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Ten years with NDM-1 metallo β -lactamase: from structural insights to inhibitor design.

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3 The worldwide emergence of metallo β -lactamase NDM-1 as carbapenemase able to hydrolyze near
4 all available β -lactam antibiotics has characterized the last decade, endangering efficacious
5 antibacterial treatments. No inhibitors for NDM-1 are available in therapy, nor promising compounds
6 are in the pipeline for future NDM-1 inhibitors.
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10 We report the studies dedicated to the design and development of effective NDM-1 inhibitors. The
11 discussion for each agent moves from the employed design strategy to the ability of the identified
12 inhibitor to synergize β -lactam antibiotics. A structural analysis of NDM-1 mechanism of action
13 based on selected X-ray complexes is also reported: the intrinsic flexibility of the binding site and the
14 comparison between penicillins/cephalosporins and carbapenems mechanisms of hydrolysis are
15 evaluated.
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19 Despite the valuable progresses in terms of structural and mechanistic information, the design of a
20 potent NDM-1 inhibitor to be introduced in therapy remains challenging. Certainly, only the deep
21 knowledge of NDM-1 architecture and of the variable mechanism of action that NDM-1 employs
22 against different classes of substrates could orient a successful drug discovery campaign.
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29 Keywords: NDM-1 Metallo β -lactamase; structure-based drug design; enzyme inhibitors, biological
30 activity, bacterial resistance, structural analysis.
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3 Bacteria multidrug resistance poses a real menace to public health, calling for new discoveries and
4 innovation in antibiotic research.^{1,2} In Enterobacteriaceae, drug resistance is mainly attributed to the
5 expression of a large number of diverse β -lactamases (BLs), enzymes able to hydrolyze β -lactam
6 antibacterials. Several drug design campaigns led, so far, to the development of β -lactam drugs
7 resistant to BLs (i.e., methicillin, last generation cephalosporins, and carbapenems) and to the design
8 of BLs inhibitors to be co-administered with β -lactam antibacterials, thus protecting them from BLs
9 hydrolysis.³ However bacteria promptly reply to last developed antimicrobials *via* the production of
10 BLs with broader spectrum of action, leaving few alternatives for the treatment of resistant
11 infections.^{4,5} In particular carbapenemases, BLs able to hydrolyze even the last resort antibiotics (i.e.
12 carbapenems) are rapidly disseminating worldwide.⁶

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14 According to Ambler's classification,^{7,8} BLs are categorized in class A, B, C and D, with classes A,
15 C and D being serine BLs (SBLs) (e.g., KPC, AmpC and OXA enzymes),⁹⁻¹¹ and class B being
16 metallo BLs (MBLs) (e.g., VIM, IMP, NDM).¹² Among them, class B carbapenemases are the most
17 worrisome, since they catalyze the hydrolysis of nearly all available β -lactam antibiotics.^{13,14} Despite
18 the enormous research effort to design effective drugs to counteract their extensive hydrolytic ability,
19 currently no clinical inhibitor able to reverse the resistance mediated by MBLs has been approved in
20 therapy.^{15,16}

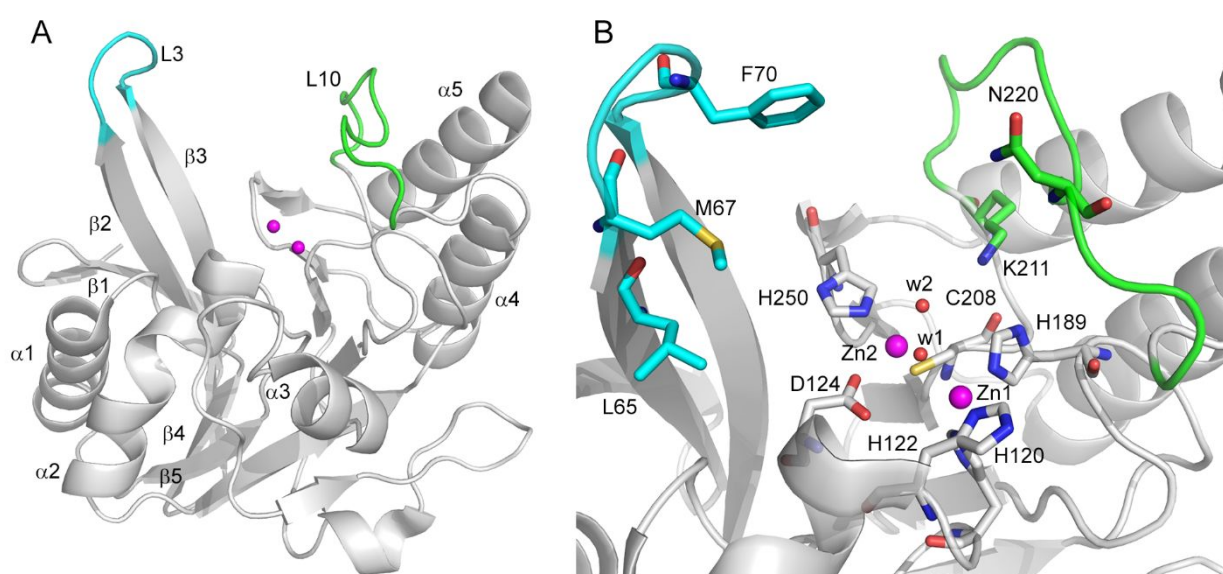
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22 The hydrolysis performed by MBL is catalyzed by one or two zinc atoms located in the active site.
23 Depending on the number of zinc atoms, MBLs are separated into three subclasses: B1, B2 and
24 B3.^{12,17} Among these, B1 subclass is the most clinically relevant and includes New Delhi Metallo- β -
25 lactamase-1 (NDM-1), an enzyme that represents a serious threat to human health in light of its
26 substrate promiscuity, broad-spectrum of action, appearance of variants and transferability.¹⁸
27 Furthermore, NDM-1 is characterized by a unique cellular localization conferring to the protein higher
28 stability to adverse condition like Zn depletion.¹⁹

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30 Since its discovery in 2008,²⁰ NDM-1 has experienced the fastest and widest geographical spread
31 among MBLs and bacterial infections harbouring plasmid-encoded NDM-1 have rapidly emerged
32 worldwide.^{1,6,21} NDM-1 production confers resistance to all β -lactam antibiotics, with the only
33 exception of monobactams (i.e. aztreonam).²² However, monobactams can be inactivated by many
34 SBLs normally co-produced with NDM-1, thus expanding bacteria resistance.²³ Resistance genes
35 encoding for MBLs are rapidly spread through plasmids and have also been reported to be located on
36 gene cassettes, further facilitating the horizontal transmission to other microorganisms.^{24,25}
37 Nevertheless, plasmids carrying NDM-1 genes are often associated with additional resistance markers
38 encoding other antibiotic-resistance mechanisms, including those for quinolones, aminoglycosides,
39 rifampicin, chloramphenicol, and macrolides.²⁶⁻²⁹ As a consequence, clinical strains producing
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3 NDM-1 are only susceptible to last line antibacterial agents, e.g. colistin, tigecycline or fosfomycin,
4 which all have toxicity limitations.³⁰
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8 **Structure and catalytic activity of NDM-1**

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10 Structurally, NDM-1 belongs to the subclass B1 of MBL family, characterized by a distinctive $\alpha\beta/\beta\alpha$
11 sandwich fold. The active site, delimited by flexible loops (loop 3 and 10), contains two divalent zinc
12 ions bridged by a hydroxide ion (**Figure 1A**). The first zinc ion (Zn1) is coordinated by His120,
13 His122, His189 and the bridging hydroxide, corresponding to w1 (**Figure 1B**), whereas the second
14 zinc ion (Zn2) is coordinated by Asp124, Cys208 and His250. Moreover, an apical water molecule
15 (w2) is in close proximity, as reported (**Figure 1B**; numbering as from UNIPROT and NDM-1 X-ray
16 structures on pdb).^{31–34} In the binding site, Zn1 orientates the carbonyl group of the substrate for the
17 nucleophilic attack to occur, while Zn2 interacts with the amide nitrogen and the carboxyl group,
18 characteristics of β -lactam antibiotics. The aforementioned hydroxide is responsible for the
19 nucleophilic attack performed on β -lactam rings, eventually leading to substrate hydrolysis.¹²
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50 **Figure 1.** NDM-1 architecture. **A**) Overall protein folding. The two zinc ions are shown as magenta
51 spheres. Loop 3 and 10 are coloured in cyan and green, respectively (PDB code 3spu).³² The
52 secondary structures are labelled according to Groundwater *et al.* and Kim *et al.*^{22,33} **B**) Inset of the
53 active site. Critical residues and waters referred in the text are labelled. The figure was prepared
54 with Pymol 2.1.1.
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58 The NDM-1 active site appears quite open and surrounded by several loops. Among these, the hairpin
59 L3 loop, involved in substrate binding recognition, is characterized by the presence of hydrophobic
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3 residues (Leu65, Met67, Phe70 and Val73) interacting with substrate hydrophobic substituents, while
4 the L10 loop includes residues coordinating Zn²⁺ (Cys 208), as well as residues interacting with the
5 substrate carboxyl group (Lys211 and Asn220).^{31,32}
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8 The hydrolytic activity of MBLs and, in particular, of NDM-1 has been largely investigated. During
9 the catalysis, the nucleophilic hydroxide attacks the substrate carbonyl carbon, a transient adduct is
10 formed and stabilized through Zn interactions, resulting in the C-N bond cleavage (**Figure 2**).^{12,35,36}
11 After the dissociation of the product from the active site and the regeneration of the bridging
12 hydroxide, the enzyme is reactivated for a new hydrolytic reaction (**Figure 2**). Over the years,
13 numerous studies on this mechanism of action have been conducted and a few variants have been
14 described.^{17,21,31,35,37-39} Particular attention has been paid to the formation of one or two transition
15 states, to the identity of the nucleophile, to the proton donor necessary to neutralize the β -lactam
16 amide nitrogen, as well as to the substrate binding mode (see the paragraph “Structural insights on
17 NDM-1 active site”).^{31,35,37,38,40} The reaction, proceeding through the formation of a stabilized anionic
18 intermediate, has been deeply investigated by enzyme kinetics, X-ray evidences and NMR studies on
19 cephalosporin intermediates. The protonation of this anionic intermediate represents the rate limiting
20 step of the overall process.⁴¹⁻⁴³ However the nature of the proton donor still remains a controversial
21 aspect.⁴⁴⁻⁴⁶ This and other mechanistic features of NDM-1 still need a better clarification.
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24 Recently, NDM-1 X-ray structures in complex with intermediates and products of hydrolysis of
25 imipenem (IPM) and meropenem (MEM) were released, strongly suggesting a distinct mechanism
26 for carbapenem hydrolysis, with respect to that described for penicillins and cephalosporins.⁴⁷ As
27 reported by Feng *et al.*, the hydrolysis of carbapenems by NDM-1 presents several peculiar aspects
28 (**Figure 3**). First, the negative charge on pyrroline ring, consequent to the hydrolysis of the β -lactam
29 ring, is delocalized over a conjugate π -system in an equilibrium between the two intermediate EI₁ and
30 EI₂. The absence of the bridging water, necessary for the protonation of the pyrroline nitrogen,
31 favours the shift of the equilibrium toward the intermediate EI₂, which could undergo two different
32 pathways for the product release. EI₂ could be protonated on C2 to give EI₃ that evolves to EP.
33 Alternatively, EI₂ could shift to a conformation observed in EP', before undergoing protonation (EP).
34 Moreover, the absence of the bridging water affects the rate-limiting step of intermediate protonation.
35 Proton uptake comes from a solvent molecule entering the pocket from the exterior space, justifying
36 the exclusive attack of the proton in the beta position on the pyrroline ring of the carbapenem
37 intermediate.³⁶
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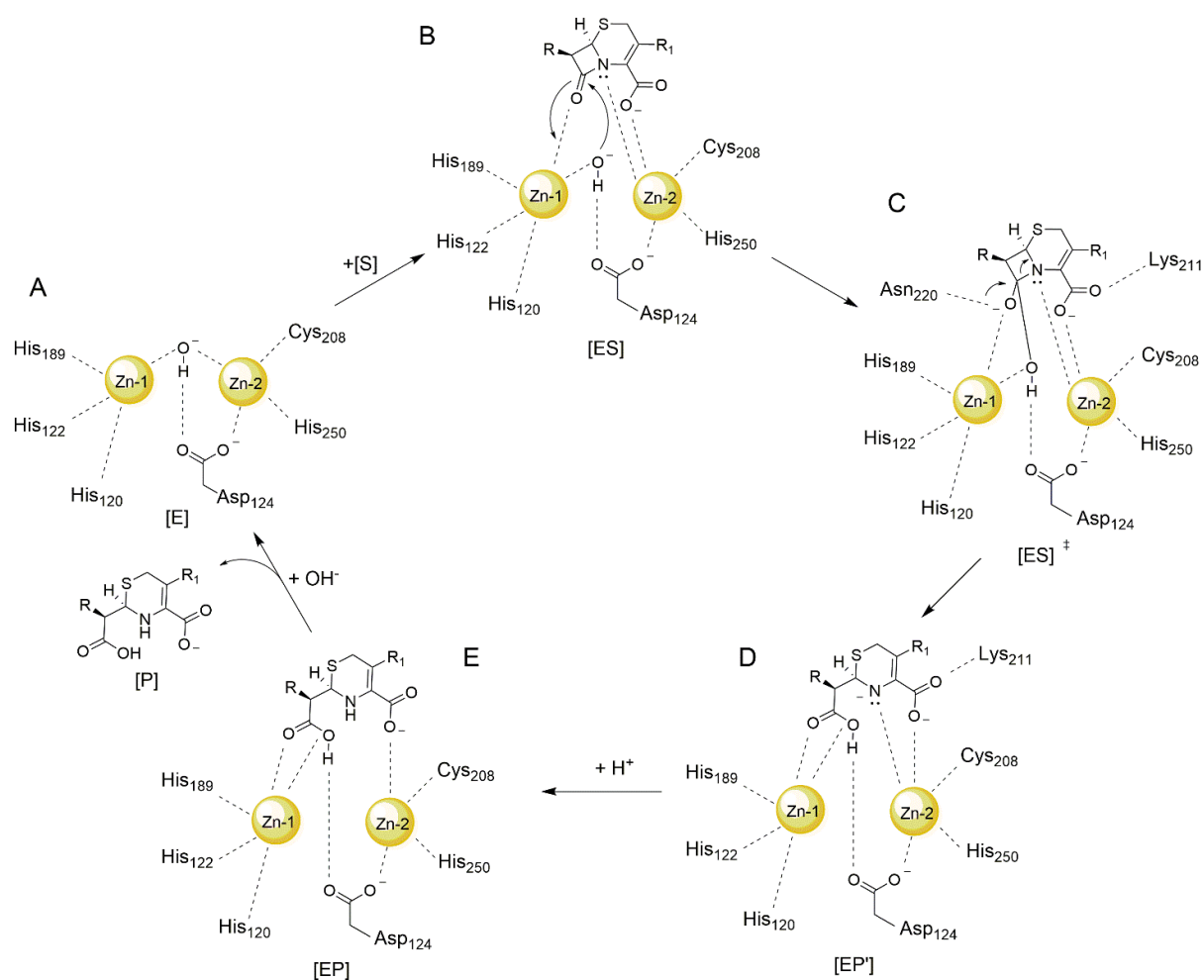


Figure 2. Hydrolytic cycle of NDM-1 on cephalosporin substrate.³⁶ A) NDM-1 catalytic site in its active state; B) Binding of cephalosporin substrate to the active site and nucleophilic attack of hydroxyl group to the β -lactam ring; C) tetrahedral transition state; D) binding of the cephalosporin hydrolyzed product to the NDM-1 active site; E) neutralisation of the hydrolyzed product, release of the inactivated cephalosporin and reactivation of NDM-1 catalytic site in its active state.

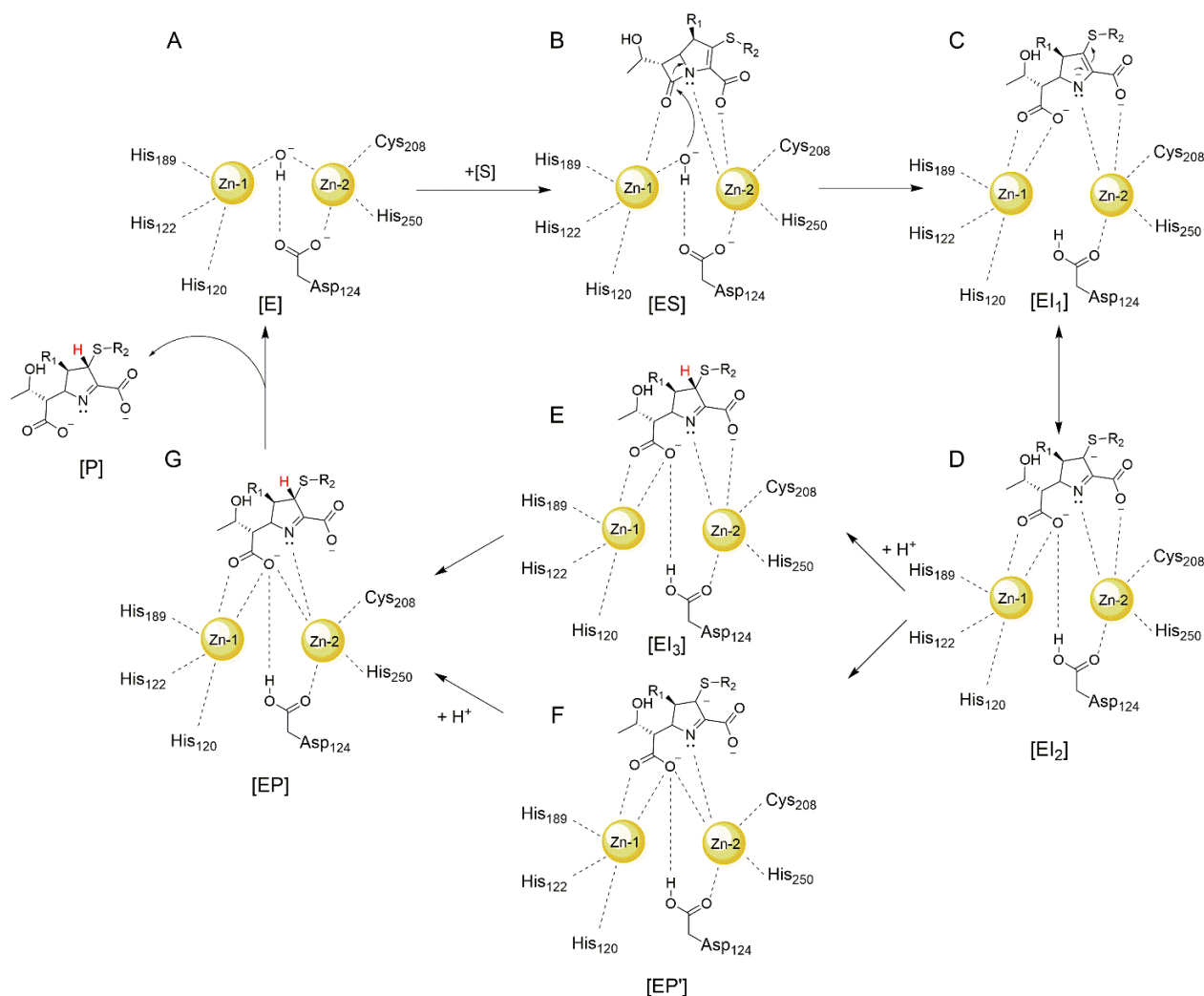


Figure 3. Hydrolytic cycle of NDM-1 on carbapenems as suggested by Feng *et al.*⁴⁷ A) NDM-1 in its active state; B) coordination of the enzyme with the carbapenem substrate and nucleophilic attack of hydroxyl to the β -lactam ring; C, D) delocalization of the negative charge on the pyrrolidine ring; E) protonation at C-3 to give intermediate IE_3 ; F) shift to configuration EP' ; G) coordination of the final hydrolysis product to NDM-1, release of the product P and regeneration of the enzyme in its active state.

In addition, Lisa *et al.*, recently reported a fully biochemical and biophysical study of IPM hydrolysis by bi-Zn(II) B1 enzyme (i.e. NDM-1 and BcII) and the mono-Zn(II) B2 and B3 BLs.³⁵ In particular, focusing on the hydrolysis of IPM (**Figure 4**), they proposed the binding of the substrate to Zn2 by means of the carboxylate group at C3 and the simultaneous detachment of the hydroxide to generate a potent nucleophile (**Figure 4, state B**).

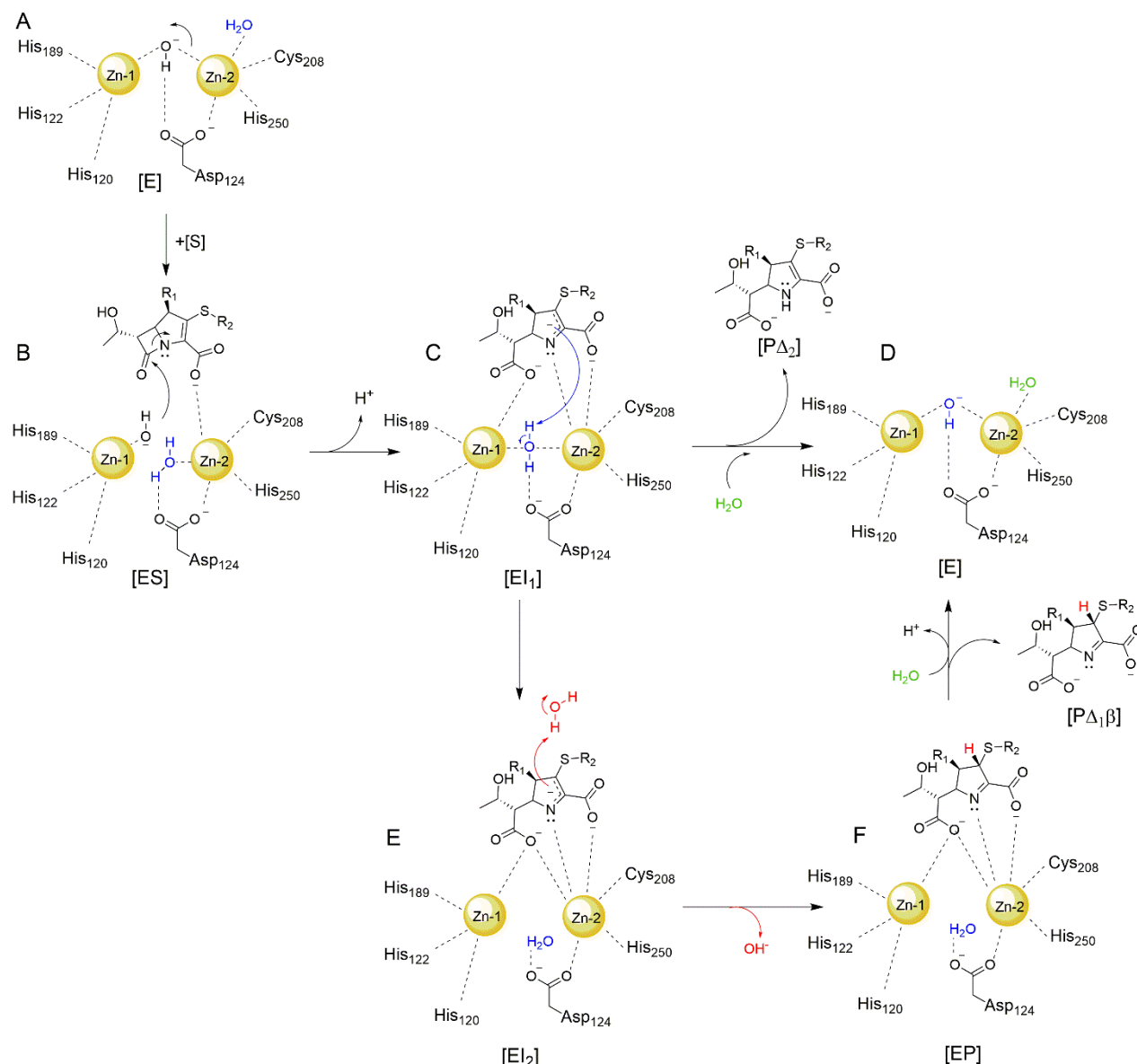


Figure 4. Hydrolytic cycle of bi-Zn(II)-MBLs (including NDM-1) on carbapenem as suggested by Lisa *et al.*³⁵ A) NDM-1 in its active state; B) binding of the substrate to Zn ions and simultaneous detachment of the hydroxide to generate the nucleophile attacking the β -lactam ring; C) protonation of the anion by means of the water molecule; D) release of the product, coordination with a water molecule and regeneration of the enzyme in the active state; E) interconversion of EI₁ to the intermediate EI₂ and protonation by means of an external water molecule; F) hydrolyzed product-enzyme coordination before product release. After the dissociation of the hydrolyzed product, a second water molecule regenerates the enzyme.

In this way the hydroxide is able to attack the β -lactam ring generating the adduct EI₁ (Figure , state C). In EI₁, the deprotonated hydrolyzed-carbapenem binds to Zn1 via the carboxylate at C7 and to Zn2 through the carboxylate at C3 and through the pyrroline ring. Subsequently, the protonation by means of a water molecule elicits the hydrolyzed product, regenerating the enzyme in its active state

(**Figure** , state **D**). Alternatively, the EI_1 can interconvert to an intermediate configuration EI_2 where the carboxylate group at C7 becomes a bridging ligand coordinating Zn2 (**Figure** , state **E**). The protonation at C2 in EI_2 by means of an external water molecule leads to the EP complex lacking a metal-bound water (**Figure** , state **F**). After the dissociation of the hydrolyzed product, a second water molecule finally regenerates the enzyme in its active state (**Figure 4**, state **D**).³⁵

Structural insights on NDM-1 active site

In the last years, many efforts have been made to get structural insights on NDM-1, to clarify the mechanism of action and to identify the residues that interact with the substrates and that could be targeted in drug design campaigns. At the time of writing this review, fifty structures were available in the Protein Data Bank (PDB), twenty-two of them in the apo form and the remaining twenty-eight complexed with β -lactam based substrates or product and only two with novel inhibitors (Table S1). Among substrates, we can recognize two main groups: penicillins/cephalosporins and carbapenems. In **Figure 5** the hydrolyzed forms of methicillin (A), cefuroxime (B) and IPM (C) within NDM-1 active site are reported.^{21,36,47}

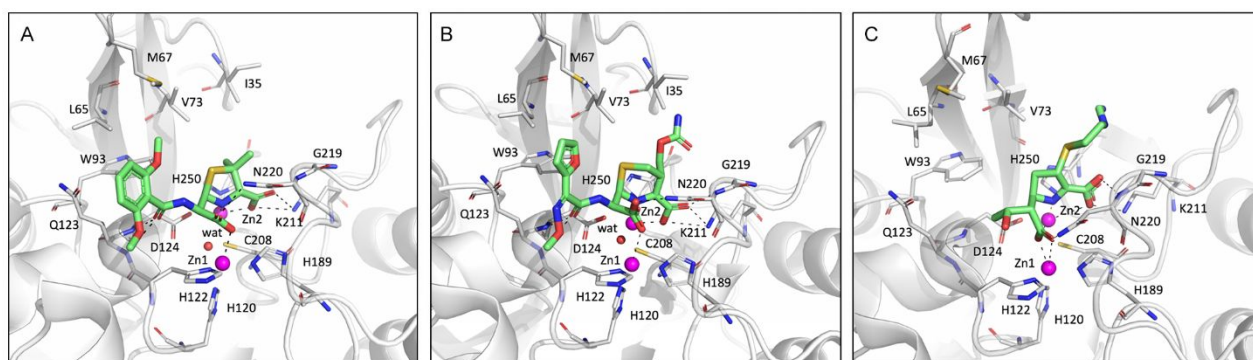


Figure 5. Close-up of hydrolyzed methicillin (A), cefuroxime (B) and IPM (C) in NDM-1 catalytic site (PDB code 4ey2,²¹ 4r10³⁶ and 5yp1⁴⁷, respectively). The ligands are represented as green capped sticks, the binding site residues as grey capped sticks, the zinc ions are shown as magenta spheres, the water molecule as a red smaller sphere. The hydrogen and coordination bonds are represented in black dashed lines. The figures were prepared using Pymol 2.1.1.

Apart from the different substituents, the three molecules occupy, in general, the same position in the protein binding site. Nevertheless, small differences can be observed when comparing methicillin and cefuroxime with IPM.

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3 The hydrolysis mediated by the nucleophile hydroxide (see **Figure 2** and **Figure 3**) generates the C6-
4 carboxylate, which intercalates the two zinc ions and establishes polar contacts with the surrounding
5 residues. In the case of methicillin and cefuroxime, this group coordinates only Zn1 and forms a
6 hydrogen bond with Asn220 (**Figure 5A** and **Figure 5B**). The C3-carboxylate contacts Zn2, Lys211
7 and Gly219. The lactam nitrogen also coordinates Zn2. Additional hydrogen bonds are formed by the
8 methoxyloxy-phenylcarbonyl-amino moiety in methicillin and by the methoxy-iminoacetyl-amino
9 moiety in cefuroxime with Gln123 and Asp124. Hydrophobic contacts with Leu65, Val73 and Trp93
10 further stabilize the complexes. In both cases, a water molecule is coordinated by the two zinc ions
11 and it is hydrogen bonded by Asp124. In the case of cefuroxime, according to what reported by Feng
12 *et al.*,³⁶ the carbon in position 3, bearing the R₂ group, is negatively charged and assumes a sp³
13 configuration. This anionic intermediate (EI state) differs from that proposed for penicillin hydrolysis,
14 where the negative charge is generally located on the lactam nitrogen.⁴⁸ It should be considered that
15 the presence of a conjugated π -system could allow the rearrangement of the double bond from
16 position 3-4 to 4-5.³⁶ The isolation of this cephalosporate intermediate further supports the hypothesis
17 that the subsequent protonation represents the rate-limiting step in the hydrolytic process.

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29 The water molecule intercalating the two zinc ions, previously mentioned, could represent the proton
30 donor. It has been hypothesized that this water could be originally bound to Zn2 or that it could come
31 from the solvent.⁴⁷ Interestingly, the same water is absent in the NDM-1-IPM complex (**Figure 5C**).
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33 With respect to methicillin and cefuroxime, IPM presents quite similar contacts for the β -lactam core.
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35 The newly generated C6-carboxylate hydrogen bonds Asn220 and coordinates both Zn1 and Zn2.
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37 Differently from hydrolyzed penicillins and cephalosporins, in carbapenems this carboxylic group
38 intercalates the metals, generating a hexahedral coordinated Zn2. At the same time, the distance
39 between Zn2 and the C3-carboxylate increases, likely destabilizing the enzyme-intermediate
40 complex, while the lactam nitrogen still coordinates Zn2. In the present complex, Feng *et al.* also
41 observed in addition a higher flexibility of the R₂ side-chain, which further supported the hypothesis
42 of the complex being in the EP state, already protonated (possibly by a solvent water) and ready to
43 leave the active site. The peculiar position of the C6-carboxylate is also responsible for the steric
44 displacement of the mentioned water molecule that was never observed in NDM-1-carbapenemes
45 complexes.^{21,47} As also noted for methicillin and cefuroxime, the C3-carboxylate contacts Lys211
46 and Gly219. Very poor hydrophobic contacts are made by the hydroxyethyl moiety with Trp93.
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48 According to these observations, the hydrolytic mechanism for penicillin/cephalosporin and
49 carbapenem would mainly differ in the rate-limiting step of intermediate protonation, due to the
50 different nature of the proton donor. In the absence of the bridging water, an additional water molecule
51 has to participate to the process, possibly modifying the catalysis speed. For this reason, the structure
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of the antibiotic substrate directly affects the rate-limiting step. As further support, Feng and co-workers explained the higher k_{cat} for IPM with respect to MEM ($k_{\text{cat}}/K_{\text{M}}$ equal to $4.3 \cdot 10^6$ and $2.6 \cdot 10^6$ $\text{M}^{-1}\text{s}^{-1}$, respectively) with the different chemical nature of the R_2 side-chain. The IPM N-formimido group could provide a more hydrophilic environment than the MEM pyrrolidine ring, thus facilitating the entrance of a solvent molecule.⁴⁷ In this perspective, side-chains could be properly modified for the design of mechanism-based inhibitors.

Another noteworthy feature that distinguishes penicillin/cephalosporin binding mode with respect to carbapenem is the conformation of the β -hairpin L3 loop, which defines the size of the binding site groove. According to Feng *et al.*, when carbapenems are bound and hydrolyzed by NDM-1, the catalytic pocket slightly collapses with the L3 loop somehow closing the site entrance. On the contrary, when penicillins/cephalosporins are present in the pocket the L3 loop shifts backwards, allowing room for bulkier moieties (**Figure 6**). This could be likely attributed to the different extension of the R_1 side-chain, generally smaller for carbapenems.⁴⁷ The different shape and volume of the cavity in the three complexes is clearly visible in **Figure 7** with cefuroxime inducing the larger variation. The pockets were calculated by flapsite, implemented in FLAP, developed by Molecular Discovery Ltd (www.moldiscovery.com).^{49,50}

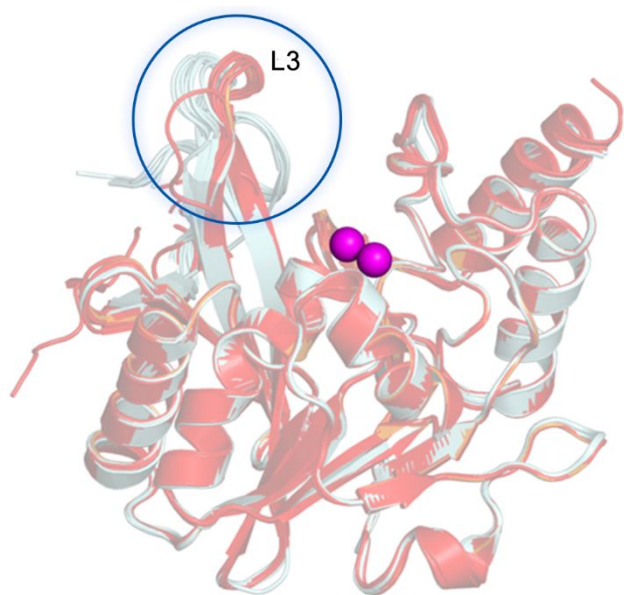
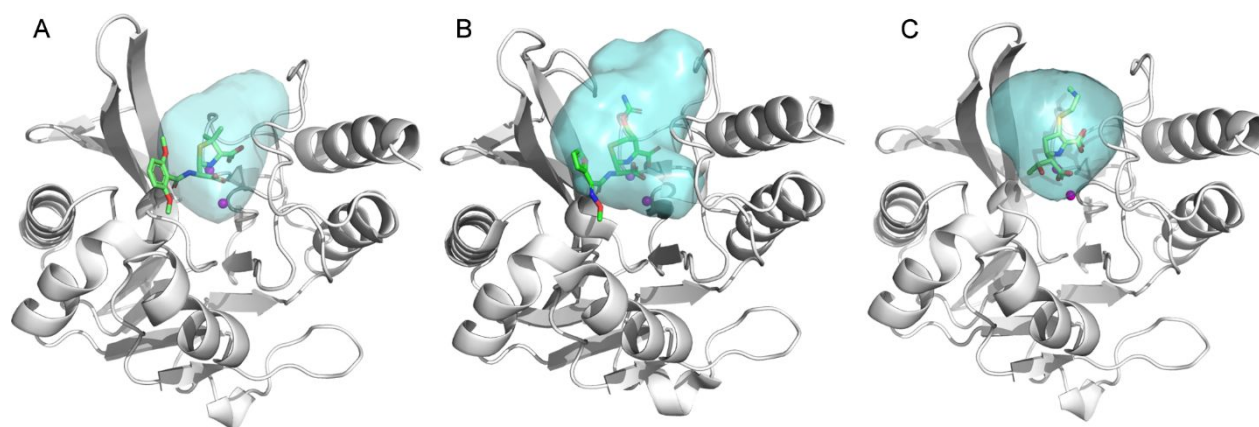
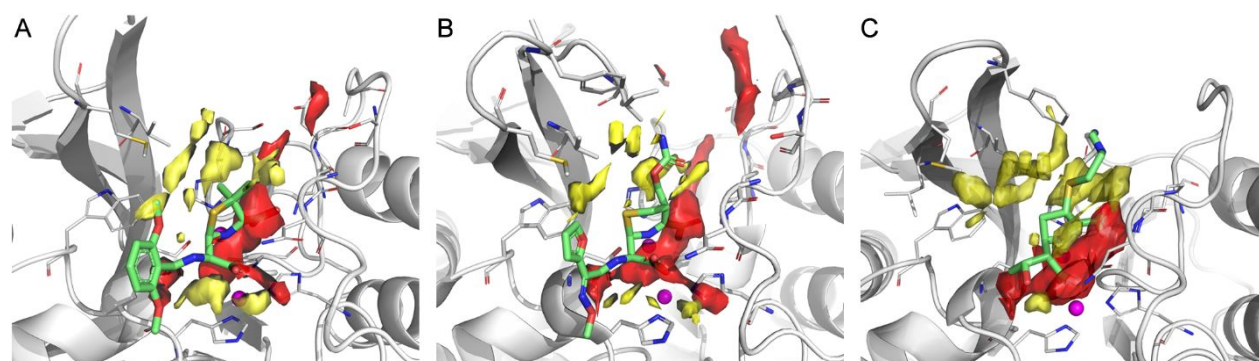


Figure 6. Superimposition of all the NDM-1 carbapenem-binding (red) and penicillin/cephalosporin (palecyan) structures reported in PDB. The L3 loop is labelled. Figures were prepared using Pymol 2.1.1.

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3 For the three pockets, the Molecular Interaction Fields (MIFs) were also determined (**Figure 8**). In
4 all cases the H-bond donor regions are properly filled by the two carboxylic groups. On the contrary,
5 the hydrophobic areas are quite poorly filled, with the only exception of the methicillin methoxy
6 group, located in a small hydrophobic contour closed to Trp93. This suggests that the design of
7 molecules having lipophilic moieties able to form stronger hydrophobic contacts with the enzyme
8 binding site could lead to the development of more effective inhibitors. It is also visible how the
9 pocket MIFs for the complexes with methicillin and cefuroxime are quite similar, while some
10 differences arise with respect to the NDM-1-IPM complex. This further supports the plasticity of the
11 binding site and the observation that a different loop arrangement occurs when carbapenems are
12 bound to the protein.
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37 **Figure 7.** Pockets calculated by flapsite for NDM-1 when complexed with methicillin (A),
38 cefuroxime (B) and IPM (C).
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55 **Figure 8.** GRID Molecular Interaction Field calculated for the NDM-1 active site when complexed
56 with methicillin (A), cefuroxime (B) and with IPM (C). Red contours correspond to hydrogen
57 bond acceptor regions, yellow contours correspond to hydrophobic areas. Only residues lining the pocket
58 have been displayed.
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NDM-1 Inhibitors

While for SBLs several mechanism-based inhibitors are available in therapy and extensive structure-based drug design efforts continues to be effective,^{51–58} a specific and efficacious inhibitor against NDM-1 is still missing in clinic. The lack of effective MBLs inhibitors could be mainly attributed to the structural diversity of the active sites among the three different MBLs classes, to the variability of the loop arrangement at the active site entrance and to the presence of several NDM-1 variants. In few years, indeed, NDM-1 has evolved in twenty new variants by single or double mutation at different positions, often enhancing the performance of NDM variant under low Zn(II) availability.^{6,59–63}

Nevertheless, we should consider the peculiar nature of MBLs binding site which might partially interfere with the design of effective and specific inhibitors, considering that the majority of substrate-protein interactions involves the two zinc ions.^{51,64} Indisputably, progresses toward a complete knowledge of the catalytic mechanism and its variability depending on the binding substrate are strictly necessary to successfully guide the rational design of clinically useful inhibitors.^{12,22,35,65}

Despite the large number of molecules disclosed as NDM-1 inhibitors, only few of them were co-crystallized with the enzyme, thus limiting our knowledge about the binding mode and the mechanism of action of reported inhibitors (Table S1).^{21,66}

Many excellent reviews have been published in the last years on NDM-1. Some of them are focused on the enzyme structural properties and on the mechanism of action, others on the epidemiology, spread and variants of NDM-1.^{12,22,67–69}

This review is aimed to provide an exhaustive report on NDM-1 inhibitors designed and developed in the last decade. We choose to focus on novel, non β -lactam like inhibitors, with particular emphasis on the most recent advances in the field. Highlights on inhibitor design, novel chemistry and proposed mechanisms of action are discussed. The inhibitors are conveniently separated and classified in groups, according to the chemical scaffold responsible for the protein recognition. The large class of non-covalent inhibitors is mainly composed by chelating agents (EDTA, AMA, NOTA), zinc coordinating agents (mercapto aliphatic acid, thiosemicarbazones, 2-mercapto-azoles, dipicolinic acids) and boronic acid derivatives. Two smaller sections are also dedicated to covalent inhibitors and to other inhibitors not ascribable to a specific chemical class.

In order to perform a systematic study from a structural and mechanistic point of view, all the discussed compounds were analysed for their structural similarity (**Figure 9**). To our knowledge, up to now, **525** NDM-1 inhibitors have been reported in literature (*see Supporting Information*). All the inhibitors were first divided into three main groups: small molecules, natural compounds and β -lactams and further clustered, based on their main chemical scaffold and similarity. In the present

review, we will focus on a systematic description of the 17 small molecules chemical clusters identified, thus including the majority of NDM-1 inhibitors so far reported in literature. Each discussed inhibitor is identified with a progressive alphanumeric code: the number indicates the library where the inhibitor belongs to, whereas the subsequent letter uniquely identifies the molecule. The reported inhibitor activity against NDM-1 is expressed in term of micromolar IC_{50} or K_i .

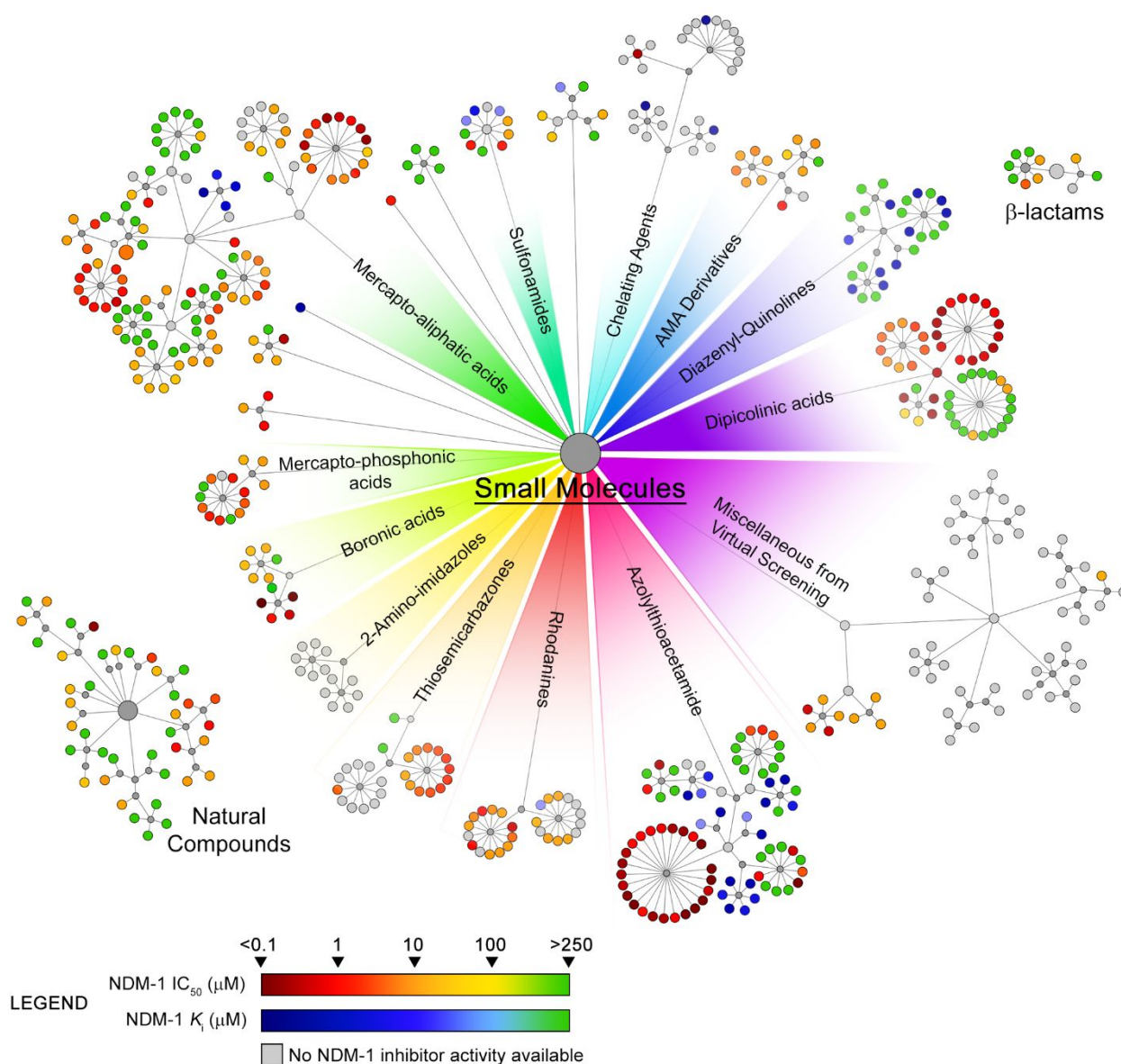


Figure 9. Dendrogram of the discussed NDM-1 inhibitors. The compounds are divided in three main groups (small molecules, natural compounds and β -lactams) and clustered according to the chemical similarity. For each molecule, the ECFP4 binary dendritic fingerprint was determined,⁷⁰ and the entire library was hierarchically clustered by Tanimoto similarity, setting a merging distance of 0.85.⁷¹ The similarity matrix was converted with Cytoscape to the corresponding dendrogram for a more rapid and intuitive visualization.⁷² In the dendrogram, each inhibitor is represented by a coloured dot at the end of each branch. Each compound is connected to the others by means of intermediate dots, closer the compounds, higher the structural similarity. All the molecules are coloured-coded according to their inhibitor activity against the enzyme, from green

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3 to red, for IC_{50} value and from green to blue for K_i value, in micromolar (see the legend). When no
4 activity against NDM-1 is reported, dots are coloured in grey.
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9 **Chelating agents as NDM-1 inhibitors**

10 *Molecules sequestering the zinc ions*

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12 **EDTA** (ethylenediamine-N,N,N',N'-tetracetic acid) is a well-known, largely used metal chelator, and
13 its capability to potentiate other antibiotics is well documented.^{73,74} Although effective, **EDTA**
14 derivatives are non-specific and highly cytotoxic, thus preventing their clinical usage.⁷⁵ The only
15 exception is represented by the correspondent disodium calcium salt (**Ca-EDTA**), actually approved
16 in Japan for the treatment of lead intoxication.⁷⁶ Yoshizumi *et al.*, inspired by the work of Aoki *et*
17 *al.*,⁷⁷ reported that **Ca-EDTA** efficaciously potentiates the antibacterial activity of IPM and MEM in
18 over-expressing NDM-1 *E. coli* strains. At the concentration of 32 $\mu\text{g/mL}$, **Ca-EDTA** was able to
19 reduce the MIC of IPM and MEM down to <2 and <4 $\mu\text{g/mL}$, respectively, whereas no synergistic
20 effects was observed in association with non β -lactams such as amikacin and ciprofloxacin. The
21 reported effect is attributed to the capability of **Ca-EDTA** to chelate the NDM-1 active site zinc ions,
22 thus blocking the enzyme and protecting the co-administered antibiotic from hydrolysis. Moreover,
23 the association of IPM/cilastin with **Ca-EDTA** was able to reduce the bacteria burden of one order
24 of magnitude in the liver of neutropenic murine model of sepsis, suggesting that the tested
25 combination could be employed in infections mediated by NDM-1 over-expressing bacteria.⁷⁸

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37 Recently, during a phenotypic screening of 500 natural extracts against an *E. coli* strain carrying
38 *bla*NDM-1, Aspergillomarasmine A (**AMA**) was identified to restore MEM activity (**Figure 10**).
39 **AMA** is a molecule that was first identified from a strain of *Aspergillus flavus oryzae* and
40 characterized for its necrotic activity on plant leaves⁷⁹ and later re-evaluated as an inhibitor of
41 angiotensin-converting enzyme (ACE).⁸⁰ In recent years, **AMA** resulted a quite interesting inhibitor
42 of NDM-1 (IC_{50} 7.0 μM) and of other MBLs as well, such as VIM-2 and IMP-7, whereas it resulted
43 completely ineffective against SBLs.⁸¹ The inhibition mediated by **AMA** is irreversible and the
44 enzymatic activity can be restored only with a supplement of Zn(II) ion. NMR and mass spectrometry
45 experiments revealed that **AMA** inhibits MBLs by sequestering the active site zinc ions, without
46 removing them from the catalytic pocket.⁸²

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54 **AMA** resulted particularly effective in targeting the less tightly bound Zn₂, whereas to sequester Zn₁
55 higher **AMA** concentrations are required.⁸³ The co-administration of **AMA** and MEM showed a
56 synergistic effect in NDM-1 expressing carbapenemase-resistant strains of Enterobacteriaceae.
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Susceptibility was restored in over 80% of clinical isolates of *Acinetobacter* and *Pseudomonas*.⁸¹ **AMA** possesses three stereogenic centers. Lederer, Moller and co-worker proposed that the absolute configuration of **AMA** was 2''R,2'R,2S or 2''S,2'S,2S.^{79,84}

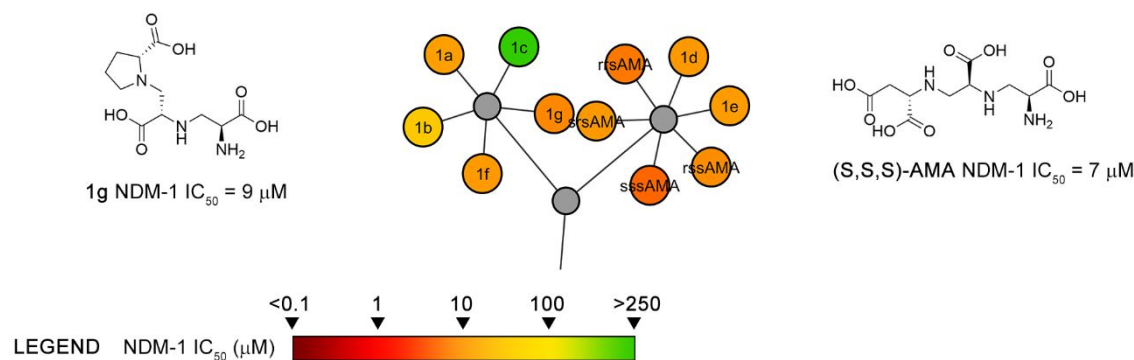
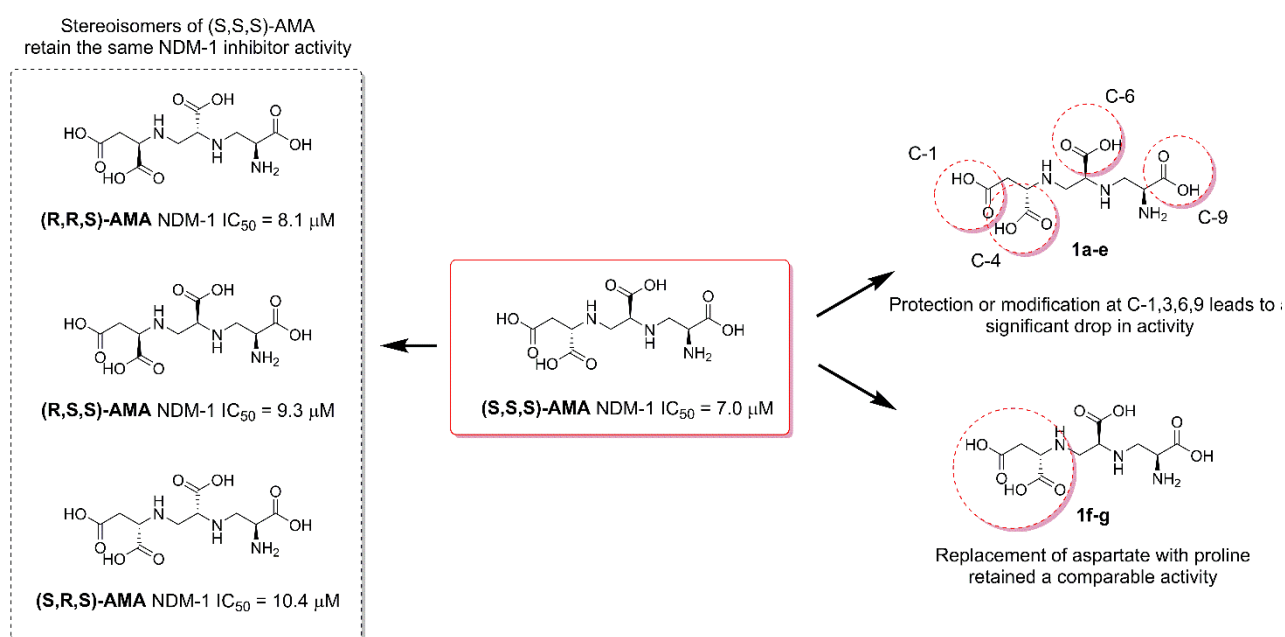


Figure 10. NDM-1 inhibitors structurally related to **AMA**.

However in 2016 Lei, Wright and co-workers carried out the first stereoselective synthesis of the molecule, reassigning the absolute configuration of the three stereocenters to (S,S,S). **(S,S,S)-AMA** showed the same inhibitory activity against NDM-1 as the first natural extract, whereas the first proposed **(R,R,S)-AMA** resulted completely inactive.^{85,86} The development of a total and stereoselective strategy for the synthesis of **AMA** opened the way to the synthetic optimization of **AMA**. Zhang and co-workers prepared seven new analogues (**1a-g**), protected or modified at the carboxyl groups in position C1 and C4 or at the amino group at the C9 position (**Figure 11**). Configurational isomers of **AMA** showed a comparable activity with respect to the natural extract suggesting that the configuration of the three stereocenters has no impact on the activity. On the contrary, the presence of carboxyl groups in C1 and C4, as well as of the carboxyl groups in C6 and C9, resulted critical for the activity, whereas the replacement of the aspartate residue with a proline retained a comparable activity (**1g**, **Figure 10**).⁸⁷ Synergy studies of **AMA** derivatives in combination with MEM on *K. pneumoniae* expressing NDM-1 showed that **AMA** stereoisomers performed better than **AMA** analogous, but only **(S,S,S)-AMA** presented the best synergic effect.⁸⁷

The capability of **AMA** to inhibit MBLs by sequestering the zinc ions suggested the use of chelating agents as a possible way to overcome MBL-mediated antibiotic resistance.⁸⁸ Somboro *et al.* explored the capability of 1,4,7-triazacyclononane-1,4,7-triacetic acid (**NOTA**, **Figure 12**) and 1,4,7,10-

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3 tetraazacyclododecane-1,4,7,10-tetraacetic acid (**DOTA**) to restore the activity of carbapenems on
4 NDM-1-producing bacteria. The MEM/**NOTA** combination restored the antibiotic susceptibility and
5 resulted 32-times better than MEM/**DOTA**. Similar synergic effect was observed with IPM/**NOTA**
6 as well.⁸⁹ Based on these promising results, Zhang *et al.* synthesized and evaluated a series of **NOTA**
7 dithiocarbamate derivatives as MBLs inhibitors (**2a-h**). Only compound **2e** (sodium 1,4,7-triazonane-
8 1,4,7-tris-carboxylodithioate, **Figure 12**) was able to restore the activity of MEM in clinical
9 carbapenem-resistant Enterobacteriaceae (CRE) carrying *bla*NDM-1. The inhibitor activity depends
10 on the capability of **2e** to chelate the zinc ion.
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41 **Figure 11.** Chemical structures and Structure Activity Relationship (SAR) of **AMA** stereoisomers
42 and derivatives.
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48 The capability of a dicarboxylic acid metal chelator (disodium 2,3-diethylmaleate, **DEM**) to
49 potentiate carbapenem activity against Enterobacteriaceae and *A. baumannii* expressing diverse MBLs,
50 including NDM-1, was phenotypically studied by Livermore *et al.*⁹⁰ **DEM** synergized with
51 carbapenems and cephalosporins against all the Enterobacteriaceae expressing MBLs. The
52 synergistic effect was more effective on strains producing VIM than NDM-1. No effect was detected
53 on SBLs expressing strains.
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58 Lately, Schnaars *et al.* reported the synthesis and the biological evaluation of a series of tris-
59 picolylamine (**TPA**) derivatives (**Figure 12**). **TPA**, a strong and selective zinc chelator, was linked
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to small peptides in order to improve its physicochemical properties (**3e-o**). These peptides were able to restore MEM activity against clinical strains of *P. aeruginosa* and *K. pneumoniae* expressing VIM-2 and NDM-1, resulting in a MIC reduction of MEM of 32-256-fold at 50 μM . The best peptide, **3k** (**Figure 12**), showed low micromolar affinity for NDM-1 and resulted active against three additional clinical strains expressing MBLs (i.e. *K. pneumoniae* VIM-1, *E.coli* NDM-1 and *E.coli* VIM-29) but not against strains expressing SBLs (i.e. GES-5, KPC-3 and OXA-48), supporting zinc chelation as mechanism of action.⁹¹

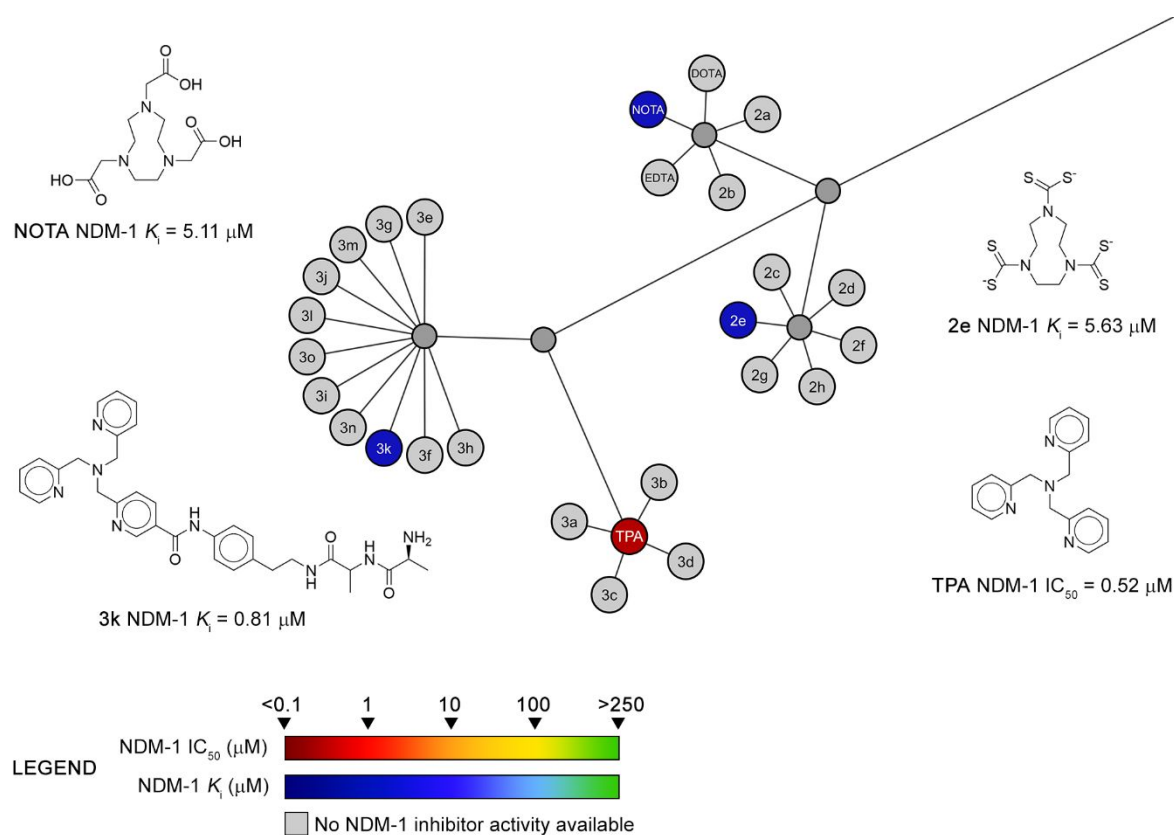


Figure 12. Chelating agent: NOTA, its derivative (**2e**), TPA and its peptide **3k**.

Molecules coordinating the zinc ions

Mercapto aliphatic acid

To design more selective and less cytotoxic MBLs inhibitors, molecules able to coordinate the zinc ions within NDM-1 binding site were designed (**Figure 13**).¹⁴

L-Captopril, a drug approved as ACE-inhibitor in the treatment of hypertension⁹² is also known as active MBLs inhibitor.⁹³ Notably, the presence of thiol moieties among MBL inhibitors is quite

common.^{94,95} Guo *et al.*, observed that **D-captopril (Figure 13)** possesses a high inhibitory activity against NDM-1 with an IC_{50} of 7.9 μM , whereas the L enantiomer resulted 25-fold less potent.⁹⁶ The binding of the drug to NDM-1 was first analysed by mass spectroscopy and a year later by X-ray crystallography. King *et al.* solved the first crystal structure of **L-captopril** in complex with NDM-1.²¹

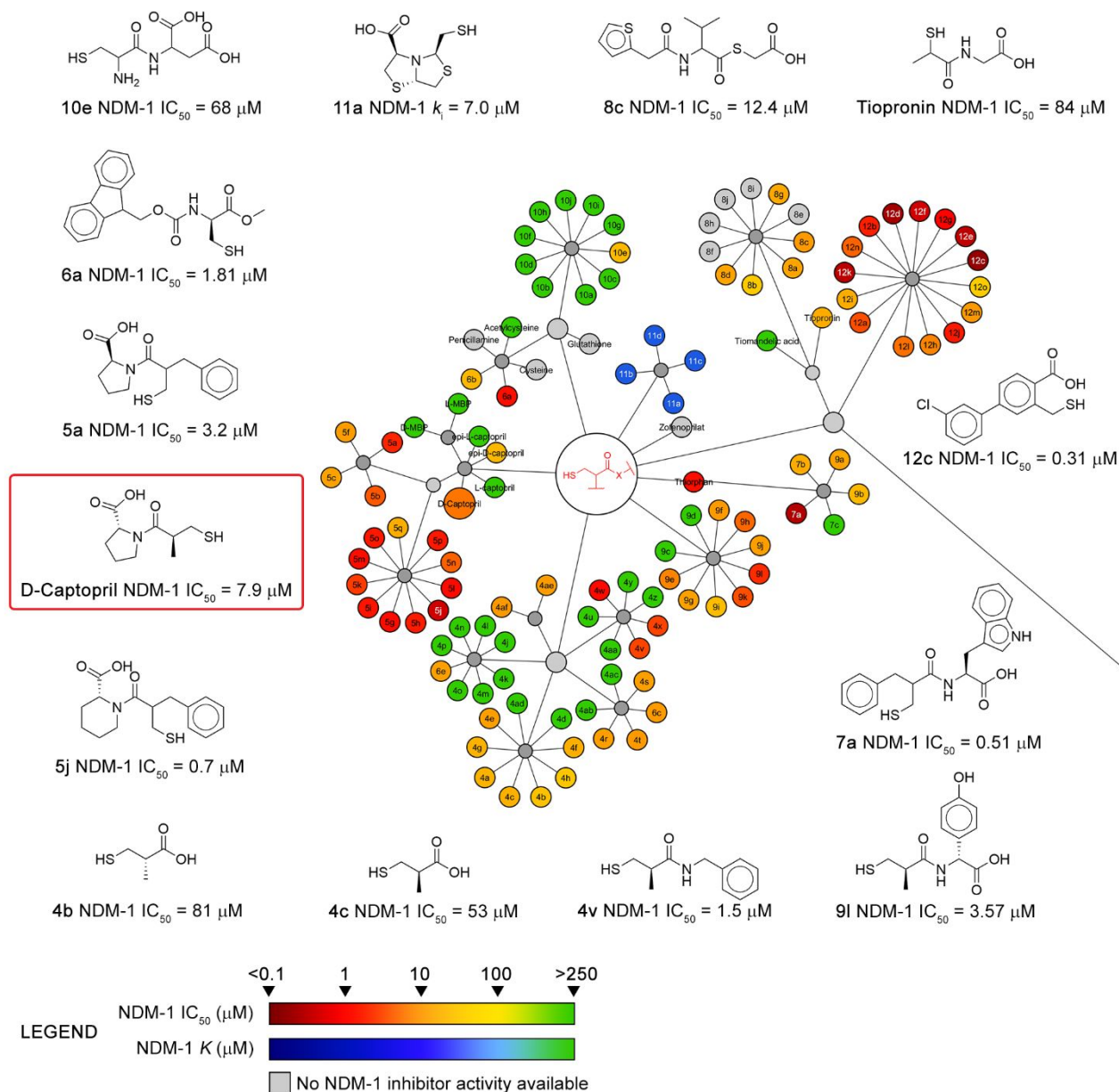
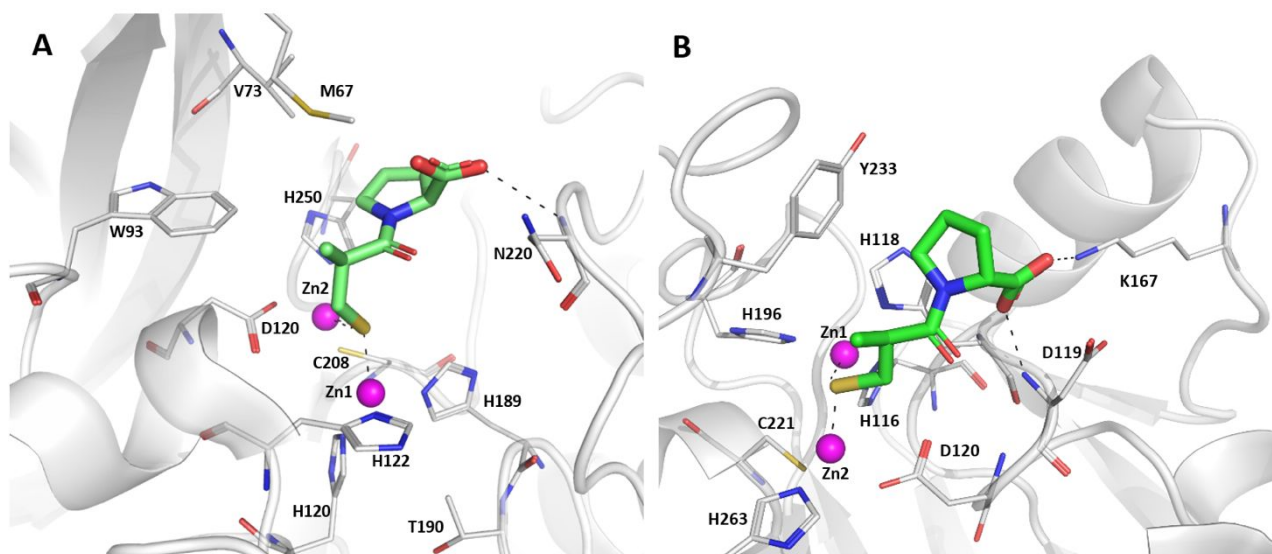


Figure 13. Mercapto aliphatic acid derivatives acting as zinc coordinating inhibitors.

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3 In X-ray structure, the thiol moiety of **L-captopril** intercalates between the two Zn ions, displacing
4 the water molecule and acting as a competitive inhibitor of NDM-1. In addition, the hydrophobic part
5 of the molecule interacts with the L3 loop, whereas the hydrophilic part of the drug is involved in a
6 hydrogen bond with Asn220, a residue involved in substrate binding and in intermediate product
7 stabilization (**Figure 14**). To estimate the binding of the more active enantiomer **D-captopril** within
8 NDM-1 active site, the crystal structure of BlaB:**D-captopril** was assumed as reference.⁹⁷ BlaB and
9 NDM-1 share a high amino acid sequence identity within the binding site as per zinc ions coordination
10 as per key amino acids involved in the catalytic activity. Therefore, it was hypothesized that **D-**
11 **captopril** could adopt the same general binding orientation in NDM-1 as that determined for BlaB.
12 Interestingly, superimposing BlaB:**D-captopril** and NDM-1:**L-captopril** X-ray structure, the two
13 diastereomers appear to bind in a different orientation, but with the thiol-moiety still intercalating
14 between the two zinc atoms and disrupting the nucleophile from its active orientation.^{21,96}
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45 **Figure 14.** **L-Captopril** binding orientation in NDM-1 (**A**) and BlaB (**B**) catalytic site (PDB code
46 4exs and 1m2x, respectively).²¹ The ligand is shown in green capped stick while the binding site
47 residues in grey capped sticks. The zinc ions are displayed as magenta spheres. The hydrogen and
48 coordination bonds are represented in black dashed lines.
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54 A study performed by Brem J. *et al.* on the inhibition of NDM-1 and other MBLs (IMP-1, VIM-2 and
55 SPM-1) by four captopril stereoisomers and the D- and L- enantiomers of captopril derivative 1-(2-
56 mercaptobenzoyl)pyrrolidine-2-carboxylic acid (**D-** and **L-MBP**) confirmed the importance of the
57 stereoisomerism for improving potency and selectivity against MBLs. **D-captopril** still remained the
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3 most active NDM-1 stereoisomer. Structural analysis showed for **D-captopril** a binding mode similar
4 to that of hydrolyzed β -lactams (PDB entry 4HL2),⁹⁸ especially penicillins.⁹⁹

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6 The ligand coordinates through the thiol moiety the two zinc ions. Thiols in MBL binding sites
7 undergo a 100-fold pK_a decrease.^{21,100} Therefore, at physiological pH the deprotonated thiolate will
8 result a better metal coordinator. An additional hydrogen bond is formed between the ligand
9 carboxylic group and the backbone nitrogen of Asn220. The carboxylic moiety, however, is quite
10 solvent exposed and the aforementioned bond does not likely stabilize the ligand, as also supported
11 by the alternative orientation assumed by Asn220 in chain B (PDB: 4exs) Hydrophobic interactions
12 are additionally formed between the methyl and pyrrolidine moieties with residues Met67 and Trp93.
13 The identification of captopril as a potent NDM-1 inhibitor able to coordinate the catalytic site zinc
14 ions represented the starting point for the development of new inhibitors bearing both thiol and
15 carboxylic moieties capable of metal ligation. In a first attempt, Klinger *et al.* screened, against NDM-
16 1, VIM-2 and IMP-7, a set of eleven approved drugs possessing a sulfhydryl moiety.¹⁰¹ Interestingly,
17 not all the selected drugs, **thiomandelic acid**, **DL-captopril**, **DL-thiorphan**, **N-acetylcysteine**,
18 **meso-2,3-dimercaptosuccinic acid**, **2,3-dimercaprol**, **D-penicillamine**, **glutathione**, **L-cysteine**,
19 **zofenoprilat** and **tiopronin** (**Figure 13**) inhibited the three considered MBLs with the same potency.
20 **D-captopril** showed a low micromolar inhibitory activity against NDM-1 in line with the affinity
21 detected *vs* VIM-2 and IMP-7. Focusing on NDM-1, **thiorphan** and **dimercaprol** resulted the most
22 active drugs but still in the low micromolar range. On the contrary, **tiopronin** showed only a modest
23 activity, whereas **N-acetylcysteine** resulted completely inactive. Thermal shift assay confirmed the
24 ligands capability of binding without sequestering the zinc ions. The binding mode of **tiopronin**
25 was confirmed by X-ray crystallography (PDB: 5A5Z).¹⁰² In the complex, the ligand thiol moiety of
26 **tiopronin** intercalates between the two zinc atoms, thus replacing the catalytic water in a similar way
27 to that observed for captopril. Compounds showing more potent inhibition and positive response in
28 thermal shift assay were further tested for synergy in combination with IPM against *E. coli*,
29 *P.aeruginosa* and *K. pneumoniae* strains over-expressing NDM-1, IMP-7 and VIM-1. **Thiorphan**
30 and **dimercaprol** were able to potentiate IPM activity reducing the MIC values from 2 to up 64-
31 fold.¹⁰¹

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33 Later, Li *et al.*, in an effort to simplify captopril structure and identify the chemical features critical
34 for molecular recognition in NDM-1, synthesized and tested a series of 3-mercapto-2-
35 methylpropanoyl amides (**4a-f**, **Figure 13**). The 3-mercapto-2-methylpropanoic acid enantiomers and
36 their methyl ester derivatives, revealing that the thiol group and the free carboxylic moiety are
37 essential for binding. The two enantiomers (**4b** and **4c**, **Figure 13**), in fact, displayed a similar affinity,
38 whereas the esterification led to a complete loss of activity. Retaining the 3-mercapto-2-
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3 methylpropanoyl moiety of captopril, the proline residue was further replaced by aliphatic and
4 aromatic amines (**4d-4ad**). Derivative **4v** (**Figure 13**) resulted the most potent NDM-1 inhibitor in
5 this series.¹⁰³
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8 Recently, Buttner *et al.* reported the investigation of a series of thiol-derivatives inspired by captopril
9 (**5a-q**, **Figure 13**). Structural modifications on the pyrrolidine ring (e.g. ring simplification,
10 contraction or expansion, ring bioisosterism and variation of the position of the acidic group) and on
11 the methyl group (e.g. introduction of an aromatic ring) were tested. SAR studies against NDM-1
12 revealed that the introduction of an unsubstituted phenyl ring (**5a**, **Figure 13**) maintained an activity
13 comparable to that of captopril, whereas the introduction of substituents on the thiophene ring led to
14 a potency decrease. All the modifications introduced on the proline-moiety of captopril led to the
15 more active derivatives **5g-o**. Interestingly, compound **5j** (**Figure 13**) resulted 7-fold more potent
16 than its enantiomer **5k**, confirming the importance of stereoisomerism in the development of NDM-
17 1 inhibitors. Docking calculations supported this evidence, predicting a key interaction between **5j**
18 and Lys211, a residue normally involved in substrate orientation and hydrolysis. Between the two
19 piperazine derivatives (**5p-q**) only **5p**, carrying a benzoyl group in position 4, resulted as potent as
20 captopril and **5j-k**. Compound **5a** and **5j** were evaluated *in vitro* in combination with IPM against
21 resistant clinical isolates. Both **5a** and **5j** showed a 16-fold MIC reduction against *E. coli* pET24a
22 T2377, but resulted ineffective against *K. pneumonia* T2301. However, captopril, assumed as the
23 reference compound, still performed best in restoring IPM activity.¹⁰⁴
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36 Other NDM-1 inhibitors, structurally related to captopril and carrying a 3-mercapto-propionic acid
37 moiety or a cysteine-based scaffold, were identified through ultrafiltration C/MS-based assay by Chen
38 *et al.* (**6a-e**, **Figure 13**), with **6a** showing low micromolar affinity for NDM-1.¹⁰⁵
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41 Similarly, combining both phenotypic and target-based screening by NMR spectroscopy on a library
42 of 92 known MBLs inhibitors, Ma *et al.* were able to identify compound **7a** (**Figure 13**) as a low
43 micromolar NDM-1 inhibitor.¹⁰⁶
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46 In an effort to discover new MBLs, Liu *et al.* synthesized and evaluated ten mercaptoacetic acid
47 thioester amino acid derivatives (**8a-j**, **Figure 13**), which showed a micromolar-nanomolar inhibition
48 of L1, a di-nuclear MBL belonging to subclass B3. Some of the thioesters resulted effective toward
49 NDM-1 and their binding mode investigated *in silico*.¹⁰⁷
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53 The authors recently published a new set of 2-substituted (S)-3-mercapto-2-methylpropanamido-
54 acetic acid derivatives (**9a-l**),¹⁰⁸ modifying a library of 3-oxoisindoline-4-carboxylate derivatives
55 active against VIM-2.¹⁰⁹ The compounds resulted to be potent nanomolar inhibitors of VIM-2 and
56 low micromolar inhibitors of NMD-1, with **9k** and **9l** being the most active in the series (**Figure 13**).
57 Kinetic enzymatic study on VIM-2 at different Zn ions concentration showed that the compounds
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3 were not strong Zn chelators, similarly to captopril. Unfortunately, no structural data against NDM-
4 1 enzyme are actually available. However, the superimposition of the available crystallographic
5 structure of VIM-2:**9I** (PDB: 5Y6E) with the X-ray structures of NDM-1 complexed with hydrolyzed
6 benzyl-penicillin and hydrolyzed cephalosporin suggested that these inhibitors bind the zinc ions and
7 the catalytically important residues. The carboxylate group of **9I** interacts in VIM-2 with Arg205, like
8 in NDM-1 the cephalosporin C4 carboxylic group interacts with Lys211, suggesting that inhibitors
9 able to mime the hydrolyzed substrate could result valuable MBL inhibitors.¹⁰⁸ Importantly, the
10 compounds showed no toxicity against HEK293T cells nor teratogenicity on embryo zebra fish.

11 Starting from the validated 3-mercapto-propionic acid moiety, Shen *et al.* recently disclosed the
12 results obtained with a series of ten oligopeptides (**10a-j**), carrying a cysteine residue as the key
13 chemical feature. The dipeptide **10e** (Cys-Asp, **Figure 13**) presented the highest potency. None of
14 the compounds showed antibacterial activity *per se*, but **10a**, **10b**, **10e** and **10g** in combination with
15 ertapenem showed synergic activity against *E. coli* and *P.aeruginosa* strains overexpressing NDM-
16 1. In particular, **10e** reduced the MIC of ertapenem to < 128 μ M against *E. coli* and *P.aeruginosa*
17 strains, at a concentration of 25 μ M. The binding mode of **10e** within the NDM-1 active site was
18 investigated by docking calculations, suggesting the formation of key interactions between the thiol
19 and Zn1 and His120, and between the aspartate and Zn2.¹¹⁰

20 A new chemical scaffold (bisthiazolidine, BZTs) was designed by Gonzales *et al.*, combining the
21 mercapto-propionic acid moiety with features of β -lactam substrates (**11a-d**, **Figure 13**). BZTs
22 bicyclic system could mime a non-cleavable β -lactam ring. While the bridging nitrogen and the
23 carboxylate interacting with Zn2 are retained, other zinc-binding groups are additionally inserted in
24 the structure. The four bisthiazolidines disclosed by the authors resulted to act as low micromolar
25 competitive inhibitors. *In vitro* NMR studies on NDM-1 producing *E. coli* strains, demonstrated that
26 the compounds are able to inhibit the hydrolysis of IPM by NDM-1 with micromolar affinity. The
27 crystal structure of the NDM-1:**11a** complex (PDB 4u4l)¹¹¹ was also resolved. **11a** orients the thiol
28 group between the two Zn ions and displaces the bridging water molecule. The carboxylic group does
29 not directly bind the Zn ions, but interacts with Lys211 by means of a water molecule.¹¹² The four
30 BZTs **11a-d** were able to reduce up to ten thousand folds the count of viable cells with respect to the
31 antibiotic alone, when assessed against NDM-1-producing clinical isolates of *K. pneumoniae*, *A.*
32 *baumannii*, and *P. rettgeri* in combination with IPM. BZTs also demonstrated to have a broad-
33 spectrum of action against other MBLs subclasses and the ability to preserve β -lactam activity against
34 important pathogens.¹¹³

35 Recently, Cain *et al.* reported the successful application of an *in silico* fragment-based design for the
36 development of B1 MBLs (NDM-1, VIM-2 and IMP-1) inhibitors. Combining fragments in the
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binding site, the benzyl thiol derivative **12c** (**Figure 13**) was identified as a possible NDM-1 competitive inhibitor. Docking calculations predicted that **12c** H-bonds through the carboxylate group to Lys224 and Zn2, the thiol group coordinates Zn1 and Zn2, while the aryl ring is involved in π - π stacking interaction with Trp93. When tested, compound **12c** showed a low micromolar affinity for NDM-1 and a submicromolar potency against VIM-2 and IMP-1. The replacement of the distal aromatic ring with substituents or heterocycles did not affect the potency of the designed inhibitors with respect to the starting lead. Compounds **12c** and **12i-o** were assayed in biological tests in combination with MEM against *E. coli* and *K. pneumoniae* NDM-1 producing strains. The compounds reduced the MIC of MEM alone by 2-16-fold, with compound **12n** being the best candidate.¹¹⁴ Since mercapto-carboxylic acids demonstrated to be valuable MBLs inhibitor scaffolds, Skagseth *et al.* explored the importance of the carboxylic group by bioisosteric replacement (**Figure 15**). Starting from compound **13a** (**Figure 15**), the carboxylic group was replaced by phosphonate esters, phosphonic acid and tetrazoles. The effect of the chain length and of the mercapto functionality were also explored (**13a-p**) against VIM-2 and NDM-1. With respect to NDM-1, almost all the compounds resulted more active than the reference one **13a**.

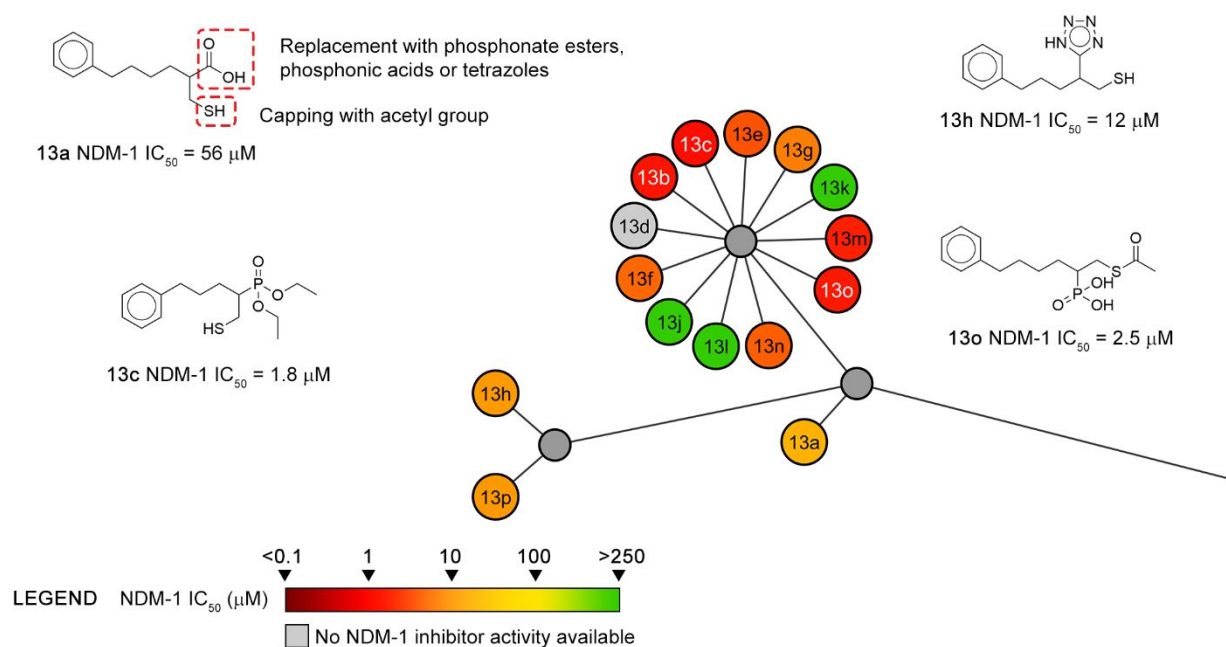


Figure 15. Mercapto aliphatic acid derivatives as NDM-1 inhibitors: exploring carboxylate bioisosters.

The most active compounds always presented a thiol (free or acetylated) and a phosphonic acid or ester in their structure. Tetrazole derivatives (**13h**, **Figure 15**) generally resulted less effective than

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3 phosphonate compounds. Analogues **13c**, **13o** and **13p** were successfully crystallized only with VIM-
4 2. Therefore, to assess the binding mode of these inhibitors within NDM-1 active site, docking
5 calculations were performed and the binding mode compared to the X-ray pose observed in VIM-2.
6 The inhibitors were predicted to bind the two catalytic zinc ions through the thiol functionality and
7 Asn233 residue through the phosphonate group, as for VIM-2. However, the phenyl ring of the
8 inhibitors resulted less stabilized by hydrophobic interactions in NDM-1 with respect to VIM-2,
9 somehow explaining the corresponding slightly lower activity. All the inhibitors were tested for
10 synergic activity with MEM against MBL-producing clinical strains of *P. aeruginosa* and *K.*
11 *pneumoniae* showing only modest biological activity.¹¹⁵
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20 *Isatin- β -thiosemicarbazones and spiro[indole]thiadiazoles*

21 Recently, following a drug repurposing approach, Song *et al.* identified **methisazone** (**Figure 16**) as
22 a weak NDM-1 inhibitor.¹¹⁶ **Methisazone**, an old drug used for the treatment of smallpox
23 infections,¹¹⁷ is structurally related to isatin, an endogenous natural product with a wide range of
24 biological activities. Moving from this, Song *et al.* synthesized and tested *in vitro* several isatin- β -
25 thiosemicarbazone derivatives, all sharing the methisazone scaffold. All the thirteen compounds
26 (**14a-n**) showed a low micromolar NDM-1 inhibitor activity, with **14n** (**Figure 16**) being the most
27 active one. Docking calculations predicted the sulphur atom to be oriented at coordinating distances
28 from zinc ions.¹¹⁶
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36 Falconer *et al.* reported a series of zinc-selective 3'H-spiro[indoline-3,2'-[1,3,4]thiadiazol]-2-one
37 derivatives (structurally related to isatin-3-thiosemicarbazones) able to potentiate the antibacterial
38 activity of β -lactams in *E. coli* strains overexpressing various MBLs (**15a-m**). One of the disclosed
39 analogues, compound **15a**, was already reported to perturb iron homeostasis in bacterial cells.¹¹⁸ The
40 researchers, interested in exploring the zinc versus iron specificity, introduced a range of chemical
41 modifications on **15a** main core. Selective modifications at the R1 position resulted in a zinc-specific
42 profile. The most selective compound **15i** (**Figure 16**), in combination with MEM against clinical
43 isolate of *K. pneumoniae* harbouring *bla*NDM-1, restored susceptibility to the carbapenem. Moreover,
44 compound **15i** resulted able to potentiate the activity of other carbapenems as well e.g. IPM,
45 doripenem, and biapenem, whereas synergism was not observed in combination with non-
46 carbapenem β -lactams.¹¹⁹
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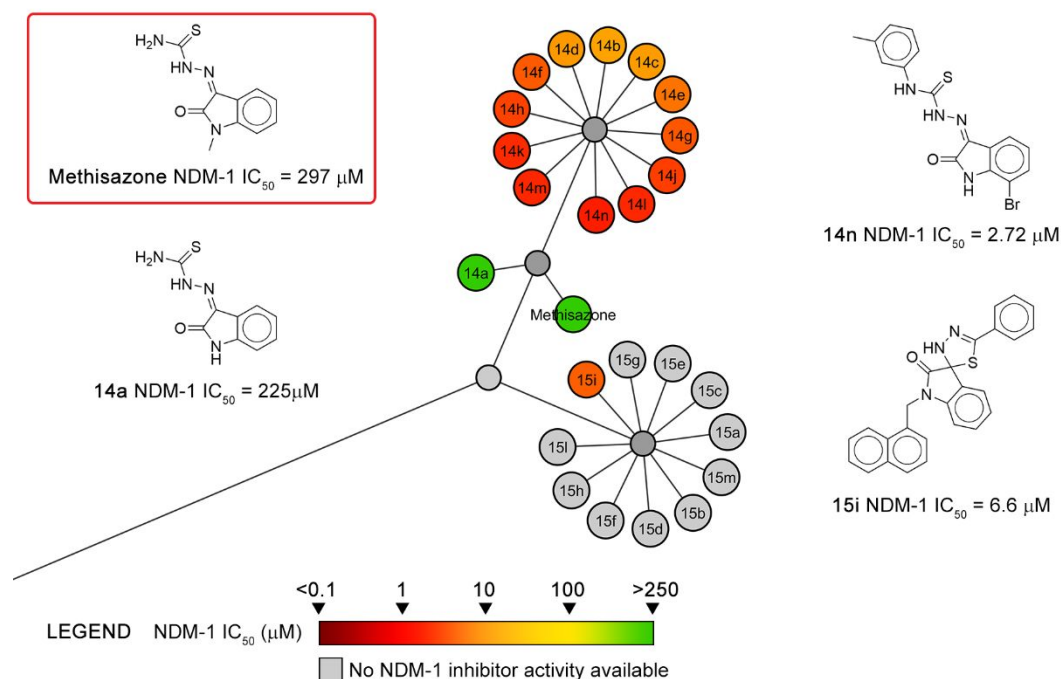


Figure 16. Methisazone optimization: exploring isatin-3-thiosemicarbazone and 3'H-spiro[indoline-3,2'-[1,3,4]thiadiazol]-2-one as valuable chemical scaffolds.

Azolythioacetamide

Starting from a previous work on azolythioacetamide as MBLs inhibitors,^{120,121} Zhang *et al.* reported the synthesis and evaluation of new diaryl-substituted azolythioacetamides (**16a-r**, **Figure 17**) as sub-micromolar inhibitors of NDM-1. Thirteen derivatives resulted to behave as mixed, low micromolar inhibitors toward NDM-1 and four of them showed broad-spectrum activity against other MBLs such as CcrA, ImiS and L1. Docking predictions for **16d** and **16i** (**Figure 17**) suggested that the deprotonated triazoles coordinate the two zinc ions, whereas the N-phenylthioacetamide moiety binds to an alternative binding site. In particular, the 2-phenolyl hydroxyl group of **16i** resembles the hydrolyzed benzyl-penicillin as observed in the crystal structure of NDM-1, thus mimicking the C3 carboxylate and interacting with Lys211.¹²² Based on these results, Zhai *et al.* replaced the azolythioacetamide scaffold with triazolylthioacetamide in a library of twenty-four new derivatives (**17a-x**, **Figure 17**), which all showed sub-micromolar IC_{50} . Kinetic characterization of compounds **17v** and **17r** (**Figure 17**) revealed a partially mixed mechanism of inhibition with K_i of 0.49 and 0.63 μM , respectively.¹²³ Docking calculations on these two inhibitors suggested binding orientations similar to the azolythioacetamides analogues.¹²²⁻¹²³ To enrich the structure-activity relationship among azolythioacetamide derivatives (**18a-ab**, **Figure 17**), the authors explored four homologous

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2
3 of the azolyl ring (triazole, oxadizole, thiadiazole, and 1-amino-triazole) and structural modifications
4 on the aromatic portion of the central scaffold.¹²⁴ Compounds **18a-s**, possessing unsubstituted
5 benzimidazole or benzoxazole rings, resulted to selectively inhibit B2 ImiS (IC₅₀ in the low-sub
6 micromolar range), without showing any significant activity against NDM-1. On the contrary, the
7 introduction of a nitro group in position 5 on the benzimidazole scaffold (**18t-ab**, **Figure 17**)
8 improved the activity toward NDM-1, suggesting that the nitro group could be involved in binding
9 the Zn ions. Docking calculations on compound **18aa** (**Figure 17**), in fact, suggested a completely
10 different binding mode with respect to that observed for ImiS analogue inhibitors. The triazole ring
11 of **18aa** does not interact with the two Zn ions, whereas the nitro group is able to intercalate Zn1 and
12 Zn2 in NDM-1 active site. Kinetic studies performed on the best inhibitor revealed a competitive and
13 uncompetitive mixed inhibition kinetic pattern that need further investigation. Finally, synergy
14 studies, conducted in combination with IPM against clinical strains of *E. coli* expressing ImiS and
15 NDM-1, showed a 2-4 folds MIC reduction consistent with the *in vitro* activity.

16
17 The effectiveness of the 2-mercapto-triazole scaffold was further validated by a recent structure-based
18 virtual screening performed by Spyrakis *et al.* on a large database of available chemicals.¹²⁵ All the
19 31 potential active candidates were characterized by the presence of electron-donor groups able to
20 coordinate the zinc ions. The best inhibitors **19a** and **19b** (**Figure 17**), sharing a 2-mercapto-triazole
21 moiety showed a *K_i* against NDM-1 of 0.72 and 1 μM, respectively. Based on the docking prediction,
22 compounds **19a** and **19b** interact with the zinc ions via the thiol and the nitrogen of the triazole ring,
23 whereas the substituent in position 5 on the heterocyclic ring points toward the hydrophobic hot spots
24 of the catalytic pocket (loop 3). Further interactions involved nitrogen-1 of the ring with Lys211.
25 Moreover, compound **19b** contacts both zinc ions with the thiol moiety and forms additional
26 interaction with Asn220. Both compounds **19a** and **19b** were tested in combination with MEM via
27 microdilution drug–drug interaction assays against *E. coli* clinical isolate carrying *bla*NDM-1, and
28 against *E. coli* BL21 (DE3) recombinant strain overproducing NDM-1. Both of them reduced the
29 MIC of MEM in the clinical isolate and in the recombinant strain up to 16-fold. Inhibitors possess a
30 full synergic profile as *per* FICI (Fractional Inhibitory Concentration Index) results.¹²⁵ The work
31 performed by Spyrakis *et al.* represents, among others here cited, a successful story of *in silico* studies
32 applied to NDM-1 inhibition.^{67,125–127} The application of high-throughput docking methods along
33 with the availability of large chemicals databases can represent a powerful tool in the identification
34 of new NDM-1 inhibitors, allowing the identification of new compounds to inhibit clinically-relevant
35 MBLs.

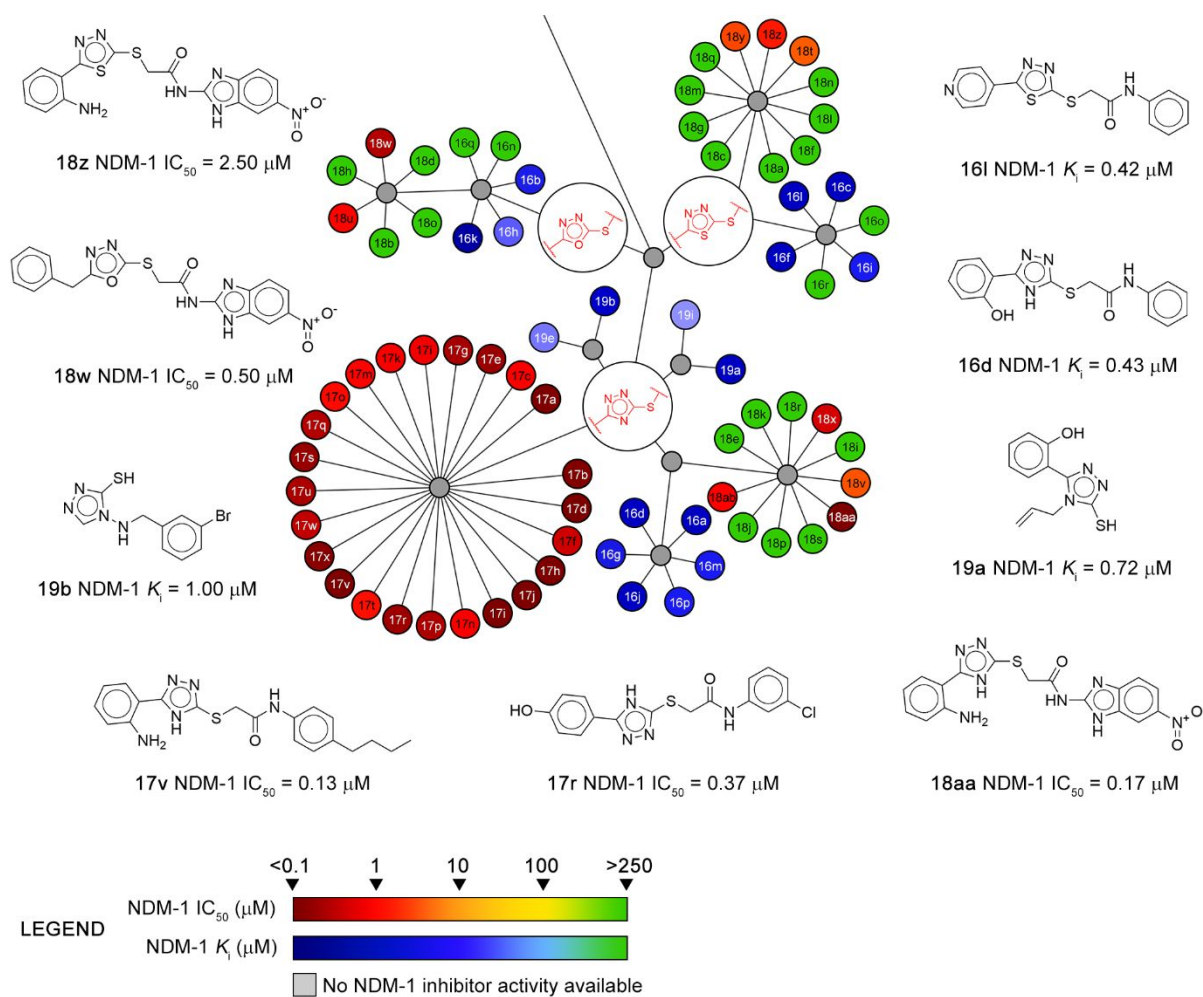


Figure 17. 2-mercapto-azoles derivatives as NDM-1 inhibitors.

Rhodanine

Rhodanines have been reported as effective non transitional state analogues of SBLs¹²⁸ and Penicillin Binding Proteins (PBPs).¹²⁹ Recently, Spicer *et al.* observed the capability of this chemical scaffold to inhibit also B1 MBLs, as VIM-2 and IMP-1.¹³⁰ In an effort to develop broad-spectrum MBL inhibitors, Xiang *et al.* designed and synthesized twenty-six rhodanine derivatives (**20a-aa**, **Figure 18**), exploring diverse aromatic rings and substituents on the core ring.¹³¹ The compounds were assessed for their enzymatic activity against B1 MBLs (NDM-1 and VIM-2), B2 MBL (ImiS) and B3 MBL (L1). In particular, for NDM-1, compounds **20b**, **20g**, **20i-l**, **20n-q**, and **20t-z** showed an interesting potency, with **20o** (**Figure 18**) being the most active. All the compounds showed submicromolar/nanomolar activity against L1 and VIM-2 and low micromolar activity against ImiS. In particular, **20y** (**Figure 18**) resulted the most potent broad-spectrum inhibitor in the series. The binding mode of **20y** in NDM-1 predicted by docking simulation is shown in **Figure 19**. The nitro

group contacts a zinc ion and Asp124, while the benzene ring at the R1 position forms π - π stacking interaction with Phe70. Further studies performed by Brem *et al.* suggested that thienolate, the hydrolysis product of rhodanine, has activity against MBLs as well.¹³²

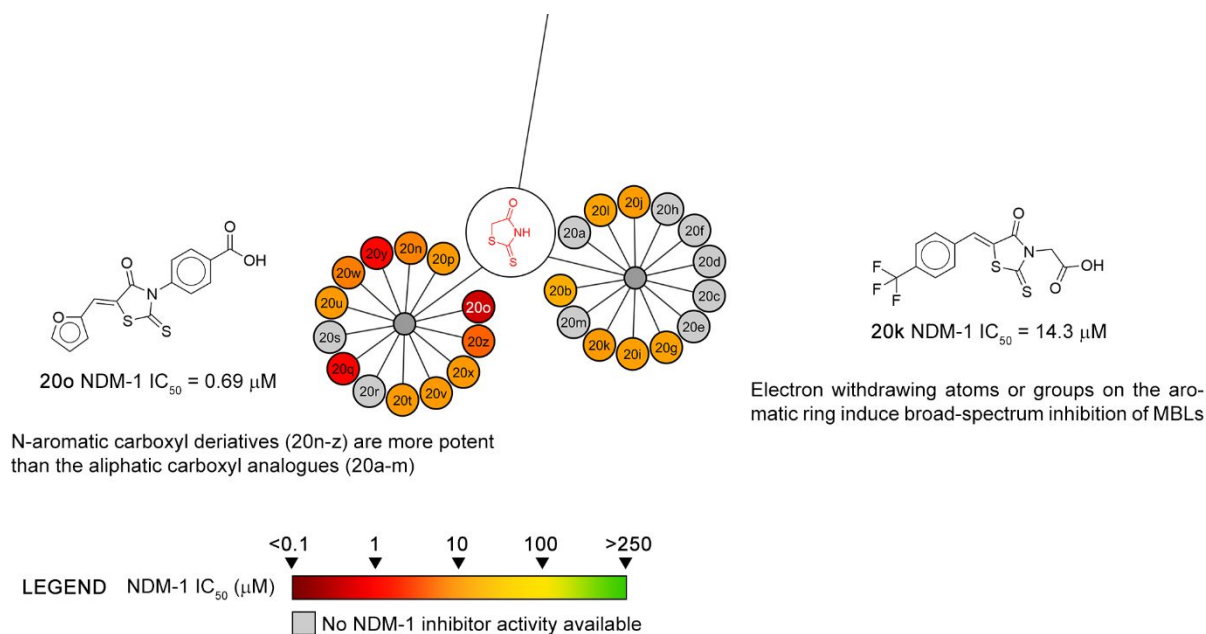


Figure 18. Rhodanine derivatives: chemical structure and inhibitor activity against NDM-1.

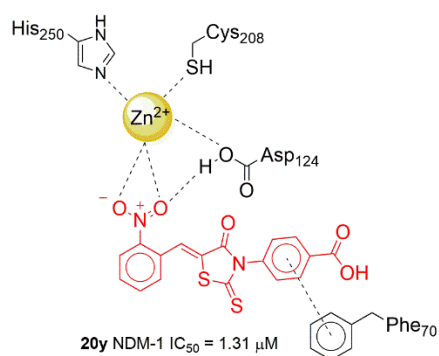


Figure 19. Derivative 20y predicted binding mode and enzymatic inhibitor activity vs NDM-1.

Following this finding, the authors prepared thienolate analogues (20aa) of 20t, finding that the compounds were able to inhibit only VIM-2 and L1, but not NDM-1 and ImiS. The structure–activity relationship revealed that N-aromatic carboxyl (20n-z) derivatives are more potent than the aliphatic carboxyl analogues (20a-m), implying that the phenyl ring may interact with the hydrophobic pocket of MBLs. In addition, diaryl-substituted rhodanines with electron-accepting atoms or groups (20t-z)

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2
3 exhibit broad-spectrum inhibition of MBLs. The co-administration of the compounds at a
4 concentration of 32 $\mu\text{g}/\text{mL}$ with cefazolin resulted in a 4-8 fold MIC reduction in *E.coli* strains
5 expressing NDM-1.¹³¹
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7

10 *Dipicolinic acid*

11
12 Chen *et al.* recently reported the results obtained with a fragment-based drug discovery approach, by
13 which 2,6-dipicolinic acid was identified (**DPA**, **Figure 20**) as a valuable chemical scaffold for the
14 development of new NDM-1, and related MBLs (IMP-1 and VIM-2), inhibitors.¹³³ **DPA** showed an
15 IC_{50} of 520 nM toward NDM-1 and was chosen for further chemical elaborations. Forty-seven **DPA**
16 derivatives (**21a-aq**, **Figure 20**) were synthesized and divided into three subseries. The first series
17 consisted of compounds obtained by substituting one of the carboxylic moieties of **DPA** with various
18 amide (**21a-r**, **Figure 20**). The second series consisted of **DPA** derivatives substituted in position 4
19 with aliphatic and aromatic rings connected with an amine linker (**21s-ab**, **Figure 20**). Finally, the
20 third series consisted of biphenyl-DPA derivatives (**21ac-aq**, **Figure 20**). The first series (**21a-r**)
21 resulted poorly active against NDM-1, with the only exception of compounds **21i** and **21l**. The second
22 series (**21s-ab**) resulted more potent, with IC_{50} in the low micromolar range. More interestingly, the
23 third series (**21ac-aq**) showed sub-micromolar IC_{50} . Among all the prepared derivatives, **21af** was
24 the best identified inhibitor with nanomolar affinity. Further investigations revealed that, whereas
25 **DPA** displayed a propensity to chelate metal ion from NDM-1, **DPA**-derivatives (such as **21aq**) can
26 form a stable NDM-1:Zn(II):inhibitor ternary complex. MIC assays revealed the ability of **21aq** to
27 reduce IPM MICs up to 32-fold vs *E. coli* and up to 16-fold vs *K. pneumoniae* strains carrying
28 *bla*NDM-1.¹³³
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32 Starting from the **DPA** scaffold, Hinchliffe *et al.* recently reported the discovery of 6-
33 phosphonomethylpyridine-2-carboxylates as MBLs inhibitors (**22c-f**, **Figure 20**).¹³⁴ Compounds
34 containing a phosphonate moiety are known to chelate zinc ions and to inhibit metalloenzymes.¹³⁵ In
35 addition, some phosphonates have been already reported as SBLs inhibitors, resembling the
36 tetrahedral intermediate of the hydrolytic path.¹³⁶⁻¹¹⁵ The authors replaced one of the **DPA** carboxylic
37 groups with a phosphonate, resulting in compounds **22c-e**. In compounds **22a** and **22b** one of the
38 carboxylic group of **DPA** was removed without introducing the phosphonate, to evaluate the effect
39 of the two carboxylic moieties in **DPA**. In **22f** both carboxylic groups were removed, introducing the
40 phosphonate, to estimate the prevalence of the two groups. All the six compounds were assayed for
41 their inhibitor activity against four MBLs (VIM-2, NDM-1, IMP-1 and L1). Focusing on NDM-1,
42 compounds **22a-b** resulted inactive, highlighting the importance of having two carboxylic moieties.
43
44 On the contrary, phosphonates **22c-e** showed interesting submicromolar activity. The presence of
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both carboxylic and phosphonic acids seemed to be an important feature to achieve inhibition, whereas the presence of phosphonic acid alone (**22f**) was not enough to maintain potency ($IC_{50} > 1000 \mu\text{M}$). The superposition of the IMP-1:**22c** complex with NDM-1:hydrolyzed cephalixin showed how **22c** (**Figure 20**) replicates some aspects of interactions of MBLs with their β -lactam substrates. Compound **22c** was assessed for *in vitro* studies in combination with MEM against clinical isolates overexpressing MBL. At a concentration of 64 mg/L, **22c** was able to reduce the MIC of MEM up to 256 folds against *K. pneumoniae* expressing NDM-1.¹³⁴

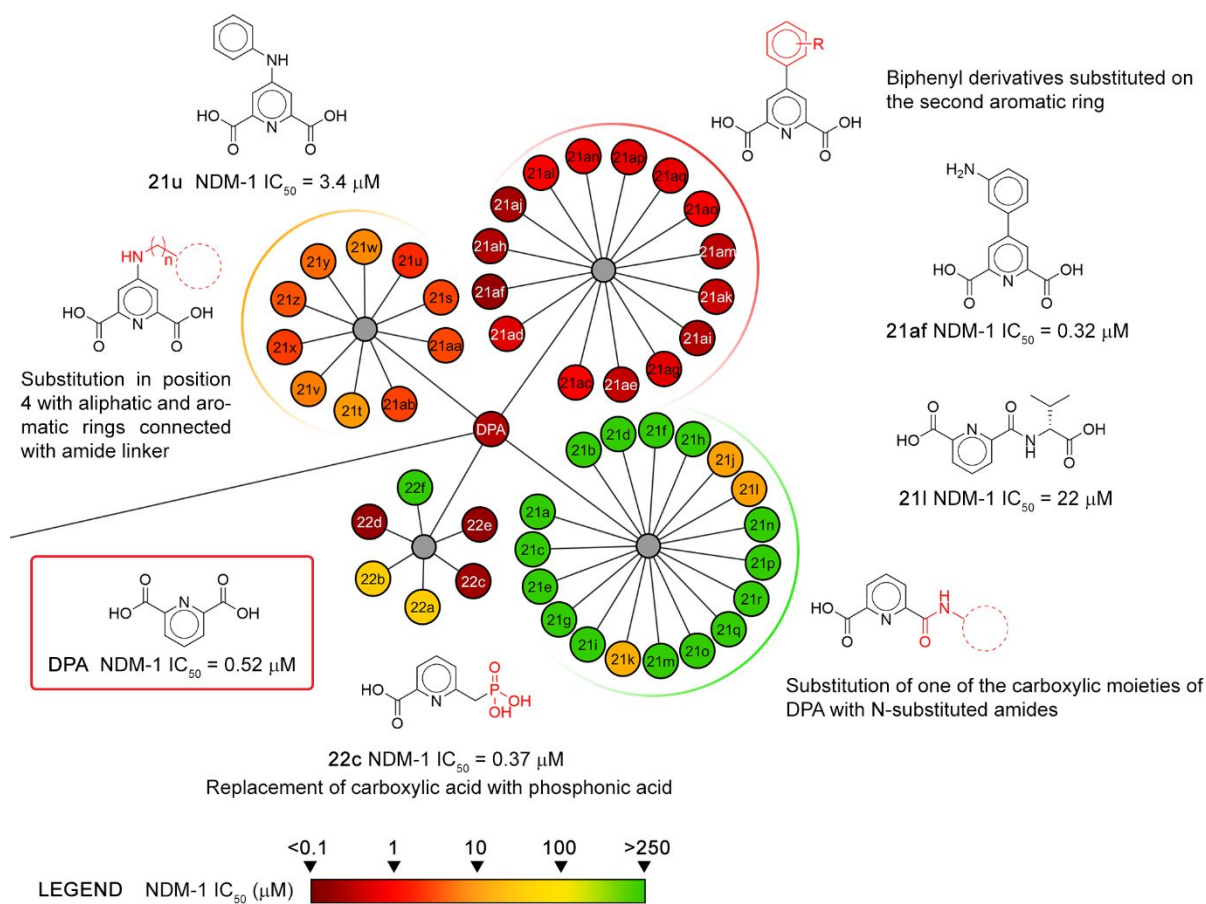


Figure 20. Detail of NDM-1 inhibitors dendrogram, focusing on dipicolinic acid (DPA) derivatives.

Cyclic and acyclic boronic acids

Inhibitors able to mimic the substrate transition state are well described in the literature for both SBLs and PBPs.⁵¹ Tetrahedral intermediates as boronic acid derivatives mimic the transient oxyanionic specie produced by the nucleophilic attack of the catalytic serine on the β -lactam carbonyl. The

hydrolysis catalysed by MBLs evolves through the formation of a tetrahedral intermediate as well, therefore this inhibition strategy could be exploited also to target MBLs. Vaborbactam (VAB; formerly RPX7009) is a cyclic boronic acid with potent inhibitory activity against class A and C BLs. It is used in therapy in combination with MEM to restore the antibiotic activity against *K. pneumoniae* carbapenemase (KPC-2). However, VAB does not inhibit class B nor class D carbapenemases.^{137,138} To identify more potent broad-spectrum inhibitors Brem J. *et al.* investigated the activity of other cyclic boronic acid derivatives (**23a-e**, **Figure 21**) against a panel of SBLs and MBLs (including NDM-1). All five compounds showed submicro/nanomolar inhibitor activity against NDM-1 and other MBLs and SBLs, acting as the first reported dual inhibitors. In particular, derivatives **23c** and **23e**, bearing an aromatic side chain in a position corresponding to β -lactam R₁ side-chain, resulted potent NDM-1 inhibitors (**Figure 21**).

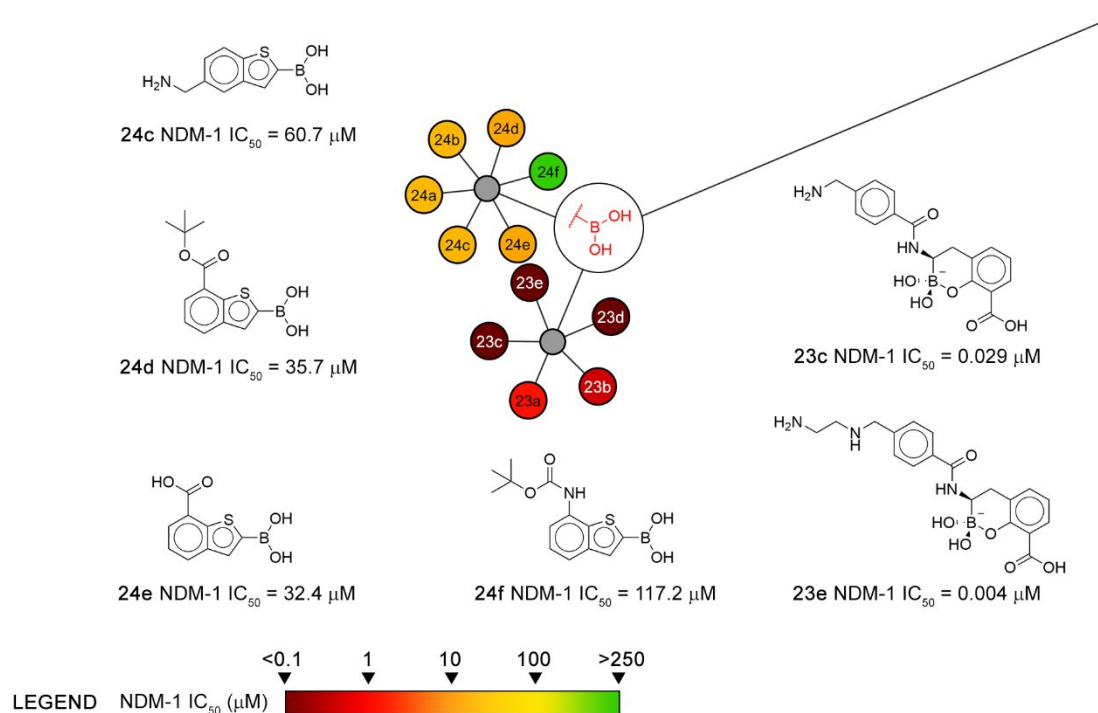


Figure 21. Cyclic and acyclic boronic acids as dual BLs inhibitors

The X-ray crystallographic structures of BcII and VIM-2 in complex with **23c** revealed binding modes similar to those observed in B1 MBLs-hydrolyzed β -lactams complexes: (i) the C-3 carboxylate coordinates both Zn²⁺ and Lys211 (NDM-1 and BcII) or Arg205 (VIM-2); (ii) the bicyclic

phenyl-boronate ring of **23c** is positioned similarly to the cephalosporin dihydrothiazine ring establishing hydrophobic interactions with the conserved Trp87 and Phe61 residues; (iii) the side chain of **23c** assumes the same orientation and binding mode of the side chain of cephalosporins; (iv) the C-6 carboxylate of the hydrolyzed β -lactam coordinates Zn1 and H-bonds with Asn220 side chain; (v) the two ‘exocyclic’ boron-bound hydroxyls mime the binding modes of the oxyanion intermediate (**Figure 22A**). Compound **23c** was tested in biological assays in combination with MEM against recombinant *K. pneumonia* and clinical strains of *K. pneumonia* and *E. coli*. These strains all carry NDM-1, together with multiple SBLs of different classes. **23c** was able to reduce the MIC of MEM in all the NDM-1 expressing strains, in the best case up to 64 folds.¹³⁹

Interestingly, boronic acids have been used for many years for rapid BLs detection in phenotypic screening, chromogenic tests and double-disk diffusion tests. To this extend, Santucci *et al.* recently reported the development and characterization of a small library of acyclic boronic acids (**24a-f**, **Figure 21**) targeting both SBLs and MBLs, NDM-1 included.^{140,141} The described compounds showed a low micromolar inhibitor activity against SBLs (i.e. AmpC, CTX-M-15 and KPC-2), while compounds **24d** and **24e** showed activity also toward MBLs, thus representing the first case of acyclic boronic acids with an extended spectrum profile (Class A-D). From docking calculations, **24a-f** were predicted to coordinate the two zinc atoms by means of the boronic group and to interact with key catalytic residues (**Figure 22B**). The co-administration of **24f** with ceftazidime to clinically isolated *E. coli* strains overexpressing NDM-1 revealed a reduction of the ceftazidime MIC up to 32 folds.¹⁴²

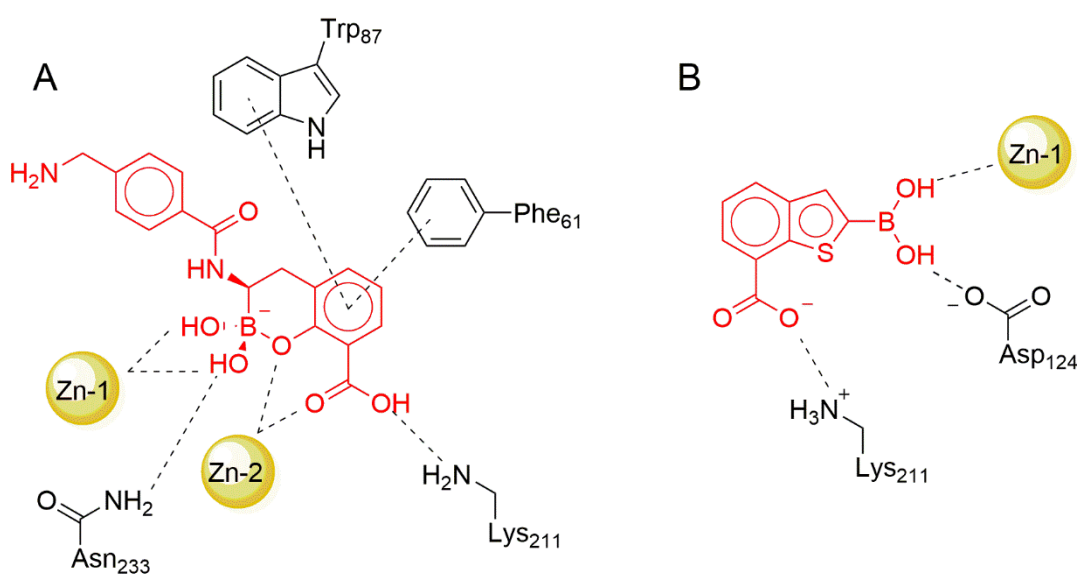


Figure 22. A) Compound **23c** binding mode within BcII active site;¹³⁹ B) Compound **24e** predicted binding mode within NDM-1 active site.¹⁴²

1.1. Covalent inhibitors

Several β -lactams have been reported to perform a covalent and irreversible inhibition toward MBLs.^{129,143} Thomas *et al.* observed how **cefactor** (**Figure 23**) is able to inhibit in a time-dependent and irreversible manner NDM-1, with millimolar affinity. Unfortunately, supratherapeutic doses (>60 folds than the therapeutic plasma concentration) are needed to effectively inhibit NDM-1, thus preventing the use of this drug for the treatment of NDM-1-mediated bacterial infections. In particular, kinetic analysis, site-directed mutagenesis and mass spectrometer assays revealed that at lower concentration, **cefactor** behaves as a typical substrate and is released after hydrolysis, whereas at higher concentration it accesses an alternative binding mode, involving Lys211, leading to irreversible inactivation.¹⁴⁴

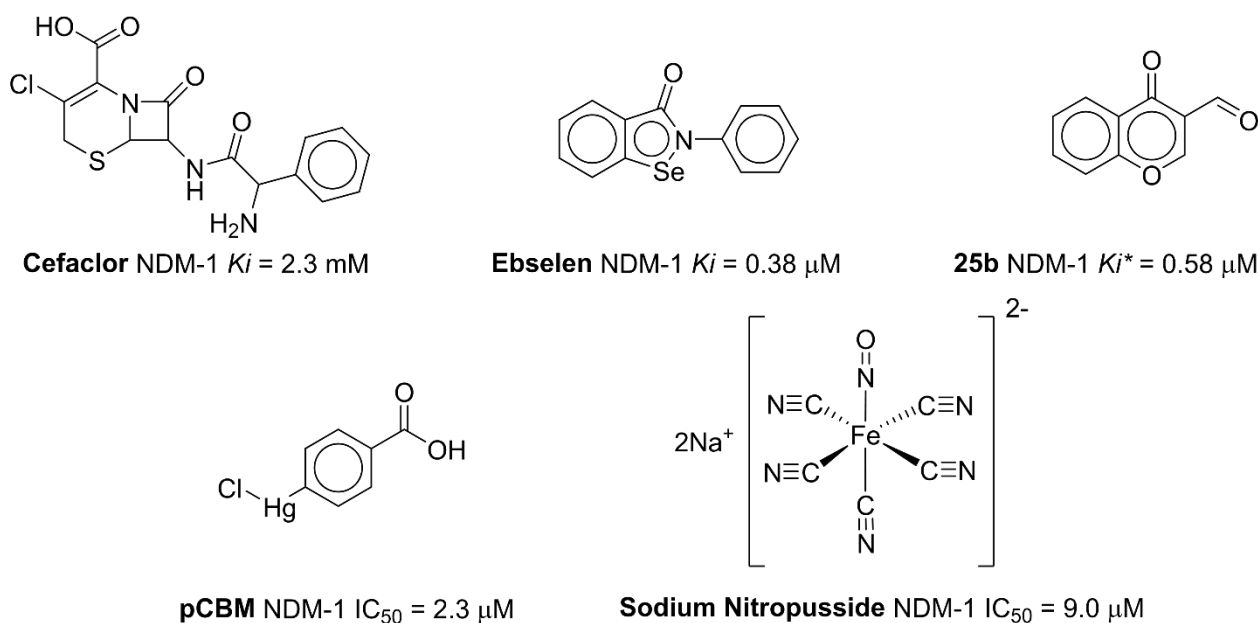


Figure 23. Covalent NDM-1 inhibitors: chemical structures and affinities.

In 2015, Chen *et al.*, through a cell-based screening, reported the discovery of **ebselen** (**Figure 23**) as a new promising NDM-1 inhibitor. **Ebselen** is a drug currently in human clinical trials for the treatment of cerebral ischemia and stroke, with low toxicity in animal model ($LD_{50} > 6180$ mg *per os*).¹⁴⁵ **Ebselen** is a selenium-containing compound able to inhibit the activity of NDM-1 in a time- and concentration-dependent manner, suggesting a covalent reversible interaction with the enzyme. Mass spectrometer studies revealed the capability of **ebselen** to tightly bind NDM-1 *via* the formation of a covalent bond with Cys208 side-chain, disrupting the coordination with Zn^{2+} that is consequently

removed from the active site (**Figure 24**). **Ebselen** is also able to reduce the MIC of ampicillin and MEM by 16- and 128-fold, respectively, thus restoring the activity of the two antibiotics on NDM-1 producing *E.coli* strains.¹⁴⁶ Recently, Jin *et al.* reported the successful structural optimization of **Ebselen**, through the generation of a library of forty-six 1,2-benzisoselenazol-3(2*H*)-one derivatives.¹⁴⁷ One of these compounds exhibited potent synergic activity with MEM against a panel of clinical NDM-1-producing Enterobacteriaceae isolates.

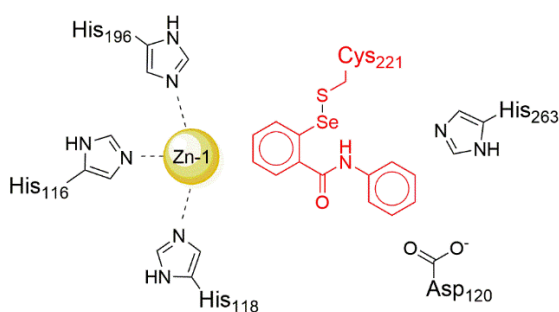


Figure 24. Covalent binding of Ebselen with Cys221 in NDM-1 active. Adapted with permission from Chiou, J.; Wan, S.; Chan, K. F.; So, P. K.; He, D.; Chan, E. W. C.; Chan, T. H.; Wong, K. Y.; Tao, J.; Chen, S. Ebselen as a Potent Covalent Inhibitor of New Delhi Metallo- β -Lactamase (NDM-1). *Chem. Commun.* **2015**, 51 (46), 9543–9546. Copyright 2015 Royal Chemical Society.

Christopeit *et al.* identified, by surface plasmon resonance (SPR), a set of four fragments inhibiting both NDM-1 and VIM-2. Compound **25a**, 3-cyanochromone, resulted the best fragment targeting NDM-1 with a K_d of 181 μ M.¹⁴⁸ The compound was modified in the 3-formyl-chromone derivative (**25b**, **Figure 23**),¹⁴⁹ which showed a strong time dependent IC_{50} , going from 200 μ M with no incubation to 2 μ M after a 10 min incubation. The covalent inhibition mode was confirmed and studied by mass spectrometry and mutagenesis, highlighting the involvement of Lys211 in the formation of a Schiff base with the aldehyde in position 3 of the chromone. Surprisingly, **25b** resulted a selective inhibitor of NDM-1, without showing any significant activity against VIM-2. The absence of Lys211 in VIM-2 avoids the capability of **25b** to covalently bind NDM-1, explaining its spectrum of activity.

Thomas *et al.* reported in 2013 the development of an effective high-throughput screening and counter screening assay that led to the identification of another NDM-1 covalent inhibitor targeting a conserved active-site cysteine. Starting from a library of 1280 compounds, ten NDM-1 inhibitors (**pCBM**, **nitroprusside** and **26a-h**) were identified. Only **pCBM** (*p*-chloromercuribenzoic acid, **Figure 23**) and **nitroprusside** (**Figure 23**) were assessed as effective NDM-1 inhibitors.¹⁵⁰

1.2. Other inhibitors

Beside the NDM-1 inhibitors described so far, other chemical scaffolds were identified as potential NDM-1 inhibitors during the last years.

Thakur *et al.* selected 35 natural compounds from various plant sources and whose antibacterial activity is well documented in literature. Combining docking simulations with *in vitro* assays, **nimbolide**, **margolone**, **margolonone**, **isomargolonone**, **acetyl aleuritic acid** and **harmane** were identified, and deserve some interest in the development of potent inhibitors active against NDM-1 (*see Supporting Information*).¹²⁷

Wang *et al.* reported the identification of new NDM-1 inhibitors (**27a-c**, **28a-aq**) by multi-step virtual screening performed on a library of over 2 millions of drug-like compounds. Compounds **27a-c** showed low micromolar affinity vs NDM-1 (**Figure 25**). In series 28, only compound **28x** resulted active against NDM-1 (**Figure 25**).¹²⁶

Shen *et al.*, found that thiophene-carboxylic acid derivatives (**29a-e**, **Figure 25**) possess modest NDM-1 inhibition potency but synergic activity in combination with MEM.¹⁵¹

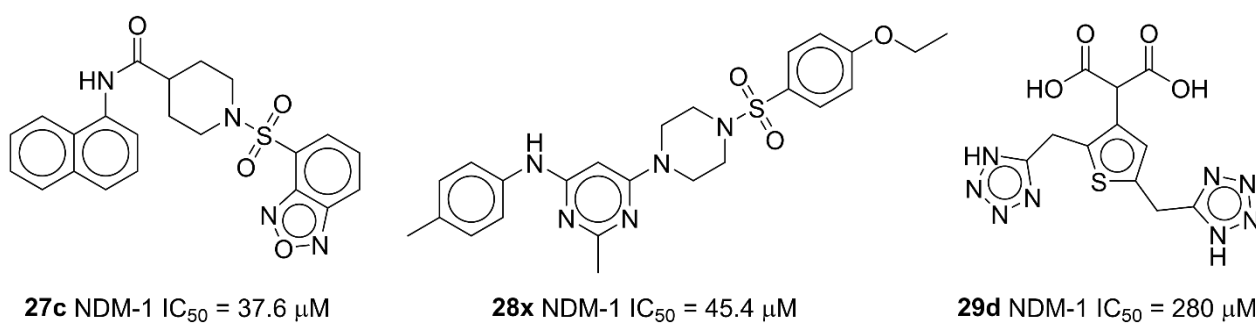


Figure 25. Chemical structure and NDM-1 inhibitor activity of compounds **27c**, **28x** and **29d**.

Brindisi *et al.* reported a structure-based high throughput docking analysis on three MBLs (i.e. NDM-1, IMP-1 and VIM-2), looking for inhibitors active against multiple MBLs. The study led to the identification of **30a**, an aryl-methane-sulfonamide derivative linked to a quinoline ring by a hydrazine linker (**Figure 26Figure**). From docking calculations, **30a** is predicted to interact with the zinc ions through the methanesulfonamide moiety. The tricyclic system forms π - π interactions with Tyr67 in VIM-2 and Phe70 in NDM-1, while the dioxole ring oxygen H-bonds Lys216. The chemical structure of **30a** was then modified at the zinc-binding group, the dioxoquinoline ring and

the hydrazine linker. Derivatives **30b**, **30k**, **30l**, **30m**, **30o** and **30p** showed improved activity against VIM-2, whereas **30h**, **30n**, **30o** and **30v** were comparable to the lead compound **30a** (Figure 26).⁶⁸

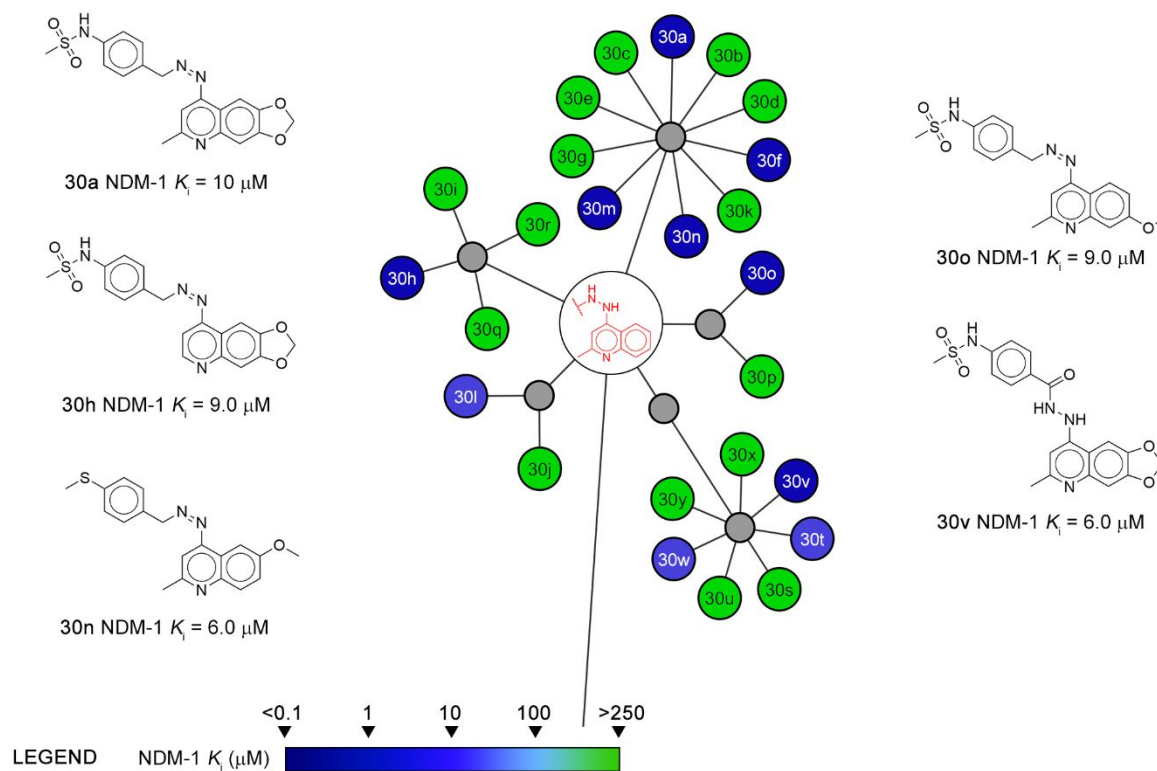


Figure 26. Chemical structure and NDM-1 enzymatic inhibitor activity of the most representative members of quinoline derivatives.

Khan *et al.* recently reported the discovery of novel non- β -lactam NDM-1 inhibitors by multistep virtual screening approach. Five chemical compounds (**31a-e**) with higher fitness score and binding energies were identified. The five compounds possess chemical features able to coordinate metal ions such as acylthiosemicarbazone (for **31a**, Figure 27), sulfonylacylazide (for **31b**, Figure 27) or sulfonylurea (for **31c**, Figure 27). The five compounds showed nanomolar IC_{50} against isolated NDM-1 and the capability of forming strong complexes with the enzyme. The MICs of the five inhibitors, in combination with ceftazidime, ceftoxitin, MEM and IPM, were determined against *E. coli* NDM-1 expressing strains, revealing the ability for **31a-e** to synergize ceftazidime, ceftoxitin and carbapenems.⁶⁷

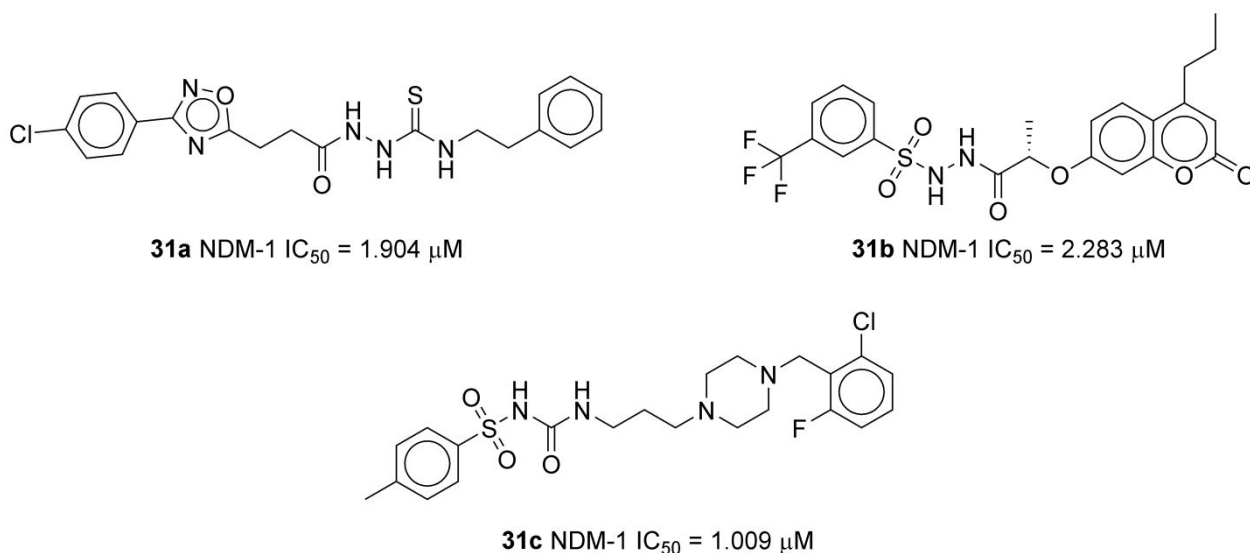


Figure 27. Chemical structure and NDM-1 enzymatic inhibitor activity of compounds **31a**, **b**, **c**.

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Worthington *et al.* recently reported the identification of a 2-aminoimidazole able to effectively reduce the MIC of some antibiotics against multi-drug resistant *Acinetobacter baumannii* (MDRAB) and methicillin-resistant *Staphylococcus aureus* (MRSA), but showing low efficacy against *K. pneumoniae* NDM-1 producing strain.¹⁵² A library of 2-aminoimidazole analogues was screened for the capability to synergize IPM and MEM against a *K. pneumoniae* strain, and a first series of six aryl 2-aminoimidazole (**32a-f**) was identified. Analogues with linear alkyl substituents on the phenyl ring were found to be considerably more active, while the presence of butyl, t-butyl or phenyl substituents was detrimental. The lead compound **32d** (**Figure 28**) was able to reduce the MIC of both IPM and MEM by 16-fold at 30 μM, and by 256-fold at higher concentration. A second series of compounds substituted at position 4 and 5 was synthesized (**32g-n**). Only compound **32h** (**Figure 28**) was able to reduce the MIC of IPM and MEM by 8-fold, suggesting substitution at position 5 is unfavourable. Checkerboard assays of **32d** in combination with IPM and MEM confirmed the synergic activity. Further mechanistic studies are ongoing to confirm that the synergic effect is related to the inhibition of NDM-1.¹⁵³

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Recently, in March 2018, Everett *et al.* described the discovery of **ANT431** (**Figure 28**), a nanomolar, competitive inhibitor of NDM-1 and VIM-2. Biological studies performed on *E. coli* BL21(DE3) harbouring *bla*NDM-1 showed a strong potentiation of MEM antibacterial activity with a MIC reduction of 128-fold. The co-administration of 30 μg/mL of **ANT431** with MEM was able to restore bacteria susceptibility to the antibiotic in NDM-1 overexpressing isolates. **ANT431** showed a suitable pharmacokinetic profile for *in vivo* study, that is, high water solubility for intravenous administration,

good metabolic stability, moderate inhibition of CYP2C9 and CYP3A4 and no toxicity against human cell lines.¹⁵⁴

Finally, Liu *et al.*, screened 75 natural compounds against recombinant NDM-1, identifying **magnolol** (a natural compound isolated from magnolia bark) a potent inhibitor. **Magnolol (Figure 28)** inhibits NDM-1 enzyme activity with low micromolar affinity. The inhibitory activity is not affected by the supplement of zinc, suggesting that magnolol mode of action is not related to a metal-depletion mechanism. When administered in combination with MEM the compound was able to restore the antibiotic susceptibility in NDM-1-expressing *E.coli* ZC-YN3 strain with a 4-fold MIC reduction (from 16 to 4 $\mu\text{g/mL}$).¹⁵⁵

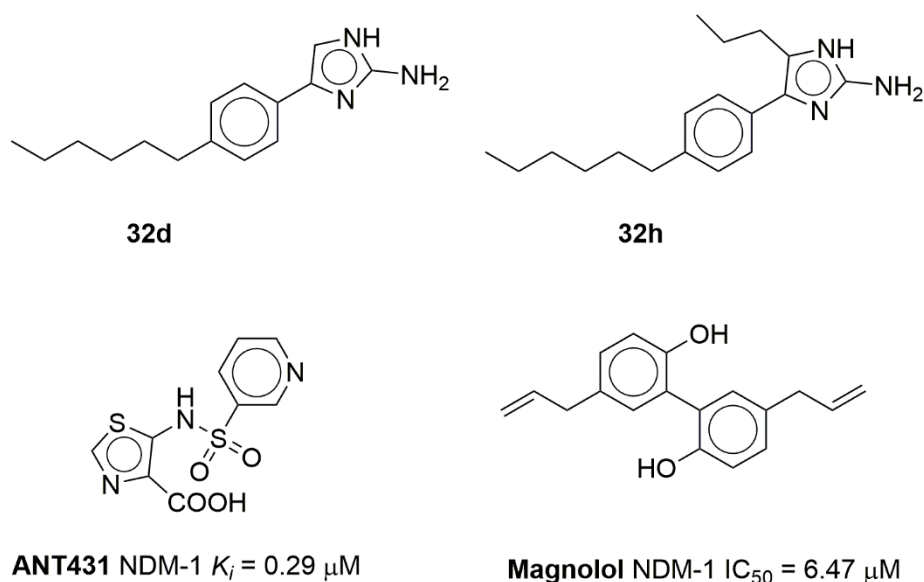


Figure 28. Chemical structure of compounds 32d,h, ANT431 and magnolol.

Conclusions

The discovery of a molecule able to restore the efficacy of available β -lactams toward resistant infections caused by NDM-1-expressing strains would have an enormous impact on human health and consistent social and economic returns. Unfortunately, despite the massive efforts dedicated over the years by many researchers all around the world, none of the new disclosed NDM-1 inhibitors has yet reached the clinic, and only a very few of them are currently under development.

Difficulties arise, primarily, from the nature of the protein itself and the related selectivity and toxicity issues, and from the variability in the mechanism by which β -lactams (penicillin, cephalosporins,

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3 carbapenems) are hydrolyzed. As here described, coordinating the enzyme zinc ions bears the risk of
4 inactivating essential human proteins as well, e.g. the metallo-proteases. Moreover, the flexibility of
5 the enzyme, in terms of mutation rate and hydrolysis mechanism, promotes the development of
6 resistant infections. This adaptability is also supported by a large and shallow active site, able to
7 efficaciously orient almost any kind of β -lactam antibiotic. The design and development of molecules
8 able to target this open cavity resulted actually quite difficult and often ineffective, in particular when
9 structure-based drug design approaches are applied. The unexpected loop adjustment at the binding
10 site entrance, the aforementioned flexibility of the pocket, as well as the water reorganization upon
11 ligand binding make *in silico* prediction, as well as rational drug design strategies are often unreliable.
12 A massive effort for the 3D resolution of the currently available inhibitor in NDM-1 active site is
13 essential to develop new structure-based strategies and try to understand/predict the receptor
14 flexibility. Apart from the difficulty to overcome selectivity issues and to properly fit such a large
15 binding site, in fact, the clarification of the hydrolytic mechanism and of the binding mode of active
16 inhibitors is crucial for the development of antibiotic less susceptible to the enzyme action or of more
17 effective inhibitors.

18
19 At the moment, the most promising molecules share the presence of electron donor chemotypes able
20 to coordinate the two metals, and of making hydrogen-bonds and/or salt bridges with the hydrogen
21 bond donor residues of the binding site. Among these, the most common have mercapto-azolyl,
22 aminotriazole, tetrazole, carboxylate, sulfonyl, and sulfonamide groups. However, recent findings on
23 the evolution of NDM-1 variants coordinating Zn more tightly pose questions on how strategies
24 involving the metal coordination can really counteract these enzymes. At the same time, the evidences
25 of the ability of NDM-1, in light of its peculiar cellular localization, to resist to Zn depletion, open to
26 new opportunities in bacterial targeting, i.e. enhancement of site-specific metal chelation elicited by
27 the immune system and/or interference of bacterial lipidation.^{19,156}

28
29 Particular attention must be deserved to the group of boronic acids derivatives: known to inhibit
30 SBLs, they demonstrated to inactivate MBLs as well, mimicking the tetrahedral oxyanion formed
31 during β -lactam hydrolysis and disrupting the active nucleophile in the binding site.¹⁵⁷ Currently, they
32 represent a productive route toward broad-spectrum inhibitors, simultaneously inhibiting
33 mechanistically different types of BLs.

34
35 We believe that only a strongly integrated effort, combining drug design strategies with a deeper
36 understanding of the enzyme mechanism of action, and looking at new alternative/additional bacterial
37 targets could lead to the identification of that key molecule or combination able to restore bacteria
38 susceptibility to antibiotics.

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Associated content

Supporting Information

The supporting information is available free of charge on the ACS Publications website.

Table S1 reports the X-ray structures for apo and complexed NDM-1 available in the Protein Data Bank (PDF). S2_NDM-1 inhibitors.xls reports the code, SMILE, NDM-1 IC₅₀ or K_i and DOI of the publication of each NDM-1 inhibitor discussed in the present review (XLS).

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List of abbreviation

AMA, Aspergillomarasmine A; BL, β -Lactamase; BZT, bisthiazolidine; CcrA, metallo- β -lactamase from *Bacteroides fragilis*; CRE, carbapenem-resistant Enterobacteriaceae; DOTA, 1,4,7,10-tetraazacyclododecane-1,4,7,10-tetraacetic acid; DPA, 2,6-dipicolinic acid; ESBL, extended spectrum β -lactamase; EDTA, Ethylenediaminetetraacetic acid; FIC, Fractional inhibitory concentration; GES, Guiana Extended Spectrum; GIM-1, German imipenemase; IC₅₀, concentration inhibiting the 50% of the enzyme; ImiS, IMIpenem-hydrolysing β -lactamase-S; IMP, imipenemase; IPM, imipenem; K_i, inhibition constant; KPC, Klebsiella Pneumoniae Carbapenemase; MBL, Metallo β -Lactamase; MBP, 1-(2-mercaptobenzoyl)pyrrolidine-2-carboxylic acid; MDRAB, Multidrug-resistant *Acinetobacter baumannii*; MEM, meropenem; MIC, minimum inhibition concentration; MIF, Molecular Interaction Field; MRSA, Methicillin-Resistant *Staphylococcus Aureus*; NDM-1, New Delhi MBL-1; NOTA, 1,4,7-triazacyclononane-1,4,7-triacetic acid; PBP, penicillin binding proteins; pCBM, p-chloromercuribenzoic acid; SAR, structure–activity relationship; SBL, serine based β -lactamase; SPR, surface plasmon resonance; VAB, vaborbactam; VIM, Verona integron-borne metallo- β -lactamase.

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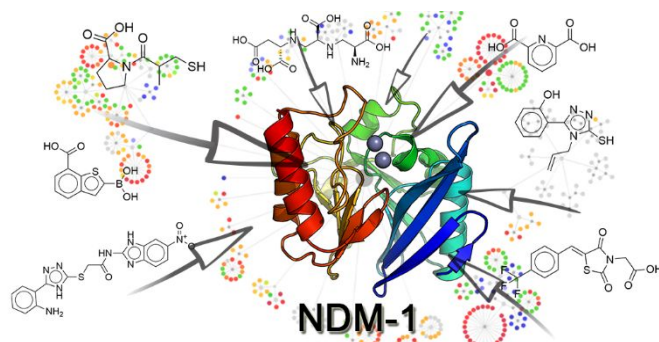
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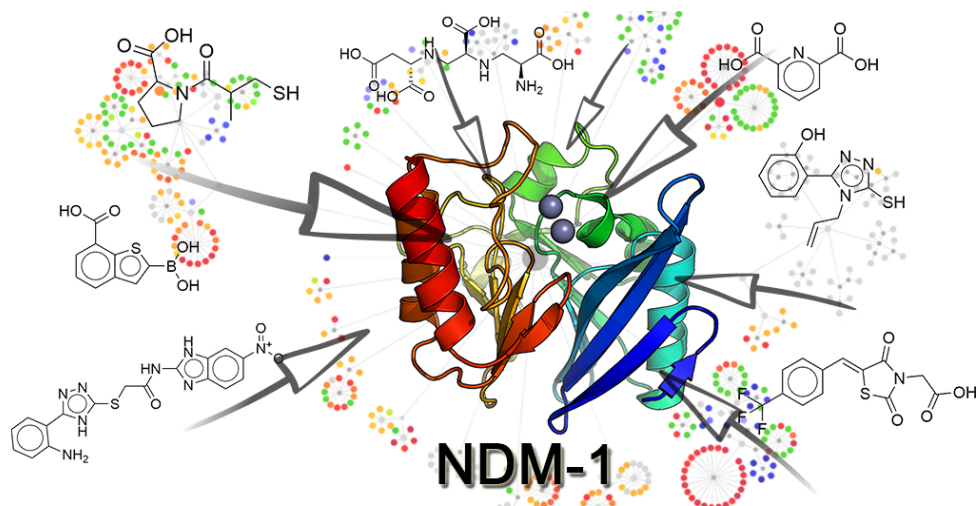
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23 Table of contents

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