Pharmacological Interrogation of the *C. elegans* Pharyngeal Cuticle

Reveals Small Molecule Amyloid Disruptors

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Abstract

Understanding how to pharmacologically manipulate amyloids is an essential step towards managing dozens of amyloid-based human diseases. Here, we present a pipeline that yields small molecule antagonists of amyloidogenesis. Screens for small molecules that perturb the development of the nematode *C. elegans* revealed 24 distinct small molecule scaffolds that crystalize on the non-luminal face of the pharyngeal cuticle. Consistent with the amyloid-like nature of the pharyngeal cuticle, 25% of these scaffolds are known to bind human amyloids with nanomolar affinity. The growing crystals preferentially disrupt the amyloid-like material within the cuticle but leave its chitin-based matrix relatively intact. We screened a collection of drugs and natural products for those that suppress crystal formation and found 45 distinct scaffolds, 33% of which are known amyloid busters. Screening for pharmacological suppressors of crystal formation therefore represents an inexpensive high-throughput *in vivo* approach that enriches for small molecules with amyloid-busting potential.

Introduction

Intrinsic disorder within proteins is increasingly recognized as exceptionally useful to

biological systems. Intrinsically disordered regions (IDRs) of proteins, or entirely

intrinsically disordered proteins (IDPs), can establish multivalent interactions with other

IDRs along their unstructured peptide chains (Fung et al., 2018). The amino acid

sequence within IDRs often exhibits repeating patterns of physicochemical properties

along the protein chain that facilitate interactions with multiple binding partners

(Vernon and Forman-Kay, 2019). These properties can include hydrogen bonding

capability, π bonding capability, hydrophobicity, and electric charge. By establishing

multivalent interactions, IDR-rich proteins can transition from a soluble state into phase-

separated states such as liquid condensates (aka liquid-liquid phase separated (LLPS)

material), gels, or insoluble amyloid or non-amyloid fibres (Banani et al., 2017). Some

examples of intracellular machines that rely on phase-separated material includes germ

granules (Brady et al., 2017), P-bodies (Banani et al., 2016) and the nuclear pore

complex (Schmidt and Gorlich, 2016). Extracellularly, IDR-rich proteins can self-assemble

into a growing list of matrices that include the webs of spiders (Jin and Kaplan, 2003;

Slotta et al., 2007), glues secreted by molluscs (Wei et al., 2014b), key elements of the

squid beak (Tan et al., 2015), and the recoiling component that surrounds arteries

(Muiznieks et al., 2018). The extent to which biology exploits intrinsic disorder is only

beginning to be appreciated.

   Despite the functionality of intrinsically disordered proteins, their existence carries

increased risk to biological systems. IDRs can fall down a well of insolubility wherein

phase-separated IDR-rich proteins adopt a kinked β-structure that organizes into

insoluble amyloid fibrils (Chiti and Dobson, 2017) or amyloid-like aggregates (McAlary et

al., 2019). Over 50 human diseases are linked to amyloid formation (Chiti and Dobson,

2017). In some cases, such as Alzheimer's Disease, it remains less clear whether amyloid

plaques are causative in the disease (Makin, 2018). In other cases, such as Creutzfeldt-

Jakob disease and multiple forms of amyloidosis, amyloid formation is central to disease

etiology (see (Chiti and Dobson, 2017) and (Iadanza et al., 2018) for in depth review).

Much effort has been devoted to identifying pharmacological agents that directly or

indirectly modulate the amyloid state associated with human disease. A few examples

of clinically-studied anti-amyloid molecules include doxycycline as a potential treatment

for ATTR (transthyretin amyloidosis) (Obici et al., 2012) and AL immunoglobulin light

chain amyloidosis (D'Souza et al., 2020; Kumar et al., 2012), CuATSM, which disrupts

SOD1 aggregation (Farrawell et al., 2019), is being clinically tested against amyotrophic

lateral sclerosis (ALS) (Rowe et al., 2018), and the monoclonal antibody aducanumab,

which targets Aβ amyloid (Sevigny et al., 2016) and has been recently been approved by

the FDA as a treatment for Alzheimer's in a controversial decision (Mullard, 2021).

Despite these examples, there is a paucity of effective treatments for the vast majority

of amyloid and aggregation-based human diseases.

We have recently generated a spatiotemporal blueprint for the construction of the

pharyngeal cuticle of the free-living nematode *Caenorhabditis elegans* (Kamal et al.,

Manuscript Submitted). The worm's pharyngeal cuticle is a flexible non-collagenous

chitin-rich matrix that is repeatedly shed and rebuilt at each larval stage (Altun and Hall,

2020; Cox et al., 1981). The blueprint reveals that successive waves of abundant IDR-rich

protein families are likely incorporated into the developing cuticle during the molting

period. These IDR-rich proteins are predicted to be capable of phase-separation, and we

demonstrated this to be true *in vitro* for an exemplar (Kamal et al., Manuscript

Submitted). Computational analyses also indicate that many of these IDR-rich proteins

have amyloidogenic features such as an enrichment in π and hydrogen-bonding

capability, in addition to having protofilament formation propensity (Kamal et al.,

Manuscript Submitted). We speculate that the IDR-rich proteins may form liquid

coacervates to fill a chitin matrix during pharyngeal cuticle construction in much the

same way that the squid beak is constructed (Tan et al., 2015).

Our previous small molecule screens with *C. elegans* revealed many compounds

visibly accumulate within the heads of the worm (Burns et al., 2015; Kwok et al., 2006).

The accumulation is obvious with the use of a low magnification dissection light

microscope and has been observed by other labs (Galford and Jose, 2020; Risi et al.,

2019). Depending on the small molecule structure, the accumulated objects form either

birefringent irregular objects, globular non-birefringent spheres, or a mixture of the two

(Kamal et al., 2019). We previously demonstrated that the birefringent objects: i) are

obvious within minutes of exposure of the animal to the small molecule; ii) contain the

exogenous small molecule; iii) grow over time; iv) are formed exclusively in association

with the pharynx of the worm; and v) are not due to the consumption of precipitate in

the media by the worm (Kamal et al., 2019). Given their birefringent nature and their

growth over time, we refer to these objects as crystals. The crystals kill younger animals

likely because of a combination of factors; they perforate the plasma membrane of

surrounding cells and rapidly grow to occlude the pharynx lumen (Kamal et al., 2019).

Here, we show that crystal-forming molecules can be grouped into 24 distinct

structural scaffolds, six of which have been previously shown to bind amyloid with high

affinity. Transmission electron microscopy, pulse-chase experiments and mutant

analyses reveal that crystals form in tight association with the non-luminal face of the

pharyngeal cuticle. We used multiple dyes and reporters to show that crystal growth

disrupts the amyloid-like components of the cuticle without a concomitant effect on the

surrounding chitin matrix. A screen of 2558 clinically approved drugs and natural

products for those that could suppress crystal formation yielded 45 distinct small

molecule scaffolds. 15 (33%) of these have been previously shown to block amyloid

formation. Finally, we have identified substructural elements that can convert select

small molecule scaffolds from crystal-forming molecules to suppressors of crystal

formation and vice-versa, suggesting that crystal-forming molecules and their

suppressors likely compete for the same environment within the pharyngeal cuticle. This

work reveals the pharyngeal cuticle to be a novel platform with which to identify small

molecules that interact with IDR-rich material. We deduce that the complex *in vivo*

environment in which these small molecule interactions occur has the potential to

reveal novel small molecule modulators of pathogenic amyloid formation.

Results

64 Small Molecules Induce Crystal Formation in *C. elegans*

We previously identified 48 compounds that form crystals in the heads of animals

(Kamal et al., 2019). For example, incubating wild type worms in 30 μM of the worm-

active #190 small molecule (aka wact-190) for three hours results in obvious crystal

formation (Figure 1a-f). More recently, we assembled a distinct custom library of 1178

small molecules containing 175 unique core structures that are based upon scaffolds we

previously identified as being worm bioactive (Burns et al., 2015) (Supplementary

Datafile 1). We screened this library for molecules that kill L1 larvae in our standard 6-

day viability assay and identified 88 lethal molecules. We re-screened these lethal hits

against the *sms-5(0)* mutant, which we had previously shown to resist crystal-formation

(Kamal et al., 2019). We identified 16 molecules that: i) kill wild type; ii) fail to kill *sms-*

5(0) mutants; and iii) form crystals in association with the pharynx (Figure 1 g and h;

Supplemental Figure 1).

   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 0.6 or more (see

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

another and 12 singletons (Figure 1g). Visual inspection reveals 24 distinct structural

families that each harbor a distinct core scaffold (Figure 1; Supplemental Figure 1). Nine

of these scaffolds contain either an oxadiazole, acetophenone, piperazine, or

benzofuran substructure (Figures 1g and 1h; Supplemental Figure 1). In addition to

other physicochemical properties that we previously described (Kamal et al., 2019), we

found the crystalizing molecules are also enriched in aromatic rings relative to non-

crystalizing molecules (p=9E-8) (Figure 1i). As discussed below, an enrichment of π

bonding capability among the crystalizing compounds (as reflected in their aromaticity)

provides insight into why the crystals grow where they do.

A search of the patent and academic literature using the SciFinder search tool

(Somerville, 1998) revealed that six of the 24 scaffolds are found in molecules that bind

amyloid protein. We performed the informatic searches with the core scaffold and not

the entire molecule because the small molecule crystallizers are non-drug molecules

that have not been widely studied, unlike common drugs and natural products (see

below). Scaffolds (a), (b), and the wact-102 scaffold have been shown to bind Abeta42

amyloid aggregates with low nanomolar affinity (Watanabe et al., 2009; Yang et al.,

2014). Scaffolds (b), (g) and the wact-415 scaffold have been shown to bind prion

amyloid aggregates with low nanomolar affinity (Geissen et al., 2011). Finally, wact-498

is a flavonoid, which is an intensively studied class of molecules that have therapeutic

potential for treating amyloid-related neurodegeneration (reviewed (Ayaz et al., 2019)).

In particular, isoflavone analogs of wact-498 can disrupt Abeta42 plaque formation in a

C. elegans model of the human disease (Gutierrez-Zepeda et al., 2005) and have been

shown to directly bind Abeta42 *in vitro* (Hirohata et al., 2012).

Crystals Emanate from the Non-Luminal Face of the Pharyngeal Cuticle

For much of our studies of crystal formation, we use either wact-190 as our canonical

crystal-forming molecule because it is structurally stable and behaves reproducibly or

wact-469 because of its fluorescent properties (Kamal et al., 2019). To better

understand the locale of crystal formation, we examined wact-190 objects by

transmission electron microscopy (TEM). Through the examination of serial sections, we

found that unusual objects form in close association with the non-luminal face of the

pharyngeal cuticle (Figures 2a-k). We presume these unusual objects to be the crystals

that we see by light microscopy, which also appear to extend from the non-luminal face

of the cuticle (see Figure 1f for example). As the objects extend in space, they can be

seen either piercing the plasma membrane (Figures 2c, c', i and j) or adjacent to the

plasma membrane like a finger pushing on the skin of a balloon (Figures 2f,f'). In either

case, the extension of the object from the pharyngeal cuticle is coincident with the

distortion of the plasma membrane inwards towards the cytoplasm.

We note the irregular amorphous material in the space between the objects and the

plasma membrane that are routinely observed in the experimental samples (e.g., pink

arrowhead in Figure 2h). This material is remarkably similar to that which forms

between the old cuticle that separates from the newly synthesized cuticle during

apolysis (for example, see Figure 8 of (Wright and Thomson, 1981)). This suggests that

the debris may be a consequence of disrupted cuticle.

The larval stages of *C. elegans* are defined by cuticle molts where the animal sheds its

old cuticle and grows a new one underneath (Knight et al., 2002). If we are correct in our

interpretation that objects form in association with the pharyngeal cuticle, then

removing larval worms from a solution of the object-forming compound should result in

the shedding of the crystals along with the old cuticle during the subsequent molt. If

instead the crystals initially form within the plasma membrane or in the cytoplasm, then

the crystals should remain after the molt. We used an established pulse-chase protocol

to determine whether the crystals were likely associated with the pharyngeal cuticle

(Figure 2l; see methods for details) (Kamal et al., Manuscript Submitted). Briefly, we

incubated third larval stage (L3) animals with a pulse of the fluorescent crystalizing

molecule wact-469 for three hours, transferred the animals to a rinse plate, and then a

chase plate without wact-469. We counted the number of animals with and without

fluorescent signal at the beginning and then at the end of the 18 hour chase (Figure 2l).

After the chase, very few animals that were initially L3s had fluorescent signal (Figure

2m-o). By contrast, when the pulse-chase experiment was done with young adults,

which do not molt, the fluorescent signal persisted (Figure 2p-r).

We investigated the site of crystal formation using a third approach. Previous work

showed that RNAi targeting *mlt-9* results in animals that remain attached to their shed

anterior exocuticle and pharyngeal cuticle (Frand et al., 2005; Kamal et al., Manuscript

Submitted). We investigated whether attached shed pharyngeal cuticle would

accumulate fluorescent crystals when incubated in wact-469 for 3 hours and found that

it did (Figure 2s-t). Together, these data indicate that wact-190 birefringent crystals

form in tight association with the non-luminal face of the pharyngeal cuticle and can

distort the plasma membrane of cells that line the pharynx lumen (Figures 2u-x).

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 binders (Bennhold, 1922;

Divry, 1927; Larbig et al., 2007; Vassar and Culling, 1959), specifically bind the

pharyngeal cuticle (Kamal et al., Manuscript Submitted). Similarly, the blue fluorescent

Calcofluor white (CFW) and the yellow-red fluorescent Eosin Y (EY), which bind chitin

(Harrington and Raper, 1968) and its deacetylated derivative chitosan (Baker et al.,

2007) respectively, specifically bind the pharyngeal cuticle (Kamal et al., Manuscript

Submitted).

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

three hours followed by 2 hours of incubation of the dyes (see methods). We found that

the amyloid dye patterns are often disrupted by the nascent objects (Figure 3). We also

observe a similar pattern in the background where a single IDR-rich protein (ABU-14) is

tagged with GFP (George-Raizen et al., 2014) (Supplemental Figure 2). By contrast, the

chitin and chitosan dyes are relatively unperturbed (Figure 3; Supplemental Figure 2). In

some instances, the birefringent crystal overlaps with amyloid stain (blue arrows, Figure

3). In other cases, there is little overlap between the birefringent signal and the amyloid

stain (orange arrows, Figure 3).

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

dyes bind to *in vitro* precipitated small molecules (see methods). None of the dyes

fluoresced brightly in association with the *in vitro* precipitated small molecules (Figure

3g). 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 3). 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 (e.g. Figure 2h). 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.

Crystal Formation is Suppressed by Canonical Amyloid Dyes and Disruptors

To better understand the interaction between crystals and the pharyngeal cuticle, we

screened Microsource's Spectrum library of 2558 drugs and natural products for those

that might suppress crystal formation. We reasoned that suppressors of crystal

formation with common mechanisms of action might lead to insight into 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

(Burns et al., 2015)). We previously established wact-190's lethality in young larvae is

dependent on crystal formation (Kamal et al., 2019). Control (solvent-only) wells are

overgrown with worms after six days (Supplementary Table 1). By contrast, wells with

wact-190 (3.75 μM) contain either arrested or dead L1s at the assay endpoint

(Supplementary Table 1 and (Kamal et al., 2019)).

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 (Burns et al., 2015)) (Supplementary

Table 1). To assess the structural diversity of the suppressors, we built a structural

similarity network of the molecules (Figure 4a). A Tanimoto coefficient cut-off of 0.8

revealed 45 distinct core scaffolds, 18 of which are represented by multiple molecules

(Figure 4a-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 4a; Supplementary Table 1). The majority of these

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

(see Figure 4b for p values). A benzaldehyde substructure is significantly enriched

among the suppressors (2.8 fold enrichment, p=2.3E-14; blue highlight in Figure 4b). Of

note, we found that several of the suppressors are fluorescent and of these, all

specifically stain the pharyngeal cuticle (Figure 4c and Supplemental Figure 4).

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 of amyloid disruptors within the Spectrum library. We

therefore randomly selected 100 molecules from the remaining 2473 Spectrum library

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 5a). 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 5b).

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

enriched in amyloid disruptors relative to the randomly selected set.

We further explored the idea that amyloid interactors might suppress crystal

formation. First, we asked whether wact-190-associated lethality is suppressed by the

canonical amyloid-binding dyes CR and ThS, neither of which are present in the

Spectrum library. Indeed, we found that CR and ThS robustly suppresses 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 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). Together, the data suggests that amyloid-

binding molecules may outcompete crystalizing molecules for interaction with the

pharyngeal cuticle.

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

Inspection of the structures of crystallizers and suppressors revealed that the former

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

hydroxyl groups ($p<1E$-10) (Figure 6a-b). The crystallizers are also more halogenated

than the suppressors (Figure 6c). 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 6d). In addition, the wact-415 crystalizing scaffold is

similar to that of ThS, which also suppresses crystal formation (Figure 6d). These

observations raised the possibility that both classes of molecules (crystallizers and

suppressors) compete for the same environment within the cuticle, which would be

consistent with their localization to that structure.

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 (Sterling and Irwin, 2015) 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 2; Figure 6e). This is comparable to the 36%

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

bioactive small molecules (Kamal et al., 2019). 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 3; Figure 6f). 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. Furthermore, the data further supports the model that

crystallizers and suppressors likely compete for the same niche.

Discussion

Crystal accumulation within the heads of *C. elegans* is commonly observed in small

molecule screens and assays. Here, we investigated this phenomenon in detail and show

that: i) many crystal-forming molecules have a core scaffold known to bind amyloid; ii)

crystals grow on the non-luminal face of the pharyngeal cuticle; iii) crystals can displace

amyloid dye-binding material within the pharyngeal cuticle; and iv) crystal formation is

antagonized by small molecules known to interact with amyloid material. We have

shown in companion work that the pharyngeal cuticle is rich in proteins with intrinsically

disordered regions (IDRs) with both phase-separation and amyloidogenic potential

(Kamal et al., Manuscript Submitted). Together, the data suggests that these small

molecule interactions occur in an environment abundant with amyloid-like material.

Despite being associated with IDR-rich proteins, IDR-rich material is not sufficient for

crystal growth. For example, the hypodermis that makes the body cuticle secretes

abundant intrinsically disordered proteins with amyloidogenic potential (see Figure 6 of

(Kamal et al., Manuscript Submitted)), yet crystal formation is restricted to the

pharyngeal cuticle. Similarly, the eggshell is rich in chitin (Zhang et al., 2005), but does

not develop birefringent crystals (see Supplemental Figure 3 in (Kamal et al., 2019)).

Hence, the niche in which crystals grow is complex and likely requires more than just

amyloid-like material and chitin.

The physicochemical properties of the small molecules that crystalize provide insight

into why these molecules may accumulate specifically within the pharyngeal cuticle.

Relative to the non-crystal-forming compounds tested, the crystal-forming compounds

are rich with π bonding capability, hydrogen bond acceptors, and polar surface areas

(this work and (Kamal et al., 2019)). Our companion analyses show that the pharyngeal

secretome is highly enriched in π-bonding capability relative to the remaining proteome

and is only surpassed by one other group of proteins (the collagens) (Kamal et al.,

Manuscript Submitted). What further distinguishes the pharynx secretome relative to all

other protein groups is that its proteins are enriched in polar uncharged residues with

hydrogen bond donor capability (i.e., Ns, Qs, Ss, Ts, and Ys) (($p<$1E-11) (Kamal et al.,

Manuscript Submitted)). Hence, there is unique complementarity between the crystal-

forming compounds and their niche within the pharyngeal cuticle.

Our finding that select crystallizing molecules and their respective suppressors have

identical core structures was unexpected. This suggests that both classes of molecules

compete for the same niche. We speculate that the suppressors' enrichment of

hydrogen bonding capability (relative to the crystallizers) may facilitate additional

interactions with the niche. In turn, the suppressors might prophylactically mask the

niche to prevent crystal seeding. This finding also suggests that it might be possible to

convert any crystallizing molecule into a suppressor by generating analogs with

hydrogen bond-donor capability. Given that a large fraction of suppressors antagonize

amyloid formation, converting crystalizing molecules to suppressors represents an

additional route towards identifying novel anti-amyloid agents.

Many crystal suppressors are known antagonists 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 (Caughey et al., 1998;

Lee et al., 2015; Yuan and Gao, 2013). The porphyrins ring is thought to disrupt the

intrapeptide π-π interactions of the amyloidogenic peptide that is necessary to achieve

superstructure (Yuan and Gao, 2013). Given that the crystalizing molecules are rich in π

bonding capability, it may be that porphyrins suppress crystal formation by disrupting

the crystallizing molecule's ability to establish π bonds with other molecules of the same

type.

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

polyphenolic secondary metabolites synthesized by plants (Panche et al., 2016). Many

flavonoid structures have been shown to antagonize amyloid formation *in vitro* (Akaishi

et al., 2008; Choi et al., 2020; Yin et al., 2011), in culture (Kimura et al., 2018), and *in*

vivo (Ahmad et al., 2017; Kim et al., 2010; Wei et al., 2014a) (see (Hole and Williams,

2021) for a comprehensive and recent review). 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 (Chen et al., 2018).

Flavonoid interaction with Abeta42 is driven by hydrophobic and hydrogen bond

interactions that antagonize the peptide's ability to adopt a β-sheet secondary structure

(Wang et al., 2015). Whether the flavonoids interact with amyloidogenic proteins within

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

A third of the suppressor scaffolds are proven amyloid disruptors, suggesting that

other molecules within the collection might also disrupt amyloids. It will be a future

priority to determine whether the collection contains novel scaffolds that can disrupt

disease-related amyloids. Notably, screens for suppressors of the crystal-induced death

of *C. elegans* is inexpensive and adaptable to high throughput methodologies.

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 drugs must act. Crystal suppression therefore represents a novel approach to

reveal new candidate amyloid disruptors.

Methods

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

C. elegans strains were cultured and synchronized as previously described (Kamal et al., 2019). Six day viability assays were conducted as previously described (Burns et al., 2015). 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 (George-Raizen et al., 2014), 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$_3$. Transmission electron microscopic (TEM) analysis was performed as previously described (Kamal et al., 2019).

Identification of New Crystallizing Molecules and Crystal Counts

A library of 1178 commercially available analogs of *C. elegans*-lethal molecules from the previously reported worm-active (aka wactive) library (Burns et al., 2015) 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* (Dulovic et al., 2020) as previously described (Burns et al., 2015), 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 (Kamal et al., 2019).

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.) comprised 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 (Burns et al., 2015), 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 [10 µM] (see

(Burns et al., 2015)) 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.

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

449 **Informatic Analyses**

450 Structural similarity networks were constructed based on pairwise similarity scores

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

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

453 visualized using Cytoscape (Cline et al., 2007) as previously described (Burns et al.,

454 2015). For each network generated, a range of Tanimoto coefficient cut-offs were tested

455 to determine which cut-off yielded a network that clustered obvious structural analogs

456 together as determined by manual inspection. Suppressors were analysed for the

457 presence of substructures (Figure 4b) using Filter-it version 1.0.2 from Silicos-it.

458 Structures were drawn using ChemDraw (PerkinElmer Informatics). A random Spectrum

459 network (Supplemental Figure 5) was generated by assigning all molecules within the

460 Spectrum library a random number using excel, then sorting the molecules in order of

461 the random number, then choosing the top 100 molecules that did not include any of

462 the 85 Spectrum suppressors.

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

464 100 randomly chosen molecules by searching that compound and the word 'amyloid' in

465 both a pubmed search and a google search. We inspected the search results for

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

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

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

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

close structural analogs that have a demonstrable 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 (O'Boyle et al., 2011) was used for the analog searches.

Using SmiLib v2.0 (Schüller et al., 2007), 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 (Sterling and Irwin, 2015). 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.

Pulse Chase Analyses

Pulse chase experiments were performed as previously described (Kamal et al.,

Manuscript Submitted). Briefly, synchronized 'L3' or 'adult' were washed with M9 to

remove bacteria. Worms were transferred using siliconized tips with the ends cut with

flame-sterilized scissors to avoid injuring the worms. 50 μL of packed worms from

centrifugation were used per sample, ensuring that the number of worms did not

exceed 1000 because the number of worms can affect stain intensity. The tubes with

worms and dye, wactive, or control, were incubated on a nutator for 3 hours in the dark

at room temperature, rinsed several times, then spotted onto the clear (agar) surface of

6 cm plates seeded with OP50. 30 minutes later, 20-30 worms were picked onto a

second plate lightly seeded with OP50. The staining of the cuticle for each was then

semi-quantitatively assessed on an epifluorescent microscope. These data represent the

pre-chase counts. The remaining animals on the original 6 cm plate are incubated for a

total of 18 hours at 20°C, after which dye staining of the cuticle was quantified again.

These data represent the post-chase counts.

Generating *mlt-9(RNAi)* Cuticle Defects

mlt-9 RNAi was carried out as described previously (Frand et al., 2005; Kamath et al.,

2003) with some modifications as described in (Kamal et al., Manuscript Submitted).

Briefly, after plating 6,500 synchronized L1s on *mlt-9(RNAi)*-inducing HT115 *E. coil*

clones, the plates were stored at 16°C in the dark for 90 hours and then used in

dye/wactive experiments. Note that approximately 50% of *mlt-9(RNAi)*-treated worms

exhibit the expected cuticle defects. Performing mock RNAi with the empty L4440

plasmid failed to yield worms with obvious cuticle defects.

Dye Staining

Dye staining experiments were performed as previously described (Kamal et al.,

Manuscript Submitted). Briefly, Congo Red (CR) (Fisher chemical C580-25; CAS 573-58-0)

staining of worms was done with final concentration of 287 µM, made from a 14.4 mM

stock (i.e. a final concentration that is 0.02% made from a 1% stock (w/v) dissolved in

DMSO). Thioflavin S (ThS) (SIGMA, T1892) staining of worms was done with a final

concentration of 2.25 mM (made from a 225 mM stock) (i.e., a final concentration that

is a 0.1% solution from a 10% stock (w/v, dissolved in DMSO)). Note that ThS is a

complex mixture of molecules with two major species of 377.1 MW and 510.1 MW and

several other minor species (Enthammer et al., 2013). Given that the ratio of molecules

is unknown, we used an average MW of 443.6 for ThS in our calculations of molarity.

Eosin Y (EY) (Sigma-Aldrich, E4009) staining of worms was done with a final

concentration of 217 µM (from a working stock of 7.23 mM) (i.e. a final concentration of

0.15 mg/ml made from a 5 mg/mL stock (dissolved in 70% ethanol). Care must be taken

to remove excess EY dye from the worm sample by running worms on seeded plates for

at least 15 minutes prior to observation. Note that eosin Y stock should be stored at -

20°C and before its use, should be incubated at 55°C for ~2 minutes and vigorously

vortexed to ensure its solvation. Calcofluor White (CFW) (Fluorescent Brightener 28,

Sigma-Aldrich, CAS 4404-43-7) staining of worms was done with a final concentration of

52 µM (from a working stock of 10.4 mM) (i.e. a final concentration of 0.005% made

from a 1% stock (w/v, dissolved in DMSO 1% stock)). Unless otherwise noted, all staining

experiments were done in 500 µL of NGM for 3 hours in the dark, and then mounted

and imaged as described above.

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 @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 themselves, 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 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.

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 pulse-

chase and *mlt-9* experiments, the dye-staining experiments, the *in vitro* precipitation

experiments, and the detailed analysis of CR, ThS, EY, and CFW-suppression of death

and crystal formation. DH determined whether the fluorescent Spectrum suppressors

specifically stain the pharyngeal cuticle. DHH and KCQN performed the transmission

electron microscopy. 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. PJR and MK composed figures and wrote the

manuscript with input from co-authors. PJR supervised and secured funding for the

project.

Competing Interests

The authors declare no competing interests.

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Figure 1. 24 Small Molecule Scaffolds are Capable of Crystal Formation. A. A

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

is green. **B.** A schematic of the corpus that is the subject of panels C-F. The central

lumen is indicated in dark grey, the channels and buccal cavity are in cream. The black

dashed line corresponds to the approximate cross sections shown in Figure 2. **C-D.**

Photos of worms taken at the working dissection microscope illustrating the

obviousness of wact-190 crystal formation relative to the control. The orange boxed

area corresponds to the area highlighted in A and B. The scale bar in C also applies to D.

E. Anterior-most region of a worm treated with solvent only. Orange arrows indicate the

buccal cavity cuticle, the green arrows highlight the buccal collar, and the white arrows

indicate the cuticle that lines the channels. Differential interference contrast (DIC) and

birefringent (BIRE) images are shown. The scale bar in E applies to all images in the

upper right-hand side. **F.** Anterior-most region of a worm treated with 30 μM wact-190

for 24 hours. The notation is the same as that in E. Blue arrowheads highlight the

birefringent crystals. **G.** An unsupervised structural similarity network of the crystalizing

molecules. Each node represents a small molecule, labelled with a wactive number. The

link represents a Tanimoto structural similarity coefficient of the core scaffold of 0.6 or

higher on the Tanimoto scale. The lower-case labels indicate groups of molecules with

the same core scaffolds as indicated in H. Note that the unsupervised network links the

non-piperazine wact-128 to the piperazine cluster and leaves the piperazine wact-220 as

a singleton because of structural differences beyond the piperazine group in the

scaffold. **H.** Markush representations of the core scaffolds of structural analogs able to

crystalize in the worm. R, X, Y, and Z groups are shown in Supplemental Figure 1. The 15

singletons shown correspond to the 12 singleton nodes shown in G, plus three

additional molecules (wact-81, wact-390, and wact-611) within the largest cluster of G.

Asterisks indicate literature-based evidence for analogs with the same core scaffold able

to bind amyloid fibrils *in vitro* as described in the main text and in Supplemental Figure

1. **I.** Crystalizing molecules from the wactive library (Burns et al., 2015) have significantly

more aromatic rings (calculated using Open Babel (O'Boyle et al., 2011)) compared to

non-crystalizing molecules from the same library (p=9E-8). The mean and standard error

is shown.

Figure 2. Wact-190 Crystals Form in Association with the Pharyngeal Cuticle. A-B.

Transmission electron microscopy of cross sections of wild type worms incubated with

either 30 μM wact-190 (A) or solvent control (DMSO; B). The scale bar in B also applies

to A. **C-F.** Serial sections of the area indicated in the blue box in 'A' ('C' is the actual

section of the series highlighted in 'A'). The scale in C applies to C-F. **C'.** An enlargement

of the area boxed in 'C' showing how the object (blue arrowhead) is disrupting the

plasma membrane. **F'.** An enlargement of the area boxed in 'F' showing how the object

(blue arrowhead) is juxtaposed to the plasma membrane (black arrowheads). **G-K.** Serial

sections of the area indicated in the pink box in 'A' ('K' is the section of the series

highlighted in 'A'). The scale in G applies to G-K. **L.** A timeline of the pulse-chase

experiment. **M-N.** Examples of third larval stage animals that have been incubated in

fluorescent wact-469 (60 μM) before the chase (M) or after the chase (N). The scale in

M applies to M-Q'. **O.** Quantification of the fraction of animals with fluorescent wact-

469 crystals. The asterisk indicates a significant difference ($p<0.001$) relative to pre-

chase using a Student's t-test. Standard error of the mean is shown. **P-R.** Analogous to

M-O, but done with young adult animals. **S&T.** *mlt-9(RNAi)* animals with incompletely

separated pharyngeal cuticle (black arrows) exposed to either DMSO (S) or wact-469 (60

μM) (T) for 3 hours. wact-469 crystals are indicated with green arrows. The scale in S

applies to S-T'. **U-X.** The interpretation of how and where crystals form in relation to the

pharyngeal cuticle and the plasma membrane of the underlying marginal cells. The

relative concentration of wact-190 is depicted in shades of blue; the darker the shade,

the greater the relative concentration. The legend for the arrows and asterisks in U-X

are indicated below panels G and K.

Figure 3. 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, but 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.

A

B

(a) flavonoid
(n=10; 3.8X p=9.6E-04)

(g) progestin
(n=3; 0.9X *p*=0.449)

(n) gossypol
(n=2; 29X *p*=1.0E-03)

(b) diphenyl
(n=5; 1X *p*=0.497)

(h) chalcone
(n=3; 9.7X *p*=3E-03)

(o) anthraquinone (n=2;
4.6X *p*=7E-03)

(c) gallin
(n=4; 23X; *p*=6.5E-06)

(i) phenethylphenol
(n=3; 8.7X *p*=4E-03)

(p) benzenesulfonamide
(n=3; 17.4X *p*=3.8E-04)

(e) naphthalen-1,4-dione
(n=3; 8.7X *p*=4.0E-03)

(j) hydroxyquinoline
(n=2; 6.4X *p*=3.6E-02)

(q) salicylanilide
(n=3; 17.4X *p*=3.8E-04)

(f) isoflavone
(n=4; 3.6X *p*=2.3E-02)

(m) porphyrin
(n=3; 29X *p*=4.0E-05)

(r) celastrol
(n=2; 29X *p*=1.0E-03)

C

CFW | curcu. | merge | CFW | harmal. | merge | CFW | erythro. | merge
animal 1 | animal 2 | animal 3

5 μm

Figure 4. 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 structural similarity coefficient of 0.8 or

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

formation. See Supplementary Table 1 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 4 for additional examples and controls. The scale

in 'C' applies to all images in the series.

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 have been 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 have been 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. Crystallizers and Suppressors can Share Identical Core Structures. A-C.

Graphs of the indicated physicochemical features of crystallizers and suppressors. A

single and double asterisk indicate $p<0.001$ and $p<1.0E-10$, respectively. Standard error

of the mean is shown. **D.** Crystallizers and suppressors that share an identical or similar

core structure. **E.** Core scaffolds of suppressing molecules that can be turned into

crystallizers (see Supplemental Table 2 for additional details). **F.** Core scaffolds of

crystallizing molecules that can be turned into suppressors (see Supplemental Table 3

for additional details).

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	% crystals	n	SD	p value	Evidence for anti-amyloid activity (PubMed ID or Patent Number) [e]	Targeted Amyloid in Study
		solvent control	OG	0	0	100	4	0	na	none found	na
s1	a	RHAMNETIN	OG	OG	0	0	2	0	0.0E+00	16248550	Abeta42
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
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	4.0E-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
s12	b	2,3,4-TRIHYDROXY-4'-ETHOXYBENZOPHENONE	OG	OG	0	14	3	12	2.3E-04	none found	na
s13	b	3,4-DIDESMETHYL-5-DESHYDROXY-3'-ETHOXYSCLEROIN	OG	OG	0	20	4	13	1.7E-05	none found	na
s14	b	CLOFOCTOL	OG	OG	0	0	2	0	0.0E+00	none found	na
s15	b	ROSOLIC ACID	OG	OG	0	70	2	1	1.6E-04	none found	na
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
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
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
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
s27	f	ISOOSAJIN	OG	OG	0	21	2	13	1.2E-02	none found	na
s28	f	MUNDULONE ACETATE	OG	OG	0	13	2	13	1.1E-02	none found	na
s29	f	KOPARIN	OG	OG	0	12	2	11	7.5E-03	none found	na
s30	g	PREGNENOLONE SUCCINATE	OG	OG	0	0	3	0	0.0E+00	none found	na
s31	g	DESOGESTREL	OG	OG	0	17	2	8	4.4E-03	none found	na
s32	g	NORGESTIMATE	OG	OG	0	10	2	1	2.5E-05	none found	na
s33	h	2',4'-DIHYDROXYCHALCONE	OG	OG	0	0	3	0	0.0E+00	none found	na
s34	h	4'-HYDROXYCHALCONE	OG	OG	0	0	2	0	0.0E+00	none found	na
s35	h	PHLORETIN	OG	OG	0	5	2	2	1.8E-04	none found	na
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
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
s42	k	BENZYL BENZOATE	OG	OG	0	8	2	1	4.3E-05	none found	na
s43	m	HAEMATOPORPHYRIN	OG	OG	0	0	2	0	0.0E+00	34570963	Abeta42
s44	m	PROTOPORPHYRIN IX	OG	OG	0	7	2	6	2.1E-03	34570963	Abeta42
s45		CHLOROPHYLLIDE Cu COMPLEX Na SALT	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
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-03	none found	na
s50	r	CELASTROL	OG	OG	0	7	3	7	1.9E-05	none found	na
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
s54	p	GLIMEPIRIDE	OG	OG	0	4	3	2	1.9E-07	none found	na
s55	p	GLIPIZIDE	OG	OG	0	28	2	9	8.3E-03	none found	na
s56	q	RAFOXANIDE	OG	OG	0	8	2	12	8.2E-03	none found	na
s57	q	CLOSANTEL	sick	sick	0	0	3	0	0.0E+00	none found	na
s58	q	OXYCLOZANIDE	OG	OG	0	27	4	30	2.6E-03	none found	na
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-06	none found	na
s61		DIFFRACTAIC ACID	OG	OG	0	46	2	6	5.9E-03	none found	na
s62		BROMOCRIPTINE MESYLATE	OG	OG	0	0	2	0	0.0E+00	none found	na
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	5.2E-03	none found	na
s66		NIFUROXAZIDE	OG	OG	0	24	4	32	3.1E-03	none found	na
s67		NITAZOXANIDE	OG	OG	0	3	3	6	8.4E-06	none found	na
s68		HARMALINE	OG	OG	0	36	2	1	4.4E-05	none found	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	7.1E-03	none found	na
s71		APOMORPHINE HYDROCHLORIDE	OG	sick	0	25	2	1	1.3E-04	none found	na
s72		USNIC ACID	OG	OG	0	4	2	6	1.9E-03	none found	na
s73		BITHIONATE SODIUM	sick	sick	0	0	2	0	0.0E+00	none found	na
s74		CITRININ	OG	OG	0	13	4	26	4.9E-04	none found	na
s75		EBSELEN	OG	OG	0	21	2	6	3.3E-03	none found	na
s76		CANDESARTAN CILEXTIL	OG	OG	0	0	2	0	0.0E+00	none found	na
s77		TOTAROL	OG	OG	0	0	2	0	0.0E+00	none found	na
s78		CURCUMIN	OG	OG	0	3	3	4	2.9E-06	15590663, 17472706, 18189141 (lots)	Abeta42
s79		4,4'-DIMETHOXYDALBERGIONE	OG	OG	0	0	2	0	0.0E+00	none found	na
s80		DIHYDROGAMBOGIC ACID	OG	OG	0	12	2	8	4.0E-03	none found	na
s81		ISORESERPINE	OG	OG	0	6	2	1	9.0E-05	none found	na
s82		SAFROLE	OG	OG	0	12	2	16	1.7E-02	none found	na
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
s85		SIROLIMUS	OG	OG	0	11	2	16	1.6E-02	none found	na

Supplemental Table 1. 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.

	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)c1ccc(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(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 2. 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]
					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)
1		DMSO (n=6)			OG	OG	OG	let	let	let	100 +/- 0
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)
12	OC-12	MolPort-003-855-287	O=C(c1cc(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)
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)
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)
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)
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 3. Halogenated 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.

(a) wact-51 23766818 21755599
wact-425

(b) wact-184 23766818
wact-158
wact-135

(b) wact-177 23766818
wact-13-21
wact-13-7
wact-13-6
wact-13-3

(c) wact-58
wact-507
wact-153

(c) wact-10-2
wact-154
wact-558

(c) wact-156
wact-106
wact-8-3
wact-8-4
wact-711

wact-81
wact-611

(d) wact-712-1
wact-157

(d) wact-713
wact-190
wact-174

(e) wact-2
wact-136
wact-113
wact-165
wact-570

(f) wact-167
wact-169

(g) 21755599 US9095596
wact-391
wact-416
wact-709-5
wact-709-4
wact-709-9
wact-709-6
wact-709-8
wact-709-2

(h) wact-86
wact-134

(i) wact-6
wact-49
wact-220
wact-381
wact-50
wact-91

wact-15
wact-24
wact-37
wact-40
wact-102 WO 2015090122 24936678
wact-105
wact-120
wact-128
wact-390
wact-393
wact-415 21755599
wact-469
wact-498 23766818 29191087 32616652

Supplemental Figure 1. Crystallizing Small Molecules Grouped According to Structural

Similarity. Molecules belonging to structurally distinct families are boxed together. The

15 singletons are unboxed. The cluster that each boxed set of molecules belong to,

which corresponds to notation in Figure 1g, is indicated in the upper left-hand corner.

The pubmed IDs or patent numbers that provides evidence of binding to amyloid are

indicated in pink.

Supplemental Figure 2. 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 3. Larger wact-190 Crystals Often Fail to Overlap with Cuticle

Markers. Legend is the same as that described for Figure 3 and Supplemental Figure 2.

Supplemental Figure 4. 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.

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

Supplemental Figure 5. 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 structural similarity coefficient 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.

Supplementary Data File 1.

The 'RL1200' library and associated screening data that revealed 16 additional

crystalizing molecules. See methods and main text for details. 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.