	5.3E-04	16627944, 11344119, 11913969	TTR amyloid					
s21	d	OCTINOXATE	OG	OG	0	12	2	17	1.8E-02	none found	na	yes	1.66	4	0.5	1.5E-02
s22	d	DIIODOTYROSINE DIHYDRATE	OG	OG	0	11	2	7	2.7E-03	US20050038117A1	multiple					
s23	e	LAWSONE	OG	OG	0	22	2	7	4.4E-03	30704121	TTR amyloid	no	0.98	4	0.1	3.4E-01
s24	e	ANTHRACENE-1,4-DIONE	OG	OG	0	21	2	13	1.3E-02	none found	na					
s25	e	1,4-NAPHTHOQUINONE	OG	OG	0	0	2	0	0.0E+00	20709023, 31016960	Abeta42					
s26	f	ISOPOMIFERIN	OG	OG	0	2	3	3	6.1E-07	none found	na	no	1.25	4	0.2	1.1E-02
s27	f	ISOOSAJIN	OG	OG	0	21	2	13	1.2E-02	none found	na	no	1.42	3	0.1	2.9E-04
s28	f	MUNDULONE ACETATE	OG	OG	0	13	2	13	1.1E-02	none found	na	no	1.27	3	0.2	2.2E-02
s29	f	KOPARIN	OG	OG	0	12	2	11	7.5E-03	none found	na	no	1.00	3	0.1	4.4E-01
s30	g	PREGNENOLONE SUCCINATE	OG	OG	0	0	3	0	0.0E+00	none found	na	no	0.96	4	0.1	2.2E-01
s31	g	DESOGESTREL	OG	OG	0	17	2	8	4.4E-03	none found	na	yes	1.60	3	0.1	1.1E-02
s32	g	NORGESTIMATE	OG	OG	0	10	2	1	2.5E-05	none found	na	no	1.43	3	0.1	2.4E-04
s33	h	2',4'-DIHYDROXYCHALCONE	OG	OG	0	0	3	0	0.0E+00	none found	na	no	1.29	4	0.2	1.6E-02
s34	h	4'-HYDROXYCHALCONE	OG	OG	0	0	2	0	0.0E+00	none found	na	no	1.12	3	0	6.8E-09
s35	h	PHLORETIN	OG	OG	0	5	2	2	1.8E-04	none found	na	no	1.33	3	0.1	3.3E-04
s36	i	DIENESTROL	OG	OG	0	0	2	0	0.0E+00	none found	na					
s37	i	ONONETIN	OG	OG	0	0	3	0	0.0E+00	none found	na					
s38	i	DIETHYLSTILBESTROL	OG	OG	0	0	3	0	0.0E+00	15469931	amyloidosis	yes	2.41	4	0.6	1.5E-03
s39	j	CLIOQUINOL	OG	OG	0	9	2	13	9.9E-03	14676042, 21199452, 24591589	Abeta42					
s40	j	NITROXOLINE	OG	OG	0	53	4	35	3.7E-02	none found	na					
s41	k	MYCOPHENOLIC ACID	OG	OG	0	12	2	10	6.8E-03	none found	na	no	0.91	3	0	1.2E-04
s42	k	BENZYL BENZOATE	OG	OG	0	8	2	1	4.3E-05	none found	na	no	1.27	4	0.2	1.3E-02
s43	m	HAEMATOPORPHYRIN	OG	OG	0	0	2	0	0.0E+00	34570963	Abeta42	yes	2.17	4	0.7	9.4E-03
s44	m	PROTOPORPHYRIN IX	OG	OG	0	7	2	6	2.1E-03	34570963	Abeta42					
s45	m	CHLOROPHYLLIDE Cu COMPLEX Na	OG	OG	0	0	2	0	0.0E+00	none found	na					
s46	n	GOSSYPOL-ACETIC ACID COMPLEX	OG	OG	0	0	2	0	0.0E+00	none found	na					
s47	n	GOSSYPOL	OG	OG	0	0	3	0	0.0E+00	21858698, 25043951, 32210536	IAPP	yes	6.02	3	4.6	3.7E-02
s48		DEMECLOCYCLINE HYDROCHLORIDE	OG	sick	0	6	2	9	4.4E-03	21068391, 28338670	β-2 microglobulin fibril					
s49	r	DIHYDROCELASTROL	OG	OG	0	23	4	27	1.3E-02	none found	na	yes	1.90	4	0.1	1.2E-06
s50	r	CELASTROL	OG	OG	0	7	3	7	1.9E-05	none found	na	no	1.09	3	0.1	1.2E-02
s51	o	ALIZARIN	OG	OG	0	13	2	6	2.3E-03	34033711	insulin fibrils					
s52	o	PURPURIN	OG	OG	0	6	3	11	1.2E-04	34033711, 31562564	Insulin fibrils, Tau peptide					
s53	p	GLICLAZIDE	OG	OG	0	0	2	0	0.0E+00	none found	na	no	1.07	4	0.1	6.0E-02
s54	p	GLIMEPIRIDE	OG	OG	0	4	2	2	1.9E-07	none found	na	no	0.95	3	0	4.4E-02
s55	p	GLIPIZIDE	OG	OG	0	28	2	9	8.3E-03	none found	na	no	1.04	3	0	1.8E-02
s56	q	RAFOXANIDE	OG	OG	0	8	2	12	8.2E-03	none found	na	yes	23.16	3	4.1	5.2E-05
s57	q	CLOSANTEL	sick	sick	0	0	3	0	0.0E+00	none found	na	yes	28.00	3	6.7	2.0E-04
s58	q	OXYCLOZANIDE	OG	OG	0	27	4	30	2.6E-03	none found	na	no	1.42	3	0.1	9.8E-04
s59		LEOIDIN	OG	OG	0	8	2	4	7.3E-04	US9463195B2	β-2 microglobulin					
s60		TENIPOSIDE	OG	OG	0	27	2	0	1.7E-05	none found	na	no	0.93	3	0	7.2E-03
s61		DIFFRACTAIC ACID	OG	OG	0	46	2	6	5.9E-03	none found	na	no	1.16	3	0.1	2.0E-02
s62		BROMOCRIPTINE MESYLATE	OG	OG	0	0	2	0	0.0E+00	none found	na	no	0.74	3	0.1	7.9E-05
s63		ADAPALENE	OG	OG	0	10	2	10	5.7E-03	28011763	Abeta42					
s64		ERYTHROSINE SODIUM	OG	OG	0	4	3	3	1.1E-06	21354256, 28137461	lysozyme fibrils					
s65		ITRACONAZOLE HYDROCHLORIDE	OG	sick	0	25	2	8	3.3E-03	none found	na	no	0.78	3	0.1	5.4E-02
s66		NIFUROXAZIDE	OG	OG	0	24	4	32	3.1E-03	none found	na	no	0.97	3	0.1	2.4E-01
s67		NITAZOXANIDE	OG	OG	0	3	3	6	8.4E-06	none found	na	no	0.96	3	0.1	1.3E-01
s68		HARMALINE	OG	OG	0	36	2	1	4.4E-05	none found	na	unc	na	3	na	na
s69		alpha-MANGOSTIN	OG	OG	0	0	3	0	0.0E+00	21958557; 28429536; 32419519	Abeta42; amyloidosis					
s70		THIOSTREPTON	OG	OG	0	8	2	11	7.6E-03	none found	na	no	0.76	3	0.3	1.0E-01
s71		APOMORPHINE HYDROCHLORIDE	OG	sick	0	25	2	1	1.3E-04	none found	na	unc	na	3	na	na
s72		USNIC ACID	OG	OG	0	4	2	6	1.9E-03	none found	na	no	1.30	4	0.2	1.4E-02
s73		BITHIONATE SODIUM	sick	sick	0	0	2	0	0.0E+00	none found	na	unc	na	3	na	na
s74		CITRININ	OG	OG	0	13	4	26	4.9E-04	none found	na	yes	1.56	3	0.6	4.7E-02
s75		EBSELEN	OG	OG	0	21	2	6	3.3E-03	none found	na	no	1.03	3	0	1.4E-01
s76		CANDESARTAN CILEXTIL	OG	OG	0	0	2	0	0.0E+00	none found	na	yes	3.00	3	0.8	1.7E-03
s77		TOTAROL	OG	OG	0	0	2	0	0.0E+00	none found	na	yes	1.72	3	0.1	1.6E-06
s78		CURCUMIN	OG	OG	0	3	3	4	2.9E-06	15590663, 17472706, 18189141	Abeta42	no	0.39	4	0.3	1.6E-03
s79		4,4'-DIMETHOXYDALBERGIONE	OG	OG	0	0	2	0	0.0E+00	none found	na	no	1.24	3	0.2	1.6E-02
s80		DIHYDROGAMBOGIC ACID	OG	OG	0	12	2	8	4.0E-03	none found	na	no	0.78	3	0.1	1.5E-04
s81		ISORESERPINE	OG	OG	0	6	2	1	9.0E-05	none found	na	no	0.62	3	0.1	8.1E-05
s82		SAFROLE	OG	OG	0	12	2	16	1.6E-02	none found	na	no	0.92	3	0.1	1.1E-02
s83		TRICLABENDAZOLE	OG	OG	0	20	4	28	1.3E-03	34547896	TTR amyloid					
s84		ARIPIPRAZOLE	OG	sick	0	6	2	8	3.4E-03	none found	na	yes	2.26	3	1.2	4.2E-02
s85		SIROLIMUS	OG	OG	0	11	2	16	1.6E-02	none found	na	no	0.46	3	0	4.9E-07

Supplemental Table 5. 85 Spectrum Suppressors of Small Molecule Crystallization in the Pharynx Cuticle.
[a]The node ID is the label of the node shown in Figure 4a.
[b]The cluster letter is that given to scaffold clusters shown in Figure 4a and 4b.
[c]The viability assay is the standard six day viability assay described in the methods. The number of replicates (n) is shown, and the mode is shown. OG, a culture overgrown with worms; sick, a culture with 11-50 worms; 0, a culture with 0-10 worms.
[d]The crystal formation assay is described in the methods section.
[e]The pubmed ID or patent number is shown that provides evidence for a primary role in fibril inhibition.
[f]Hits equate to those molecules that significantly ($p<0.05$) antagonize Aβ42 secondary fibril formation by more than 50% that of the solvent control as measured by the time of half (T-half) saturated signal (see methods).

	Trivial Name	MolPort ID	Analog Smiles	Suppressor Analog[a]	48 hour crystal assay[b]			
					mean	n	sem	type
1	DMSO	negative control	na	na	0	6	0	-
2	wact-190	positive control	na	na	100	6	0	cry
3	RS-15	MolPort-001-814-824	c1cc2c(oc3ccc(cc3c2=O)Br)cc1	alpha-MANGOSTIN	100	4	0	cry
4	RS-50	MolPort-003-712-626	O=C1c2cc(ccc2C(=O)c2c1cccc2)F	PURPURIN/ALIZARIN	87	4	3	cry
5	RS-9	MolPort-002-211-224	O=C(c1ccc(OCC)cc1)c1ccc(cc1Cl)Cl	DDE	67	5	9	sph
6	RS-14	MolPort-000-690-079	c1(cc2c(oc3ccc(cc3c2=O)F)cc1)F	alpha-MANGOSTIN	66	4	12	cry
7	RS-11	MolPort-008-682-078	O=C(c1ccc(OCC)cc1)c1ccccc1Cl	DDE	60	3	19	sph
8	RS-40	MolPort-000-628-186	O=C1c2c(cccc2C(=O)c2c1cccc2)Cl	PURPURIN/ALIZARIN	56	5	7	cry
9	RS-6	MolPort-002-120-487	O=C(c1ccc(OC)cc1)c1ccc(cc1Cl)Cl	DDE	51	5	10	sph
10	RS-13	MolPort-001-814-873	O=C(c1ccc(cc1)F)C=Cc1c(cccc1)Cl	4'-HYDROXYCHALCONE	45	3	11	sph
11	RS-7	MolPort-002-120-597	O=C(c1ccc(OC)cc1)c1ccccc1Cl	DDE	41	3	10	sph
12	RS-41	MolPort-000-628-197	O=C1c2cccc(c2C(=O)c2c1cccc2Cl)Cl	PURPURIN/ALIZARIN	35	5	3	cry
13	RS-8	MolPort-002-209-464	O=C(c1ccc(OCC)cc1)c1ccc(cc1)Cl	DDE	26	5	6	cry
14	RS-10	MolPort-003-801-426	O=C(c1ccc(OC)c(c1)Cl)c1ccccc1	DDE	22	5	8	sph
15	RS-1	MolPort-000-153-180	O=C(c1ccc(OC)cc1)c1cccc(c1)Cl	DDE	14	5	7	sph
16	RS-46	MolPort-002-139-631	O=C1c2c(cccc2C(=O)c2c1cccc2)Br	PURPURIN/ALIZARIN	6	2	6	cry
17	RS-2	MolPort-000-153-182	O=C(c1ccc(OC)cc1)c1ccc(cc1)Cl	DDE	0	5	0	-
18	RS-5	MolPort-001-773-641	O=C(c1ccc(OC)cc1)c1ccc(cc1)F	DDE	0	4	0	-
19	RS-12	MolPort-009-323-013	O=C(c1ccc(OC)cc1Cl)c1ccccc1	DDE	0	5	0	-
20	RS-16	MolPort-000-153-368	O=C(Cc1ccccc1)c1ccc(cc1)Cl	ONONETIN	0	4	0	-
21	RS-18	MolPort-001-785-660	O=C(Cc1ccc(cc1)Cl)c1ccccc1	ONONETIN	0	4	0	-
22	RS-21	MolPort-002-498-703	O=C(Cc1ccc(c(c1)F)F)c1ccccc1	ONONETIN	0	4	0	-
23	RS-24	MolPort-003-899-970	O=C(Cc1ccc(cc1)F)c1ccc(cc1)Cl	ONONETIN	0	2	0	-
24	RS-26	MolPort-011-192-811	O=C(Cc1ccc(cc1)F)c1ccc(cc1Cl)Cl	ONONETIN	0	2	0	-
25	RS-27	MolPort-011-790-797	O=C(Cc1ccc(cc1Cl)Cl)c1ccc(cc1)Cl	ONONETIN	0	2	0	-
26	RS-28	MolPort-011-912-385	O=C(Cc1ccc(cc1)Cl)c1cccc(c1)F	ONONETIN	0	4	0	-
27	RS-29	MolPort-011-912-395	O=C(Cc1cccc(c1)F)c1cccc(c1)F	ONONETIN	0	4	0	-
28	RS-30	MolPort-011-912-620	O=C(Cc1ccc(cc1Cl)Cl)c1ccc(cc1)F	ONONETIN	0	4	0	-
29	RS-31	MolPort-012-334-336	O=C(Cc1ccc(cc1)Cl)c1ccc(cc1Cl)Cl	ONONETIN	0	2	0	-
30	RS-32	MolPort-013-275-146	O=C(Cc1cccc(c1)F)c1ccc(cc1)F	ONONETIN	0	4	0	-
31	RS-33	MolPort-013-289-535	O=C(Cc1cccc(c1)F)c1ccc(c(c1)Cl)Cl	ONONETIN	0	4	0	-
32	RS-38	MolPort-026-446-172	O=C(Cc1ccc(c(c1)F)F)c1ccc(cc1)Cl	ONONETIN	0	2	0	-
33	RS-45	MolPort-002-136-236	O=C1c2c(c(c(c(c2C(=O)c2c1cccc2)F)F)F)F	PURPURIN/ALIZARIN	0	2	0	-
34	RS-47	MolPort-002-250-630	O=C1c2c(c(c(c2C(=O)c2c1cccc2)Cl)Cl)Cl)Cl	PURPURIN/ALIZARIN	0	4	0	-
35	RS-48	MolPort-002-904-427	O=C1c2c(ccc(c2C(=O)c2c1cccc2)F)F	PURPURIN/ALIZARIN	0	4	0	-

Supplemental Table 6. Reduced Analogs of Suppressors.
Suppressors are listed in order of their ability to induced object formation.
[a]DDE, 3,4-DIDESMETHYL-5-DESHYDROXY-3'-ETHOXYSCLEROIN
[b]N, the number of trials (at least 20 animals were counted in each trial); SEM, standard error of the mean; type (of object) is either birefringent crystals (cry) or non-birefringent globular spheres (sph).

	Trivial Name	MolPort ID	Analog Smiles	Wactive Analog	6 day viability assay[a]						crystal counts[b]	Aβ42 Secondary Fibril Inhibition Assay[c]				
					DMSO trial 1 (n=3)	DMSO trial 2 (n=3)	DMSO trial 3 (n=3)	w190 trial 1 (n=3)	w190 trial 2 (n=3)	w190 trial 3 (n=3)	w190 average +/- SEM (N=5, n>20)	Hit?	T-half mean	n	SD	p value
1		DMSO (n=6)			OG	OG	OG	let	let	let	100 +/- 0	no	1.00	4	0	1
2	OC-1	MolPort-000-132-940	c1cc(c2nc(c3cccnc3)no2)c(cc1)O	wact-10-2	OG	OG	OG	let	let	let						
3	OC-2	MolPort-001-849-559	c1cccc(OCc2nc3ccccc3s2)c1O	wact-15	let	OG	OG	let	let	let						
4	OC-4	MolPort-000-369-009	c1ccccc1c1nnc(c2c(cccc2)O)o1	wact-51	OG	OG	OG	let	let	let						
5	OC-5	MolPort-000-156-303	O=C(c1ccccc1)Nc1cccc(c1)O	wact-128	OG	OG	OG	let	let	let						
6	OC-6	MolPort-000-516-315	O=C(c1ccccc1)Nc1ccc(cc1)O	wact-128	OG	OG	OG	let	let	let						
7	OC-7	MolPort-000-677-289	O=C(c1ccc(cc1)O)Nc1ccccc1	wact-128	OG	OG	OG	let	let	let						
8	OC-8	MolPort-001-011-775	O=C(c1ccccc1)Nc1ccccc1O	wact-128	OG	OG	OG	let	let	let						
9	OC-9	MolPort-001-781-621	O=C(c1c(cccc1)O)Nc1ccccc1	wact-128	OG	OG	OG	let	let	let						
10	OC-10	MolPort-001-783-472	O=C(c1c(cccc1)O)Nc1ccc(cc1)O	wact-128	OG	OG	OG	let	let	let						
11	OC-11	MolPort-002-323-598	O=C(c1ccc(cc1)O)Nc1ccc(cc1)O	wact-128	OG	OG	OG	OG	OG	OG	57 +/- 16 (p<0.3)	no	1.15	4	0.13	2.9E-02
12	OC-12	MolPort-003-855-287	O=C(c1c(ccc1)O)Nc1ccccc1	wact-128	OG	OG	OG	let	let	let						
13	OC-13	MolPort-046-069-921	O=C(c1ccccc1)Nc1ccc(cc1O)O	wact-128	OG	OG	OG	let	let	let						
14	OC-14	MolPort-008-388-876	c1cccc(c1c1nc(c2cccs2)no1)O	wact-169	OG	OG	OG	let	let	let						
15	OC-16	MolPort-001-900-048	c1cccc(c1c1nc(c2ccccc2)no1)O	wact-184	sick	OG	OG	let	let	let						
16	OC-17	MolPort-002-222-727	Brc1ccc(cc1)c1noc(c2ccc(cc2)O)n1	wact-184	OG	OG	OG	sick	OG	OG	0 +/- 0 (p=0)	yes	11.71	4	3.01	1.9E-04
17	OC-18	MolPort-000-519-488	c1ccccc1c1csc(Nc2cc(ccc2)O)n1	wact-393	sick	OG	OG	sted/dea	sick	let						
18	OC-20	MolPort-001-998-500	c1cc(c(cc1c1csc(Nc2ccccc2)n1)O)O	wact-393	OG	OG	OG	OG	OG	OG	46 +/- 17 (p<0.02)	no	1.40	4	0.17	1.5E-03
19	OC-21	MolPort-001-998-519	c1cc(cc(c1c1csc(Nc2ccc(cc2)O)n1)O)O	wact-393	OG	OG	OG	sick	OG	OG	24 +/- 7 (p<0.001)	no	1.46	4	0.30	1.1E-02
20	OC-22	MolPort-002-013-480	c1cc(ccc1c1csc(Nc2ccc(cc2)O)n1)O	wact-393	OG	OG	OG	sick	OG	OG	23 +/- 7 (p<0.001)	no	1.37	4	0.32	3.0E-02
21	OC-23	MolPort-002-176-399	Br.Oc1ccc(Nc2nc(cs2)-c2ccccc2)cc1	wact-393	OG	OG	OG	let	let	let						
22	OC-24	MolPort-002-973-587	c1cccc(c1c1csc(Nc2ccccc2)n1)O	wact-393	OG	OG	OG	let	let	let						
23	OC-25	MolPort-001-945-190	O=C(Nc1ccc(c(c1)O)c1nc2ccccc2s1)c1ccccc1	wact-415	OG	OG	OG	let	let	sick						
24	OC-26	MolPort-001-945-191	O=C(c1c(cccc1)F)Nc1ccc(c(c1)O)c1nc2c(cccc2)s1	wact-415	sick	OG	OG	let	let	let						
25	OC-27	MolPort-003-180-443	c1ccccc1c1nnc(c2ccc(cc2)O)o1	wact-425	OG	OG	OG	let	let	let						
26	OC-29	MolPort-010-675-363	Clc1ccc(cc1)c1noc(c2c(nccc2)O)n1	wact-712-1	OG	OG	OG	let	let	let						

Supplemental Table 7. Hydroxylated Analogs of Crystal-Forming Molecules.

[a]OG, the majority of the wells in the trial were over-grown with more than 50 animals in each well; sick, the majority of the wells in the trial were sick with between 11 and 50 animals in each well; let, the majority of the wells in the trial had 10 or fewer animals.

[b]N is the number of trials; n is the number of animals counted in each trial; SEM is the standard error of the mean; the p value shown is from a Student's T-test between the experimental sample and the wact-190-only control.

[c]Hits equate to those molecules that significantly ($p<0.05$) antagonize Aβ42 secondary fibril formation by more than 50% that of the solvent control as measured by the time of half (T-half) saturated signal (see methods).

Supplemental Figure 1. Crystallizing Small Molecules Grouped According to Structural

Similarity. Small molecules belonging to structurally distinct families are boxed

together. The 18 singletons are unboxed. The cluster that each boxed set of molecules

belong to corresponds to the notation in Figure 3 and is indicated in the upper left-hand

corner. Wactive names highlighted in pink have core scaffolds that are known to interact

with amyloids (see methods and Supplemental Data File 1 for details). Molecule names

that are underlined were discovered from a screen of the RLL1200 small molecule

library.

Supplemental Figure 2. Further Details on the Biophysical Characterization of wact-190

and wact-416 *in vitro* **Crystals. A-C.** Different aspects of the 3D packing arrangement of

wact-190 crystals from the a, b, and c aspects, respectively. **D.** The fitting pattern of

wact-190 was obtained from the PXRD instrument. **E-G.** Different aspects of the 3D

packing arrangement of wact-416 crystals from the a, b, and c aspects, respectively. **D.**

The fitting pattern of wact-416 was obtained from the PXRD instrument. Panels (D) and

(H) show the experimental powder diffraction profile (°), the calculate curve by using the

reported structure (green line), the peak positions (|), and the normalized difference

curve (I_o-I_c) (black curve).

Supplemental Figure 3. Crystal-Induced Disruption of the ABU-14::sfGFP Pharyngeal

Cuticle Marker. A-C. Images of animals expressing ABU-14::sfGFP (the

extrachromosomal array, which we integrated as *trIs113*, was a kind gift from David

Raizen) and stained with the indicated dyes. The imaging channel is indicated (lower

left) as is the 3-hour wactive treatment (left-hand side of micrograph series). DIC,

differential interference contrast; bire, birefringence; CFW, calcofluor white. Merge 1 is

the merge of ABU-14::GFP and the CFW signal. Merge 2 is the merge of the signals from

ABU-14::GFP and the birefringence signal. Blue arrows indicate overlapping signals of

the amyloid-binding dye and birefringence; orange arrows show a lack of amyloid-

binding dye signal associated with birefringence signal. 60 μM of wact-190 and wact-390

was used in all experiments relevant to panels A-C.

Supplemental Figure 4. Larger wact-190 Crystals Often Fail to Overlap with Cuticle

Markers. Legend is the same as that described for Figure 4 and Supplemental Figure 3.

Supplemental Figure 5. Fluorescent Suppressors Specifically Localize to the Pharyngeal

Cuticle. A. Calcofluor white (CFW) is used as counter-stain control for each of the

molecules (60 μM) examined. **B-C.** B. Whole animal pictures illustrating the specificity of

the localization of the indicated suppressor molecules. The intestine exhibits

autofluorescence from gut granules, as illustrated in the no-dye control pictures (C). ac,

anterior corpus; i, intestine.

Supplemental Figure 6. The Construction and Analysis of a Random Network from the

Spectrum Library. A. A structural similarity network of the 100 randomly chosen

Spectrum library molecules. The nodes (circles) represent a drug or natural product

whose number corresponds to the identity indicated in panel B. The links (straight lines)

represent a Tanimoto score of structural similarity of 0.8 or more (see methods). A bold

red outline indicates that the molecule is a known disruptors of amyloid fibril formation

(see panel B for details). **B.** The 100 molecules randomly chosen from the Spectrum

Library that were used the build the network depicted in panel A. The node ID is the

label of the node shown in panel A. The PubMed ID is shown for those molecules for

which evidence could be found of a primary role in fibril inhibition.

Supplemental Figure 7. A-E. Behaviour of 2 mM Aβ42 Incubated with Small Molecules

under Different Aggregation Conditions. A. Dichlorophen **B.** Candesartan Cilexetil **C.**

Closantel **D.** Gossypol **E.** OC-11, OC-17, OC-20, OC-21, OC-22 in **i.** unseeded conditions or

with **ii.** 1 mM monomer equivalent pre-formed seed (heavy seeded). Heavy seeded

conditions isolate elongation as the dominant mechanism of aggregation, as the

availability of fibril ends is so high that further amyloid formation only occurs via this

route. By comparison, light seeded conditions (main text) are dominated by secondary

nucleation and elongation, while under unseeded conditions primary nucleation,

secondary nucleation and elongation are operative.

Supplemental Figure 1

pink indicates the scaffold has been showin to interact with amyloids

A

B

Node ID	Name of Molecule	Evidence for direct disruption of amyloid fibrils (PMID)	Targeted Amyloid
1	1,3-DIDEACETYL-7-DEACETOXY-7-OXOKHIVORIN	none	na
2	3-ACETAMIDOCOUMARIN	none	na
3	4,6-DIMETHOXYTOLUQUINONE	none	na
4	5-AMINOPENTANOIC ACID HYDROCHLORIDE	none	na
5	6,4'-DIMETHOXYFLAVONE	none	na
6	7-METHOXYCHROMONE	none	na
7	7,8-DIMETHOXYFLAVONE	none	na
8	8-HYDROXYCARAPINIC ACID	none	na
9	8beta-HYDROXYCARAPIN, 3,8-HEMIACETAL	none	na
10	ACETOHEXAMIDE	none	na
11	ACTINOQUINOL SODIUM	none	na
12	AMLEXANOX	none	na
13	ANAZOLENE SODIUM	none	na
14	ANDROGRAPHOLIDE	none	na
15	APRAMYCIN SULFATE	none	na
16	AVANAFIL	none	na
17	BEPHENIUM HYDROXYNAPTHOATE	none	na
18	BETULINIC ACID	none	na
19	BOLDINE	none	na
20	CAPOBENIC ACID	none	na
21	CARYOPHYLLENE [t(-)]	none	na
22	CEFAZOLIN SODIUM	none	na
23	CEFDINIR	none	na
24	CHLORPROTHIXENE HYDROCHLORIDE	none	na
25	CLOXYQUIN	none	na
26	CORTISONE	none	na
27	CRUSTECDYSONE	none	na
28	CYCLOPAMINE	none	na
29	CYCLOTHIAZIDE	none	na
30	CYPERMETHRIN	none	na
31	CYTISINE	none	na
32	DENATONIUM BENZOATE	none	na
33	DERRUSNIN	none	na
34	DIHYDROCELASTROL	none	na
35	DIPLOSALSALATE	none	na
36	DIRITHROMYCIN	none	na
37	DRONEDARONE HYDROCHLORIDE	none	na
38	EBASTINE	none	na
39	EBSELEN	none	na
40	ELLAGIC ACID	none	na
41	EPICATECHIN MONOGALLATE	none	na
42	ERGOTAMINE TARTRATE	none	na
43	ESTRADIOL ACETATE	none	na
44	ESTRADIOL-3-SULFATE, SODIUM SALT	none	na
45	ESTRAMUSTINE	none	na
46	ESTROPIPATE	none	na
47	ETHOXYQUIN	none	na
48	ETHOXZOLAMIDE	none	na
49	FENOLDOPAM MESYLATE	none	na
50	FENSPIRIDE HYDROCHLORIDE	none	na
51	FLAVANONE	none	na
52	FORMONONETIN	none	na
53	GLIQUIDONE	none	na
54	HALAZONE	none	na
55	HIERACIN	none	na
56	HYDROCORTISONE	none	na
57	IODIXANOL	none	na
58	IODOQUINOL	19664688	Abeta42
59	ISOBUTAMBEN	none	na
60	ISOGUVACINE HYDROCHLORIDE	none	na
61	IVERMECTIN	none	na
62	IZALPININ	none	na
63	LANSOPRAZOLE	none	na
64	LOVASTATIN	none	na
65	MEROGEDUNIN	none	na
66	MEROPENEM	none	na
67	METHAZOLAMIDE	none	na
68	METHYLPHENIDATE HYDROCHLORIDE	none	na
69	MONOBENZONE	none	na
70	MOROXYDINE HYDROCHLORIDE	none	na
71	N-METHYLBENZYLAMINE HYDROCHLORIDE	none	na
72	NATAMYCIN	none	na
73	OCTOPAMINE HYDROCHLORIDE	none	na
74	OLSALAZINE SODIUM	none	na
75	ORNIDAZOLE	none	na
76	PALMIDROL [5mM]	none	na
77	PANTOPRAZOLE	none	na
78	PHENYLBUTAZONE	none	na
79	PHENYLETHYL ALCOHOL	none	na
80	PODOFILOX	none	na
81	PREDNISOLONE SODIUM PHOSPHATE	none	na
82	PYRITHYLDIONE	none	na
83	PYROCATECHUIC ACID	none	na
84	QUINOLINIC ACID	none	na
85	SEROTONIN HYDROCHLORIDE	none	na
86	SHIKIMIC ACID	none	na
87	SULFAMETER	25043951	IAPP
88	SULFAMETHAZINE	none	na
89	TANSHINONE IIA SULFONATE SODIUM	none	na
90	THIMEROSAL	none	na
91	THYMOQUINONE	none	na
92	TILMICOSIN	none	na
93	TOLNAFTATE	none	na
94	TRETINOIN	none	na
95	TRICHLOROETHYLENE	none	na
96	TRIMEDLURE	none	na
97	TYROSINE HYDROCHLORIDE	none	na
98	URIDINE	none	na
99	VALSARTAN	none	na
100	VANITIOLIDE	none	na

 Supplementary Data File 1

 Tab 1 (the screen of RLL1200 for crystalizing small molecules) contains the information

 on the RLL1200 library for which we screened for new crystalizing molecules. Red cells

 on the table indicate that the culture is dead (fewer than 12 animals remaining); orange

 and yellow indicate that the culture is sick (between 12 and 50 animals), and green

 indicate that the culture is growing well. OG, over-grown; L, larvae; A, adults. The 16 hits

 are in the top 16 rows.

 Tab 2 (16 new crystallizers) contains the screening and follow-up data for the 16

 molecules identified as crystallizers along with the associated counts (see Methods and

 main text for details). Red cells in the table indicate that the culture is dead (fewer than

 12 animals remaining); orange and yellow indicate that the culture is sick (between 12

 and 50 animals), and green indicate that the culture is growing well. OG, over-grown; L,

 larvae; A, adults.

 Tab 3 (Spectrum Screen for Crystallizers) contains the information of the Spectrum

 library for which we screened for new crystalizing small molecules. Only two candidate

 crystallizers resulted from the screen with dehydrovariabilin being the only reproducible

 hit.

 Tab 4 (Spectrum Screen for Suppressors of wact-190 Crystals). The hits are shown in

 the first 85 rows of data. Purple cells on the table indicate that the culture is dead

(fewer than 12 animals remaining); gray indicate that the culture is sick (between 12 and

50 animals), and green indicate that the culture is growing well. OG, over-grown; L,

larvae; A, adults.

Tabs 5 and 6-10 (Supplemental Tables 1, and 3-7, respectively). We include copies of

these tables here to allow for ease of copying the SMILES and other information.

Tab 11 (The display item of Supplemental Figure 6b) is included here to allow for ease

of copying any pertinent information.

Tab 12 (The physicochemical properties of the wactive library). The first 48 rows of

data show the true positives (crystallizers) from the wactive library.

Tab 13 (Student's T-Test comparing the physicochemical properties of the wactive

library and RLL1200 crystallizers).