Potent New Small-Molecule Inhibitor of Botulinum Neurotoxin Serotype A Endopeptidase Developed by Synthesis-Based Computer-Aided Molecular Design

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Abstract

Botulinum neurotoxin serotype A (BoNTA) causes a life-threatening neuromuscular disease known as botulism. Current treatment for post exposure of BoNTA uses antibodies that are effective in neutralizing the extracellular toxin to prevent further intoxication but generally cannot rescue already intoxicated neurons. Effective small-molecule inhibitors of BoNTA endopeptidase (BoNTAe) are desirable because such inhibitors potentially can neutralize the intracellular BoNTA and offer complementary treatment for botulism. Previously we reported a serotype-selective, small-molecule BoNTAe inhibitor with a K\text{app} value of 3.8 ± 0.8 μM. This inhibitor was developed by lead identification using virtual screening followed by computer-aided optimization of a lead with an IC50 value of 100 μM. However, it was difficult to further improve the lead from micromolar to even high nanomolar potency due to the unusually large enzyme-substrate interface of BoNTAe. The enzyme-substrate interface area of 4,840 Å² for BoNTAe is about four times larger than the typical protein-protein interface area of 750–1,500 Å². Inhibitors must carry several functional groups to block the unusually large interface of BoNTAe, and syntheses of such inhibitors are therefore time-consuming and expensive. Herein we report the development of a serotype-selective, small-molecule, and competitive inhibitor of BoNTAe with a K\text{I} value of 760 ± 170 nM using synthesis-based computer-aided molecular design (SBCAMD). This new approach accounts the practicality and efficiency of inhibitor synthesis in addition to binding affinity and selectivity. We also report a three-dimensional model of BoNTAe in complex with the new inhibitor and the dynamics of the complex predicted by multiple molecular dynamics simulations, and discuss further structural optimization to achieve better in vivo efficacy in neutralizing BoNTA than those of our early micromolar leads. This work provides new insight into structural modification of known small-molecule BoNTAe inhibitors. It also demonstrates that SBCAMD is capable of improving potency of an inhibitor lead by nearly one order of magnitude, even for BoNTAe as one of the most challenging protein targets. The results are insightful for developing effective small-molecule inhibitors of protein targets with large active sites.


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Introduction

Botulism is a life-threatening neuromuscular disease that occurs in at least five forms—food-borne botulism, infant botulism, wound botulism, adult enteric infectious botulism, and inhalation botulism. The disease is caused by the specific action of botulinum neurotoxins. Seven antigenically distinct botulinum neurotoxins (serotypes A to G) are known, but primarily serotypes A, B, E, and F have been reported to cause botulism in humans. Botulinum neurotoxin serotype A (BoNTA) is a protein produced by the spore-forming anaerobic bacterium, Clostridium botulinum. The lethal doses of BoNTA for a 70-kg human are estimated as 0.9 μg by inhalation and 70 μg by ingestion [1]. BoNTA inhibits the release of acetylcholine from presynaptic nerve terminals at neuromuscular junctions, causing flaccid paralysis and frequently leading to prolonged mechanical ventilation with serious medical sequelae or death following respiratory arrest [2]. Despite its toxicity, the purified and diluted BoNTA has been used as medical treatment for cholinergic nerve and muscle dysfunctions [3,4]; BoNTA (marketed as Botox) also can temporarily reduce facial frown lines. However, overdose with BoNTA can develop systemic botulism [5].
Current post-exposure treatment of botulism relies on administration of antibodies against the toxins. The available antitoxin is an equine product that causes allergic reactions in ~10% of patients [6]. In late 2005, a solution of human antibodies was licensed as “BabyBIG” to treat infant botulism [7], but to date generic botulism immune globulin injections are still unavailable. Furthermore, antibodies are effective in neutralizing the extracellular toxin to prevent further intoxication but generally cannot rescue already intoxicated neurons. There is a need to develop complementary, post-exposure treatments such as small-molecule antidotes that potentially can neutralize the intracellular toxin.

Structurally, BoNTA consists of a light chain (Mr ~50,000) and a heavy chain (Mr ~100,000) that are linked by a disulfide bond. The light-chain is a zinc endopeptidase that specifically cleaves SNAP-25, a neuronal protein required for acetylcholine release [8]. The BoNTA endopeptidase (BoNTAe) has been a target for developing small-molecule inhibitors of the toxin [9–15]. However, developing potent inhibitors is as difficult as developing small-molecule inhibitors of protein-protein complexes. The latter has been a known challenge for decades [16]. The difficulty arises because, upon binding, the substrate wraps around the circumference of BoNTAe constituting an unusually large substrate enzyme interface area of 4,840 Å² (Figure 1) [17]. This interface requires molecules possessing several functional groups to block it. Consequently, syntheses of such molecules are time-consuming and costly. The extent of the challenge can be appreciated by comparing the interface area (4,840 Å²) of BoNTAe to the typical protein-protein interface area of 750–1500 Å² [16]. Because of the micromolar range (see Section 3.1). To date, the most potent inhibitors reported to date typically have inhibitory potencies in the low nanomolar range. BoNTAe inhibitors reported to date typically have inhibitory potencies in the low micromolar range (see Section 3.1). To date, the most potent BoNTAe inhibitor has been an elegantly designed peptidic analog that mimics GlnArgAlaThrLysMetLeu, and this peptide mimetic (HPM) has a Ki value of 41 nM [18]. Nevertheless, some of the reported micromolar small-molecule inhibitors already demonstrate ex vivo efficacy in protecting cells against BoNTA [9,11]. Our micromolar small-molecule BoNTAe inhibitor leads also demonstrate in vivo efficacy at a concentration of 2 mg/kg in protecting mice against 5 LD50 challenge of BoNTAe (manuscript in preparation). These results suggest that BoNTAe is a viable target for developing small-molecule antidotes to BoNTA.

Previously we reported a serotype-selective, small-molecule BoNTAe inhibitor with a Ki value of 3.8±0.8 μM [10]. This inhibitor was developed by lead identification using virtual screening followed by optimization of a lead with an IC50 value of 100 μM [19]. However, we were unable to further improve the lead from micromolar to even high-nanomolar potency using conventional computer-aided molecular design (CAMD), despite the use of a high-resolution BoNTAe crystal structure (free and in complex with a peptidic substrate analog) [20] and advanced terascale computer simulation techniques [10].

In this article, we report the development of a serotype-selective, small-molecule, and competitive inhibitor of BoNTAe with a Ki value of 760±170 nM by using a new approach, termed synthesis-based computer-aided molecular design (SBCAMD), to address the challenge in synthesis. We also report a three-dimensional (3D) model of the high-nanomolar inhibitor in complex with BoNTAe and the dynamics of the complex predicted by multiple molecular dynamics simulations (MMDSS). On the basis of the 3D model, we discuss insights into further structural optimization to achieve Ki values comparable to that of HPM and the prospect of small-molecule BoNTAe inhibitors as effective antidotes to neutralize the intracellular BoNTA. We also discuss the advantages of both SBCAMD and CAMD in drug discovery.

Results

Inhibitor Design

MMDSs on our early lead 1 (Figure 2) [10] suggested that structures like analog 2 (Figure 2) have higher affinities for BoNTAc than 1. This is because (1) one diphenylmethanol group of 2 can adopt the Venus-flytrap-like conformation to grasp Arg363 of BoNTAc more tightly via cation-pi interactions than the phenyl group of 1; (2) the other diphenylmethanol group can fill the large void of the BoNTAc active site and interact with Arg231 via cation-pi interactions, whereas 1 cannot reach Arg231; (3) two ammonium groups of 2 rather than only one ammonium group of 1 can interact with four carboxylates (Glu55, Glu64, Glu164, and Glu257) at the active site.

However, we could not make 2 using the scheme shown in Figure S1 in a short period, nor could we make analog 6 (Figures 2 and S2), a thiopeptide analog of 2, given the same time constraint. We subsequently replaced the pyrrole ring of 2 with a benzene ring to avoid the problem of making 2. This transformation resulted in analogs 3–5 (Figure 2) that can be made with facile syntheses described in the schemes shown in Figure S3, Figure S4, and Figure S5, although these molecules are more bulky than 2 and carry an aromatic hydroxamate that has a relatively low affinity for zinc due to pi-electron delocalization. We initially hoped that the bulkiness problem could be remedied by the flexibility of the BoNTAc active site and therefore made 3–5 with ease. However, biological evaluation showed that none of these analogs was active in inhibiting BoNTAc at an inhibitor concentration of 10 μM (Table 1). Although change of an aromatic hydroxamate to an aliphatic hydroxamate does not require too much synthetic effort, we did not pursue this modification, as it would make these molecules even more bulky.

Alternatively, we made analog 7 (Figure 2), as a truncated analog of 6 according to the scheme shown in Figure S6. Unexpectedly, 7 precipitated in the inhibition assay buffer even though dimethyl sulfoxide was used to dissolve 7. Gratifyingly, a different truncation of 6 led to the syntheses of analogs 8 and 9 (Figure 2) according to Schemes I–III of Figure 3. Encouragingly, both 8 and 9 showed 35% inhibition of BoNTAc at an inhibitor concentration of 10 μM (Table 1). These results inspired the design of analog 10a (Figure 2). The replacement of the thiopeptide ring of 8 by a pyrrole ring in 10a was due to our synthetic experience and available intermediates of the unsuccessful synthesis of 2. In making 10a according to Schemes I and IV of Figure 3, we had to protect the pyrrole nitrogen atom in order to improve the yield of the Sonagashira coupling [21]. However, we could not cleave the β-methoxybenzyl or benzyl group from the pyrrole nitrogen atom, nor could we protect the nitrogen atom using tosyl chloride. Nonetheless, according to the inhibitor-bound BoNTAc complexes generated by MMDSs, we conjectured that the benzyl group of 10b could interact favorably with the serotype-specific Phe194 via the pi-pi interaction. We therefore completed the synthesis of 10a without cleaving the benzyl group to give 10b. More encouragingly, 10b at 10 μM showed 64% inhibition of BoNTAc (Table 1). A structure-activity relationship study on a series of homologues of 10b with two identical alkylamino chain lengths varying from 6 to 10 methylene groups identified N,N-bis(7-aminohexyl)-1-benzyl-5-(3-hydroxy-3-diphenylpropyl)-4-(3-hydroxyamino)-3-oxopropyl)-1H-pyrrrole-2-carboxamide (AHP, see Figure 2) as the most potent of the series (see Section 2.4 for characterization of AHP). To confirm the conjecture about the interaction of the benzyl group with Phe194, we also made analog 11 with a methyl group attached to the pyrrole nitrogen atom of 11 (Figures 2 and 3). Indeed, 11 at 1 μM showed only 8% inhibition of BoNTAc,
Figure 1. Large enzyme-substrate interface of BoNTAe. A: top view of the active site showing the substrate binding at the large pocket. B: side view of the active site showing the substrate wrapping around the circumference of BoNTAe. Active-site residues of BoNTAe (Zn$^{2+}$, H223, H227, E262, F163, F194, R363, and D370) are shown in light blue sphere or light blue stick model. The SNAP-25 substrate (146–204) is shown in red stick model. BoNTAe is shown in grey surface model with 15% transparency.

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Figure 2. Chemical structures of BoNTAe inhibitors and their analogs resulted from SBCAMD.
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whereas AHP exhibited 54% inhibition under the same conditions (Table 1).

Computer Simulation

Twenty different molecular dynamics simulations (each lasted 10 ns) were carried out for the AHP-BoNTAe complex to probe the intermolecular interactions of the design inhibitor using the PMEMD module of the AMBER 8 program [22] (see Section 4.4). The initial complex structure was generated by manually docking AHP into the BoNTAe active site with (1) the hydroxamate group near the active-site zinc ion, (2) the diphenylmethanol group near Arg363, (3) the benzyl group near Phe194, (4) one ammonium group near Glu56 and Glu164, and (5) the other ammonium group near Glu257. The BoNTAe structure used for the docking was taken from the crystal structure of an inhibitor-bound BoNTAe (Protein Data Bank Code: 3BOO [20]) in which conformations of missing residues 62–67 were taken from the crystal structure of a BoNTAe mutant in complex with SNAP-25 (Protein Data Bank Code: 1XTG [17]).

For each of the 20 simulations, 200 instantaneous conformations were saved at 5-ps intervals during the last 1-ns period. A total of 4,000 instantaneous conformations of AHP-BoNTAe from the 20 simulations were subjected to a cluster analysis using the averagelinkage algorithm (epsilon = 2.0 Å and RMS on all atoms of alpha-carbon atoms) [23] implemented in the PTRAJ module of the AMBER 10 program [22]. Only one cluster of the BoNTAe conformations and five clusters of the AHP conformations was identified. All 4,000 instantaneous conformations of AHP-BoNTAe were subjected to a second-round cluster analysis using the averagelinkage algorithm (epsilon = 2.0 Å and RMS on all atoms of AHP). This analysis identified five clusters of the AHP conformations. The numbers of the AHP conformations in Clusters 1–5 are 2400, 600, 721, 200, and 79, respectively. Of the three most populated clusters (Figure 4), the AHP conformations in Clusters 1 and 3 are similar, and the one in Cluster 2 is unique. All inhibitor conformations in Clusters 1–3 have one ammonium group forming a salt bridge to Asp370, although this group was placed away from Asp370 but close to Glu257 in the initial conformation used in the MMDSs. For the inhibitor conformations in Cluster 2, the other ammonium group moved away from Glu56 and Glu164, and the ammonium group of Lys66 moved close to the two carboxylates to form salt bridges, although the ammonium groups of AHP and Lys66 were placed close to and away from the carboxylates in the initial conformation, respectively. For the inhibitor conformations in Clusters 1 and 3, the Glu56-interacting ammonium group of AHP and the Lys66 ammonium group remained in the same locations as those in the initial conformation.

To investigate whether AHP adopts different conformations found in Clusters 1 and 2 or one of the two, a second round of 20 10-ns-long simulations on AHP-BoNTAe were carried out using the representative conformation of AHP-BoNTAe in Cluster 2 as an initial conformation. The same cluster analyses of the second-round simulations identified again one cluster of the BoNTAe conformations and five clusters of the AHP conformations. The numbers of the inhibitor conformations in Clusters 1–5 of the second-round simulations are 459, 201, 2762, 178, and 400, respectively. Interestingly, the most populated inhibitor conformation (Cluster 3) of the second-round simulations is nearly identical to the third most popular inhibitor conformation (Cluster 2) of the first-round. However, the most popular inhibitor conformation (Cluster 1) of the first-round simulations disappeared in the second-round, suggesting that AHP adopts only one conformation in the BoNTAe active site.

Deviations for all alpha-carbon atoms between the representative conformation of Cluster 3 of the second-round simulations and the free BoNTAe crystal structure (Protein Data Bank Code: 3BON [20]) that was aligned over the representative conformation were computed and plotted against temperature factors of the corresponding alpha-carbon atoms (Figure 5). A similar plot was also obtained from the average conformation of Cluster 3 of the second-round simulations (Figure 5). It is worth noting that only alpha-carbon atoms were used for the alignment and that no energy minimization was performed on the representative or average conformation. As apparent from these correlation plots, the alpha-carbon deviations of the representative and average conformations are consistent with temperature factors for all residues except for terminal residues or residues that are involved in crystal contact such as residues 197–213, 244–257, 283–295, and 375–387. The representative conformation of AHP-BoNTAe in Cluster 3 of the second-round simulations has a free-and-cool root mean square deviation (C&F RMSD) of 1.06 Å for all alpha-carbon atoms of the protein relative to those of the crystal structure. The C&F RMSD [24] is the RMSD of residues that are not involved in crystal contact and have temperature factors lower than the average temperature factors, and it is used to minimize the structural difference caused by crystal packing [25–27] and high temperature factors. Consistently, the average conformation of AHP-BoNTAe in Cluster 3 of the second-round simulations has a C&F RMSD of 0.85 Å. These results suggest that the average or representative conformation in Cluster 3 of the second-round simulations best represents the AHP-BoNTAe complex structure in water. The coordinates of the average and representative conformations are available from Datasets S1 and S2 of Supporting Information.

In the representative conformation of AHP-BoNTAe (Figures 6A and 6B), the hydroxamate group coordinates the zinc ion and has (1) a hydrogen bond to Glu224, (2) a one-water-mediated hydrogen-bond network to Tyr366, and (3) a one-water-mediated hydrogen-bond network to Arg363; the two hydroxamate-linking methylene groups have van der Waals interactions with the methyl and methylene groups of Thr220 and Glu224, respectively; the diphenylmethanol group has (1) cation-pi interactions with Arg365, (2) pi-pi interactions with Tyr366, Phe194, and Phe196, and the ammonium group of Lys66...
(3) a hydrogen bond to Asp370, and (4) a three-water-mediated hydrogen-bond network to Asp203; the benzyl group has pi-pi interactions with Phe194 and Phe419; the pyrrole-substituted carbonyl oxygen atom has a one-water-mediated hydrogen-bond network to Gln162; one ammonium group has a salt bridge with Asp370 and an intramolecular cation-pi interaction with the diphenylmethanol group; the other ammonium group is placed at the midpoint to the carboxylates of Glu55, Glu64, and Glu164 and has ionic interactions with these carboxylates; the alkyl chain of the Glu55-interacting ammonium group has van der Waals interactions with the methylene groups of Glu164, Lys66, and Glu162.

In the average conformation of AHP-BoNTAe (Figure 6C), there is significant contraction for the benzyl group and the alkyl ammonium group that interacts with Glu55, Glu64, and Glu164. The contraction of the benzyl group indicates that it spins in a hydrophobic pocket constituted by Val70, Ile161, Phe194, Val373, and Phe419. It also indicates that the alkyl ammonium group is highly mobile in interacting with Glu55, Glu64, and Glu164. The inhibitor dynamics revealed by the MMDSs suggests that the binding of AHP to BoNTAe is partly entropy-driven. It also suggests that the electron density for the benzyl group will be slightly disordered and that the electron

Figure 3. Syntheses of BoNTAe inhibitors 8, 9, 10b, 11, and AHP. Scheme I: synthesis of intermediate 14; Scheme II: synthesis of 8; Scheme III: synthesis of 9; Scheme IV: syntheses of 10b, 11, and AHP.
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density for one alkyl ammonium group will be significantly disordered in the crystal structure of AHP-BoNTAe to be determined.

Chemical Synthesis
AHP, an achiral molecule possessing five functional groups (hydroxamate, diphenylmethanol, benzyl, and two ammonium groups) designed to interact with the active-site residues of BoNTAe, was made readily with a 10-step synthesis outlined in Schemes I and IV of Figure 3. This synthesis began with methyl 4-formyl-1H-pyrrole-2-carboxylate (33) that has a pyrrole ring as a frame to support the five functional groups in different orientations. This expensive commercially available starting material was, however, made in house from 2-(trichloroacetyl)-pyrrole using a two-step synthesis according to published protocols [28,29]. To introduce the diphenylmethanol group to the pyrrole ring via the Sonogashira coupling [21], I₂ and CF₃CO₂Ag in CHCl₃ [29] were used to iodinate intermediate 33 to give the desired intermediate 34, which was separable from methyl 4-formyl-3,5-diiodo-1H-pyrrole-2-carboxylate and methyl 4-formyl-5-iodo-1H-pyrrole-2-carboxylate through column chromatography. Another reported procedure [30] was also effective in converting 33 to 34 in a similar yield. N-Benzylation of 34 followed by the Sonogashira coupling [21] with 1,1-diphenylprop-2-yne-1-ol gave intermediate 36x with both diphenylmethanol and benzyl groups linked to the pyrrole ring, which was confirmed by the heteronuclear multiple bond coherence (HMBC) spectroscopy. Saponification of 36x followed by amidation using intermediate 14y gave intermediate 38z with two protected alkylamino groups linked to the pyrrole ring, wherein 14y was obtained from N-(7-bromohexyloxy)phthalimide in a high yield via a two-step synthesis outlined in Scheme I of Figure 3. Wittig olefination of 38z gave intermediate 39z with an ethyl ester as a precursor of the desired hydroxamate group. The two unsaturated bonds of 39z were reduced by dry 10% Pd-C in ethyl acetate to give intermediate 40z. The hydrogenation reaction was very sensitive to moisture; wet Pd-C or Raney nickel resulted in unidentified products. The final product (AHP) was obtained by treating 40z with excess of 50% aqueous hydroxylamine for 24 hours [31]. This treatment converted the ethyl ester and N-phenylphthalimides to hydroxamic acid and amines, respectively [32,33]. High performance liquid chromatography (HPLC) purification using TFA-containing solvent yielded pure AHP in its TFA salt form. Caution should be taken in removing TFA-containing eluent after HPLC, as the diphenylmethyl hydroxy group of AHP is prone to elimination under acidic conditions (see Section 4.2.7).

Biological Testing
According to HPLC-based kinetics assays described in Section 4.3 [34], AHP has a Kᵢ value of 760±170 nM, which was calculated from slopes of Dixon plots (Figure 7) with Kᵢ = Kᵢ/[slope]/V_MAX/[S], where [S] is the substrate concentration [35] and kinetic constants for the substrate were taken from reference [36]. Unlike inhibitor 1 as we reported previously [10], AHP has linear Dixon plots (Figure 7) indicating that AHP is a competitive inhibitor of BoNTAe and its Kᵢ value can thus be obtained from the fractional inhibition method or the Cheng and Prusoff method [35,37]. Indeed, both methods yielded a Kᵢ value of 760±170 nM, consistent with the value from the Dixon plots. AHP did not inhibit botulinum neurotoxin serotype B endopeptidase (BoNTBc) at concentrations up to 5 μM at which AHP showed >80% inhibition of BoNTAe. As described in Section 4.3, the BoNTAe inhibition assay buffer was supplemented by 25 μM ZnCl₂, whereas the BoNTBc inhibition assay buffer contained no exogenous zinc ion. AHP at 5 μM showed >80% inhibition of BoNTAe in the presence of 5-molar excess of exogenous zinc, but it did not show any BoNTBc inhibition in the absence of exogenous zinc. These results preclude the possibility that AHP nonspecifically inhibited BoNTAe through depleting the active-site zinc divalent cation via zinc chelation. Clearly, AHP is a serotype-selective, small-molecule, and competitive inhibitor of BoNTAe with a Kᵢ value of 760±170 nM.
Discussion

Relative Potencies of BoNTAe Inhibitors

A mixture of two regioisomeric small molecules has been reported to have a $K_i$ value of 600±100 nM in inhibiting BoNTAe [39]; however, there has been no report for the separation of the mixture. To our knowledge, the most potent BoNTAe inhibitor has been HPM, a peptidic inhibitor with a $K_i$ value of 41 nM [10]. A small-molecule BoNTAe inhibitor, 2,4-dichlorocinnamic hydroxamate DCCH, was reported to have initially a $K_i$ value of 300±12 nM [39] and most recently an IC$_{50}$ value of 39 or 81 μM depending on assay conditions [40]. Using the assay conditions described in Section 4.3 that are different from those reported in [39,40], we found that the IC$_{50}$ values of AHP and DCCH are <1 μM and 34 μM, respectively, and that AHP is >34-fold more potent in inhibiting BoNTAe than DCCH [39] and one order of magnitude less potent than HPM [18].

Insights into BoNTAe Inhibitor Design

While crystal structures of HPM-BoNTAe and DCCH-BoNTAe have been reported [18,41], the results of the crystal structure of AHP-BoNTAe is currently underway. The results described in Section 2.2 suggest that the computer model of AHP-BoNTAe is suitable for qualitative comparison of the binding of AHP at the BoNTAe active site with those of HPM and DCCH.

As apparent from the cross-section view of the inhibitor-bound BoNTAe active site (Figure 8), DCCH occupies a small portion of the active-site region where the Arg198-containing hydrolysis product binds [17]; AHP occupies the bottom half of that region; HPM occupies nearly the entire region. The rank order of occupancy in the active site for the three inhibitors agrees well with the rank order of the inhibitory potency described in Section 3.1. From structural point of view, this agreement suggests that effective BoNTAe inhibitors have volumes that are comparable to or more than that of AHP. The “bulkiness” requirement observed is consistent with the reported nanomolar inhibitors of BoNTBe [42]. Therefore, we anticipate that optimization of known small-molecule BoNTAe inhibitors by small structural perturbations alone is unlikely to lead to effective BoNTAe inhibitors.

To obtain more potent nanomolar small-molecule BoNTAe inhibitors, we think that new functional groups have to be introduced to AHP to occupy the upper portion of the active-site region. However, the more functional groups are introduced, the more challenging the inhibitor synthesis will become. In addition, adding more functional groups can hamper cell permeability. For these reasons, sophisticated computer simulations such as MMDSs employing the cationic dummy atom approach to simulating zinc proteins [19,43–45] are needed to identify new functional groups. These groups must have high affinities for the BoNTAe active site and low molecular weights to maintain cell permeability. In our view, for a realistic prospect of obtaining nanomolar BoNTAe inhibitors able to antagonize the intracellular BoNTAe, the design and optimization of current BoNTAe inhibitor leads may need new approaches such as the nonbonded bivalence approach [46] that dimerizes composite inhibitors by intermolecular interactions (self-assembly) rather than covalent bonds in order to improve both affinity and permeability.

Synthesis-Based Computer-Aided Molecular Design

Despite the use of high-performance computing to predict inhibitor affinity and serotype selectivity in developing our small-molecule BoNTAe inhibitors, we recognized that the development process is still a brute force process for at least two reasons. First, exquisitely designed inhibitors such as inhibitor 2 may not be synthetically accessible within a reasonable amount of time. Second, like analog 7, newly made inhibitors may not dissolve in an assay buffer under a high ionic strength condition. Identification of these problems a priori is beyond the scope of current computer simulations. The best way to circumvent these problems is to make and test more inhibitors with good affinities predicted by computer simulations. This requires facile synthesis of more of such inhibitors, which is, however, different from high-throughput screen of any available chemicals. Therefore, the ability to obtain nanomolar BoNTAe inhibitors relies more on expeditious syntheses of inhibitor analogs with good affinities than on exquisite design of high-affinity inhibitor analogs using free energy perturbation calculations that can compute the absolute binding free energy [10].

With these considerations, we pursued synthesis-based computer-aided molecular design (SBCAMD) that accounts the practicality and efficiency of inhibitor synthesis in addition to binding affinity and selectivity. The general form of our proposed approach comprises (1) identification of an inhibitor lead with the aid of computer simulations (e.g., identifying 2 by MMDSs); (2) transformation of the lead to molecules that can be made in a...
Figure 6. Close-up view of the intermolecular interactions of AHP with the active-site residues of BoNTAe. A (top): representative conformation generated by the second-round MMDSs; B (middle): diagram of the intermolecular interactions between AHP and BoNTAe; C (bottom): average conformation generated by the second-round MMDSs.

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reasonable amount of time (e.g., converting 2 to inhibitors 5–10); (3) re-evaluation of the synthetically accessible molecules with computer simulations (e.g., confirming the intermolecular interactions of AHP through MMDSs), this step may not be necessary if inhibitor synthesis takes less time than computer simulations; (4) synthesis and evaluation of the molecules from Step 2 or 3 (e.g., synthesizing and testing AHP).

From synthetic chemistry point of view, SBCAMD uses a facile synthetic scheme to transform commercially available or known chemicals into a molecule that fits or likely fits the binding site of a drug target. In this case, the target molecule is determined with consideration of its synthetic effort. In contrast, CAMD uses retrosynthetic analysis [47] to repeatedly transform a target molecule as a potential inhibitor of a drug target into simpler precursors until commercially available or known molecules are reached. In this case, like a natural product, the target molecule is pre-determined regardless of its synthetic effort.

SBCAMD is proposed to work with large-binding-pocket targets, while CAMD works best with small-binding-pocket targets. There are knowingly a number of factors (such as solubility in an assay buffer) that are beyond the scope of current computer simulations, but govern the potency of an inhibitor. Therefore, the more inhibitors are tested, the more likely a better inhibitor can be identified. The CAMD approach works well with small-binding-pocket targets, even though it does not address practicality and efficiency of chemical synthesis for each “computer-identified” inhibitor to be tested. This is because inhibitors for this kind of targets are structurally simple and often commercially available or can be made without too much synthetic effort. When bulky inhibitors are needed to bind a large protein pocket, such inhibitors are structurally complex and generally commercially unavailable. Therefore, inhibitor syntheses inevitably become the rate determine step of the development process, and hence SBCAMD comes into play.

More case studies are certainly needed, however, in our view, SBCAMD holds promise in developing small-molecule BoNTAe inhibitors or other small-molecules inhibitors that bind at large interfaces, because it aims to reduce the number of chemicals to be tested relative to the number of chemicals used in the high throughput screen and the time and cost to make each chemical to be tested.

Conclusion

We developed a serotype-selective, small-molecule, and competitive inhibitor of BoNTAe with a $K_i$ of $760 \pm 170$ nM. We also developed a 3D model of BoNTAe in complex with the inhibitor, which supports the concept underlying the design of the inhibitor. These developments were made possible by the use of a new approach (SBCAMD) that aims to reduce the number of

Figure 7. Dixon plots for competitive inhibition of BoNTAe by AHP.
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Figure 8. Cross-Section Views of HPM, AHP, and DCCH bound in the BoNTAe active site. Left: HPM with carbon in yellow obtained from the crystal structure of 3DS9 [18]; middle: AHP with carbon in green obtained from the MMDS-generated model; right: DCCH with carbon in blue obtained from the crystal structure of 2IMA [41]. Oxygen, nitrogen, and zinc are shown in red, blue, and light blue, respectively. BoNTAe is shown in white surface model with 15% transparency.
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chemicals to be tested as well as the time and cost to make each chemical to be tested. The results provide insights into developing effective small molecules that can neutralize the intracellular BoNTA to provide a therapy complimentary to current antibody therapy for treating botulism. This work offers an example of the use of SBCAMD to improve expeditiously the potency of an inhibitor lead by nearly one order of magnitude for BoNTAe that is arguably one of the most challenging protein targets.

Materials and Methods

Reagents

Hexanes (Hex), ethyl acetate (EtOAc), and TFA were purchased from Fisher Scientific (Pittsburgh, PA) and used without purification. CF3CO2Ag and l,l-diphenylprop-2-yn-1-ol were purchased from Aldrich Chemical Co Inc (Milwaukee, WI). Dry Pd-C catalyst was purchased from Stem Chemicals Inc (Newburyport, MA). All other commercially available reagents were used as received. Recombinant BoNTAe was provided by Dr. Leonard Smith of the United States Army Medical Research Institute of Infectious Diseases, Fort Detrick, MD. BSA, HEPES buffer, and zinc chloride were purchased from Sigma-Aldrich (St. Louis, MO). Dithiothreitol was obtained from BioRad (Hercules, CA).

Chemical Synthesis

General description. The 1H (400 MHz) and 13C NMR (100 MHz) spectra were recorded on a Mercury 400 spectrometer from Varian (Palo Alto, CA). Chemical shifts are reported in ppm using either tetramethylsilane or the solvent peak as an internal standard. Data are reported as follows: chemical shift, multiplicity (s = singlet, d = doublet, t = triplet, br = broad triplet, q = quartet, m = multiplet), coupling constant, and integration. High-resolution mass spectra were obtained from Varian (Palo Alto, CA). Chemical shifts are reported in ppm using either tetramethylsilane or the solvent peak as an internal standard. Data are reported as follows: chemical shift, multiplicity (s = singlet, brs = broad singlet, d = doublet, t = triplet, m = multiplet), coupling constant, and integration. High-resolution mass spectra were obtained from Varian (Palo Alto, CA). Chemical shifts are reported in ppm using either tetramethylsilane or the solvent peak as an internal standard. Data are reported as follows: chemical shift, multiplicity (s = singlet, brs = broad singlet, d = doublet, t = triplet, m = multiplet), coupling constant, and integration. High-resolution mass spectra were obtained from Varian (Palo Alto, CA). Chemical shifts are reported in ppm using either tetramethylsilane or the solvent peak as an internal standard. Data are reported as follows: chemical shift, multiplicity (s = singlet, brs = broad singlet, d = doublet, t = triplet, m = multiplet), coupling constant, and integration. High-resolution mass spectra were obtained from Varian (Palo Alto, CA). Chemical shifts are reported in ppm using either tetramethylsilane or the solvent peak as an internal standard. Data are reported as follows: chemical shift, multiplicity (s = singlet, brs = broad singlet, d = doublet, t = triplet, m = multiplet), coupling constant, and integration. High-resolution mass spectra were obtained from Varian (Palo Alto, CA). Chemical shifts are reported in ppm using either tetramethylsilane or the solvent peak as an internal standard. Data are reported as follows: chemical shift, multiplicity (s = singlet, brs = broad singlet, d = doublet, t = triplet, m = multiplet), coupling constant, and integration. High-resolution mass spectra were obtained from Varian (Palo Alto, CA). Chemical shifts are reported in ppm using either tetramethylsilane or the solvent peak as an internal standard. Data are reported as follows: chemical shift, multiplicity (s = singlet, brs = broad singlet, d = doublet, t = triplet, m = multiplet), coupling constant, and integration. High-resolution mass spectra were obtained from Varian (Palo Alto, CA). Chemical shifts are reported in ppm using either tetramethylsilane or the solvent peak as an internal standard. Data are reported as follows: chemical shift, multiplicity (s = singlet, brs = broad singlet, d = doublet, t = triplet, m = multiplet), coupling constant, and integration. 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High-resolution mass spectra were obtained from Varian (Palo Alto, CA). Chemical shifts are reported in ppm using either tetramethylsilane or the solvent peak as an internal standard. Data are reported as follows: chemical shift, multiplicity (s = singlet, brs = broad singlet, d = doublet, t = triplet, m = multiplet), coupling constant, and integration. High-resolution mass spectra were obtained from Varian (Palo Alto, CA). Chemical shifts are reported in ppm using either tetramethylsilane or the solvent peak as an internal standard. Data are reported as follows: chemical shift, multiplicity (s = singlet, brs = broad singlet, d = doublet, t = triplet, m = multiplet), coupling constant, and integration. High-resolution mass spectra were obtained from Varian (Palo Alto, CA). Chemical shifts are reported in ppm using either tetramethylsilane or the solvent peak as an internal standard. Data are reported as follows: chemical shift, multiplicity (s = singlet, brs = broad singlet, d = doublet, t = triplet, m = multiplet), coupling constant, and integration. High-resolution mass spectra were obtained from Varian (Palo Alto, CA). Chemical shifts are reported in ppm using either tetramethylsilane or the solvent peak as an internal standard. Data are reported as follows: chemical shift, multiplicity (s = singlet, brs = broad singlet, d = doublet, t = triplet, m = multiplet), coupling constant, and integration. High-resolution mass spectra were obtained from Varian (Palo Alto, CA). Chemical shifts are reported in ppm using either tetramethylsilane or the solvent peak as an internal standard. Data are reported as follows: chemical shift, multiplicity (s = singlet, brs = broad singlet, d = doublet, t = triplet, m = multiplet), coupling constant, and integration. High-resolution mass spectra were obtained from Varian (Palo Alto, CA). Chemical shifts are reported in ppm using either tetramethylsilane or the solvent peak as an internal standard. Data are reported as follows: chemical shift, multiplicity (s = singlet, brs = broad singlet, d = doublet, t = triplet, m = multiplet), coupling constant, and integration. High-resolution mass spectra were obtained from Varian (Palo Alto, CA). Chemical shifts are reported in ppm using either tetramethylsilane or the solvent peak as an internal standard. Data are reported as follows: chemical shift, multiplicity (s = singlet, brs = broad singlet, d = doublet, t = triplet, m = multiplet), coupling constant, and integration. High-resolution mass spectra were obtained from Varian (Palo Alto, CA). Chemical shifts are reported in ppm using either tetramethylsilane or the solvent peak as an internal standard. Data are reported as follows: chemical shift, multiplicity (s = singlet, brs = broad singlet, d = doublet, t = triplet, m = multiplet), coupling constant, and integration. High-resolution mass spectra were obtained from Varian (Palo Alto, CA). Chemical shifts are reported in ppm using either tetramethylsilane or the solvent peak as an internal std...
carboxylic acid (2.19 g, 99%). 1H NMR (CDCl3) δ 9.60 (brs, 1H), 7.56 (s, 1H), 7.34–7.30 (m, 4H), 7.20–7.13 (m, 4H), 7.11 (s, 1H), 7.06 (d, J = 7.2 Hz, 2H), 4.07 (q, J = 7.2 Hz, 2H), 3.90 (t, J = 7.8 Hz, 2H), 3.86 (t, J = 7.2 Hz, 2H), 3.60 (s, 9H), and 2.89 (t, J = 7.4 Hz, 2H). A 10% Pd-C (40 mg) was added to the resulting suspension. The resulting solution was filtered through Celite, concentrated, re-dissolved in MeOH, and purified by HPLC (eluting time: 20 min).

**4-ethyl-3-thio-2-propynylphenyl-2-carboxylic acid.** To a stirred solution of 19 (0.46 g, 0.94 mmol) in MeOH (15 mL) Raney-Ni (1.0 mL as MeOH slurry) was added, and the stirring was continued under a balloon of hydrogen for 17 hours. The metal catalyst was removed with a magnet, the catalyst was washed with MeOH. The washings and the aliquot were combined, concentrated in vacuo, purified by MPLC (gradient Hex to EtOAc) to give 20 as an oil (0.42 g, 91%). 1H NMR (CDCl3) δ 7.45 (d, J = 7.8 Hz, 4H), 7.41 (s, 1H), 7.34–7.30 (m, 4H), 7.23 (t, J = 7.2 Hz, 2H), 4.09 (q, J = 7.2 Hz, 2H), 2.77–2.70 (m, 4H), 2.23–2.18 (m, 3H), 2.52 (t, J = 7.5 Hz, 2H), 1.56 (s, 9H), and 1.21 (t, J = 7.2 Hz, 3H). 13C NMR (CDCl3) δ 172.93, 161.79, 147.52, 146.65, 136.99, 134.24, 131.66, 128.36, 127.30, 126.15, 81.65, 78.03, 60.82, 44.10, 35.05, 28.47, 23.36, 23.08, and 14.41.

5-(3,3-Diethyl-2-propynyl)-4-(3-hydroxy-3-propynyl)thiophene-2-carboxylic acid.** To a stirred solution of 19 (171 mg, 0.17 mmol) in MeOH/THF (2 mL each) containing 50% aqueous NH2OH (1 mL) and a catalytic amount (two crystals) of KCN was heated at 65°C for 24 hours. The resulting solution was filtered through Celite, concentrated, redissolved in MeOH, and purified by HPLC (elu-ting time: 20 minutes) to give of 8-2TFA (23 mg, 14%). Both semi-preparative and analytical HPLC retention times of 8-2TFA are 14.83 minutes (see Figure S7 for chromatograms of 8-2TFA before and after the HPLC purification).

**5-(3,3-Diethyl-2-propynyl)-4-(3-hydroxyaminomethyl)-3-oxopropylthiophene-2-carboxamide.** A stirred solution of 23 (171 mg, 0.17 mmol) in MeOH/THF (2 mL each) containing 50% aqueous NH2OH (1 mL) and a catalytic amount (two crystals) of KCN was heated at 65°C for 24 hours. The resulting solution was filtered through Celite, concentrated, redissolved in MeOH, and purified by HPLC (elu-ting time: 20 minutes) to give 8-2TFA (23 mg, 14%). Both semi-preparative and analytical HPLC retention times of 8-2TFA are 14.83 minutes (see Figure S7 for chromatograms of 8-2TFA before and after the HPLC purification).
A solution of oxalyl chloride (2.00 g, 16 mmol) in CH₂Cl₂ (3 mL) was added into the mixture during a period of 1 hour at 0°C. After the mixture was warmed up to room temperature, stirring continued for 24 hours. The solvent was removed in vacuo, and the residue was dissolved in EtOAc (150 mL), washed with brine (4×30 mL). The organic layer was dried over MgSO₄, filtered, and concentrated in vacuo. MPLC purification (Hex:EtOAc/5:1) of the residue gave 25 as a colorless oil (24.00 g, 81%).¹ H NMR (CDCl₃) δ 7.23 (d, J = 5.4 Hz, 1H), 6.93 (d, J = 5.4 Hz, 1H), 4.17 (q, J = 7.2 Hz, 2H), 3.61 (s, 2H), and 1.27 (t, J = 7.2 Hz, 3H); ¹³C NMR (CDCl₃) δ 170.37, 133.84, 128.90, 129.93, 111.78, 61.32, 35.30, and 14.43.

Ethyl 2-2-bromo-5-chlorocarboxylic acid (26). A solution of oxalyl chloride (20.0 g, 161 mmol) in CH₂Cl₂ (3 mL) was added dropwise into a solution of Ach (206 mg, 1.064 g, 8 mmol) in CH₂Cl₂ (6 mL) at 0°C. After the mixture was stirred for 1 hour, a solution of 25 (1.00 g, 4 mmol) in CH₂Cl₂ (2 mL) was added into the mixture during a period of 1 hour at 0°C. The mixture was filtered, the residue was dissolved in H₂O (20 mL), and extracted with EtO (10 mL). The organic layer was washed with brine (3×15 mL), dried over MgSO₄, and concentrated in vacuo. MPLC purification (Hex:EtOAc/20:1) of the residue gave 26 as a colorless oil (38 mg). The mixture was stirred under a balloon of hydrogen for 12 hours at room temperature and filtered through Celite. Concentration of the filtrate gave 30 as a colorless oil (22 mg, quantitative yield).¹ H NMR (CDCl₃) δ 6.71 (s, 1H), 7.45–7.60 (m, 10H), 6.20 (d, J = 7.4 Hz, 1H), 4.09 (q, J = 7.2 Hz, 2H), 3.60 (d, J = 7.2 Hz, 2H), 3.46 (s, 2H), and 1.19 (t, J = 7.2 Hz, 3H); ¹³C NMR (CDCl₃) δ 170.63, 167.35, 150.56, 144.62, 141.88, 139.31, 137.52, 131.02, 129.93, 128.73, 128.44, 127.30, 126.78, 124.68, 104.60, 61.42, 34.13, 29.40, and 14.35.

1-(3,3-Diphenylallyl)-4-(2-ethoxy-2-oxoethyl)thiophene-2-carboxylic acid (31). To a solution of 29 (22 mg, 0.052 mmol) in benzene (6 mL) was added p-TSA hydrate (9 mg, 0.052 mmol). After the mixture was stirred at 70°C for 1 hour, it was poured into H₂O (20 mL) and extracted with EtO (50 mL). The organic layer was washed with brine (2×15 mL), dried over MgSO₄, and concentrated in vacuo to give 31 as a colorless oil (22 mg, quantitative yield).¹ H NMR (CDCl₃) δ 7.51 (s, 1H), 7.32–7.51 (m, 10H), 6.10 (t, J = 7.4 Hz, 1H), 3.37 (t, J = 6.1 Hz, 2H), 2.75 (t, J = 7.8 Hz, 2H), 2.43 (q, J = 8.0 Hz, 2H), and 1.21 (t, J = 7.2 Hz, 3H); ¹³C NMR (CDCl₃) δ 170.69, 167.27, 151.13, 144.20, 137.27, 131.21, 129.05, 128.38, 128.02, 126.72, 61.39, 50.75, 37.13, 34.05, 27.20, and 14.37.

Ethyl 2-(5-bis-(1,1,3,5-tetramethyldioxoimido-2-yl)ethyl)carbamomyl)-3,3-diphenylallyl-3-(3-hydroxy-3,3-diphenylpropyl-1-ynyl)thiophene-2-carboxylic acid (32). A mixture of 31 (22 mg, 0.054 mmol), BOP (36 mg, 0.081 mmol), NMM (8 mg, 0.081 mmol), HOBt (11 mg, 0.081 mmol), and 14 (47 mg, 0.081 mmol) in anhydrous DMF (4 mL) was stirred at room temperature under N₂ for ~24 hours. When the reaction was over by TLC monitoring, the mixture was poured into H₂O (10 mL) and then extracted with EtO (70 mL). The organic layer was washed with brine (3×10 mL), dried over MgSO₄, and concentrated in vacuo. MPLC purification (Hex:EtOAc 4:1) of the residue gave 32 as a yellow amorphous solid (32 mg, 74% based on recovery of starting material).¹ H NMR (CDCl₃) δ 7.86–7.80 (m, 4H), 7.31–7.15 (m, 10H), 7.13 (s, 1H), 4.08 (q, J = 7.2 Hz, 2H), 3.95 (q, J = 8.0 Hz, 1H), 3.67 (t, J = 7.4 Hz, 2H), 3.44 (brt, 4H), 3.33 (s, 2H), 2.70 (t, J = 7.6 Hz, 2H), 2.40 (q, J = 7.6 Hz, 2H), 1.70–1.57 (m, 8H), 1.36–1.23 (m, 2H), and 1.20 (t, J = 7.2 Hz, 3H); ¹³C NMR (CDCl₃) δ 170.91, 168.70, 164.02, 144.60, 143.40, 136.64, 132.39, 130.87, 129.36, 128.80, 128.04, 126.39, 123.38, 61.15, 50.66, 38.27, 37.32, 34.18, 29.27, 29.63, 29.58, 29.37, 28.82, 27.06, 26.54, and 14.40.

N-(3,3-Diphenylallyl)-4-(2-hydroxymino)-2-oxoethyl-thiophene-2-carboxamide (9). To a stirred solution of 31 (18 mg, 0.018 mmol) in THF/MeOH (1.5 mL/1.5 mL), 1 mL of 50% aqueous NH₂OH was added, followed by catalytic amount (two crystals) of KCN. The resulting mixture was stirred for 23 hours at room temperature, and then filtered through a short Celite column. HPLC purification (eluting time: 30 minutes) of the filtrate gave 9-ZTFA as a white amorphous solid.
(18 mg, quantitative yield). The semi-preparative and analytical HPLC retention times of 9-TFMA were 17.70 and 15.07 minutes, respectively (see Figure S0 for chromatograms of 9-TFMA before and after the HPLC purification). 1H NMR (DMSO-d6) δ 10.62 (s, 1H), 7.65 (t, 1H), 5.72–7.50 (m, 4H, 7.36 (s, 1H), 7.30–7.24 (m, 9H), 7.06–7.02 (m, 2H), 5.69 (s, 2H), 3.80 (s, 3H), and 3.65 (s, 1H). 13C NMR (CDCl3) δ 183.16, 160.72, 144.07, 136.84, 129.18, 128.33, 129.91, 127.99, 127.05, 126.23, 124.96, 116.97, 103.33, 75.37, 75.27, 52.15, and 50.38. 1H-13C HMBC (CDCl3): there is a correlation between the pyrrole proton and the carbonyl carbon of the methyl ester, and there is no correlation between the pyrrole proton and the benzylic carbon.

1-Benzyl-4-formyl-5-(3-hydroxy-3,3-diphenylprop-1-ynyl)-1H-pyrrole-2-carboxylic acid (37x). To a solution of 36x (0.49 g, 1.09 mmol) in MeOH (20 mL) and water (6 mL) was added KOH (0.18 g, 3.27 mmol) and stirred at 60°C for 2 hours. The solvent was removed in vacuo. The residue obtained was acylated with 2 N HCl to pH 2.3 and extracted with EtOAc (3×15 mL). The combined organic layer was dried over MgSO4, filtered and then concentrated in vacuo to give 37x as a light brown solid. The crude product was subjected to the next reaction without further purification. 1H NMR (CDCl3) δ 7.92 (s, 1H), 7.52–7.50 (m, 4H), 7.45 (s, 1H), 7.30–7.18 (m, 9H), 7.06–6.99 (m, 2H), and 5.64 (s, 2H).

1-Benzyl-2-N-bis(6-(3-dioxoisoindolin-2-yl)hexyl)-4-formyl-5-(3-hydroxy-3,3-diphenylprop-1-ynyl)-1H-pyrrole-2-carboxamide (38x). A solution of 37x (0.35 g, 0.81 mmol), 14x (0.46 g, 0.97 mmol), BOP (0.73 g, 1.61 mmol), HOBT (0.22 g, 1.61 mmol) in anhydrous DMF (3 mL) and NMM (2 mL) was stirred at room temperature for 16 hours. The reaction mixture was partitioned between water and CH2Cl2 (20 mL). The organic layer was dried over MgSO4, filtered and concentrated in vacuo. MPLC purification (Hex:EtOAc/40:60) of the residue gave 38x as a pale yellow oil. (0.40 g, 41%). 1H NMR (CDCl3) δ 9.86 (s, 1H), 7.92–7.75 (m, 4H), 7.70–7.62 (m, 2H), 7.56–7.54 (m, 4H), 7.27–7.21 (m, 6H), 7.15–7.14 (m, 3H), 7.02–6.98 (m, 2H), 6.53 (s, 1H), 5.34 (s, 2H), 3.68–3.52 (m, 2H), 3.28–3.18 (m, 2H), 3.04–2.94 (m, 2H), 1.68–1.59 (m, 2H), 1.58–1.46 (m, 2H), 1.42–1.27 (m, 6H), 1.18–1.04 (m, 4H), and 1.02–0.94 (m, 2H). 13C NMR (CDCl3) δ 185.34, 168.68, 162.62, 144.57, 136.84, 134.15, 132.26, 139.07, 138.87, 126.11, 127.79, 127.29, 126.20, 125.18, 123.42, 109.14, 72.74, 75.31, 75.10, 49.57, 45.39, 37.96, 28.57, 27.13, 26.73, 26.48, and 26.28.

ethyl-3-(1-benzyl-5-bis(6-(1,3-dioxoisoindolin-2-yl)hexyl) carbamoyl)-2-(3-hydroxy-3,3-diphenylprop-1-ynyl)-1H-pyrrole-3-yl)acrylate (39x). To a stirred solution of 38x (0.33 g, 0.37 mmol) in benzene (20 mL) was added (ethoxycarbonylmethylene)triphenylphosphorane (0.3 g, 0.92 mmol). The resulting mixture was stirred under reflux for 16 hours. The reaction mixture was cooled to room temperature and the solvent was removed in vacuo. MPLC purification (Hex:EtOAc/50:50) of the residue gave 39x as a pale yellow oil (0.30 g, 85%). 1H NMR (CDCl3) δ 7.86–7.79 (m, 4H), 7.72–7.65 (m, 5H), 7.57–7.55 (m, 4H), 7.31–7.22 (m, 6H), 7.20–7.15 (m, 3H), 7.06–6.98 (m, 2H), 6.42 (s, 1H), 6.25 (d, J = 15.6 Hz, 1H), 5.33 (s, 2H), 4.18 (q, J = 7.2 Hz, 2H), 3.70–3.58 (m, 4H), 3.44 (s, 1H), 3.32–3.02 (m, 4H, 1.70–1.50 (m, 4H), and 1.49–1.12 (m, 15H). 13C NMR (CDCl3) δ 168.68, 167.65, 163.07, 144.63, 137.59, 136.76, 134.14, 132.32, 129.03, 128.98, 127.89, 128.66, 128.61, 120.86, 127.76, 127.57, 125.76, 124.97, 123.42, 119.74, 115.04, 108.54, 102.26, 77.18, 75.34, 64.61, 60.36, 49.60, 35.80, 31.86, 28.64, 26.75, and 14.44.

ethyl 3-(1-benzyl-5-bis(6-(1,3-dioxoisoindolin-2-yl)hexyl) carbamoyl)-2-(3-hydroxy-3,3-diphenylprop-1-ynyl)-1H-pyrrole-3-yl)propanoate (40x). To a stirred solution of 39x (0.15 g, 0.16 mmol) in EtOAc (20 mL) was added 10% dry Pd-C (0.015 g). The resulting mixture was stirred at room temperature for 48 hours under a balloon of hydrogen. The reaction mixture was filtered through Celite and the filtrate was concentrated to give 40x as a colorless oil. The crude product was subjected to the next reaction without further purification. 1H NMR of the crude product is as follows. 1H NMR (CDCl3) δ 7.77–7.75 (m, 4H), 7.64–7.62 (m, 4H), 7.27–7.06 (m, 13H), 6.71 (d, J = 7.2 Hz, 2H), 6.05 (s, 1H), 5.09 (s, 2H), 3.98 (q, J = 6.8 Hz, 2H), 3.57 (t, J = 7.2 Hz, 4H), 3.19 (t, J = 6.8 Hz, 2H), 2.56 (t, J = 7.6 Hz, 2H), 2.41–2.37 (m, 4H), 2.26–2.24 (m, 2H), 1.56–1.33 (m, 4H), and 1.30–1.11 (m, 15H).

X-Vio-Bis(6-aminoxy)-1-benzyl-5-(3-hydroxy-3,3-diphenylpropyl)-4-(3-hydroxyamino)-3-oxopropyl)-1H-pyrrole-2-carboxamide (10b). To a stirred solution of 40x (0.15 g, 0.16 mmol) in MeOH:THF (3 mL each) was added 50% aqueous hydroxy-
amine (4 mL) followed by KCN (0.04 g, 0.62 mmol). The resulting mixture was stirred at 35°C for 24 hours. After the solvent was removed in vacuo, the residue was subjected to HPLC purification (eluting time: 45 minutes). The eluent from HPLC was concentrated and partitioned between ethyl acetate (10 mL) and water (10 mL). The aqueous layer was washed with EtOAc (20 mL). The combined organic layer was dried over MgSO₄, filtered and then concentrated in vacuo. MPLC purification (Hex:EtOAc/50:50) of the residue gave 39y as a pale yellow oil (0.30 g, 53%). ¹H NMR (CDCl₃) δ 7.75–7.66 (m, 6H), 7.67–7.57 (m, 9H), 7.28–7.25 (m, 4H), 7.20–7.15 (m, 2H), 6.55 (s, 1H), 5.36 (s, 1H), 3.62–3.50 (m, 7H), 3.34 (s, J = 6.8 Hz, 4H), 1.66–1.38 (m, 5H), and 1.36–1.04 (m, 12H). ¹C NMR (CDCl₃) δ 185.15, 168.66, 162.58, 144.92, 134.12, 132.21, 129.97, 128.53, 127.98, 127.28, 126.19, 125.49, 123.35, 108.30, 102.92, 75.49, 74.83, 49.30, 45.20, 38.04, 33.85, 31.60, 28.64, and 26.88.

(6-Ethyl-3-(5-(bis(7-(1,3-dioxoisindolin-2-yl)heptyl)carbamoyl)-3-hydroxy-3,3-diphenylpropyl)-1-methyl-1H-pyrrole-3-yl) acrylate (39y). To a stirred solution of 38y (0.30 g, 0.4 mmol) in benzene (10 mL) was added (ethoxycarbonylmethylene)triphenylphosphorane (0.31 g, 0.9 mmol). The resulting mixture was stirred under reflux for 16 hours. The reaction mixture was cooled to room temperature and the solvent was removed in vacuo. MPLC purification (Hex:EtOAc/50:50) of the residue gave 39y as a pale yellow oil (0.22 g, 68%). ¹H NMR (CDCl₃) δ 7.75–7.66 (m, 4H), 7.63–7.57 (m, 9H), 7.28–7.25 (m, 4H), 7.19–7.18 (m, 2H), 6.31 (s, 1H), 6.17 (d, J = 16.0 Hz, 1H), 4.82 (s, 1H), 4.03 (q, J = 6.8 Hz, 2H), 3.62–3.53 (m, 7H), 3.35 (t, J = 7.2 Hz, 4H), 1.64–1.48 (m, 5H), and 1.36–1.15 (m, 15H). ¹C NMR (CDCl₃) δ 168.64, 167.64, 163.06, 145.15, 136.84, 134.08, 132.20, 129.58, 124.97, 128.75, 126.25, 123.60, 123.32, 119.97, 115.60, 108.00, 102.65, 76.55, 75.07, 60.26, 49.20, 45.20, 38.03, 33.72, 28.86, 28.63, 26.90, and 14.58.

Ethyl 3-(5-(bis(7-(1,3-dioxoisindolin-2-yl)heptyl)carbamoyl)-3-hydroxy-3,3-diphenylpropyl)-1-methyl-1H-pyrrole-3-ylpropanoate (40y). To a stirred solution of 39y (0.11 g, 0.12 mmol) in EtOAc (10 mL) was added dry powdered 10% Pd-C (0.01 g). The resulting mixture was stirred at room temperature for 48 hours under a balloon of hydrogen. The reaction mixture was filtered through Celite and the filtrate was concentrated to give 40y as a colorless oil (0.10 g, 90%). The crude product was subjected to the next reaction without further purification. ¹H NMR (CDCl₃) δ 7.82–7.80 (m, 4H), 7.70–7.68 (m, 4H), 7.46–7.44 (m, 4H), 7.32–7.20 (m, 6H), 6.03 (s, 1H), 4.04 (q, J = 6.8 Hz, 2H), 3.63 (t, J = 7.2 Hz, 4H), 3.44–3.36 (m, 7H), 2.60–2.52 (m, 4H), 2.46–2.39 (m, 4H), 2.04 (s, 1H), 1.68–1.60 (m, 4H), 1.58–1.49 (m, 4H), and 1.30–1.17 (m, 15H).

N,N'-Bis(7-aminoheptyl)-5-(3-hydroxy-3,3-diphenylpropyl)-4-(3-hydroxymino)-3-oxopropyl-1-methyl-1H-pyrrole-2-carboxamide (11). To a stirred solution of 40y (0.10 g, 0.11 mmol) in MeOH:THF (4 mL each) was added 50% aqueous hydroxylamine (4 mL) followed by KCN (0.04 g, 0.55 mmol). The resulting mixture was stirred at 35°C for 24 hours. After the solvent was removed in vacuo, the residue was subjected to HPLC purification (eluting time: 40 minutes). The eluent from HPLC was concentrated in vacuo at room temperature to remove the organic solvents. The resulting aqueous solution was lyophilized to give 11-2TFA as a white sticky solid (0.032 g, 33%). The semi-preparative and analytical HPLC retention times of 11-2TFA are 16.52 and 11.35 minutes, respectively (see Figure S10 for chromatograms of 11-2TFA before and after the HPLC purification). ¹H NMR (DMSO-d₆) δ 9.78 (brs, 1H), 7.71 (brs, 6H), 7.51–7.49 (m, 4H), 7.29–7.25 (m, 4H), 7.17–7.14 (m, 2H), 5.96 (s, 1H), 3.35–3.29 (m, 7H), 2.73–2.70 (m, 4H), 2.43 (m, 2H), 2.35 (m, 4H), 2.08 (t, J = 7.2 Hz, 2H), 1.48–1.42 (m, 8H), and 1.23–1.18 (m, 12H). ¹C NMR (DMSO-d₆) δ 169.47, 164.32, 158.98 (q), 148.65, 133.40, 128.34, 126.80, 126.36, 125.04, 123.60, 123.32, 119.97, 115.60, 108.00, 102.65, 76.55, 75.07, 60.26, 49.20, 45.20, 38.03, 33.72, 28.86, 28.63, 26.90, and 14.58.
Reaction mixture was partitioned between water and CH2Cl2. The (2 mL) was stirred at room temperature for 16 hours. The HOBt (0.30 g, 2.25 mmol) in anhydrous DMF (3 mL) and NMM was added 10% dry Pd-C (0.012 g). The resulting mixture was treated as GLH \[44,55,56\]. A total of 39 crystallographically unique residues, His39, His230, and His269 were treated as HID; all other residues were generated by the PREP, LINK, EDIT, and PARM modules were included for simulations. The topology and force field parameters were obtained according to the RESP procedure \[53\] with \(1.00 \times 10^{-5}\) kcal/mol. Small-Molecule BoNTa Inhibitor The atomic charges of AHP were obtained according to the RESP procedure \[33\] with \(ab initio\) calculations at the HF/6-31G* level using the Gaussian 98 program \[54\]. The starting structure of AHP was generated by the PREP, LINK, EDIT, and PARM modules of the AMBER 5.0 program \[57\]. The complex was refined by energy minimization using a dielectric constant of 1.0 and 100 cycles of steepest-descent minimization followed by 100 cycles of conjugate-gradient minimization. The refined complex was solvated with 12,098 TIP3P water molecules (named WAT). The WAT molecules were scaled from slopes of Dixon plots with the equation \(K_i = K_{0i}/(\text{slope})/\text{N}_{\text{free}}/\text{S}\), where \(S\) was the substrate concentration \[33\]. Kinetic constants for the substrate were taken from reference \[36\]. In Vitro Evaluation of AHP Assays of endopeptidase activities of BoNTa and BoNTb were done at 37°C and contained 0.5 mM substrate, 0.5–1.5 μM recombinant BoNTa or BoNTb, 40 mM HEPEs, and 0.05% tween at pH 7.3. BoNTa inhibition assays also contained 1 mM dithiothreitol, 25 μM ZnCl2, and 0.5 mg/mL BSA, while BoNTb inhibition assays were supplemented with 1 mM dithiothreitol only. Substrate for BoNTa was an SNAP-25 fragment containing residues 187–203 with N- and C-termini acylated and amidated, respectively \[51\], while for BoNTb it was residues 60–94 of VAMP \[52\]. Inhibitors were dissolved in dimethyl sulfoxide at 10 times the final assay concentration, then diluted into the assay mixture containing substrate, followed by addition of the endopeptidase (i.e., inhibitor and endopeptidase were not preincubated). Assay times and endopeptidase concentrations were adjusted so that less than 10% of the substrate was hydrolyzed. Assays were stopped by acidification with TFA and analyzed by reverse-phase HPLC as described \[34\]. Inhibition of BoNTa by AHP was determined in three independent experiments using nine concentrations of AHP in each. \(K_i\) was calculated from slopes of Dixon plots with the equation \(K_i = K_{0i}/(\text{slope})/\text{N}_{\text{free}}/\text{S}\), where \(S\) was the substrate concentration \[33\]. 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Kinetic constants for the substrate were taken from reference \[36\].
box of 216,000 TIP3P molecules, whose hydrogen atom charge was set to 0.4170, where any water molecule was removed if it had an oxygen atom closer than 2.2 Å to any solute atom or a hydrogen atom closer than 2.0 Å to any solute atom, or if it was located further than 9.0 Å along the x-, y-, or z-axis from any solute atom. The solvated complex system was energy-minimized for 100 cycles of steepest-descent minimization followed by 100 cycles of conjugate-gradient minimization to remove close van der Waals contacts in the system, then heated from 0 to 300 K at a rate of 10 K/ps under constant temperature and volume, and finally simulated independently with a unique seed number for initial velocities at 300 K under constant temperature and pressure using the PMEMD module of the AMBER 8.0 program [22] with the AMBER force field (ff99SB) [59,60].

All simulations used (1) a dielectric constant of 1.0, (2) the Berendsen coupling algorithm [61], (3) a periodic boundary condition at a constant temperature of 300 K and a constant pressure of 1 atm with isotropic molecule-based scaling, (4) the Particle Mesh Ewald method to calculate long-range electrostatic interactions [62], (5) a time step of 1.0 fs, (6) the SHAKE-bond-length constraints applied to all the bonds involving the H atom, (7) saving the image closest to the middle of the “primary box” to the restart and trajectory files, (8) formatted restart file, and (9) default values of all other inputs of the PMEMD module. These simulations were carried out on a cluster of 300 Apple Xserves each equipped with two G5 processors at a clock rate of 2.0/2.3 GHz.

Average structures were obtained by using the CARNAL module of the AMBER 5.0 program. Cluster analyses were performed by using the PTRAJ module of the AMBER 10 program [22]. RMSDs were calculated by using the McLachlan algorithm [63] as implemented in the ProFit program (V2.6, http://www.bioinf.org.uk/software/profit/). The CaRMSDs were obtained by (1) generating symmetry mates within 12 Å using PyMol 0.99rc6 [64], (2) identifying not-free residues that have a distance of <3.0 Å between any non-hydrogen atom of the structure in the primary cell and any non-hydrogen atom of the symmetry mates, (3) identifying hot residues that have alpha-carbon atoms with B factors greater than the average B factor for alpha carbons, (4) identifying short peptides with up to four residues that are between two hot residues, between two not-free residues, or between a hot and a not-free residue, (5) deleting the hot and not-free residues and the short peptides from the crystal structure and from the structure to be compared, and (6) computing the alpha-carbon RMSD of the truncated proteins using the ProFit program.

Supporting Information

Figure S1 Synthesis toward Analog 2.
Found at: doi:10.1371/journal.pone.0007730.s001 (0.21 MB PDF)

Figure S2 Synthesis toward Analog 6.
Found at: doi:10.1371/journal.pone.0007730.s002 (0.07 MB PDF)

Figure S3 Synthesis of Analog 3.
Found at: doi:10.1371/journal.pone.0007730.s003 (0.10 MB PDF)

References