

1-(2-Hydroxybenzoyl)-thiosemicarbazides are promising antimicrobial agents targeting D-alanine- D-alanine ligase *in bacterio*.

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ABSTRACT. The bacterial cell wall and the enzymes involved in peptidoglycan synthesis are privileged targets for the development of novel antibacterial agents. In this work, a series of 1-(2-hydroxybenzoyl)-thiosemicarbazides inhibitors of D-Ala-D-Ala ligase (Ddl) were designed and synthesized in order to target resistant strains of bacteria. Among these, the 4-(3,4-dichlorophenyl)-1-(2-hydroxybenzoyl)-3-thiosemicarbazide **29** was identified as a potent Ddl inhibitor with activity in the micromolar range. This compound, possessing strong antimicrobial activity including against multidrug resistant strains, was proven to act through a bactericidal mechanism and demonstrated very low cytotoxicity on THP-1 human monocytic cell line. Inhibition of Ddl activity by **29** was confirmed *in bacterio* using UPLC-MS/MS by demonstrating an increase in D-Ala intracellular pools accompanied by a commensurate decrease in D-Ala-D-Ala. Further structure-activity relationships (SARs) studies provided evidence that the hydroxyl substituent in the 2-position (R₁) of the benzoylthiosemicarbazide scaffold is essential for the enzymatic inhibition. This work thus highlights the 1-(2-hydroxybenzoyl)-thiosemicarbazide motif as a very promising tool for the development of novel antibacterial compounds acting through an interesting mechanism of action and low cytotoxicity.

Keywords: D-alanine-D-alanine ligase inhibitors, Benzoylthiosemicarbazides, Antimicrobial agents, Antibiotics, Structure-activity relationships.

1. INTRODUCTION

In an era of growing antibiotic resistance, the search for effective molecules with novel mechanisms of action is a priority.¹ Today, the bacterial cell wall and the enzymes involved in peptidoglycan biosynthesis, a major cell wall structural component, constitute validated targets of

many antimicrobial agents.² The peptidoglycan is a polymeric network which alternates *N*-acetylglucosamine (GlcNAc) and *N*-acetylmuramic acid (MurNAc) disaccharide units cross-linked via peptide bonds³ thanks to the catalytic activity of *D,D*-transpeptidases. These enzymes catalyze the reticulation of the peptide chains ending in *D*-Ala-*D*-Ala, with subsequent elimination of the terminal *D*-Ala residue and transfer of the remaining peptide chain on the lateral amino group of another peptide of an adjacent glycan chain. This last step of peptidoglycan biosynthetic pathway is inhibited by β -lactams antibiotics (such as penicillins), which act as suicide inhibitors of the transpeptidases,⁴ and by glycopeptides (vancomycin) that directly bind the terminal *D*-Ala-*D*-Ala moiety, creating a steric hindrance that prevents the access of *D,D*-transpeptidases to their substrate.⁵ However, the frequent resistance associated with the use of these antibiotics revealed the need to target other enzymes acting on earlier steps of peptidoglycan synthesis.⁶ Among these, *D*-alanine-*D*-alanine ligase (Ddl) represents a very interesting target.

Ddl is present in both Gram-negative and -positive bacteria and catalyzes the formation of *D*-Ala-*D*-Ala dipeptide, an early step in peptidoglycan synthesis. Two isoforms exist for *E. coli* and *S. typhimurium*, DdlA and DdlB.⁷ Alternative ligases, catalyzing the formation of *D*-Ala-*D*-Lac (VanA, -B and -D types) or *D*-Ala-*D*-Ser (VanC, -E, -G and -L types), were also described in vancomycin-resistant enterococci.^{5,8} Therefore, the discovery of inhibitors that are active not only on Ddl but also on these alternative ligases would increase their potential spectrum of activity. Today, various crystallographic structures of DdlB in presence of inhibitors, or in the *apo* form, are available and could thus contribute to the rational development of novel antibiotics.⁹⁻¹² Over the past few years, four main classes of Ddl inhibitors were described.⁶ First, analogues of the substrate *D*-Ala were reported¹³⁻¹⁷ including *D*-cycloserine (DCS, **Figure 1**),¹⁸⁻²¹ the only inhibitor used in the past as a therapeutic agent. However, its use is rather limited due to its known

neurotoxicity.²² This cyclic analogue of D-Ala acts as a competitive and reversible inhibitor of Ddl ($K_i = 25 \mu\text{M}$ against *M. tuberculosis* Ddl)¹⁹ and exhibits relatively high MIC values (50 mg/L against *M. tuberculosis*).²³ Secondly, compounds that mimic the transition state of the enzymatic reaction were reported. These latter inhibit Ddl by acting as false substrates. Interestingly, these compounds allowed crystallographic studies of the enzyme-inhibitor complex thus affording important structural information for drug design.²⁴⁻²⁵ Third, analogues of the reaction product D-Ala-D-Ala also showed interesting Ddl inhibition.^{13, 26} Fourth, inhibitors showing no structural resemblance with the substrate, the reaction intermediate or the product were discovered by screening chemical libraries or by rational drug design.²⁷⁻³⁶ For instance, thanks to a high-throughput screening against *S. aureus* Ddl (StaDDI), compound **1** (**Figure 1**) was identified ($K_i = 4 \mu\text{M}$). Although modestly active, this compound was used in structural studies and revealed a novel binding mode at an allosteric site.¹² This study thus paves the way to the development of original Ddl inhibitors acting via new mechanisms of inhibition. However, even if the most potent molecules reported so far showed inhibitory potencies in the micromolar range, only a few of them were evaluated for their antibacterial activity, which unfortunately usually remained very low.

An initial *de novo* design study carried out previously in our group allowed identifying the 2-phenylbenzoxazole series, exemplified by molecule **2** (**Figure 1**), as promising Ddl inhibitors. This series, however, revealed to be deprived of any antibacterial activity.³³ In the present work, we performed a screening of our internal library of compounds and identified the 1-(2-hydroxybenzoyl)-4-phenyl-3-thiosemicarbazide **3** (**Figure 1**) as an interesting tool compound with an IC_{50} of $0.80 \mu\text{M}$ against Ddl (*E. faecalis*) and relatively weak but reasonable antimicrobial potency on *S. aureus* ATCC 25923 and *E. faecalis* ATCC 29212 with MIC values of 128 mg/L and 512 mg/L respectively. We found from the literature that this compound was, in fact,

previously reported to be a very weak carbonic anhydrase inhibitor I and IX ($K_i > 80 \mu\text{M}$ on both isoforms)³⁷ and to have some antibacterial activities evaluated against usual random strains, although no information were given regarding its mode of action³⁸. These encouraging results prompted us to further develop and study this series of compounds, particularly their mode of action as antibacterials.

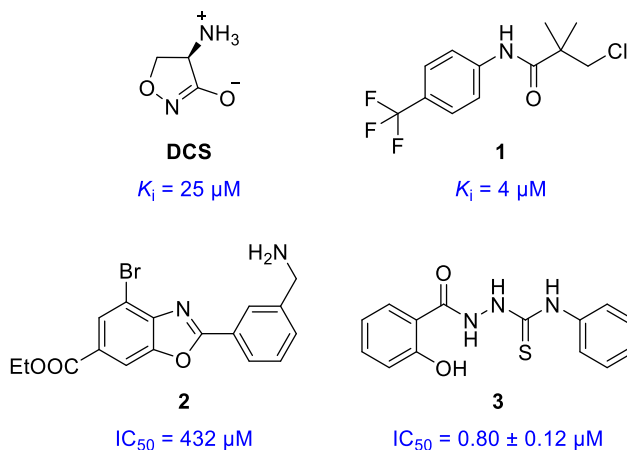


Figure 1. Chemical structure and affinity for Ddl or inhibitory potency of DCS (*M. tuberculosis* Ddl)¹⁹, 3-chloro-2,2-dimethyl-N-[4-(trifluoromethyl)phenyl]propanamide **1** (*S. aureus* Ddl)¹² and 2-phenylbenzoxazole **2** (*E. faecalis* Ddl)³³ reported in the literature. The IC_{50} of 1-(2-hydroxybenzoyl)-4-phenyl-3-thiosemicarbazide **3** (*E. faecalis* Ddl) is presented as the mean $\pm$ SD of experiments realized in triplicate, $n=2$.

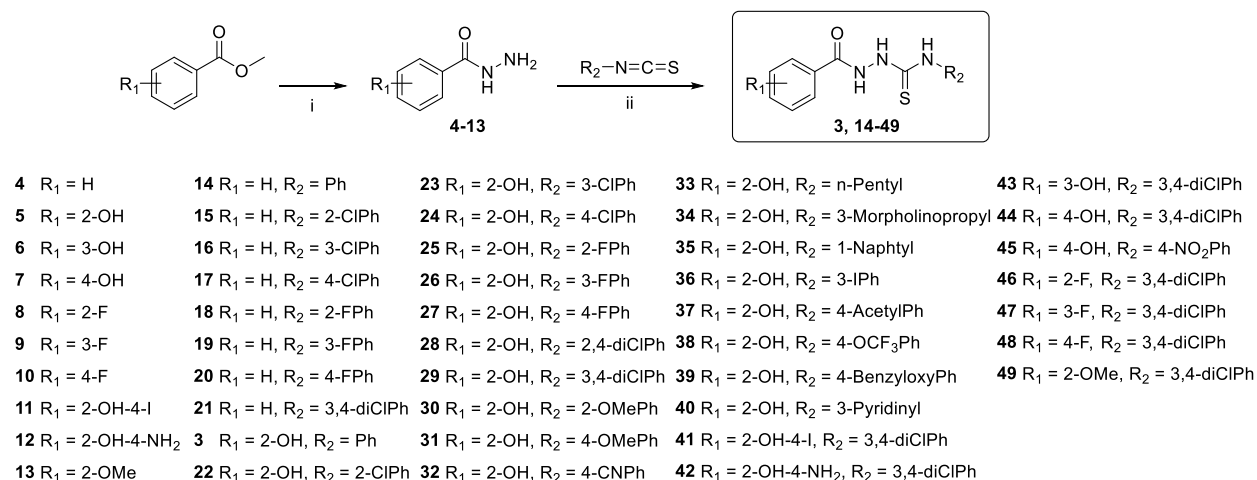
Various pharmacomodulations of compound **3** were investigated to improve the Ddl inhibition and the antibacterial potency, and to establish qualitative structure-activity relationships. The mechanism of action towards Ddl was also studied and the activity against Gram-positive and negative, sensitive or resistant strains to current therapeutics was determined. Finally, the *in vivo* biochemical mechanism was determined by UHPLC-MS/MS dosage of intracellular L-Ala, D-Ala

and D-Ala-D-Ala levels in response to 4-(3,4-dichlorophenyl)-1-(2-hydroxybenzoyl)-3-thiosemicarbazide **29**.

2. CHEMISTRY

The synthesis of benzoylthiosemicarbazides **3** and **14-49** was carried out according to a two-step procedure presented in **Scheme 1**. First, the benzohydrazides **4-13** were obtained according to the literature by refluxing hydrazine hydrate and the appropriate methyl benzoate in ethanol or were commercially available (**4** and **8**).³⁹⁻⁴⁰ Then, these benzohydrazides were reacted with various isothiocyanates in refluxing methanol or at room temperature.⁴¹⁻⁴² The targeted benzoylthiosemicarbazides **3** and **14-49** were collected by filtration and recrystallized from ethanol if necessary.

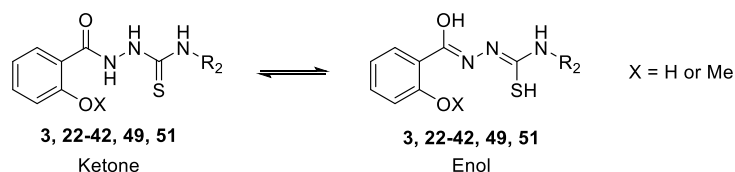
Scheme 1. Synthetic route for the preparation of the benzoylthiosemicarbazides **3** and **14-49** and their precursors **4-13**.^a



^a Reagents and conditions: (i) 65% hydrazine hydrate (5 equiv), EtOH, reflux, 2.5 h-24 h (ii) MeOH, reflux or r.t., 0.5 h-24 h.

The three labile protons (NH) of the thiosemicarbazide linker were visible on ^1H NMR in DMSO at approximately 9.72 ppm, 9.94 ppm and 10.47 ppm depending on the substituents of the thiosemicarbazide motif. The ^1H NMR spectrum of 1-(2-hydroxybenzoyl)-thiosemicarbazides **3**, **22-42** showed a duplication of two labile proton signals of the -NH-NH- functionality, probably reflecting an equilibrium between two of the potential tautomeric forms of this molecule (**Scheme 2**), as well as the 1-(2-methoxybenzoyl)-thiosemicarbazide **49** and the 1-(2-hydroxynaphthoyl)-thiosemicarbazide **51**. As this peak splitting can only be seen for the benzoylthiosemicarbazides bearing a substituent containing an oxygen in the 2-position (see Supporting Information), intramolecular H-bonding was suggested to explain this enol form stabilization allowing to observe both peaks in ^1H NMR. The existence of this keto-enol equilibrium for 1-(2-hydroxybenzoyl)-thiosemicarbazides was already mentioned in the literature.⁴³

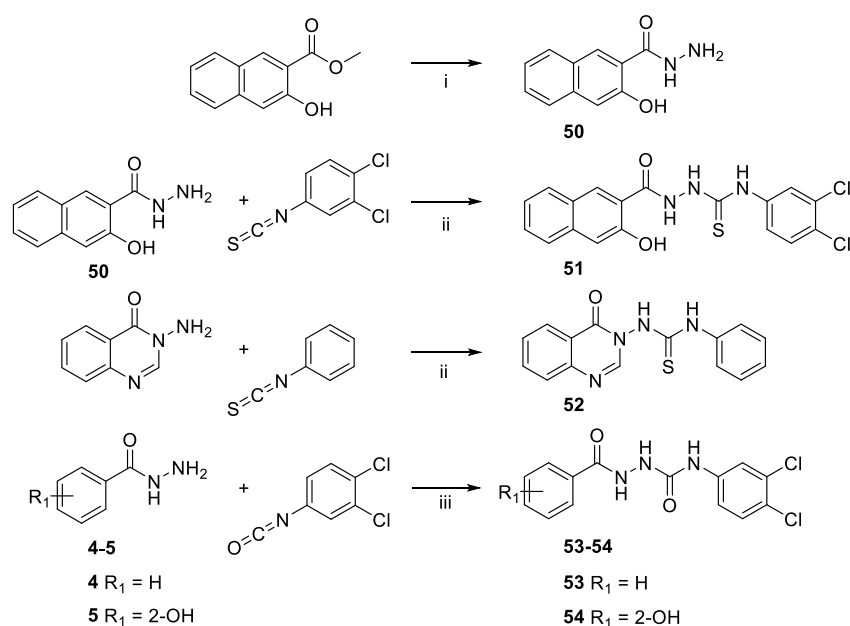
Scheme 2: Potential keto-enol equilibrium for compounds bearing a substituent containing an oxygen in the 2-position is visible in ^1H NMR spectrum.



To better understand the structure-activity relationships (SARs) in this series, other analogues were also prepared. First, the left part of the model compound **3** was rigidified by introducing a quinazolinone moiety and extended with the replacement of the phenyl by a naphthyl group, as depicted in **Scheme 3**. After obtaining the naphthohydrazide precursor **50**, the syntheses of **51-52** were thus carried out following the previous procedure for thiosemicarbazides synthesis. We then also investigated the replacement of the thiocarbonyl moiety by a carbonyl group to obtain the semicarbazide motif. To this end, the commercially available benzohydrazide **4** and 2-

hydroxybenzohydrazide **5** were added to 3,4-dichloro isocyanate in methanol at reflux to afford respectively 2-benzoyl-*N*-(3,4-dichlorophenyl)hydrazine-1-carboxamide **53** and *N*-(3,4-dichlorophenyl)-2-(2-hydroxybenzoyl)hydrazine-1-carboxamide **54** (**Scheme 3**) following the adapted known procedure.⁴⁴

Scheme 3. Synthesis of new structural analogues.^a



^a Reagents and conditions: (i) 65% hydrazine hydrate (5 equiv), EtOH, reflux, 1 h (ii) EtOH, reflux, 4 h- 20 h (iii) MeOH, reflux, 17 h.

The structures and purities were assessed by ¹H NMR, ¹³C NMR, HRMS and HPLC. The analysis of spectral data of the target compounds are provided in the experimental section. These molecules were subsequently evaluated on Ddl using purified *His*-tagged Ddl and their antimicrobial activity was assessed on sensitive and resistant bacteria.

3. PHARMACOLOGICAL EVALUATION AND DISCUSSION

3.1. Enzymatic assay

3.1.1 Optimization. Prior to the evaluation of compounds **3**, **14-49** and **51-54** towards recombinant *His*-tagged Ddl from *E. coli*, the colorimetric malachite green assay⁴⁵ was optimized for the determination of inorganic phosphate generated during the reaction catalyzed by Ddl. The linearity zone (**Figure 2a**), the optimal working conditions (**Figure 2b**), the tolerance to DMSO (**Figure 2c**) and the K_m values for the two D-Ala sites (**Figure 2d**) were determined. The linearity zone for the phosphate concentrations is from 0 to 40 μM . Working conditions are 20 min of incubation time with D-Ala, 20 mg/L of enzyme concentration and 10% of DMSO. A detailed description of the assay optimization can be found in the Supporting Information.

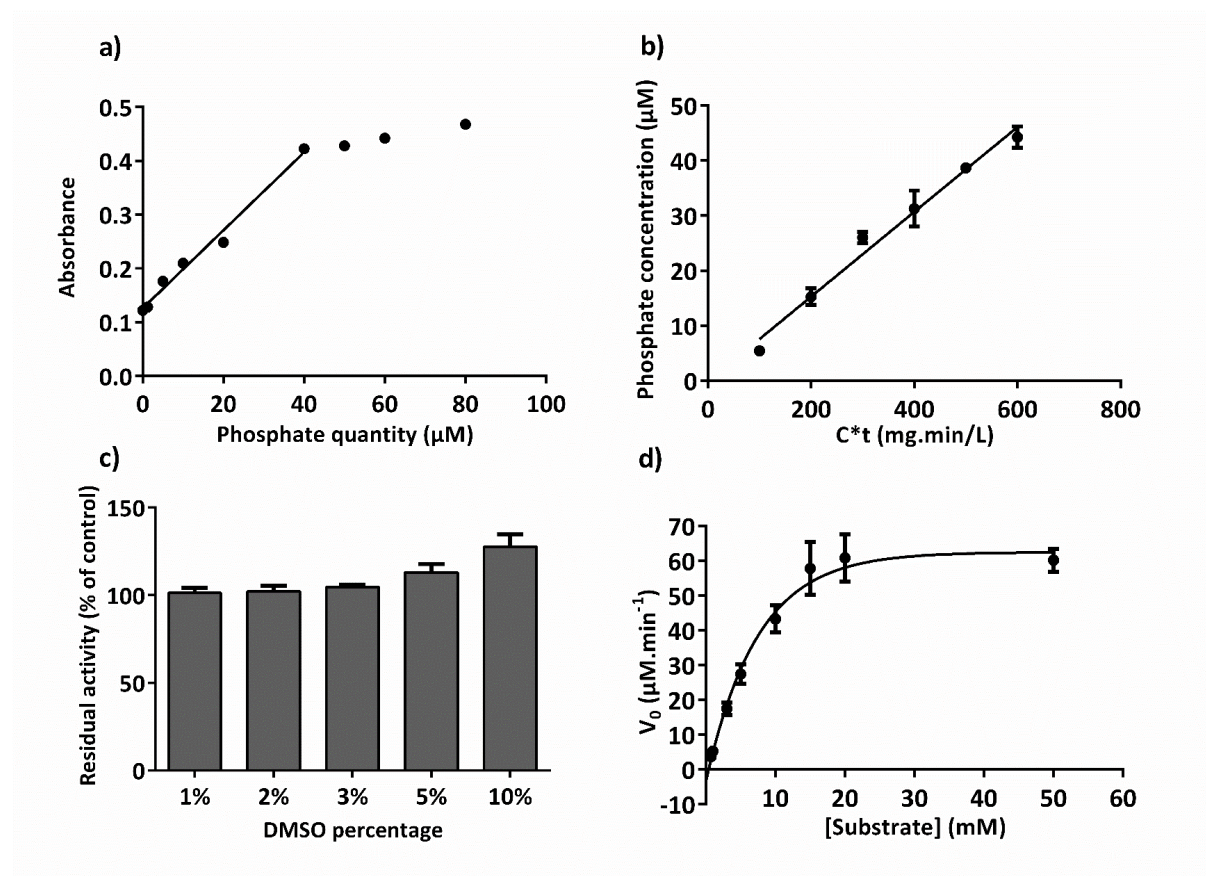


Figure 2. Optimization of the enzymatic assay. D-Ala and ATP concentrations were set respectively at 1 mM and 500 μM . Buffer composition was 20 mM Tris.HCl (pH 7.4), 10 mM MgCl_2 , 10 mM KCl. **(a)** Evolution of the absorbance as a function of phosphate concentrations in

μM . Inorganic phosphate (0-80 μM) was incubated with malachite green for 25 min. Absorbance was monitored at 650 nm. **(b)** Evolution of phosphate concentration (μM) in relationship with the product of enzyme concentration (mg/L) and time (min). Concentrations of Ddl were 5-20 mg/L. Incubation time with the substrate was 0-30 min. **(c)** Evaluation of DMSO influence on the enzymatic activity. DMSO concentrations (v/v) were 1, 2, 3, 5 and 10%. **(d)** Velocity of the enzyme ($\mu\text{M}.\text{min}^{-1}$) as a function of substrate concentration (mM). Substrate concentrations were 0.45-30 fold the theoretical K_{m2} (value reported in the literature).^{7, 46} Apparent $K_m = 5.62 \text{ mM}$.

3.1.2. Activity of inhibitors on the purified enzyme. A primary screening at 10 μM ([D-Ala] = 1 mM) was performed in triplicate to select inhibitors that lowered the Ddl activity of 30% or more (Ddl inhibition $\geq 30\%$). Then, for the most active compounds, an IC_{50} was determined after 30 min of incubation with Ddl (**Table 1**). DCS was used as a reference and it showed an IC_{50} of 262 μM in our hands, similar to the published data.⁶

Table 1. Structures, Ddl inhibitory activities and some physicochemical parameters of compounds **3**, **14-49** and **51-54**.

3, 14-49, 53-54 51 52

Compd	X	R ₁	R ₂	IC ₅₀ (μM) ^a	LogD ^b (pH=7.4)	TPSA ^b	S (mmol/L) ^b (pH=7.4)
3	S	2-OH	Phenyl	0.80 $\pm$ 0.12	2.31	105.48	0.94
14	S	H	Phenyl	n.a.	2.14	85.25	0.82
15	S	H	2-Chlorophenyl	n.a.	2.63	85.25	0.2
16	S	H	3-Chlorophenyl	n.a.	2.87	85.25	0.07

17	S	H	4-Chlorophenyl	n.a.	2.69	85.25	0.05
18	S	H	2-Fluorophenyl	n.a.	2.17	85.25	0.5
19	S	H	3-Fluorophenyl	n.a.	2.37	85.25	0.3
20	S	H	4-Fluorophenyl	n.a.	2.19	85.25	0.26
21	S	H	3,4-Dichlorophenyl	n.a.	3.57	85.25	0.002
22	S	2-OH	2-Chlorophenyl	0.79 ± 0.14	2.79	105.48	0.31
23	S	2-OH	3-Chlorophenyl	0.63 ± 0.13	3.13	105.48	0.07
24	S	2-OH	4-Chlorophenyl	0.83 ± 0.16	2.87	105.48	0.12
25	S	2-OH	2-Fluorophenyl	0.97 ± 0.18	2.22	105.48	0.46
26	S	2-OH	3-Fluorophenyl	0.10 ± 0.15	2.50	105.48	0.25
27	S	2-OH	4-Fluorophenyl	0.84 ± 0.17	2.28	105.48	0.23
28	S	2-OH	2,4-Dichlorophenyl	0.58 ± 0.15	3.40	105.48	0.04
29	S	2-OH	3,4-Dichlorophenyl	1.54 ± 0.30	3.63	105.48	0.008
30	S	2-OH	2-Methoxyphenyl	0.55 ± 0.08	2.36	114.71	0.65
31	S	2-OH	4-Methoxyphenyl	0.71 ± 0.13	2.18	114.71	0.72
32	S	2-OH	4-Cyanophenyl	0.51 ± 0.11	2.02	129.27	0.64
33	S	2-OH	Pentyl	0.93 ± 0.15	2.75	105.48	0.32
34	S	2-OH	3-Morpholinopropyl	*	0.71	117.95	13.4
35	S	2-OH	1-Naphthyl	0.52 ± 0.14	3.37	105.48	0.08

36	S	2-OH	3-Iodophenyl	0.73 ± 0.12	3.23	105.48	0.03
37	S	2-OH	4-Acetylphenyl	0.37 ± 0.04	2.08	122.55	0.47
38	S	2-OH	4-Trifluoromethoxyphenyl	0.70 ± 0.16	2.89	114.71	0.08
39	S	2-OH	4-Benzoyloxyphenyl	0.99 ± 0.99	3.54	114.71	0.04
40	S	2-OH	Pyridin-3-yl	*	1.32	118.37	3.82
41	S	2-OH-4-I	3,4-Dichlorophenyl	0.93 ± 0.12	4.31	105.48	0.007
42	S	2-OH-4-NH ₂	3,4-Dichlorophenyl	0.99 ± 0.99	3.01	131.5	0.009
43	S	3-OH	3,4-Dichlorophenyl	n.a.	3.30	105.48	0.01
44	S	4-OH	3,4-Dichlorophenyl	n.a.	3.25	105.48	0.01
45	S	4-OH	4-Nitrophenyl	n.a.	1.89	154.31	0.45
46	S	2-F	3,4-Dichlorophenyl	n.a.	3.26	85.25	0.003
47	S	3-F	3,4-Dichlorophenyl	n.a.	3.49	85.25	0.003
48	S	4-F	3,4-Dichlorophenyl	n.a.	3.50	85.25	0.003
49	S	2-OMe	3,4-Dichlorophenyl	n.a.	4.08	62.39	0.001
51	/	/	3,4-Dichlorophenyl	0.56 ± 0.07	4.54	105.48	0.0001
52	/	/	Phenyl	n.a.	1.95	88.82	0.75
53	O	H	3,4-Dichlorophenyl	n.a.	3.00	70.23	0.002
54	O	2-OH	3,4-Dichlorophenyl	n.a.	3.66	90.46	0.01
DCS	/	/	/	262 ± 43.4	/	/	/

^a IC₅₀ values are presented as the (mean $\pm$ SD) of measures performed in triplicate (n $\geq$ 2)

^b LogD, TPSA (topological polar surface area) and S (solubility) were calculated with ACD/Labs® program

* Ddl inhibition of 30% at 10 μ M

n.a. = not active; 100% residual activity at 10 μ M

Firstly, compared to the parent compound **3**, it can be observed that removal of the hydroxyl group in the 2-position always leads to inactive compounds (**14-21**), independently of the nature of the substituent present on the right part (R_2) of the molecule (**Table 1**). When this hydroxyl group is replaced by a bioisosteric fluorine **46-48** ($R_1 = F$) or a methoxyl group **49** ($R_1 = OMe$), no inhibition is found either. Further comparison of the hydroxy-benzoylthiosemicarbazides **29**, **43** and **44** possessing the hydroxyl function in the 2-, 3- and 4-position, respectively, also clearly reveals that only the 2-position is tolerated. However, it seems that an additional substituent on the left phenyl (**41-42**), or its replacement by a naphthyl group (**51**), allows to keep the activity if the 2-OH is still present. This feature indicates that there is still enough space in the inhibitor binding pocket and could be important for further structural modifications.

It thus appears from these first SAR modifications that a hydroxyl group in this 2-position is key for Ddl inhibition. Because its replacement by a fluorine leads to inactive compounds, it may be inferred that (i) it probably contributes to the stabilization of the inhibitor inside the Ddl cavity through H-bonding with residues bearing H-bond acceptor groups and (ii) it could stabilize a particular conformation by intramolecular H-bonding. This hypothesis was further validated by the X-ray structure of a representative benzoylthiosemicarbazide **29**. As observed from **Figure 3**, this compound co-crystallized with one DMSO molecule from the crystallization solvent. The analysis of the X-ray structure of **29** revealed that the hydroxyl group on the aromatic ring was, as

suggested, intramolecularly H-bonded to the thiosemicarbazide NH (N-H...O interaction) leaving the OH available for an additional intermolecular H-bond with the DMSO sulfoxide function. The OH group in the 2-position thus probably plays a key role both as an intramolecular H-bond acceptor and an intermolecular H-bond donor. The inactivity of compound **49** bearing a 2-methoxy substituent reinforces this hypothesis.

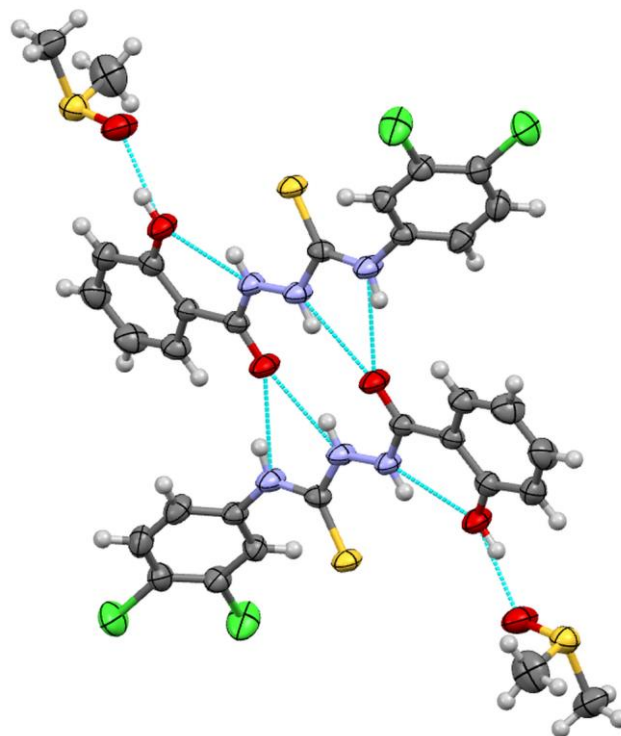


Figure 3. View of the molecular interaction (H-bonds represented as dashed lines) within the crystal packing of compound **29** (ORTEP representation for each molecule, 50% probability representation).

Thereafter, we investigated the effect of the modulation on the right part (R_2) of the benzoylthiosemicarbazide scaffold. In this position an electron-withdrawing (Cl, F, CN, I ...) or electron-donating (MeO, BnO ...) substituent is introduced at the phenyl ring (**22-32** and **36-39**). Subsequent Ddl inhibition is always in the same range to that of the parent compound **3** (in the submicromolar range). Interestingly, the introduction of a pentyl (**33**) or a naphthyl (**35**) group in

the same position also leads to potent Ddl inhibitors, in similar range that previously tested molecules. On the contrary, introduction of more hydrophilic substituents such as 3-morpholinopropyl (**34**) or pyridin-3-yl (**40**) decreases the Ddl inhibition as this compound exhibits only a maximum Ddl inhibition of 30% at the highest concentration. The data obtained thanks to these pharmacomodulations on R₂ suggest that no critical interaction is made between this part of the molecule and the enzymatic cavity apart from hydrophobic interactions.

Finally, the importance of the thiosemicarbazide linker was assessed. Its replacement by a semicarbazide function, with (**54**) and without (**53**) the hydroxyl substituent in the 2-position of the aromatic ring (R₁), as well as the complete replacement of the 4-phenylthiosemicarbazide in **3** with a 1-(4-oxoquinazolin-3(4H)-yl)thiourea scaffold (**52**), to evaluate a cyclized structure, afford inactive derivatives.

Furthermore, according to the literature, the inhibition of Ddl by compound **3**, chosen for its good aqueous solubility, was tested in the presence and absence of 0.01% Triton X-100 to double-check that the activity was not an artefact due, for instance, to drug aggregation.⁴⁷⁻⁴⁸ No change in Ddl inhibition was noticed, therefore proving that the activity was the result of a specific interaction to Ddl.

These results highlight the importance of the thiosemicarbazide template and the 2-OH benzoyl group for the proper recognition inside the Ddl enzyme cavity.

3.1.3. Study of the binding mode. A residual activity of Ddl of about 25% was always observed for active compounds after 30 min of incubation with the inhibitor. To gain a deeper understanding of the mechanism of action in this series a detailed study of the binding mode was investigated. Compound **3** was selected for its good aqueous solubility and adequate lipophilicity (**Table 1**). First, upon increasing the incubation time of the inhibitor with the enzyme from 10 to 120 min

(**Figure 4a**), we first noticed that, although the IC_{50} of **3** was not modified, the maximum inhibition percentage increased from 60% (10 min incubation) up to more than 90% (90 min incubation). Then, the reversibility of the inhibition was assessed using a rapid dilution assay.⁴⁹ To this end, **29** was selected as a model compound for subsequent studies given its activity on Ddl and bacteria (see below). As observed from **Figure 4b**, the enzymatic activity was recovered after a rapid and large dilution of the enzyme-inhibitor complex, thus proving the reversible interaction of our inhibitors with Ddl.

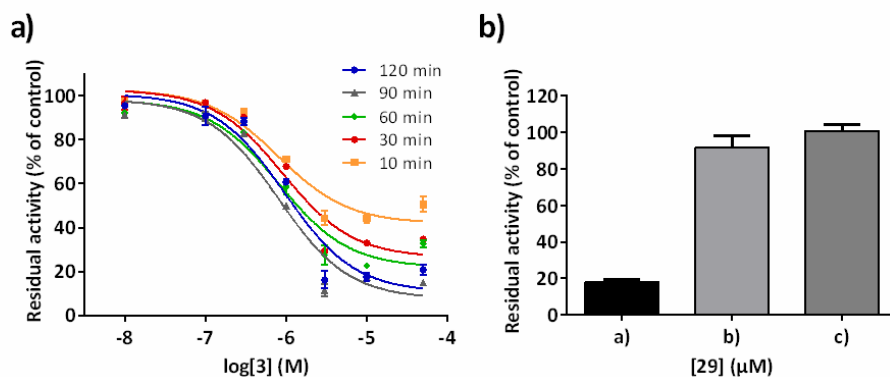


Figure 4. (a) IC_{50} of benzoylthiosemicarbazide **3** with increasing incubation time (10, 30, 60, 90 and 120 min) of Ddl with the inhibitor. (b) Rapid dilution method with a) 3 μ M of **29** and 200 mg/L of Ddl-His₆; b) 0.3 μ M of **29** and 20 mg/L of Ddl-His₆ and c) rapid dilution of a) allows for the recovery of the activity compared to the control b). All values are presented as the (mean $\pm$ SD) of measures performed in triplicate.

Next, competition studies were carried out with **29** against both D-Ala and ATP (**Figure 5a** and **5b**). Regarding competition against D-Ala, as Ddl binds two D-Ala molecules in two distinct binding sites,⁵⁰ we assumed that, at concentrations where the substrate occupies both sites (1 mM $\sim K_{m2}$), K_{m1} is negligible compared to K_{m2} .^{15, 46} When a saturating concentration of ATP (500

μM) was used, two K_m values for D-Ala were found ($K_{m1} = 487.2 \mu\text{M}$ and $K_{m2} = 10.5 \text{ mM}$). When a concentration of D-Ala of 50 mM was used, a K_m value for ATP of 691 μM could be approximated. Detailed information regarding these measurements can be found in the available Supporting Information.

Upon increasing concentrations of **29**, a decrease of the V_{max} value was observed on both graphs (**Figure 5**). Moreover, we noticed that the V/K_m value also changes with increasing concentrations of **29** (see Supporting Information) thus suggesting a mixed non-competitive inhibition profile for this compound towards both D-Ala ($\alpha > 1$, inhibitor preferentially binds the free enzyme) and ATP ($\alpha < 1$, inhibitor preferentially binds the enzyme-ATP complex). This mechanism of action led us to hypothesize an interaction of **29** at an allosteric site rather than at the active site. This assumption is further supported by the recent identification of such an allosteric site on Ddl together with the identification of Ddl inhibitors with similar kinetic profile.¹²

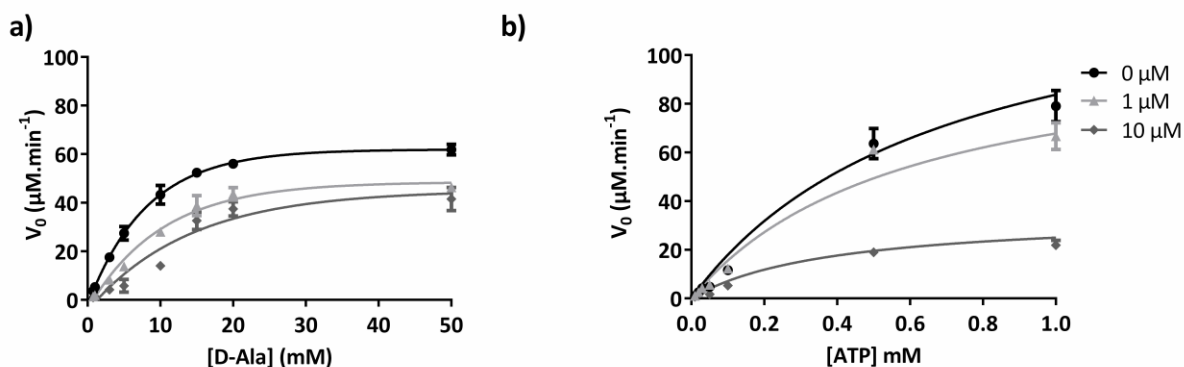


Figure 5. Competition studies of model inhibitor **29** at three concentrations (0 μM , 1 μM and 10 μM) with (a) D-Ala: enzyme velocity ($\mu\text{M} \cdot \text{min}^{-1}$) as a function of [D-Ala] (mM). (b) ATP: enzyme velocity ($\mu\text{M} \cdot \text{min}^{-1}$) as a function of [ATP] (mM). All values are presented as the (mean $\pm$ SD) of measures performed in triplicate.

3.2. Biological activities

3.2.1. *In vitro* antibacterial activity. The MICs of compounds **3**, **14-48** and **51-54** against two Gram-positive bacterial strains, *S. aureus* ATCC 25923 and *E. faecalis* ATCC 29212 were determined using maximal concentrations of 100 μ M and 400 μ M respectively (see details in the Supporting Information available) with 1% DMSO (v:v). Unfortunately, compounds **46-48** were not soluble at these concentrations. The most active compounds are **28** with a MIC of 50 μ M (17.81 mg/L) against both strains, **29** with a MIC of 100 μ M (35.62 mg/L) and 50 μ M (17.81 mg/L) against *S. aureus* ATCC 25923 and *E. faecalis* ATCC 29212 respectively, **37-38** with MICs of 25 μ M (8.23 and 9.28 mg/L) against *S. aureus* ATCC 25923 and 50 μ M (16.47 and 18.56 mg/L) against *E. faecalis* ATCC 29212, and, finally, **40** with a MIC of 50 μ M (14.42 mg/L) against both strains (**Table 2**). The benzoylthiosemicarbazides **22-27**, **32**, **39** and **41** have MICs ranging from 100 μ M to 400 μ M. In fact all these molecules have better *in vitro* activities than DCS, the reference antibiotic targeting Ddl. The other compounds assayed showed no biological activities at these concentrations.

Table 2. MIC values of active benzoylthiosemicarbazides against fully susceptible Gram-positive reference strains.

Compd	MIC (mM/(mg/L))			
	<i>S. aureus</i> ATCC		<i>E. faecalis</i> ATCC	
	25923 ^a		29212 ^a	
	mM	mg/L	mM	mg/L
22	> 0.1	> 32.18	0.4	128.72
23	0.1	32.18	0.4	128.72

25	> 0.1	> 30.53	0.2	61.06
26	> 0.1	> 30.53	0.2	61.06
27	> 0.1	> 30.53	0.2	61.06
28	0.05	17.81	0.05	17.81
29	0.1	35.62	0.05	17.81
32	> 0.1	> 31.23	0.1	31.23
37	0.025	8.23	0.05	16.47
38	0.025	9.28	0.05	18.56
39	0.1	39.34	> 0.4	> 157.38
40	0.05	14.42	0.05	14.42
41	0.1	48.21	> 0.4	> 192.85
DCS	0.313	32	1.25	128

^a *Staphylococcus aureus*, *S. aureus*; *Enterococcus faecalis*, *E. faecalis*.

The active compounds on Ddl, **3**, **22-42** and **51** were also assayed against various Gram-positive and negative bacteria, including clinical isolates resistant to current antibiotics and strains expressing alternative ligases (*E. faecalis* JH2-2::C1,⁵¹ BM 4390,⁵² BM 4575⁵³). MICs are shown in **Table 3**.

Table 3. MIC values of active compounds **3**, **22-42** and **51** against Gram-positive resistant strains.

MIC (mM/(mg/L)) of:

Compd	<i>E. faecalis</i> ^a			<i>S. aureus</i> ^b				
	BM 4390	JH2-2::C1	BM 4575	MU 50	NRS 119	SA 325	SA 481	VRS-1
22	> 0.1	> 0.1	> 0.1	> 0.1	0.1/32.18	0.1/32.18	0.1/32.18	0.1/32.18
23	> 0.1	> 0.1	> 0.1	> 0.1	> 0.1	0.1/32.18	> 0.1	> 0.1
28	0.025/8.90	0.05/17.81	0.025/8.90	0.05/17.81	0.025/8.90	0.05/17.81	0.05/17.81	0.025/8.90
29	0.05/17.81	0.1/35.62	0.05/17.81	0.1/35.62	0.05/17.81	0.05/17.81	0.1/35.62	0.05/17.81
38	> 0.1	0.1/37.12	> 0.1	> 0.1	0.1/37.12	0.1/37.12	> 0.1	> 0.1
VAN ^c	0.7/ 1024	0.35/ 512	N.D.	0.005/ 8	0.0007/1	N.D.	N.D.	>0.175/> 256
LZD ^c	N.D.	N.D.	N.D.	0.003/ 1	0.19/ 64	N.D.	N.D.	N.D.
CIP ^c	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	0.77/ 256	N.D.

^a VRE (Vancomycin resistant *enterococcus*): *E. faecalis* BM 4390⁵² (*vanB* genotype, *in vitro* mutant of a clinical isolate with inactive Ddl; constitutive expression of D-Ala-D-Lac); *E. faecalis* JH2-2::C1⁵¹ (*vanB* genotype, engineered derivative of JH2-2; constitutive expression of Ddl and of the VanB ligase); *E. faecalis* BM 4575⁵³ (*vanE* genotype, clinical isolate, constitutive expression of Ddl and of the VanE D-Ala-D-Ser ligase).

^b *S. aureus* MU 50: MRSA (methicillin resistant *S. aureus*) and VISA (vancomycin intermediate resistant *S. aureus*); *S. aureus* NRS 119: MRSA resistant to linezolid (clinical isolate)⁵⁴; *S. aureus* SA 325: CA-MRSA (community-acquired MRSA) resistant to erythromycin; *S. aureus* SA 481: HA-MRSA (hospital-acquired MRSA) resistant to ciprofloxacin and moxifloxacin; VRS-1: VRSA (vancomycin resistant *S. aureus*, *vanA* genotype) and HA-MRSA.

^c VAN, vancomycin; LZD, linezolid; CIP, ciprofloxacin.

All the tested compounds were inactive against Gram-negative bacteria (*Klebsiella pneumoniae* ATCC 700603, *Escherichia coli* ATCC 25922 and *Pseudomonas aeruginosa* PAO1). Compound **28** was equipotent against all Gram-positive strains, including those expressing alternative ligases (*E. faecalis* BM 4390, BM 4575, JH2-2::C1; VRSA VRS-1) or resistant to glycopeptides, oxazolidinones, or fluoroquinolones, with MICs of 25-50 μ M. The benzoylthiosemicarbazide **29** showed MICs of 50-100 μ M, whatever the strain tested. Compound **22** displayed MIC of 100 μ M towards *S. aureus* NRS 119, SA 325, SA 481 and VRS-1, and compound **23** showed MIC of 100 μ M towards *S. aureus* SA 325, but these latter were not active on *E. faecalis* and the other staphylococci at 100 μ M. Finally, compound **38** displayed MIC of 100 μ M for *E. faecalis* JH2-2::C1, *S. aureus* NRS 119 and SA 325. These data suggest that compounds **28**, **29** and **38** may also be active on alternative ligases. Moreover, the ability of 2-hydroxybenzoyl-thiosemicarbazides derivatives to prevent the growth of various bacterial strains resistant to a wide range of antibiotics such as methicillin, linezolid, erythromycin, ciprofloxacin and moxifloxacin highlights them as attractive molecules warranting further development.

Interestingly, none of the benzoylthiosemicarbazides that are inactive on ligase exhibits antibacterial activity (see data in the Supporting Information). This supports our hypothesis that Ddl is the bacterial target of these compounds and could explain in part the antibacterial activity reported previously by other groups for benzoylthiosemicarbazide analogues.^{38, 55-56} Particularly, Siwek *et al.* and Plech *et al.* recently reported that 4-benzoylthiosemicarbazides derivatives could act as topoisomerase IV and DNA gyrase inhibitors.^{57, 58} However, no convincing concordance was found in their work between the antimicrobial activity and the inhibition of their presumed targets. The present analysis may therefore suggest that Ddl could be the bacterial target of these derivatives.

3.2.2. *Killing curve for compound 29.* To determine if the model compound **29** was bactericidal, killing curves were performed over 24 hours for *S. aureus* ATCC 25923 exposed to increasing concentrations of inhibitor. As shown in **Figure 6**, a bactericidal effect was reached when using a 10^6 CFU/mL starting inoculum after 24 h of incubation with concentrations of 2 or 5× the MIC (0.2 and 0.5 mM), suggesting that the compound is slowly bactericidal. A complete eradication of bacteria was obtained at 5× MIC.

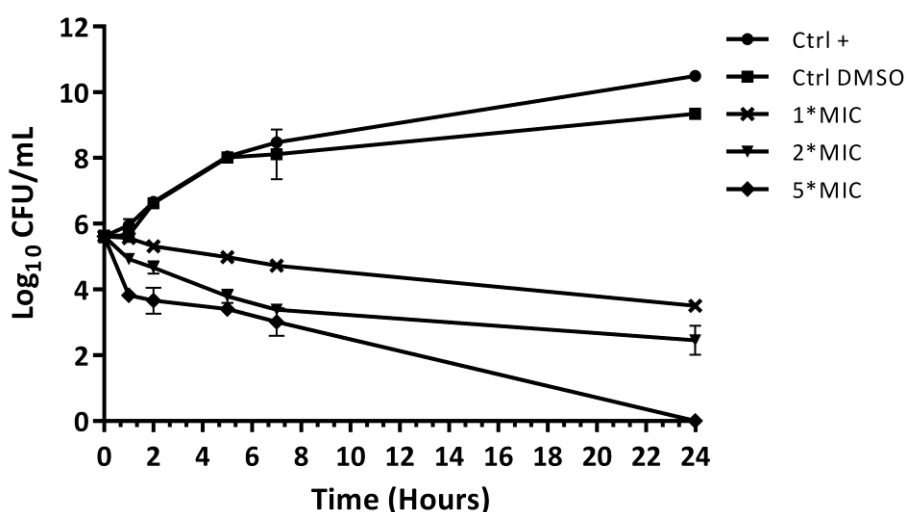


Figure 6. Time-kill curves of *S. aureus* ATCC 25923 incubated with the model inhibitor **29**. The strain was incubated with growth media (●) as positive control, with 5% DMSO (■) as growth control; with molecule **29** at 1× the MIC (×), 2× the MIC (▼), and 5× the MIC (◆). All values are presented as the (mean ± SD) of measures performed in triplicate.

3.2.3. *Determination of in vivo L-Ala, D-Ala and D-Ala-D-Ala levels in presence of model compound 29.* In order to demonstrate that Ddl is effectively the *in vivo* biochemical target of our 1-(2-hydroxybenzoyl)-thiosemicarbazides, the effect of **29** on intracellular levels of L-Ala, D-Ala and D-Ala-D-Ala was evaluated by UHPLC-MS/MS. To this end we used an LC-MS/MS

methodology adapted from the literature in order to quantify these metabolites *in vivo*.^{17, 59-60} Briefly, the strategy involves the derivatization of L-Ala, D-Ala and D-Ala-D-Ala with Marfey's reagent⁶¹ on *S. aureus* extracts followed by the chromatographic separation and detection of Marfey's derivatives in positive electrospray ionization (ESI) mode with multiple reaction monitoring (MRM) for the transition corresponding to a neutral loss of 45 Da $[M+H-45]^+$, the Marfey's terminal protonated amide. Based on preliminary experiments, we chose to expose bacteria to 2× MIC of **29** for limited periods of time, i.e. conditions where only a modest decrease in bacterial counts was observed ($\Delta \log \text{CFU/mL} = 1$). The metabolite levels (L-Ala, D-Ala and D-Ala-D-Ala) were analyzed over 30 min.

As shown in **Figure 7**, the $[\text{D-Ala}]/[\text{D-Ala-D-Ala}]$ ratio increased over time in these conditions. This experiment thus proves that 1-(2-hydroxybenzoyl)-thiosemicarbazides exert their antimicrobial activity by targeting Ddl *in bacterio*.

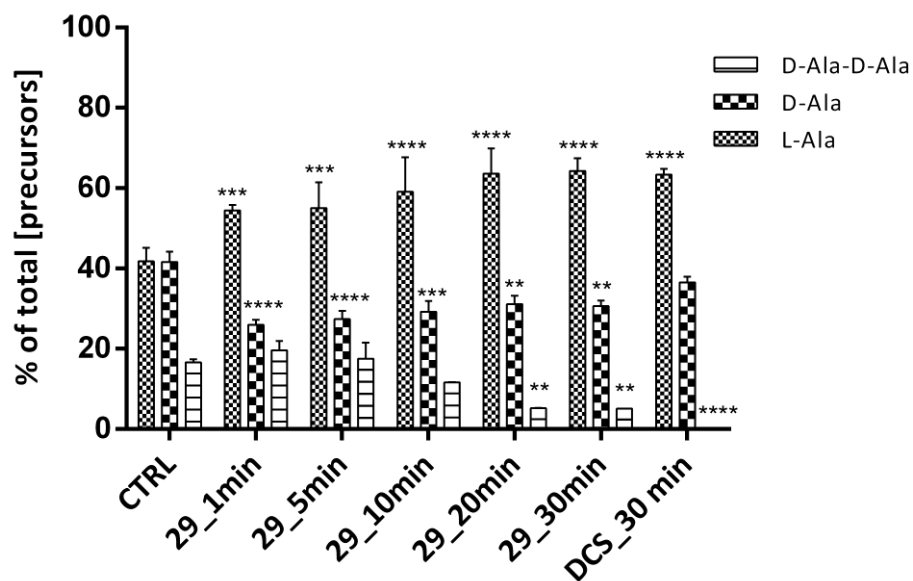


Figure 7. Evolution over time of *S. aureus* L-Ala, D-Ala and D-Ala-D-Ala levels in presence of 2×MIC of compound **29** compared to the control (DMSO 5%) and the reference antibiotic, DCS

(2×MIC). All values are presented as the (mean ± SD) of measures performed in triplicate. A multiple comparison (two-way ANOVA) led to the following statistical results: **** extremely significant (P value < 0.0001), *** extremely significant (P value from 0.0001 to 0.001), ** very significant (P value from 0.001 to 0.01), * significant (P value from 0.01 to 0.05), no asterisk means not significant (P value ≥ 0.05).

3.2.4. Cytotoxicity of model compound 29. The representative inhibitor **29** was then assayed for its potential cytotoxicity on THP-1 human monocytic cell line. **Figure 8** shows the evolution of cell survival as a function of time and inhibitor concentration. A significant but moderate (12-25%) decrease in viability was observed after 24 h of incubation over the range of concentrations investigated. This suggests that the compound is well tolerated at the concentrations showing antibacterial activity (1× MIC or 0.1 mM).

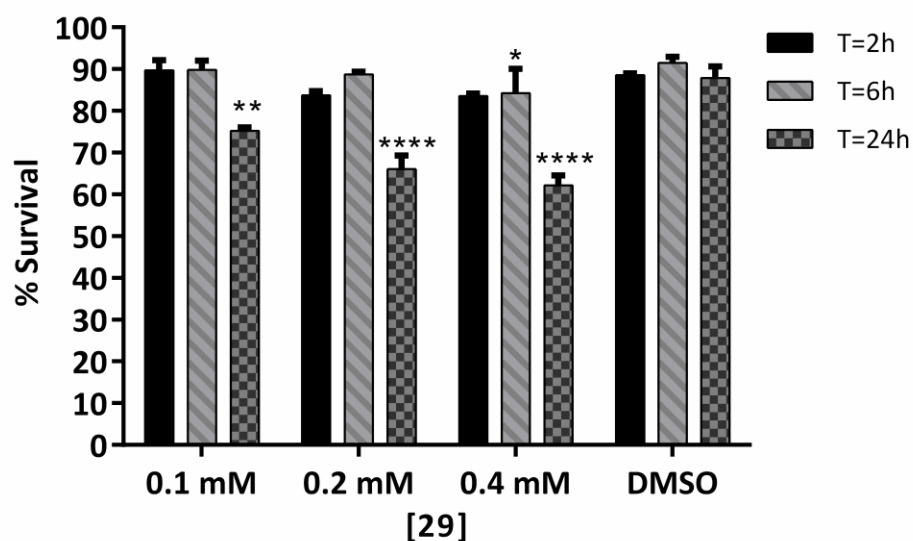


Figure 8. Cytotoxicity on THP-1 human monocytic cell line. Percentage of cell survival as a function of time (2 h, 6 h and 24 h) and compound **29** concentration (0.1 mM - 1× MIC, 0.2 mM - 2× MIC and 0.4 mM - 4× MIC) compared to the control (DMSO 1%). All values are presented as

the (mean $\pm$ SD) of measures performed in triplicate. A multiple comparison (two-way ANOVA) led to the following statistical results: ***** extremely significant (P value < 0.0001), *** extremely significant (P value from 0.0001 to 0.001), ** very significant (P value from 0.001 to 0.01), * significant (P value from 0.01 to 0.05), no asterisk means not significant (P value $\geq$ 0.05).

3.2.5. Selectivity profile of 29. Finally, these encouraging results prompted us to investigate the selectivity of **29**. To this effect, we tested its inhibitory activity against various enzymes and receptors at 10 μ M, i.e. a concentration approx. 7 times higher than its IC₅₀ towards Ddl (**Table 4**). From these data we can conclude that the 4-(3,4-dichlorophenyl)-1-(2-hydroxybenzoyl)-3-thiosemicarbazide **29** is highly selective for Ddl as none of the investigated enzymes or receptors are impacted in these conditions apart from the angiotensin converting enzyme, ACE, that is weakly inhibited (66%) by this compound. Despite that the literature describes the parent benzoylthiosemicarbazide **3** as a CA I and CA IX inhibitor, carbonic anhydrase II was not impacted by **29**.

These results demonstrate that the benzoylthiosemicarbazide motif is a selective and efficient pharmacological tool to target Ddl.

Table 4. Selectivity profile of compound **29**.

Enzyme or receptor	Radioligand	Control inhibitor (IC ₅₀ , nM)	% Inhibition
5-HT _{1A} (h)	[³ H]8-OH-DPAT	[³ H]8-OH-DPAT (0.6)	NI
ACE (h)	-	Captopril (0.7)	66
Acetylcholinesterase (h)	-	Galanthamine (520)	NI
Arg1 (h)	-	S-(2-boronoethyl)-l-cysteine (13 μ M)	NI
β -Lactamase (<i>Bacillus cereus</i>)	-	Clavulanic acid (11)	NI

Carbonic anhydrase II (h)	-	Acetazolamide (29)	NI
CB ₁ (h)	[³ H]CP 55940	CP55940 (0.58)	NI
COX ₁ (h)	-	Diclofenac (8)	NI
DNA Gyrase (<i>E. coli</i> and <i>S. aureus</i>)	-	-	NI ^a
GABA _{A1} ($\alpha 1, \beta 2, \gamma 2$) (h)	[³ H]Muscimol	Muscimol (75)	NI
IDO (h)	-	1-L-Methyltryptophan (37 μ M)	NI
Lck kinase (h)	-	Staurosporine (31)	NI
LDH (h)	-	Oxamic acid (577 μ M)	NI
M ₁ (h)	[³ H]Pirenzepine	Pirenzepine (22)	NI
MAG lipase (h)	[³ H]-2-OG	Disulfiram (363)	NI
MAO-A (h)	-	Clorgiline (40)	NI
PDE3A (h)	-	Milrinone (490)	NI
PHGDH (h)	-	1-(4-Chlorophenyl)-2-morpholino-2-thioxoethanone (8.7 μ M)	NI
sPLA ₂ (type V) (h)	-	Oleyloxyethyl phosphorylcholine (20 μ M)	NI
Potassium Channel hERG (h)	[³ H]Dofetilide	Terfenadine (80)	NI
PPAR α (h)	[³ H]WY 14643	GW7647 (52)	NI
Thrombin (h)	-	PPACK (0.103)	NI
Topo IV (<i>E. coli</i> and <i>S. aureus</i>)	-	-	NI ^a

^a from reference⁵⁷; NI = inhibition $\leq$ 30% at 10 μ M; Significance criteria (Eurofins Cerep): $\geq$ 50% of inhibition

3.3. Molecular docking

Because the binding mode of **29** was established to be non-competitive, we performed a preliminary molecular docking study at the known allosteric site of Ddl. To this end, we used the

structure of StaDdl available in the Protein Databank (PDB code: 2I80)¹² and docked **29** by mean of the automated Gold program with the aim to understand at the molecular level the interactions stabilizing the benzoylthiosemicarbazide in Ddl. To be consistent with the potential existence of tautomeric forms in this series of compounds, both tautomers of the model benzoylthiosemicarbazide **29** were investigated.

As a result, the binding mode of **29** in both tautomeric forms (**Figure 9a**) supports the hypothesis that the right part of the inhibitor (R₂) could partially occupy a hydrophobic pocket (color code in green) open to the substrate binding site, and that no crucial interaction is made by this aromatic moiety apart from stabilizing hydrophobic interactions. At the bottom of the allosteric site, a quadrupolar T-shape interaction between Phe313 and the phenol ring of **29** ensures an additional stabilization. Moreover, it can be observed that both tautomers fit very well this pocket thanks to an almost planar geometry stabilized through H-bond interactions between the thiosemicarbazide function and the 2-hydroxyphenyl moiety. This intramolecular H-bond was already mentioned in the X-ray structure of **29** (**Figure 3**). In the “keto” form (**Figure 9b**), the hydroxyl in the 2-position of **29** would be stabilized through H-bonding with the carbonyl oxygen of Pro311 backbone, whereas in the “enol” form (**Figure 9c**), the compound would be stabilized through H-bonds between the carbonyl oxygen of Pro311 and the thiol function, and between the carbonyl oxygen of Leu94 and the enol function. Whether the “keto” or the “enol” tautomeric form is being considered, this molecular modeling analysis strongly supports the SAR reported earlier in this work, particularly regarding the key role of the hydroxyl function in the 2-position of the aryl-thiosemicarbazide for the proper conformation and interaction with Ddl.

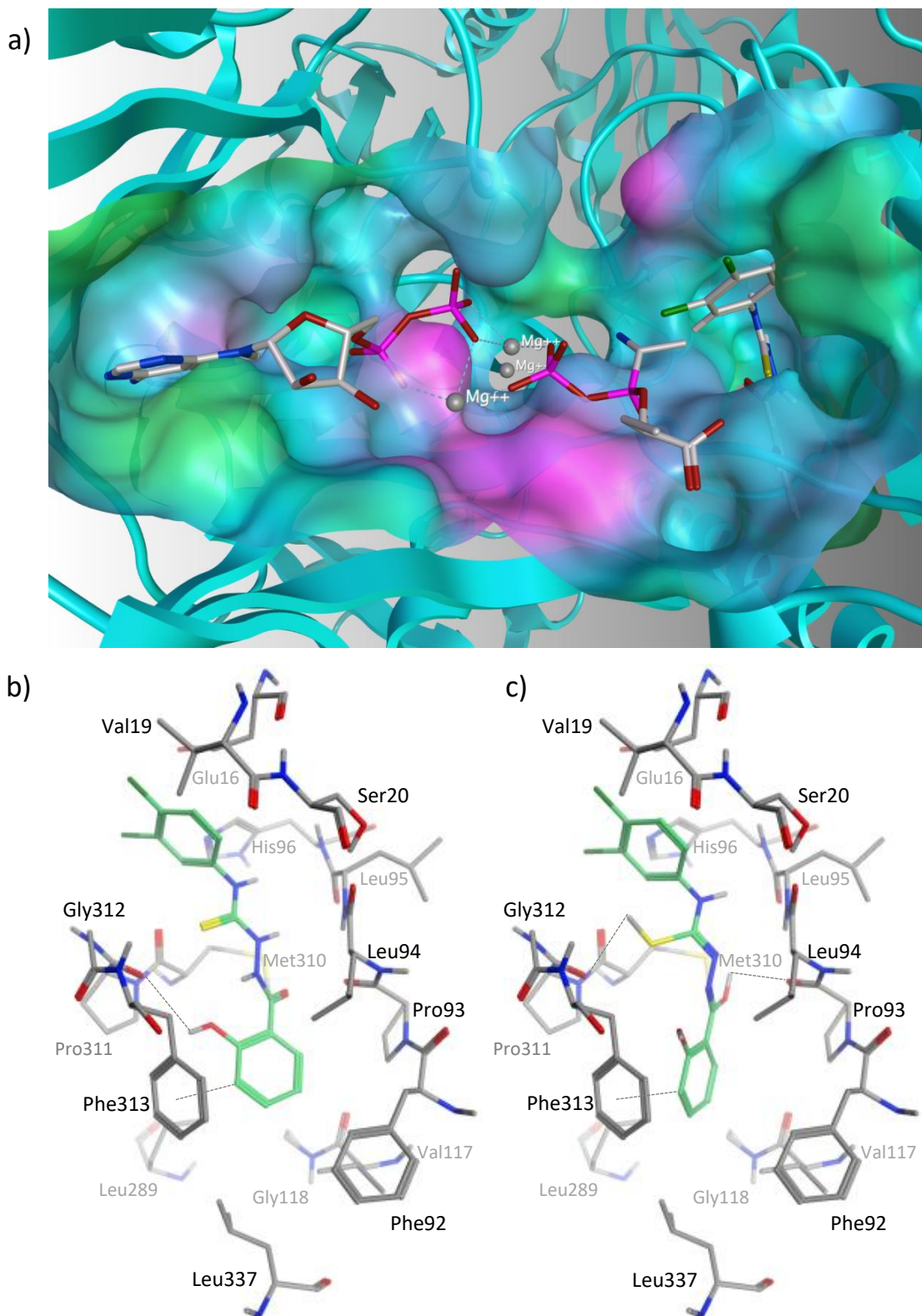


Figure 9: Docking of the model compound **29** at the allosteric site of Ddl. **(a)** The lipophilic protein surface was built from the inhibitor-bound StaDdl crystal structure, with green and

magenta representing lipophilic and hydrophilic residues, and cyan for the neutral ones. Carbon, oxygen, nitrogen, phosphorus, chlorine and hydrogens are colored in grey, red, blue, magenta, green and white respectively. Mg^{2+} ions are represented by grey spheres; ADP, methylphosphinophosphate, and compound **29** by sticks. **(b)** Ketone form of the model benzoylthiosemicarbazide **29**. **(c)** Enol form of the model benzoylthiosemicarbazide **29**. Carbon atoms of **29** and residues are shown in green and grey, respectively.

4. CONCLUSIONS

This work thus allowed the identification of novel D-Ala-D-Ala ligase inhibitors with antibacterial effects on sensitive and resistant strains. This novel benzoylthiosemicarbazide series was synthesized via a straightforward procedure. Pharmacomodulations around the parent compound **3** were performed and led to interesting structure-activity relationships, particularly (i) the 2-hydroxy substituent (R_1) on the benzoylthiosemicarbazide derivatives is essential for the enzymatic inhibition, (ii) no crucial interaction is made between the right part of the thiosemicarbazide scaffold (R_2) and the enzymatic cavity and (iii) the thiosemicarbazide linker is essential for a proper recognition by Ddl.

Moreover, the antibacterial results showed that several compounds displayed promising biological activities against Gram-positive bacterial strains. Among them, the benzoylthiosemicarbazide **28** exhibited strong antibacterial potency against all tested sensitive and resistant Gram-positive species with low MIC values between 25 μ M (8.91 mg/L) and 50 μ M (17,81 mg/L). The ability of our compounds to prevent the growth of various bacterial strains, resistant to a wide range of currently used antibiotics, paves the way to the development of new antimicrobial agents that should be less sensitive to resistance mechanisms. A major parameter for the development of these novel drugs is lipophilicity. Indeed, an optimally balanced $\log D_{7.4}$ value

is needed to allow the molecules to enter bacteria and remain soluble in body fluids. The theoretical $\log D_{7.4}$ for all benzoylthiosemicarbazides were calculated by mean of the ACD/Labs® program and are presented in **Table 1**. Our best compounds **28** and **29** against sensitive and resistant bacterial strains indeed possessed two of the highest calculated $\log D_{7.4}$ among the benzoylthiosemicarbazide derivatives ($X = S$) of 3.40 and 3.63, respectively. In addition, the drug's ability to permeate cells was estimated by the calculation of the polar surface area (PSA). TPSA is a 2-dimensional estimation of the compound's PSA.⁶² It can be observed from **Table 1** that all the active molecules on bacteria showed TPSA from 105.48 to 129.27 Å², which is very encouraging given that low values ($PSA < 75 \text{ Å}^2$) are usually linked to non-specific toxicity⁶³ and high values ($PSA > 140 \text{ Å}^2$) to poor membrane permeability⁶⁴.

As emphasized in the *in vitro* evaluation, only Ddl inhibitors possessing a 2-hydroxy substituent ($R_1 = 2\text{-OH}$) and a thiosemicarbazide linker were able to stop bacterial growth. Furthermore, it seemed that the presence of a halogen group on the phenyl ($R_2 = X\text{-phenyl}$) on the right part of the molecule is beneficial to the antimicrobial activity, as observed for compounds **22-23**, **25-29**, **38** and **41**. It was also observed that electron-donating groups did not favor the antibacterial efficiency given that compounds **30-31**, **33** and **34** are inactive.

The model compound **29** was proved to act through a bactericidal mechanism. Moreover, a high specificity towards bacterial species compared to cytotoxicity as evaluated on THP-1 human monocytic cell line was also noticed. Indeed, 99% of bacteria are killed after 24 hours of incubation at 0.1 mM ($1\times$ the MIC value) compared to only 12 % of cells.

An additional selectivity study of this compound allowed us to conclude that this 1-(2-hydroxybenzoyl)-thiosemicarbazide motif is highly selective for Ddl as only one of the twenty-three investigated systems, angiotensin converting enzyme, was slightly inhibited at 10 µM.

Finally, we demonstrated through the quantification of D-Ala, L-Ala and D-Ala-D-Ala *via* LC-MS that Ddl was effectively the *in bacterio* target of our benzoylthiosemicarbazides. This striking result, not only validates this series of 1-(2-hydroxybenzoyl)-thiosemicarbazides as novel antibacterial agents but also opens new perspectives for the development of novel antibiotics deprived of issues related to resistance mechanisms.

5. EXPERIMENTAL SECTION

5.1. Chemistry

All reagents were purchased from chemical suppliers if commercially available and used without purification. Syntheses were performed under atmospheric pressure unless specified otherwise. Thin-layer chromatography (TLC) was performed using silica gel 60 F254 plates, with observation under UV. The ^1H and ^{13}C Nuclear Magnetic Resonance spectra were recorded respectively on an AVANCE II 400 MHz or 100 MHz Bruker spectrometer with CDCl_3 (residual internal CHCl_3 δ_{H} = 7.26) or $\text{DMSO}-d_6$ (residual internal DMSO δ_{H} = 2.50 ppm) as solvent. All coupling constants are measured in hertz (Hz), and the chemical shifts (δ_{H} and δ_{C}) are quoted in parts per million (ppm) relative to TMS (δ_0), which was used as the internal standard. Data are reported as follows: chemical shift, multiplicity (s = singlet, d = doublet, t = triplet, q = quartet, quint = quintet, br = broad, m = multiplet), coupling constant (Hz) and integration. Labile protons are not always visible in ^1H NMR spectrum. Melting points were measured on an Electrothermal IA9000 apparatus. High-resolution mass spectroscopy was carried out on an LTQ-Orbitrap XL hybrid mass spectrometer (Thermo Fisher Scientific, Bremen, Germany). Data were acquired in positive ion mode using full-scan MS with a mass range of 100-1000 m/z. The orbitrap operated at 30.000 resolution (FWHM definition). All experimental data were acquired using daily external calibration prior to data acquisition. Appropriate tuning of the electrospray ion source was done.

The following electrospray inlet conditions were applied: flow rate, 100 $\mu\text{L min}^{-1}$; spray voltage, 5 kV; sheath gas (N_2) flow rate, 20 a.u.; auxiliary gas (N_2) flow rate, 10 a.u.; capillary temperature, 275°C; capillary voltage, 45 V; tube lens, 80 V. High performance liquid chromatography analyses were performed on a Merck-Hitachi apparatus with quaternary pump, automatic autosampler and UV-vis detector. The column was a Lichrospher C18 endcapped with 5 μm particles size, 250 mm long and 4.6 mm diameter. The purity of the products was determined along two methods, an isocratic system with acetonitrile/water (50:50) as mobile phase (reading at 254 nm) and the other using an elution gradient of 5 to 80 % in acetonitrile (reading at 210 nm). The HPLC purities of the final compounds that underwent biological assessment were $\geq 95\%$.

5.1.1. General procedure for the preparation of benzohydrazides (4-13). Various benzohydrazides **5-7** and **9-13** were obtained according to known procedures^{40, 65} except for benzohydrazides **4** and **8** which were commercially available. A solution of the methyl benzoate (1 equiv) in ethanol was added dropwise to 65 % hydrazine monohydrate (5 equiv). The reaction mixture was then heated under reflux and stirred overnight. The reaction progress was followed up by TLC. Crude product was collected by filtration after cooling of the reaction medium and finally washed with cold ethanol unless specified otherwise. The desired benzohydrazides were used without any further purification.

The analysis of spectral data (^1H and ^{13}C NMR), the yields, HRMS, Mp and R_f of these precursors are presented in Supplementary Information.

5.1.2. General procedure for the preparation of thiosemicarbazides (3, 14-48 and 51-52). A series of thiosemicarbazides **3**, **14-48** and **51-52** were prepared according to a procedure adapted from the literature⁴⁰⁻⁴¹ by adding an isothiocyanate (1 equiv) dropwise to a solution of benzohydrazide (1 equiv) in methanol. The reaction mixture was stirred at room temperature and

its progress was followed by TLC. The precipitate was then collected by filtration, washed with cold ethanol and then recrystallized from ethanol as many times as necessary to obtain a pure product.

Target compounds are presented below, the analysis of spectral data (^1H and ^{13}C NMR), the yields, HRMS, Mp and R_f of other compounds are however presented in Supplementary Information.

*1-(2-Hydroxybenzoyl)-4-phenyl-3-thiosemicarbazide (3).*⁶⁶ This compound was synthesized according to the general procedure described above using synthesized 2-hydroxybenzohydrazide **5** (0.29 g, 1.93 mmol) and phenyl isothiocyanate (0.26 g, 1.93 mmol) in methanol (20 mL). After 7 h of reaction, the pure product was collected as a white powder (0.16 g, 28 %). R_f 0.75 (PE/EtOAc 4:6). Mp: 187.8-190.0°C. ^1H NMR (400 MHz, $\text{DMSO}-d_6$): δ_{H} (ppm) 6.92-7.01 (m, 2H, Ar), 7.17 (dd, $J = 7.4$ Hz, 1H, ArH), 7.37 (dd, $J = 7.8$ Hz, 2H, ArH), 7.44-7.56 (m, 3H, Ar), 7.91 (d, $J = 5.6$ Hz, 1H, Ar), 9.7-10.5 (m, 1.7H and 0.3H, NH), 10.6-11.5 (brs, 0.7H and 0.3H, NH), 11.91 (s, 1H, OH). ^{13}C NMR (100 MHz, $\text{DMSO}-d_6$): δ_{C} (ppm) 115.13 (Ar), 117.12 (Ar), 118.87 (Ar), 125.07 (Ar), 125.79 (Ar), 128.09 (Ar), 128.81 (Ar), 134.01 (Ar), 139.07 (Ar), 159.39 (Ar), 168.94 (C=O), 180.85 (C=S). HRMS (ESI⁺): m/z calcd for $\text{C}_{14}\text{H}_{14}\text{N}_3\text{O}_2\text{S}$ ($\text{M}+\text{H}$)⁺ 288.08012, found 288.08008.

*1-Benzoyl-4-phenyl-3-thiosemicarbazide (14).*⁶⁷ This compound was synthesized according to the general procedure described above using commercial benzohydrazide **4** (0.54 g, 4 mmol) and phenyl isothiocyanate (0.54 g, 4 mmol) in methanol (20 mL). After 17 h of reaction, the pure product was collected as white needles (0.82 g, 76 %). R_f 0.3 (PE/EtOAc 5:5). Mp: 162.6-163.1°C. ^1H NMR (400 MHz, $\text{DMSO}-d_6$): δ_{H} (ppm) 7.17 (dd, $J = 7.3$ Hz, 1H, ArH), 7.34 (dd, $J = 7.7$ Hz, 2H, ArH), 7.45 (m, 2H, ArH), 7.51 (dd, $J = 7.5$ Hz, 2H, ArH), 7.59 (dd, $J = 7.3$ Hz, 1H, ArH), 7.97 (d, $J = 7.4$ Hz, 2H, ArH), 9.73 (s, 1H, NH), 9.83 (brs, 1H, NH), 10.56 (s, 1H, NH). ^{13}C NMR

(100 MHz, DMSO- d_6): δ_C (ppm) 125.22 (Ar), 125.80 (Ar), 128.03 (Ar), 128.29 (Ar), 131.91 (Ar), 132.56 (Ar), 139.06 (Ar), 165.95 (C=O), 181.05 (C=S). HRMS (ESI⁺): m/z calcd for C₁₄H₁₄N₃OS (M+H)⁺ 272.08521, found 272.08499.

4-(3,4-Dichlorophenyl)-1-(2-hydroxybenzoyl)-3-thiosemicarbazide (29).⁶⁸ This compound was synthesized according to the general procedure described above using synthesized 2-hydroxybenzohydrazide **5** (0.43 g, 2.55 mmol) and 3,4-dichlorophenyl isothiocyanate (0.52 g, 2.55 mmol) in methanol (10 mL). After 24 h of reaction, the pure product was collected as white needles (0.56 g, 63 %). R_f 0.19 (PE/EtOAc 4:6). Mp: 200.0-201.0°C. ¹H NMR (400 MHz, DMSO- d_6): δ_H (ppm) 6.91-7.02 (m, 2H, ArH), 7.47 (ddd, J = 7.6 Hz, J = 0.8 Hz, 1H, ArH), 7.54 (dd, J = 8.8 Hz, J = 2.1 Hz, 1H, ArH), 7.60 (d, J = 9.2 Hz 1H, ArH), 7.80-7.96 (m, 2H, ArH), 9.90-10.30 (m, 2H, NH), 10.5-11.5 (brs, 1H, NH), 11.88 (s, 1H, OH). ¹³C NMR (100 MHz, DMSO- d_6): δ_C (ppm) 120.13 (Ar), 122.46 (Ar), 124.14 (Ar), 128.90 (Ar), 130.74 (Ar), 132.03 (Ar), 134.02 (Ar), 135.05 (Ar), 135.32 (Ar), 139.45 (Ar), 144.55 (Ar), 164.73 (Ar), 174.01 (C=O), 186.05 (C=S). HRMS (ESI⁺): m/z calcd for C₁₄H₁₂Cl₂N₃O₂S (M+H)⁺ 356.00218, found 356.00235.

5.1.3. General procedure for the preparation of semicarbazides (53-54).⁴⁴ The semicarbazides **53** and **54** were prepared by adding an isocyanate (1 equiv) to a benzohydrazide (1 equiv) in methanol. The reaction mixture was stirred under reflux and its progress was followed up by TLC. The precipitate was then collected by filtration and washed with cold methanol.

2-Benzoyl-N-(3,4-dichlorophenyl)hydrazine-1-carboxamide (53).⁶⁹ This compound was synthesized according to the general procedure described above using commercial benzohydrazide **4** (0.37 g, 2.72 mmol) and 3,4-dichlorophenyl isocyanate (0.51 g, 2.72 mmol) in methanol (20 mL). After 17 h of reaction, the pure product was collected as white needles (0.28 g, 32 %). R_f 0.54 (PE/EtOAc 5:5). Mp: 214.5-215.0°C. ¹H NMR (400 MHz, DMSO- d_6): δ_H (ppm) 7.36-7.54

(m, 4H, ArH), 7.58 (ddd, $J = 7.3$ Hz, $J = 2.2$ Hz, 1H, ArH), 7.87 (d, $J = 2.2$ Hz, 1H, ArH), 7.91 (d, $J = 7.3$ Hz, 2H, ArH), 8.44 (brs, 1H, NH), 9.18 (brs, 1H, NH), 10.31 (s, 1, NH). ^{13}C NMR (100 MHz, DMSO- d_6): δ_{C} (ppm) 118.66 (Ar), 119.68 (Ar), 123.14 (Ar), 127.56 (Ar), 128.38 (Ar), 130.44 (Ar), 130.80 (Ar), 131.83 (Ar), 132.46 (Ar), 140.02 (Ar), 159.94 (C=O), 166.43 (C=O). HRMS (ESI $^{+}$): m/z calcd for $\text{C}_{14}\text{H}_{12}\text{Cl}_2\text{N}_3\text{O}_2$ (M+H) $^{+}$ 324.03011, found 324.03021.

N-(3,4-dichlorophenyl)-2-(2-hydroxybenzoyl)hydrazine-1-carboxamide (**54**). This compound was synthesized according to the general procedure described above using synthesized 2-hydroxybenzohydrazide **5** (0.40 g, 2.65 mmol) and 3,4-dichlorophenyl isocyanate (0.50 g, 2.67 mmol) in methanol (20 mL). After 17 h of reaction, pure product was collected as white powder (0.34 g, 37 %). R_{f} 0.74 (PE/EtOAc 5:5). Mp: 254.0-256.0°C. ^1H NMR (400 MHz, DMSO- d_6): δ_{H} (ppm) 6.89-6.99 (m, 2H, ArH), 7.38-7.47 (m, 2H, ArH), 7.51 (d, $J = 8.8$ Hz, 1H, ArH), 7.87 (d, $J = 2.3$ Hz, 1H, ArH), 7.89 (dd, $J = 7.9$ Hz, $J = 1.5$ Hz, 1H), 8.59 (s, 1H, NH), 9.24 (brs, 1H, NH), 10.45 (brs, 1H, NH), 11.92 (brs, 1H, OH). ^{13}C NMR (100 MHz, DMSO- d_6): δ_{C} (ppm) 114.65 (Ar), 117.29 (Ar), 118.67 (Ar), 118.92 (Ar), 119.68 (Ar), 123.28 (Ar), 128.36 (Ar), 130.47 (Ar), 130.85 (Ar), 134.11 (Ar), 139.87 (Ar), 155.17 (Ar), 159.30 (C=O), 168.60 (C=O). HRMS (ESI $^{+}$): m/z calcd for $\text{C}_{14}\text{H}_{12}\text{Cl}_2\text{N}_3\text{O}_3$ (M+H) $^{+}$ 340.02502, found 340.02505.

5.1.4 X-ray crystal structure determination of compound 29. A single crystal of compound **29** was obtained by slow evaporation from a solution of MeOH/DMSO. Data were then collected at room temperature on a Gemini diffractometer (Oxford Diffraction Ltd) equipped with a Ruby CCD detector using Enhance (Cu) X-ray Source. Data collection program: CrysAlis CCD (Oxford Diffraction Ltd), data reduction: CrysAlis RED (Oxford Diffraction Ltd), structure solution: SHELXS, structure refinement (on F^2): SHELXL-97,⁷⁰ data analysis: PLATON.⁷¹ A multi-scan procedure was applied to correct for absorption effects. Hydrogen atom positions were calculated

and refined isotropically using a riding model. Crystal size 0.04 x 0.06 x 0.60 mm; monoclinic, $P2_1/c$, $a = 10.9037(2)$, $b = 6.7368(1)$, $c = 26.5219(6)$ Å, $\beta = 96.558(2)^\circ$, $V = 1935.45(6)$ Å³, $Z = 4$, $\rho_{calc} = 1.491$ g cm⁻³, $F_{000} = 896$, λ Cu K α = 1.54184 Å, $\theta_{max} = 66.6^\circ$, 10601 total measured reflections, 3391 independent reflections ($R_{int} = 0.034$), 3056 observed reflections ($I > 2 \sigma(I)$), $\mu = 5.229$ mm⁻¹, 253 parameters, R_I (observed data) = 0.0434, R_I (all data) = 0.1242, $S = \text{GooF} = 1.06$, $\Delta/s.u. = 0.000$, residual $\rho_{max} = 0.40$ e Å⁻³, $\rho_{min} = -0.41$ e Å⁻³.

5.2. Biology

All the graphs were obtained with *GraphPad Prism 6* software (San Diego, CA). The reagents used for the enzymatic assay (BIOMOL[®] Green reagent, phosphate standard 800 µM) were purchased from Enzo Life Sciences, Inc (Farmingdale, NY). The UV spectra were recorded at room temperature on a Spectramax[®] M2E spectrophotometer (Molecular Devices, LLC, Sunnyvale, CA) in 96-well plates. The enzyme used was *Enterococcus faecalis* polyHis-DdlB produced and purified by our care. *E. faecalis* BM 4390, *E. faecalis* JH2-2::C1 and *E. faecalis* BM 4575 were received from Prof Patrice Courvalin, Institut Pasteur, Paris, France. *S. aureus* MU 50, VRS-1 and *S. aureus* NRS 119 were obtained from the NARSA (Network on Antimicrobial Resistance in Staphylococcus Aureus), BEI Resources, Manassas, VA. *S. aureus* SA 325 and *S. aureus* SA 481 were received from Prof. Peter Appelbaum, Hershey Medical Center, Hershey, PA. D-Ala, L-Ala and Marfey's reagent (1-fluoro-2,4-dinitrophenyl-L-5-alanine amide) were purchased from TCI Europe N.V. (Zwijndrecht, Belgium) and D-Ala-D-Ala from Fluorochem Ltd (Derbyshire, UK). Solvent used in LC-MS runs had the quality required for such analyses. LC-MS/MS was performed on a UHPLC system (Acquity H-Class, Waters) coupled to a tandem-quadrupole mass spectrometer (Xevo TQ-S, Waters). All chromatographic separations were achieved on an Acquity UPLC[®] BEH C18 column (1.7 µm, 2.1 mm × 50 mm, Waters, Milford,

Massachusetts) equipped with an inline filter. All centrifuge operations were performed on an Eppendorf 5810R refrigerated centrifuge.

5.2.1. Production and purification of the recombinant His-tagged DdlB.

5.2.1.1 Construction of expression vector for *Enterococcus faecalis* Ddl. *Enterococcus faecalis* JH2-2 total DNA⁷² was extracted as described.⁷³ The *ddl* gene was amplified by PCR using the Phusion® High-Fidelity DNA Polymerase (New England Biolabs, Ipswich, MA) and a pair of primers including a NcoI (5'-GAGGAATTAACCATGGCTAAGATTATTTTGTG-3') and an PstI (5'-CCCATATGGTACCAGCTGCAGTTTAAACGATTCAAAGCTAACTG-3') restriction sites (underlined). The *ddl* gene was cloned into the expression pBAD/Myc-His-A vector (Invitrogen) under the control of the L-arabinose inducible promoter⁷⁴ between the NcoI and PstI restriction sites. The sequence of the PCR fragment was completely checked on both strains using the pBAD forward and reverse sequencing primers. The resulting plasmid encoding a protein with a C-terminal 6-His tag served to transform the *E. coli* LMG194 expression strain (Invitrogen⁷⁵).

5.2.1.2 Overproduction of the Ddl-His₆ enzyme. The production and purification of Ddl-His₆ enzyme were performed according to previous work from our group.³³ Transformed bacteria *E. coli* LMG194 containing the pBAD/Ddl-Myc-His plasmid were inoculated by adding 1/50 of preculture (performed overnight) in minimal medium (RM media, Invitrogen⁷⁶) containing 0.2% glucose and 100 mg/L ampicillin. This culture was placed in the incubator and grown at 37°C until an optical density (OD) at 600 nm of 0.4. At this point, L-arabinose was added to the culture to reach 2% of the final concentration and the latter was placed for overnight growth at 20°C under shaking. All subsequent steps were performed at 4°C. Bacteria were then harvested by centrifugation, resuspended in a 30-fold smaller volume of buffer A (50 mM Hepes pH 8.0, 5 mM MgCl₂·6H₂O, 10 mM imidazole (U.V. = 0) and 10% glycerol). Phenylmethylsulfonyl fluoride

(PMSF) 100 mM, a serine protease inhibitor, was added to the bacterial suspension (100× dilution) as well as benzonase (10.000× dilution). Lyse was performed by 3 successive passages in a French Press operating at 1000-1500 psi (SLM Aminoco). Cellular debris, or insoluble fraction, were removed by centrifugation (30 min, 18 000 g). The supernatant, or soluble fraction, was then filtered through a 0.45 µm filter and contained the desired protein.

5.2.1.3 Purification of the Ddl-His₆ enzyme. 30 mL of supernatant were injected on the Ni-NTA column (HisTrap GE Healthcare) previously washed with cold buffer A (50 mM Hepes pH 8.0, 5 mM MgCl₂.6H₂O, 10 mM imidazole (U.V. = 0) and 10% glycerol). Proteins having low natural affinity for Ni were eluted by 20 mL of 10% buffer B (50 mM Hepes pH 8.0, 5 mM MgCl₂.6H₂O, 500 mM imidazole (U.V. = 0), 300 mM NaCl and 10% glycerol), then His-tagged protein was recovered thanks to an elution gradient of buffer B (50 mL, 10% to 100%). Eluate was dialyzed overnight against a 142.8-fold higher volume of buffer C (50mM Hepes pH 7.2, 150 mM KCl, 5 mM MgCl₂.6H₂O, 5 mM glutathione reduced form (GSH) and 20% glycerol) at 4°C. The His-tagged protein purity was checked by SDS-polyacrylamide gel electrophoresis (Novex Tris-Glycine Gels 14%, Invitrogen⁷⁷): a single band at 42 kDa was observed after Coomassie Blue staining. The purified protein concentration was measured by the method of Bradford using bovine serum albumin as standard (Pierce™ BCA Protein Assay Kit, ThermoFisher Scientific) and determined to be 2.04 mg/mL. Pure fractions were stored in buffer C at -80°C.

5.2.2. Inhibition of the Ddl-His₆ enzyme.

The activity of DdlB was monitored with the colorimetric malachite green method in which orthophosphate generated during the reaction is measured, performed exactly as described in the literature.⁴⁵

5.2.2.1 Screening of the compounds. Each compound was tested at a concentration of 10 μ M for its ability to inhibit DdlB activity. Assays were performed with a pre-incubation of 30 min at 30°C between the enzyme, the inhibitor and the ATP. Then, the substrate was added and incubated with the mixture for 20 min at 30°C. The composition of this mixture (final volume: 50 μ L) was 20 mM Tris.HCl (pH 7.4), 10 mM MgCl₂, 10 mM KCl, 10 μ M inhibitor, 500 μ M ATP, 1 mM of D-Ala and 20 mg/L of purified DdlB. All compounds were soluble in the assay mixture containing 10% DMSO. After the incubation, 100 μ L of Biomol® Green reagent containing 10% DMSO were added and the absorbance was read at 650 nm after 25 min.

5.2.2.2 Determination of the IC₅₀. For compounds showing significant inhibitory activity at 10 μ M (> 70 %) with respect to a similar assay without the inhibitor, IC₅₀ values were determined under similar conditions to the screening. Each compound was tested at 7 concentrations (10⁻⁸, 10⁻⁷, 3.10⁻⁷, 10⁻⁶, 3.10⁻⁶, 10⁻⁵ and 3.10⁻⁵ or 5.10⁻⁵M). The absorbance was read at 650 nm after 25 min of reaction with the Biomol® Green reagent, 10 min of incubation with the substrate and a preincubation with the inhibitor, the enzyme and ATP of 30 min at 30°C. Additionally, we performed several IC₅₀ by varying incubation time with our hit compound. Inhibitor **3** was preincubated with the enzyme for 10, 30, 60, 90 and 120 min before the reaction was initiated as described above (the same final concentrations were those described for IC₅₀).

5.2.2.3 Rapid dilution assay. The reversibility of the enzymatic inhibition by benzoylthiosemicarbazide **29** was evaluated by the rapid dilution method. Three conditions were tested with similar assay composition to those used for the screening: a positive control medium without inhibitor (20 mg/L of Ddl), a medium with 3 μ M of **29** and 200 mg/L of the enzyme, and a negative control with 3 μ M of **29** and 20 mg/L of the enzyme. After a preincubation of 30 min at 30°C between the enzyme, the inhibitor **29** and the ATP, the concentrated medium was diluted

10 times to mimic the composition of the control with 3 μ M of **29** and 20 mg/L of the enzyme. The absorbance was then read after 20 min of incubation with the substrate at 30°C and the addition of Biomol® Green reagent.

5.2.2.4 Competition with D-Ala. Kinetics for D-Ala were performed with compound **29** at 3 concentrations (0 μ M, 1 μ M and 10 μ M) and increasing concentrations in substrate (0.75, 1, 3, 5, 10, 15, 20 and 50 mM) and 500 μ M of ATP. The operating conditions were similar to the ones previously described. Before the quenching by Biomol® Green reagent, the wells containing 3, 5, 10, 15, 20 and 50 mM of D-Ala were diluted 10 times with respect to the linearity zone.

5.2.2.4 Competition with ATP. Kinetics for ATP were performed with compound **29** at 3 concentrations (0 μ M, 1 μ M and 10 μ M), increasing concentrations in cofactor (10, 20, 30, 50, 100, 500 and 1000 μ M) and 50 mM of D-Ala. The operating conditions were similar to the ones previously described except for the D-Ala concentration. Before the quenching by Biomol Green reagent, the wells containing 30, 50, 100, 500 and 1000 μ M of ATP were diluted 10 times to respect the linearity zone.

5.2.2.5 Selectivity assays. The inhibitory activities of **29** were assessed according to the literature for the following enzymes: Arginase 1 (Arg1)⁷⁸, indoleamine 2,3-dioxygenase (IDO)⁷⁹, lactate dehydrogenase (LDH)⁸⁰, monoacylglycerol lipase (MAGL)⁸¹, and phosphoglycerate dehydrogenase (PHGDH)⁸². Other enzymes and receptors binding assays were performed at Eurofins Cerep (France). Their criteria for significance is $\geq 50\%$ inhibition.

5.2.3. Microbiological evaluation.

5.2.3.1 Antimicrobial activity. MICs were determined by microdilution method in cation-adjusted Muller-Hinton broth (CAMHB) (Becton-Dickinson, NJ, USA), following the recommendations of the US Clinical and Laboratory Standards Institute (CLSI)⁸⁴, using an initial

inoculum of 10^6 bacteria/mL, with a final concentration of 1% DMSO (this concentration was proved not to impair bacterial growth). The potential antimicrobial agents were prepared in a two-fold dilution series in CAMHB with 2 % DMSO (Sigma-Aldrich), and then diluted with the same volume of bacterial suspension. Microwell plates with 96 wells were then incubated for 18-24 h at 37°C. The MIC was taken as the lowest concentration of potential antimicrobial agent that prevented the visible growth of bacteria.^{29, 33}

5.2.3.2 Time-kill studies. Time-kill curves were performed according to CLSI method.⁸⁵ *S. aureus* ATCC 25923 was grown overnight at 37°C in CAMHB under shaking. The bacterial suspension was then centrifuged for 7 min at 4000 rpm and the supernatant recollected. Cells were diluted in medium to obtain $2 \cdot 10^6$ CFU/mL. Compound **29** in DMSO, adjusted to a concentration of 1, 2 or 5 times the MIC, was then added to obtain a starting inoculum of 10^6 CFU/mL with 5% DMSO (5% DMSO alone was tested in parallel). The positive control contained only 10^6 CFU/mL. Aliquots (20 μ L) of the cultures were removed at 0 h, 1 h, 2 h, 5 h, 7 h and 24 h of incubation. A series of 10-fold dilutions were prepared in phosphate buffer saline (PBS) and plated on tryptic soy agar (TSA). The number of viable cells on TSA was determined after 24 h of incubation at 37°C. The rate of killing was determined by calculating the reduction of viable bacteria ($\log_{10}$ CFU/mL) at different sampling times for all the inhibitor concentrations. Bactericidal activity is defined as a ≥ 3 - $\log_{10}$ reduction of the initial CFU amount in 24 h.

5.2.3.3 LC-MS/MS analysis of L-Ala, D-Ala and D-Ala-D-Ala levels in bacterio.

Preparation of bacterial extracts. The bacterial sample was prepared according to the literature for *S. aureus* strains.⁶⁰ *S. aureus* ATCC 25923 (2 $\times$ 25mL) was grown overnight at 37°C in MHB 5% DMSO under shaking. The bacterial suspension was then centrifuged for 7 min at 4000 rpm and the cells pellet was resuspended in 20 mL of MHB 5% DMSO. The appropriate volume of

this solution was added to 200 mL of MHB 5% DMSO to obtain an absorbance of 0.05 at 600 nm (OD_{600}) and the culture was subsequently incubated at 37°C under shaking at 300 rpm until the OD_{600} reached 0.6. Compound **29** was then added to 60 mL-portions of this culture to a final concentration of 2× MIC (0.2 mM) so that the incubation time ranges from 0, 5, 10, 20 to 30 minutes. Control cultures were grown without antibiotic or with 2× MIC of DCS (0.63 mM). After the incubation time, all flask were cooled in an ice/water bath and three 10 mL-aliquots of each were poured into cold centrifugation tubes. Bacteria were then pelleted at 4000 rpm for 10 min at 4°C and cell pellets washed with 400 μ L of M9 minimal medium (Na_2HPO_4 30 g/L, KH_2PO_4 15 g/L, NH_4Cl 5 g/L and NaCl 2.5 g/L). These centrifugation/washing steps were repeated 3 times. After the third wash, cell pellets were resuspended in 100 μ L of M9 minimal medium and 400 μ L of ice-cold lysis solvent (MeOH/ H_2O /formic acid, 80:20:0.1 v/v) were then added. After 5-10 minutes on ice by vortexing occasionally, the lysed bacteria were centrifuged at 4000 rpm for 10 min at 4°C. Supernatants (~500 μ L) were then harvested and kept on ice for the subsequent derivatization of 45 μ L-samples of each triplicate.

Derivatization with Marfey's reagent and optimization in LC, MS and MS/MS. The optimization of the LC-MS/MS method and the derivatization procedure were carried out according to the literature.⁵⁹ First, L-Ala, D-Ala and D-Ala-D-Ala metabolites purchased from commercial source were derivatized with Marfey's reagent either alone or as a mixture to optimize the separation and the MS and MS/MS parameters. Calibration curves were performed with dilutions of these samples in water or bacterial extracts from 15 to 0 μ M. All the derivatization and the following steps were carried out under dark condition (absence of light).⁸³ These mixtures were then desalted on a C18 SPE column prior to MS and MS/MS optimization. The optimized MS parameters are described hereunder. The MS/MS detection was done with electrospray ionization (ESI) in the positive mode

and multiple reaction monitoring (MRM). The capillary voltage was set to 3.0 kV, the source offset was 50 V, the cone gas flow was 150 L/h, the source block temperature was 150°C and the nitrogen desolvation gas was heated to 500°C with a flow rate of 1000 L/h. Four transitions were followed: two corresponding to the neutral loss of 45 Da-Marfey's terminal protonated amide [M+H-45]⁺ for the quantification: 342.20>297.20 with cone voltage at 25.0 V and collision energy at 15.0 eV (D-Ala and L-Ala, quantitative ion product) ; 413.25>368.20 with cone voltage at 25.0 V and collision energy at 15.0 eV (D-Ala-D-Ala, quantitative ion product) and two transitions for the qualification : 342.20>205.35 with cone voltage at 25.0 V and collision energy at 30.0 eV (D-Ala and L-Ala, qualitative ion product) ; 413.25>251.25 with cone voltage at 25.0 V and collision energy at 25.0 eV (D-Ala-D-Ala, qualitative ion product). The dwell time was set to 0.034 s. The tandem mass spectrometer was operated with MassLynx/Target Lynx Software version 4.1 (Waters). Finally, the chromatographic conditions were set as followed: the elution was performed at 0.5 mL/min at a temperature of 40°C with a starting gradient of 90% solvent A (0.1% formic acid in water) and 10% solvent B (acetonitrile). After 1 min, the gradient linearly ramped to 64.5% solvent A and 35.5% solvent B until 8 min. The proportion of B was then return to 10% and reequilibration was done during 2 min before the next injection. UHPLC-MS/MS analysis was performed with an injection volume of 2 µL for each derivatized sample.

5.2.3.4 Determination of toxicity for mammalian cells. Cell viability was determined on human THP-1 cells by use of the Trypan blue exclusion assay.⁸⁶ Human myelomonocytic THP-1 cells (ATCC TIB-202)⁸⁷ were cultivated in RPMI-1640 medium supplemented with 10% fetal calf serum (Gibco/Life Technologies Corporation (Paisley, UK)) as described previously.⁸⁸ Compound **29** was added to cell suspension to obtain final concentrations of 10⁻⁴ M, 2.10⁻⁴ M and 4.10⁻⁴ M at 1% DMSO (1, 2 and 5 times the MIC for *S. aureus* ATCC 25923). The medium was incubated at

37°C in a 5% CO₂ atmosphere and aliquots (50 µL) were removed at 2 h, 4 h and 24 h. Trypan blue solution 0.4% (Gibco/Life Technologies Corporation (Paisley, UK)) was then added in a 1:1 (v:v) proportion to the cell suspension. After 5 min of incubation with the dye, the percentage of dead cells was calculated as the number of cells stained in blue vs the total number of cells as counted using optical microscopy.

ASSOCIATED CONTENT

Supporting Information. Optimization of the colorimetric malachite green assay. MIC values of derivatives **3**, **14-49** and **51-54** against Gram-positive sensitive strains. MIC values of active compounds on Ddl **3**, **22-42** and **51** against Gram-positive resistant strains. ¹H NMR spectra of compound **14** and **3** illustrating the possible keto-enol equilibrium. Experimental data of benzohydrazides precursors **4-13** and **50**. Experimental data of thiosemicarbazides **14-28**, **30-49** and **51-52**. PDB Coordinates for Computational Models.

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Conceived and designed the experiments: AA, LT, RF, FVB. Protein production and purification: AA, BJ, SL. Compounds synthesis and characterization: AA, LT. Enzymatic assays: AA, LT. Biological activities: AA. UHPLC-MS/MS experiments: AA, LP. Crystal growth and X-ray structure determination: AA, JW. Manuscript preparation: AA, RF, FVB. All authors have given approval to the final version of the manuscript. ‡ AA and LT contributed equally to this work.

The authors declare no competing financial interest.

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ABBREVIATIONS

CAMHB, cation-adjusted Muller-Hinton broth; CA-MRSA, community-acquired MRSA; CFU, colony-forming unit; CIP, ciprofloxacin; DCS, D-cycloserine; Ddl, D-alanine-D-alanine ligase; DD-ligases, D-Ala-D-Ala, D-Ala-D-Lac and D-Ala-D-Ser ligases; GlcNAc, N-acetylglucosamine; HA-MRSA, hospital-acquired MRSA; LZD, linezolid; MurNAc, N-acetylmuramic acid; Ph, Phenyl; PE, petroleum ether; S, solubility; StaDDI, *S. aureus* Ddl; TPSA, topological polar surface area; TSA, tryptic soy agar; VAN, vancomycin; VISA, vancomycin intermediate resistant *S. aureus*; VRSA, vancomycin resistant *S. aureus*.

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