

# Synthesis and antibacterial activity of monocyclic 3-carboxamide tetramic acids

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## Full Research Paper

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Keywords:  
acylation; antibacterial; drug discovery; natural products; tetramate

*Beilstein J. Org. Chem.* **2013**, *9*, 1899–1906.  
doi:10.3762/bjoc.9.224

Received: 25 June 2013  
Accepted: 23 August 2013  
Published: 19 September 2013

This article is part of the Thematic Series "Natural products in synthesis and biosynthesis".

Guest Editor: J. S. Dickschat

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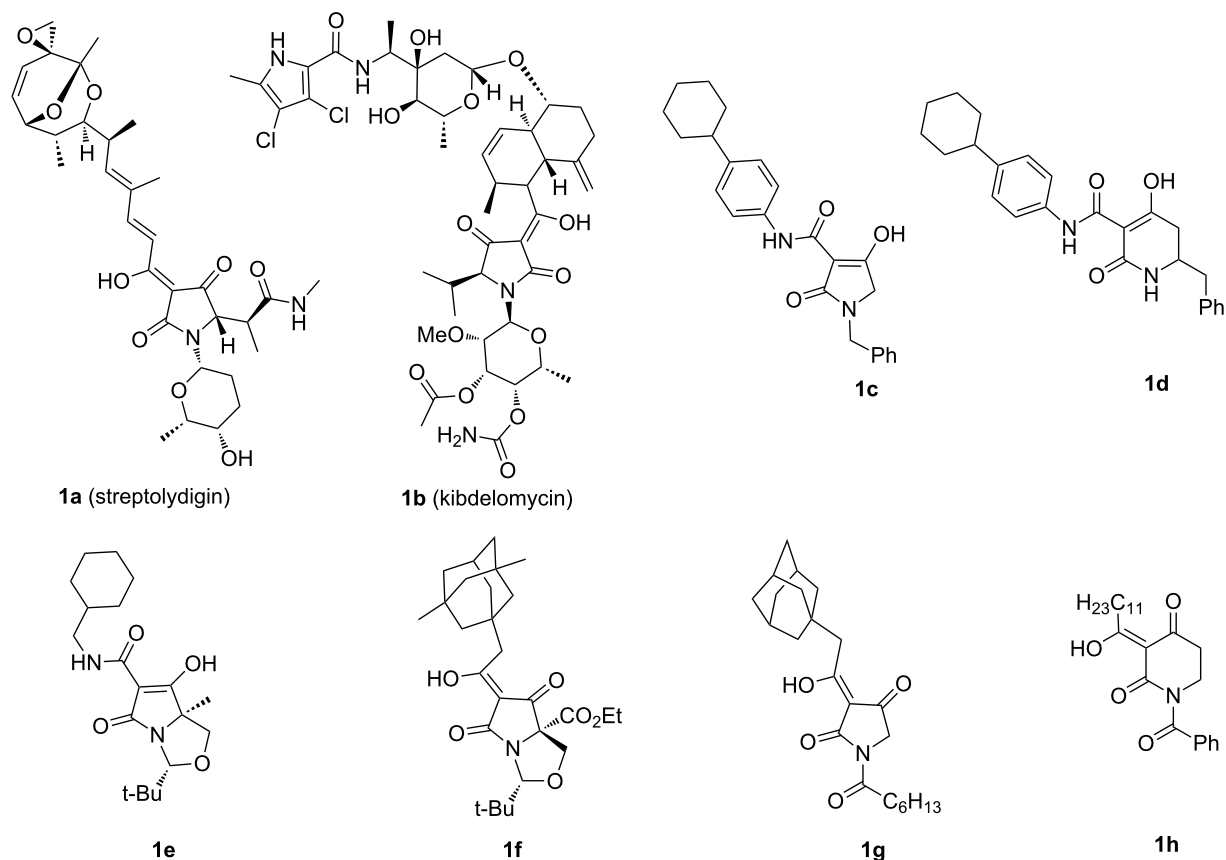
## Abstract

A chemical library of carboxamide-substituted tetramates designed by analogy with antibacterial natural products, a method for their rapid construction, and the evaluation of their antibacterial activity is reported.

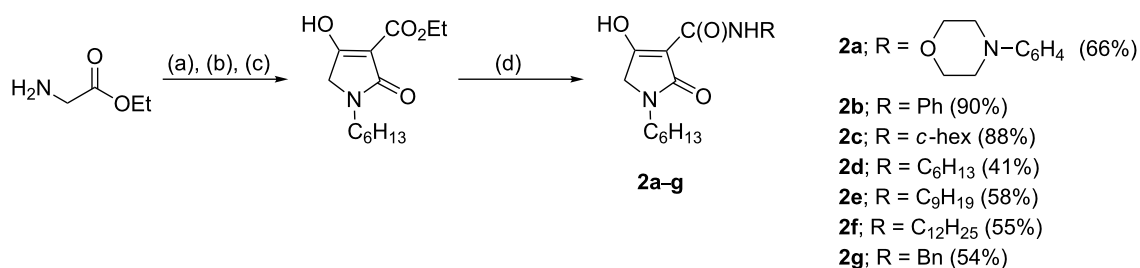
## Introduction

The discovery of new antibiotic families with novel modes of action is a promising way to overcome resistant or virulent bacteria, since novel modes of action might be expected to slow target-based endogenous resistance [1]. In this regard, natural products play a major role by providing a biologically validated starting point [2]. Recently discovered antibiotic lead compounds of major interest include platensimycin (a FabF inhibitor) [3], R207910 (an ATP synthase inhibitor) [4] and moiramide B (a bacterial acetyl-CoA carboxylase inhibitor) [5]. Both natural 3-acyltetramic acids, for example streptolydigin **1a** (bacterial RNA polymerase (RNAP) inhibitory activity) [6] and kibdelomycin **1b** (bacterial type II topoisomerase inhibitory activity) [7] and unnatural systems, such as 3-carboxamide tetramic acid **1c** and 3-carboxamide piperidine-2,4-dione **1d** (undecaprenyl pyrophosphate synthase (UPPS) inhibitory

activity) [8] exhibit high levels of antibacterial activity (Figure 1). All these systems share a  $\beta$ -dicarbonyl core. A drug discovery programme inspired by these natural products, as promoted by Waldmann [9], was of interest to us. We have recently focused on the construction and evaluation of libraries derived from tetramic acid scaffolds and discovered that bicyclic 3-carboxamide **1e**, bicyclic 3-acyl **1f** and monocyclic 3-acyl **1g** exhibit a dual targeting ability at RNAP and UPPS, while 3-acyl piperidine-2,4-dione **1h** only targets UPPS [10]. Although tetramates are well-known as a core component in many natural products that continue to excite interest [11–14], we carried out a more detailed study of the synthesis, tautomeric behaviour and antibiotic activity of related monocyclic 3-carboxamide tetramic acid systems **2** and **3** (Schemes 1–3), the results of which are outlined below. In



**Figure 1:** Some antibiotic natural and unnatural tetramic acids.



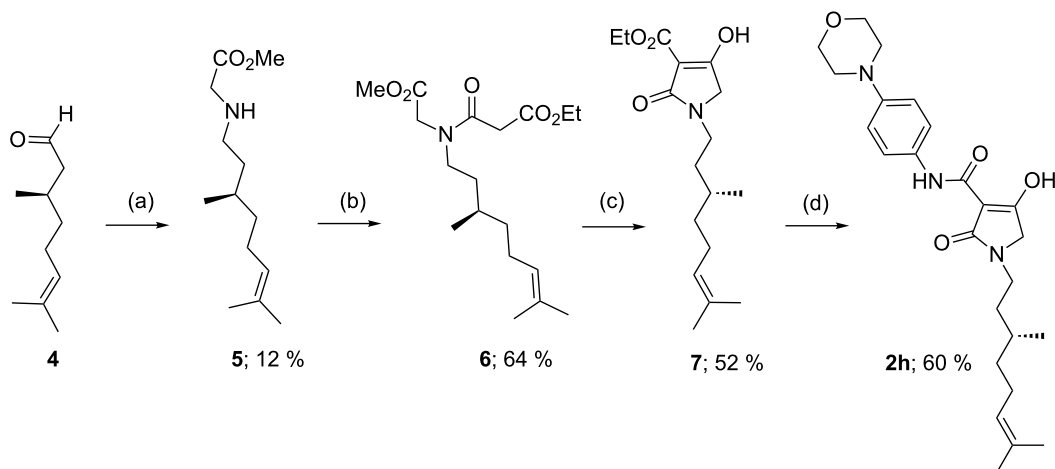
**Scheme 1:** Synthesis of simple 3-carboxamide tetramic acids. Reaction conditions: (a) triethylamine (2.0 equiv), 1-bromohexane (0.5 equiv), EtOH, reflux; (b) monoethyl malonate (1.1 equiv), DCC (1.1 equiv),  $CH_2Cl_2$ , rt; (c) NaOMe (1.1 equiv), benzene, EtOH, reflux; (d)  $RNH_2$  (1.0 equiv), toluene, reflux.

system **2**, the N(1) and C(5) substituents were chosen in order to probe the effect of the length of the *N*-alkyl chain on antibiotic activity. The substituents of system **3** were chosen in order to probe the effect of a C(3) substituent containing a sulfur heteroatom, which we had earlier seen results in enhanced antibacterial activity compared with the oxygen counterpart [10], for two types of amide substituent and a range of C(3) carboxamides.

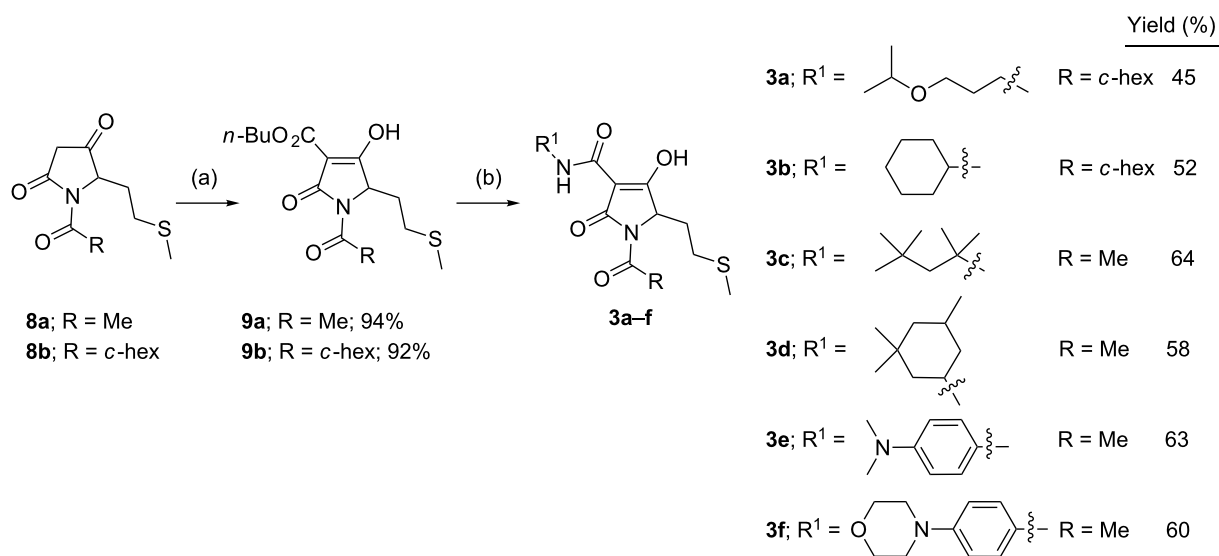
## Results and Discussion

### Synthesis

The synthesis of the required tetramic acid systems **2a–g** (Scheme 1), **2h** (Scheme 2) and **3a–f** (Scheme 3) was achieved by Dieckmann cyclisation of the required *N*-alkyl-*N*-malonyl glycine (readily prepared from glycine). A similar strategy for the base-mediated cyclisation of *N*-acetoacetyl amino acid esters leading to 3-acetyltetramates has been reported, which give



**Scheme 2:** Synthesis of *N*-alkyl 3-carboxamide tetramic acid. Reaction conditions: (a) 1. glycine methyl ester-HCl (1.0 equiv), Et<sub>3</sub>N (1.2 equiv), MgSO<sub>4</sub> (2.0 equiv), THF, rt. 2. NaBH<sub>4</sub> (2.0 equiv), MeOH, rt; (b) ethyl malonyl chloride (1.05 equiv), Et<sub>3</sub>N (1.2 equiv), CH<sub>2</sub>Cl<sub>2</sub>, rt; (c) KO<sup>t</sup>-Bu (1.1 equiv), THF, reflux; (d) amine (1.0 equiv), toluene, reflux; (e) butyl chloroformate (1.2 equiv), DMAP (2.2 equiv), CH<sub>2</sub>Cl<sub>2</sub>, rt.



**Scheme 3:** Synthesis of C(5)-alkyl 3-carboxamide tetramic acids. Reaction conditions: (a) butyl chloroformate (1.2 equiv), DMAP (2.2 equiv), CH<sub>2</sub>Cl<sub>2</sub>, rt; (b) RNH<sub>2</sub> (1.0 equiv), toluene, reflux.

N–H rather than *N*-alkyl systems [15–17]. Tetramate **7** was obtained from amino acid **6**, except that the key intermediate **5** was obtained by reductive amination (Scheme 2) of (*R*)-citronellal (**4**), which although proceeding in poor yield gave enough material with which to proceed [18]. By contrast, *N*-acyl derivatives could not be easily prepared by an equivalent approach because of the difficulty of a controlled double acylation on N(1). Although the synthesis of *N*-acetyl 3-alkoxycarbonyls from *N*-hydroxysuccinimide esters of *N*-acetyl amino acids has been reported [19], we wished to exploit an alternative approach based upon C-acyloxymethylation of enolates fol-

lowed by amine exchange, which had been shown to be very effective in a pyroglutamate series, since it offered synthetic simplicity and the potential for generality [20,21]. We found that an approach based upon direct acylation of methyl thioethers **8a,b** (these were readily obtained from the required *N*-acetylmethionine by DCC/DMAP coupling with Meldrum's acid and cyclisation under reflux) was possible, which made use of the high acidity of the tetramate system. Thus, conversion to the *n*-butyloxycarbonyl derivatives *N*-acyl **9a,b** by using 1.2 equivalents of butyl chloroformate along with 2.2 equivalents of 4-(dimethylamino)pyridine (DMAP) proceeded in good

yields (over 90%) (Scheme 3) [10]. With the 3-alkoxycarbonyl tetramic acid core systems **7** and **9** in hand, conversion to 3-carboxamides **2a–g** and **3a–f** by direct ester–amide exchange under reflux in toluene was readily achieved, providing access to a range of amides in good to excellent yield (Schemes 1–3). This process neatly complements a strategy we had earlier used for the introduction of amine substituents in pyroglutamates by a conjugate addition of amines [22].

## Tautomerism

Tautomerism in tricarbonyl 3-acyltetramate systems is known to be complex and strongly dependent on the identity of the side chain acyl group [23]. 3-Acyl ( $X = \text{CH}_2$ ) [10,24,25], 3-carboxamide ( $X = \text{NH}$ ) [8,10] and 3-alkoxycarbonyl ( $X = \text{O}$ ) tetramic acids (Figure 2) have been found to exist as a pair of external conformers (AB and CD) in slow equilibrium ( $\text{AB} \rightleftharpoons \text{CD}$ ), each consisting of a pair of internal tautomers in rapid equilibrium ( $\text{A} \rightleftharpoons \text{B}$  and  $\text{C} \rightleftharpoons \text{D}$ ). The tautomerisation of 3-acyltetramic acids has been shown to be mainly affected by substitution on N(1) rather than the functionalities on the 3-acyl and C(5) positions. Thus, the dominant tautomer of N-unsubstituted and N-alkyltetramates is D, while N-acyltetramates exist as a mixture of external tautomers AB and D in approximately equal ratio [23]. By contrast, it was found that the tautomerisation of 3-carboxamides and 3-alkoxycarbonyls was not affected by substitution on N(1). Therefore, the dominant tautomer of 3-carboxamide tetramates is tautomer A (over 80%) with a minor contribution of tautomer D, while 3-alkoxycarbonyltetramates exist as only tautomer A (>99%). In order to understand this phenomenon, the ground state energy of simplified 3-carboxamides **11a,b** and 3-alkoxycarbonyls **12a,b** was calculated and compared with that of 3-acyl derivatives **10a,b**

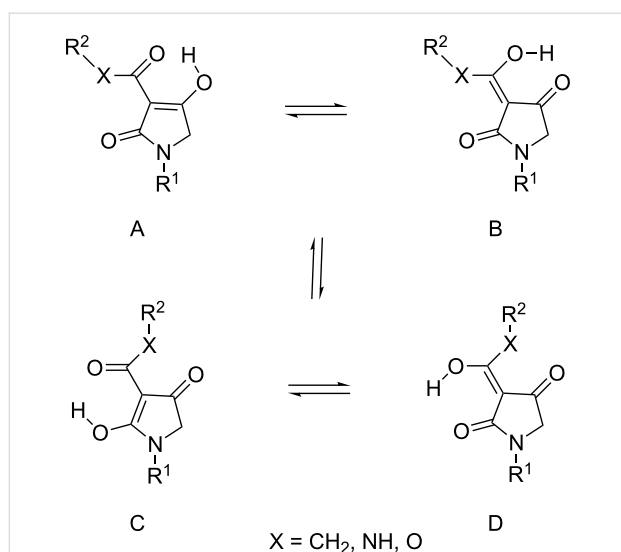


Figure 2: Tautomerism of tetramates.

(Table 1). To the best of our knowledge, such a detailed analysis has not been previously reported. In the calculation for N-alkyl 3-acyltetramate **10a**, the ground-state energies of tautomers B and D, which shows preference for tautomer D, is considerably lower than those of tautomers A and C. This outcome supports experimental NMR observations (>80% of tautomer D and <20% of tautomer B, Table 1, entry 1). On the other hand, the ground state energy of tautomer C of N-acyl **10b** is considerably higher than that of tautomers A, B and D, also supporting the NMR observations (tautomer AB:D = about 50:50, Table 1, entry 2). However, tautomer A of 3-carboxamides was the most stable for both of N-alkyl tetramate **11a** and N-acyl tetramate **11b** (>80% of tautomer A and <20% of tautomer D, Table 1, entry 3 and entry 4), while for 3-alkoxycarbonyltetramates **12a,b**, tautomer A was the most stable, and significantly more stable than tautomers B–D. These findings support the conclusion that 3-alkoxycarbonyls exist only as tautomer A (Table 1, entry 5 and entry 6).

Table 1: Calculated energy of the ground state of 3-acyltetramic acids **10a,b**, 3-carboxamide tetramic acids **11a,b** and 3-alkoxycarbonyl tetramic acids **12a,b**.

Entry	Compound	Calcd relative energy (kcal/mol) <sup>a,b</sup>			
		Form A	Form B	Form C	Form D
1	<b>10a</b>	+4.16	+1.61	+4.30	0
2	<b>10b<sup>c</sup></b>	+1.59	+0.17	+5.62	0
3	<b>11a</b>	−0.51	+0.42	+1.74	0
4	<b>11b</b>	−0.91	−0.15	+3.82	0
5	<b>12a</b>	−3.58	+1.75	−1.41	0
6	<b>12b</b>	−6.24	−0.64	+3.20	0

<sup>a</sup>The energy difference between each tautomer related to tautomer D.

<sup>b</sup>Calculated by using DFT B3LYP (6-31G\*) in Spartan 02. <sup>c</sup>Reported in our previous paper [10].

## Antibacterial activity

The antibiotic activities of tetramates **2a–h** and **3a–f** along with analogues **1c** and **1d** (reported by Novartis [8]) were determined against 4 species of Gram-positive bacteria, consisting of 4 strains of *Staphylococcus aureus*, including a methicillin-resistant strain (MRSA, S2), vancomycin susceptible *Enterococcus faecalis* (VSE, E1), vancomycin resistant *E. faecium* (VanA VRE, E2), and 2 strains of *Streptococcus pneumoniae*,

including multi-drug resistant strain (MDRSP, P9), as well as 3 species of Gram-negative bacteria, consisting of *Pseudomonas aeruginosa* and 2 strains of *Haemophilus influenzae*, including an efflux-negative strain, and 2 strains of *Escherichia coli*, including an efflux-negative strain (Table 2). Relevant physicochemical properties of the analogues are also shown in Table 3. These were used to elaborate structure–activity relationships (SAR) [26]. In the assay against Gram-negative bacteria, no activity against *E. coli* and *P. aeruginosa* was found (MIC > 64 µg/mL, data not shown), consistent with the inactivity of 3-acyl and 3-carboxamide tetramic acids against these strains seen earlier [7,8,10]. This result is most likely explained by their poor cell permeability as a result of their hydrophobic character [14,27]. However, activities against another Gram-negative bacterium, *H. influenzae*, were found, the magnitude of which depended on the substituent. An SAR consistent with transportation by the efflux pump was found [28]. Analogues **2e,h** and **1c,d**, for which activity differences between efflux-positive (H3) and negative (H4) *H. influenzae* strains are large, are more lipophilic compared with other active analogues (rel-PSA < 13.5, c log P

> 2.79 and c log D (7.4) > 1.41). On the other hand, analogues **2** and **3** show a broad-spectrum activity against Gram-positive bacteria, although the activity depends on the substituent identities. Importantly, the variation of antibacterial activity for analogues **2** and **3** was less pronounced in the resistant strains MRSA, VRE and MDRSP (normally less than 8 times variation, with the exception of analogues **2e** and **3b**), while the activities of Novartis analogue **1c** against MRSA [8], amoxicillin against MDRSP and ciprofloxacin against MRSA and VRE were significantly lower (more than 250 times compared with the activity against the most sensitive strain). Among the various substituent groups, *N*-alkyl phenyl derivatives **2a,b,h** were active, while *N*-acetyl phenyl derivatives **3e,f** were inactive or only very weakly active. This SAR might be accounted for by their physicochemical properties: the less lipophilic character of *N*-acetyl **3e,f** (rel-PSA > 17.0%, c log P < 0.80 and c log D (7.4) < −1.20) compared with those of *N*-alkyl **2a,b,h** (rel-PSA < 15.0%, c log P > 1.77 and c log D (7.4) > 0.41) might make penetration of the bacterial cell membrane more difficult. However, 3-carboxamides **2c–g** and **3a–d**, all possessing alkyl substituents, including a benzyl group on the

**Table 2:** In vitro antibiotic activity (MIC, µg/mL) of tetramic acids.<sup>a,b</sup>

	S1	S26	S4	S2	E1	E2	P1	P9	P9B	H3	H4
<b>2a<sup>c</sup></b>	4	8	8	8	8	8	16	8	32	16	4
<b>2b<sup>c</sup></b>	1	1	1	2	2	4	4	4	– <sup>d</sup>	2	0.5
<b>2c<sup>c</sup></b>	8	8	8	8	8	8	16	8	8	4	0.25
<b>2d<sup>c</sup></b>	2	2	2	2	2	2	4	1	4	1	0.12
<b>2e<sup>c</sup></b>	2	16	16	16	8	0.5	4	1	4	>64	≤0.1
<b>2f</b>	>64	>64	>64	>64	>64	>64	16	8	16	>64	>64
<b>2g</b>	8	8	8	8	16	8	64	16	8	4	0.25
<b>2h</b>	2	2	2	2	2	2	8	4	>64	>64	8
<b>3a</b>	>64	>64	32	>64	16	16	8	8	8	>64	>64
<b>3b</b>	4	8	2	8	1	2	0.5	0.5	0.5	8	1
<b>3c</b>	8	32	32	16	8	16	8	8	8	32	4
<b>3d</b>	8	64	32	32	8	16	8	8	4	64	4
<b>3e</b>	>64	>64	>64	>64	>64	>64	64	64	64	>64	64
<b>3f</b>	>64	>64	>64	>64	>64	>64	>64	>64	>64	>64	>64
<b>1c<sup>c</sup></b>	0.1	0.12	1	<b>64</b>	≤0.1	≤0.1	2	2	2	>64	0.5
<b>1d</b>	8	64	32	64	32	4	64	64	>64	>64	16
<b>Line<sup>c</sup></b>	2	2	2	2	2	2	1	0.5	0.5	16	4
<b>Cip</b>	0.1	0.5	0.12	<b>16</b>	1	<b>32</b>	1	1	1	0.5	≤0.1
<b>Amox</b>	– <sup>d</sup>	– <sup>d</sup>	– <sup>d</sup>	– <sup>d</sup>	– <sup>d</sup>	– <sup>d</sup>	>0.03	<b>8</b>	– <sup>d</sup>	– <sup>d</sup>	– <sup>d</sup>
<b>Caz</b>	8	16	16	– <sup>d</sup>	– <sup>d</sup>	– <sup>d</sup>	– <sup>d</sup>	– <sup>d</sup>	– <sup>d</sup>	– <sup>d</sup>	– <sup>d</sup>

<sup>a</sup>Abbreviation; **S1**; *S. aureus* 1, ATCC13709 in vivo (methicillin sensitive), **S26**; *S. aureus* 26, ATCC25923 (vancomycin susceptible), **S4**; *S. aureus* 4, Oxford, **S2**; *S. aureus* 2, (MRSA in vivo), **E1**; *E. faecalis* 1, ATCC29212 VanS (vancomycin susceptible), **E2**; *E. faecium* 1, VanA (vancomycin resistant), **P1**; *S. pneumonia* 1, ATCC49619 (erythromycin susceptible), **P9**; *S. pneumonia* 9, (multi-drug resistant), **P9B**; *S. pneumonia* 9 in presence of 2.5% horse blood, **H3**; *H. influenzae* 3, ATCC31517 MMSA, **H4**; *H. influenzae* 4, LS2 Efflux knock out, **Line**; linezolid, **Cip**; ciprofloxacin, **Amox**; amoxicillin, **Caz**; ceftazidime. <sup>b</sup>All analogues are inactive (MIC > 64 µg/mL) against *E. coli* 1, ATCC25922 (non pathogenic strain), *E. coli* 50, Ec49 No efflux and *P. aeruginosa* 1, ATCC27853. <sup>c</sup>The activity was reported in our previous publication [10]. <sup>d</sup>Not determined.

**Table 3:** Physicochemical properties of 3-carboxamide tetramic acids.<sup>a,b</sup>

	MW	MSA	PSA	rel-PSA	c log P	c log D (7.4)	HD/HA	RB
<b>2a<sup>c</sup></b>	387	599	82.1	13.7	1.77	0.41	2/5	8
<b>2b<sup>c</sup></b>	302	462	69.6	15.1	1.85	0.64	2/3	7
<b>2c<sup>c</sup></b>	308	509	69.6	13.7	1.28	−0.15	2/3	7
<b>2d<sup>c</sup></b>	310	540	69.6	12.9	1.69	0.23	2/3	11
<b>2e<sup>c</sup></b>	353	632	69.6	11.0	2.88	1.42	2/3	14
<b>2f</b>	395	725	69.6	9.6	4.07	2.61	2/3	17
<b>2g</b>	316	492	69.6	14.1	1.47	−0.04	2/3	8
<b>2h</b>	442	691	82.1	11.9	2.79	1.41	2/5	9
<b>3a</b>	427	662	95.9	14.5	0.90	−1.32	2/5	10
<b>3b</b>	409	613	86.7	14.1	1.84	−0.19	2/4	6
<b>3c</b>	371	590	86.7	14.7	0.84	−1.13	2/4	7
<b>3d</b>	383	586	86.7	14.8	1.06	−0.96	2/4	5
<b>3e</b>	377	530	90.0	17.0	0.80	−1.20	2/5	6
<b>3f</b>	419	577	99.2	17.2	0.46	−1.54	2/6	6
<b>1c</b>	390	568	69.6	12.3	3.51	2.03	2/3	5
<b>1d</b>	405	591	78.4	13.3	3.63	2.96	3/3	5

<sup>a</sup>MW; molecular weight, MSA; molecular surface area, PSA; polar surface area, %PAS; relative polar surface area = (PSA/MSA) × 100, c log P; calculated partition coefficient, c log D (7.4); calculated distribution coefficient at pH 7.4, HD; hydrogen-bond donor count, HA; hydrogen-bond acceptor count, RB; rotatable bond count. <sup>b</sup>Tautomer A was selected for the calculation. <sup>c</sup>Reported in our previous publication [10].

amide function, are also active to Gram-positive strains. Furthermore, the activities of *n*-alkyl **2d–f** depended on the chain length, with a marked drop-off in activity for the longer chain **2f**. In addition, the activity of the more lipophilic analogues **2a,d–f,h** (PSA ≤ 13.7%, c log P ≥ 1.69 and c log D (7.4) ≥ 0.23) in the presence of 2.5% horse blood was shifted to high MICs even though that of less lipophilic analogues **2c,g** and **3a–e** (PSA ≥ 13.7%, c log P ≤ 1.84 and c log D (7.4) ≤ −0.04) was maintained. This serum-protein binding signifi-

cantly affected the activity against *S. aureus* S26, since almost all analogues showed inactivity (MIC > 64 µg/mL) in the presence of 10% human serum with the exception of **2a** (32 µg/mL) and **2b** (64 µg/mL) (data not shown).

After screening to find the most active compound, tetramate **2b** was selected for a detailed investigation and its antibiotic activity against various drug-resistant strains was further evaluated with reference antibiotics (Table 4). Tetramate **2b** was

**Table 4:** Antibiotic activity of tetramic acid **2b**.<sup>a</sup>

Strains	Phenotype	MIC (µg/mL)					
		<b>2b</b>	Moxi	Amox	Ery	Vanco	Caz
<i>S. pneumoniae</i> Pn7	EryR	2	0.125	<b>4</b>	<b>16</b>	0.25	– <sup>c</sup>
<i>S. pneumoniae</i> Pn10	PenR, EryR	2	0.125	<b>4</b>	<b>&gt;32</b>	0.5	– <sup>c</sup>
<i>S. pneumoniae</i> Pn11	PenR	2	0.125	<b>4</b>	<0.03	0.25	– <sup>c</sup>
<i>S. pneumoniae</i> Pn19	EryR	2	0.06	0.06	<b>&gt;32</b>	0.5	– <sup>c</sup>
<i>S. pneumoniae</i> Pn21	EryR	2	0.06	0.125	<b>4</b>	0.25	– <sup>c</sup>
<i>S. pneumoniae</i> Pn31	EryR	0.13	<0.03	<0.03	<b>16</b>	0.5	– <sup>c</sup>
<i>S. aureus</i> Sa5	ermR PK2 <sup>b</sup>	1	≤0.03	– <sup>c</sup>	– <sup>c</sup>	– <sup>c</sup>	<b>32</b>
<i>S. aureus</i> Sa18	FQR	1	<b>32</b>	– <sup>c</sup>	– <sup>c</sup>	– <sup>c</sup>	<b>16</b>
<i>S. aureus</i> Sa40	mecA <sup>b</sup>	1	≤0.03	– <sup>c</sup>	– <sup>c</sup>	– <sup>c</sup>	<b>32</b>

<sup>a</sup>Abbreviation: EryR; erythromycin resistant, PenR; penicillin resistant, FQR; fluoroquinolone resistant, Moxi; moxifloxacin, Amox; amoxicillin, Ery; erythromycin, Caz; ceftazidime. <sup>b</sup>Methicillin-resistant strain. <sup>c</sup>Not determined.

found to be active against virulent and resistant strains, such as methicillin and fluoroquinolone-resistant *S. aureus* and penicillin and/or erythromycin-resistant *S. pneumoniae*. Remarkably, tetramate **2b** maintained the activities against all the strains and was highly effective against erythromycin resistant *S. pneumoniae* Pn31 (MIC = 0.125 µg/mL). By way of comparison, the activities of moxifloxacin (a fourth generation fluoroquinolone) to *S. aureus* Sa18 (MIC = 32 µg/mL), amoxicillin (β-lactam) to *S. pneumoniae* Pn7, Pn10 and Pn11 (MIC = 4 µg/mL), erythromycin to *S. pneumoniae* Pn7, Pn10, Pn19, Pn21 and Pn31 (MIC ≥ 4 µg/mL) and ceftazidime (a third generation cephalosporin) to *S. aureus* Sa5, Sa18 and Sa40 (MIC ≥ 16 µg/mL) were substantially decreased.

Lipophilic efficiency (LipE) has been used to assess the suitability of drug candidates as CB agonists [29], and the usage of a similar calculation for the data presented in this work (with  $\text{LipE} = \text{pMIC}(\text{nM}) - c \log P$ ) (see Table S1 and Figure S1 in Supporting Information File 1; pMIC values were calculated according to a literature protocol [30]), facilitated the identification of compounds with potential for optimisation. According to Figure S1, strongly active compounds can be found at  $c \log P$  values of 1–2, 3 or 4, and for the highly susceptible strain H4, for example, compounds of interest would be **2b–e** and **2g**.

## Conclusion

We have prepared monocyclic 3-carboxamide tetramic acids from 3-alkoxycarbonyl tetramic acids based on a direct ester–amide exchange by using butyl chloroformate with DMAP, thereby providing a general access to this type of system. The tautomerization of 3-alkoxycarbonyl and 3-carboxamide tetramic acids compared to 3-acyltetramic acids has been investigated. It has been found that 3-alkoxycarbonyl and 3-carboxamide tetramic acids prefer tautomer A, while the preference of 3-acyltetramic acids depends on the N(1)-functionality. Of particular interest is that 3-carboxamide analogues, especially **2b**, have shown bioactivity against various Gram-positive bacteria including clinically resistant strains such as MRSA, fluoroquinolone-resistant *S. aureus*, MDRSP, penicillin and erythromycin-resistant *S. pneumonia* and VRE as well as Gram-negative *H. influenzae*. Further optimisation, especially for overcoming high plasma-protein binding, is warranted but these compounds may be suitable for an evaluation for topical use [31,32]. Significantly, these results suggest that a drug discovery approach based upon deconstruction–reconstruction inspired by suitable natural products with demonstrable biological activity provides a route for the rapid assembly of compound libraries, which, even if not fully optimized, provide a useful starting point for further elaboration.

## Experimental

**General.** Melting points were determined with a Stuart Scientific SMP1 melting point device and are uncorrected. The  $^1\text{H}$  and  $^{13}\text{C}$  NMR spectra were obtained by using a Bruker Avance AV400 (400 MHz and 100 MHz, respectively) with residual solvent peaks as the internal reference. Mass spectra (MS) and high-resolution mass spectra (HRMS) were obtained with Micro Mass LCT and GCT spectrometers under the conditions of electrospray ionization (ESI) and chemical ionization (CI) respectively, and values were reported as a ratio of mass to charge in Daltons.

**Synthesis.** The synthesis of monocyclic precursor tetramate compounds from glycine has been reported in our previous publication [33].

**Calculations.** Density Functional B3LYP (6-31G\*) in Spartan 02 was used for the calculation of the energy in equilibrium geometry at ground state. MarvinSketch Version 5.3.8. (<http://www.chemaxon.org>) was used for the calculation of the van der Waals molecular surface area (MSA), the polar surface area (PSA), the calculated partition coefficient ( $c \log P$ ) under VG method, the calculated distribution coefficient at pH 7.4 [ $c \log D (7.4)$ ] under VG method, the hydrogen-bond donor count, the hydrogen-bond acceptor count, and the rotatable bond count.

**Antibacterial activity.** Antibiotic activity was measured by using standard methodology (Clinical and Laboratory Standards Institute. Methods for antimicrobial susceptibility test for bacteria that grow aerobically, approved standard M7-A7, 7th ed., CLSI, Wayne, PA, 2006): compounds were diluted in DMSO to obtain 2.56 mg/mL, then 100 µL were diluted in Mueller-Hinton broth to 0.256 mg/mL and assayed against the bacterial panel by incubation in 96-well microplates at 37 °C for 24 h. The MIC was determined by visually reading the first concentration where no growth (no turbidity) appeared.

## Supporting Information

### Supporting Information File 1

Experimental details, calculated energies (Spartan) for selected compounds and NMR spectra.

[<http://www.beilstein-journals.org/bjoc/content/supplementary/1860-5397-9-224-S1.pdf>]

## Acknowledgements

We are particularly grateful for valuable input by Drs Phil Dudfield and John Lowther, and for funding by Galapagos SASU (France).

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