

1 **Ambroxol Hydrochloride Inhibits the Interaction between Severe Acute Respiratory**  
2 **Syndrome Coronavirus 2 Spike Protein's Receptor Binding Domain and Recombinant**  
3 **Human ACE2.**

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## 34 **Abstract**

35           Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), the causative agent  
36 of coronavirus disease 2019 (COVID-19), enters the host cells through two main pathways, both  
37 involving key interactions between viral envelope-anchored spike glycoprotein of the novel  
38 coronavirus and the host receptor, angiotensin-converting enzyme 2 (ACE2). To date, SARS-  
39 CoV-2 has infected up to 26 million people worldwide; yet, there is no clinically approved drug or  
40 vaccine available. Therefore, a rapid and coordinated effort to re-purpose clinically approved  
41 drugs that prevent or disrupt these critical entry pathways of SARS-CoV-2 spike glycoprotein  
42 interaction with human ACE2, could potentially accelerate the identification and clinical  
43 advancement of prophylactic and/or treatment options against COVID-19, thus providing  
44 possible countermeasures against viral entry, pathogenesis and survival. Herein, we discovered  
45 that Ambroxol hydrochloride (AMB), and its progenitor, Bromhexine hydrochloride (BHH), both  
46 clinically approved drugs are potent effective modulators of the key interaction between the  
47 receptor binding domain (RBD) of SARS-CoV-2 spike protein and human ACE2. We also found  
48 that both compounds inhibited SARS-CoV-2 infection-induced cytopathic effect at micromolar  
49 concentrations. Therefore, in addition to the known TMPRSS2 activity of BHH; we report for the  
50 first time that the BHH and AMB pharmacophore has the capacity to target and modulate yet  
51 another key protein-protein interaction essential for the two known SARS-CoV-2 entry pathways  
52 into host cells. Altogether, the potent efficacy, excellent safety and pharmacologic profile of both  
53 drugs along with their affordability and availability, makes them promising candidates for drug  
54 repurposing as possible prophylactic and/or treatment options against SARS-CoV-2 infection.

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## 67 Introduction

68 The coronavirus disease 2019 (COVID-19) caused by severe acute respiratory syndrome  
69 coronavirus 2 (SARS-CoV-2) has emerged as a global pandemic and infected over 26 million  
70 individuals, with characteristics ranging from asymptomatic, mild, moderate to severe symptoms,  
71 with some people experiencing diverse multi-organ pathologies, substantial morbidity, and  
72 mortality<sup>1-4</sup>. Presently, there is no Food and Drug Administration (FDA) approved drug or vaccine  
73 available for treatment of COVID-19<sup>5</sup>. Although, there are several clinical studies investigating the  
74 possibility of repurposing existing clinically approved drugs as treatment options for COVID-19<sup>5-9</sup>;  
75 there still remains an urgent call for the rapid development of antiviral drugs for the prevention  
76 and/or treatment of COVID-19.

77 SARS-CoV-2 enters the host cells through two main pathways, both involving key  
78 interactions between viral envelope-anchored spike (S) glycoprotein of the novel coronavirus  
79 and the host receptor, angiotensin-converting enzyme 2 (ACE2), a membrane-bound  
80 metalloprotease<sup>10-13</sup>. The first pathway involves receptor mediated endocytosis process; while  
81 the second pathway, involves cell fusion also consisting of host receptor recognition and  
82 attachment of surface unit S1 to the peptidase domain of ACE2. Here, SARS-CoV-2 S protein is  
83 primed at the S1/S2 and the S2' site by a plasma membrane-associated type II transmembrane  
84 serine protease (TMPRSS2), which triggers fusion of viral and cellular membranes, an essential  
85 step for release of the viral contents into the host cell cytosol<sup>14,15</sup>. X-ray crystallography and  
86 structural studies of human ACE2 revealed two domains; the N-terminal zinc metallopeptidase  
87 domain (MPD), which binds to the viral receptor binding domain (RBD) within the S  
88 glycoprotein, and a C terminal "collectrin-like" domain<sup>16-18</sup>. The crucial interaction between the  
89 MPD of human ACE2 and RBD of SARS-CoV-2 S glycoprotein has been characterized as an  
90 initial and critical step in viral infection<sup>10-13</sup>. Therefore, repurposing clinically approved drugs that  
91 could potentially prevent or disrupt this key interaction between SARS-CoV-2 S glycoprotein  
92 and human ACE2, could accelerate the clinical advancement of prophylactic and/or treatment  
93 options against COVID-19, thus providing possible countermeasures against viral entry,  
94 pathogenesis and survival.

95 Ambroxol hydrochloride ((AMB) 4-[(2-amino-3,5-dibromophenyl) methylamino]cyclohexan-  
96 1-ol; hydrochloride)<sup>19</sup>, belonging to the benzylamine structural class, is a demethylated active  
97 metabolite of Bromhexine hydrochloride (BHH)<sup>20</sup>. Both AMB and its progenitor, BHH are widely  
98 prescribed drugs used to treat respiratory tract infections and disorders<sup>21-24</sup>, clinically indicated  
99 for their secretolytic activity for treatment of acute and chronic bronchopulmonary diseases

100 associated with abnormal mucus secretion and impaired mucus transport<sup>20,21,24</sup>. Traditionally,  
101 AMB and BHH have been available, affordable and used as over the counter drugs, with no  
102 significant adverse effects<sup>24,25</sup>. Furthermore, AMB and BHH have been extensively investigated in  
103 translational studies because of their multiple activities including mucociliary clearance activity,  
104 mucokinetic properties, stimulation of surfactant production, anti-inflammatory and antioxidative  
105 actions, and the local anesthetic effect<sup>22,23,26–28</sup>. More recent studies have shown that AMB and  
106 BHH both induce cellular autophagic-lysosome pathway<sup>29–31</sup>, critical processes in the host  
107 defense machinery against viral infections<sup>32</sup>. Additional studies have also shown the involvement  
108 of AMB in the modulation of homeostasis of ions such as, sodium, hydrogen, and calcium<sup>33</sup>.  
109 Moreover, AMB gained renewed interest as a potential drug for the clinical development of  
110 therapeutics for neurodegenerative diseases<sup>34</sup>, due to its potential to act as a chaperone, pH-  
111 dependent, mixed-type inhibitor of glucocerebrosidase (GCase), and its involvement in  
112 mechanisms for mitochondria, lysosomal biogenesis, and secretory pathway<sup>31, 33, 34</sup>. Other than  
113 the plethora of molecular impact and physiologic functions of the AMB pharmacophore mentioned  
114 above, reports have also shown that AMB could inhibit viruses that cause influenza and rhinovirus  
115 infections<sup>35,36</sup>. In addition, AMB's progenitor BHH is an established potent inhibitor of TMPRSS2<sup>37</sup>,  
116 one of the key proteases for viral fusion into host cells. BHH's activity against TMPRSS2 and lung  
117 protective properties makes it an attractive drug for the prevention and/or treatment of coronavirus  
118 infections<sup>38,39</sup>. To date, COVID-19 clinical trials investigating the impact of BHH (and/or in  
119 combination with other drugs) on SARS-CoV-2 infection are ongoing or completed in some  
120 countries [NCT04273763; NCT04340349; NCT04355026; NCT04424134; NCT04405999 and  
121 IRCT202003117046797N4]. However, the exact mechanism of action of the BHH and AMB  
122 pharmacophore against SARS-CoV-2 infection needs to be elucidated.

123 In this study, we evaluated the effects of AMB, and its progenitor, BHH, on the  
124 interaction between recombinant human ACE2 (rhACE2) and the RBD of the S protein of  
125 SARS-CoV-2. We also determined the effect of both compounds on SARS-CoV-2 infection-  
126 induced cytopathic effect (CPE) *in vitro* and assessed their cytotoxicity, in comparison to other  
127 clinically approved drugs. Herein, we discovered that AMB and BHH, effectively modulated the  
128 rhACE2's interaction with Spike (RBD) protein in the micromolar range. We also found that both  
129 compounds inhibited SARS-CoV-2 infection-induced CPE at certain concentrations. Therefore,  
130 in addition to the known TMPRSS2 activity of BHH<sup>37</sup>; we report for the first time that AMB and  
131 BHH pharmacophore have the capacity to target and modulate yet another key protein-protein  
132 interaction essential for the two known SARS-CoV-2 entry pathways in to human cells.  
133 Altogether, the potent efficacy, excellent safety and pharmacologic profile of both drugs along

134 with their affordability and availability, makes them promising candidates for drug repurposing  
135 as possible prophylactic and/or treatment options against SARS-CoV-2 infection.

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## 137 **MATERIALS AND METHODS**

### 138 **MATERIALS**

#### 139 **Cell Growth Conditions and Medium**

140 African Green Monkey Kidney Vero E6 cells (ATCC# CRL-1586, American Tissue Culture Type)  
141 were maintained using medium purchased from Gibco (modified eagle's medium (MEM) Gibco  
142 (#11095); 10% fetal bovine serum (HI FBS) Gibco (#14000); Penicillin/Streptomycin (PS) Gibco  
143 (#15140); 10U/mL penicillin and 10 $\mu$ g/mL streptomycin (only in assay media)). For the SARS-  
144 CoV-2 infection induced cytopathic effect (CPE) assay, cells were grown in MEM/10% HI FBS  
145 and harvested in MEM/1% PS/supplemented with 2% HI FBS. Cells were batch inoculated with  
146 SARS-CoV-2 USA\_WA1/2020 (M.O.I.  $\sim$  0.002) which resulted in 5-10% cell viability 72 hours  
147 post infection.

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#### 149 **Compounds and Preparation of Stock Solutions**

150 We prepared 10mM stocks solutions of the inhibitors in Dimethyl sulfoxide (DMSO; D8418-  
151 Lot#SHBL5613) purchased from Sigma Aldrich. Ambroxol Hydrochloride (AMB; A9797 - Lot #  
152 BCCB1637), and Bromhexine Hydrochloride (BHH; 17343 - Lot # BCBJ8156V) were also  
153 purchased from Sigma Aldrich. Both compound samples were serially diluted 2-fold in DMSO  
154 nine times and screened in duplicates for the SARS-CoV-2 infection induced cytopathic effect  
155 assay. The reference compounds used for the CPE and cytotoxicity assays were made  
156 available by SRI. Assay Ready Plates (ARPs; Corning 3764BC) pre-drugged with test  
157 compounds (90 nL sample in 100% DMSO per well dispensed using a Labcyte (ECHO 550)  
158 were prepared in the Biosafety Level-2 (BSL-2) laboratory by adding 5 $\mu$ L assay media to each  
159 well.

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#### 161 **Method for Measuring Antiviral Effect of AMB and BHH**

162 Southern Research Institute (SRI), located in Birmingham, Alabama performed the SARS-CoV-  
163 2 infection induced cytopathic effect (CPE) assay and cytotoxicity assays through a sub-contract  
164 from Texas Southern University, Houston, Texas. The CPE reduction assay was conducted  
165 using a high throughput-screening (HTS) format as previously described<sup>40,41</sup>. Specifically, Vero  
166 E6 cells selected for expression of the SARS-CoV-2 receptor (ACE2; angiotensin-converting  
167 enzyme 2) were used for the CPE assay. Cells were grown in MEM/10% HI FBS supplemented

168 and harvested in MEM/1% PS/ supplemented with 2% HI FBS. Cells were batch inoculated  
169 with SARS-CoV-2 (M.O.I. ~ 0.002) which resulted in 5% cell viability 72 hours post infection.  
170 Compound samples were serially diluted 2-fold in DMSO nine times and screened in duplicates.  
171 Assay Ready Plates (ARPs; Corning 3764 BC black-walled, clear bottom plates) pre-drugged  
172 with test compounds (90 nL sample in 100% DMSO per well dispensed using a Labcyte (ECHO  
173 550) were prepared in the BSL-2 lab by adding 5µL assay media to each well. The plates were  
174 passed into the BSL-3 facility where a 25µL aliquot of virus inoculated cells (4000 Vero E6  
175 cells/well) was added to each well in columns 3-22. The wells in columns 23-24 contained virus  
176 infected cells only (no compound treatment). Prior to virus infection, a 25µL aliquot of cells was  
177 added to columns 1-2 of each plate for the cell only (no virus) controls. After incubating plates at  
178 37°C/5%CO<sub>2</sub> and 90% humidity for 72 hours, 30µL of Cell Titer-Glo (Promega) was added to  
179 each well. Luminescence was read using a Perkin Elmer Envision or BMG CLARIOstar plate  
180 reader following incubation at room temperature for 10 minutes to measure cell viability. Raw  
181 data from each test well was normalized to the average (Avg) signal of non-infected cells (Avg  
182 Cells; 100% inhibition) and virus infected cells only (Avg Virus; 0% inhibition) to calculate %  
183 inhibition of CPE using the following formula: % inhibition = 100\*(Test Cmpd - Avg Virus)/(Avg  
184 Cells – Avg Virus). The SARS CPE assay was conducted in BSL-3 containment with plates  
185 being sealed with a clear cover and surface decontaminated prior to luminescence reading.

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#### 187 **Determination of Cytotoxic Effect of AMB and BHH**

188 The cytotoxicity of AMB and BHH were assessed in a BSL-2 counter screen using the Cell Titer-  
189 Glo Luminescent Cell Viability Assay as previously described<sup>41</sup>. Briefly, host cells in media were  
190 added in 25µL aliquots (4000 cells/well) to each well of assay ready plates prepared with test  
191 compounds as above. Cells only (100% viability) and cells treated with hyamine at 100µM final  
192 concentration (0% viability) serve as the high and low signal controls, respectively, for cytotoxic  
193 effect in the assay. DMSO was maintained at a constant concentration for all wells (0.3%) as  
194 dictated by the dilution factor of stock test compound concentrations. After incubating plates at  
195 37°C/5%CO<sub>2</sub> and 90% humidity for 72 hours, 30µl CellTiter Glo (CTG) (G7573, Promega) was  
196 added to each well. Luminescence was read using a BMG CLARIOstar plate reader following  
197 incubation at room temperature for 10 minutes to measure cell viability.

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#### 199 **SARS-CoV-2 Spike (RBD) Protein - ACE2 Interaction Assay**

200 We purchased the SARS-CoV-2 Spike - ACE2 binding assay kits (Cat # CoV-SACE2-1, Lot#  
201 062320 7066 and Lot# 081120 7066) from RayBiotech (Norcross, GA) and adapted the

202 manufacturer's protocol<sup>42</sup> to determine the effect of AMB and BHH on the interaction between  
203 SARS-CoV-2 Spike (RBD) Protein and recombinant human ACE2. The *in vitro* enzyme-linked  
204 immunoabsorbent assay (ELISA) was performed in a transparent flat-bottom 96-well plate. We  
205 prepared 10mM stock solutions of the compounds in Dimethyl sulfoxide (DMSO), with serially  
206 diluted the compounds in DMSO as follows: 100, 50, 10, 5, 1, 0.5, and 0.1  $\mu$ M for AMB and  
207 BHH. All experiments were performed in triplicates. Each plate contained positive controls (1%  
208 DMSO) and blank controls with no ACE2. Specifically, 1  $\mu$ L of serially diluted compounds were  
209 incubated with recombinant SARS-CoV-2 Spike receptor binding domain (RBD) protein, pre-  
210 coated on the 96 well plates in 49  $\mu$ L of 1X assay diluent buffer for about 30 mins, at room  
211 temperature (22°C) with shaking at 180 rpm. Then, we added 50  $\mu$ L of ACE2 protein in 1X  
212 assay diluent buffer into the 96 well plate, and incubated for 2.5 hrs at room temperature (22°C)  
213 with shaking at 180 rpm. Thereafter, the solution was discarded and the plate was washed  
214 consecutively four times with 300  $\mu$ L 1X wash buffer, followed by the addition of the detection  
215 antibody (anti-ACE2 goat antibody). The reaction was allowed to go on for 1 hr at room  
216 temperature (22°C) with shaking at 180rpm. Then, the solution was discarded and the wash  
217 step was repeated as described above. Next, the HRP-conjugated anti-goat IgG was added to  
218 each well, and the reaction plate was further incubated for 1 hr at room temperature (22°C) with  
219 shaking at 180rpm. Again, the solution was discarded and the wash step was repeated as  
220 described above. Then, 100 $\mu$ L of 3,3',5,5'-tetramethylbenzidine (TMB) one-step substrate was  
221 added to each well, and reaction mixtures were incubated in the dark at room temperature  
222 (22°C) with shaking at 180rpm for 30 mins. The reaction was stopped by the addition of 50  $\mu$ L  
223 stop solution. The absorbance was read at 405 nm using a Beckman Coulter DTX880  
224 multimode plate reader. The background hydrolysis was subtracted and the data was fitted to a  
225 special bell-shaped dose-response curve equation using GraphPad prism software 8.4.3.

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## 236 RESULTS

### 237 Effects of AMB and BHH on Spike (RBD) Glycoprotein and rhACE2 Interaction

238 The interaction of human ACE2 and the receptor binding domain (RBD) of the SARS-CoV-2 S  
239 protein has been reported as a critical step in viral infection for both the endocytosis and non-  
240 endocytosis pathways of viral entry into host cells<sup>10-15, 43</sup>. We evaluated the effect of AMB and  
241 its progenitor, BHH on the binding affinity of rhACE2 and RBD of SARS-CoV-2 S protein at  
242 concentrations ranging from 100  $\mu$ M to 100 nM, using an adapted *in vitro* enzyme-linked  
243 immunoabsorbent assay (ELISA)<sup>42</sup>. We observed a unique dose-response curve for both  
244 compounds (using the special bell shape curve model). AMB displayed the highest inhibition of  
245 S (RBD)-rhACE2 protein interaction at lower micromolar concentrations (ranging from 100nM to  
246 10 $\mu$ M); compared to higher concentrations of AMB from 50  $\mu$ M (Figure 1B). Interestingly, we  
247 found that BHH inhibited the binding of SARS-CoV-2's S (RBD) protein to rhACE2 receptor at  
248 lower concentrations ranging from 100 nM to 10  $\mu$ M; but enhanced the interaction at higher  
249 concentrations of BHH from 50  $\mu$ M (Figure 1A). Hence, the bell shaped model generated two  
250 IC<sub>50</sub> values (IC<sub>50\_1</sub> and IC<sub>50\_2</sub>) as shown in Table 4. Unlike BHH, we did not observe a stimulation  
251 or enhancement of binding of SARS-CoV-2's Spike (RBD) protein to rhACE2 receptor for its  
252 metabolite – AMB, at the concentrations we tested. However, using the bell curve model, the  
253 graphpad software generated a second IC<sub>50\_2</sub> at 232  $\mu$ M for AMB, greater than the highest  
254 concentration tested (100  $\mu$ M). Moreover, the unconventional dose response curve observed in  
255 this protein interaction assay, could be intrinsic to the mode of inhibition or an indicator of  
256 additional binding site(s) and/or target(s), for the BHH and AMB, such as other sites on rhACE2  
257 or the Spike (RBD) protein. To our knowledge, these finding is the first report to reveal that AMB  
258 inhibits and interferes with the binding between rhACE2 receptor and SARS-CoV-2 S (RBD)  
259 glycoprotein *in vitro*; while BHH inhibits this critical interaction at lower concentrations and  
260 enhances at higher concentrations (Table 4). These results suggest that AMB might be a  
261 promising lead for clinical development of novel SARS-CoV-2 entry inhibitors and potential  
262 COVID-19 therapeutics (Figure 2). Altogether, these results reveal a new pharmacologic mode  
263 of action and novel target for AMB and its progenitor, BHH.

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### 265 Efficacy of Ambroxol Hydrochloride (AMB) and Bromhexine Hydrochloride (BHH) against 266 SARS-CoV-2 infection induced Cytopathic Effect (CPE) in Vero E6 cells.

267 The rapid identification and repurposing of clinically approved drugs with antiviral activity against  
268 SARS-CoV-2 infection could potentially accelerate their consideration as potential treatment  
269 options for COVID-19. Here in, we evaluated the *in vitro* antiviral activity of AMB, and its



270 progenitor, BHH, using a standard luminescent-based high-throughput screening (HTS)  
271 platform<sup>40,41</sup> for SARS-CoV-2 infection induced CPE in African Green Monkey Kidney Vero E6  
272 cells. We found that, BHH inhibited SARS-CoV-2 infection induced CPE *in vitro* with 50%  
273 Inhibitory Concentration (IC<sub>50</sub>) value at about 21.72 µM; while AMB's IC<sub>50</sub> was greater than 30  
274 µM, the highest concentration tested (Table 1). At this maximum concentration, AMB displayed  
275 14.25% inhibition of SARS-CoV-2 induced CPE. Compared to its metabolite; BHH exhibited the  
276 highest maximum inhibition at about 91.08% inhibition at 30 µM (Table 1). Additional higher  
277 concentrations need to be tested in future studies to determine the actual IC<sub>50</sub> value of AMB  
278 against SARS-CoV-2 infection induced CPE in Vero E6 cells. Furthermore, we compared the  
279 antiviral effects of AMB and BHH with five other known inhibitors of SARS-CoV-2 *in vitro*:  
280 Calpain Inhibitor IV, Chloroquine, Remdesivir, Hydroxychloroquine and Aloxistatin. We found  
281 that the IC<sub>50</sub> for most of the reference compounds (Calpain Inhibitor IV (0.29µM), Chloroquine  
282 (3.56µM), Hydroxychloroquine (5.16µM), Remdesivir (8.54µM)) were lower than the IC<sub>50S</sub> values  
283 for BHH and AMB. However, the IC<sub>50</sub> of Aloxistatin (21.78 µM) was similar to that of BHH (21.72  
284 µM) (Table 1 and 2). The IC<sub>50</sub> values that we observed for the reference compounds are  
285 consistent with earlier reports<sup>44-47</sup>. While writing this manuscript, we found that other cellular  
286 studies tested BHH and AMB at certain or single concentrations<sup>48-50</sup>; however, this is the first  
287 study to our knowledge to conduct the IC<sub>50</sub> evaluation for BHH and AMB against the novel  
288 SARS-CoV-2 infection induced CPE.

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### 290 **Cytotoxicity Effects of AMB and BHH in Vero E6 cells.**

291 Using a Cell Titer-Glo Luminescent Cell Viability Assay<sup>41</sup>, we determined the cytotoxicity of AMB  
292 and BHH. We also assessed the cytotoxic effects of the reference compounds in Vero E6 cells  
293 and observed that, the 50% cytotoxic concentration (CC<sub>50</sub>) of AMB and BHH were greater than  
294 30 µM. In comparison to the other reference compounds tested, AMB and BHH displayed  
295 slightly higher percent maximum and minimum viability at the concentrations tested (Table 3).  
296 Between the two compounds, we observed a higher percent minimum viability for AMB  
297 (113.95%), compared to its progenitor, BHH (103.87%) at 30 µM (Table 3). These cytotoxicity  
298 results are consistent with the known clinical safety profiles of both compounds, with AMB  
299 showing better pharmacokinetic and safety profiles compared to BHH<sup>51</sup>.

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## 304 DISCUSSION

305 The emergence of novel SARS-CoV-2 strains has imposed an urgent call to accelerate the  
306 repurposing and advancement of existing clinically safe and approved drugs as effective  
307 prophylactic and/or therapeutic agents for combating the COVID-19 pandemic. The crystal  
308 structure of full length human ACE2 revealed that the RBD on SARS-CoV-2 S1 binds directly to  
309 the metallopeptidase domain (MPD) of ACE2 receptor<sup>10-13</sup>. In this study, we explored the  
310 possibility of a clinically safe and approved drug, AMB and its progenitor, BHH as potential  
311 effectors of the interaction between SARS-CoV-2's Spike protein receptor binding domain and  
312 recombinant human ACE2 receptor, a critical first step in the two significant pathways required  
313 for viral entry into host cells<sup>10-15,43</sup> and initiation of pathogenesis (Figure 2). Using a sensitive  
314 ELISA<sup>42</sup>, we found that AMB and its progenitor, BHH modulates the interaction of rhACE2 and S  
315 (RBD) protein, with AMB being the most potent effector. Significant inhibition of the interaction  
316 between SARS-CoV-2's S (RBD) protein and rhACE2 by AMB at nanomolar to micromolar  
317 concentrations provides strong evidence that this pharmacophore could serve as a promising  
318 lead for the discovery and clinical development of novel SARS-CoV-2 entry inhibitors and  
319 potential COVID-19 therapeutics. On the other hand, we found that BHH, enhances this key  
320 interaction between Spike (RBD) protein and rhACE2 at higher concentrations; while inhibiting  
321 at lower concentrations. To our knowledge, this is the first experimental study revealing this  
322 class of compounds as potent effectors of the binding of Spike (RBD) protein to rhACE2, a new  
323 pharmacologic mode of action for potentially modulating viral entry into host cells. *In vivo*  
324 pharmacodynamics and pharmacokinetic studies are warranted to further explore the  
325 physiologic relevance of the inhibitory activity of AMB, as well as the dual inhibitory and  
326 enhancement activities of BHH in the context of SARS-CoV-2 infection.

327 Our findings regarding the "paradoxical behavior" of BHH *in vitro* biochemical assay, are  
328 consistent with a recent report by Hörnich, B.F. et. al., that revealed that BHH enhanced SARS-  
329 CoV-2 S-mediated fusion in 293T cells at the concentrations tested<sup>48</sup>. Moreover, the  
330 unconventional dose-response curve that we observed in our interaction studies suggests that  
331 there may be more than one binding site for interaction of rhACE2 and Spike (RBD) protein for  
332 BHH and its metabolite-AMB, resulting in the potent inhibition of interaction at lower micromolar  
333 concentrations; compared to the impact at higher concentrations. This may also explain the  
334 enhancement of interaction by BHH at higher concentrations. Interestingly, a molecular dynamic  
335 study by Silva de Souza et al.<sup>52</sup>, revealed that two different regions within the RBD of SARS-CoV-  
336 2 interact differently with hACE2 in the presence of high salt concentrations (E1, is more  
337 hydrophobic; while E2 favors more polar interactions). Hence, suggesting that these differences

338 may impact how effectors modulate these sites and affect the binding between RBD to hACE2.  
339 Future computational modeling and X-ray co-crystallization studies of the compounds with  
340 rhACE2 and Spike (RBD) may provide additional insight into the mode of inhibition (for AMB)  
341 and/or enhancement in the case of BHH. Besides, this will facilitate the rational design of novel  
342 drugs that could inhibit this interaction and in turn, prevent viral entry into human cells. In addition,  
343 synthesis of more potent inhibitors in the AMB-containing, benzylamine structural class and SAR  
344 studies could accelerate the discovery of novel anti-SARS-CoV-2 agents.

345 Furthermore, we investigated the effect of AMB and BHH on SARS-CoV-2 infection  
346 induced CPE *in vitro*, using a simple and rapid cellular high throughput screening assay<sup>40,41</sup>.  
347 Although, AMB was found to be the most potent against rhACE2-RBD interaction in the  
348 biochemical assay compared to BHH; however, in the cellular CPE assay, AMB had a higher IC<sub>50</sub>  
349 than BHH for antiviral activity. Additionally, we observed that the IC<sub>50</sub> values of the compounds in  
350 the cellular CPE assay were much higher than the IC<sub>50s</sub> in the rhACE2-Spike(RBD) protein  
351 interaction assay, although the special bell curve model produced two IC<sub>50s</sub> due to the mode of  
352 inhibition at lower concentrations versus higher concentrations. Therefore, *in vivo*  
353 pharmacokinetic and pharmacodynamics studies will be required to ascertain half maximal  
354 effective concentrations (EC<sub>50</sub>) for both drugs. Consistent with our study, a high throughput screen  
355 of clinically approved drugs by Tourte et. al.<sup>50</sup> also identified AMB as an inhibitor of SARS-CoV-2  
356 infection *in vitro* at 10 µM. Our findings for percent inhibitions for AMB in the CPE assay in Vero  
357 E6 cells are also consistent with a recent study by Bradfute, S.B. et. al.<sup>49</sup>, in which they reported  
358 that AMB could inhibit SARS-CoV-2 infection *in vitro* at high concentrations<sup>49</sup>. Our biochemical  
359 findings are most complementary to the report by Hornich, B.F. et. al., that observed inhibition of  
360 SARS-CoV-2-S-mediated fusion in the presence of 50 µM AMB<sup>48</sup>; but observed a dose  
361 dependent enhancement of SARS-CoV-2-S-mediated fusion by BHH at the concentrations  
362 tested<sup>48</sup>. Furthermore, a computational transcriptomics study by Napolitano, F. et al.<sup>53</sup>, found that  
363 AMB induced an opposite transcriptional profile compared to that induced by SARS-CoV-2  
364 infection *in vitro*, suggesting that it may be playing a role in counteracting viral infection<sup>53</sup>.  
365 Altogether, our findings provide a novel protein-protein interaction target and strong supporting  
366 evidence that may explain the mechanism of action for the AMB and BHH pharmacophore (Figure  
367 2).

368 In addition, we conducted a comparative analysis of the dose-response curves of antiviral  
369 activity and cytotoxicity of AMB and BHH with five other known inhibitors of SARS-CoV-2 *in vitro*,  
370 which we refer to as “reference compounds.” We found that the IC<sub>50</sub> range for BHH and AMB were  
371 similar to that of Aloxistatin (Table 1 and 2); but higher than the other reference compounds,

372 namely, Chloroquine, Hydroxychloroquine, Remdesivir, and Calpain Inhibitor IV. On the other  
373 hand, when we assessed the cytotoxicity of AMB and BHH in Vero E6 cells, we observed that  
374 both compounds displayed higher percent maximum and minimum viability at the concentrations  
375 tested (Table 3) compared to the other reference compounds. Moreover, AMB had a slightly  
376 higher percent minimum viability compared to BHH, consistent with other reported safety studies  
377 for both compounds, that demonstrate that AMB has superior safety profile than BHH<sup>51</sup>. Thus,  
378 considering that AMB is safe and clinically approved, our findings that AMB significantly inhibited  
379 binding of rhACE2 receptor with SARS-CoV-2 Spike (RBD) protein and moderately inhibited  
380 SARS-CoV-2 infection induced CPE at the concentration tested, strongly supports the notion that  
381 AMB could be a safe drug option for the clinical advancement of counter measures against  
382 COVID-19. In addition, AMB and its progenitor – BHH, could be used as chemical probes to study  
383 the biology of host-pathogen interaction in the context of SARS-CoV-2 infections, particularly in  
384 the pre-clinical development of novel entry inhibitors. Our findings not only provides strong *in vitro*  
385 evidence and mechanism, for the proposed use of AMB as a therapeutic option for the treatment  
386 of COVID-19; but also sheds light on the relevance of this pharmacophore as potential  
387 prophylactic options for prevention of SARS-CoV-2 infection.

388 Both AMB and BHH have been used in the clinic for treatment of respiratory conditions  
389 and are extensively studied, because of their multiple pharmacologic effects and safety profile<sup>20-24</sup>.  
390 In addition to their impact on lung physiology and function with regards to mucociliary clearance,  
391 mucokinetic properties, and stimulation of surfactant production, they have also been shown to  
392 elicit anti-inflammatory, antioxidative and anesthetic effects<sup>20-24</sup>. Additional studies have reported  
393 that both compounds induce cellular autophagic-lysosome pathway<sup>29-31</sup>. Reports have also  
394 shown the involvement of AMB in modulation of the homeostasis of ions such as sodium,  
395 hydrogen, and calcium<sup>33, 51</sup>. Additionally, AMB has gained attention clinically as a potential drug to  
396 repurpose for treatment of neurodegenerative diseases<sup>31, 34</sup>. Moreover, AMB is known to inhibit  
397 certain viruses *in vitro* and *in vivo*, with one proposed mechanism as that of preventing the  
398 release of RNA into the cytoplasm by increasing the endosomal pH<sup>35,36</sup>. This may suggest the  
399 possibility of additional mechanisms of action beyond viral entry pathways, that is, post-entry of  
400 virus into host cells. Given the ongoing COVID-19 pandemic and the lack of clinically approved  
401 vaccine or drugs; AMB and its progenitor, BHH could be possible drug leads, because of earlier  
402 reports of BHH's inhibitory activity against TMPRSS2 at low micromolar concentrations<sup>37</sup>.  
403 However in a recent study, unlike Camostat, another known TMPRSS2 inhibitor; AMB and BHH  
404 did not reverse TMPRSS2-mediated enhancement of SARS-CoV-2 infection in 293Tcells<sup>48</sup>.  
405 Suggesting that AMB and BHH, may have additional modes/sites of action<sup>48</sup>. Hence, our finding

406 that AMB and BHH is an effector of the RBD-rhACE2 interaction could shed more light on the  
407 mode of SARS-CoV-2 inhibition.

408 The clinical advancement of the AMB pharmacophore could potentially accelerate their  
409 consideration for repurposing as potential antiviral agents against COVID19, in non-human  
410 primate (NHP) models of SARS-CoV-2 infection, and in clinical trials. Ongoing COVID19 clinical  
411 trials [NCT04273763; NCT04340349; and NCT04355026; NCT04424134; NCT04405999]  
412 investigating the impact of BHH use prophylactically and/or for treatment in combination therapy  
413 for SARS-CoV-2 infection may provide more insight on the relevance of this pharmacophore in  
414 counteracting viral entry, pathogenesis and survival. To date, the only published clinical trials  
415 results of BHH, is that of a completed open-label randomized clinical trial conducted in Tabriz,  
416 North West of Iran<sup>54</sup>. This small sample-size study, revealed that early administration of oral BHH  
417 decreases the intensive care unit transfer, intubation, and the mortality rate in patients with  
418 COVID-19<sup>54</sup>. Additional large scale and multi-country trials are needed to assess and ascertain  
419 the effect of BHH and/or AMB on clinical outcomes and mortality in COVID-19 patients. Moreover,  
420 previous studies by others have shown that both AMB and BHH could enhance the lung levels of  
421 certain antibiotics when used in combination<sup>29,30</sup>, suggesting that combination therapy with other  
422 known antimicrobials with antiviral activity against SARS-CoV-2 could be explored in COVID-19  
423 clinical studies. Therefore, we propose the clinical evaluation and comparative analysis of the  
424 impact of AMB or BHH (or in combination with other available therapeutics) to reduce COVID19  
425 morbidity and mortality.

426 Overall, the abundance of clinical evidence on the pharmacologic spectrum of activity of  
427 AMB, combined with its extensive clinical safety profile, affordability and availability, makes this  
428 an attractive and promising drug for targeting the binding of SARS-CoV-2 Spike (RBD) to  
429 rhACE2, an essential biologic interaction for viral entry into host cells<sup>10-13</sup>. The unique potential  
430 of AMB and/or BHH in modulating the two currently known viral entry pathways, makes this  
431 pharmacophore promising as possible prophylactic agents against SARS-CoV-2 infection. One  
432 of the main strengths of our study is the use of a rapid and sensitive ELISA, to identify and  
433 characterize two existing clinical drugs as novel inhibitors of the critical interaction between  
434 SARS-CoV-2 Spike (RBD) protein and rhACE2. However, our study has some limitations such  
435 as the use of Vero E6 cells that were selected for high expression of human ACE2 in the  
436 antiviral assay<sup>40,41</sup>. Besides, future studies exploring structural activity relationship (SAR) with  
437 derivatives of AMB, with a similar pharmacophore, improved efficacy and similar/better safety  
438 profile, will facilitate the discovery and pre-clinical development of new chemical molecules as  
439 potential options for COVID-19 prevention and/or treatment. SAR studies will also provide

440 additional insight into the mode of action of this pharmacophore and aid in the rational  
441 design/discovery of new countermeasures against SARS-CoV-2 infection.

442

#### 443 **CONCLUSION AND SIGNIFICANCE**

444 Repurposing clinically approved drugs with novel mechanisms of action and/or multiple  
445 cellular targets could potentially disrupt viral pathogenesis, survival and/or prevent the viral entry  
446 and interaction with host receptor, ACE2. This approach to drug discovery could accelerate the  
447 clinical development of anti-COVID-19 prophylactics/treatments, thus providing  
448 countermeasures against COVID-19 and its impact on population health, healthcare systems,  
449 and the global economy<sup>55</sup>. Our novel findings of AMB and BHH as modulators of the binding of  
450 rhACE2 with SARS-CoV-2 Spike (RBD) protein provide new insights into the mode of action  
451 and additional molecular target(s) for AMB and its progenitor, BHH. Thus, validating this  
452 chemical class as promising leads for clinical development of novel SARS-CoV-2 entry  
453 inhibitors that could be used for potential COVID-19 prevention and/or treatment. Additionally,  
454 because these pharmacophore was shown earlier to have activity against TMPRSS2; and now  
455 we found that it inhibits rhACE2-RBD interaction, thus, probably targeting more than one  
456 protein. Therefore, this pharmacophore represents a favorable drug class that could possibly  
457 be studied as lead series in the development of countermeasures for limiting SARS-CoV-2 drug  
458 resistance in the future. Also its clinical efficacy as a secretolytic and anti-inflammatory agent  
459 makes it a promising drug for COVID-19 treatment due to lung injury. Therefore, we propose  
460 additional pharmacologic and clinical studies to further explore AMB and/or its derivatives as  
461 prophylaxis and/or treatment options in the toolbox for combating this novel coronavirus.

462

463 **Author Contributions:** OAO conceived the study and performed biochemical experiments  
464 (rhACE2-Spike (RBD) protein interaction experiments); OAO and MK performed experimental  
465 design, data analysis and interpretations. OAO and MK wrote the manuscript. CCO created  
466 Figure 2a and 2b and helped to thoroughly review and edit the manuscript.

467

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470

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485 [19.pdf?sfvrsn=96b04adf\\_4](https://www.who.int/docs/default-source/coronaviruse/situation-reports/20200306-sitrep-46-covid-19.pdf?sfvrsn=96b04adf_4)
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646  
647 **Tables and Figures** (See attached)

648  
649 **Table 1.** Chemical Structure and Activity of Ambroxol Hydrochloride (AMB) and Bromhexine  
650 Hydrochloride (BHH) against SARS-CoV-2 induced Cytopathic Effect (CPE) in Vero E6 Cells.

651  
652 **Table 2.** Chemical Structure and Activity of Reference Inhibitors against SARS-CoV-2 induced  
653 Cytopathic Effect (CPE) in Vero E6 Cells.

654  
655 **Table 3.** Cytotoxicity of Ambroxol Hydrochloride (AMB) and Bromhexine Hydrochloride (BHH) in  
656 Vero E6 Cells, in Comparison to Reference Inhibitors of SARS-CoV-2.

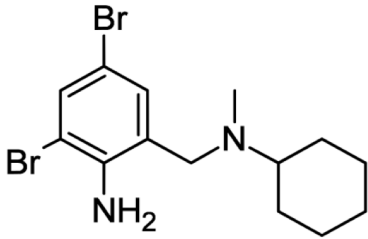
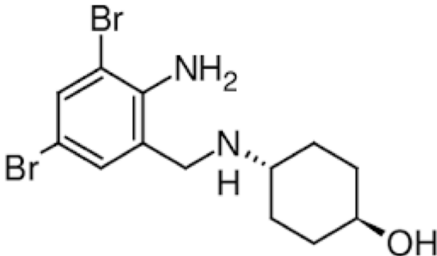
657  
658 **Table 4.** Activity of Ambroxol Hydrochloride (AMB) and Bromhexine Hydrochloride (BHH)  
659 against rhACE2 and SARS-CoV-2 Spike (RBD) protein Interaction.

660  
661 **Figure 1.** Effect of Bromhexine Hydrochloride (BHH) and Ambroxol Hydrochloride (AMB) on the  
662 interaction of rhACE2 with SARS-CoV-2 Spike (RBD) protein Interaction: A. BHH, and B. AMB.

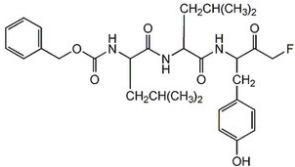
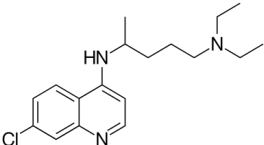
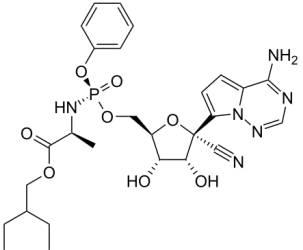
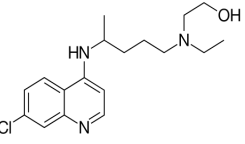
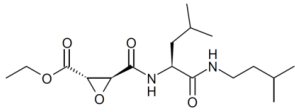
663  
664 **Figure 2.** Schematic diagram depicting SARS-CoV-2 Spike (RBD) protein interaction with  
665 human ACE2 receptor at the cellular membrane, and inhibition of the two entry pathways of  
666 virus into host cells by Ambroxol Hydrochloride (AMB) and Bromhexine Hydrochloride (BHH)  
667 pharmacophore: A. TMPRSS2 mediated pathway, and B. Endosomal pathway activated by  
668 Cathepsin L.

669  
670  
671

**Table 1.** Chemical Structure and Activity of Ambroxol Hydrochloride (AMB) and Bromhexine Hydrochloride (BHH) against SARS-CoV-2 induced Cytopathic Effect (CPE) in Vero E6 Cells.

Inhibitor ID	Screen ID	Chemical Structure		IC <sub>50</sub> (μM)	Maximum Inhibition at 30μM (%)
BHH	MDXC19T009		HCl	21.72	91.08
AMB	MDXC19T010		HCl	>30	14.25

**Table 2.** Chemical Structure and Activity of Reference Inhibitors against SARS-CoV-2 induced Cytopathic Effect (CPE) in Vero E6 Cells.

Inhibitor ID	Screen ID	Chemical Structure	IC <sub>50</sub> (μM)	Maximum Inhibition (%)	Concentration at Maximum % Inhibition (μM)
CalpainInhibitorIV	AB01968659		0.29	104.68	0.90
Chloroquine	AB00053436		3.56	151.80	30.00
Remdesivir	AB01952209		8.54	105.89	30.00
Hydroxychloroquine	AB00053257		5.16	101.28	15.00
E64d (Aloxistatin)	AB01955411		21.78	57.09	30.00

**Table 3.** Cytotoxicity of Ambroxol Hydrochloride (AMB) and Bromhexine Hydrochloride (BHH) in Vero E6 Cells, in Comparison to Reference Inhibitors of SARS-CoV-2.

Inhibitor ID	Cytotoxicity CC <sub>50</sub> (μM)	Minimum Viability (%)	Concentration at Minimum % Viability (μM)	Maximum Viability (%)	Concentration at Maximum % Viability (μM)
BHH	>30.00	103.87	30.00	133.17	0.12
AMB	>30.00	113.95	30.00	124.37	1.88
CalpainInhibitorIV	>7.17	97.74	7.17	113.22	0.45
Chloroquine	>30.00	93.52	30.00	111.43	0.06
Remdesivir	>30.00	101.07	0.120	109.76	15.00
Hydroxychloroquine	>30.00	96.10	0.470	105.31	0.12
E64d (Aloxistatin)	>30.00	97.45	30.000	104.15	0.47

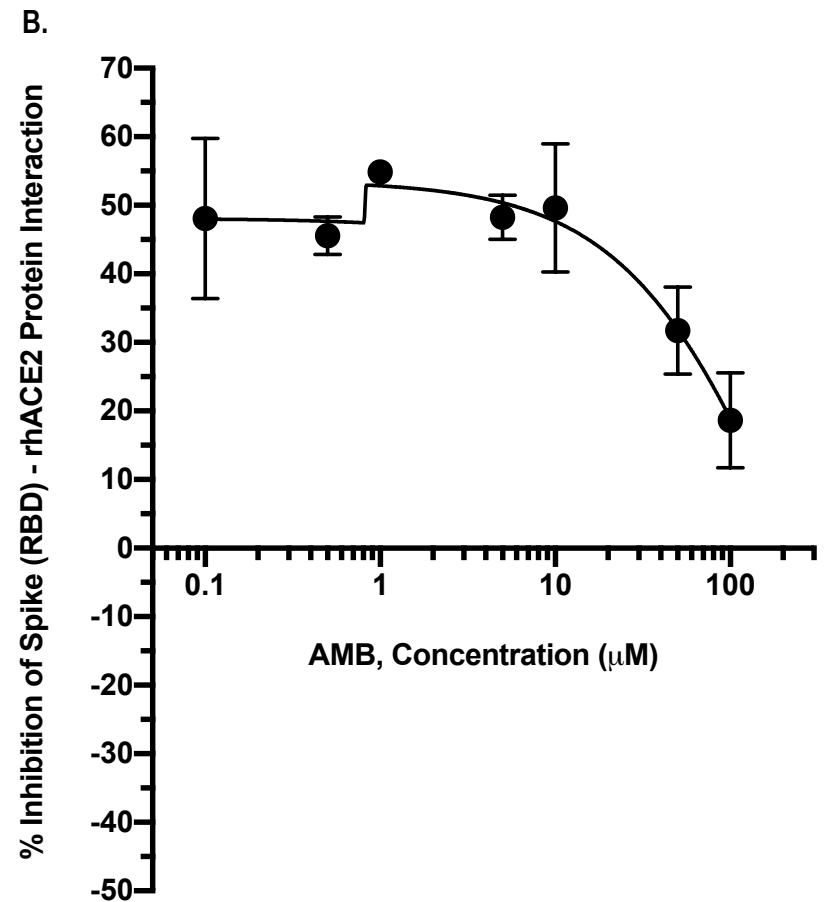
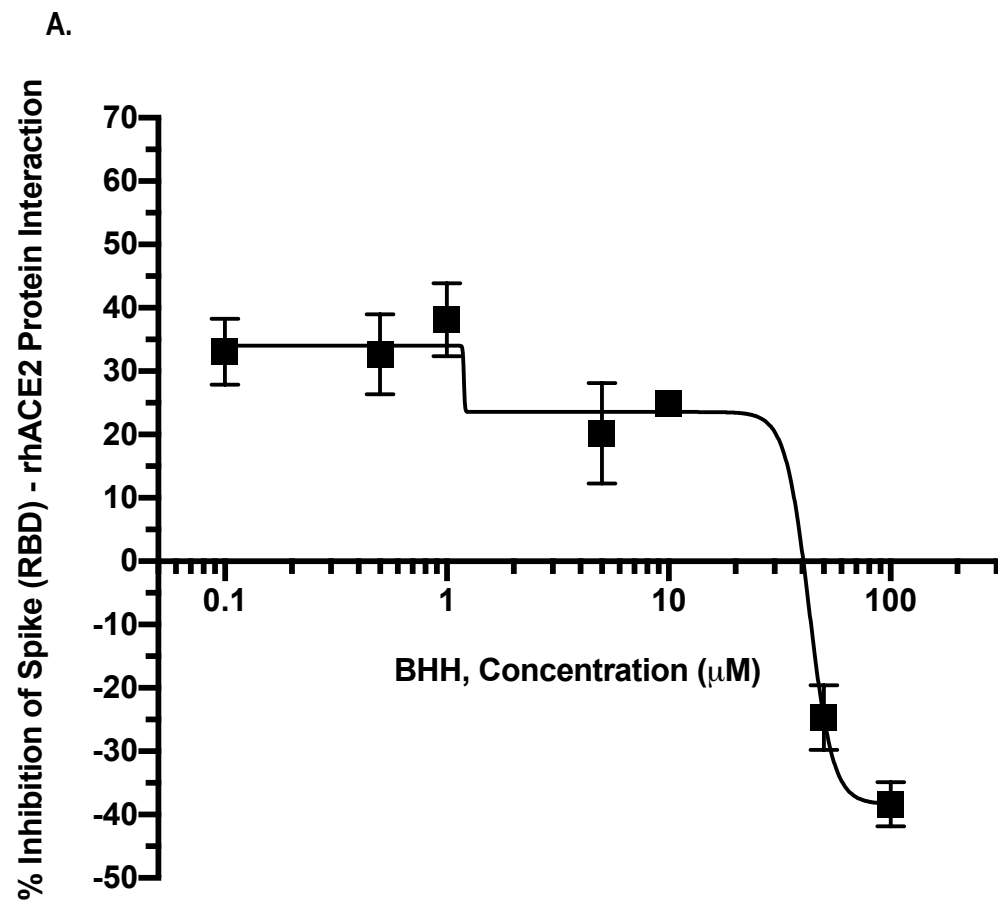
**Table 4.** Activity of Ambroxol Hydrochloride (AMB) and Bromhexine Hydrochloride (BHH) against rhACE2 and SARS-CoV-2 Spike (RBD) protein Interaction.

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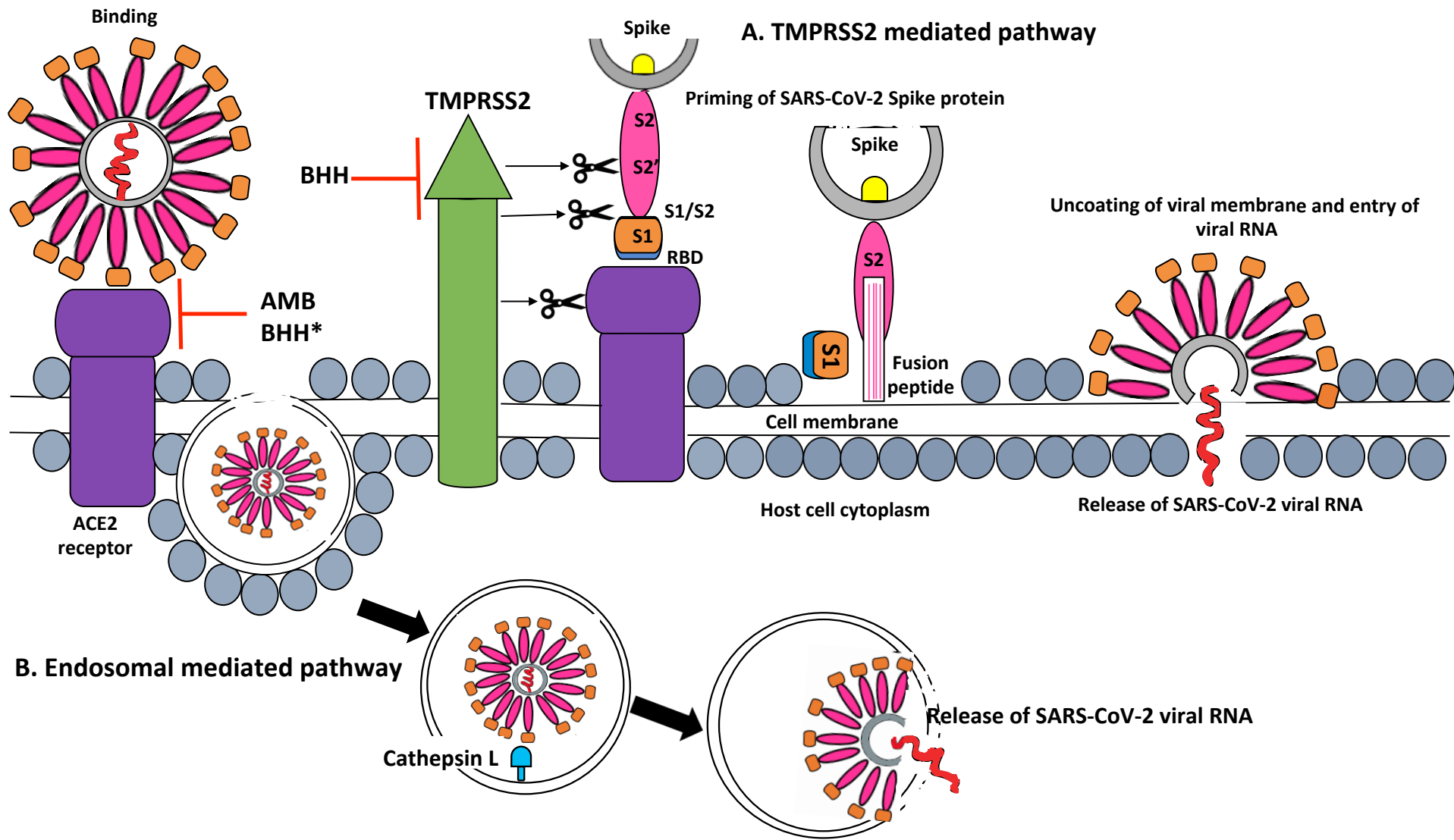
<b>Estimated Relative IC<sub>50</sub> (μM) for Spike (RBD)-rhACE2 Protein Interaction Assay</b>		
<b>Inhibitor ID</b>	<b>IC<sub>50_1</sub> (μM)</b>	<b>IC<sub>50_2</sub> (μM)</b>
BHH	1.19	42.90
AMB	0.82	231.60

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**Figure 1.** Effect of Bromhexine Hydrochloride (BHH) and Ambroxol Hydrochloride (AMB) on the interaction of rhACE2 with SARS-CoV-2 Spike (RBD) protein Interaction: A. BHH, and B. AMB.



**Figure 2.** Schematic diagram depicting SARS-CoV-2 Spike (RBD) protein interaction with human ACE2 receptor at the cellular membrane, and inhibition of the two entry pathways of virus into host cells by Ambroxol Hydrochloride (AMB) and Bromhexine Hydrochloride (BHH) pharmacophore: A. TMPRSS2 mediated pathway, and B. Endosomal pathway activated by Cathepsin L. \*At high concentrations, BHH was shown to also enhance the interaction between recombinant hACE2 and SARS-CoV-2 Spike (RBD) protein.