## SUPPORTING INFORMATION

# Systematic design of adenosine analogs as inhibitors of a *Clostridioides difficile*-specific DNA adenine methyltransferase required for normal sporulation and persistence

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# Contents

Table S1. Elemental analyses for final compounds 10-12, 14-21, and 31-42

 Table S2. Summary of X-ray data collection and refinement statistics

 Table S3. The predicted cell permeability of compounds 16, 38, and 39

Figure S1. Compounds 201-241 related to MTA

Figure S2. Raw data of MTase-Glo<sup>TM</sup> inhibition assay and ITC measurements

Figure S3. APNEA (compound 9) contains an impurity

Figure S4. Chemical stability of compound 39

References

HR-MS spectra and HPLC traces of compounds 1-42

HPLC traces of compounds 201-241

**Molecular Formula Strings** (in a separate CSV file)

T.h	Compd	Formula	Calculated, %			Found, %		
Lab code		Formula	С	Н	Ν	С	Н	Ν
MC4742	10	C24H25N5O4	64.42	5.63	15.65	64.52	5.63	15.60
MC4736	11	$C_{22}H_{23}N_5O_4$	62.70	5.50	16.62	62.82	5.50	16.55
MC4737	12	C22H23N5O4	62.70	5.50	16.62	62.81	5.51	16.56
MC4741	14	$C_{19}H_{23}N_5O_4$	59.21	6.02	18.17	59.30	6.04	18.10
MC4800	15	$C_{19}H_{24}N_6O_4$	56.99	6.04	20.99	57.11	6.05	20.92
MC4761	16	C19H23N5O5	56.85	5.78	17.45	56.97	5.78	17.39
MC4760	17	C <sub>20</sub> H <sub>25</sub> N <sub>5</sub> O <sub>5</sub>	57.82	6.07	16.86	57.92	6.08	16.81
MC4756	18	$C_{20}H_{25}N_5O_4$	60.14	6.31	17.53	60.25	6.32	17.47
MC4757	19	C <sub>21</sub> H <sub>27</sub> N <sub>5</sub> O <sub>4</sub>	61.00	6.58	16.94	61.12	6.58	16.87
MC4795	20	C15H23N5O5	50.98	6.56	19.82	51.11	6.58	19.76
MC4758	21	C22H29N5O4	61.81	6.84	16.38	61.91	6.85	16.32
MC4764	31	$C_{22}H_{28}N_6O_4$	59.99	6.41	19.08	60.09	6.42	19.01
MC4770	32	$C_{21}H_{23}N_7O_4$	57.66	5.30	22.41	57.78	5.30	22.34
MC4771	33	$C_{17}H_{24}N_6O_4$	54.24	6.43	22.33	54.36	6.44	22.26
MC4776	34	$C_{18}H_{28}N_6O_4$	55.09	7.19	21.41	55.20	7.19	21.35
MC4769	35	C17H26N6O5	51.77	6.64	21.31	51.90	6.65	21.25
MC4778	36	$C_{18}H_{29}N_7O_4$	53.06	7.17	24.06	53.18	7.18	23.99
MC4830	37	$C_{21}H_{32}N_6O_6$	54.30	6.94	18.09	54.44	6.95	18.02
MC4777	38	$C_{22}H_{34}N_6O_6$	55.22	7.16	17.56	55.34	7.18	17.50
MC4799	39	$C_{23}H_{36}N_6O_6$	56.08	7.37	17.06	56.20	7.38	17.00
MC4831	40	$C_{22}H_{34}N_6O_6$	55.22	7.16	17.56	55.35	7.17	17.49
MC4832	41	$C_{23}H_{34}N_6O_6$	56.31	6.99	17.13	56.43	7.00	17.07
MC4919	42	$C_{18}H_{28}N_6O_4$	55.09	7.19	21.41	55.22	7.19	21.34

**Table S1.** Elemental Analyses for Final Compounds 10-12, 14-21, and 31-42.

Date Collected	03/2021	06/2021	06/2021	06/2021	06/2021	06/2021	07/2021
compound	214 (MTA)	2	3	8	4	6	9
		(161; MC4679)	(162; MC4680)	(163; MC4681)	(164; MC4682)	(165; MC4683)	(168: APNEA)
PDB Code	8CXS	8CXU	8CXV	8CXY	8CXW	8CXX	8CY2
Cell dimensions (Å)	81.97, 161.16, 230.80	81.45, 161.24, 229.52	81.46, 161.34, 229.79	81.36, 161.36, 229.75	81.33, 161.63, 229.60	81.76, 161.47, 230.27	81.53, 161.81, 230.34
Resolution (Å)	41.87-2.49 (2.89-2.49)	44.86-2.28 (2.37-2.28)	44.88-2.26 (2.37-2.26)	48.71-2.19 (2.27-2.19)	46.80-2.78 (2.89-2.78)	44.29-2.34 (2.43-2.34)	45.17-2.81 (2.89 - 2.81)
<sup>a</sup> R <sub>merge</sub>	0.292 (2.295)	0.233 (1.70)	0.244 (2.09)	0.166 (1.93)	0.224 (1.51)	0.165 (1.46)	0.465 (3.28)
R <sub>pim</sub>	0.074 (0.700)	0.072 (0.733)	0.070 (0.788)	0.040 (0.575)	0.110 (0.789)	0.048 (0.499)	0.141 (1.081)
$CC_{1/2}, CC^*$	(0.469, 0.799)	(0.410, 0.762	(0.344, 0.715)	(0.762, 0.930)	(0.394, 0.752)	(0.503, 0.818)	(0.402, 0.758)
$_{p} < I \setminus QI >$	11.4 (1.3)	10.0 (0.9)	10.9 (1.0)	14.9 (1.4)	7.4 (1.1)	14.4 (1.2)	8.0 (1.1)
Completeness (%)	99.6 (94.9)	93.5 (74.8)	95.0 (90.5)	95.0 (83.4)	99.6 (99.6)	96.5 (76.0)	99.9 (99.9)
Redundancy	14.9 (10.1)	8.9 (4.8)	12.4 (6.8)	14.4 (9.1)	5.1 (4.5)	12.1 (8.1)	11.6 (9.9)
Observed reflections	1,578,071	1,147,875	1,650,078	2,167,132	390,186	1,497,945	861,139
Unique reflections	106,240	129,038	133,608	147,745	76,354	123,740	74,091
Refinement							
Resolution (Å)	2.49	2.28	2.26	2.19	2.78	2.34	2.81
No. reflections	106,072	128,797	133,381	147,569	76,256	123,583	73,994
<sup>c</sup> R <sub>work</sub> / <sup>d</sup> R <sub>free</sub>	0.179 / 0.213	0.186 / 0.222	0.177 / 0.205	0.174 / 0.203	0.184 / 0.230	0.179 / 0.206	0.171 / 0.222
No. Atoms							
Protein	13,408	13,407	13,421	13,401	13,372	13,464	13,280
DNA	1704	1704	1704	1704	1704	1704	1704
Inhibitor	60	81	81	81	87	84	84
Solvent	440	629	736	759	406	582	348
B Factors ( $Å^2$ )							
Protein	51.1	46.2	48.0	48.7	51.7	52.8	56.0
DNA	56.1	50.2	54.8	54.9	59.7	59.6	64.5
Inhibitor	53.1	55.4	54.5	48.9	64.9	70.3	65.3
Solvent	41.2	41.9	43.8	45.3	38.4	46.8	44.5
R.m.s. deviations							
Bond lengths (Å)	0.003	0.003	0.004	0.004	0.003	0.003	0.004
Bond angles (°)	0.6	0.6	0.6	0.6	0.5	0.6	0.6

Table S2. Summary of X-ray data collection at wavelength=1Å of beamline APS 222-ID and refinement statistics (\*) of space group  $P2_12_12_1$  ( $\alpha=\beta=\gamma=90^\circ$ )

\* Values in parenthesis correspond to highest resolution shell; <sup>a</sup>  $R_{merge} = \Sigma | I - \langle I \rangle | / \Sigma I$ , where I is the observed intensity and  $\langle I \rangle$  is the averaged intensity from multiple observations; <sup>b</sup>  $\langle I / \sigma I \rangle =$  averaged ratio of the intensity (I) to the error of the intensity ( $\sigma I$ ); <sup>c</sup>  $R_{work} = \Sigma | Fobs - Fcal | / \Sigma | Fobs |$ , where Fobs and Fcal are the observed and calculated structure factors, respectively; <sup>d</sup>  $R_{free}$  was calculated using a randomly chosen subset (5%) of the reflections not used in refinement.

Date Collected	09/2021	11/2021	11/2021	11/2021	03/2022	03/2022	03/2021
Inhibitor	14	18	19	16	15	39	1
	(174; MC4741)	(178; MC4756)	(179; MC5757)	(181; MC4761)	(197; MC4800)	(199; MC4799)	(101; MC4624)
PDB Code	8CXZ	8CY0	8CY1	8CY4	8CY3	8CY5	8CXT
Cell dimensions (Å)	81.44, 161.43, 229.71	81.37, 160.86, 230.38	81.25, 161.57, 229.93	81.31, 161.76, 229.95	81.24, 161.24, 229.58	81.55, 161.23, 230.29	82.21, 161.67, 230.80
Resolution (Å)	45.89-2.35 (2.43-2.35)	47.01-2.65 (2.74-2.65)	44.89-2.38 (2.48-2.38)	44.10-2.34 (2.43-2.34)	46.9-2.65 (2.74-2.65)	47.03-2.50 (2.58-2.50)	44.23-2.61 (2.74-2.61)
<sup>a</sup> R <sub>merge</sub>	0.210 (1.36)	0.281 (1.89)	0.282 (1.80)	0.251 (1.73)	0.279 (1.64)	0.244 (1.35)	0.337 (2.535)
R <sub>pim</sub>	0.071 (0.519)	0.116 (0.926)	0.100 (0.728)	0.076 (0.661)	0.083 (0.646)	0.057 (0.642)	0.063 (0.678)
CC <sub>1/2</sub> , CC*	(0.356, 0.724)	(0.363, 0.730)	(0.374, 0.738)	(0.472, 0.801)	(0.387, 0.747)	(0.431, 0.776)	(0.468, 0.799)
$^{b} < I/\sigma I >$	12.4 (1.2)	8.1 (1.1)	8.0 (0.81)	10.2 (0.95)	8.6 (0.8)	12.7 (1.0)	11.3 (1.2)
Completeness (%)	99.5 (97.4)	99.8 (99.6)	96.2 (77.7)	96.6 (86.9)	97.3 (85.5)	99.3 (93.4)	100.0 (99.8)
Redundancy	12.7 (6.6)	6.6 (4.5)	8.6 (4.9)	10.9 (6.3)	11.3 (6.0)	12.6 (4.4)	23.8 (9.7)
Observed reflections	1,588,738	582,034	1,012,216	1,339,925	966,027	1,329,225	2,164,493
Unique reflections	125,490	88,696	117,552	122,653	85,741	105,385	91,039
Refinement							
Resolution (Å)	2.35	2.65	2.38	2.34	2.65	2.50	2.61
No. reflections	125,292	88,571	117,266	121,299	85,314	105,232	90,810
<sup>c</sup> R <sub>work</sub> / <sup>d</sup> R <sub>free</sub>	0.174 / 0.204	0.173 / 0.221	0.182 / 0.227	0.173 / 0.207	0.190 / 0.226	0.177 / 0.210	0.189 / 0.224
No. Atoms							
Protein	13,424	13,368	13,386	13,402	13,368	13,397	13,241
DNA	1704	1704	1704	1704	1704	1704	1704
Inhibitor	84	87	90	87	87	105	78
Solvent	849	498	747	818	305	609	136
B Factors ( $Å^2$ )							
Protein	53.2	58.3	58.1	51.1	74.9	65.0	68.9
DNA	61,2	68.0	68.1	58,0	85.9	73.0	73.5
Inhibitor	53.4	62.8	63.2	55.1	78.4	66.9	79.8
Solvent	48.0	47.7	51.0	45.8	60.4	55.2	56.2
R.m.s. deviations							
Bond lengths (Å)	0.003	0.003	0.003	0.003	0.003	0.002	0.003
Bond angles (°)	0.6	0.5	0.6	0.6	0.5	0.5	0.6

Table S2 (Continues) Summary of X-ray data collection at wavelength=1Å of beamline APS 22-ID and refinement statistics (\*) of space group  $P2_12_12_1$  ( $\alpha=\beta=\gamma=90^\circ$ )

\* Values in parenthesis correspond to highest resolution shell; <sup>a</sup>  $R_{merge} = \Sigma | I - \langle I \rangle | / \Sigma I$ , where I is the observed intensity and  $\langle I \rangle$  is the averaged intensity from multiple observations; <sup>b</sup>  $\langle I / \sigma I \rangle =$  averaged ratio of the intensity (I) to the error of the intensity ( $\sigma I$ ); <sup>c</sup>  $R_{work} = \Sigma | Fobs - Fcal | / \Sigma | Fobs |$ , where Fobs and Fcal are the observed and calculated structure factors, respectively; <sup>d</sup>  $R_{free}$  was calculated using a randomly chosen subset (5%) of the reflections not used in refinement.

Compound		Caco2 permeability (Papp)		Human inte	estinal absorption	
		pkCSM (×10⁻ <sup>6</sup> cm/s)	PreADMET (×10 <sup>-6</sup> cm/s)	pkCSM (%)	PreADMET (%)	References
16	-	1.77	1.68	63.9	74.4	-
38	-	1.85	1.93	60.6	73.5	-
39	-	1.78	1.57	61.5	76.2	-
7	Nitrobenzylthioinosine	0.79	0.33	73.9	64.9	In cells <sup>1</sup>
9	APNEA	1.81	1.45	62.1	74.0	In cells/tissues <sup>2,3</sup> In vivo <sup>4,5</sup>
13	A2AR-agonist-1	1.81	0.54	70.0	75.7	In vivo <sup>6</sup>

**Table S3**. The predicted cell permeability of compounds 16, 38, and 39

We have performed *in silico* cell permeability prediction using two different tools: pkCSM (https://biosig.lab.uq.edu.au/)<sup>7</sup> and PreADMET (https://preadmet.webservice.bmdrc.org/). Both tools enable the prediction of Caco-2 cell permeability and human intestinal absorption.



Compound	name	Reference/note	Compound	name	Reference/note
201 (dcSAM)	Decarboxyliertes SAM	a gift from Dr. Bernard Blessington, Bradford University, Bradford, UK	221	TL106 N6-benzylthioethyl-2'-deoxyadenosine	Qian et al. <i>Chem. Commun. 54</i> , 13945-13948, 2018
202 (da-SAM)	Deaminiertes SAM (epimeric mixture)	iBorchardt el al. <i>J. Med.</i> <i>Chem.</i> <b>19</b> , 1104-1110, 1976	222	TL104 N6-hydroxyethyl-2'-deoxyadenosine	Brock et al. <i>Chem. Res. Toxicol.</i> <b>17</b> , 1047-1056, 2004
203 (DMTA)	5'-dimethylthioadenosine	Borchardt, R.T. <i>J. Am.</i> <i>Chem. Soc.</i> <b>101</b> , 458-463, 1979	223	TL100-2 N6-(S-(homocysteinyl)-ethyl)-2'- deoxyadenosine	N/A
204	sinefungin	a gift from Dr. M. Niedenthal, Lilly Research Laboratories, Indianapolis, IN, USA	224 (AEA)	5'-aminoethyladenosine	N/A
205	Aza-SAM	a gift from Dr. Mike Blackburn, The University of Sheffield, Sheffield, U.K.)	225 (CMTA)	5'-carboxymethylthioadenosine	Gillet et al. <i>Experientia</i> <b>35</b> , 1007- 1009, 1979
206	L-SAH (not used in the assay – reaction product)	Sigma-Aldrich	226	5'-deoxy-5'-chloroadenosine	Kikugawa et al. <i>J. Med. Chem.</i> <b>15</b> , 387-390, 1972
207	D-SAH	Sigma-Aldrich	227	5'-phthalimidoadenosine	M. Pignot, Dissertation, TU Dortmund, Germany, 1999
208 (dc-SAH)	Decarboxyliertes SAH	Pignotet al. <i>Eur. J. Org.</i> <i>Chem.</i> <b>3</b> , 549–555, 2000	228	5'-deoxy-5'-acetylthioadenosine	Pignot et al. <i>Eur. J. Org. Chem.</i> <b>3</b> , 549–555, 2000
209	5-'-adenosyl-L-cysteine	Sigma-Aldrich	229	(South)-SAH	a gift from Dr. Victor Marquez, National Cancer Institute, Frederick, MD, USA
210 (CPTA)	5'-carboxypropyl-thioadenosine (deaminiated SAH, daSAH)	Pignotet al. <i>Eur. J. Org.</i> <i>Chem.</i> <b>3</b> , 549–555, 2000	230	(North)-SAH	a gift from Dr. Victor Marquez, National Cancer Institute, Frederick, MD, USA
211	CPTA methylester	Pignotet al. <i>Eur. J. Org.</i> <i>Chem.</i> <b>3</b> , 549–555, 2000	231	5'-ethylthioadenosine	Kikugawa et al. <i>J. Med. Chem.</i> <b>15</b> , 387-390, 1972
212 (AETA)	5'-aminoethylthioadenosine	Goedecke et al. <i>Nat. Struct.</i> <i>Biol.</i> <b>8</b> , 121-125, 2001	232	5'-propythioadenosine	Kikugawa et al. <i>J. Med. Chem.</i> <b>15</b> , 387-390, 1972
213 (CETA)	5'-carboxyethylthioadenosine	Srivastava et al. <i>Med.</i> <i>Chem. Lett.</i> <b>17</b> , 6239-6244, 2007	233	5'-butylthioadenosine	Kikugawa et al. <i>J. Med. Chem.</i> <b>15</b> , 387-390, 1972
214 (MTA)	5'-methylthioadenosine	Sigma-Aldrich	234	5'-methylbutylthioadenosine [as epimeric mixture from 5'- butylthioadenosine ( <b>233</b> )]	Gillet et al. <i>Experientia</i> 35, 1007- 1009, 1979
215	5'-thioadenosine	Pignotet al. <i>Eur. J. Org.</i> <i>Chem.</i> <b>3</b> , 549–555, 2000	235	5'-methylpropylthioadenosine [as epimeric mixture from 5'- propylthioadenosine (232)]	Gnegy and Lotspeich, <i>J. Med.</i> <i>Chem.</i> <b>19</b> , 1191-1195, 1976
216	Adenosine (not used)	Sigma-Aldrich	236	5'-methylethylthioadenosine [as epimeric mixture from 5'- ethylthioadenosine ( <b>231</b> )]	Gnegy and Lotspeich, <i>J. Med.</i> <i>Chem.</i> <b>19</b> , 1191-1195, 1976, 1976
217	L-methionine	Sigma-Aldrich	237 (AEAA)	5'-aminoethylamino-5'- deoxyadenosine	M. Kolb et al. <i>J. Med. Chem.</i> <b>25</b> , 550-556, 1982
218	5'-aminoadenosine	M. Pignot, Dissertation, TU Dortmund, Germany, 1999	238 (phETA)	5'-phenylethythio-5'-deoxyadenosine	Kai <i>et al.</i> Chem. Commun. <b>50</b> , 8586-8589, 2014
219	N6-methyl-2'-deoxyadenosine	MBI Fermentas, Vilnius, Lithuania	239 (ML43)	Bisubstrate inhibitor	New synthesis (see next page)
220	TL107-2 N6-(S-(homocysteinyl)-methyl)- 2'-deoxyadenosine	Wahnon et al. <i>J. Am. Chem.</i> Soc. <b>123</b> , 976-977, 2001	240	5'-iodo-5'-deoxyadenosine	TCI Europe, Zwijndrecht, Belgium
			241	5'-tosyladenosine	Sigma-Aldrich

**Figure S1. (A)** Screen of CamA inhibition against SAM analogs at [I]=50  $\mu$ M, in the presence of 40  $\mu$ M co-substrate SAM. Three compounds, **203** (dMTA), **204** (sinefungin) and **214** (MTA), have inhibitions at >50% CamA activity. Compounds **207**, **211**, **215**, **225** and **227** might interfere with the Promega MTase-Glo<sup>TM</sup> luminescent assay used in the study (see Figure S3). (**B**) Compound information (see HPLC traces of compounds 201-241).



Figure S2. Raw data of MTase-GloTM inhibition assay (top panels) and ITC measurements (bottom panels). (A) Related to Figure 3. (B) Related to Figure 4. (C) Related to Figure 5. (D) Related to Figure 6.



**Figure S3. APNEA (compound 9) contains an impurity that interferes with MTase-Glo<sup>TM</sup> assay.** (**A**) Schematic steps of CamA-mediated methylation. After the methylation reaction is complete, the MTase-Glo<sup>TM</sup> Reagent and Detection Solution (provided by Promega) convert SAH to ATP and measure the light from the luciferase reaction. (B) Standard curves for the Promega bioluminescence assay as a function of SAH concentrations in the range of above or below 1  $\mu$ M (left and right panels) (*N* = 2). (**C**) Enzymatic activity of CamA wild-type (WT) and catalytic mutant (N165A) (left: the raw reading of luminescence signal; right: converted SAH concentration). There is no component in the methylation reaction that interference with the luminescent assay. (**D**) Adenosine acts like SAH in the MTase-Glo<sup>TM</sup> assay which converts nearly 100% of adenosine to ATP. (**E**) APNEA (compound **9**) contains a >5% impurity which interferes with MTase-Glo<sup>TM</sup> assay.



Figure S4. Evaluation of compound 39 stability in assay buffer. We assessed the stability of compound 39 in a water solution containing 50 mM Tris-HCl pH 7.5 and 100 mM NaCl, similar to the enzymatic inhibition assay buffer. Specifically, we dissolved the compound in the buffer (c = 0.5mg/mL), incubated the solution at 37 °C and then performed analytical HPLC under the same conditions described in the Experimental section. HPLC runs were performed at time 0 and after 1, 2, 4, 8, 24, and 48 h of incubation (A). As a comparison, the hydrolysis/deprotection product of 39, i.e. compound 42, was also dissolved in the same buffer and analyzed via HPLC (B). There is no significant difference between the HPLC profiles of compound 39 at different incubation times and no hydrolysis product formation was observed at any time point, thereby compound **39** is chemically stable under the tested conditions. This observation agrees with that tert-butyl carbamate moiety is resistant to hydrolysis under physiological pH conditions<sup>8</sup>. Indeed, given the presence of the additional oxygen, three possible resonance structures can be found which contribute to the increased stability of carbamates compared to amides<sup>9</sup>. Moreover, carbamates are being increasingly chosen as peptide mimetic groups because of their metabolic stability and many examples of carbamatecontaining drugs, such as the anthelminthic drugs albendazole and mebendazole, the chemotherapeutic mitomycin C, and the antiasthma agent zafirlukast<sup>10</sup>.

## References

- (1) Griffiths, M. et al. Cloning of a human nucleoside transporter implicated in the cellular uptake of adenosine and chemotherapeutic drugs. Nat Med. 3(1): 89-93 (1997)
- (2) Gardner, N.M. and Broadley, K.J. Analysis of the atypical characteristics of adenosine receptors mediating negative inotropic and chronotropic responses of guinea-pig isolated atria and papillary muscles. Br. J. Pharmacol. 127(7): 1619-2 (1999)
- (3) Deguchi, H. et al. Adenosine regulates tissue factor expression on endothelial cells. Thromb.Res. 91(2): 57-64 (1998)
- (4) Borowicz K. K. et al. N6-2-(4-aminophenyl)ethyl-adenosine enhances the anticonvulsive activity of antiepileptic drugs. Eur J Pharmacol. 327(2-3):125-133 (1997)
- (5) Fozard J.R. et al. Mast cell degranulation following adenosine A3 receptor activation in rats.
- Eur. J. Pharmacol. Eur. J. Pharmacol. 298(3):293-7 (1996)
- (6) Chou, A. H. et al. T1-11 and JMF1907 ameliorate polyglutamine-expanded ataxin-3-induced neurodegeneration, transcriptional dysregulation and ataxic symptom in the SCA3 transgenic mouse. Neuropharmacology 99:308-17 (2015)
- (7) Pires, D. E. V. et al. pkCSM: Predicting Small-Molecule Pharmacokinetic and Toxicity Properties Using Graph-Based Signatures. J. Med. Chem. 58 (9):4066-4072 (2015).
- (8) Wuts, P. G. M. and Greene, T. W. Chapter 7: Protection for the Amino Group in Protective Groups in Organic Synthesis, 4th ed.; Wiley: Hoboken, NJ (2006)
- (9) Cox, C. and Lectka, T. Solvent Effects on the Barrier to Rotation in Carbamates. J. Org. Chem.63, 2426-2427 (1998)
- (10) Gosh, A. K. and Brindisi, M. Organic carbamates in drug design and medicinal chemistry. J.Med. Chem. 58, 2895-2940 (2015)









Time (min)













































Time (min)

























Relative Abundance





Time (min)



































.....

420

425

m/z

415

100

80\_\_ 70

60

50-

40 30

50

0-

410

387.1780

Relative Abundance



∆m= 0.49ppm NL: 1.83E4

C<sub>20</sub> H<sub>22</sub> N<sub>6</sub> O<sub>4</sub> +H: C20 H23 N6 O4 p (gss, s /p:40) Chrg 1 R: 70000 Res .Pwr . @FWHM

#### ∆m= 0.23ppm NL: 1.83E4



R=67265

z=?

435
















































100\_

50

0-

100 \_

50-

0-

415.2165

z=?

415

R=74153 417.2216

R=58941

z=?

420

Theoretical

425

m/z

C21H27 N5 O4 +H:  $C_{21}H_{28}\,N_5\,O_4$ p (gss, s /p:40) Chrg 1 R: 76000 Res .Pwr . @FWHM

## <sub>NL:</sub> Δm= 2.06 ppm 1.81E4

436.1955

R=75932

z=?

435

437.1985

R=73915

z=?

C21H27 N5 O4 +Na: C21H27 N5 O4 Na1 p (gss, s /p:40) Chrg 1 R: 76000 Res .Pwr . @FWHM

19









ОН



































































R=66726

z=?

m/z

506

20-

0-

502

504

R=53309

z=?

-

508

R=49380

z=?

510

R=43887 R=55197

512

z=?

z=?

Δm=0.20 ppm







100 -

90 80\_ 70

60 50-40












































































Time (min)























Reversed phase HPLC analysis of compounds from Figure S1. Compounds were analyzed by reversed phase HPLC (MZ-Aqua Perfect C-18 column, 250 x 4.6 mm, 5  $\mu$ m, 120 Å, equipped with a C-18 pre-column, 8.0 mm x 4.0 mm, 5  $\mu$ m, 120 Å) using acetonitrile gradient A (0% – 7% in 15 min and 7% – 70% in 5 min) or gradient B (4.9% – 52.5% in 30 min and 52.5 – 70% in 1 min) in aqueous TFA solution (0.01 % TFA) with a flow of 1 mL/min and detection at 260 nm.



**201** (dcSAM), gradient A



202 (daSAM), gradient A



204 (sinefungin), gradient A







206 (L-SAH), gradient B



208 (dc-SAH), gradient B







209 (5'-adenosyl-L-cysteine), gradient B



210 (CPTA), gradient B



211 (CPTA methylester), gradient B



212 (AETA), gradient A



213 (CETA), gradient B



215 (5'-thioadenosine), gradient B



214 (MTA), gradient B



216 (adenosine), gradient B



218 (5'-aminoadenosine), gradient A



**219** (*N*6-methyl-2'-deoxyadenosine), gradient B



**220** (TL-107-2), gradient B



221 (TL-106), gradient B







223 (TL-100-2), gradient B



224 (AEA), gradient A



225 (CMTA), gradient B



226 (5'-deoxy-5'-chloroadenosine), gradient B



228 (5'-deoxy-5'-acetyladenosine), gradient B



227 (5'-phthalimidoadenosine), gradient B



229 (South-SAH), gradient B



## 230 (North-SAH), gradient B



## 232 (5'-propylthioadenosine), gradient B



## 234 (5'-methylbutylthioadenosine), gradient B



## 231 (5'-ethylthioadenosine), gradient B



233 (5'-butylthioadenosine), gradient B









236 (5'-methylethylthioadenosine), gradient A





238 (phETA), gradient B



240 (5'-iodo-5'-deoxyadenosine), gradient B



239 (Bisubstrate inhibitor), gradient B



241 (5'-tosyladenosine), gradient B

