

# Design and synthesis of 1-(4-benzoylphenyl)imidazole derivatives as new potent 20-HETE synthase inhibitors

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**Abstract**—Structural modification of the novel 20-HETE synthase inhibitor **1** ( $IC_{50}$  310 nM) is described. Introduction of a side chain with a carboxylic acid at the terminal position to **1** resulted in increased ability to inhibit human renal microsomal production of 20-HETE (**7c**:  $IC_{50}$  7.9 nM), with good selectivity toward CYP2D6 and cyclooxygenases (COX)-1 and -2.  
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20-Hydroxy-5,8,11,14-eicosatetraenoic acid (20-HETE) is a major metabolite of arachidonic acid (AA) produced in the kidney.<sup>1</sup> Its biological properties have recently been extensively studied. The formation of 20-HETE from AA is catalyzed by cytochrome P450 (CYP) 4A isozymes (CYP4A1, 4A2, 4A3, and 4A8) in rat kidney<sup>2</sup> and cerebral artery,<sup>3</sup> and by CYP4A11 and 4F2 in human liver and kidney.<sup>4</sup> 20-HETE plays an important role in the regulation of vascular and tubular functions in kidneys and the regulation of vascular tone in the brain.<sup>3,5–7</sup> Therefore, 20-HETE is now considered to be a promising new target for the treatment of renal and cerebrovascular diseases. Several nonspecific 20-HETE synthase inhibitors such as 1-aminobenzotriazole (1-ABT),<sup>8</sup> and suicide-type inhibitors such as 17-octadecynoic acid (17-ODYA),<sup>9</sup> *N*-methylsulfonyl-12,12-dibromododec-11-enamide (DDMS), 12,12-dibromododec-11-enoic acid (DBDD),<sup>10</sup> and sodium 10-undecynyl sulfate (10-SUYS)<sup>11</sup> have been reported, however they received only limited therapeutic evaluation (Fig. 1).

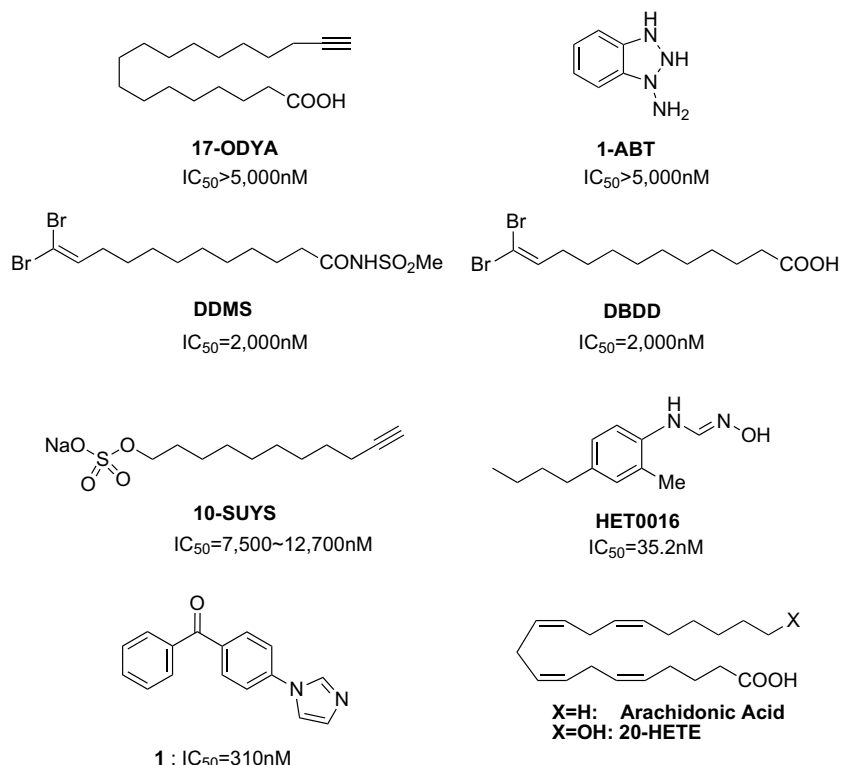
We previously described the evaluation of *N*-hydroxyphenylformamidinium derivative HET0016 (Fig. 1) as a selective 20-HETE synthase inhibitor.<sup>12–15</sup> We describe here an evaluation of phenylimidazole derivative **1**, which was obtained along with HET0016 by random

screening of our in-house chemical library (Fig. 1). AA is metabolized to 20-HETE by oxidation of the  $\omega$ -carbon atom with the oxygen atom coordinated to the heme iron atom of 20-HETE synthases. Accordingly, compound **1** should inhibit 20-HETE synthase activity through coordination of its imidazole ring to the active-site heme iron atom of the enzyme, as with well-known azole CYP inhibitors. On the other hand, AA has a characteristic carboxylic acid moiety opposite the hydrophobic terminal, which is recognized by 20-HETE synthase. Therefore, to improve the potency and selectivity of **1**, we examined the introduction of a carboxy moiety with a suitable linkage to the site opposite the imidazole ring of compound **1**.

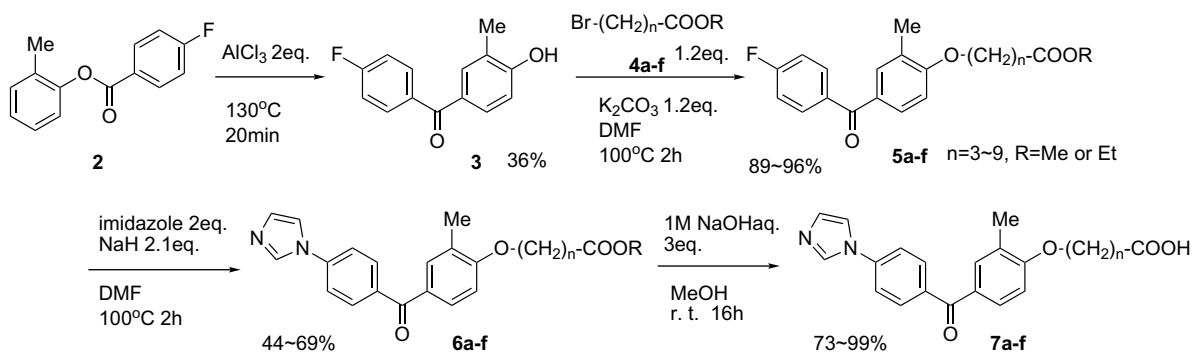
Introduction of a carboxy side chain to the 4- and 6-positions of **1**, which may correspond to the expanded and folded conformations of AA,<sup>16</sup> was accomplished by Fries rearrangement of the *o*- and *p*-cresol 4-fluorobenzoate (**2** and **8**) followed by introduction of an imidazole ring and carboxyalkyl moiety (Schemes 1 and 2). Heating of **2** with powdered aluminum chloride without solvent<sup>17</sup> gave the benzophenone derivative **3**. Alkylation of **3** by  $\omega$ -bromoalkanoates **4a–f** with potassium carbonate in dimethylformamide at 100 °C gave the corresponding esters **5a–f**. Subsequent treatment of **5a–f** with imidazole and sodium hydride in dimethylformamide at 100 °C gave the corresponding imidazole derivatives **6a–f**. The ester group of **6a–f** was hydrolyzed by 1 M sodium hydroxide solution in methanol at room temperature to give the carboxylic acids or sodium salts

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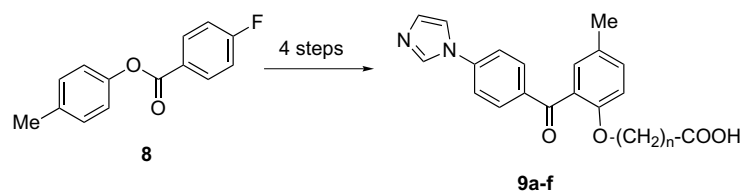
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**Figure 1.** Structures of reported 20-HETE synthase inhibitors and compound **1**.  $IC_{50}$  values are for the production of 20-HETE from AA by rat renal microsome.



**Scheme 1.**

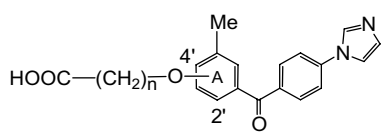


**Scheme 2.**

**7a–f.** Corresponding 2'-carboxyalkyl derivatives **9a–f** were prepared from *p*-cresol ester **8** in the same way.

Introduction of a  $\omega$ -carboxyalkoxy moiety with 3–9 methylene groups to the 4'-position of compound **1** (**7a–f**) enhanced the 20-HETE synthase inhibitory activ-

ity 4- to 40-fold (Table 1). However, introduction of the same moieties at the 2'-position (**9a–f**) resulted in a great loss of activity (1/8 to less than 1/30). These results suggest that the region around the 2'-position of compound **1** is spatially limited in the coordination to 20-HETE synthase. The length of the carboxyalkoxy moiety of

**Table 1.** Inhibitory activities of **7a–f** and **9a–f** toward 20-HETE synthase


No.	n	IC <sub>50</sub> (nM) <sup>a</sup>	
		7	9
<b>a</b>	3	13 <sup>b</sup>	>10,000
<b>b</b>	4	12	8384
<b>c</b>	5	7.9 <sup>b</sup>	3290
<b>d</b>	6	22	2461
<b>e</b>	7	44	4797
<b>f</b>	9	73 <sup>b</sup>	6743

<sup>a</sup> IC<sub>50</sub> value for the production of 20-HETE from AA by human renal microsome (n = 2).

<sup>b</sup> Sodium salt.

**7a–f** was clearly correlated with the activity. A sequential increase in the number of methylene groups from 3 to 5 gradually enhanced the activity. The optimal compound **7c** (n = 5) showed an IC<sub>50</sub> value of 7.9 nM, which is about 2-fold more potent than **7a** (n = 3). An increase in the number of methylene groups in **7c** was sensitively associated with the loss of activity. Compound **7d** (n = 6, IC<sub>50</sub> = 22 nM) was about three times weaker than **7c**, and **7f** (n = 9) was about ten times weaker than **7c**.

Superimposition of the crystal structure of the optimal compound **7c**<sup>18</sup> with the predicted crystal structure of AA<sup>16</sup> was performed using the Molecular Operating Environment (MOE 2004. 03) method.<sup>19</sup> Their 3-D structures nearly overlapped (Fig. 2). The carboxy moiety of AA and that of **7c** were consistent with each other. The imidazole ring of **7c** and the C<sub>20</sub> carbon atom of AA, which is the position oxidized by 20-HETE syn-

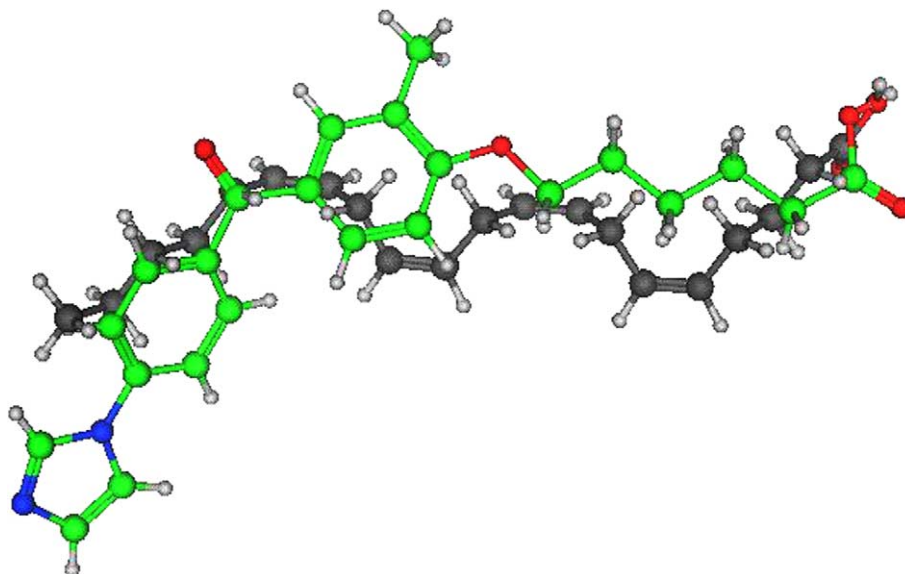
thase, were also well accorded. These results suggest that AA might be located in the active site of 20-HETE synthase with a expanded conformation rather than a folded conformation, which is thought to be more stable in solution.<sup>16</sup> Selectivity for drug-metabolizing enzymes (CYP2D6 was inhibited 50.7% by **7c** and 71.1% by **1** at 1 μM) was also improved by the introduction of a carboxyalkoxy moiety, and **7c** did not inhibit the activities of cyclooxygenases-1 and -2 (COX-1 and COX-2), even at higher concentrations (100 μM). These results indicate that **7c** is a potent and selective inhibitor of the formation of 20-HETE from AA.

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**Figure 2.** Superposition of a predicted crystal structure of AA and the crystal structure of **7c**. The superimposition of arachidonic acid (gray) and **7c** (green) was studied using the Molecular Operating Environment (MOE 2004.03) method.

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19. Molecular Operating Environment (MOE 2004.03) Chemical Computing Group, Inc., 1255 University St. Suite 1600, Montreal, Quebec, Canada H3B 3X3.