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DPAGT1 Inhibitors of Capuramycin Analogues and Their Antimigratory Activities of Solid Tumors

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KEYWORDS. Capuramycin analogues, DPAGT1 inhibitor, Antimigratory activity, Snail zinc-finger transcription factors, E-Cadherin, Synergistic effect, Computational chemistry

ABSTRACT:

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3 Capuramycin displays narrow spectrum of antibacterial activity by targeting bacterial translocase I
4 (MraY). In our program of development of new *N*-acetylglucosaminephosphotransferase1 (DPAGT1)
5 inhibitor, we have identified that a capuramycin phenoxy piperidinyl benzylamide analogue (CPPB) inhibits
6 DPAGT1 enzyme with an IC₅₀ value of 200 nM. Despite a strong DPAGT1 inhibitory activity, CPPB does
7 not show cytotoxicity against normal cells and a series of cancer cell lines. However, CPPB inhibits
8 migrations of several solid cancers including pancreatic cancers that require high DPAGT1 expression in
9 order for tumor progression. DPAGT1 inhibition by CPPB leads to a reduced expression level of Snail, but
10 does not reduce E-cadherin expression level at the IC₅₀ (DPAGT1) concentration. CPPB displays a strong
11 synergistic effect with paclitaxel against growth-inhibitory action of a patient-derived pancreatic
12 adenocarcinoma, PD002: paclitaxel (IC₅₀ 1.25 μM) inhibits growth of PD002 at 0.0024-0.16 μM in
13 combination with 0.10-2.0 μM of CPPB (IC₅₀ 35 μM).
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30 INTRODUCTION

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33 Capuramycin (CAP (**1**), Figure 1) is a nucleoside antibiotic, which has a narrow-spectrum of activity
34 against Gram-positive bacteria including *Mycobacterium tuberculosis* (Mtb).¹⁻³ To date, medicinal
35 chemistry efforts on capuramycin have been focused on developing a new TB drug; new capuramycin
36 analogues have been synthesized to improve bacterial phospho-MurNAc-pentapeptide translocase I (MraY
37 and MurX for *Mycobacterium* spp.) enzyme as well as antimycobacterial activities.^{1,4,5} Somewhat recently,
38 the anti-*Clostridioides difficile* (formerly *Clostridium difficile*) activity of a capuramycin analogue has been
39 reported.⁶ Capuramycin is a specific inhibitor of MraY with the IC₅₀ value of 0.13 μM,⁷ however, some
40 other nucleoside antibiotics (*e.g.*, muraymycin A1 and tunicamycins) display activity against MraY, WecA
41 (polyprenyl phosphate-GlcNAc-1-phosphate transferase), and its human homologue, DPAGT1 (*N*-
42 acetylglucosaminephosphotransferase1)-type phosphotransferases.⁸⁻¹⁴ MraY is an essential enzyme for
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3 growth of the vast majority of bacteria that catalyzes the transformation from UDP-MurNAc-pentapeptide
4 (Park's nucleotide) to prenyl-MurNAc-pentapeptide (lipid I).¹⁵ WecA catalyzes the transformation from
5 UDP-GlcNAc to decaprenyl-P-P-GlcNAc, the first membrane-anchored glycopospholipid that is
6 responsible for the biosynthesis of mycolylarabinogalactan in *Mycobacterium tuberculosis* (Mtb). WecA is
7 an essential enzyme for the growth of Mtb and some other bacteria. Biochemical studies of WecA enzyme
8 are hampered by lack of selective inhibitor molecules.⁹ Tunicamycin shows inhibitory activity against these
9 phosphotransferases with the IC₅₀ values of 2.9 μM (MraY/MurX), 0.15 μM (WecA), and 1.5 μM
10 (DPAGT1).^{9,10} CPZEN-45, an antimycobacterial MraY inhibitor, was reported to exhibit WecA inhibitory
11 activity (IC₅₀ ~0.084 μM).¹⁶ We showed that 2'-O-methyl capuramycin (OM-CAP (**2**), formerly UT-01320,
12 Figure 1) does not exhibit MraY/MurX inhibitory activity, but displays a strong WecA inhibitory activity
13 (IC₅₀ 0.060 μM).^{1,9} *In vitro* cytotoxicity of tunicamycin has been documented in a number of articles.¹⁷
14 Acute toxicity of tunicamycin due to its narrow therapeutic window (LD₅₀: 2.0 mg/kg, LD₁₀₀: 3.5 mg/kg
15 mice, IP) discourages scientists from developing tunicamycin for new antibacterial, antifungal, or anti-
16 cancer agents.^{18,19} A large number of scientists believe that cytotoxicity of tunicamycin is attributable to its
17 interaction with DPAGT1, which catalyzes the first and rate limiting step in the dolichol-linked
18 oligosaccharide pathway in *N*-linked glycoprotein biosynthesis (Figure 2).^{10,12} In contrast, OM-CAP (**2**)
19 possesses the same level of DPAGT1 inhibitory activity (IC₅₀ 4.5 μM) to tunicamycins (IC₅₀ 1.5 μM), but
20 it does not show cytotoxicity against healthy cells (*e.g.*, Vero and HPNE cells) at 50 μM and some cancer
21 cell lines (*e.g.*, L1210, KB, AsPC-1, PANC-1, LoVo, SK-OV-3) at 10 μM. A sharp difference in the
22 cytotoxicity profiles between tunicamycins (**11**, Figure 1) and OM-CAP (**2**) raises the question of whether
23 selective inhibition of DPAGT1 enzyme function in certain cells/organs by small molecules does not cause
24 unacceptable level of toxicity against human during chemotherapy. We have recently engineered the
25 structure of muraymycin to yield strong DPAGT1 inhibitors; one of these analogues, APPB (**12**, Figure 1),
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3 showed a promising antiproliferative effect on a series of solid cancer cell lines that required overexpression
4 of the *DPAGT1* gene in their growth and cancer progression.^{11,13,14} The design of APPB was originated from
5 the discovery of DPAGT1 inhibitors of capuramycin analogues. In this article, we report structure-activity
6 relationship (SAR) studies of capuramycin to identify novel DPAGT1 inhibitors, and *in vitro* anti-invasion
7 and anti-metastasis activity of a new capuramycin analogue DPAGT1 inhibitor, CPPB (capuramycin
8 phenoxyperidinybenzylamide analogue, **5**) (Figure 1). A unique synergistic effect was observed against
9 a patient-derived pancreatic adenocarcinoma, PD002 in a combination of CPPB with paclitaxel. We
10 demonstrated key interactions of CPPB with DPAGT1 via molecular docking studies. Lastly, we report a
11 semi-synthetic method to deliver enough CPPB for future *in vivo* studies.
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34 RESULTS AND DISCUSSION

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37 **Chemistry and Structure activity relationship (SAR).** Sankyo (currently Daiichi-Sankyo) and Sequella
38 have reported several capuramycin (CAP, **1**) analogues that have improved *MraY* enzyme and bacterial
39 growth inhibitory activities.^{2,3,5,20} Their SAR studies rely on a capuramycin biosynthetic intermediate, A-
40 500359E, which allows delivery of novel amide molecules (R_1 group) having an ester (R_2) functional group
41 (Figure 3). The capuramycin analogue, SQ992, has an interesting antibacterial characteristic with
42 antimycobacterial activity *in vivo*.²¹ We have accomplished a total chemical synthesis of capuramycin and
43 its analogues.²² To date, we have identified an novel analogue possessing improved *MraY* inhibitory
44 activity, Cap-3-amino-1,4-benzodiazepine-2-one analogue,²³ and a selective *WecA* inhibitor, OM-Cap (**2**),
45 via our total synthetic approach (Figure 3).^{1,9} Since our first report on a total synthesis of capuramycin, a
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3 few improvements of the synthetic scheme have been made: we introduced acid-cleavable protecting groups
4 for the uridine ureido nitrogen (3-position in **a**) and primary alcohol (6''-position in **c**) (Scheme 1).²³ The
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6 MDPM and MTPM groups can simultaneously be removed with 30% TFA to form the key synthetic
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8 intermediate **A** for capuramycin. In our on-going SAR of capuramycin, commercially available protecting
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10 groups (BOM and chloroacetyl groups) for the ureido nitrogen (3-position) and C6''-alcohol were decided
11
12 to apply in our SAR tactics. Success of hydrogenolytic cleavage of the BOM group and tolerability of the
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14 chloroacetyl group were difficult to predict in capuramycin synthesis. To establish the new protecting group
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16 strategy, we first demonstrated the synthesis of *iso*-capuramycin (I-Cap) (Scheme 2A). Syntheses of all
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18 building blocks and the experimental procedures for their synthetic steps in Scheme 2 and 3 are summarized
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20 in Supporting Information (SI). Highlights of syntheses of new capuramycin analogues are illustrated in
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22 Scheme 2 and 3. The (*S*)-cyanohydrin **13** was subjected to NIS-AgBF₄ promoted α -selective mannosylation
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24 with the thioglycoside **14** to yield the α -mannosylated cyanohydrin **15** in 78% yield.²² The cyano group of
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26 **15** was hydrated using HgCl₂-aldoxime in aq. EtOH, and the BOM and chloroacetyl groups of the generated
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28 amide were deprotected stepwisely: dechloroacetylation with thiourea followed by hydrogenation with 10%
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30 Pd-C in AcOH-ⁱPrOH-THF provided the C6''-free alcohol **16** in 53% overall yield. Oxidation-elimination
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32 reaction of **16** with SO₃•pyridine in a solvent system (CH₂Cl₂/Et₃N/DMSO = 10/2/1) provided the α,β -
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34 unsaturated aldehyde **17** in quantitative yield (determined by ¹H NMR analysis). After all volatiles were
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36 removed, the aldehyde **17** was oxidized to the corresponding carboxylic acid **18** by using NaClO₂ in the
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38 presence of NaH₂PO₄ and 2-methyl-2-butene.²⁴ The resulting carboxylic acid **18** was coupled with (*2S*-
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40 aminocaprolactam by using a standard peptide-forming reaction condition (HOBt, EDCI, and NMM) to
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42 yield the coupling product **19** in 70% overall yield from **16**. Saponification of **19** by using Et₃N in MeOH
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44 provided I-Cap (**3**) in quantitative yield. Similarly, dimethyl-capuramycin (DM-CAP) was synthesized in
45
46 31% overall yield from the cyanohydrin-acetonide **20**. CAP (**1**) and its three analogues, OM-CAP (**2**), I-

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3 CAP (**3**), and DM-CAP (**4**) were evaluated in enzyme inhibitory assays against bacterial
4 phosphotransferases, *MraY* and *WecA*, and archaeal and human dolichyl-phosphate *GlcNAc-1-*
5 phosphotransferases, *AglH* and *DPAGT1*.^{7,9,11} CAP is a selective *MraY* inhibitor that does not display
6 inhibitory activity against *WecA*, *AglH*, and *DPAGT1* (Table 1). Previously, OM-CAP (**2**) was identified
7 as a selective *WecA* inhibitor (IC_{50} 0.060 μ M) that does not possess *MraY* inhibitory activity (IC_{50} >50 μ M
8 (entry 2 in Table 1).⁹ In this program, it was realized that OM-CAP (**2**) has inhibitory activity against *AglH*
9 and *DPAGT1* with the IC_{50} values of 2.5 and 4.5 μ M, respectively (entry 2). I-CAP (**3**) showed enzyme
10 inhibitory activity against *MraY*, *WecA*, *AglH*, and *DPAGT1* with the IC_{50} between 8.5-30 μ M
11 concentrations (entry 3). On the contrary, DM-CAP (**4**) showed only a weak *WecA* inhibitory activity (IC_{50}
12 35.0 μ M) (entry 4). In recent reports on co-crystal structures of *DPAGT1* with tunicamycin (PDB: 5O5E
13 and 6BW6), the fatty acid chain of tunicamycin is occupied in the hydrophobic tunnel (the proposed
14 dolichol-phosphate (Dol-P) binding site).^{25,26} We speculated that introduction of pharmacologically
15 amenable hydrophobic groups that occupy the proposed Dol-P binding site is essential to exhibit strong
16 *DPAGT1* inhibitory activity. In virtual screening of a hydrophobic group (excluding fatty acids) using the
17 structure of *DPAGT1* with bound tunicamycin (PDB: 6BW6), an analogue (*e.g.*,
18 (((trifluoromethoxy)phenoxy)piperidinyl)benzylamide) of (((trifluoromethoxy)phenoxy)piperidin-1-
19 yl)phenol group (*i.e.* **34** in Scheme 3) found in a new anti-TB drug, delamanid,^{27,28} was suggested to be a
20 reasonable fatty acid surrogate, whose capuramycin derivatives (capuramycin
21 phenoxypiperidinylbenzylamide (CPPB, **5**), *iso*-capuramycin phenoxypiperidinylbenzylamide (I-CPPB, **6**),
22 *O*-methyl capuramycin phenoxypiperidinylbenzylamide (OM-CPPB, **7**), demethyl capuramycin
23 phenoxypiperidinylbenzylamide (DM-CPPB, **8**), capuramycin phenoxypiperidinylbenzylamine (CPPA, **9**),
24 and *iso*-capuramycin phenoxypiperidinylbenzylamine (I-CPPA, **10**)) could bind to *DPAGT1* with high
25 affinity. However, the docking program used in these studies is not able to distinguish between low- and
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3 high-binding molecules: all (((trifluoromethoxy)phenoxy)piperidin-1-yl)phenyl)methanamino derivatives
4 provided “good” GlideScores of between -12.9~-16.6 (see Table S1 in SI). Therefore, we decided to
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6 synthesize all analogues (CPPB, I-CPPB, OM-CPPB, DM-CPPB, CPPA, and I-CPPA) identified in the
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8 virtual screening and evaluate their phosphotransferase inhibitory activity.
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12 The carboxylic acid intermediate **32** for CAP (**1**) was subjected to peptide coupling reaction with
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14 (((trifluoromethoxy)phenoxy)piperidin-1-yl)phenyl)methylamine (**34**), providing the protected CPPB, **37**.
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16 Saponification of **37** and purification by reverse HPLC yielded CPPB (**5**) in 95% overall yield from **37**.
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18 Similarly, I-CPPB (**6**), OM-CPPB (**7**), and DM-CPPB (**8**) were synthesized from the mannuronic acid
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20 derivatives **18**, **33**, and **31** in 24-34% overall yield (Scheme 3A). Capuramycin
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22 phenoxy-piperidinylbenzylamine analogues, CPPA (**9**) and I-CPPA (**10**), were synthesized via reductive
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24 aminations of the aldehydes **29** and **17** with the amine **34**, furnishing the desired products in 63-65% overall
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26 yield from **26** and **16** after saponification. *MraY*, *WecA*, *AglH*, and *DPAGT1* enzyme inhibitory activity
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28 assays for the six (((trifluoromethoxy)phenoxy)piperidin-1-yl)phenyl)methylamine analogues revealed that
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30 CPPB (**5**) and I-CPPB (**6**) are high nM range *DPAGT1* inhibitors (entries 5 and 6 in Table 1), however, the
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32 *O*-methylation and demethylation analogues (OM-CPPB (**7**) and DM-CPPB (**8**)) turned out to be very low-
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34 or no-*DPAGT1* inhibitor (entries 7 and 8). The secondary amine analogues, CPPA (**9**) and I-CPPA (**10**), did
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36 not inhibit all phosphotransferases tested in Table 1 at 50 μM concentration (entries 9 and 10). CPPB was
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38 determined to be three times stronger *DAPGT1* inhibitor (IC_{50} 0.20 μM) than I-CPPB (entry 5 vs. 6). I-
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40 CPPB did not display *MraY* inhibitory activity, but showed a very weak *WecA* and *AglH* enzyme inhibitory
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42 activity (entry 6). Interestingly, difference in these phosphotransferase inhibitory profiles between CPPB
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44 and I-CPPB correlate with their antimycobacterial activity: CPPB possessing *MraY*/*WecA* inhibitory
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46 activity killed *Mycobacterium tuberculosis* H₃₇Rv, *Mycobacterium avium* 2285, *Mycobacterium*
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48 *smegmatis* (ATCC607) with the MIC values 6.25-12.5 $\mu\text{g}/\text{mL}$. In contrast, I-CPPB, which does not have
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MraY inhibitory activity, did not show growth inhibitory activity against these *Mycobacterium* spp. at 50 $\mu\text{g/mL}$.

Insert Scheme 1 and Scheme 2

Insert Table 1

Cytotoxicity of new capuramycin analogues, CPPB (5) and I-CPPB (6). In the capuramycin analogue series, the degree of MraY inhibitory activity correlates with their antimycobacterial activity.^{7-9,13} Antimycobacterial capuramycin analogues display low *in vitro* cytotoxicity against mammalian cells, and have been recognized as safe drug leads that have acceptable tolerability in animal models.^{2,3} The toxicity of tunicamycin (**11**, Figure 1) has been studied extensively *in vitro*: tunicamycin inhibits growth in many cancer cell lines without selectivity, and has a narrow therapeutic window demonstrated in *in vivo* studies using mice.^{18,29} The toxicity of tunicamycin is believed to be attributable to its ability to inhibit DPAGT1 enzyme function.^{10,30} However, in our studies, tunicamycin's toxicity could not be explained solely by its inhibition of DPAGT1. Our DPAGT1 inhibitor, APPB (**12**, Figure 1) inhibits DPAGT1 with greater than 30-times the inhibitory activity of tunicamycin, and inhibits growth of selected solid cancer cell lines at low μM concentrations with selective cytotoxicity (IC_{50} normal cells / cancer cells) of >35 .¹⁰ The LD_{50} value of APPB is >20 mg/kg (mouse), whereas it is 2.0 mg/kg (mouse) for tunicamycin.^{10,18} Capuramycin-based DPAGT1 inhibitors, CPPB (**5**) and I-CPPB (**6**), identified in this program inhibited DPAGT1 enzyme with the IC_{50} values of 0.2 and 0.6 μM , respectively. Unlike the MraY-antimycobacterial activity relationship observed for CAP analogues, the DPAGT1 inhibitors, CPPB and I-CPPB, did not show antiproliferative activity against L1210 (a leukemia cell), HPNE (a normal pancreatic ductal cell), and Vero (a normal kidney cell) at 50 μM . They showed various levels of growth inhibitory activity against several solid cancer cell

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3 lines such as KB (HeLa, a cervix carcinoma), SiHa (a cervical squamous cell carcinoma), HCT-116 (a
4 colorectal adenocarcinoma), DLP-1 (a colorectal adenocarcinoma), Capan-1 (a pancreatic ductal
5 adenocarcinoma), PANC-1 (a pancreatic ductal carcinoma), AsPC-1 (a pancreatic adenocarcinoma), PD002
6 (a patient-derived pancreatic adenocarcinoma) in MTT assays (IC_{50} 15-45 μ M, Table 2). A lower DPAGT1
7 inhibitor, tunicamycin (**11**), showed growth inhibition of all cell lines in Table 2 with the IC_{50} values of
8 0.78-7.5 μ M concentrations (entry 5 in Table 2). Cellular behavior and morphological changes of a patient-
9 derived metastatic pancreatic adenocarcinoma, PD002 treated with CPPB were monitored over time via
10 IncuCyte[®] live cell analysis imaging system (Figure 4A). Interestingly, 10-13% of phase area confluent of
11 PD002 culture (time 0h) remained the same after 72h for the CPPB-treated cells (50 μ M), whereas, ca. 70%
12 of confluence was reached for the control PD002 culture (PBS) (Figure 4B vs.4C). Although morphological
13 changes were subtle over time (0-72h), cell viability assessed by the MTT reduction assay revealed that
14 PD002 cells treated with CPPB (50 μ M) was significantly decreased (Table 2). Exposure of CPPB (0.2-20
15 μ M) inhibited cell proliferation of PD002: ca. 20% of cell proliferation was inhibited at time 72h. These
16 results may indicate that DPAGT1 inhibitors may have cytostatic effect against certain cancerous tumors that
17 require DPAGT1 overexpression for their growth.
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43 *Insert Figure 4*
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47 **Cell migratory inhibition by CPPB (5).** DPAGT1 catalyzes the first step in *N*-glycan biosynthesis of
48 mammalian cells (Figure 2). Aberrant *N*-glycosylation is common in many solid cancers and important for
49 the epithelial to mesenchymal transition program (EMT, a mechanism of metastases).¹⁰ We found high
50 levels of DPAGT1 protein expression in a series of pancreatic cancers (*e.g.*, PANC-1, Capan-1, and AsPC-
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3 1). Dysregulation of DPAGT1 enzyme leads to disturbances in cell-cell adhesions and may increase
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5 epithelial to mesenchymal transition (EMT): these processes increase migratory and invasive capabilities of
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7 malignant neoplasms that are the initiation of metastasis in cancer progression, especially pancreatic
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9 cancer.^{31,32} Interestingly, there is significant crosstalk between DPAGT1 and the Wnt/ β -catenin and Snail
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11 pathway where DPAGT1 overexpression leads to 1) accumulation of β -catenin in the cytoplasm and then
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13 translocation into the nucleus, and 2) reduction of the Snail expression levels, preventing epithelial-
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15 mesenchymal transition by suppressing the E-cadherin expression (a cell-cell adhesion glycoprotein).^{10,31,32}
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17 As such, aberrations in these pathways occur in numerous cancers, thus, discovery of small molecules
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19 directed towards inhibition of the Wnt and Snail pathways represents an important area of anticancer
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21 therapeutics.³³⁻³⁵ In order to obtain insights into anti-metastatic ability of DPAGT1 inhibitors, we explored
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23 the degree of cell migration in several commercially available cell lines (Capan-1, PANC-1, and AsPC-1),
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25 a patient-derived pancreatic ductal adenocarcinoma cell line (PD002), a cervical carcinoma (SiHa), and a
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27 colorectal adenocarcinoma (HCT-116) to determine the effects on cellular motility. After 24h of three
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29 treatment doses (0.05, 0.1, and 0.2 μ M) with CPPB (**5**), inhibition of migration (closing the gap) was
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31 measured in a scratch assay (wound healing assay).³⁶ Only the images for PD002 are shown in Figure 5 and
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33 all other images obtained through these experiments are illustrated in Supporting Information (SI). The
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35 pancreatic cancer cell lines treated with CPPB migrated far less than the PBS treated (control) cells (Figure
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37 5A-D). In these assays, the wound-healing rate of the untreated PD002 cells was 63% in 24h. In sharp
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39 contrast, CPPB treated cells inhibited the wound-healing effectively at its IC_{50} level against DPAGT1 (0.2
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41 μ M): the wound-healing rate was approximately 20% (Figure 5B). We thoroughly evaluated migration
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43 inhibition ability of CPPB compared to gemcitabine, one of the main chemotherapy drugs used to treat
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45 pancreatic cancer, and tunicamycin using PD002 cells. Gemcitabine shows a wound-healing rate of 43% at
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47 0.2 μ M, and tunicamycin shows 35% at 0.2 μ M (SI). Thus, it was concluded that CPPB is more effective in
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3 inhibiting cancer cell migration than gemcitabine and tunicamycin. These trends were further confirmed by
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5 an endpoint migration assays via Boyden chambers for PD002.^{37,38} In these assays, the cell migrations of
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7 PD002 treated with CPPB (0.1 μ M) were inhibited on a higher level compared to those with tunicamycin
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9 and gemcitabine at the same concentration (0.1 μ M) (Figure 6).
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15 *Insert Figure 5*

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17 *Insert Figure 6*
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22 **Inhibition of a zinc-finger transcription factor, Snail1 (Snail) in the selected cancer cell lines by**
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24 **CPPB.** Snail protein is one of the most important transcription factor that induces epithelial to mesenchymal
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26 transition (EMT), which converts epithelial cells into migratory mesenchymal cells that are more efficient
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28 at metastasizing.³⁹ EMT induced by overexpression of Snail produces cancer stem-like properties in a
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30 number of solid organ cancers. Aberrant expression of Snail leads to loss of expression of E-cadherin.⁴⁰
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32 Thus, suppression of Snail expression or inhibition of Snail functions represents a potent targeted
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34 therapeutic strategy for many cancers.^{41,42}
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38 Immunofluorescence assays using an anti-Snail antibody revealed that the fluorescence intensity of Snail
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40 was strong in a series of pancreatic cancer cells (PANC-1, AsPC-1, Capan-1, and PD002), and the
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42 expression of Snail was decreased by the treatment with CPPB in a concentration dependent manner. Among
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44 pancreatic cancer cell lines, only the data for PD002 and PANC-1 are shown in Figure 7A and 7B (see SI
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46 for AsPC-1 and Capan-1). The Snail expression level of a non-metastatic pancreatic cancer, PANC-1, was
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48 much lower than metastatic pancreatic cancers (*e.g.*, PD002 and Capan-1). A few other types of cancer cells
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50 such as a colorectal cancer (HCT-116) and a cervical cancer (SiHa) were examined by similarly designed
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52 immunofluorescence assays or Western blot assays (Figures 7C and 7D). The Snail expression in SiHa was
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3 inhibited by treatment of CPPB in a concentration dependent manner; at the IC₅₀ concentration (0.2 μM
4 against DPAGT1), CPPB effectively inhibited the Snail expression (Figure 7D). In contrast, the Snail
5 expression level in HCT-116 was not noticeably changed by the treatment of CPPB between 0.05 and 2.0
6 μM concentrations. Interestingly, cell migration of HCT-116 was not inhibited by CPPB demonstrated in
7 the wound healing (scratch) assays (Figure 5F). At the concentrations tested in the scratch assays (0.05-2.0
8 μM), the E-Cadherin expression levels of PD002, PANC-1, and HCT-116 were not changed significantly
9 (Figure 8). To support the above discussion based on the immunofluorescent staining (Figure 7 and 8), the
10 relative expression levels of Snail and E-cadherin in PD002, PANC-1, and HCT-116 treated with CPPB
11 were measured by Western blot analyses (Figure 9). The relative expression levels were obtained by using
12 Image Studio™ Lite quantification software, and these quantified data were summarized in SI (see Figure
13 S5). PD002 and PANC-1 treated with CPPB (0 to 2.0 μM) lead to a dose dependent decrease in Snail. The
14 E-Cadherin expression level of a metastatic pancreatic cancer, PD002 was increased in a CPPB
15 concentration depended manner (0 to 2.0 μM), whereas, a non-metastatic pancreatic cancer, PANC-1
16 exhibited the same expression level of E-Cadherin at 0-2.0 μM concentrations of CPPB (Figure 9A and 9B).
17 A low DPAGT1 expressed-colon cancer, HCT-116 did not display noticeable difference in the expression
18 levels of Snail and E-Cadherin at 0-2.0 μM CPPB concentrations (Figure 9C).
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44 *Insert Figure 8*

45 *Insert Figure 9*

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52 **Inhibition of DPAGT1 by CPPB.** CPPB decreased the DPAGT1 expression level in all pancreatic cancer
53 cell lines examined in Figure 5: the DPAGT1 expression was apparently inhibited by the IC₅₀ concentration
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3 of CPPB (0.2 μM) (only the data for PD002 and PANC-1 shown Figure 10 and see Figure S4 in SI) for
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5 AsPC-1 and Capan-1). An important observation is that the DPAGT1 expression of the pancreatic cancer
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7 cell lines could not completely be inhibited at a high concentration of CPPB (2-20 μM) (Figures 9 and 10).
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10 In MTT assays, we realized that all pancreatic cancers tested remained viable at 20 μM concentration of
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12 CPPB (Table 2). We confirmed that the DPAGT1 expression level in a colorectal adenocarcinoma, HCT-
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14 116 is significantly lower than that in the pancreatic cancer cell lines (PD002 and PANC-1); DPAGT1 was
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16 not detectable in Western blot assays for the lysate obtained by a standard protocol (50 $\mu\text{g}/30 \mu\text{L}$ of total
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18 protein sample). A 10 times concentrated HCT-116 cell lysate (prepared by ultracentrifugation, 130,000xg
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20 for 1h) enabled us to detect DPAGT1 in Western blotting. By treatment of HCT-116 with CPPB at 0.1-20
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22 μM concentration, the DPAGT1 expression levels of HCT-116 remained higher fluorescence intensity in
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24 immunofluorescent assay (Figure 10C) and 20-90% in Western blot assays (Figure 9C). These data imply
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26 that the inhibitory effect of CPPB on cell migration varies depending on degree of inhibition of the DPAGT1
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28 expression: immunofluorescent assays at 0.2-2.0 μM concentrations of CPPB, the degree of DPAGT1
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30 expression was decreased by the following order: PANC-1 > PD002 >> HCT-116. Migration inhibition
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32 observed in the scratched assays (Figure 5) is well-correlated with the degree of the DPAGT1 expression
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34 inhibition. Although CPPB decreased the protein expression of DPAGT1 without significantly decreasing
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36 its gene (*DPAGT1*) expression, tunicamycin decreased both the gene expression of *DPAGT1* and DPAGT1
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38 protein expression (Figure 11). These down-regulation in *DPAGT1* gene expression by tunicamycin may be
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40 attributable to its high cytotoxicity against mammalian cells without selectivity.
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3 **Synergistic effect of CPPB with paclitaxel.** The FOLFIRINOX (a combination of folinic acid, 5-
4 fluorouracil, irinotecan, and oxaliplatin) and nab-paclitaxel (albumin-bound paclitaxel)-gemcitabine
5 regimens have been adopted into clinical practice for patients with metastatic pancreatic cancers.⁴³ Median
6 progression-free survival was reported in one study of patients with metastatic pancreatic cancer to be 6.4
7 months in the FOLFIRINOX group and 3.3 months in the gemcitabine group.^{43,44} Over the past years, the
8 clinical data have not supported that FOLFIRINOX is associated with any better (or worse) survival rates
9 compared to the nab-paclitaxel-gemcitabine regimen as there have been no head-to-head trials.⁴⁵ However,
10 the inclusion of paclitaxel and its derivatives in combination regimens remains an important therapeutic
11 strategy in pancreatic cancer chemotherapy since nab-paclitaxel-gemcitabine is associated with less adverse
12 effects (toxicity in patients) than FOLFIRINOX.⁴⁶ In this regard, we were very interested in synergistic or
13 additive effects of DPAGT1 inhibitor in combination with paclitaxel. The synergistic or antagonistic
14 activities of CPPB were assessed *in vitro* via checkerboard technique.^{47,48} In these experiments, CPPB
15 displayed strong synergistic effects with paclitaxel in a wide range of concentrations against PD002. Table
16 3 summarizes the results of FIC index analyses for selected combinations of CPPB (IC₅₀ 35.0 μM) plus
17 paclitaxel (IC₅₀ 1.25 μM) that showed synergistic combination (ΣFIC<0.5). The FIC index below 0.50 was
18 observed for 20 combinations of two molecules out of 96 different concentrations (see Figure S6 in SI). The
19 IC₅₀ value of paclitaxel against PD002 was lowered (0.024-0.61 μM) in combination with CPPB (0.1-2.0
20 μM).

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53 **Interaction of CPPB with DPAGT1 (Modeling Studies).** DPAGT1 encompasses ten transmembrane
54 segments, three loops on the ER (endoplasmic reticulum) side, and five loops on the cytoplasmic side. Four
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3 loops (CL-1, CL-5, CL-7, and CL-9) on the cytoplasmic side form the UDP-GlcNAc-binding domain.^{25,26}
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5 The hydrophobic tunnel created by the transmembrane segments (TM-4, TM-5 and CL-9) within the lipid
6 bilayer is predicted to interact with dolychol-phosphate (Dol-P). The weak DPAGT1 inhibitors, *O*-methyl
7 capuramycin (OM-CAP) and *iso*-capuramycin (I-CAP) (Table 1), yielded low docking scores (Glide
8 Scores) using Schrödinger's Glide program: the score for OM-CAP was -12.4 and for I-CAP was -10.9.
9
10 These scores predicted that OM-CAP and I-CAP possess significantly lower affinity for DPAGT1 than
11 CPPB, which showed a docking score of -16.6 (see Table S1 in SI).⁴⁹⁻⁵¹ The docked CPPB-DPAGT1
12 structure illustrated in Figure 12 shows several key interactions. The C2'-OH acts as a donor in a hydrogen
13 bond to the Glu56 carboxylate. This interaction is likely be lost when the C2'-OH is methylated. Pi-stacking
14 interactions are observed between 1) Phe249 and the uracil ring, and 2) Trp122 and the
15 trifluoromethoxybenzene in the hydrophobic moiety. Asn185 and Ash252 (protonated Asp) form hydrogen-
16 bond(s) to the primary amide and the dihydropyran-hydroxy (C3''-OH) group, respectively. Additional
17 hydrogen-bonds between the uridine ureido group and the backbone amides (Gln44 and Leu46) strengthen
18 the ligand interaction. In this program, capuramycin (CAP), a strong MraY inhibitor with no DPAGT1
19 inhibitory activity, was successfully engineered to be a relatively strong DPAGT1 inhibitor by introducing
20 a hydrophobic functional group, (((trifluoromethoxy)phenoxy) piperidin-1-yl)phenyl)methylamine at the
21 C6''-position. This hydrophobic group allows the preferable conformation of the uridine-
22 enopyranosiduronic moiety in the DPAGT1 binding domain, resulting in increased interactions with Asn185,
23 Ash252, Glu56, and Phe249.
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3 **A semi-synthesis of CPPB from A500359F.** Pharmacological studies of CPPB (**5**) and its related
4 analogues using appropriate animal models will be a focus of our future research efforts. Previously, a
5 natural product A-5003659E was used to develop novel capuramycin analogues with strong MraY
6 inhibitory activity (Hotoda et. al. 2003) (Figure 3).⁵² Its free-carboxylic acid analogue, A-500359F was also
7 isolated from the capuramycin-producing strain, *Streptomyces griseus* Sank 60196. Saponification of A-
8 5003659E to A-500359F was established by the Sankyo group.²⁰ Although, the currently available synthetic
9 schemes for capuramycin analogues (e.g., Scheme 3) include a relatively short number of chemical
10 steps,^{22,23,53} a semi-synthetic approach is more feasible to deliver a large quantities of CPPB for
11 pharmacological studies. To establish semi-synthesis of CPPB, A-500359F was first synthesized from the
12 CAP-synthetic intermediate **32** (Scheme 3A) in a single step. Amide-forming reaction of synthetic A-
13 500359F with (((trifluoromethoxy)phenoxy) piperidin-1-yl)phenyl)methylamine (**34**) was performed under
14 an optimized condition using EDCI, glyceracetone-Oxyma, and NMM in DMF.⁵⁴ All coupling reagents
15 could be removed by partitions between CHCl₃ and water and evaporation. The crude product was passed
16 through DOWEX 50Wx4 column (MeOH : NH₄OH = 4 : 1) to provide CPPB with >95% purity, which was
17 further purified by C₁₈-reverse HPLC (MeOH : H₂O = 65 : 35) to yield pure CPPB (Scheme 4).
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41 42 43 44 **CONCLUSION**

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47 This paper describes the identification of a new DPAGT1 inhibitor of capuramycin analogue,
48 capuramycin phenoxy piperidinyl benzylamide (CPPB, **5**) and its isostere I-CPPB (**6**). Previously,
49 tunicamycin is the only DPAGT1 inhibitor that has been widely applied to the studies associated with
50 protein misfolding *in vitro*.^{55,56} Tunicamycin displays cytotoxicity against cancer and healthy cells with low
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3 selectivity ratio.¹⁰ One of cytotoxicity mechanisms of tunicamycin is believed to be its ability to inhibit
4 DPAGT1 enzyme functions. The DPAGT1 expression levels vary depending on the cell types; renal cancers
5 and lymphomas express low-levels of DPAGT1, whereas, a majority of solid cancers express high-levels.⁵⁷
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7 Thus, the observed antiproliferative activity of tunicamycin against all types of cancer cells are difficult to
8 understand solely by its DPAGT1 inhibitory activity. In our studies, CPPB showed ~7.5 times stronger
9 DPAGT1 inhibitory activity than tunicamycin. However, unlike tunicamycin, CPPB did not inhibit growth
10 of cancer cell lines at the IC₅₀ values observed for tunicamycin (0.45 -7.5 μM). CPPB is a cell-permeable
11 molecule which was demonstrated by IncuCyte[®] live cell analyses and immunofluorescence assays. In this
12 article, we have studied effectiveness of CPPB on the expression levels of Snail, E-cadherin, and DPAGT1
13 primary in pancreatic cancers (Figures 7-10). CPPB decreased the Snail expression in commercially
14 available pancreatic cancer cell lines (PANC-1, AsPC-1, and Capan-1) and a patient-derived pancreatic
15 ductal adenocarcinoma cell line (PD002) in a dose dependent manner. On the other hand, the E-cadherin
16 expression level was increased in PD002 (a metastatic pancreatic cancer cell) or was not noticeably changed
17 in PANC-1 at between 0.05-0.2 μM of CPPB. These biochemical data may support that a selective DPAGT1
18 inhibitor, CPPB is effective in inhibiting metastasis spread of the pancreatic cancer cells observed in scratch
19 and transwell assays (Figures 5 and 6). Other than pancreatic cancers, a lower DPAGT1 expression cell, a
20 colorectal adenocarcinoma (HCT-116) and a higher DPAGT1 expression cell, a cervical carcinoma (SiHa)
21 were examined. CPPB did not inhibit migration of HCT-116, but strongly inhibited migration of SiHa in
22 scratch assays at 0.2 μM (IC₅₀ concentration against DPAGT1). These observations were supported by the
23 biochemical analyses of the Snail and E-cadherin expression levels. Snail plays an important role in cancer
24 progression. The accumulated evidences on Snail indicate that over-expression of Snail promotes drug
25 resistance, tumor recurrence and metastasis.⁴⁰ Although, only limited data have been generated in this
26 article, CPPB's Snail inhibitory activity observed in pancreatic and a several high DPAGT1-expressed cell
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lines suggests that selective DPAGT1 inhibitors have the potential to develop into less toxic anticancer therapeutics than anticancer drugs that are cytotoxic to all dividing cells in the body. CPPB is not cytotoxic against a series of cancer and healthy cell lines at 10 μM or higher concentrations. However, it showed a cytostatic activity against pancreatic cancers and a strong synergistic effect with paclitaxel; cytotoxic activity of paclitaxel was improved over 250-times against PD002 in combination with CPPB (0.2-2.0 μM). Docking studies of CPPB with the available DPAGT1 crystal structures provided insight into unique interactions, and thus, structure-based molecule design may be a fruitful approach to improve CPPB's DPAGT1 affinity. A collaboration with Daiichi-Sankyo is essential to efficiently produce CPPB for *in vivo* studies using large-animal models such as dogs, pigs, and monkeys. We have demonstrated a semi-synthesis of CPPB from a capuramycin biosynthetic intermediate, A-500359F, that will secure a production of large amount of CPPB (Scheme 4). Our total synthetic scheme is amenable to produce gram-quantity of CPPB (Scheme 3). Extensive synergistic, toxicity, and pharmacokinetic studies of CPPB will be performed using preclinical animal models, and these data including detailed evaluation on *in vivo* efficacy against pancreatic and cervical cancers will be reported elsewhere.

EXPERIMENTAL SECTION

Chemistry. General Information. All chemicals were purchased from commercial sources and used without further purification unless otherwise noted. THF, CH_2Cl_2 , and DMF were purified via Innovative Technology's Pure-Solve System. All reactions were performed under an Argon atmosphere. All stirring was performed with an internal magnetic stirrer. Reactions were monitored by TLC using 0.25 mm coated commercial silica gel plates (EMD, Silica Gel 60F₂₅₄). TLC spots were visualized by UV light at 254 nm, or developed with ceric ammonium molybdate or anisaldehyde or copper sulfate or ninhydrin solutions by heating on a hot plate. Reactions were also monitored by using SHIMADZU LCMS-2020 with solvents: A:

0.1% formic acid in water, B: acetonitrile. Flash chromatography was performed with SiliCycle silica gel (Purasil 60 Å, 230-400 Mesh). Proton magnetic resonance ($^1\text{H-NMR}$) spectral data were recorded on 400, and 500 MHz instruments. Carbon magnetic resonance ($^{13}\text{C-NMR}$) spectral data were recorded on 100 and 125 MHz instruments. For all NMR spectra, chemical shifts (δH , δC) were quoted in parts per million (ppm), and J values were quoted in Hz. ^1H and ^{13}C NMR spectra were calibrated with residual undeuterated solvent (CDCl_3 : $\delta\text{H} = 7.26$ ppm, $\delta\text{C} = 77.16$ ppm; CD_3CN : $\delta\text{H} = 1.94$ ppm, $\delta\text{C} = 1.32$ ppm; CD_3OD : $\delta\text{H} = 3.31$ ppm, $\delta\text{C} = 49.00$ ppm; $\text{DMSO-}d_6$: $\delta\text{H} = 2.50$ ppm, $\delta\text{C} = 39.52$ ppm; D_2O : $\delta\text{H} = 4.79$ ppm) as an internal reference. The following abbreviations were used to designate the multiplicities: s = singlet, d = doublet, dd = double doublets, t = triplet, q = quartet, quin = quintet, hept = heptet, m = multiplet, br = broad. Infrared (IR) spectra were recorded on a Perkin-Elmer FT1600 spectrometer. HPLC analyses were performed with a Shimadzu LC-20AD HPLC system. HR-MS data were obtained from a Waters Synapt G2-Si (ion mobility mass spectrometer with nanoelectrospray ionization). All assayed compounds were purified by reverse HPLC to be $\geq 95\%$ purity.

(2S,3S,4S,5R,6R)-2-((1S)-((2R,5R)-3-Acetoxy-5-(3-((benzyloxy)methyl)-2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)-4-methoxytetrahydrofuran-2-yl)(cyano)methoxy)-6-((2-chloroacetoxy)methyl)tetrahydro-2H-pyran-3,4,5-triyl triacetate (15). To a stirred suspension of **13** (0.17 g, 0.38 mmol), **14** (0.37 g, 0.75 mmol), MS3Å (0.50 g) and SrCO_3 (0.28 g, 1.88 mmol) in CH_2Cl_2 (9.4 mL) were added AgBF_4 (0.037 g, 0.19 mmol) and NIS (0.25 g, 1.13 mmol) at 0 °C. After being stirred for 19h, the reaction mixture was added Et_3N (1.0 mL) and passed through a silica gel pad (hexanes/ $\text{EtOAc} = 1/4$). The filtrate was concentrated *in vacuo*. The crude mixture was purified by silica gel column chromatography (hexanes/ $\text{EtOAc} = 2/1$ to $1/2$) to afford **15** (0.24 g, 78%): $^1\text{H NMR}$ (400 MHz, $\text{Chloroform-}d$) δ 7.40 – 7.27 (m, 6H), 6.07 (d, $J = 4.7$ Hz, 1H), 6.00 (d, $J = 8.2$ Hz, 1H), 5.51 (d, $J = 9.8$ Hz, 1H), 5.47 (d, $J = 9.6$ Hz, 1H), 5.37 (dd, $J = 3.4, 2.0$ Hz, 1H), 5.28 (d, $J = 10.2$ Hz, 1H), 5.22 – 5.15 (m, 2H), 4.84 (d,

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3 $J = 3.2$ Hz, 1H), 4.71 (s, 2H), 4.41 (dd, $J = 5.5, 3.2$ Hz, 1H), 4.39 – 4.35 (m, 1H), 4.33 (d, $J = 6.0$ Hz, 1H),
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5 4.27 (d, $J = 2.3$ Hz, 1H), 4.14 (d, $J = 1.7$ Hz, 2H), 4.03 – 4.01 (m, 1H), 3.93 (ddd, $J = 8.9, 5.9, 2.4$ Hz, 1H),
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7 3.47 (s, 3H), 2.20 (s, 3H), 2.19 (s, 3H), 2.07 (s, 3H), 2.02 (s, 3H); ^{13}C NMR (101 MHz, CDCl_3) δ 170.20,
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9 169.84, 169.50, 166.92, 162.19, 150.97, 137.75, 137.46, 128.32 (2C), 127.72, 127.69 (2C), 113.96, 103.58,
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11 96.29, 88.68, 80.93, 80.09, 72.30, 70.42, 69.60, 68.46, 67.94, 65.16, 64.35, 63.58, 59.26, 40.61, 31.58,
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13 20.70, 20.66, 20.62, 20.57; HRMS (ESI+) m/z calcd for $\text{C}_{35}\text{H}_{41}\text{ClN}_3\text{O}_{17}$ $[\text{M} + \text{H}]$ 810.2125, found: 810.2151.

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17 **(2R,3S,4S,5R,6R)-2-((1R)-1-((2S,5R)-3-Acetoxy-5-(2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)-4-**
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19 **methoxytetrahydrofuran-2-yl)-2-amino-2-oxoethoxy)-6-(hydroxymethyl)tetrahydro-2H-pyran-3,4,5-**
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21 **triyli triacetate (16).** To a stirred solution of **15** (0.24 g, 0.29 mmol) in a 9:1 mixture of EtOH and H_2O (2.9
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23 mL) were added HgCl_2 (0.16 g, 0.59 mmol) and acetaldoxime (0.18 mL, 2.9 mmol). After being stirred for
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25 13h at r.t., the reaction mixture was concentrated *in vacuo*. The residue was quenched with aq. NaHCO_3 ,
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27 and extracted with CHCl_3 . The combined organic extracts were dried over Na_2SO_4 and concentrated *in*
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29 *vacuo*. The crude product was purified by silica gel column chromatography (hexanes/EtOAc = 1/2 to
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31 $\text{CHCl}_3/\text{MeOH} = 96/4$) to afford the amide (0.21 g, 87%). To a solution of the amide (0.21 g, 0.26 mmol) in
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33 a 1:1 mixture of THF and MeOH (2.6 mL) was added thiourea (0.059 g, 0.77 mmol). After being stirred for
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35 11h at 50 °C, the reaction mixture was concentrated *in vacuo*. The residue was diluted with H_2O and
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37 extracted with CHCl_3 . The combined organic extracts were dried over Na_2SO_4 and concentrated *in vacuo*.
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39 The crude product was purified by silica gel column chromatography ($\text{CHCl}_3/\text{MeOH} = 98/2$ to $97/3$ to $96/4$)
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41 to afford the primary alcohol (0.15 g, 75%). To a stirred solution of the primary alcohol (0.15 g, 0.19 mmol)
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43 and AcOH (0.040 mL) in a 1:1 mixture of THF and i PrOH (2.0 mL) was added 10% Pd/C (0.12 g) under
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45 N_2 . H_2 gas was introduced and the reaction mixture was stirred under H_2 atmosphere for 3h, the solution
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47 was filtered through Celite and concentrated *in vacuo*. The crude product was purified by silica gel column
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49 chromatography ($\text{CHCl}_3/\text{MeOH} = 97/3$ to $92/8$) to afford **16** (0.10 g, 81%): ^1H NMR (400 MHz,
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3 Chloroform-*d*) δ 9.08 (brs, 1H), 7.60 (d, $J = 8.2$ Hz, 1H), 6.87 (brs, 1H), 6.12 (brs, 1H), 6.00 (d, $J = 8.1$ Hz,
4 1H), 5.87 (d, $J = 3.6$ Hz, 1H), 5.55 – 5.52 (m, 1H), 5.26 – 5.22 (m, 2H), 5.20 (t, $J = 6.0$ Hz, 1H), 5.00 (d, J
5 = 1.7 Hz, 1H), 4.53 (dd, $J = 6.5, 2.3$ Hz, 1H), 4.46 (d, $J = 2.3$ Hz, 1H), 4.06 (dd, $J = 5.5, 3.7$ Hz, 1H), 3.76
6 – 3.71 (m, 1H), 3.69 – 3.57 (m, 2H), 3.44 (s, 3H), 2.17 (s, 3H), 2.15 (s, 3H), 2.09 (s, 3H), 2.04 (s, 3H); ^{13}C
7 NMR (101 MHz, CDCl_3) δ 171.42, 170.46, 170.46, 170.40, 163.10, 150.03, 139.50, 103.61, 97.15, 96.95,
8 88.50, 81.26, 80.96, 75.33, 72.91, 69.67, 68.89, 65.54, 61.27, 59.05, 50.86, 20.82, 20.75, 20.67, 20.59;
9 HRMS (ESI+) m/z calcd for $\text{C}_{25}\text{H}_{34}\text{N}_3\text{O}_{16}$ [$\text{M} + \text{H}$] 632.1939, found: 632.1963.
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20 **(2*S*,3*S*,4*S*)-3,4-Diacetoxy-2-((1*R*)-1-((2*S*,5*R*)-3-acetoxy-5-(2,4-dioxo-3,4-dihydropyrimidin-1(2*H*)-
21 *yl*)-4-methoxytetrahydrofuran-2-yl)-2-amino-2-oxoethoxy)-3,4-dihydro-2*H*-pyran-6-carboxylic acid**
22 **(18)**. To a stirred solution of **16** (0.10 g, 0.16 mmol) and DMSO (0.11 mL, 1.57 mmol) in a 5:1 mixture of
23 CH_2Cl_2 and Et_3N (0.80 mL) was added $\text{SO}_3 \cdot \text{pyridine}$ (0.25 g, 1.57 mmol). After being stirred for 3h at r.t.,
24 the reaction mixture was added H_2O (0.16 mL) and passed through a silica gel pad ($\text{CHCl}_3/\text{MeOH} = 92/8$)
25 to provide the crude **17**. To a stirred solution of the crude mixture in *t*-BuOH (1.0 mL) and 2-methyl-2-butene
26 (0.5 mL) was added a solution of NaClO_2 (0.071 g, 0.78 mmol) and $\text{NaH}_2\text{PO}_4 \cdot 2\text{H}_2\text{O}$ (0.12 g, 0.78 mmol) in
27 H_2O (1.0 mL). After being stirred for 4h at r.t., the reaction was quenched with H_2O and extracted with
28 $\text{CHCl}_3/\text{MeOH}$ (9/1). The combined organic extracts were dried over Na_2SO_4 and concentrated *in vacuo*.
29 The crude product was purified by silica gel column chromatography ($\text{CHCl}_3/\text{MeOH} = 9/1$) to afford **18**
30 (0.078 g, 85%): ^1H NMR (400 MHz, Methanol-*d*₄) δ 7.77 (d, $J = 8.1$ Hz, 1H), 5.94 (d, $J = 11.7$ Hz, 1H),
31 5.94 (s, 1H), 5.78 (t, $J = 2.1$ Hz, 1H), 5.66 (dd, $J = 4.5, 2.5$ Hz, 1H), 5.56 (ddd, $J = 4.7, 3.2, 1.6$ Hz, 1H),
32 5.32 (d, $J = 3.3$ Hz, 1H), 4.99 (t, $J = 5.2$ Hz, 1H), 4.85 (d, $J = 2.1$ Hz, 1H), 4.60 (dd, $J = 5.2, 2.0$ Hz, 1H),
33 3.95 (t, $J = 5.0$ Hz, 1H), 3.39 (s, 3H), 2.13 (s, 3H), 2.08 (s, 3H), 2.05 (s, 3H); ^{13}C NMR (101 MHz, MeOD)
34 δ 172.79, 172.06, 171.60, 167.79, 166.01, 152.05, 148.16, 140.97, 104.23, 103.98, 97.91, 88.13, 83.38,
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82.91, 76.56, 71.95, 65.17, 65.06, 59.41, 20.75, 20.63, 20.57; HRMS (ESI+) m/z calcd for C₂₃H₂₈N₃O₁₅ [M + H] 586.1520, found: 586.1549.

(2S,3S,4S)-2-((1R)-1-((2S,5R)-3-Acetoxy-5-(2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)-4-methoxytetrahydrofuran-2-yl)-2-amino-2-oxoethoxy)-6-(((S)-2-oxoazepan-3-yl)carbamoyl)-3,4-dihydro-2H-pyran-3,4-diyl diacetate (19). To a stirred solution of **18** (31 mg, 0.053 mmol), 2-(S)-aminocaprolactam (26 mg, 0.16 mmol), HOBt (21 mg, 0.16 mmol) and NMM (58 μ L, 0.53 mmol) in DMF (0.26 mL) was added EDCI (51 mg, 0.26 mmol). After being stirred for 6h at r.t., the reaction was quenched with aq. NaHCO₃, and extracted with CHCl₃/MeOH (9/1). The combined organic extracts were dried over Na₂SO₄ and concentrated *in vacuo*. The crude product was purified by silica gel column chromatography (CHCl₃/MeOH = 95/5) to afford **19** (30 mg, 82%): ¹H NMR (400 MHz, Methanol-*d*₄) δ 7.68 (d, J = 8.2 Hz, 1H), 6.02 (t, J = 2.1 Hz, 1H), 5.91 (d, J = 4.2 Hz, 1H), 5.89 (d, J = 6.3 Hz, 1H), 5.73 (dd, J = 4.4, 2.5 Hz, 1H), 5.68 – 5.65 (m, 1H), 5.51 (d, J = 3.0 Hz, 1H), 5.01 (d, J = 4.6 Hz, 1H), 4.76 (d, J = 2.0 Hz, 1H), 4.62 (d, J = 12.5 Hz, 1H), 4.60 – 4.57 (m, 1H), 3.98 (d, J = 6.1 Hz, 1H), 3.35 (s, 3H), 2.11 (s, 3H), 2.08 (s, 3H), 2.05 (s, 3H), 2.03 – 1.98 (m, 2H), 1.91 – 1.83 (m, 2H), 1.65 – 1.56 (m, 2H), 1.44 – 1.37 (m, 2H); ¹³C NMR (101 MHz, MeOD) δ 176.12, 172.32, 171.66, 171.29, 171.21, 165.96, 160.96, 151.90, 144.61, 141.42, 106.25, 103.54, 98.81, 88.77, 83.41, 79.28, 77.39, 74.79, 64.91, 64.49, 59.26, 57.36, 53.25, 42.36, 32.19, 29.75, 28.94, 20.54, 20.41, 20.32; HRMS (ESI+) m/z calcd for C₂₉H₃₈N₅O₁₅ [M + H] 696.2364, found: 696.2391.

(2S,3S,4S)-2-((1R)-2-Amino-1-((2S,5R)-5-(2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)-3-hydroxy-4-methoxytetrahydrofuran-2-yl)-2-oxoethoxy)-3,4-dihydroxy-N-((S)-2-oxoazepan-3-yl)-3,4-dihydro-2H-pyran-6-carboxamide (3). A solution of **19** (30 mg, 0.043 mmol) in a 5:1 mixture of MeOH and Et₃N (0.60 mL) was stirred for 5h at r.t., and concentrated *in vacuo*. The crude mixture was purified by reverse-phase HPLC [column: Luna® (C18, 10 μ m, 100 Å , 250 x 10 mm), solvents: 15:85 MeOH:H₂O, flow rate:

3.0 mL/min, UV: 254 nm, retention time: 20 min] to afford I-CAP (**3**, 24 mg, 98%): ^1H NMR (400 MHz, Methanol- d_4) δ 7.92 (d, J = 8.1 Hz, 1H), 6.02 (d, J = 3.8 Hz, 1H), 5.88 (d, J = 5.1 Hz, 1H), 5.74 (d, J = 8.1 Hz, 1H), 5.23 (d, J = 5.6 Hz, 1H), 4.67 (d, J = 2.0 Hz, 1H), 4.59 – 4.54 (m, 2H), 4.38 (t, J = 4.2 Hz, 1H), 4.29 (t, J = 5.1 Hz, 1H), 3.98 (t, J = 5.0 Hz, 1H), 3.84 (t, J = 4.6 Hz, 1H), 3.43 (s, 3H), 2.06 – 1.99 (m, 2H), 1.89 – 1.81 (m, 2H), 1.62 – 1.45 (m, 2H), 1.44 – 1.33 (m, 2H); ^{13}C NMR (101 MHz, MeOD) δ 176.27, 173.46, 166.15, 161.85, 152.32, 144.23, 141.91, 109.37, 102.82, 101.22, 90.27, 83.49, 81.02, 78.93, 74.54, 68.51, 63.53, 58.67, 53.35, 42.48, 32.36, 29.91, 29.06; HRMS (ESI+) m/z calcd for $\text{C}_{23}\text{H}_{32}\text{N}_5\text{O}_{12}$ [M + H] 570.2048, found: 570.2071.

(2S,3S,4S,5R,6R)-2-((S)-((3aR,4R,6R,6aR)-6-(3-((Benzyloxy)methyl)-2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)-2,2-dimethyltetrahydrofuro[3,4- d][1,3]dioxol-4-yl)(cyano)methoxy)-6-((2-chloroacetoxy)methyl)tetrahydro-2H-pyran-3,4,5-triyl triacetate (21**). To a stirred suspension of **20** (0.24 g, 0.56 mmol), **14** (0.55 g, 1.12 mmol), MS3Å (0.72 g), and SrCO_3 (0.41 g, 2.80 mmol) in CH_2Cl_2 (14.0 mL) were added AgBF_4 (0.055 g, 0.28 mmol) and NIS (0.25 g, 1.12 mmol) at 0 °C. After being stirred for 12h, the reaction mixture was added Et_3N (1.0 mL), and passed through a silica gel pad (hexanes/EtOAc = 1/4). The filtrate was concentrated *in vacuo*. The crude mixture was purified by silica gel column chromatography (hexanes/EtOAc = 6/4 - 4/6) to afford **21** (0.39 g, 88%): ^1H NMR (400 MHz, Chloroform- d) δ 7.37 – 7.28 (m, 5H), 7.20 (d, J = 8.1 Hz, 1H), 5.82 (d, J = 8.1 Hz, 1H), 5.61 (d, J = 1.6 Hz, 1H), 5.50 (d, J = 9.8 Hz, 1H), 5.42 (d, J = 9.8 Hz, 1H), 5.35 – 5.27 (m, 1H), 5.23 (dd, J = 10.0, 3.3 Hz, 1H), 5.07 (d, J = 1.9 Hz, 1H), 5.00 (d, J = 3.5 Hz, 1H), 4.98 (dd, J = 6.4, 1.6 Hz, 1H), 4.84 (d, J = 7.1 Hz, 1H), 4.69 (s, 2H), 4.43 (dd, J = 7.1, 3.6 Hz, 1H), 4.20 (dd, J = 12.2, 4.3 Hz, 1H), 4.17 – 4.07 (m, 2H), 4.05 (d, J = 1.6 Hz, 2H), 3.97 – 3.92 (m, 1H), 2.16 (s, 3H), 2.02 (s, 3H), 1.98 (s, 3H), 1.59 (s, 3H), 1.39 (s, 3H); ^{13}C NMR (101 MHz, CDCl_3) δ 169.80, 169.57, 169.47, 166.80, 162.08, 150.84, 140.89, 137.67, 128.33 (2C), 127.91, 127.77, 127.63 (2C), 115.23, 114.72, 102.84, 96.56, 96.30, 86.55, 84.15, 80.95, 72.42, 70.41, 69.41, 68.39**

(2C), 66.04, 65.35, 62.90, 40.52, 27.03, 25.20, 20.73, 20.64, 20.59; HRMS (ESI+) m/z calcd for $C_{35}H_{41}ClN_3O_{16}$ [M + H] 794.2175, found: 794.2198.

(2R,3S,4S,5R,6R)-2-((R)-2-Amino-1-((3aR,4S,6R,6aR)-6-(2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)-2,2-dimethyltetrahydrofuro[3,4-*d*][1,3]dioxol-4-yl)-2-oxoethoxy)-6-(hydroxymethyl)tetrahydro-2H-pyran-3,4,5-triyl triacetate (22). To a stirred solution of **21** (0.39 g, 0.49 mmol) in a 9:1 mixture of EtOH and H₂O (4.9 mL) were added HgCl₂ (0.27 g, 0.98 mmol) and acetaldoxime (0.30 mL, 4.9 mmol). After being stirred for 12h at r.t., the reaction mixture was concentrated *in vacuo*. The residue was diluted with aq.NaHCO₃, and extracted with CHCl₃. The combined organic extracts were dried over Na₂SO₄ and concentrated *in vacuo*. The crude product was purified by silica gel column chromatography (hexanes/EtOAc = 1/2 to CHCl₃/MeOH = 97/3) to afford the amide (0.36 g, 91%). To a solution of the amide (0.36 g, 0.45 mmol) in a 1:1 mixture of THF and MeOH (4.5 mL) was added thiourea (0.10 g, 1.34 mmol). After being stirred for 11h at 50 °C, the reaction mixture was concentrated *in vacuo*. The residue was diluted with H₂O, and extracted with CHCl₃. The combined organic extracts were dried over Na₂SO₄ and concentrated *in vacuo*. The crude product was purified by silica gel column chromatography (CHCl₃/MeOH = 98/2 to 97/3 to 96/4) to afford the primary alcohol (0.25 g, 76%). To a stirred solution of the alcohol (0.25 g, 0.34 mmol) and AcOH (0.08 mL) in a 1:1 mixture of THF and ⁱPrOH (4.0 mL) was added 10% Pd/C (0.20 g) under N₂. H₂ gas was introduced and the reaction mixture was stirred under H₂ atmosphere. After being stirred for 4h at r.t., the reaction mixture was filtered through Celite and concentrated *in vacuo*. The crude product was purified by silica gel column chromatography (CHCl₃/MeOH = 96/4 to 92/8) to afford **22** (0.17 g, 80%): ¹H NMR (400 MHz, Chloroform-*d*) δ 9.45 (brs, 1H), 7.34 (d, *J* = 8.0 Hz, 1H), 6.72 (brs, 1H), 6.17 (brs, 1H), 5.78 (d, *J* = 8.0 Hz, 1H), 5.60 (d, *J* = 1.7 Hz, 1H), 5.43 (dd, *J* = 10.1, 3.5 Hz, 1H), 5.33 (dd, *J* = 3.5, 1.7 Hz, 1H), 5.20 (t, *J* = 10.1 Hz, 1H), 5.12 – 5.05 (m, 1H), 5.03 (dd, *J* = 6.4, 1.7 Hz, 1H), 4.98 (s, 1H), 4.46 (d, *J* = 5.8 Hz, 1H), 4.33 (t, *J* = 5.1 Hz, 1H), 3.88 (dt, *J* = 10.1, 4.0

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3 Hz, 1H), 3.60 – 3.53 (m, 2H), 2.14 (s, 3H), 2.07 (s, 3H), 2.02 (s, 3H), 1.55 (s, 3H), 1.35 (s, 3H); ^{13}C NMR
4 (101 MHz, CDCl_3) δ 170.68, 170.40, 170.28, 170.24, 163.27, 150.13, 142.81, 114.72, 102.85, 96.39, 87.34,
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6 84.26, 80.35, 71.92, 69.35, 68.64, 66.03, 61.16, 27.25, 25.42, 20.83, 20.77, 20.74; HRMS (ESI+) m/z calcd
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8 for $\text{C}_{25}\text{H}_{34}\text{N}_3\text{O}_{15}$ [M + H] 616.1990, found: 616.2018.
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13 **(2S,3S,4S)-2-((R)-2-Amino-1-((3aR,4S,6R,6aR)-6-(2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)-2,2-**
14 **dimethyltetrahydrofuro[3,4-d][1,3]dioxol-4-yl)-2-oxoethoxy)-6-(((S)-2-oxoazepan-3-yl)carbamoyl)-**
15 **3,4-dihydro-2H-pyran-3,4-diyl diacetate (23).** To a stirred solution of **22** (0.17 g, 0.27 mmol) and DMSO
16 (0.19 mL, 2.72 mmol) in a 5:1 mixture of CH_2Cl_2 and Et_3N (1.4 mL) was added $\text{SO}_3 \cdot \text{pyridine}$ (0.43 g, 2.72
17 mmol). After being stirred for 3h at r.t., the reaction mixture was added H_2O (0.27 mL) and passed through
18 a silica gel pad ($\text{CHCl}_3/\text{MeOH} = 92/8$). To a stirred solution of the crude mixture in $t\text{BuOH}$ (1.0 mL) and 2-
19 methyl-2-butene (0.5 mL) was added a solution of NaClO_2 (0.12 g, 1.36 mmol) and $\text{NaH}_2\text{PO}_4 \cdot 2\text{H}_2\text{O}$ (0.21
20 g, 1.36 mmol) in H_2O (1.0 mL). After being stirred for 5h at r.t., the reaction was extracted with
21 $\text{CHCl}_3/\text{MeOH}$ (9/1). The combined organic extracts were dried over Na_2SO_4 and concentrated *in vacuo*.
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23 The crude product was purified by silica gel column chromatography ($\text{CHCl}_3/\text{MeOH} = 9/1$) to afford the
24 acid (0.13 g, 81%). To a stirred solution of the acid (28 mg, 0.049 mmol), 2-(S)-aminocaprolactam (24 mg,
25 0.15 mmol), HOBT (20 mg, 0.15 mmol) and NMM (54 μL , 0.49 mmol) in DMF (0.25 mL) was added EDCI
26 (47 mg, 0.25 mmol). After being stirred for 14h at r.t., the reaction was quenched with aq. NaHCO_3 , and
27 extracted with $\text{CHCl}_3/\text{MeOH}$ (9/1). The combined organic extracts were dried over Na_2SO_4 and
28 concentrated *in vacuo*. The crude product was purified by silica gel column chromatography ($\text{CHCl}_3/\text{MeOH}$
29 = 95/5) to afford **23** (30 mg, 89%): ^1H NMR (400 MHz, Methanol- d_4) δ 7.79 (d, $J = 8.0$ Hz, 1H), 5.98 (t, J
30 = 2.0 Hz, 1H), 5.84 (d, $J = 2.8$ Hz, 1H), 5.78 (d, $J = 8.0$ Hz, 1H), 5.62 (dd, $J = 4.5, 2.6$ Hz, 1H), 5.51 – 5.48
31 (m, 1H), 5.45 (d, $J = 3.1$ Hz, 1H), 4.74 (d, $J = 2.8$ Hz, 1H), 4.71 (dd, $J = 6.2, 2.9$ Hz, 1H), 4.65 (dd, $J = 6.2,$
32 3.3 Hz, 1H), 4.59 – 4.55 (m, 2H), 3.76 – 3.67 (m, 4H), 2.09 (s, 3H), 2.04 (s, 3H), 1.86 (d, $J = 13.4$ Hz, 3H),
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3 1.63 – 1.52 (m, 3H), 1.51 (s, 3H), 1.45 – 1.34 (m, 3H), 1.25 (s, 3H); ¹³C NMR (101 MHz, MeOD) δ 176.35,
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5 172.24, 171.62, 171.28, 166.24, 161.14, 151.99, 144.75, 142.76, 115.34, 106.38, 102.91, 98.75, 93.55,
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7 87.12, 85.94, 82.02, 78.13, 67.16, 64.99, 64.46, 56.04, 53.46, 46.10, 42.52, 42.43, 32.25, 29.89, 29.08,
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9 27.47, 25.47, 20.61, 20.52; HRMS (ESI+) *m/z* calcd for C₂₉H₃₈N₅O₁₄ [M + H] 680.2415, found: 680.2432.

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12 **(2*S*,3*S*,4*S*)-2-((1*R*)-2-Amino-1-((2*S*,5*R*)-5-(2,4-dioxo-3,4-dihydropyrimidin-1(2*H*)-yl)-3,4-**
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14 **dihydroxytetrahydrofuran-2-yl)-2-oxoethoxy)-3,4-dihydroxy-*N*-((*S*)-2-oxoazepan-3-yl)-3,4-dihydro-**
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16 **2*H*-pyran-6-carboxamide (4).** A solution of **23** (30 mg, 0.044 mmol) in a 4:1 mixture of TFA and H₂O
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18 (0.88 mL) was stirred for 4h at r.t., and concentrated *in vacuo*. A solution of the crude diol in a 5:1 mixture
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20 of MeOH and Et₃N (0.88 mL) was stirred for 9h at r.t., filtered, and concentrated *in vacuo*. The crude mixture
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22 was purified by reverse-phase HPLC [column: Luna® (C18, 10 μm, 100 Å, 250 x 10 mm), solvents: 15:85
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24 MeOH:H₂O, flow rate: 3.0 mL/min, UV: 254 nm, retention time: 16 min] to afford DM-CAP (**4**, 22 mg,
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26 90%): ¹H NMR (400 MHz, Methanol-*d*₄) δ 7.94 (d, *J* = 8.1 Hz, 1H), 6.03 (d, *J* = 4.5 Hz, 1H), 5.85 (d, *J* =
27
28 3.7 Hz, 1H), 5.73 (d, *J* = 8.2 Hz, 1H), 5.19 (d, *J* = 6.7 Hz, 1H), 4.68 (d, *J* = 1.7 Hz, 1H), 4.61 (dd, *J* = 11.2,
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30 1.4 Hz, 1H), 4.54 (dd, *J* = 5.8, 1.7 Hz, 1H), 4.36 (t, *J* = 4.5 Hz, 1H), 4.30 (t, *J* = 5.5 Hz, 1H), 4.12 (t, *J* = 4.4
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32 Hz, 1H), 3.97 (t, *J* = 5.7 Hz, 1H), 3.90 (t, *J* = 6.5 Hz, 1H), 3.43 – 3.38 (m, 1H), 3.03 (t, *J* = 7.0 Hz, 1H), 2.70
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34 – 2.64 (m, 1H), 2.07 – 1.97 (m, 2H), 1.81 (d, *J* = 15.2 Hz, 2H), 1.62 (q, *J* = 11.9, 10.7 Hz, 1H), 1.39 (s, 1H);
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36 ¹³C NMR (101 MHz, MeOD) δ 176.85, 174.05, 166.21, 162.02, 152.21, 144.60, 141.91, 108.72, 102.50,
37
38 101.60, 90.76, 84.77, 79.50, 75.68, 71.40, 63.63, 60.06, 53.44, 42.50, 31.89, 29.82, 29.14; HRMS (ESI+)
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40 *m/z* calcd for C₂₂H₃₀N₅O₁₂ [M + H] 556.1891, found: 556.1912.

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43 **(2*S*,3*S*,4*S*)-2-((1*R*)-1-((2*S*,5*R*)-4-Acetoxy-5-(2,4-dioxo-3,4-dihydropyrimidin-1(2*H*)-yl)-3-**
44
45 **methoxytetrahydrofuran-2-yl)-2-amino-2-oxoethoxy)-6-((4-(4-(4-**
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47 **(trifluoromethoxy)phenoxy)piperidin-1-yl)benzyl)carbamoyle)-3,4-dihydro-2*H*-pyran-3,4-diyl**
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49 **diacetate (37).** To a stirred solution of **32** (55 mg, 0.094 mmol), **34** (0.10 g, 0.28 mmol), HOBT (38 mg,
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0.28 mmol) and NMM (95 μ L, 0.94 mmol) in DMF (0.47 mL) was added EDCI (90 mg, 0.47 mmol). After being stirred for 7h at r.t., the reaction mixture was quenched with aq.NaHCO₃, and extracted with CHCl₃/MeOH (9/1). The combined organic extracts were dried over Na₂SO₄ and concentrated *in vacuo*. The crude product was purified by silica gel column chromatography (CHCl₃/MeOH = 95/5) to afford **37** (76 mg, 87%): ¹H NMR (400 MHz, Methanol-*d*₄) δ 7.71 (d, *J* = 8.1 Hz, 1H), 7.23 (d, *J* = 8.5 Hz, 2H), 7.19 (d, *J* = 8.8 Hz, 2H), 7.03 (d, *J* = 9.1 Hz, 2H), 6.97 (d, *J* = 8.7 Hz, 2H), 5.97 (t, *J* = 2.1 Hz, 1H), 5.91 (d, *J* = 8.1 Hz, 1H), 5.87 (d, *J* = 3.8 Hz, 1H), 5.74 (dd, *J* = 4.5, 2.4 Hz, 1H), 5.67 (ddd, *J* = 4.5, 2.8, 1.7 Hz, 1H), 5.43 (d, *J* = 2.8 Hz, 1H), 5.28 (dd, *J* = 5.1, 3.8 Hz, 1H), 4.70 (d, *J* = 1.9 Hz, 1H), 4.54 (dq, *J* = 7.5, 3.8 Hz, 1H), 4.42 (d, *J* = 14.5 Hz, 1H), 4.38 (dd, *J* = 6.2, 1.9 Hz, 1H), 4.33 (d, *J* = 14.4 Hz, 1H), 3.82 – 3.79 (m, 1H), 3.48 (td, *J* = 9.0, 6.8, 3.5 Hz, 3H), 3.13 – 3.06 (m, 2H), 3.05 (s, 3H), 2.09 (s, 3H), 2.09 (s, 3H), 2.06 (s, 3H), 1.87 (dtd, *J* = 12.3, 8.2, 3.6 Hz, 3H); ¹³C NMR (101 MHz, MeOD) δ 172.85, 171.84, 171.43, 171.17, 166.07, 162.39, 157.61, 152.11, 151.92, 144.94, 143.92, 141.57, 130.89, 130.02 (2C), 123.59 (2C), 118.04 (2C), 117.98 (2C), 106.19, 103.75, 98.26, 89.36, 83.17, 78.98, 76.60, 74.71, 73.98, 64.75, 59.35, 48.18, 48.16, 31.43 (2C), 20.70, 20.52, 20.49; HRMS (ESI+) *m/z* calcd for C₄₂H₄₇F₃N₅O₁₆ [M + H] 934.2970, found 934.2998.

(2*S*,3*S*,4*S*)-2-((1*R*)-2-Amino-1-((2*S*,5*R*)-5-(2,4-dioxo-3,4-dihydropyrimidin-1(2*H*)-yl)-4-hydroxy-3-methoxytetrahydrofuran-2-yl)-2-oxoethoxy)-3,4-dihydroxy-*N*-(4-(4-(4-(trifluoromethoxy)phenoxy)piperidin-1-yl)benzyl)-3,4-dihydro-2*H*-pyran-6-carboxamide (5). A solution of **37** (76 mg, 0.082 mmol) in a 5:1 mixture of MeOH and Et₃N (1.6 mL) was stirred for 6h at r.t., and concentrated *in vacuo*. The crude mixture was purified by reverse-phase HPLC [column: Luna® (C18, 10 μ m, 100 Å, 250 x 10 mm), solvents: 65:35 MeOH:H₂O, flow rate: 3.0 mL/min, UV: 254 nm, retention time: 18 min] to afford CPPB (**5**, 63 mg, 95%): ¹H NMR (400 MHz, Methanol-*d*₄) δ 7.86 (d, *J* = 8.1 Hz, 1H), 7.20 (dd, *J* = 10.9, 8.6 Hz, 4H), 7.02 (d, *J* = 9.1 Hz, 2H), 6.97 (d, *J* = 8.7 Hz, 2H), 5.98 (dd, *J* = 3.3,

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3 1.0 Hz, 1H), 5.80 (d, $J = 4.4$ Hz, 1H), 5.76 (d, $J = 8.2$ Hz, 1H), 5.21 (d, $J = 4.6$ Hz, 1H), 4.68 (d, $J = 2.0$ Hz,
4 1H), 4.54 (dp, $J = 7.3, 3.6$ Hz, 1H), 4.48 (dd, $J = 5.2, 2.0$ Hz, 1H), 4.44 (d, $J = 14.5$ Hz, 1H), 4.39 (t, $J = 3.9$
5 Hz, 1H), 4.33 (d, $J = 14.6$ Hz, 1H), 4.20 (t, $J = 4.7$ Hz, 1H), 4.06 – 4.02 (m, 1H), 3.66 (t, $J = 5.1$ Hz, 1H),
6 3.52 – 3.45 (m, 3H), 3.19 (s, 3H), 3.08 (ddd, $J = 12.3, 8.6, 3.4$ Hz, 3H), 2.15 – 2.07 (m, 2H), 1.86 (dtd, $J =$
7 12.2, 8.3, 3.5 Hz, 3H); ^{13}C NMR (101 MHz, MeOD) δ 173.68, 166.16, 163.31, 157.62, 152.18, 152.08,
8 144.15, 141.83, 130.91, 129.76 (2C), 123.58 (2C), 118.03 (4C), 109.58, 102.74, 100.64, 90.83, 83.32, 80.35,
9 77.51, 74.27, 74.01, 67.61, 63.48, 58.61, 48.20 (2C), 43.51, 31.47 (2C); HRMS (ESI+) m/z calcd for
10 $\text{C}_{36}\text{H}_{41}\text{F}_3\text{N}_5\text{O}_{13}$ [M + H] 808.2653, found 808.2675.

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22 **(2*S*,3*S*,4*S*)-2-((1*R*)-1-((2*S*,5*R*)-3-Acetoxy-5-(2,4-dioxo-3,4-dihydropyrimidin-1(2*H*)-yl)-4-**
23 **methoxytetrahydrofuran-2-yl)-2-amino-2-oxoethoxy)-6-((4-(4-**
24 **(trifluoromethoxy)phenoxy)piperidin-1-yl)benzyl)carbamoyl)-3,4-dihydro-2*H*-pyran-3,4-diyl**
25 **diacetate (35).** To a stirred solution of **18** (33 mg, 0.056 mmol), **34** (62 mg, 0.17 mmol), HOBt (23 mg,
26 0.17 mmol) and NMM (62 μL , 0.56 mmol) in DMF (0.28 mL) was added EDCI (54 mg, 0.28 mmol). After
27 being stirred for 14h at r.t., the reaction was quenched with aq.NaHCO₃, and extracted with CHCl₃/MeOH
28 (9/1). The combined organic extracts were dried over Na₂SO₄ and concentrated *in vacuo*. The crude product
29 was purified by silica gel column chromatography (CHCl₃/MeOH = 95/5) to afford **35** (43 mg, 82%): ^1H
30 NMR (400 MHz, Methanol-*d*₄) δ 7.69 (d, $J = 8.2$ Hz, 1H), 7.22 (d, $J = 8.5$ Hz, 2H), 7.19 (d, $J = 8.6$ Hz, 2H),
31 7.02 (d, $J = 9.0$ Hz, 2H), 6.98 (d, $J = 8.4$ Hz, 2H), 5.99 – 5.97 (m, 1H), 5.95 (d, $J = 5.8$ Hz, 1H), 5.91 (d, J
32 = 8.1 Hz, 1H), 5.74 – 5.71 (m, 1H), 5.66 – 5.63 (m, 1H), 5.46 (d, $J = 3.2$ Hz, 1H), 5.05 (t, $J = 4.7$ Hz, 1H),
33 4.78 (d, $J = 2.0$ Hz, 1H), 4.57 – 4.52 (m, 1H), 4.49 (d, $J = 14.5$ Hz, 1H), 4.39 – 4.34 (m, 1H), 4.30 (d, $J =$
34 14.7 Hz, 1H), 3.84 – 3.80 (m, 1H), 3.64 (s, 3H), 3.53 – 3.45 (m, 2H), 3.13 – 3.06 (m, 2H), 2.83 (t, $J = 6.5$
35 Hz, 1H), 2.10 (s, 3H), 2.07 (s, 3H), 2.06 (s, 3H), 1.87 (dtd, $J = 12.7, 8.5, 3.5$ Hz, 3H); ^{13}C NMR (101 MHz,
36 MeOD) δ 172.92, 171.74, 171.36, 170.39, 166.18, 162.23, 157.56, 152.06, 151.81, 145.05, 140.90, 130.78,
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3 129.96 (2C), 123.52 (2C), 117.96 (2C), 117.92 (2C), 105.75, 103.47, 98.22, 88.92, 82.72, 78.21, 76.44,
4
5 73.95, 67.92, 64.42, 61.21, 58.65, 58.20, 48.10 (2C), 43.57, 31.38 (2C), 20.60, 20.44, 20.39; HRMS (ESI+)
6
7 *m/z* calcd for C₄₂H₄₇F₃N₅O₁₆ [M + H] 934.2970, found 934.2991.

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10 **(2*S*,3*S*,4*S*)-2-((1*R*)-2-Amino-1-((2*S*,5*R*)-5-(2,4-dioxo-3,4-dihydropyrimidin-1(2*H*)-yl)-3-hydroxy-4-**
11
12 **methoxytetrahydrofuran-2-yl)-2-oxoethoxy)-3,4-dihydroxy-*N*-(4-(4-**
13
14 **(trifluoromethoxy)phenoxy)piperidin-1-yl)benzyl)-3,4-dihydro-2*H*-pyran-6-carboxamide (6). A**
15
16 solution of **35** (43 mg, 0.046 mmol) in a 5:1 mixture of MeOH and Et₃N (0.92 mL) was stirred for 6h at r.t.,
17
18 and concentrated *in vacuo*. The crude mixture was purified by reverse-phase HPLC [column: Luna® (C18,
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20 10 μm, 100 Å, 250 x 10 mm), solvents: 65:35 MeOH:H₂O, flow rate: 3.0 mL/min, UV: 254 nm, retention
21
22 time: 19 min] to afford I-CPPB (**6**, 35 mg, 93%): ¹H NMR (400 MHz, Methanol-*d*₄) δ 7.79 (d, *J* = 8.2 Hz,
23
24 1H), 7.19 (d, *J* = 8.6 Hz, 4H), 7.02 (d, *J* = 9.1 Hz, 2H), 6.98 (d, *J* = 8.5 Hz, 2H), 5.98 (d, *J* = 3.6 Hz, 1H),
25
26 5.94 (d, *J* = 5.1 Hz, 1H), 5.77 (d, *J* = 8.0 Hz, 1H), 5.36 (d, *J* = 5.8 Hz, 1H), 4.67 – 4.65 (m, 1H), 4.61 (d, *J*
27
28 = 2.8 Hz, 1H), 4.48 (dd, *J* = 8.6, 4.6 Hz, 1H), 4.36 – 4.33 (m, 1H), 4.27 (dd, *J* = 5.4, 2.7 Hz, 1H), 3.71 –
29
30 3.65 (m, 2H), 3.51 (d, *J* = 4.4 Hz, 2H), 3.48 (s, 3H), 3.25 – 3.18 (m, 2H), 2.13 – 2.00 (m, 3H), 1.92 – 1.76
31
32 (m, 3H); ¹³C NMR (101 MHz, MeOD) δ 173.68, 166.15, 163.30, 157.62, 152.18, 152.08, 144.15, 141.83,
33
34 130.90, 129.76 (2C), 123.58 (2C), 118.10 (2C), 118.02 (2C), 109.57, 102.73, 100.63, 90.83, 83.32, 80.35,
35
36 77.51, 74.27, 74.01, 67.61, 63.48, 58.61, 48.20 (2C), 43.51, 31.47 (2C); HRMS (ESI+) *m/z* calcd for
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38 C₃₆H₄₁F₃N₅O₁₃ [M + H] 808.2653, found 808.2668.

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41 **(2*S*,3*S*,4*S*)-2-((1*R*)-2-Amino-1-((2*S*,5*R*)-5-(2,4-dioxo-3,4-dihydropyrimidin-1(2*H*)-yl)-3,4-**
42
43 **dimethoxytetrahydrofuran-2-yl)-2-oxoethoxy)-6-((4-(4-(4-(trifluoromethoxy)phenoxy)piperidin-1-**
44
45 **yl)benzyl)carbonyl)-3,4-dihydro-2*H*-pyran-3,4-diyl diacetate (38). To a stirred solution of **33** (38 mg,**
46
47 0.068 mmol), **34** (75 mg, 0.20 mmol), HOBt (28 mg, 0.20 mmol) and NMM (75 μL, 0.68 mmol) in DMF
48
49 (0.34 mL) was added EDCI (65 mg, 0.34 mmol). After being stirred for 7h at r.t., the reaction was quenched
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with aq. NaHCO₃, and extracted with CHCl₃/MeOH (9/1). The combined organic extracts were dried over Na₂SO₄ and concentrated *in vacuo*. The crude product was purified by silica gel column chromatography (CHCl₃/MeOH = 95/5) to afford **38** (53 mg, 86%): ¹H NMR (400 MHz, Methanol-*d*₄) δ 7.75 (d, *J* = 8.2 Hz, 1H), 7.24 (d, *J* = 8.6 Hz, 2H), 7.19 (d, *J* = 8.8 Hz, 2H), 7.02 (d, *J* = 9.1 Hz, 2H), 6.98 (d, *J* = 8.5 Hz, 2H), 5.98 (d, *J* = 2.0 Hz, 1H), 5.96 (d, *J* = 8.1 Hz, 1H), 5.85 (d, *J* = 2.9 Hz, 1H), 5.71 – 5.66 (m, 2H), 5.43 (d, *J* = 2.3 Hz, 1H), 4.70 (d, *J* = 1.9 Hz, 1H), 4.57 – 4.51 (m, 1H), 4.45 – 4.40 (m, 2H), 4.34 (d, *J* = 14.4 Hz, 1H), 3.86 (dd, *J* = 4.9, 2.9 Hz, 1H), 3.79 (t, *J* = 6.5 Hz, 1H), 3.60 (dd, *J* = 6.9, 4.9 Hz, 1H), 3.50 (td, *J* = 7.6, 7.0, 3.3 Hz, 2H), 3.46 (s, 3H), 3.11 (dd, *J* = 8.9, 3.6 Hz, 1H), 3.08 (s, 3H), 2.83 (t, *J* = 6.5 Hz, 1H), 2.14 (dd, *J* = 8.7, 5.4 Hz, 1H), 2.10 (s, 3H), 2.07 (s, 3H), 1.87 (dtd, *J* = 12.5, 8.2, 3.5 Hz, 2H); ¹³C NMR (101 MHz, MeOD) δ 172.98, 171.81, 171.42, 166.22, 162.30, 157.62, 152.12, 151.87, 145.11, 140.96, 130.85, 130.02 (2C), 123.58 (2C), 118.03 (2C), 117.98 (2C), 105.81, 103.54, 98.28, 88.98, 82.79, 82.54, 78.28, 76.50, 74.02, 64.59, 64.49, 61.28, 58.72, 58.27, 48.17 (2C), 43.64, 42.08, 31.45 (2C), 20.67, 20.51; HRMS (ESI+) *m/z* calcd for C₄₁H₄₇F₃N₅O₁₅ [M + H] 906.3021, found 906.3045.

(2*S*,3*S*,4*S*)-2-((1*R*)-2-Amino-1-((2*S*,5*R*)-5-(2,4-dioxo-3,4-dihydropyrimidin-1(2*H*)-yl)-3,4-dimethoxytetrahydrofuran-2-yl)-2-oxoethoxy)-3,4-dihydroxy-*N*-(4-(4-(4-(trifluoromethoxy)phenoxy)piperidin-1-yl)benzyl)-3,4-dihydro-2*H*-pyran-6-carboxamide (7). A solution of **38** (53 mg, 0.059 mmol) in a 5:1 mixture of MeOH and Et₃N (1.2 mL) was stirred for 6h at r.t., and concentrated *in vacuo*. The crude mixture was purified by reverse-phase HPLC [column: Luna® (C18, 10 μm, 100 Å, 250 x 10 mm), solvents: 65:35 MeOH:H₂O, flow rate: 3.0 mL/min, UV: 254 nm, retention time: 21 min] to afford OM-CPPB (**7**, 46 mg, 96%): ¹H NMR (400 MHz, Methanol-*d*₄) δ 7.89 (d, *J* = 8.1 Hz, 1H), 7.22 (d, *J* = 8.4 Hz, 2H), 7.19 (d, *J* = 8.7 Hz, 2H), 7.02 (d, *J* = 9.1 Hz, 2H), 6.96 (d, *J* = 8.5 Hz, 2H), 5.98 (dd, *J* = 3.0, 1.2 Hz, 1H), 5.85 (d, *J* = 3.3 Hz, 1H), 5.76 (d, *J* = 8.1 Hz, 1H), 5.22 (d, *J* = 4.1 Hz, 1H), 4.67 (d, *J* = 1.9 Hz, 1H), 4.57 – 4.51 (m, 1H), 4.46 (dd, *J* = 6.8, 2.0 Hz, 1H), 4.43 (d, *J* = 14.9 Hz, 1H),

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3 4.40 (d, $J = 3.7$ Hz, 1H), 4.32 (d, $J = 14.5$ Hz, 1H), 4.08 (t, $J = 4.2$ Hz, 1H), 3.90 (t, $J = 4.1$ Hz, 1H), 3.70
4
5 (t, $J = 5.5$ Hz, 1H), 3.52 – 3.47 (m, 2H), 3.45 (s, 3H), 3.13 (s, 3H), 3.08 (td, $J = 9.1, 4.6$ Hz, 2H), 2.15 – 2.09
6
7 (m, 2H), 1.91 – 1.82 (m, 2H); ^{13}C NMR (101 MHz, MeOD) δ 173.61, 166.17, 163.21, 157.62, 152.09,
8
9 151.92, 144.02, 141.57, 130.94, 129.89 (2C), 123.59 (2C), 118.03 (2C), 117.98 (2C), 109.78, 102.61,
10
11 100.76, 88.94, 83.23, 82.71, 78.58, 77.02, 74.02, 67.27, 63.42, 60.07, 58.70, 58.37, 48.18, 47.87, 45.76,
12
13 43.53, 31.46 (2C); HRMS (ESI+) m/z calcd for $\text{C}_{37}\text{H}_{43}\text{F}_3\text{N}_5\text{O}_{13}$ [M + H] 822.2809, found 822.2838.

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17 **(2*S*,3*S*,4*S*)-2-((*R*)-2-Amino-1-((3*aR*,4*S*,6*R*,6*aR*)-6-(2,4-dioxo-3,4-dihydropyrimidin-1(2*H*)-yl)-2,2-**
18
19 **dimethyltetrahydrofuro[3,4-*d*][1,3]dioxol-4-yl)-2-oxoethoxy)-6-((4-(4-(4-**
20
21 **(trifluoromethoxy)phenoxy)piperidin-1-yl)benzyl)carbamoyl)-3,4-dihydro-2*H*-pyran-3,4-diyl**
22
23 **diacetate (36).** To a stirred solution of **31** (27 mg, 0.047 mmol), **34** (52 mg, 0.14 mmol), HOBt (19 mg,
24
25 0.14 mmol) and NMM (52 μL , 0.47 mmol) in DMF (0.24 mL) was added EDCI (45 mg, 0.24 mmol). After
26
27 being stirred for 11h at r.t., the reaction was quenched with aq. NaHCO_3 , and extracted with $\text{CHCl}_3/\text{MeOH}$
28
29 (9/1). The combined organic extracts were dried over Na_2SO_4 and concentrated *in vacuo*. The crude product
30
31 was purified by silica gel column chromatography ($\text{CHCl}_3/\text{MeOH} = 95/5$) to afford **36** (37 mg, 84%): ^1H
32
33 NMR (400 MHz, Methanol-*d*₄) δ 7.69 (d, $J = 8.1$ Hz, 1H), 7.20 (t, $J = 9.5$ Hz, 4H), 7.02 (d, $J = 9.2$ Hz, 2H),
34
35 6.98 (d, $J = 8.5$ Hz, 2H), 5.99 (t, $J = 2.0$ Hz, 1H), 5.87 (d, $J = 3.0$ Hz, 1H), 5.83 (d, $J = 8.1$ Hz, 1H), 5.66
36
37 (dd, $J = 4.4, 2.5$ Hz, 1H), 5.57 – 5.54 (m, 1H), 5.41 (d, $J = 3.0$ Hz, 1H), 4.78 (d, $J = 2.3$ Hz, 1H), 4.70 (dd,
38
39 $J = 6.3, 3.1$ Hz, 1H), 4.63 (dd, $J = 6.4, 3.5$ Hz, 1H), 4.57 – 4.52 (m, 1H), 4.39 (s, 2H), 3.79 (t, $J = 6.5$ Hz,
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41 1H), 3.64 (s, 1H), 3.49 (ddd, $J = 10.9, 6.4, 3.6$ Hz, 2H), 3.09 (ddd, $J = 12.4, 8.6, 3.4$ Hz, 2H), 2.83 (t, $J =$
42
43 6.5 Hz, 1H), 2.16 – 2.09 (m, 2H), 2.08 (s, 3H), 2.05 (s, 3H), 1.87 (dtd, $J = 12.1, 8.1, 3.5$ Hz, 2H), 1.53 (s,
44
45 3H), 1.21 (s, 3H); ^{13}C NMR (101 MHz, MeOD) δ 172.59, 171.76, 171.36, 166.16, 162.38, 157.61, 152.04,
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47 151.92, 145.03, 142.46, 130.80, 129.66 (2C), 123.59 (2C), 118.05 (2C), 118.02 (2C), 115.67, 106.20,
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3 103.33, 98.57, 92.78, 86.55, 85.61, 81.72, 77.88, 73.99, 64.84, 64.58, 61.28, 48.20 (2C), 43.59, 31.47 (2C),
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5 27.52, 25.45, 20.66, 20.51; HRMS (ESI+) m/z calcd for $C_{42}H_{47}F_3N_5O_{15}$ [M + H] 918.3021, found 918.3053.

6
7 **(2S,3S,4S)-2-((1R)-2-Amino-1-((2S,5R)-5-(2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)-3,4-**
8
9 **dihydroxytetrahydrofuran-2-yl)-2-oxoethoxy)-3,4-dihydroxy-N-(4-(4-(4-**
10
11 **(trifluoromethoxy)phenoxy)piperidin-1-yl)benzyl)-3,4-dihydro-2H-pyran-6-carboxamide (8).** A
12
13 solution of **35** (37 mg, 0.040 mmol) in a 4:1 mixture of TFA and H₂O (0.80 mL) was stirred for 4h at r.t.,
14
15 and concentrated *in vacuo*. A solution of the crude alcohol in a 5:1 mixture of MeOH and Et₃N (0.80 mL)
16
17 was stirred for 10h at r.t., and concentrated *in vacuo*. The crude mixture was purified by reverse-phase
18
19 HPLC [column: Luna® (C18, 10 μm, 100 Å, 250 x 10 mm), solvents: 35:65 MeOH:H₂O, flow rate: 3.0
20
21 mL/min, UV: 254 nm, retention time: 15 min] to afford DM-CPPB (**8**, 29 mg, 91%): ¹H NMR (400 MHz,
22
23 Methanol-*d*₄) δ 7.92 (d, *J* = 8.1 Hz, 1H), 7.20 (d, *J* = 3.1 Hz, 2H), 7.18 (d, *J* = 3.5 Hz, 2H), 7.02 (d, *J* = 9.1
24
25 Hz, 2H), 6.96 (d, *J* = 8.6 Hz, 2H), 6.01 (d, *J* = 4.4 Hz, 1H), 5.80 (d, *J* = 3.0 Hz, 1H), 5.73 (d, *J* = 8.1 Hz,
26
27 1H), 5.14 (d, *J* = 6.7 Hz, 1H), 4.66 (d, *J* = 1.8 Hz, 1H), 4.57 – 4.51 (m, 1H), 4.50 (dd, *J* = 6.7, 1.7 Hz, 1H),
28
29 4.41 – 4.31 (m, 3H), 4.16 (dd, *J* = 6.6, 5.0 Hz, 1H), 4.04 (dd, *J* = 4.9, 3.0 Hz, 1H), 3.88 (dd, *J* = 6.7, 4.5 Hz,
30
31 1H), 3.47 (t, *J* = 6.2 Hz, 2H), 3.27 (d, *J* = 7.2 Hz, 1H), 3.07 (ddd, *J* = 17.0, 8.1, 4.0 Hz, 2H), 2.37 – 2.29 (m,
32
33 1H), 2.16 – 2.07 (m, 2H), 1.86 (dtd, *J* = 12.3, 8.2, 3.5 Hz, 2H); ¹³C NMR (101 MHz, MeOD) δ 174.07,
34
35 170.14, 166.22, 163.14, 157.62, 152.12, 151.99, 144.89, 141.84, 131.07, 129.64 (2C), 123.58 (2C), 118.08
36
37 (2C), 118.03 (2C), 116.78, 108.52, 102.45, 101.32, 91.15, 84.20, 78.81, 75.49, 74.02, 71.19, 69.27, 63.69,
38
39 60.09, 47.81 (2C), 31.46 (2C); HRMS (ESI+) m/z calcd for $C_{35}H_{39}F_3N_5O_{13}$ [M + H] 794.2496, found
40
41 794.2522.

42
43 **(2R)-2-(((2S,3S,4S)-3,4-Dihydroxy-6-(((4-(4-(4-(trifluoromethoxy)phenoxy)piperidin-1-**
44
45 **yl)benzyl)amino)methyl)-3,4-dihydro-2H-pyran-2-yl)oxy)-2-((2S,5R)-5-(2,4-dioxo-3,4-**
46
47 **dihydropyrimidin-1(2H)-yl)-4-hydroxy-3-methoxytetrahydrofuran-2-yl)acetamide (9).** To a stirred
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3 solution of **16** (5.8 mg, 0.0092 mmol) and DMSO (0.065 mL, 0.92 mmol) in a 5:1 mixture of CH₂Cl₂ and
4
5 Et₃N (0.5 mL) was added SO₃•pyridine (15 mg, 0.092 mmol). After being stirred for 2h at r.t., the reaction
6
7 mixture was added H₂O (0.1 mL) and passed through a silica gel pad (CHCl₃/MeOH = 93/7) to afford the
8
9 crude **17**: this was used without purification. To a stirred solution of the crude **17** and **34** (17 mg, 0.046
10
11 mmol) in CH₃CN (0.5 mL) was added NaB(CN)H₃ (5.8 mg, 0.092 mol). After being stirred for 3h at r.t.,
12
13 the reaction was quenched with aq.NaHCO₃, and extracted with CHCl₃/MeOH (9/1). The combined organic
14
15 extracts were dried over Na₂SO₄ and concentrated *in vacuo*. The crude product was passed through a silica
16
17 gel pad (CHCl₃/MeOH = 9/1). The solution of the crude product in a 5:1 mixture of MeOH and Et₃N (0.5
18
19 mL) was stirred for 8h at r.t., and concentrated *in vacuo*. The crude mixture was purified by reverse-phase
20
21 HPLC [column: Luna® (C18, 10 μm, 100 Å, 250 x 10 mm), solvents: 65:35 MeOH:H₂O, flow rate: 3.0
22
23 mL/min, UV: 254 nm, retention time: 15 min] to afford CPPA (**9**, 4.6 mg, 65% for 3 steps): ¹H NMR (400
24
25 MHz, Methanol-*d*₄) δ 8.02 (d, *J* = 8.1 Hz, 1H), 7.24 (d, *J* = 8.5 Hz, 2H), 7.19 (d, *J* = 8.5 Hz, 2H), 7.03 (d, *J*
26
27 = 8.9 Hz, 2H), 6.99 (d, *J* = 8.5 Hz, 2H), 5.90 (d, *J* = 5.4 Hz, 1H), 5.76 (d, *J* = 7.8 Hz, 1H), 5.73 (d, *J* = 8.1
28
29 Hz, 1H), 5.06 (d, *J* = 6.6 Hz, 1H), 4.57 (dd, *J* = 6.4, 3.0 Hz, 1H), 4.52 (td, *J* = 4.4, 1.7 Hz, 1H), 4.33 (t, *J* =
30
31 5.2 Hz, 1H), 4.26 (d, *J* = 26.3 Hz, 1H), 4.18 (d, *J* = 1.6 Hz, 1H), 3.90 – 3.77 (m, 3H), 3.55 – 3.50 (m, 2H),
32
33 3.49 (s, 3H), 3.15 – 3.06 (m, 3H), 2.16 – 2.07 (m, 3H), 1.86 (m, *J* = 8.8, 4.3 Hz, 3H); ¹³C NMR (101 MHz,
34
35 MeOD) δ 174.07, 165.86, 163.68, 157.58, 151.26, 144.88, 142.07, 131.25, 129.37 (2C), 123.22 (2C), 118.03
36
37 (4C), 109.57, 102.60, 100.40, 90.92, 83.37, 80.46, 77.56, 74.63, 73.77, 73.15, 67.78, 63.30, 58.33, 48.19
38
39 (2C), 43.21, 30.74 (2C); HRMS (ESI+) *m/z* calcd for C₃₆H₄₃N₃F₅O₁₂ [M + H] 794.2860, found 794.2877.

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41
42 **(2R)-2-(((2S,3S,4S)-3,4-Dihydroxy-6-(((4-(4-(4-(trifluoromethoxy)phenoxy)piperidin-1-**
43
44 **yl)benzyl)amino)methyl)-3,4-dihydro-2H-pyran-2-yl)oxy)-2-((2S,5R)-5-(2,4-dioxo-3,4-**
45
46 **dihydropyrimidin-1(2H)-yl)-3-hydroxy-4-methoxytetrahydrofuran-2-yl)acetamide (10)**. To a stirred
47
48 solution of **26** (4.6 mg, 0.0073 mmol) and DMSO (0.052 mL, 0.73 mmol) in a 5:1 mixture of CH₂Cl₂ and
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Et₃N (0.5 mL) was added SO₃•pyridine (12 mg, 0.073 mmol). After being stirred for 2h at r.t., the reaction mixture was added H₂O (0.1 mL) and passed through a silica gel pad (CHCl₃/MeOH = 93/7) to afford the crude **29**. To a stirred solution of the crude **29** and **34** (13 mg, 0.036 mmol) in CH₃CN (0.5 mL) was added NaB(CN)H₃ (4.6 mg, 0.073 mol). After being stirred for 3h at r.t., the reaction was quenched with aq.NaHCO₃, and extracted with CHCl₃/MeOH (9/1). The combined organic extracts were dried over Na₂SO₄ and concentrated *in vacuo*. The crude product was passed through a silica gel pad (CHCl₃/MeOH = 9/1). A solution of the crude product in a 5:1 mixture of MeOH and Et₃N (0.5 mL) was stirred for 8h at r.t., and concentrated *in vacuo*. The crude mixture was purified by reverse-phase HPLC [column: Luna® (C18, 10 μm, 100 Å, 250 x 10 mm), solvents: 65:35 MeOH:H₂O, flow rate: 3.0 mL/min, UV: 254 nm, retention time: 15 min] to afford I-CPPA (**10**, 3.6 mg, 63% for 3 steps): ¹H NMR (400 MHz, Methanol-*d*₄) δ 8.04 (d, *J* = 8.1 Hz, 1H), 7.23 (d, *J* = 8.4 Hz, 2H), 7.19 (d, *J* = 8.7 Hz, 2H), 7.03 (d, *J* = 9.1 Hz, 2H), 6.98 (d, *J* = 8.5 Hz, 2H), 5.94 (d, *J* = 3.6 Hz, 1H), 5.74 (d, *J* = 8.1 Hz, 1H), 5.72 (d, *J* = 8.1 Hz, 1H), 5.06 (s, 1H), 4.59 – 4.52 (m, 2H), 4.43 – 4.38 (m, 1H), 4.28 (t, *J* = 5.4 Hz, 1H), 4.25 (t, *J* = 4.4 Hz, 1H), 4.21 (d, *J* = 1.5 Hz, 1H), 4.14 (dd, *J* = 8.3, 4.9 Hz, 1H), 3.88 – 3.85 (m, 2H), 3.82 (d, *J* = 8.2 Hz, 2H), 3.53 (s, 3H), 3.13 (ddd, *J* = 12.3, 8.7, 3.3 Hz, 2H), 2.11 (d, *J* = 9.7 Hz, 3H), 1.87 (ddt, *J* = 13.3, 8.9, 4.1 Hz, 3H); ¹³C NMR (101 MHz, MeOD) δ 173.92, 165.98, 162.46, 157.87, 151.93, 143.90, 140.73, 130.53, 129.43 (2C), 123.29 (2C), 118.10 (2C), 117.87 (2C), 109.98, 103.08, 100.53, 91.27, 83.47, 80.53, 78.03, 74.70, 73.54, 67.84, 63.75, 58.42, 57.46, 48.20, 43.48 (2C), 31.49 (2C); HRMS (ESI+) *m/z* calcd for C₃₆H₄₃N₃F₅O₁₂ [M + H] 794.2860, found 794.2885.

(2*S*,3*S*,4*S*)-2-((1*R*)-2-Amino-1-((2*S*,5*R*)-5-(2,4-dioxo-3,4-dihydropyrimidin-1(2*H*)-yl)-4-hydroxy-3-methoxytetrahydrofuran-2-yl)-2-oxoethoxy)-3,4-dihydroxy-3,4-dihydro-2*H*-pyran-6-carboxylic acid (A-500359F). A solution of **32** (18 mg, 29 μmol) in a 5:1 mixture of MeOH and Et₃N (0.5 mL) was stirred for 5h at r.t., and concentrated *in vacuo*. The crude mixture was purified by reverse-phase HPLC [column:

Luna® (C18, 10 μm , 100 \AA , 250 x 10 mm), solvents: 15:85 MeOH:H₂O, flow rate: 3.0 mL/min, UV: 254 nm, retention time: 14 min] to afford A-500359F (12 mg, 96%): ¹H NMR (400 MHz, Deuterium Oxide) δ 7.75 (d, J = 8.1 Hz, 1H), 5.88 (d, J = 8.1 Hz, 1H), 5.80 (dd, J = 2.5, 1.6 Hz, 1H), 5.78 (d, J = 4.0 Hz, 1H), 5.25 (d, J = 3.2 Hz, 1H), 4.71 (d, J = 2.1 Hz, 1H), 4.48 (dd, J = 5.7, 2.1 Hz, 1H), 4.43 (dd, J = 4.5, 2.5 Hz, 1H), 4.30 (dd, J = 5.1, 4.0 Hz, 1H), 4.12 (ddd, J = 4.8, 3.3, 1.7 Hz, 1H), 3.73 (t, J = 5.4 Hz, 1H), 3.35 (s, 3H); ¹³C NMR (101 MHz, D₂O) δ 173.32, 168.26, 166.06, 151.29, 144.11, 140.79, 108.44, 101.93, 98.62, 89.42, 81.99, 78.20, 75.00, 72.10, 64.43, 62.19, 57.93; HRMS (ESI+) m/z calcd for C₁₇H₂₂N₃O₁₂ [M + H] 460.1204, found 460.1215.

Synthesis of CPPB (5) in Scheme 4. To a stirred solution of A-500359F (11 mg, 0.024 mmol), **34** (26 mg, 0.072 mmol), Glyceroacetone-Oxyma (16 mg, 0.072 mmol)⁵⁴ and NMM (26 mL, 0.24 mmol) in DMF (0.49 mL) was added EDCI (23 mg, 0.12 mmol). After being stirred for 5h at r.t., the reaction mixture was filtered, and diluted with water. The product was extracted with CHCl₃/MeOH (9/1). The combined extracts were derived over Na₂SO₄, and concentrated *in vacuo*. The crude mixture was purified by DOWEX 50Wx4 (MeOH : NH₄OH = 4 : 1) followed by reverse-phase HPLC [column: Luna (C₁₈, 10 mm, 100 \AA , 250 x 10 mm), solvents: 65:35 MeOH : H₂O, flow rate: 3.0 mL/min, UV: 254 nm, retention time: 18 min] to afford **5** (17 mg, 92%). All physical data were identical to that of CPPB synthesized in Scheme 3A.

Expression and purification of HyMraY. The gene *mraY* of *Hydrogenivirga spp.* 128-5-R1-1 was cloned with a *N*-terminal His₆ tag into a pET22b vector. The plasmid was transformed and expressed in *E. coli* NiCo21(DE3) pLEMO competent cells. The proteins were purified using a nickel, cation exchange, and size exclusion chromatography. The final storage buffer was 20 mM HEPES pH 7.5, 100 mM NaCl, 10% glycerol, 5 mM β ME, 0.15% decyl β -D-maltopyranoside (DM).

Expression and purification of MjAgIH. The gene *mj1113* of *Methanocaldococcus jannaschii* DSM 2661 was cloned with a *N*-terminal His₉ tag into a pET33b-derived vector. The plasmid was transformed

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3 and expressed in *E. coli* NiCo21(DE3) pLEMO competent cells. The proteins were purified using cobalt
4 and size exclusion chromatography. The final storage buffer was 20 mM Tris-HCl, pH 7.5, 100 mM NaCl,
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6 5% glycerol, 5 mM β ME, 0.15% DM.
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10 **Preparation of membrane fraction P-60 containing WecA.** *E. coli* B21 wecA strain were harvested by
11 centrifugation (4,700 rpm) at 4 °C followed by washing with 0.9% saline solution (thrice).^{9,58} The washed
12 cell pellets were washed with homogenization buffer (containing 50 mM K_2HPO_4 , 5 mM $MgCl_2$, 5 mM 1,4-
13 dithio-DL-threitol, and 10% glycerol, pH = 7.2) (thrice), and approximately 5 g of pellet (wet weight) was
14 collected. The washed cell pellets were suspended in homogenization buffer and disrupted by probe
15 sonication on ice (5sec on and 2sec off for 1 min, then cool down for 1.5min, 5 cycles, cool down for 15min,
16 and then, 5sec on and 2sec off for 1min, cool down for 1.5min, 5 cycles). The resulting suspension was
17 centrifuged at 4,700 xg for 15min at 4 °C to remove unbroken cells. The lysate was centrifuged at 25,000
18 xg for 20min. at 4 °C. The supernatant was subjected to ultracentrifugation at 60,000 xg for 1h at 4 °C. The
19 supernatant was discarded, and the membrane fraction containing WecA enzyme (P-60) was suspended in
20 the Tris-HCl buffer (pH = 7.5). Total protein concentrations were approximately 8 to 10 mg/mL. Aliquots
21 were stored in Eppendorf tubes at -80 °C.
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37 **DPAGT1 expression and purification.** DPAGT1 was expressed in suspended Expi293 cells for 36h.
38 The cells were lysed by drawing through a 26g needle (10 times) and membrane protein was extracted using
39 buffer containing 1% decyl β -D-maltopyranoside detergent. DPAGT1 was purified using HA-agarose resin
40 and a superdex 200 size exclusion column.
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47 **MraY assay.** MraY assay substrates, Park's nucleotide- N^{ϵ} -C₆-dansylthiourea, neryl phosphate, were
48 chemically synthesized according to the reported procedures.⁷ Park's nucleotide- N^{ϵ} -C₆-dansylthiourea (2
49 mM stock solution, 1.88 μ L), $MgCl_2$ (0.5 M, 5 μ L), KCl (2 M, 5 μ L), Triton X100 (0.5%, 5.63 μ L), Tris-
50 HCl buffer (pH 8.0, 50 mM), neryl phosphate (0.1 M, 2.25 μ L), and inhibitor molecule (0 - 50 μ g/mL in
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Tris-HCl buffer) were placed in a 1.5 mL Eppendorf tube. To a reaction mixture, P-60 (10 μ L) was added (total volume of reaction mixture: 50 μ L adjust with Tris-HCl buffer). The reaction mixture was incubated for 2h at r.t. (26 $^{\circ}$ C) and quenched with CHCl_3 (100 μ L). Two phases were mixed via vortex and centrifuged at 25,000 xg for 10min. The aqueous phase was assayed via reverse-phase HPLC. The water phase (10 μ L) was injected into HPLC (solvent: $\text{CH}_3\text{CN}/0.05 \text{ M aq. NH}_4\text{HCO}_3 = 25:75$; UV: 350 nm; flow rate: 0.5 mL/min; column: Kinetex 5 μm C8, 100 A, 150 x 4.60 mm), and the area of the peak for lipid I-neryl derivative was quantified to obtain the IC_{50} value. The IC_{50} values were calculated from plots of the percentage product inhibition versus the inhibitor.

WecA assay. WecA assay substrate, UDP-Glucosamine- C_6 -FITC was chemically synthesized according to the reported procedures.^{9,11,59} UDP-Glucosamine- C_6 -FITC (UDP-GlcN- C_6 -FITC, 2 mM stock solution, 0.56 μ L), MgCl_2 (0.5 M, 4 μ L), β -mercaptoethanol (50 mM, 5 μ L), CHAPS (5%, 11.3 μ L), Tris-HCl buffer (pH 8.0, 50 mM), undecaprenyl phosphate (4 mM, 1.4 μ L), and inhibitor molecule (0 - 50 $\mu\text{g}/\text{mL}$ in Tris-HCl buffer) were placed in a 1.5 μ L Eppendorf tube. To a reaction mixture, P-60 (10 μ L) was added (total volume of reaction mixture: 50 μ L adjust with Tris-HCl buffer). The reaction mixture was incubated for 2h at 37 $^{\circ}$ C and quenched with n-butanol (150 μ L). Two phases were mixed via vortex and centrifuged at 10,000 xg for 3min. The upper organic phase was assayed via reverse-phase HPLC. The organic phase (30 μ L) was injected into HPLC (solvent: gradient elution of 85:15 to 95:5 MeOH/0.05 M aq. NH_4HCO_3 ; UV: 485 nm; flow rate: 0.5 ml/ min; column: Kinetex 5 μm C8, 100 \AA , 150 x 4.60 mm), and the area of the peak for C_{55} -P-P-GlcN- C_6 -FITC was quantified to obtain the IC_{50} value. The IC_{50} values were calculated from plots of the percentage product inhibition versus the inhibitor concentration.

AgIH assay. AgIH assays were performed as the procedure described for WecA assays, but used *Mj*AgIH and α -dihydroundecaprenyl phosphate (C_{55} -dolichyl phosphate) instead of WecA and undecaprenyl phosphate. UDP-GlcN- C_6 -FITC (2 mM stock solution, 0.56 μ L), MgCl_2 (0.5 M, 4 μ L), β -mercaptoethanol

(50 mM, 5 μ L), CHAPS (5%, 11.3 μ L), Tris-HCl buffer (pH 8.0, 50 mM), C₅₅-dolichyl phosphate (4 mM, 1.4 μ L), and inhibitor molecule (0 - 50 μ g/mL in Tris-HCl buffer) were placed in a 1.5 μ L Eppendorf tube. To a reaction mixture, AgIH solution (10 μ L) was added (total volume of reaction mixture: 50 μ L adjusted with Tris-HCl buffer). The reaction mixture was incubated for 2h at 37 °C and quenched with n-butanol (150 μ L). Two phases were mixed via vortex and centrifuged at 10,000 \times g for 3min. The upper organic phase was assayed via reverse-phase HPLC. The organic phase (30 μ L) was injected into HPLC (solvent: gradient elution of 85:15 to 95:5 MeOH/0.05 M aq. NH₄HCO₃; UV: 485 nm; flow rate: 0.5 ml/min; column: Kinetex 5 μ m C8, 100 Å, 150 x 4.60 mm), and the area of the peak for C₅₅-P-P-GlcN-C₆-FITC was quantified to obtain the IC₅₀ value. The IC₅₀ values were calculated from plots of the percentage product inhibition versus the inhibitor concentration.

DPAGT1 assay. DPAGT1 assays were performed as the procedure described for AgIH assays, but used DPAGT1.

Cell lines. The human primary PDAC cell lines PANC-1 (ATCC CRL 1469); Capan-2 (ATCC HTB-80) and metastatic PDAC cell lines Capan-1 (ATCC HTB-79), AsPC-1 (ATCC CRL-1682), L1210 (ATCC CCL-219), KB (ATCC CCL-17), HeLa, SiHa (ATCC HTB-35), HCT-116 (ATCC CCL-247), DLD-1 (ATCC CCL221), hTERT-HPNE (ATCC CRL-4023), Vero (ATCC CCL-81) were purchased from the ATCC. The cell lines were cultured and maintained in the media as recommended by the supplier. The cell lines were regularly tested for mycoplasma contamination and authenticated. In addition to ATCC cell lines, Dr. Glazer's lab generated patient-derived PDAC cell line, PD002. PD002 Cells were maintained and cultured in DMEM medium supplemented with 20% FBS and 100 IU/mL penicillin and incubated at 37°C with 5% CO₂.

MTT cytotoxicity assay. To study the effect of treatment with DPAGT1 inhibitors on the growth and proliferation of cells, a fixed number of cells (5 x 10⁴ cells/well, 196 μ L) were plated in a 96 well plate. Into

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3 each well 5 μL of drug concentration was added. After 72h of incubation with drugs at 37 $^{\circ}\text{C}$, 5% CO_2 , 10
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5 μL of MTT solution (5 mg/mL in PBS) was added and incubated another 3h at 37 $^{\circ}\text{C}$, 5% CO_2 . The medium
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7 was removed, and DMSO (200 μL /well) was added. Viability was assessed on the basis of cellular
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9 conversion of MTT into a purple formazan product. The absorbance of the colored formazan product was
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11 measured at 570 nm by BioTek Synergy HT Spectrophotometer.
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15 **Kinetic proliferation assay.** To study the effect of treatment with DPAGT1 inhibitors on the growth and
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17 proliferation of cells, a fixed number of cells (2×10^4) were plated in multiple wells of a 96 well plate,
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19 incubated for 24h to let cells settle down. Then, CPPB (**5**) was added (0-50 μM). Images were obtained
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21 every 4h using an IncuCyte Live-Cell Imaging System (Essen BioScience, Ann Arbor, MI). After 72h, cell
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23 proliferation was quantified using the metric phase object confluence (POC), a measurement of the area of
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25 the field of view that is covered by cells, which is calculated by the integrated software.
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29 **Scratch assay.** A confluent monolayer was formed in 24-well plates. The monolayer was scratched by a
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31 sterile 200 μL pipette tip and washed with PBS to remove cell debris. Complete medium with CPPB (**5**) (0,
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33 0.05, 0.1, 0.2 μM) were added and scratched areas were photographed with microscope. The scratched cells
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35 were incubated at 37 $^{\circ}\text{C}$, 5% CO_2 . After 24h, medium was removed and cells were stained with a 1:1 mixture
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37 of crystal violet and PBS for 5min, washed with PBS twice, and photographed with microscope. Wound
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39 areas were measured and recovered areas were calculated.
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43 **Cell migration assays using transwell chamber.** Cell migration assay was performed using Boyden
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45 chamber (Thermo Fisher). PD002 cells ($\sim 10^4$ cells/mL) were seeded in 96-wells plate (Corning, HTS
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47 Transwell-96 Well Permeable Supports, pore size: 8 μm) in FBS free media and the lower chambers were
48
49 filled with 10% FBS medium. CPPB, tunicamycin, or gemcitabine (0.1 μM) was added to the upper
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51 chamber. The cells were incubated for 18h at 37 $^{\circ}\text{C}$ under 5% CO_2 . The cells were fixed using 4%
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3 paraformaldehyde for 0.5h and stained with 0.05% crystal violet (300 μ L/well), after 0.5h, images were
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5 captured via 10X magnification microscopy.
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8 **Reagents, antibodies, and cell treatments.** All the primary and secondary antibodies used were obtained
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10 from Cell Signaling Technology.
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12 **SDS-PAGE and Western blotting assay.** The medium of the cells grown in 10 cm cell culture plate was
13 removed, and the cells were washed once with PBS, and lysed with Pierce RIPA buffer (Thermo Scientific,
14 Cat. # 89901) containing 1x Pierce protease and phosphatase inhibitors (Thermo Scientific, Cat. # 88668).
15 The cell lysate was pelleted down at 15,200 xg at 4 °C for 15min, the cell supernatant was transferred to a
16 fresh Eppendorf tube, and 5 μ L of sample was quantitated by using (Quick Start Bradford Dyed Reagent,
17 Biorad, Cat. # 500-0205). 50 μ g of each protein sample was analyzed by SDS-PAGE (10% gel) followed
18 by Western blotting, and autoradiography. Precision Plus Dual Color (Biorad, Cat. # 161-0374) was used
19 as protein standard marker. Clarity Western ECL Substrate (Biorad, Cat. # 170-5060) was used to develop
20 the probe signal, and Classic Blue BX film (MidSci, Ref. # 604 5983) was used for autoradiography.
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33 **Immunofluorescent staining.** A confluent monolayer was formed in Nunc™ Lab-Tek™ II CC2™
34 chamber slide (8 well, Thermo Scientific, Cat. # 154941PK). Complete medium with CPPB (5, 0-20 μ M)
35 was added and incubated at 37 °C under 5% CO₂. After 24h, medium was removed and cells were washed
36 with PBS (3 times), then fixed with 4% paraformaldehyde in PBS for 0.5h at 4 °C. After washing with 0.2%
37 Tween-20/PBS (3 times), the cells were treated with a blocking buffer (0.2% Tween-20, 1% NGS, 1% BSA
38 in PBS) for 2h at 4 °C. The cells were treated with primary antibody in blocking buffer (0.4% v/v) for 12h
39 at 4 °C. The cells were washed with 0.2% Tween-20 in PBS (3 times) and treated with secondary antibody
40 (Donkey anti-Rabbit IgG (H+L) Highly Cross-Adsorbed Secondary Antibody, Alexa Fluor 555 (Invitrogen,
41 Cat. # A31572)) in blocking buffer (0.2% v/v) for 2h at r.t. in the dark. After additional washing (3 times)
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3 with 0.2% Tween-20/PBS, the cells were treated with DAPI Fluoromount-G[®] (SouthernBiotech, Cat. #
4 0100-20) and covered with glass slide for fluorescence microscopy analysis.
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8 **Reverse transcription-quantitative polymerase chain reaction (RT-qPCR).** Total RNA was extracted
9 from PD002 (~10⁶) cells using a RNeasy Mini kit (Qiagen, Inc., Valencia, CA, USA) after the treatment
10 with CPPB or tunicamycin (0-10 μM) for 24h. Expression was measured by Kapa probe fast qPCR Master
11 Mix (2X) (KAPA BIOSYSTEMS; Wilmington, MA, USA) with S19 as an endogenous control. Primer
12 sequences were as follow; *DPAGT1*, forward, 5'-tcagggacaaagagatctgga-3'; reverse, 5'-
13 cagcatggtttgttctaagtctt-3'. The PCR cycling conditions were performed with total 45 cycles at 95 °C for
14 10sec and 60 °C for 10sec, 72 °C for 10sec, and cooled down at 40 °C for 30sec. Relative mRNA expression
15 changes were calculated by the 2- $\Delta\Delta C_q$ method.
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26 **Synergistic effect of CPPB with paclitaxel.** The synergistic or antagonistic activities of CPPB (5) with
27 paclitaxel were assessed *in vitro* via micro dilution broth checkerboard technique.⁴⁸ PD002 cells (180 μL,
28 1x10⁴/mL) were places in each well of a 96well plate. The cells were treated with a combination of CPPB
29 (0-50 μM) and paclitaxel (5-0.024 μM), and cultured at 37 °C for 72h under 5% CO₂. Antiproliferation
30 kinetic of each well were monitored by using an IncuCyte Live-Cell Imaging System (Essen BioScience,
31 Ann Arbor, MI). At the endpoint, MTT assays were performed. The FIC index was calculated according to
32 the following equation. $\Sigma FIC = FIC_A + FIC_B = C_A/MIC_A + C_B/MIC_B$ where, MIC_A and MIC_B: MIC of drugs A
33 and B, C_A and C_B=concentrations of drugs A and B used in combination. In these interaction studies, ΣFIC
34 of less than 0.5 represents synergistic activity.
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47 **Computational methods – DPAGT1 inhibitor study.** Protein preparation: All molecular modeling and
48 docking studies were performed using the experimental structure of the human GPT (DPAGT1, H129
49 variant) with bound tunicamycin (PDB 6BW6).²⁵ The biological unit was downloaded and prepared using
50 the Protein Preparation Wizard of the Maestro Small Molecule Drug Discovery Suite (Schrödinger, LLC).⁴⁹
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3 Hydrogens were added, when applicable, and protonation and tautomeric states were assigned using the
4 Epic program.⁶⁰ Lone waters were removed and the protein was refined by optimizing H-bond assignments
5 and performing a restrained minimization using MacroModel.⁵⁰ Docking site preparation: The docking
6 receptor grid was prepared using Schrödinger's Glide program.^{51,61} The docking grid was defined as 25 Å
7 region centroid of the bound tunicamycin compound. Van der Waals radius scaling was employed with a
8 scaling factor of 1.0 and partial charge cutoff of 0.25 (default values). No docking constraints or excluded
9 volumes were defined. Hydroxyl and thiol groups within close proximity to the bound tunicamycin
10 compound ($\leq 3\text{Å}$) were defined as rotatable. Inhibitor docking: Compounds were built and prepared for
11 docking using the LigPrep program using default settings (Schrödinger, LLC). The DPAGT1 inhibitors,
12 non-inhibitors, and weak inhibitor reported herein were docked into the prepared protein using
13 Schrödinger's Glide program using XP (extra precision) settings using the grid described above.⁶² Glide XP
14 score for CPPB (5), I-CPPB (6), CPPA (9), I-CPPA (10), OM-CPPB (7), DM-CPPB (8), I-CAP (10), OM-
15 CAP (2), and CAP (1) are summarized in Table S1 in Supporting Information.
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35 ASSOCIATED CONTENT

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38 **Supporting Information** This material is available free of charge via the Internet at <http://pubs.acs.org>.

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42 NMR spectra of the compounds in the Experimental Section, all assay data, HPLC chromatogram of new
43 compounds, assay procedures, and molecular formula string (CSV)
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2
3 gratefully acknowledge Miss Shakiba Eslamimehr and Mr. David Mingle for their efforts in culturing
4
5 several cancer cell lines used in this article.
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8 9 **DEDICATION**

10 This article is dedicated to the memory of Dr. Isao Kitagawa, Professor Emeritus of Pharmaceutical sciences
11
12 at Osaka University, an inspirational scientist.
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15

16 17 **ABBREVIATIONS**

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19 THF, tetrahydrofuran; CH₂Cl₂, methylene chloride; DMSO, dimethyl sulfoxide; DMF, *N,N*-
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21 dimethylformamide; MeOH, methanol; EtOH, ethanol; iPrOH, isopropanol; *t*BuOH, *tert*-butanol; EtOAc,
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23 ethyl acetate; CHCl₃, chloroform; HRMS, high resolution mass spectrometry; HPLC, high performance
24
25 liquid chromatography; TLC, thin layer chromatography; Bu, *n*-butyl; Ts, *p*-toluenesulfonyl; DMAP, *N,N*-
26
27 dimethyl-4-aminopyridine; Boc, *tert*-butoxycarbonyl; EDCI, 1-(3-dimethylaminopropyl)-3-
28
29 ethylcarbodiimide hydrochloride; AcOH, acetic acid; Et₃N, triethylamine; NIS, *N*-iodosuccinimide; TFA,
30
31 2,2,2-trifluoroacetic acid; MS, molecular sieve; ATCC, American type culture collection; SAR, structure–
32
33 activity relationship; MIC, minimum inhibitory concentration; FIC, fractional inhibitory concentration;
34
35 MTT, 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide; OD, optical density; PBS, phosphate-
36
37 buffered saline; FBS, fetal bovine serum; NADPH, nicotinamide adenine dinucleotide phosphate; UDP-
38
39 GlcNAc, uridine diphosphate *N*-acetylglucosamine; UMP, uridine monophosphate; RT-qPCR, reverse
40
41 transcription quantitative real time polymerase chain reaction; CAP, capuramycin; OM-CAP, *O*-methyl
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43 capuramycin; DM-CAP, demethyl capuramycin; CPPB, capuramycin phenoxypiperidinylbenzylamide; I-
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45 CPPB, *iso*-capuramycin phenoxypiperidinylbenzylamide; OM-CPPB, *O*-methyl capuramycin
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47 phenoxypiperidinylbenzylamide; DM-CPPB, demethyl capuramycin phenoxypiperidinylbenzylamide;
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3 CPPA, capuramycin phenoxy piperidiny benzylamine; I-CPPA, iso-capuramycin
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5 phenoxy piperidiny benzylamine.
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Scheme, Figure, and Table and Their Legends:

Artwork

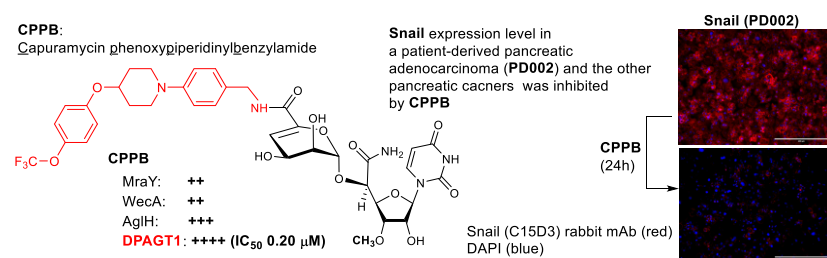


Figure 1. Development of DPAGT1 Inhibitors of Capuramycin Analogues. Structures of Capuramycin, *O*-Methyl capuramycin (OM-Cap), Capuramycin phenoxy piperidiny benzylamide analogue (CPPB), Aminouridyl phenoxy piperidiny benzylbutanamide (APPB, Previously Reported DPAGT1 Inhibitor), and Tunicamycin (Reference Molecule).

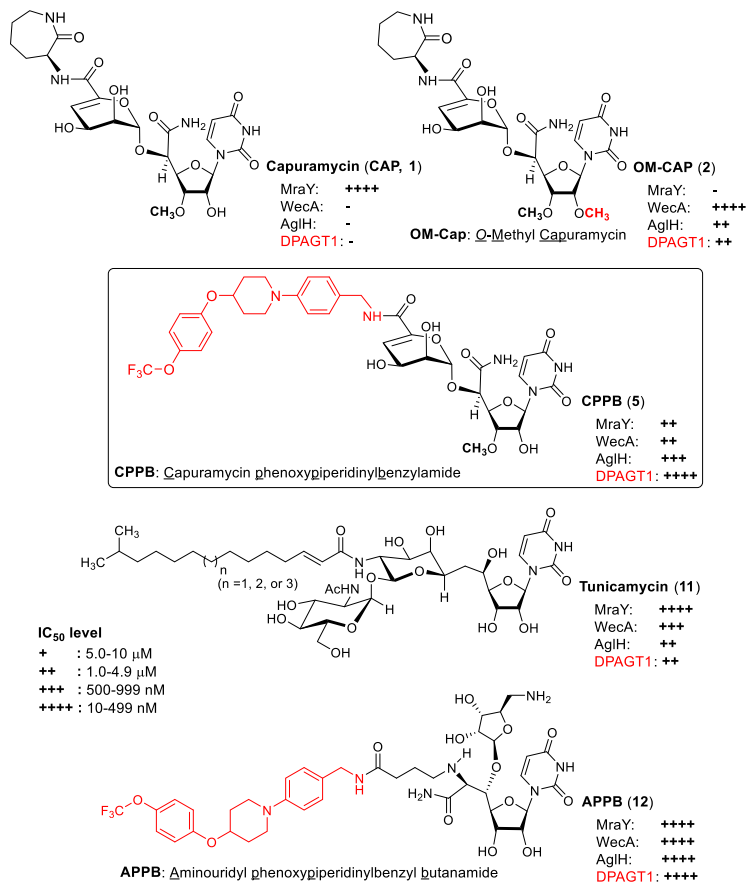
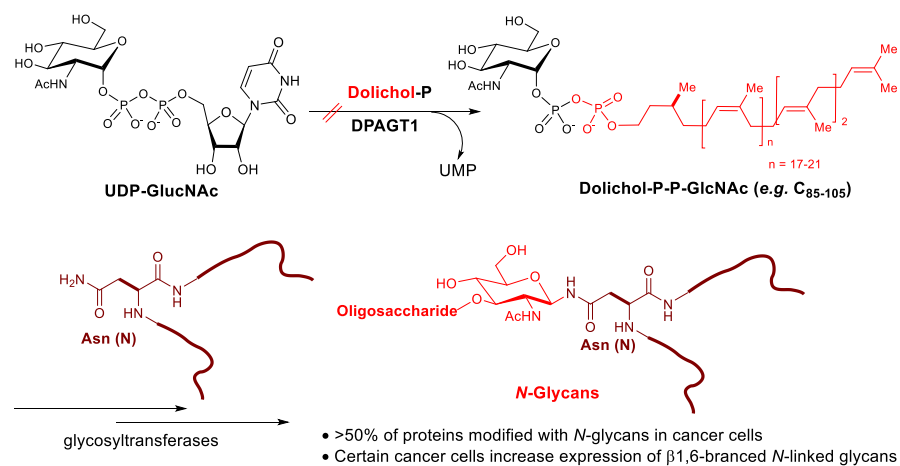
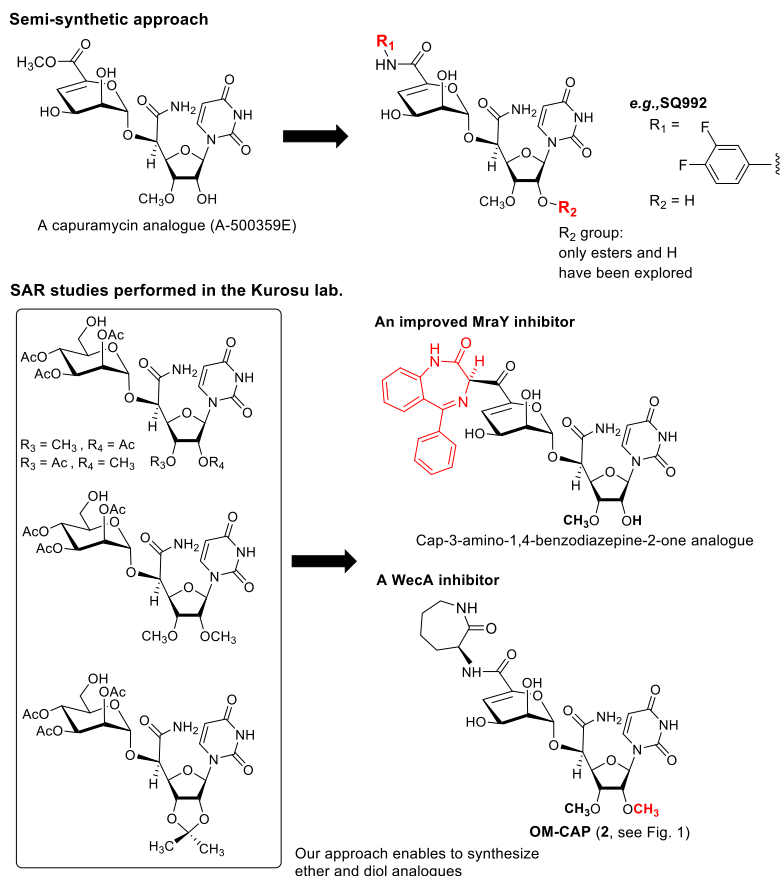
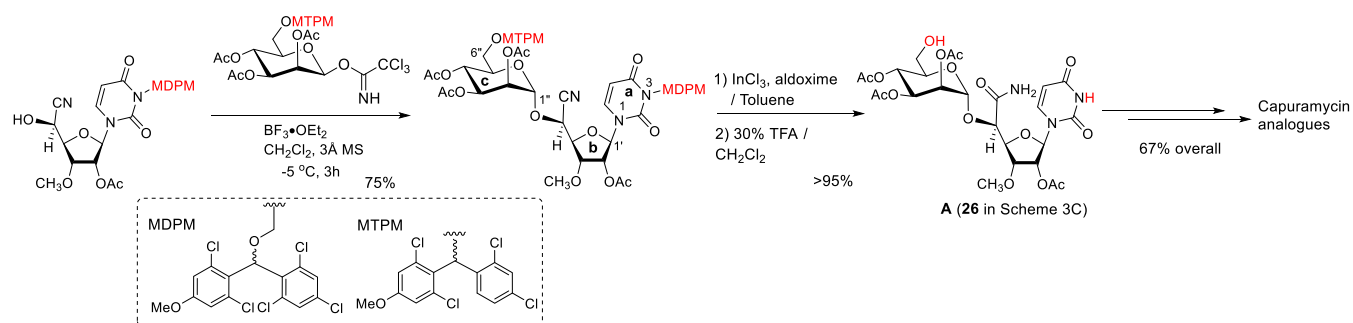


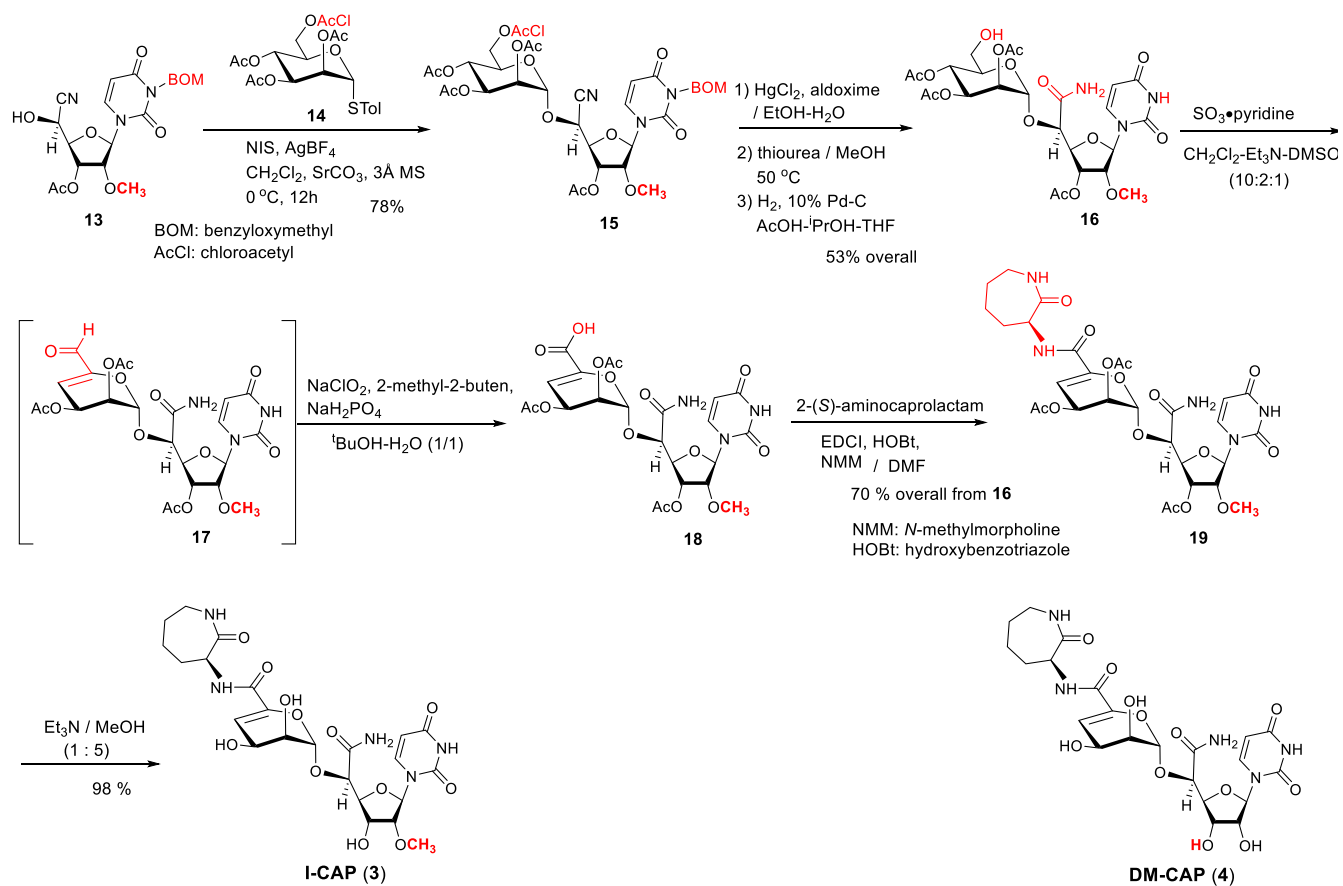
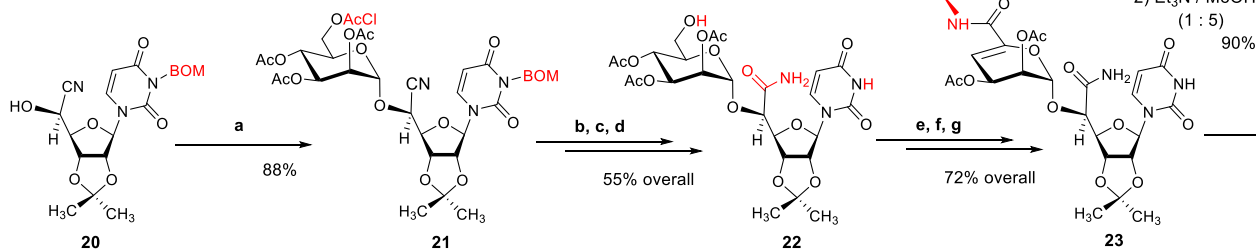
Figure 2. DPAGT1 in *N*-Glycan Biosynthesis.

1
2
3 **Figure 3.** General Strategy of SAR of Capuramycin.
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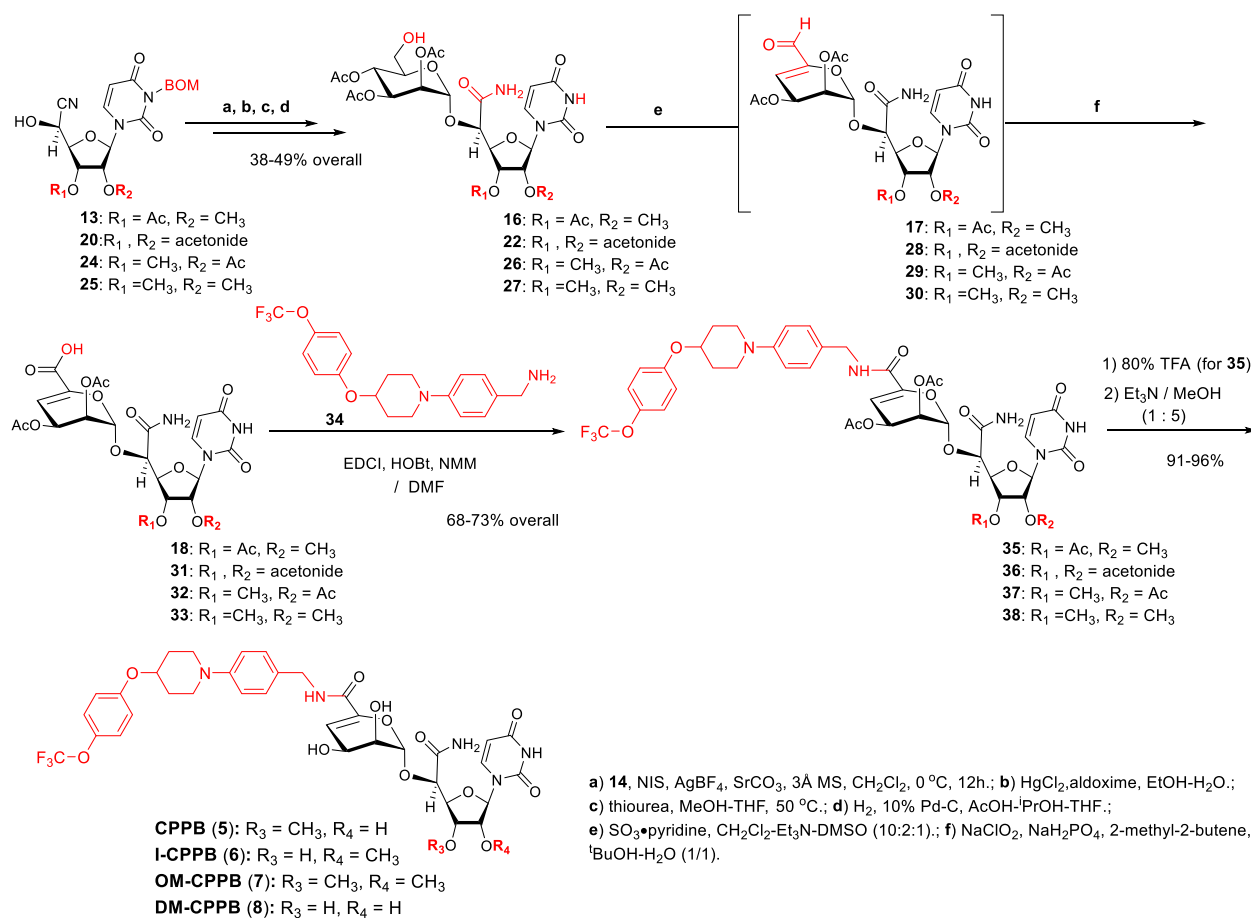
Scheme 1. An Improved Synthesis of Capuramycin Analogues Developed in The Kurosu Lab.

A: Synthesis of *iso*-capuramycin (I-CAP)**B: Synthesis of demethyl-capuramycin (DM-CAP)**

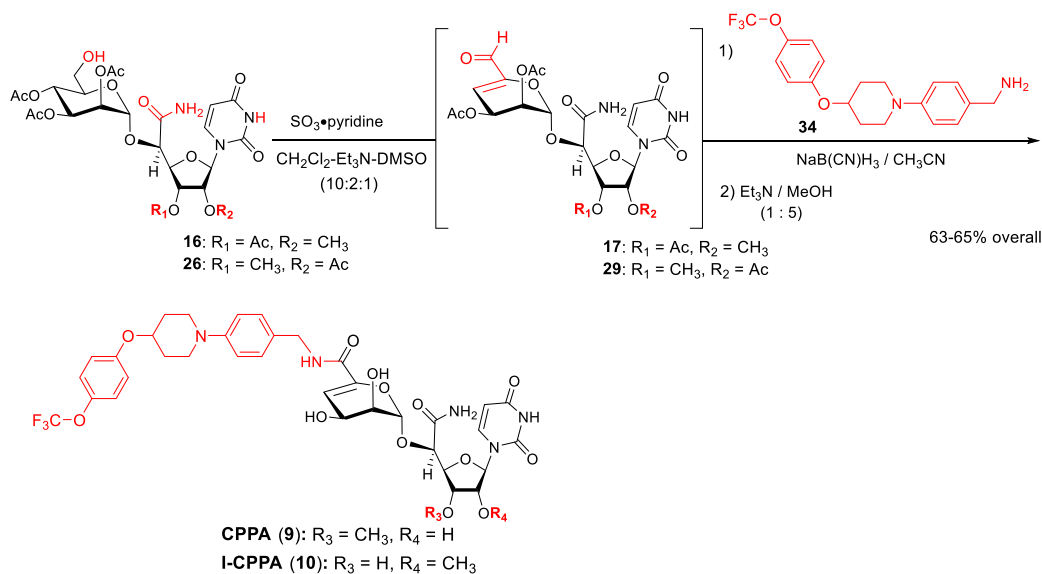
a) 14, NIS, AgBF₄, SrCO₃, 3Å MS, CH₂Cl₂, 0 °C, 12h.; b) HgCl₂, aldoxime, EtOH-H₂O.; c) thiourea, MeOH-THF, 50 °C.; d) H₂, 10% Pd-C, AcOH-ⁱPrOH-THF.;

Scheme 2. Syntheses of *iso*-Capuramycin (I-CAP, 3) and Demethyl-capuramycin (DM-CAP, 4).

A: Synthesis of capuramycin phenoxypiperidinylbenzylamide analogues, CPPB, *iso*-CPPB (I-CPPB), and demethyl-CPPB (DM-CPPB)



B: Synthesis of capuramycin phenoxypiperidinylbenzylamine analogues, CPPA, *iso*-CPPA (I-CPPA)



Scheme 3. Syntheses of Capuramycin phenoxypiperidinylbenzylamine (CPPA, **9**) and *iso*-Capuramycin phenoxypiperidinylbenzylamine (I-CPPA, **10**).

Table 1. Phosphotransferase Enzyme Inhibitory Activities of Capuramycin Analogues.^a

Entry	Compound	IC ₅₀ (μM) ^a			
		MraY (<i>Hydrogenivirga</i> sp.)	WecA (<i>E. coli</i>)	AgIH (<i>M. jannaschii</i>)	DPAGT1 (Human)
1	Capuramycin (CAP, 1)	0.13	>50	>50	>50
2	<i>O</i> -Methyl capuramycin (OM-CAP, 2)	>50	0.060	2.5	4.5
3	<i>iso</i> -Capuramycin (I-CAP, 3)	8.5	30.0	20.0	11.5
4	Demethyl capuramycin (DM-CAP, 4)	>50	35.0	>50	>50
5	Capuramycin phenoxypiperidinylbenzylamide (CPPB, 5)	10.3	0.10	0.15	0.20
6	<i>iso</i> -Capuramycin phenoxypiperidinylbenzylamide (I-CPPB, 6)	>50	20.0	15.0	0.60
7	<i>O</i> -Methyl capuramycin phenoxypiperidinylbenzylamide (OM-CPPB, 7)	5.0	10.0	30.0	20.0
8	Demethyl capuramycin phenoxypiperidinylbenzylamide (DM-CPPB, 8)	>50	30.0	>50	>50
9	Capuramycin phenoxypiperidinylbenzylamine (CPPA, 9)	>50	>50	>50	>50
10	<i>iso</i> -Capuramycin phenoxypiperidinylbenzylamine (I-CPPA, 10)	>50	>50	>50	>50
11	Tunicamycin (11)	2.9	0.15	13.2	1.5

^aAll assay protocols are summarized in Experimental Section as well as SI.

Table 2. Cytotoxicity of Capuramycin, Capuramycin Analogues, and Tunicamycin.

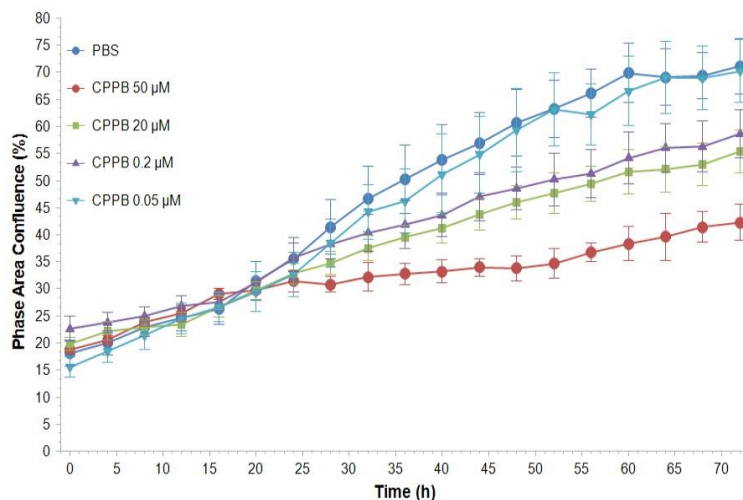
Entry	Compound	IC ₅₀ (μM) ^a										
		L1210	KB	SiHa	HCT-116	DLD-1	Capan-1	PANC-1	AsPC-1	PD002	HPNE	Vero
1	CAP (1)	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50
2	OM-CAP (2)	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50
3	CPPB (5)	>50	35.0	15.0	15.0	25.0	30.0	35.0	25.0	35.0	>50	>50
4	I-CPPB (6)	>50	35.0	25.0	25.0	35.0	40.0	45.0	30.0	50.0	>50	>50
5	Tunicamycin (11)	1.70	2.50	0.92	0.92	1.25	1.50	1.50	0.45	1.50	7.5	0.78

CAP: Capuramycin.; OM-CAP: *O*-Methyl capuramycin.; CPPB: Capuramycin phenoxypiperidinylbenzylamide.; I-CCB: *iso*-Capuramycin phenoxypiperidinylbenzylamide.; L1210 (ATCC® CCL-219™): mouse lymphocytic leukemia.; KB (ATCC® CCL-17™): HeLa, human cervical carcinoma.; SiHa (ATCC® HTB-35™): human cervical squamous cell carcinoma.; HCT-116 (ATCC® CCL-247™): colorectal adenocarcinoma.; DLD-1 (ATCC® CCL221™): colorectal adenocarcinoma.; Capan-1 (ATCC® HTB-79™): pancreatic ductal adenocarcinoma.; PANC-1 (ATCC® CRL-1469™): pancreatic ductal carcinoma.; AsPC-1 (ATCC® CRL-1682™): pancreatic adenocarcinoma.; PD002: a pancreatic adenocarcinoma staged at T3N1M0 from a 55 years old Caucasian male in 2011 (provided by Dr. Glazer (University of Tennessee Health Science Center).); hTERT-HPNE (ATCC® CRL-4023™): normal pancreatic ductal cell.; Vero (ATCC® CCL-81™): normal Cercopithecus aethiops kidney cell.

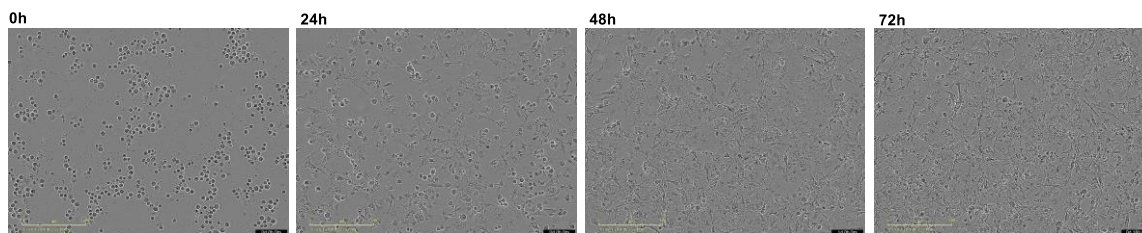
^aIC₅₀ values were determined via MTT assay.

Figure 4. Kinetic Proliferation Assays for PD002 Treated with CPPB Monitored by IncuCyte[®] Live Cell Analysis.^a

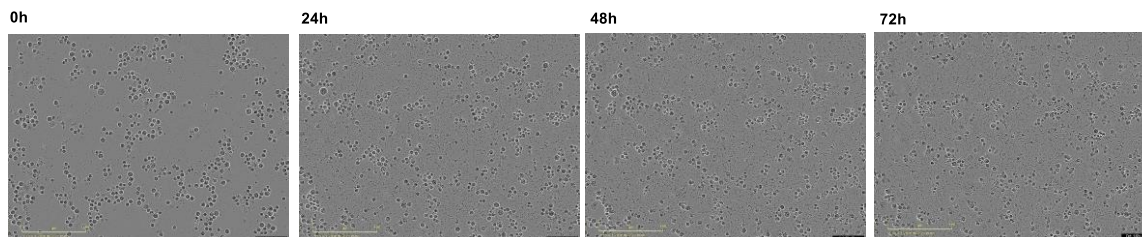
A: Phase area confluence of PD002 treated with CPPB



B: PD002 (PBS)

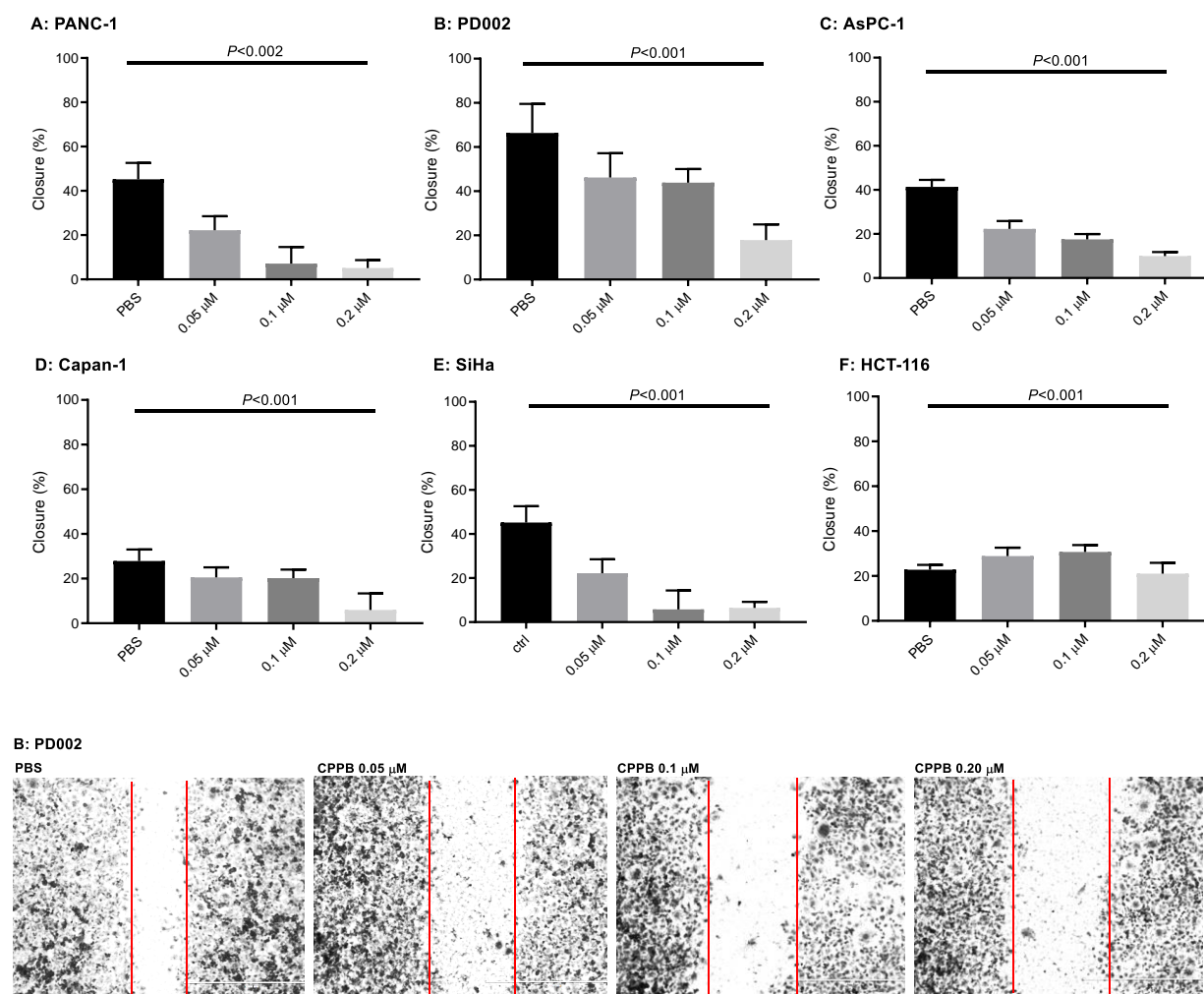


C: PD002 (CPPB 50 μM)



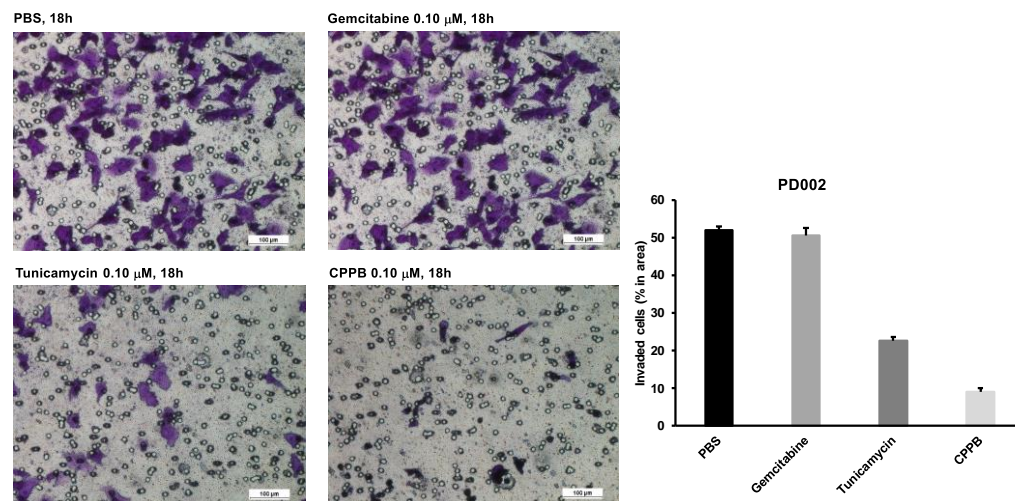
^aImages were obtained every 4h using an IncuCyte Live-Cell Imaging System (Essen BioScience, Ann Arbor, MI). After 72h, cell proliferation was quantified using the metric phase object confluence (POC), the area of the field of view that is covered by cells (phase area confluence %) is calculated by the integrated software.

Figure 5. Analyses of Migration inhibition of Pancreatic Cancers (PANC-1, PD002, AsPC-1, and Capan-1), a Cervical carcinoma (SiHa), a Colorectal Adenocarcinoma (HCT-116) by Treatment with CPPB in Wound Healing (Scratch) Assays.^a



^aAll images were acquired at 24h and these are summarized in SI (only the data for PD002 shown). *P* values were obtained from T score calculator.

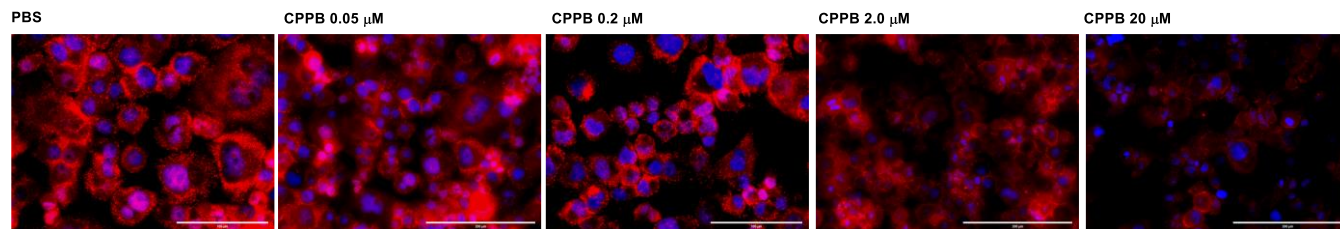
Figure 6. Cell Migration Inhibition of PD002 by Gemcitabine, Tunicamycin, and CPPB via Transwell Chamber.^a



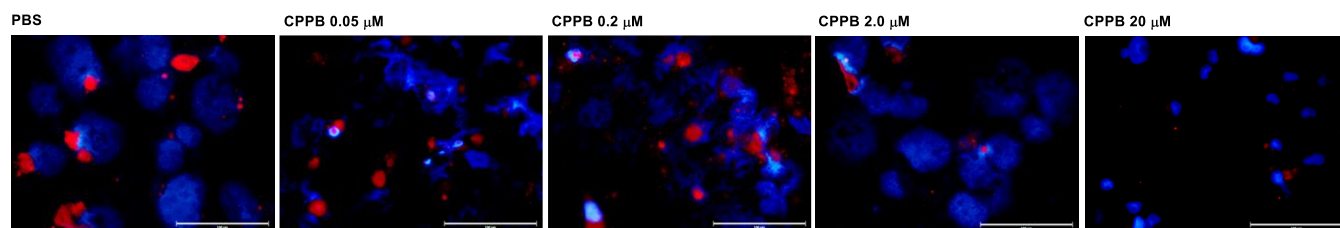
^aThe cells were fixed using 4% paraformaldehyde for 0.5h and stained with 0.05% crystal violet (300 μ L/well), after 0.5h, the images were captured via 10X magnification microscopy.

Figure 7. Immuno-fluorescent staining: Effect of a DPAGT1 Inhibitor, CPPB, on Snail in Pancreatic Cancer Cells (PD002 and PANC-1) and a Colorectal Adenocarcinoma (HCT-116). Western Blotting Assay for a Cervical Cancer (SiHa).^a

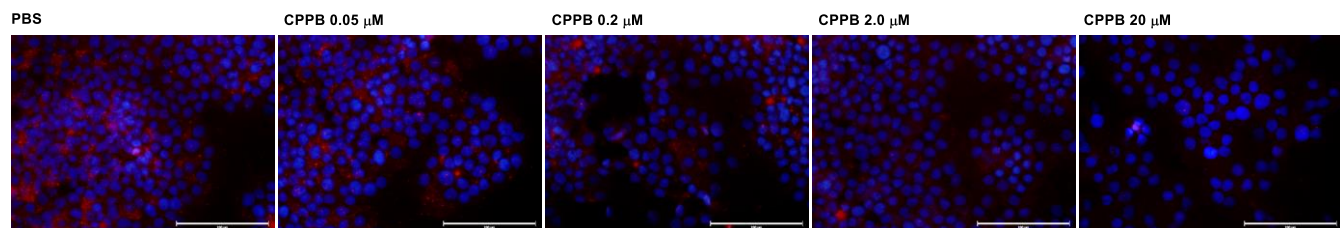
A: Snail (PD002)



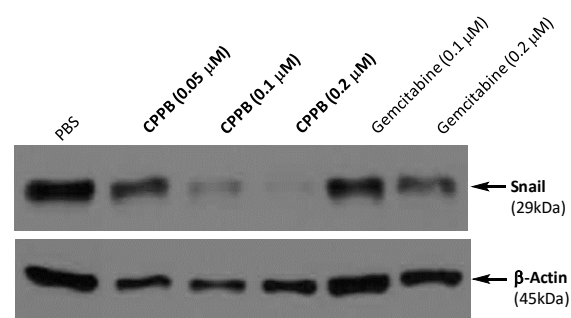
B: Snail (PANC-1)



C: Snail (HCT-116)

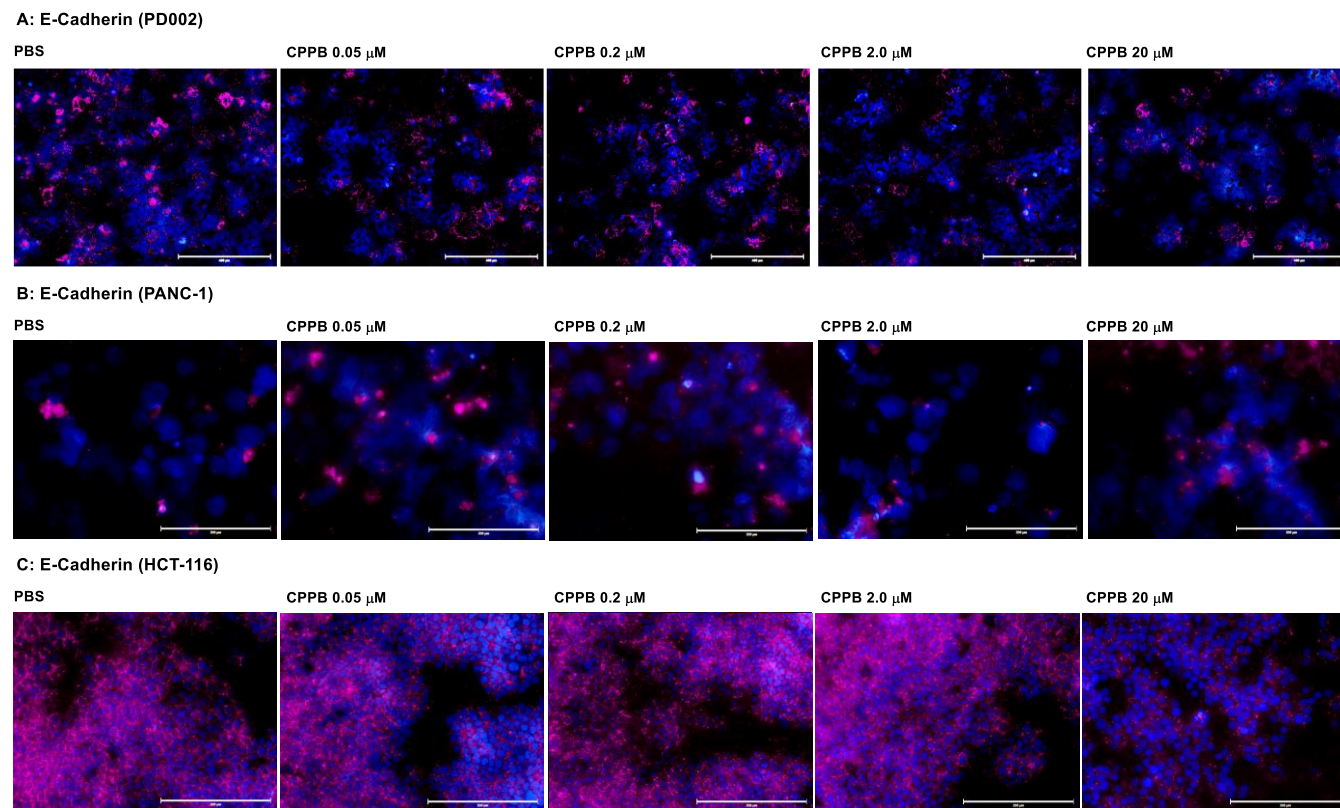


D: Western blotting assay for Snail (SiHa)



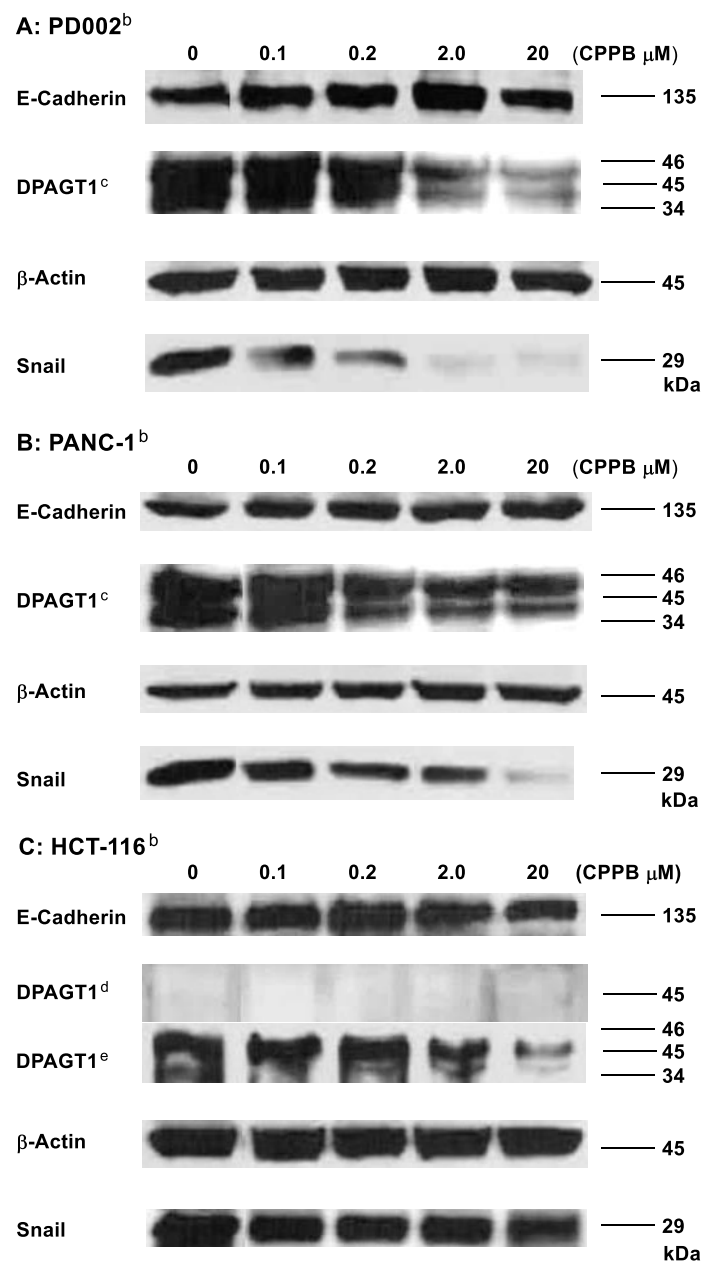
^aFluorescence microscopy images at 40x. The cells (1×10^5) were treated with CPPB (0.05, 0.2, 2.0, and 20 μM) or PBS for 24h. For immunofluorescent studies: the cells were treated with Snail (C15D3) rabbit mAb (Cell Signaling Technology), followed by Goat anti-Rabbit IgG (H+L) Cross-Adsorbed Secondary Antibody, Alexa FluorTM568 (red). DAPI (4',6-diamidino-2-phenylindole), a blue fluorescent DNA dye, was used to mark the nucleus. 40x. For Western blotting assays: The cells were treated with Snail (C15D3) rabbit mAb (Cell Signaling Technology), followed by secondary antibody, horseradish peroxidase (HRP)-linked antibody (Cell Signaling Technology).

Figure 8. Immunofluorescent Staining: Effect of a DPAGT1 inhibitor, CPPB, on E-Cadherin in Pancreatic cancer cells (PD002 and PANC-1) and a Colorectal Adenocarcinoma (HCT-116).^a



^aFluorescence microscopy images at 20x. The cells (1×10^5 - 6) were treated with CPPB (0.05, 0.2, 2.0, and 20 μ M) or PBS for 24h. The cells were treated with E-cadherin (4A2) mouse mAb (Cell Signaling Technology), followed by secondary antibody, goat anti-mouse IgG (H+L), Alexa Fluor™ Plus 647 (Invitrogen). DAPI (4',6-diamidino-2-phenylindole), a blue fluorescent DNA dye, was used to mark the nucleus. 40x

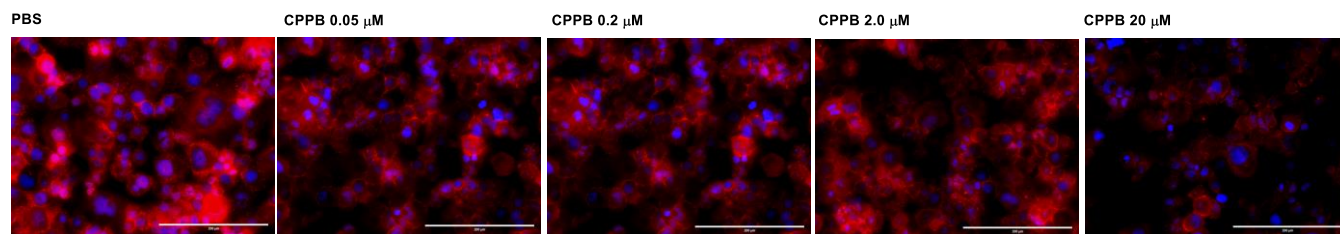
Figure 9. Western blot Analyses of DPAGT1, Snail, and E-Cadherin in PD002, PANC-1, and HCT-116 treated with CPPB.^a



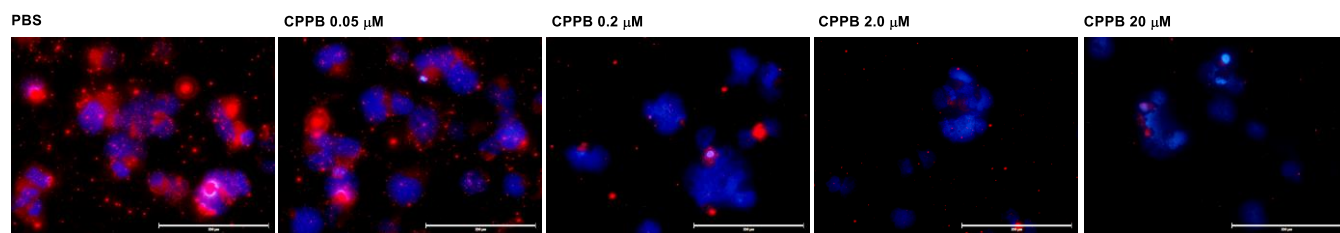
^aThe relative expression level was quantified by using Image Studio™ Lite quantification software ($n = 3$, $p < 0.001$, see SI); ^bAll cell lysates were prepared to be 1.5 mg total protein/mL by 15,200 xg, 30min at 4 °C unless indicated. ^cAt least three isoforms of DPAGT1 were detected.; ^dDPAGT1 was not detectable at 30 μ L (1.5 mg total protein /mL).; ^eThe cell lysate was prepared by ultracentrifugation (130,000 xg for 1h at 4 °C). 30 μ L of the lysate was analyzed.

Figure 10. Immunofluorescent staining: The DPAGT1 Expression Level in the Selected Cancer Cell Lines (PD002 and PANC-1) and a Colorectal Adenocarcinoma (HCT-116) Treated with CPPB.^a

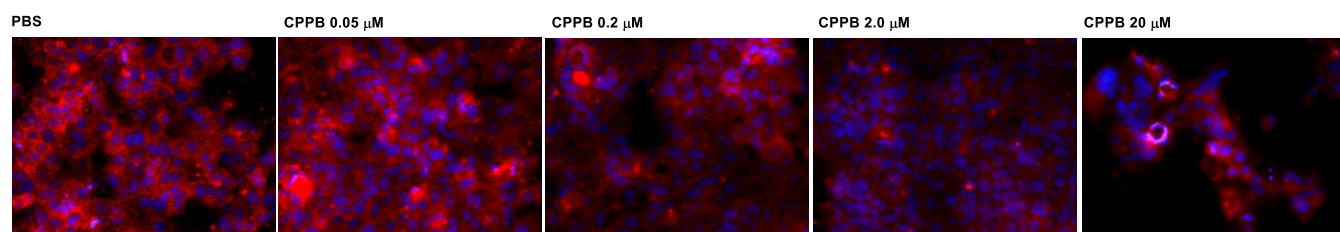
A: DPAGT1 (PD002)



B: DPAGT1 (PANC-1)

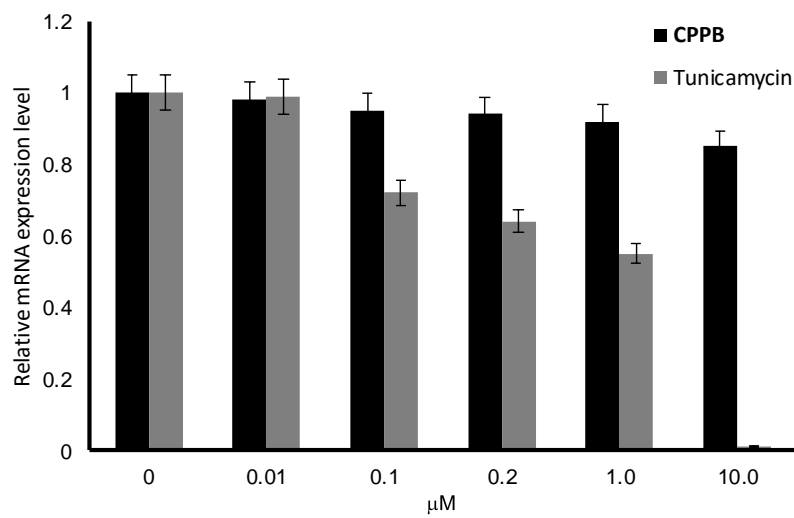


C: DPAGT1 (HCT-116)



^aFluorescence microscopy images at 20x. The cells (1×10^5) were treated with CPPB (0.05, 0.2, 2.0, and 20 μ M) or PBS for 72h. The cells were treated with DPAGT1 polyclonal antibody (Invitrogen, PA5-72704), followed by secondary antibody, Donkey anti-rabbit IgG (H+L), Alexa Fluor™ 555 (red) (Invitrogen). DAPI (4',6-diamidino-2-phenylindole), a blue fluorescent DNA dye, was used to mark the nucleus.

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2
3 **Figure 11.** RT-qPCR Analyses of *DPAGT1* Expression Level in PD002 Treated with CPPB.^a
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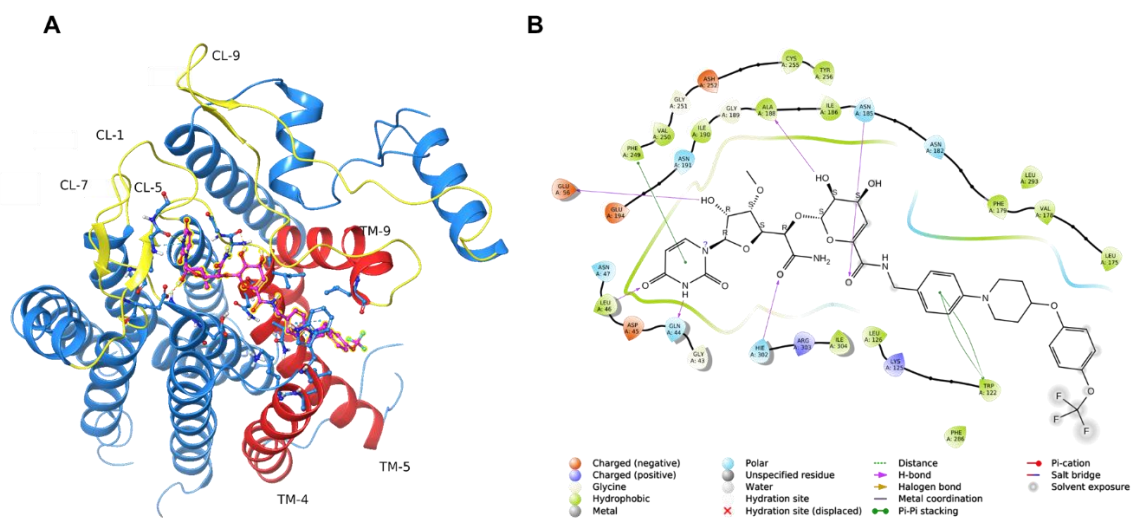


22 ^a~5 x10⁶ of PD002 was applied. Incubation time: 24h at 37 °C. At 10 μM, tunicamycin killed PD002 in 100%.
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Table 3. Fractional Inhibitory Concentration (FIC) of a Combination of CPPB and Paclitaxel against a Patient-derived Pancreatic Adenocarcinoma PD002.^a

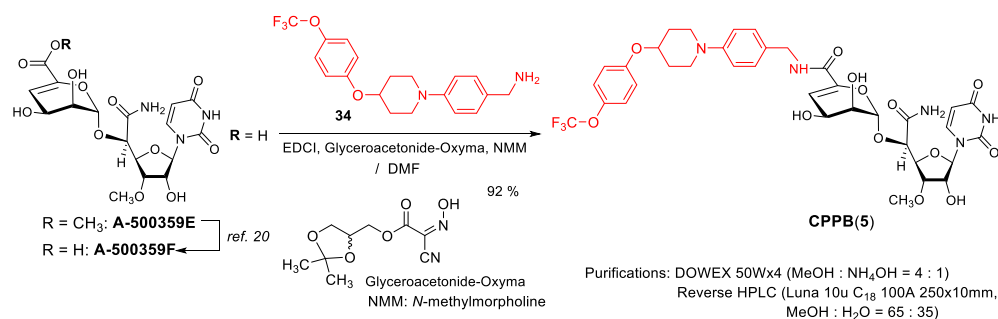
Entry	Combination of A and B ^b	C _A and C _B (μM) ^c	ΣFIC ^d
1	A: CPPB	0.10	0.50
	B: Paclitaxel	0.63	
2	A: CPPB	0.10	0.13
	B: Paclitaxel	0.16	
3	A: CPPB	0.20	0.0096
	B: Paclitaxel	0.0049	
4	A: CPPB	0.20	0.021
	B: Paclitaxel	0.020	
5	A: CPPB	0.20	0.26
	B: Paclitaxel	0.031	
6	A: CPPB	2.0	0.021
	B: Paclitaxel	0.020	
7	A: CPPB	2.0	0.037
	B: Paclitaxel	0.039	
8	A: CPPB	2.0	0.26
	B: Paclitaxel	0.31	

^aΣFIC index for the wells at growth–no growth interface. ^bThe IC₅₀ values of CPPB and paclitaxel against PD002 are 35.0 and 1.25 μM, respectively. ^cC_A and C_B are concentrations of A and B. ^dΣFIC is the sum of fractional inhibitory concentration calculated by the equation $\Sigma FIC = FIC_A + FIC_B = C_A/IC_{50A} + C_B/IC_{50B}$. Cellular behavior of PD002 treated with paclitaxel or a combination with paclitaxel and CPPB was monitored over time by IncuCyte[®] live cell analysis (Supporting Information).

Figure 12. Modeling CPPB-DPAGT1 Interaction to Design New Inhibitor Molecules.^a

^aDocking studies were performed using the human DPAGT1 with bound tunicamycin (PDB: 6BW6) (PMID 29459785). The biological unit was downloaded and prepared using the Protein Preparation Wizard of the Maestro Small Molecule Drug Discovery Suite (Schrödinger, LLC). The docking receptor grid was prepared using Schrödinger's Glide program. (PMID 15027866, PMID 15027865). CPPB was built and prepared for docking using the LigPrep program using default settings (Schrödinger, LLC). **A:** Predicted binding pose of CPPB (highlighted ball & stick model) into DPAGT1. Key active site loops (yellow) and transmembrane regions (orange) are indicated. **B:** 2D ligand interaction diagram of the docked CPPB-DPAGT1 complex with key predicted interactions shown.

CL: cytoplasmic loop.; TM: transmembrane segment



Scheme 4. A Semi-synthesis of CPPB from Synthetic A-500359F, a Metabolite of *S. griseus* SANK60196.

DPAGT1 Inhibitors of Capuramycin Analogues and Their Antimigratory Activities of Solid Tumors

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