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Intermolecular interactions of the extended recognition site of VIM -2 metallo- β -lactamase with 1,2,4-triazole-3-thione inhibitors. Validations of a polarizable molecular mechanics potential by ab initio QC

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**Intermolecular interactions of the extended recognition site
of VIM-2 MBL with 1,2,4-triazole-3-thione inhibitors.
Validations of a polarizable molecular mechanics/dynamics
potential by ab initio QC:**

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3 **Intermolecular interactions of the extended recognition site of VIM-2**
4 **Metallo- β -Lactamase with 1,2,4-triazole-3-thione inhibitors. Validations**
5 **of a polarizable molecular mechanics/dynamics potential by ab initio QC.**
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31 Molecular dynamics on the complexes of inhibitors with Zn-metalloproteins are a
32 privileged area of applications of polarizable molecular mechanics potentials.
33 With which accuracy could these reproduce the QC intermolecular interaction
34 energies in the mono- and the dizinc binding sites? If convincing, this could pave
35 the way for PMM to emulate QM/MM procedures for full-fledged MD simulations
36 on the entirety of the protein complexes. We considered the complexes of the
37 extended recognition site of a Zn-dependent metallo- β -lactamase, VIM-2,
38 responsible for nosocomial disease, with five newly synthesized inhibitors sharing
39 an original dizinc binding group, 1,2,4-triazole-3-thione (TZT). We considered the
40 energy-minimized structures of each of the five VIM-2 complexes obtained with
41 the SIBFA potential. Energy decomposition analyses (EDA) at the HF level
42 enabled to compare the QC and the SIBFA ΔE values and their contributions in
43 the two mono-zinc cores and the dizinc core, with and without TZT, totaling
44 thirty complexes. With one exception, the $\Delta E(QC)$ values were reproduced with
45 relative errors <1.5%. We next considered the complex of the whole inhibitor
46 with substituents in the *ortho* position and in the hydrazine site, with an
47 extended model of VIM-2 recognition site, totaling up to 280 atoms. $\Delta E(SIBFA)$
48 could closely reproduce $\Delta E(QC)$. EDA analyses were resumed on the complexes
49 of each inhibitor arm with its interacting VIM-2 residues. As a last step, EDA
50 results at the correlated level with the B3LYP-D3 and ω -B97X-D functionals were
51 analyzed for the mono- and dizinc sites enabling comparisons with dispersion-
52 augmented $\Delta E(SIBFA)$ and correlated multipoles and polarizabilities.
53
54
55

56 **Key words:** metallo- β -lactamases; 1,2,4-triazole-3-thione inhibitors; polarizable
57 molecular mechanics/dynamics; ab initio quantum chemistry; intermolecular
58 interactions.
59
60

Introduction.

Zn(II)-metalloenzymes [1-3] should constitute a privileged domain of application for accurate, quantum-chemistry (QC) grounded polarizable molecular mechanics/dynamics (PMM/PMD) potentials [4-10]. The need for such potentials is made clear by the non-anisotropy and non-additivity of $\Delta E(QC)$ and its individual contributions, unraveled by numerous energy-decomposition analyses (EDA) of mono- and polyligated Zn(II) complexes [11-15].

Classical, non-polarizable point-charge force-fields cannot account for such effects. For such complexes, the most reliable approach is multilevel QM/MM [16-18] or QM coupled with Effective Fragment Potentials or Fragment-Based approaches [19-21]. In spite of very noteworthy recent computational speedup of the QM part [22], the CPU time remains dominated by it. In addition, the long-range effects extend far beyond the QM core, so that a polarizable MM periphery is desirable.

Semi-empirical DFT-Tight -Binding approaches are a worthy alternative [23, 24] but unless coupled to Molecular Mechanics to handle the periphery of the zinc cores have not been extended so far to long-duration Molecular Dynamics (MD).

On account of such limitations, it would be rewarding if polarizable potentials could act as a surrogate for QC in the actual QM core, and not only at its periphery. Some of the above-mentioned papers have evaluated how well the Sum of Interactions Between Fragments Ab initio computed (SIBFA) procedure could reproduce non-anisotropy and non-additivity of $\Delta E(QC)$ in a diversity of mono- and polyligated Zn(II) complexes [11-13, 15]. These validations were extended to Zn-metalloprotein complexes, for which the numerical values of $\Delta E(QC)$ and their trends in series of related inhibitors could be closely accounted for [25-27].

But is it possible to further fine-tune this potential, revisiting first the zinc core(s) and subsequently the periphery where the arms of diverse inhibitors bind and confer enhanced affinity and selectivity for a targeted metalloprotein?

Metallo- β -lactamases (MBL), which emerged three decades ago, are a class of Zn-metalloenzymes responsible for acquired resistance to many β -lactam antibiotics in bacterial opportunistic pathogens [Reviewed in 28-31] and against which there are presently no clinically useful inhibitors yet, whence a major health concern worldwide [32].

Among these, VIM subtypes (Verona-Integron Metallo-beta-lactamase), which are among the most widespread metallo-carbapenemases in Europe and North America, are able to hydrolyze almost all marketed β -lactams [32]. VIM-2 is an MBL enzyme produced by Gram-negative opportunistic pathogens exhibiting multi-drug resistance phenotypes and which are responsible for nosocomial infections. The present paper is a continuation of a previous work [33] which focused on the mono- and dizinc cores of the L1 and VIM-2 MBL enzymes and their interaction energies with an original Zn-binding motif, the 1,2,4-triazole-3-thione (TZT) heterocycle. TZT has a monoanionic pentacyclic ring with an extracyclic sulfur atom. The Zn(II) cation of the His3-binding site is bound by

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3 one ring nitrogen (N^2), on which the anionic charge is partly delocalized, and the
4 Zn(II) cation of the Cys-Asp-His binding site is bound by the extracyclic S atom.
5 As a step forward, we now consider the interaction energies of five novel MBL
6 inhibitors, synthesized and tested in our Laboratories [34]. They all have the
7 same TZT acting as an anchor in the dizinc core, and two arms substituting the
8 ring C^5 and the hydrazone end. These substituents are denoted as R1 and R2
9 (Figure 1).
10

11
12 Three inhibitors, MV4690, 4390 and 5064, have an R2 *o*-benzoic substituent.
13 Compound JMV5069 has a *m*-biphenyl arm possessing a carboxylate at the *meta*
14 position of the second phenyl ring. Compound JMV4684 displays a 2,4-
15 dihydroxy-phenyl as R2 substituent.

16 As R1 substituent, compound 4690 has a 2-hydroxy-5-methoxy-phenyl, while
17 compound 4390 possesses an unsubstituted benzene ring. Both compounds 4684
18 and 5069 have a 2,5-dihydroxy-phenyl moiety. Compound 5064 contains a 3,5-
19 dichlorophenyl substituent (Figure 1).
20

21
22 The synthesis of a large number of TZT-based inhibitors was very recently
23 reported, along with their inhibitory potencies on several clinically relevant MBLs.
24 Along with VIM-2 and VIM-4, these included NDM-1 (New-Delhi Metallo- β -
25 lactamase), and IMP-1 (Imipenemase). The free energies of binding of nine of
26 these for VIM-2 were in addition measured by Isothermal Calorimetry, enabling
27 to derive the separate contributions of enthalpy and entropy to ΔG [34].
28

29
30 A major objective is SIBFA MD simulations on the complexes of a diversity of TZT
31 grounded inhibitors, completed with free energy perturbation (FEP) studies [35,
32 36]. It should be attained by the integration of this potential and its gradients,
33 now effective in a massively parallel computer code, Tinker-HP [37]. Following
34 SAPT/DFT-based analyses of $\Delta E(QC)$, it recently enabled the first SIBFA MD
35 simulations on liquid water and comparison with experimental observables
36 [Naseem-Khan et al., to be submitted]. Extensions to a diversity of biologically-
37 relevant fragments are underway [El Ahdab et al., work in progress].
38

39
40 Considering the non-isotropy and non-additivity issues, and in view of safe FEP
41 computations, it is essential to ensure beforehand that $\Delta E(SIBFA)$ can reproduce
42 as closely as possible $\Delta E(QC)$ and its individual contributions in a diversity of
43 complexes making up extended recognition sites of Zn-metalloproteins. These
44 concern on the one hand the interactions of the TZT anchor with the mono- and
45 dizinc cores, and on the other hand those of each arm with its interacting VIM-2
46 partners around the binuclear core.
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48
49 The present comparisons will be done on the SIBFA energy-minimized complexes
50 of VIM-2 with each inhibitor. In a first step, an extended recognition site is
51 extracted encompassing the inhibitor and the VIM-2 relevant residues, together
52 with the closest fourteen 'discrete' water molecules. For each inhibitor, five
53 single-point SIBFA and QC calculations are then performed on this site. They
54 bear on: the uncomplexed site a) without and b) with the discrete waters; c) the
55 site complexed with the sole TZT anchor and without the waters; and the site
56 complexed with the complete inhibitor d) without and e) with the structural
57 waters.
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59 Proceeding in this step-wise fashion could be highly instructive to trace possible
60 shortcomings in the last stage, e), to one of the preceding stages.

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4 Due to its 'proof of concept' nature, the present study will mostly focus on
5 comparisons with QC HF ΔE calculations. Preliminary results from correlated
6 calculations will be evaluated only at the end of this study. This choice is
7 motivated by the following:

8 -Energy Decomposition Analyses (EDA) on multimolecular complexes delivering
9 separate values of the first-order Coulomb (E_C) and exchange-repulsion (E_X) and
10 second-order polarization (E_{pol}) and charge-transfer (E_{ct}) can presently only be
11 done with EDAs at the HF level, specifically with the Reduced Variational Space
12 (RVS) method [38]. The released ALMOEDA procedure [39], used in the last part
13 of this work, does enable EDA for multimolecular complexes and at several
14 possible correlation levels. However, it does not provide a separation of E_C and E_X
15 within the first-order of ΔE , E_1 . Were shortcomings of E_1 (SIBFA) to be found in
16 some of these complexes, it would not enable to trace back whether they
17 originate from E_C , E_X , or possibly both;

18 -the automated Least-Squares Fit (LSQF) procedure integrated in the SIBFA code
19 should enable to fit equally well the separate ΔE (HF) contributions and those
20 from correlated ΔE , such as from Symmetry Adapted Perturbation Theory (SAPT
21 [40, 41] provided correlated multipoles and polarizabilities are used. Previous
22 papers on ligand-alkali cation complexes [42, 43], on stacked and H-bonded
23 cytosine and guanine dimers [44] and on cation channeling along the z axis of
24 stacked guanine tetramers [45] did show these to enable virtually equally as
25 good reproductions of correlated ΔE as of HF ΔE with uncorrelated multipoles and
26 polarizabilities;

27 -the present analyses should unavoidably unravel shortcomings of the potential,
28 whether regarding interactions in the Zn(II) cores or those of the arms with the
29 periphery. These should enable to refine the strategy for the next stage of SIBFA
30 calibration to be resumed at the correlated level. It would likely be hopeless to
31 undertake large-scale MD/FEP simulations if shortcomings already at the HF level
32 were not identified beforehand.

33 While in the present study ΔE (SIBFA) was shown to reproduce in consistent
34 fashion the trends of ΔE (QC) in the above-mentioned cases a-e, it overestimated
35 it after accounting for BSSE and the relative energy differences between the five
36 inhibitors left room for improvement. This led us to revisit the parameters of
37 TZT, of the benzocarboxylate arm and of imidazole, upon resorting to the LSQF
38 procedure using a Zn(II) probe approaching these ligands in-plane as well as
39 perpendicular to the plane as detailed below.

40 The first series of subsequent evaluations bear on the two mono-zinc cores and
41 the dizinc core, whether TZT-uncomplexed or TZT-complexed, as extracted from
42 the optimized complex of VIM-2 with each inhibitor. There is thus a total of thirty
43 complexes on which ΔE (SIBFA) and ΔE (HF) are done in parallel. This enables to
44 probe the 'flexibility' of the dizinc core anchoring TZT because it can partly
45 distort to allow optimizing the interactions of the arms with the periphery: how
46 well could such a flexibility be reflected by ΔE (SIBFA) and its contributions as
47 compared to the HF ones?

48 The five complexes a-e) are then reconsidered with the extended recognition site
49 to evaluate the amount of improvement now realized.

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3 Additional validations bear, for each inhibitor, on the compared $\Delta E(\text{SIBFA})$ and ΔE
4 (QC) values and of their contributions on the complexes of each arm with its
5 VIM-2 interacting partners. These interactions are either ionic, polar, cation- π , or
6 π -stacking.
7

8
9 We finally provide ALMOEDA results on the mono-and dizinc sites with two DFT
10 functionals, $\omega\text{B97X-D}$ [46] and B3LYP-D3 [47]. This enables to unravel the impact
11 of correlation/dispersion on each separate QC contribution and how well could
12 $\Delta E(\text{SIBFA})$ with correlated multipoles and polarizabilities and augmented with
13 dispersion match the QC results prior to any further refinement, whence an
14 upper bound to the expectable error.
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16
17 We believe the interest of such analyses should extend far beyond the targeting
18 of MBLs, notwithstanding their essential importance as targets for drug
19 development. Thus Zn-metalloproteins when overexpressed are responsible for
20 numerous diseases, with very few efficient inhibitors at this time.
21

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23 Although this list is far from exhaustive, newly-emerging targets are matrix
24 metalloproteinases (MMP), involved in matrix invasion and metastases [48,49],
25 neural inflammation [50] and auto-immune diseases [51], histone deacetylase
26 (HDAC), involved in cancer [52], and phosphomannose isomerase (PMI) in
27 microbial and parasitic diseases [53].
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34 **Computational procedure.**

35 **Ab initio QC.**

36
37 The computations used the aug-cc-pVTZ(-f) and cc-pVTZ(-f) basis sets [54, 55
38].

39
40 The complexes of the five inhibitors with the extended recognition site were
41 computed with the G09 software [56] and included the Basis Set Superposition
42 Error (BSSE [57]) correction.

43
44 Energy Decomposition Analyses (EDA) at the HF level were done with the
45 Reduced Variation Space Analysis by Stevens and Fink [38] coded in the
46 GAMESS [58] software. The DFT computations were done with the B3LYP-D3
47 [47, 59] and the $\omega\text{-B97X-D}$ functionals [46]. EDAs at the DFT levels were done
48 with the ALMOEDA procedure [39] coded in the Q-Chem software [60].
49

50
51 **Polarizable Molecular Mechanics (PMM).** The PMM computations were done
52 with the SIBFA procedure [4]. The intermolecular interaction energy, ΔE , is
53 computed as a sum of five contributions: electrostatic multipolar (E_{MTP}), short-
54 range repulsion (E_{rep}), polarization (E_{pol}), charge-transfer (E_{ct}) and dispersion
55 (E_{disp}). Their expressions were detailed in several previous papers [4, 13, 15].
56 The distributed multipoles on the fragments making up VIM-2 (backbone and
57 side-chains) and the inhibitors (TZZ and its substituents on the R1 and R2 sites)
58 were obtained by the Generalized Distributed Multipole Analysis (GDMA) by
59 Stone [61] with the aug-cc-pVTZ(-f) basis set. The distributed polarizabilities,
60 located on the bond barycenters and the extremities of the heteroatom lone-

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3 pairs were derived from the Garmer and Stevens procedure [62] coded in
4 GAMESS.
5

6 We have resorted to the X-ray structure of the complex of VIM-2 with inhibitor
7 JMV4690 [pdb code 6YRP, Ref. 34] as a starting point for energy-minimizations
8 (EM) of the five complexes. These resorted to the Merlin software [63]. As in our
9 previous studies [25-27], the protein backbone was held rigid. We relaxed the
10 protein side-chains around their χ torsional angles. The six intermolecular
11 variables defining the orientation of the inhibitors and their torsional angles were
12 minimized. Fourteen 'discrete' water molecules were retained for each complex,
13 based on proximity criteria and their six intermolecular variables were
14 minimized. The intramolecular bond lengths and valence angles were not
15 relaxed. At the outcome of the EMs, the comparisons between SIBFA and QC
16 were on an extended recognition site of VIM2. Such sites, in addition to the
17 entirety of the inhibitors and to the dizinc binding site, encompassed all VIM-2
18 residues (backbone and/or side-chains) interacting with the inhibitors, as well as
19 the fourteen discrete waters. The same residues were retained in all five
20 complexes:
21

22 backbone atoms of Cys-221, Tyr224-Glu225; Gly232-Val234; side-chains of
23 Tyr67, Ser69, Trp87, His116, His118, Asp119, Asp120, Arg121, His196, Cys-
24 221, Tyr224, Glu225, Arg228, Asn233, His263.
25
26

27 **Refinements of the TZT, benzocarboxylate, and imidazole fragments.**

28 In light of the comparisons with the QC results on the extended recognition site, we
29 sought for further refinements of the relevant parameters for TZT, for the
30 benzocarboxylate arm (an R2 substituent in four of the five considered inhibitors),
31 but also for imidazole, which occurs four times out of six as a Zn-ligand in the dizinc
32 binding core of VIM-2. We have resorted to a procedure recently integrated into the
33 standard SIBFA software and used to calibrate the dianionic phosphate group (DPG)
34 [64] and to derive a water potential grounded on Symmetry Adapted Perturbation
35 Theory [SAPT] for molecular dynamics simulations on liquid water [Naseem-Khan et
36 al., to be submitted]. The relevant fragment specific parameters for the SIBFA E_{MTP} ,
37 E_{rep} , E_{pol} and E_{ct} contributions were optimized by Least-Squares Fit minimization of
38 the error with respect to their respective RVS counterparts E_C , E_X , E_{pol} and E_{ct} as
39 computed in all probed positions of the fragment. Minimization was done with a
40 BFGS procedure with numerically-computed gradients [65].
41
42

43 TZT was 'probed' by Zn(II) along both deprotonated ring nitrogens and sulfur upon
44 performing distance and in- and out-of-plane angular variations. The five ring atoms
45 were also probed vertically, upon performing distance variations along the
46 perpendicular passing through the probed atom. In order to ensure better control of
47 the non-additivity of E_{pol} , we have included in the optimization procedure the ten
48 complexes of TZT with the monozinc cores, that is, each of the His3 and Asp-Cys-His
49 cores in their structures extracted from their complexes with each of the five
50 inhibitors. As in previous studies [33, 64], we have similarly resorted to a Zn(II)
51 'probe' to maximize the response of the probed ligands regarding both first-order
52 (Coulomb and exchange), and second-order (polarization and charge-transfer)
53 responses. Thus benzocarboxylate was probed by Zn(II) approaching one anionic
54 carboxylate upon performing in-plane radial and angular variations, and radial
55 variations along a perpendicular to the plane passing through this oxygen, or to the
56 extracyclic C atom or the C atoms *ortho*, *para* or *meta* to it. Imidazole was probed by
57 radial variations of the approach of Zn(II) along the external bisector of its
58 deprotonated nitrogen. At equilibrium distance (1.90 Å) out-of-plane variations were
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3 done until the perpendicular to the ring was reached. To improve the control of non-
4 additivity, we included the five complexes of Zn(II) in the His3-monozinc core in its
5 energy-minimized structure with the five inhibitors.
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9 **Results and discussion.**

10 **1. Complexes of inhibitors I-V with the extended recognition site. Starting**

11 **validations.**

12
13
14 The structures of the complexes of the five inhibitors with the extended binding sites
15 are shown in Figures 2(a-e). In the first monozinc binding site, Zn(II) is bound to
16 three His residues (His116, His118 and His196) and the partially anionic ring TZT N²
17 atom *ortho* to the extracyclic S. In the second site, the other Zn(II) is bound by one
18 Asp (Asp120), one Cys (Cys221), and one His residue (His263), and by the
19 extracyclic TZT S atom. For convenience, we will denote the two Zn-sites as the
20 'blue' and the 'colored' site, respectively. The most relevant interatomic distances are
21 listed in Supp. Info 1. It is seen that the distances of each Zn-atom to its ligands can
22 vary by up to 0.2 Å. For conciseness, we will use an alternative notation for ligands
23 4690, 4390, 4684, 5064 and 5069, namely I-V, respectively.
24

25 The interactions occurring with the R1 arm, which substitutes the TZT C⁵ atom
26 involve the side-chains of residues Phe61, Trp87, and Asp119. Those occurring with
27 the R2 arm, which substitutes the N⁴-hydrazone involve the side-chains of residues
28 Arg228, His263 and the main-chain atoms of residues Glu225 or Asn233. They will
29 be analyzed in section 6.
30

31
32 Single-point computations were done on the complexes of I-V with the extended
33 recognition site, extracted from the energy-minimized complexes. As in our previous
34 studies, the same geometries were used in the validation of QC and SIBFA
35 computations. Table I compares the ΔE values in: the unligated sites a) without and
36 b) with the fourteen water molecules; c) the sites complexed with the sole TZT
37 anchor and without the waters; the sites complexed with the entire inhibitor d)
38 without and e) with the waters.
39

40 For both complexes d) and e), $\Delta E(\text{SIBFA})$ reproduces the ranking of $\Delta E(\text{QC})$
41 affinities: I > II > IV > V > III. For the first three complexes, they are much closer to
42 the BSSE-uncorrected $\Delta E(\text{QC})$ values than to the uncorrected ones, with relative
43 errors <0.5%. For the last two complexes, $\Delta E(\text{SIBFA})$ is either closer to BSSE-
44 corrected $\Delta E(\text{QC})$ or intermediate between corrected and uncorrected $\Delta E(\text{QC})$. As
45 such, even though the ranking of the five complexes is accounted for, the $\Delta E(\text{SIBFA})$
46 curve cannot parallel the $\Delta E(\text{QC})$ curves, as illustrated in Figures 3a-b.
47
48

49 Another $\Delta E(\text{QC})$ ordering is found for complexes c), involving the sole TZT anchor:
50 V > I > III > II > IV. It can also be accounted by $\Delta E(\text{SIBFA})$, which has values
51 intermediate between the uncorrected and corrected $\Delta E(\text{QC})$ values. The relative
52 errors are <2%. However, there are some undesirable features, notably the very
53 small $\Delta E(\text{SIBFA})$ values separating V from I, 1.9 kcal/mol out of 1230, compared to
54 17 in QC. The corresponding evolutions of $\Delta E(\text{SIBFA})$ and $\Delta E(\text{QC})$ are illustrated in
55 Figure 3c.
56
57

58 In the absence of the TZT anchor, for complexes a without the waters, $\Delta E(\text{SIBFA})$
59 reproduces $\Delta E(\text{QC})$ with relative errors <1% at the BSSE-corrected level. At this
60 stage, a reproduction of the $\Delta E(\text{QC})$ ordering could no longer be ensured. Close

reproduction also obtains in the presence of the waters, the values of $\Delta E(\text{SIBFA})$ being intermediate between the BSSE-corrected and uncorrected $\Delta E(\text{QC})$ values.

The results for complexes *c* are revealing. They show the modulations of the affinities of the anchoring TZT group by the additional interactions of the inhibitor arms with their VIM-2 partners and the structural waters. This implies the need to account for such modulations as closely as possible in the context of $\Delta E(\text{SIBFA})$, namely for complexes *c*, to prevent further imbalances with respect to $\Delta E(\text{QC})$ when such interactions are embodied, as in complexes *d* and *e*. This led us to the next stage of this work: is it possible to narrow down the relative errors concerning the complexes of TZT in the two monozinc sites and the dizinc site in structures a-e?

2. Automated recalibration of the TZT anchor.

We denote throughout by E_1 the sum of first-order contributions, E_C and E_X in QC and E_{MTP} and E_{rep} in SIBFA, and by E_2 the sum of second-order contributions, E_{pol} and E_{ct} .

For all four contributions, the relevant parameters are the effective radii of TZT ring nitrogens and extracyclic sulfur. These values can differ as a function of the contribution. For E_{rep} , additional parameters are the internal variables defining the positions of the lone pairs with respect to their atom bearers, their occupation numbers, and the increment of effective radii along the lone pair directions. Related lone pairs, such as the pi ones on a given atom, or the sp^3 -lone pairs of sulfur, are constrained to have the same values. For E_{ct} the additional parameters are the increments of corresponding effective radii. Regarding E_{pol} , and in the perspective of future MD simulations, the polarizability tensors were transformed into scalars, the values of which were taken as the average of the three diagonal elements. A multiplicative factor was used as an additional parameter for each scalar polarizability. Additional parameters are those concerning the Gaussian screening of the field undergone by TZT. Its original expression is given in Ref. [66]. There are four multiplicative factors: for the bond then the lone-pair polarizabilities prior to iterating, then for the bond and lone-pair polarizabilities upon iterating. To each is associated a value for the exponent of the Gaussian screening function. In the standard calibration which was performed manually in Ref. [33], all four multiplicative factors have the same values, and so do the four Gaussian exponents. To enable for more flexibility, and since we included the two mono-zinc cores in their five different geometries in the training set, all eight parameters were enabled to vary independently.

Figures 4(a-g) recast the compared QC(RVS) and SIBFA evolutions as a function of the probing position regarding: a) E_C and E_{MTP} ; b) E_X and E_{rep} ; c) E_{pol} ; d) E_{ct} ; e) E_1 ; f) E_2 ; g) ΔE . We report the selected 32 most relevant complexes of Zn(II):

1-5: in-plane binding to S, θ angle (C-S-Zn) at 105° , five 0.1 Å distance variations from 2.0 to 2.4 Å;

6-11: in-plane binding to S, Zn-S distance at 2.1 Å, six 30° θ angle variations from 60° to 240° ;

12-15: binding to S, distance at 2.1 Å, θ angle at 105° , four 60° ϕ out-of-plane angular variations from 120° to 300° ;

16-21: in-plane binding to N^2 , *ortho* to the extracyclic sulfur, along its external bisector (θ angle of 126°), six 0.1 Å distance variations from 1.7 to 2.2 Å;

22-25: in-plane binding to N^2 , distance at 1.8 Å, four 30° θ variations, from 66° to 156° ;

26-32: in-plane binding to N^2 , distance at 1.8 Å, θ at 126° , seven ϕ out-of-plane 30° angular variations from 90° to -90° .

To show control of the short-range repulsion in less relevant Zn(II) positions, we report for this contribution additional results with a more complete coverage of the volume around TZT:

33-36: in plane binding along the external bisector of the extracyclic hydrazone N;

37-61: approach along the perpendicular to TZT with distance variations from 1.8 Å till 2.2 Å. 37-41 are to N¹, *meta* to the sulfur, 42-46 to N², 47-51 to C, 52-56 to the substituted N, and 57-61 to the extracyclic N.

62-67: in-plane binding to N¹ along its external bisector, distance variations from 1.7 to 2.2 Å;

68, 69 and 70: in-plane binding to N¹, distance of 1.8 Å, θ angles of 96°, 156°, and 186°.

The LSQF-optimized SIBFA TZT parameters for E_{MTP} , E_{rep} , E_{pol} and E_{ct} are given in Supplementary Information S2.

The largest relative error of E_{MTP} with respect to E_C is 6%, occurring for in-plane binding to N² at a distance of 1.8 Å to N² (Figure 4a, position 25).

The closest QC reproductions are those of $E_X(RVS)$ by $E_{rep}(SIBFA)$ over the 70 probe positions (Figure 4b).

Those concerning E_{pol} (Figure 4c) are at positions 1-3, for the three shortest distances of approach to S (2.0-2.2 Å), and at position 12, where Zn(II) binds TZT out-of plane.

The least regular matches concern E_{ct} (Figure 4d). Positions 1-5 and 16-20 relate to the variations of the distances of Zn(II) to S and N², respectively: $E_{ct}(SIBFA)$ undergoes faster variations than $E_{ct}(RVS)$, which is much shallower and could actually start to increase in magnitude past the reported distances. It was earlier reported that in monoligated complexes of Zn(II) [66, 67] and lanthanides [68] such an increase in magnitude upon increasing distance is caused by the admixture of a state with transfer of a 'complete' electron from the ligand to the cation [69]. This is prevented in polyligated Zn(II) complexes. In positions 26-32, the underestimated values of $E_{ct}(SIBFA)$ are compensated for by $E_{pol}(SIBFA)$ within E_2 (Figure 4f).

The lowest-energy position is 22 (Figure 4g) for which Zn(II) bridges N² and N¹ at distances of 1.8 and 1.7 Å, respectively. The second minimum is at position 25, for in-plane binding to N² with a θ angle of 156°, for which Zn(II) bridges N² and S, at distances of 1.8 and 2.5 Å respectively. $\Delta E(SIBFA)$ is overestimated by 5%, due to E_{MTP} . The largest overestimation of ΔE is in the fifth second minimum (position 7) in which Zn(II) binds in-plane S at an angle of 2.1 Å, and it is caused by E_{pol} .

These results imply that further refinements to E_{pol} could be considered at a later stage, such as by enabling a relaxation of the internal coordinates defining the position of each centroid with respect to its bearer, in addition to the actual modulation of the amplitude of the polarizability. On the other hand, the strong reduction of the magnitudes of E_{pol} and E_{ct} in polyligated Zn(II) complexes due to anti-cooperativity could limit the impact of the shortcomings occurring in monoligated complexes. How well could then $\Delta E(SIBFA)$ and its contributions fare in the two monozinc cores and the dizinc core of VIM-2, whether uncomplexed or complexed by TZT?

3. Mono-zinc binding cores in geometries I-V.

Tables II(a-d) compare $\Delta E(SIBFA)$ and ΔE (QC) for each mono-zinc binding core, extracted from the VIM-2 complexes with the five inhibitors in four distinct cases: a) the 'blue' and b) the 'colored' core uncomplexed by TZT; c) and d) the 'blue' and 'colored' cores complexed by TZT, respectively. They are commented in succession.

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2
3
4 a). *'Blue core'*. $\Delta E(\text{SIBFA})$ retains values reproducing $\Delta E(\text{QC})$ to within 3 kcal/mol out
5 of 300, i.e. relative errors $< 1.5\%$. I-IV have ΔE values themselves differing by
6 $< 1.5\%$. On the other hand, $\Delta E(\text{SIBFA})$ in V is less stabilizing by 6 kcal/mol, and this
7 is consistent with $\Delta E(\text{QC})$. For all five complexes, E_1 has a lesser magnitude than E_2
8 with both approaches. With both as well, the largest E_2 versus E_1 magnitudes are
9 with IV, while it is in I that E_1 comes closer to E_2 . $E_1(\text{SIBFA})$ comes very close to
10 $E_1(\text{QC})$ (less than 1 kcal/mol out of 150) but there are error compensations, E_{MTP}
11 having larger magnitudes than E_{C} , while conversely E_{rep} is smaller than E_{X} .
12

13
14 b) *'Colored core'*. $\Delta E(\text{SIBFA})$ retains a very close numerical agreement with $\Delta E(\text{QC})$,
15 with 1% relative errors, for all five cores. The two best bound cores are those of II
16 and IV. Both E_1 and E_2 are closely reproduced as well. Again, there are
17 compensations of errors coming into play within E_1 , but this time it is E_{MTP} that is
18 smaller in magnitude than E_{C} , E_{rep} now being smaller than E_{X} . E_2 is now more than
19 three times smaller in magnitude than E_1 , in marked contrast to the situation
20 occurring in the blue cores a. This translates the very strong anti-cooperativity of E_{pol}
21 and E_{ct} , owing to the presence of two anionic ligands, overcompensating for their
22 stronger polarizabilities and electron-donating characters. Of note is, with both QC
23 and SIBFA, the rather modest increases of the magnitude of E_{ct} upon passing from
24 the 'blue' cores (all neutral imidazole ligands) to the 'colored' ones, despite these
25 having two anionic ligands with much smaller ionization potentials and much more
26 extended electronic clouds than imidazole.
27

28
29 c). *TZT-complexed blue core*. $\Delta E(\text{SIBFA})$ retains a close agreement with $\Delta E(\text{QC})$ upon
30 TZT binding to the 'blue' core. The ranking I > III > II > V > IV is the same as that
31 of $\Delta E(\text{QC})$, but this could be coincidental given the very small differences between
32 the complexes: there are very small relative errors of $\Delta E(\text{SIBFA})$ with respect to
33 $\Delta E(\text{QC})$ of 1%, but with one notable exception, V, the least favored complex, for
34 which the relative error is 3%: this is the largest relative error among all the twenty
35 considered a-d mono-zinc complexes in structures I-V. It is mostly due to
36 $E_{\text{pol}}(\text{SIBFA})$, which is 7 kcal/mol out of 130-140 smaller in magnitude than $E_{\text{pol}}(\text{QC})$,
37 while it retained very close values to it in the four other complexes. In line with a
38 conclusion from the above-reported monoligated study, a finer tuning of $E_{\text{pol}}(\text{SIBFA})$
39 in polyligated complexes would likely be enabled by additional LSQF relaxing the
40 three internal variables (the distance and the θ and ϕ angles), which define the
41 position of each polarizability with respect to their bearer, atom or barycenter, as
42 was done for the lone-pairs regarding E_{rep} .
43

44 $E_{\text{ct}}(\text{SIBFA})$ closely follows the evolutions of $E_{\text{ct}}(\text{QC})$ but is underestimated by a
45 difference of 6-8 kcal/mol with respect to it. $E_1(\text{SIBFA})$ has a noteworthy agreement
46 with $E_1(\text{HF})$, and so do both E_{MTP} and E_{rep} compared to E_{C} and E_{X} . Small
47 overestimations of $E_1(\text{SIBFA})$ can 'absorb' to some extent the corresponding
48 underestimations of E_{ct} . It is instructive to compare for each complex I-V the values
49 of E_{pol} and E_{ct} prior to, and following, complexation by TZT. We observe very modest
50 increases of their magnitudes following complexation, and much more so in the case
51 of E_{ct} . For both contributions, this reflects the strong inhibition by anti-cooperativity
52 of the contribution of TZT to E_2 , opposing its polarizability and electron-donating
53 properties.
54

55
56 d). *Complexed colored core*. $\Delta E(\text{SIBFA})$ retains very close numerical agreements with
57 $\Delta E(\text{QC})$ throughout, the largest relative error being 2.3% for complex III. $E_1(\text{SIBFA})$
58 has by up to 2% larger magnitudes than $E_1(\text{QC})$, due mostly to E_{MTP} but this is
59 compensated by smaller magnitudes of $E_2(\text{SIBFA})$ than $E_2(\text{QC})$. It is instructive, here
60 also, to compare the separate evolutions of E_{pol} and E_{ct} upon passing from the

1
2
3 uncomplexed to the complexed 'colored' core, namely complexes *b* and *d*. $E_{\text{pol}}(\text{QC})$
4 and $E_{\text{ct}}(\text{QC})$ increase by limited amounts, by about 9 and 8 kcal/mol respectively. A
5 notable exception is complex *V*, where $E_{\text{pol}}(\text{QC})$ has *diminished* in magnitude, albeit
6 by a small amount (2 kcal/mol out of 95) and $E_{\text{ct}}(\text{QC})$ has increased in magnitude by
7 half the amount observed in I-IV. Both trends are seen in SIBFA for *V*. While for I-IV
8 the magnitude increases of $E_{\text{ct}}(\text{SIBFA})$ of 7 kcal/mol are very close to those of
9 $E_{\text{ct}}(\text{QC})$, the corresponding increases of $E_{\text{pol}}(\text{SIBFA})$ are much smaller (<2 kcal/mol)
10 with even a small decrease in magnitude for *IV*. In retrospect, this suggests that a
11 similar LSQF fine-tuning of the E_{pol} parameters for formate and methanethiolate
12 should be envisaged as done for imidazole, encompassing polyligated complexes in
13 the training set. This will also be considered in forthcoming refinements at the
14 correlated level. At this stage it could be noted that the present close reproduction of
15 the QC values might exempt from this extra endeavor at this stage.
16
17

18 **4. Dizinc binding cores in geometries I-V.**

19
20 Tables III(a-b) report the BSSE-corrected $\Delta E(\text{QC})$ and $\Delta E(\text{SIBFA})$ values in the dizinc
21 core, uncomplexed (a) and complexed (b) by TZT. RVS analyses could not be
22 performed for size reasons. We have resorted to QC calculations with both aug-cc-
23 pVTZ(-f) and cc-pVTZ(-f) basis sets.
24

25 *a) Uncomplexed cores.*

26 There is a very striking agreement of $\Delta E(\text{SIBFA})$ and $\Delta E(\text{QC})$, actually better with the
27 aug-cc-pVTZ(-f) basis set, the relative errors being <1%. To some extent, it stems
28 from mutual compensations from the separate mono-zinc cores, since $\Delta E(\text{SIBFA})$
29 was found to smaller and larger magnitudes than $\Delta E(\text{HF})$ in the blue and the colored
30 cores, respectively.
31

32 *b) TZT-complexed cores.*

33 $\Delta E(\text{SIBFA})$ remains able to reproduce $\Delta E(\text{QC})$ with relative errors <1%. Such
34 accuracy was far from granted at the outset. Given the small magnitude of such an
35 error, it would be illusory, here again, to compare the rankings of the ΔE values in
36 the five complexes. A preference in favor of complex *V* nevertheless emerges from
37 both $\Delta E(\text{QC})$ and $\Delta E(\text{SIBFA})$. Complex *IV* is the one with the least $\Delta E(\text{SIBFA})$ versus
38 $\Delta E(\text{QC})$ stabilization. This can be traced back again to the outcome from complex *IV*
39 in the colored mono-zinc core, the relative underestimation mostly stemming from
40 $E_{\text{pol}}(\text{SIBFA})$ in this complex. This was discussed in paragraph 3 above with possible
41 means towards a finer tune-up. It provides an illustration of the insight afforded by
42 EDAs in a segmental approach.
43
44
45
46

47 **5. Reconsidered complexes of inhibitors I-V with the extended recognition** 48 **site.**

49
50 Table IV recasts the results of the first section of this study, starting with the TZT-
51 uncomplexed cores within the extended VIM-2 recognition site (a) and ending up
52 with the complexes of the entirety of ligands I-V with the site, without (d) and with
53 (e) the water molecules. For the complexes of the TZT anchor with site (c) as well as
54 those of the entirety of the ligand (c and d), $\Delta E(\text{SIBFA})$ has come closer numerically
55 to BSSE-corrected $\Delta E(\text{QC})$ than at the outset, as can be seen by comparing Tables I
56 and IV. There remains an exception, that of TZT in complex *IV*, for which $\Delta E(\text{SIBFA})$
57 has a smaller (by 0.6%) value than $\Delta E(\text{QC})$. Again, this can be traced back to the
58 situation with its complex with the 'blue' site in this very structure *IV*, identifying E_{pol}
59 as the cause for the underestimation. The compared evolutions of $\Delta E(\text{SIBFA})$ and
60

1
2
3 $\Delta E(QC)$ in complexes c, d and e are reported in Figures 5a-c. A significant
4 improvement of the shape of $\Delta E(SIBFA)$ curve relative to $\Delta E(QC)$ is visible in Figures
5 5b-c, as compared to Figures 3b-c.
6

7 **6. Separate interactions of the two arms with VIM-2 residues around the** 8 **dizinc binding site.** 9

10 We have further considered the complexes of R1 and R2 arms with their interacting
11 partners. These are of four types: ionic, H-bonding, π -stacking and cation- π . How
12 well, prior to any recalibration than that of imidazole and benzocarboxylate, could
13 $\Delta E(SIBFA)$ and its contributions match the $\Delta E(QC)$ results? The results are reported
14 in Tables Va-e regarding ligands I-V.
15
16

17 **Ligand I (4690).** The benzocarboxylate arm interacts with its ring perpendicular to
18 the Arg228 side-chain, and *oblique* to the Tyr67 side-chain. In both cases $\Delta E(SIBFA)$
19 can match $\Delta E(QC)$. Of note are the very strong stabilization energies of the Arg228
20 complex, even though the extracyclic carboxylate does not directly interact. ΔE has
21 positive values with the neutral Tyr67 side-chain owing to the absence of
22 dispersion/correlation, an accurate SIBFA calibration which is planned as a next
23 stage in light of SAPT analyses. Lesser accuracy is observed with the His263 side-
24 chain, with which a parallel stacked arrangement takes place, and with the Asn233
25 main-chain, with the carboxylate group as a proton acceptor from the amino group.
26 These are, rather surprisingly, mainly caused by E_{MTP} in both cases. This could
27 possibly be due to the calibration of the parameters of its penetration component
28 (reported in Ref. 43), in which the charge-quadrupole component was given a
29 negligible weight. This is presently being reconsidered in the context of SAPT
30 recalibration with correlated multipoles, and it will be instructive to reconsider this
31 issue when this is completed in turn. Related overestimations with His263 side-chain
32 and VIM-2 backbones are also encountered with the other ligands (see below).
33

34 The R1 substituent interacts with its ring perpendicular to the Phe61 side-chain, and
35 oblique to the Trp87 one, with an H-bond interaction taking place between the
36 extracyclic methoxy group and the Trp87 imino nitrogen. Overestimations of E_{MTP}
37 could again be noted. Such complexes might thus also have to be reevaluated with
38 SAPT.
39

40 **Ligand II (4390).** Similar remarks are found as with ligand I, the geometries of the
41 two complexes being closely related: regarding benzocarboxylate, close $\Delta E(SIBFA)$
42 and $\Delta E(QC)$ values for Arg228, overestimated E_{MTP} values with His263 side-chain and
43 Asn233 main-chain, as well as regarding the interactions of R1 with Phe61 and Trp87
44 side-chains.
45
46

47 **Ligand III (4684).** The N-hydrazone-connected 2,4-dihydroxy-phenyl group
48 interacts with Arg228 by an H-bond between its para-hydroxyl oxygen and one
49 Arg228 amino group ($d_{O-H}=2.29 \text{ \AA}$). It has its ring perpendicular to the Tyr36 ring
50 and nearly parallel to that of His263. $\Delta E(SIBFA)$ matches well $\Delta E(QC)$ but there are
51 again E_{MTP} overestimations in the His263 complex, and to a lesser extent, in the
52 Tyr67 one. $E_{pol}(SIBFA)$ appears underestimated.
53

54 The C-connected 2,5-dihydroxy-phenyl group (substituent R1) has its meta-O
55 hydroxyl accepting a proton from the imino group of Trp87 ($d_{OH}=2.05 \text{ \AA}$) with its
56 ring oblique to the indole and perpendicular to the Phe61 ring. $E_{pol}(SIBFA)$ is
57 underestimated, while E_{MTP} is overestimated regarding the interaction with Phe61.
58 There is an overall acceptable match of $\Delta E(SIBFA)$ to $\Delta E(QC)$, pending the forecast
59 refinements.
60

Ligand IV (5064). The interactions of the benzocarboxylate arm with Arg228 and His263 are similar to those found with ligands I and II, the best numerical agreement being with Arg228. As with these two ligands, the $\Delta E(\text{SIBFA})$ values for its interaction with the Asn233 backbone are overestimated, again due to E_{MTP} .

The dichlorobenzene R1 arm interacts with Asp119 and Trp87 through one Cl substituent, acting simultaneously as an electron acceptor from Asp86 by its 'sigma hole' ($d_{\text{Cl-O}}=2.86 \text{ \AA}$) and as an H-bond acceptor from the imino proton of Trp56 ($d_{\text{Cl-H}}=2.49 \text{ \AA}$). It interacts in a near-perpendicular arrangement with Phe31 side-chain. Even though the summed $\Delta E(\text{SIBFA})$ energies of R1 with the three side-chains are similar to the $\Delta E(\text{QC})$ values (14.9 vs. 14.5 kcal/mol, respectively), improvements regarding its interaction with each residue appear necessary.

Ligand V (5069). The first phenyl ring of the R2 substituent interacts by perpendicular π -stacking with the Tyr67 side-chain, and simultaneously by a cation- π interaction with the Arg228 side-chain which binds perpendicular to it. As in the related π -stacking complexes with the other ligands, there are partial compensations between overestimated E_{MTP} and underestimated E_{pol} values.

The *m*-benzocarboxylate arm interacts with the main-chain of Glu225 and with the Arg228 and His263 side-chains. Its interaction with the Arg228 side-chain is much stronger than the one between the first phenyl ring and this residue, clearly due to the greater proximity of the carboxylate group and its greater overlap. It is noted that the summed $\Delta E(\text{SIBFA})$ value of this ring with the Arg228 and His263 side-chains is the same (-40 kcal/mol) than that of $\Delta E(\text{QC})$, but it is due to compensations between its under- and its overestimations with them, thus an additional incentive for further refinements of the aromatic entities.

The 2,5-dihydro-phenyl R1 arm binds in an oblique π -stacking arrangement to Trp87 with an additional H-bond of the *meta*-hydroxyl oxygen with the Trp87 imino proton ($d_{\text{OH}}=2.09 \text{ \AA}$), with very close $\Delta E(\text{SIBFA})$ and $\Delta E(\text{QC})$ values. It also has a perpendicular π -stacking interaction with Phe61 side-chain.

7. Networks of structural waters.

There are tightly bound 'discrete' water molecules in the recognition site, which can either bind to both the ligand and protein residues, or mediate the interaction between them. They can be endowed with much higher dipole moments than liquid water [70-72], and possibly impact the ordering of relative affinities of ligands to a given target [70, 72]. For ligands I, II, and IV, we could identify related networks of discrete waters in the vicinity of their common benzocarboxylate arm and of its VIM-2 partners.

Thus, with the present notation, in the case of ligand I (4690), water *W1* donates one proton to one carboxylate oxygen and the other to the main-chain carbonyl of Asn233. It acts as an H-bond acceptor from the imino proton of His196, from the hydroxyl group of Tyr224 and from water *W2*. *W2* is in turn acceptor from the partly acidic H connected to the His263 C *ortho* to the Zn-binding nitrogen, and to *W3*. *W3* acts as an H-bond donor to the main-chain CO of Ile223, and as an H-bond acceptor from *W5*. *W5* acts as an acceptor from the main-chain NH of Glu225, and as a donor to *W4*. *W4* is also an acceptor from the imino cationic Arg228 side-chain and the partly acidic H belonging to the CH bond *meta* to the carboxylate, and acts as an H-bond donor to the anionic Glu225 side-chain. The simultaneous involvement of *W4* as an H-bond acceptor from a cationic side-chain and an H-bond donor to an anionic side-chain should explain its particularly large dipole moment of 2.94 Debye. With ligands II (4390) and IV (5064) the corresponding *W4* molecule is also the one with the largest dipole moment, namely 3.09 and 3.20 Debye, respectively.

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2
3
4 A similar network is found in the high-resolution X-ray crystal structure of the VIM-2
5 complex with ligand I [34]. One water molecule does, related to *W4*, bridge the
6 imino nitrogen of Arg228 and one anionic O of Glu225 ($d_{\text{ON}}=3.10 \text{ \AA}$; $d_{\text{OO}}=3.00 \text{ \AA}$).
7 It is H-bonded to a second water, related to *W5*, which is H-bonded to the main-
8 chain N of Glu225, and to a third water, related to *W3*, bound to the main-chain O of
9 Ile169. There is also one water, related to *W1*, which binds simultaneously to one O
10 of the benzocarboxylate, to the hydroxyl of Tyr224 and the imino N of His196.
11 With ligand III (4684), devoid of an anionic *ortho* carboxylate, replaced by a
12 hydroxyl group, a similar network could be observed as well, with *W4* having a value
13 of 3.14 Debye.
14

15
16 A different network is observed with ligand V (5069), which has two phenyl rings at
17 R2, with a *meta* carboxylate on the second one. *W1* accepts a proton from the main-
18 chain NH of Asn233 and donates a proton to *W2* and the hydroxyl O of Tyr224. *W2*
19 donates a proton to one carboxylate O of R2 and to *W5*. *W5* donates a proton to this
20 O as well, and to the main-chain O of Ile223. *W3* and *W4* donate a proton to one
21 anionic O of Glu225 and to the other R2 carboxylate O, respectively. There are now
22 three water molecules with large dipole moments, *W1*, *W2*, and *W5* with values of
23 2.63, 2.73 and 2.76 Debye, respectively.
24

25 **8. Correlated ΔE calculations on the mono- and the dizinc cores.**

26
27 It is essential to extend the present validations with advanced dispersion-augmented
28 Density Functional Theory (DFT) functionals. This is a prime objective of SIBFA
29 underway in the context of SAPT. But how close an agreement could be enabled at
30 the present stage with DFT-D EDA's pending such refinements, could EDA enable to
31 monitor the changes in the magnitude of each $\Delta E(\text{QC})$ contribution upon passing
32 from HF to DFT-D, and how well could their SIBFA counterparts account for such
33 staged changes?
34

35
36 Table VI reports the ALMOEDA results on the blue and the colored mono-zinc binding
37 sites with the B3LYP-D3 and the ω -B97X-D functionals using the cc-pVTZ basis set.
38 We also report the corresponding SIBFA results with correlated multipoles and
39 polarizabilities. We have used the same parametrization as in our previous study on
40 the complexes of TZT with the zinc-binding cores of L1 [33]. The recalibration done
41 in the present study for HF having resulted into a lesser agreement, was not
42 retained. For comparison, we also report the ALMOEDA HF/cc-pVTZ results. Table VII
43 reports the corresponding results on the dizinc core.
44

45
46 *Blue Zn(II) core.* $E_1(\omega\text{B97X-D})$ is app. 7 kcal/mol larger in magnitude than $E_1(\text{B3LYP-}$
47 $\text{D3})$ but E_2 is correspondingly 4 kcal/mol smaller with $\omega\text{B97X-D}$, due essentially to
48 E_{ct} . With both functionals, E_2 , which includes dispersion through the van der Waals
49 kernel, has 30-35 kcal/mol larger magnitudes than E_1 . $E_1(\text{HF})$ is smaller in
50 magnitude than $E_1(\text{DFT-D})$, but this could result from a compensation between both
51 large E_{C} and E_{X} values at the HF level. Most of the ΔE gains upon passing to the
52 correlated levels stem from E_{pol} and E_{ct} , about 15 kcal/mol from both with the
53 $\omega\text{B97X-D}$ functional.

54 $E_1(\text{SIBFA})$ has extremely close values to $E_1(\omega\text{B97X-D})$, and follows consistent trends
55 with it in the five complexes. Comparison with Table I shows that $E_2(\text{SIBFA})$ has
56 comparable magnitudes than at the HF level, an increase in the magnitude of E_{pol}
57 being compensated by a decrease of E_{ct} . The sum of E_2 and $E_{\text{disp}}(\text{SIBFA})$ follows very
58 close trends with the five complexes as $E_2(\text{DFT-D})$. It has an approximately 5
59 kcal/mol out of 180 smaller magnitude than $E_2(\omega\text{B97X-D})$ accounting for most of the
60

1
2
3 present underestimation of $\Delta E_{\text{tot}}(\text{SIBFA})$. It reproduces the shallow behavior of
4 $\Delta E(\text{DFT-d})$ among complexes I-IV with variations of <1% and its decrease with
5 complex V, due to E_2 .
6

7 *Colored Zn(II) core.* E_1 now has extremely close values with both functionals, as well
8 as with $E_1(\text{HF})$. $E_1(\text{SIBFA})$ has also very close values to $E_1(\text{QC})$ in complexes I-IV, the
9 difference increasing, however, from <3 kcal/mol out of 460 to 7 kcal/mol out of
10 460, the corresponding relative error nevertheless remaining < 1.5%. E_2 has
11 increased by app. 8 kcal/mol with respect to its values calibrated on HF results
12 (Table I). The sum of E_2 and E_{disp} can now matches $E_2(\omega\text{B97X-D})$ to within <6
13 kcal/mol out of 155, and evolves consistent to it in complexes I-V. Overall,
14 $\Delta E_{\text{tot}}(\text{SIBFA})$ can reproduce the numerical values of $\Delta E(\omega\text{B97X-D})$ very closely, the
15 relative errors < 1.5%.
16
17

18 *Binuclear Zn(II) core.* $E_1(\omega\text{B97X-D})$ has 15 kcal/mol larger magnitudes than
19 $E_1(\text{B3LYP-D3})$ while $E_2(\omega\text{B97X-D})$ has 10.5 kcal/mol smaller magnitudes than
20 $E_2(\text{B3LYP-D3})$, resulting in only slightly larger magnitudes of $\Delta E(\omega\text{B97X-D})$ than
21 $\Delta E(\text{B3LYP-D3})$, of 3.5 kcal/mol out of 1000. The magnitude increase of DE upon
22 passing from HF to DFT-d stems first from E_{ctr} , about 40 and 50 kcal/mol with the
23 $\omega\text{B97X-D}$ and B3LYP-D3 functionals, respectively, and then from E_{pol} , about 30
24 kcal/mol.
25

26 $E_1(\text{SIBFA})$ retains extremely close values to $E_1(\omega\text{B97X-D})$, the relative errors not
27 exceeding 1.2%. $E_{\text{pol}}(\text{SIBFA})$ is also close to $E_{\text{pol}}(\text{DFT-D})$, the relative errors < 3%.
28 While as noted above, $E_{\text{ct}}(\text{SIBFA})$ is much smaller than its DFT counterparts, namely
29 nearly one half, the inclusion of $E_{\text{disp}}(\text{SIBFA})$ results into a summed E_2 matching very
30 closely the $E_2(\text{DFT-D})$ trends: its largest and smallest magnitudes are for complexes
31 IV and V, respectively, with shallow variations in I-III. $\Delta E_{\text{tot}}(\text{SIBFA})$ can match
32 $\Delta E(\text{DFT-D})$ with relative errors <2%. Figures 6a-c show the compared evolutions in
33 complexes I-V of $\omega\text{B97X-D}$ and SIBFA for E_1 , E_2 (including E_{disp} for SIBFA) and ΔE_{tot} ,
34 respectively. The trends are faithfully reproduced. We believe this is highly
35 encouraging, considering that no extra calibration was attempted to match the DFT-
36 D results at this stage.
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41 **Conclusions and Perspectives.**

42 Zn(II) metalloproteins can be responsible for numerous severe pathologies, and are
43 challenging targets for the design of novel efficient inhibitors, a need presently
44 unmet. Among these are MBLs, responsible for the acquired resistance of bacteria
45 against antibiotics which they cleave. In inhibitor-MBL complexes, the onset of very
46 strong second-order polarization and charge-transfer precludes the use of 'classical'
47 force-field simulations. Presently only QM/MM approaches could be safely considered,
48 as well as semi-empirical approaches such as DFT-TB [23, 24]. But are these
49 presently tractable to perform long-duration MD and free energy perturbation (FEP)
50 calculations to derive free energies of binding, or could not, alternatively, polarizable
51 MM be used as a surrogate to handle the inhibitor-MBL complex in its entirety?
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54 In a previous study, we showed that the SIBFA procedure closely reproduced the
55 values of $\Delta E(\text{QC})$ and its individual contributions at play in the two separate mono-
56 zinc cores and the dizinc core of two MBLs, L1 and VIM-2, both uncomplexed and
57 complexed with a 1,2,4-triazole-3-thione (TZT) moiety, a conjugated monoanionic
58 zinc-binding motif acting as an 'anchor' in the dizinc core. We have extended this
59 study by now considering five TZT-containing inhibitors synthesized and tested in our
60

Laboratories. They have two arms, R1 and R2, substituting the TZT ring C⁵- and extracyclic hydrazone, respectively. At the outcome of energy-minimization of their complexes with VIM-2, we have evaluated how closely could $\Delta E(\text{SIBFA})$ reproduce $\Delta E(\text{QC})$ in an extended recognition site made out of the dizinc core, the neighboring VIM-2 residues bound to each arm, and fourteen discrete waters. The interactions of these arms are of diverse nature, H-bonding, cation- π and π -stacking. $\Delta E(\text{SIBFA})$ reproduced correctly the variations of $\Delta E(\text{QC})$ along the series of the five complexes, and its numerical values. These were however overestimated, being closer to BSSE-uncorrected than to BSSE-corrected $\Delta E(\text{QC})$, and the differences between some complexes were larger than the corresponding $\Delta E(\text{QC})$ differences. Some of these could be traced back to the interactions of the sole TZT anchor in the five complexes, prior to including the contributions of the arms.

This issue led us to seek for refinements in its calibration. It was done by an automated procedure, which for each separate $\Delta E(\text{SIBFA})$ contribution optimizes simultaneously the relevant parameters by LSQF minimizing its difference with respect to its $\Delta E(\text{QC})$ counterpart for a diversity of TZT complexes with a Zn(II) cation probing in- and out-of-plane positions. This was extended to imidazole as well, because it is encountered as a Zn(II) ligand three times in the first mono-zinc core and once in the second. This enabled further refined reproductions of $\Delta E(\text{QC})$ and its contributions by SIBFA. For each of the five structures derived from energy-minimization with each ligand, the validations were done on the two TZT-uncomplexed as well as on the TZT-complexed mono-zinc cores and dizinc core. This represents a total of thirty complexes, fifteen uncomplexed and fifteen complexed ones. With one exception, $\Delta E(\text{SIBFA})$ could reproduce $\Delta E(\text{QC})$ with a narrowed down relative error, now <1.5%. The 'outlier' had a relative error of 2.5%. The relative weights of E_1 and E_2 were correctly accounted for, thus attesting for a good control of non-additivity.

Retaining a good control is essential because any imbalance with respect to QC at this stage could result into an amplified imbalance when the arms are included, and into their suboptimal orientation in the extended site. The present calculations showed that the anchorage of TZT in the dizinc site retains flexibility, so that it is essential to be able to account for the sensitivity of $\Delta E(\text{QC})$ and its contributions upon geometrical rearrangements, however limited.

We next revisited the complexes of the five inhibitors with the extended recognition VIM-2 site, totaling about 280 atoms. A significant improvement of the reproduction of $\Delta E(\text{QC})$ was observed with respect to the starting situation, and this could be readily seen upon comparing the evolutions displayed in Figures 5a-c to those displayed in Figures 3a-c. It concerned a) the interactions of the sole TZT with the extended binding site; and the interaction of the entirety of the inhibitor b) prior to; and c) after the inclusion of the structured waters: in a) and b) $\Delta E(\text{SIBFA})$ could match $\Delta E(\text{QC}/\text{BSSE-corrected})$ with relative errors < 1.5% and an improved parallelism could be seen in all three cases. The relative errors were amplified to 2% in case c). This appears to be due to some overestimation of the contributions to DE of water. This should be remedied in the next phase of refinements, presently underway at the correlated level.

On the other hand, the interactions of the R1 and R2 arms with their VIM-2 partners showed that some improvements remained desirable, even if the remaining errors did not impair the overall agreements noted in stage b) above.

The above comparisons also gave clues for the future refinements that are being resumed, now at the correlated level:

- the calibration of the penetration component of E_{MTP} should give more weight to the charge-quadrupole term;
- the calibration of E_{rep} should be done upon resorting to an additional probe than Zn(II), such as water. This would enable for the response of its bond-bond and lone pair-lone pair components, as it is presently dominated by the lone pair-bond component, itself limited to an actual lone pair-atom component;
- the calibration of E_{pol} should allow for a partial relaxation of the internal coordinates of the polarizability tensors connecting them to their heteroatom or bond barycenter bearers.

We have extended the validations at the correlated level, regarding at this stage the unligated mono-zinc cores and the dizinc core. We resorted to the same calibration as in our previous work and performed EDA analyses with two advanced functionals, B3LYP and ω B97X-D. Close correlations were found in the fifteen complexes. E_1 was closely accounted for. The inclusion of E_{disp} enabled the sum of $E_{ct}+E_{pol}+E_{disp}$ to match the evolutions of the summed $E_{pol}+E_{ct}$ from ALMOEDA, in which the actual dispersion is included in the van der Waals kernel. There was a constant underestimation in the dizinc core of accountable for the present underestimation of $\Delta E_{tot}(SIBFA)$ with respect to $\Delta E(DFT/\omega B97X-D)$, nevertheless limited to 2%.

The next stage of refinements is now starting, and should be reported subsequently. It resorts to SAPT-DFT on all protein and nucleic acid constitutive fragments, with Zn(II) and a dipolar molecule, water, probing a diversity of in-plane approaches, and perpendicular positions of conjugated fragments. SAPT delivers six separate contributions, including dispersion and exchange-dispersion, and their SIBFA counterparts should be able to match them by the LSQF approach, and, subsequently, more evolved approaches from applied mathematics. Other probes could be considered as well to enrich the diversity of the training set. Validations on multimolecular complexes will be done next, as in the present study, on multimolecular complexes using ALMOEDA and advanced DFT-D functionals.

We would like to reemphasize our essential motivation, namely long-duration MD on a series of drug-Zn-metalloprotein complexes, which should enable free energy perturbation studies delivering relative free energies of binding of competing inhibitors. Such studies are now rendered possible by very significant recent accelerations of the massively parallel Tinker-HP code [37]. The closer $\Delta E(SIBFA)$ to $\Delta E(QC)$ on the extended recognition sites, the safer the predictions of relative ΔG s on the complexes with the entirety of the protein.

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Table captions.

Table I. Complexes of the extended recognition site of VIM-2 with ligands I-V. Compared $\Delta E(\text{SIBFA})$ and $\Delta E(\text{QC}/\text{HF})$ on the following:

a) intermolecular interactions prior to ligand binding and without the 'discrete' water molecules; b) intermolecular interactions prior to ligand binding and with the 'discrete' water molecules; c) intermolecular interactions with the TZT anchor and without the waters; d) intermolecular interactions with the entire ligands and without the waters; e) intermolecular interactions with the entire ligands and with the waters, Energies in kcal/mol.

Table II. Mono-zinc cores of VIM-2 in their complexes with the five inhibitors. QC (HF/RVS) and SIBFA intermolecular interaction energies and their contributions. Energies in kcal/mol.

Table III. Di-zinc cores of VIM-2 in their geometries with the five inhibitors. QC (HF/RVS) and SIBFA intermolecular interaction energies without and with the TZT anchor. Energies in kcal/mol.

Table IV. Complexes of the extended recognition site of VIM-2 with ligands I-V. Compared $\Delta E(\text{SIBFA})$ and $\Delta E(\text{QC}/\text{HF})$ at the outcome of the recalibration procedure on the following:

a) intermolecular interactions prior to ligand binding and without the 'discrete' water molecules; b) intermolecular interactions prior to ligand binding and with the 'discrete' water molecules; c) intermolecular interactions with the TZT anchor and without the waters; d) intermolecular interactions with the entire ligands and without the waters; e) intermolecular interactions with the entire ligands and with the waters, Energies in kcal/mol.

Tables V(a-e). Complexes of the R1 and R2 arms of ligands I-V with VIM-2 residues of the extended recognition site. Energies in kcal/mol.

Table VI. Compared ALMOEDA and SIBFA total interaction energies in the two mono-zinc binding sites. ALMOEDA results are at the B3LYP-D, ω B97X-D and HF levels. Energies in kcal/mol.

Table VII. Compared ALMOEDA and SIBFA total interaction energies in the dizinc binding sites. ALMOEDA results are at the B3LYP-D, ω B97X-D and HF levels. Energies in kcal/mol.

Figure captions.

Figures 1(a-e). Structural formulas of the five studied VIM-2 inhibitors

Figures 2(a-e). Representation of the energy-minimized complexes of the extended recognition site of VIM-2 with the five inhibitors.

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4 **Figures 3(a-c).** Complexes of the extended VIM-2 recognition site with ligands I-V. Comparisons between $\Delta E(\text{SIBFA})$ and $\Delta E(\text{QC/HF})$ regarding: a) the entire ligand without the discrete waters; b) the entire ligand with the discrete waters; c) the sole TZT anchor.

9 **Figures 4(a-g),** Complexes of the TZT anchor with a probe Zn(II) ligand. Compared evolutions of SIBFA and QC/RVS ΔE contributions regarding: a) E_C and E_{MTP} ; b) E_X and E_{rep} ; c) E_{pol} ; d) E_{ct} ; e) E_1 ; f) E_2 ; g) DE.

13 **Figures 5(a-c).** Complexes of the extended VIM-2 recognition site with ligands I-V at the outcome of TZT, imidazole, and benzocarboxylate parameter refinements. Comparisons between $\Delta E(\text{SIBFA})$ and $\Delta E(\text{QC/HF})$ regarding: a) the entire ligand without the discrete waters; b) the entire ligand with the discrete waters; c) the sole TZT anchor.

19 **Figures 6(a-c).** Dizinc binding site. SIBFA and $\omega\text{B97X-D/ALMOEDA}$ intermolecular interaction energies prior to TZT binding. Compared evolutions in the structures of ligands I-V of: a) E_1 ; E_2 including E_{disp} for SIBFA; c) $\Delta E_{\text{tot}}(\text{SIBFA})$ and $\Delta E(\omega\text{B97X-D})$.

Supporting information.

26 **S1.** List of Zn-TZT and ligand-VIM-2 distances in the complexes of the extended recognition site with ligands I-V.

29 **S2.** LSQF-optimized SIBFA TZT parameters for a) E_{MTP} ; b) E_{rep} ; c) E_{pol} ; d) E_{ct} .

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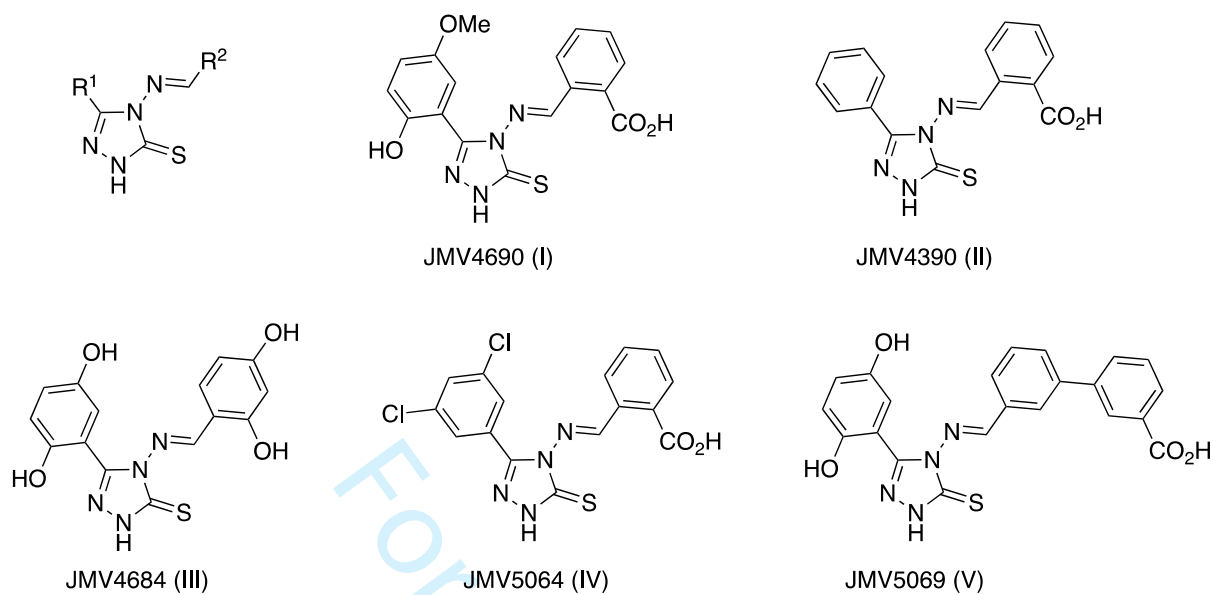
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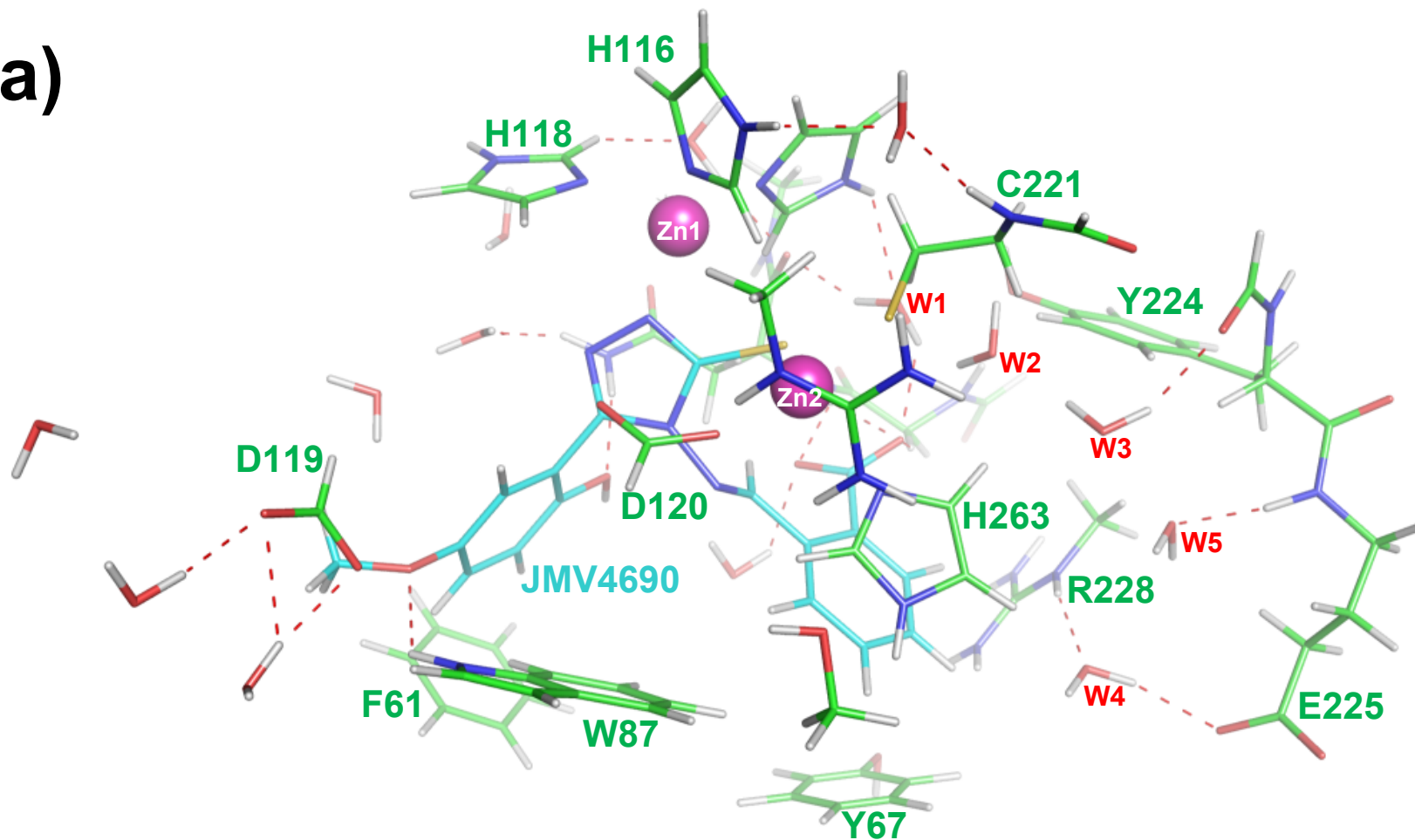
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Figure 1

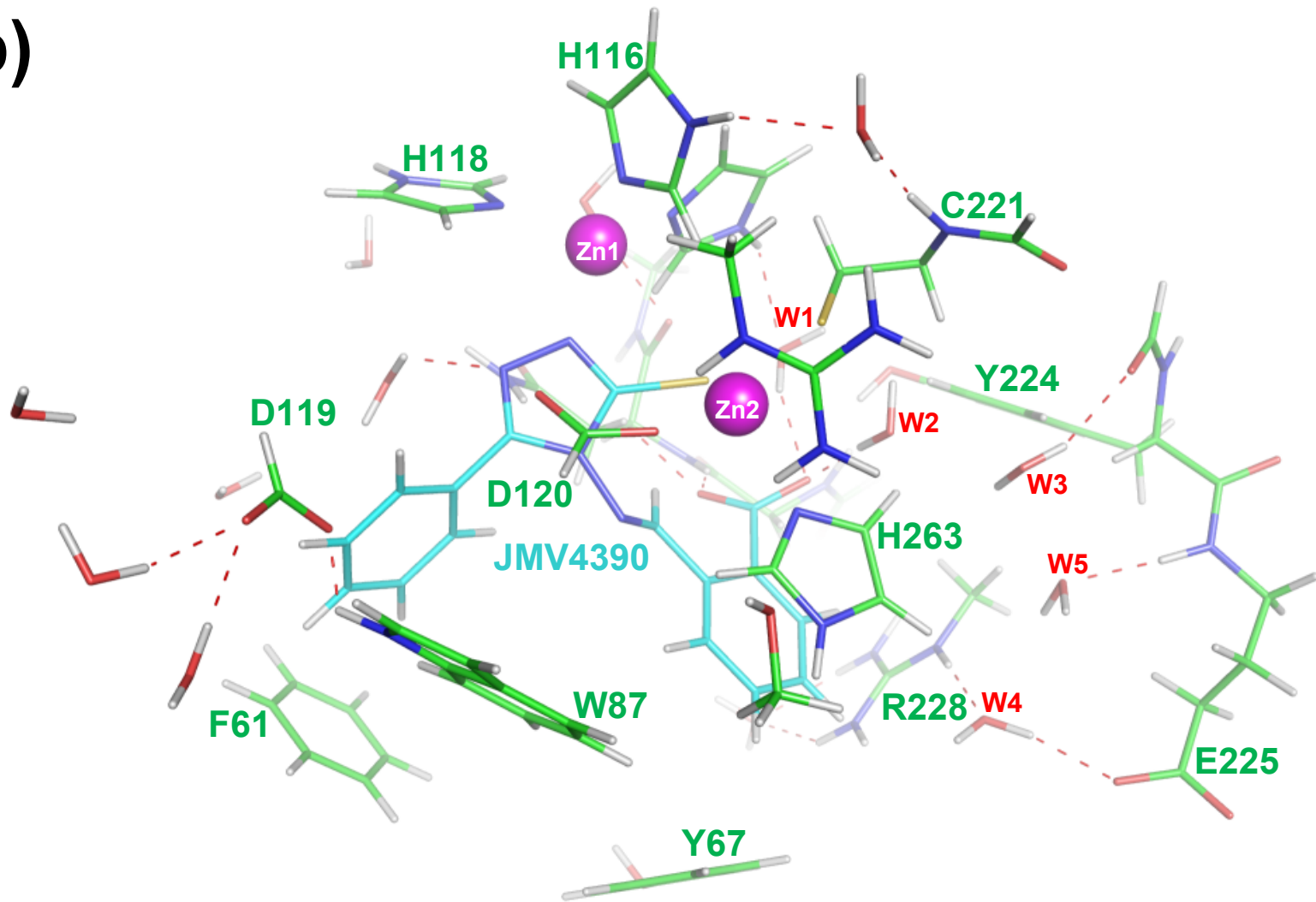


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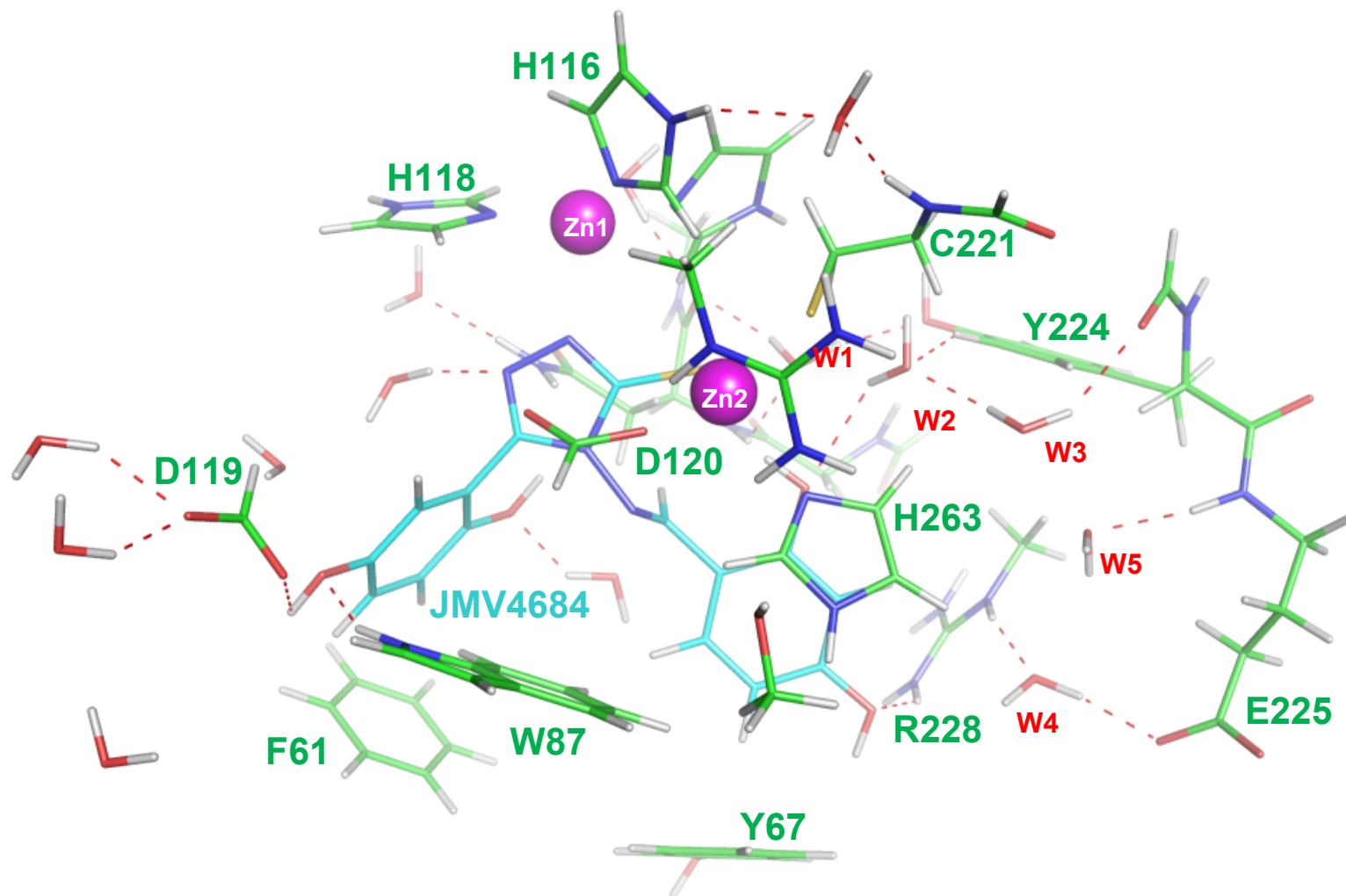


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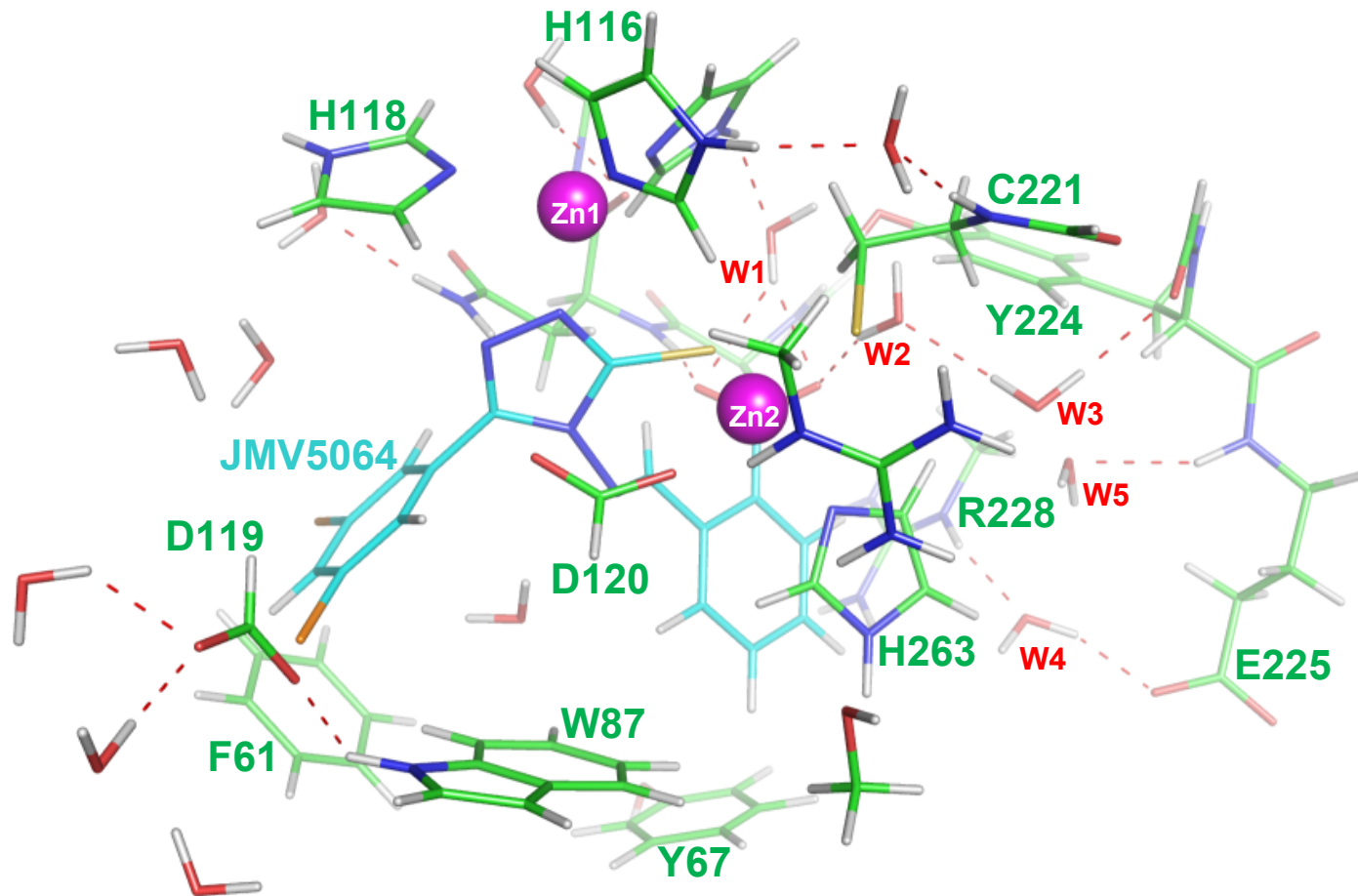


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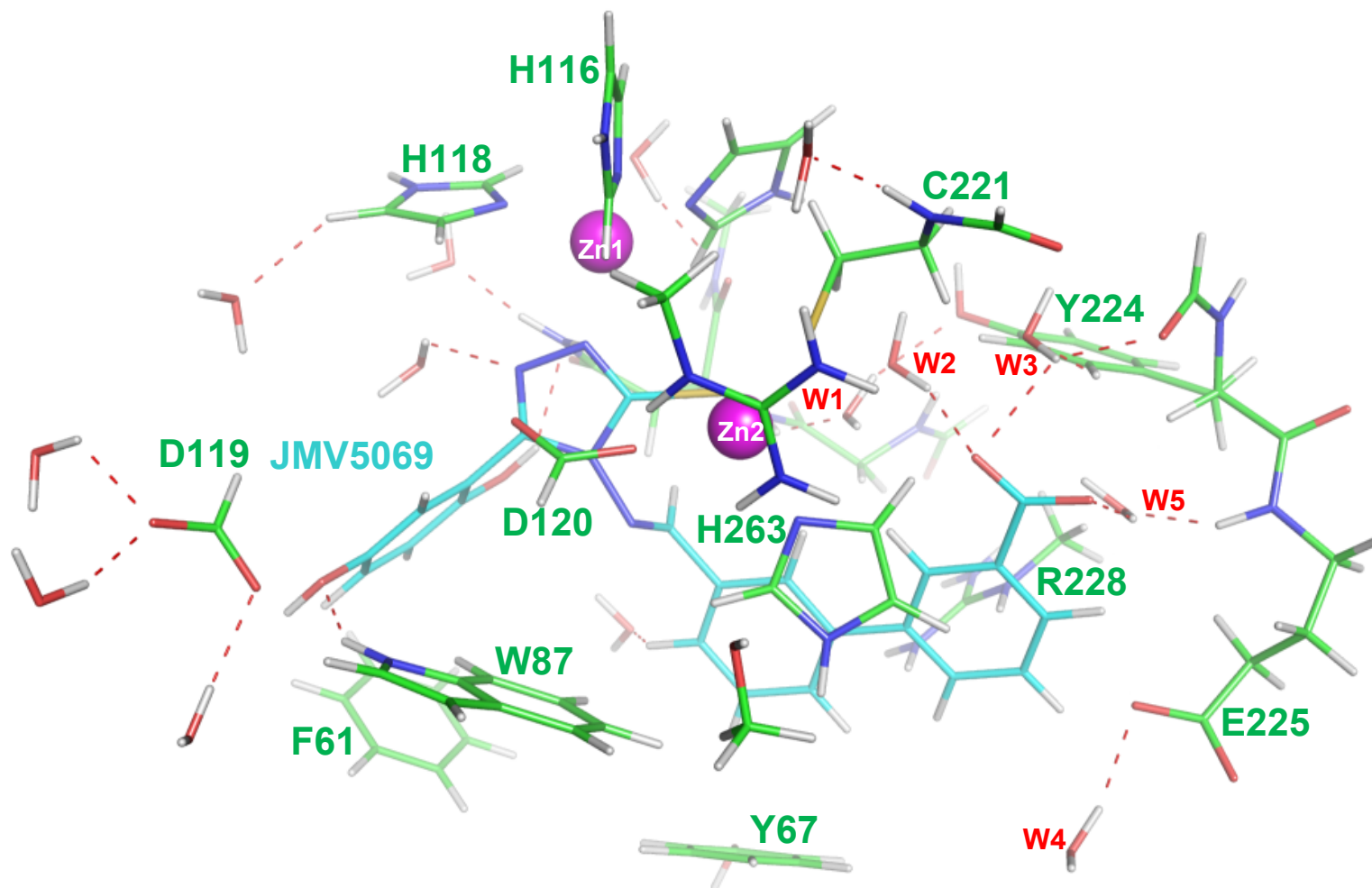


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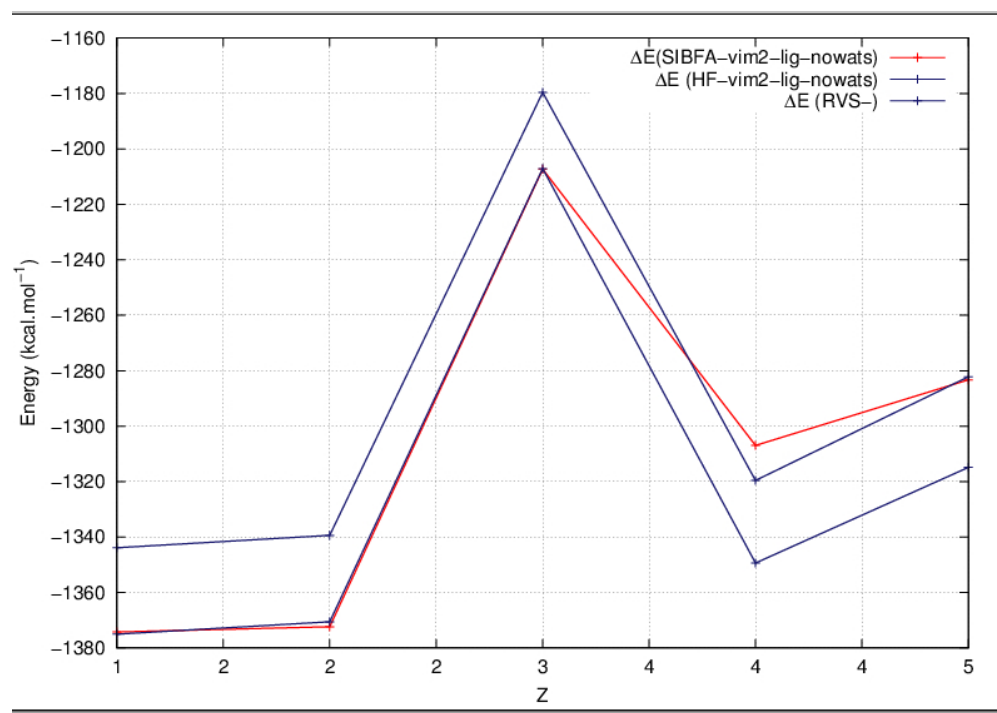


Figure 3a

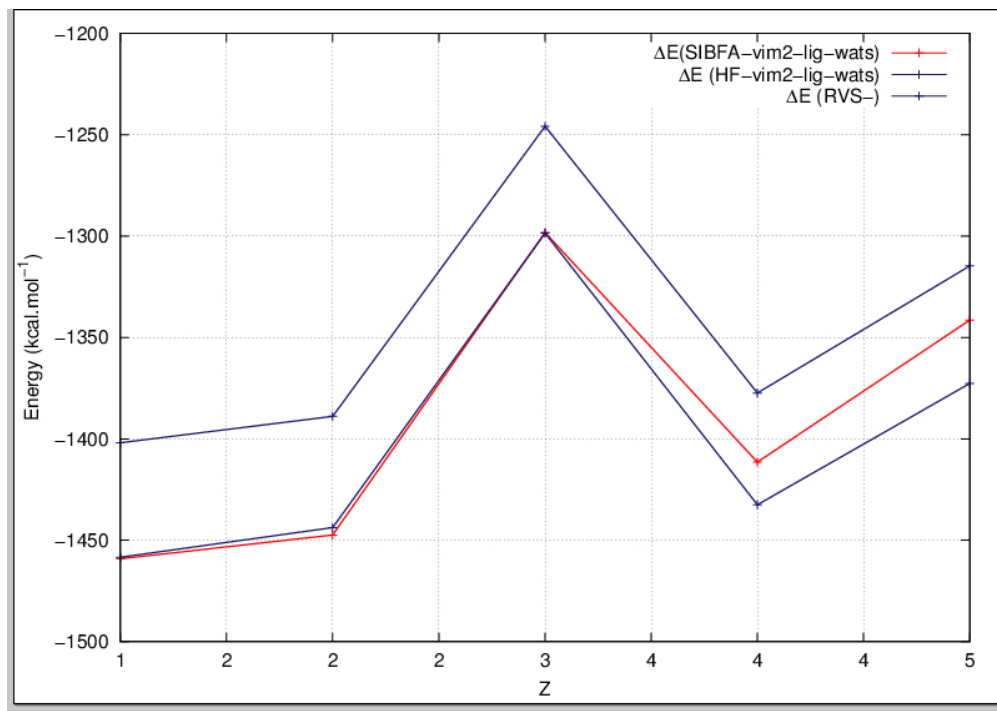


Figure 3b

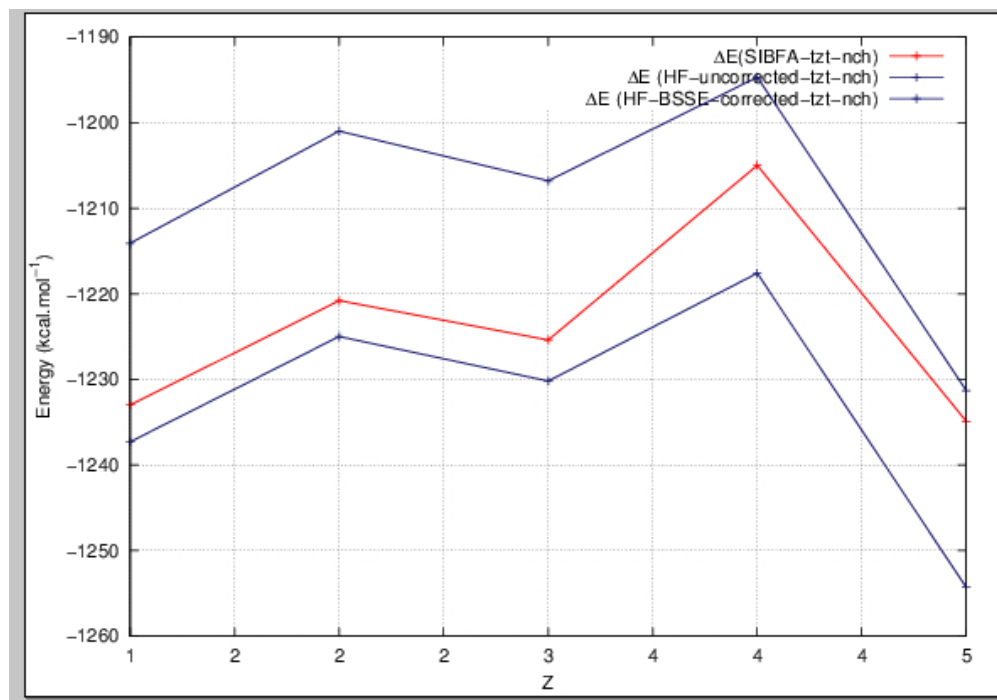


Figure 3c

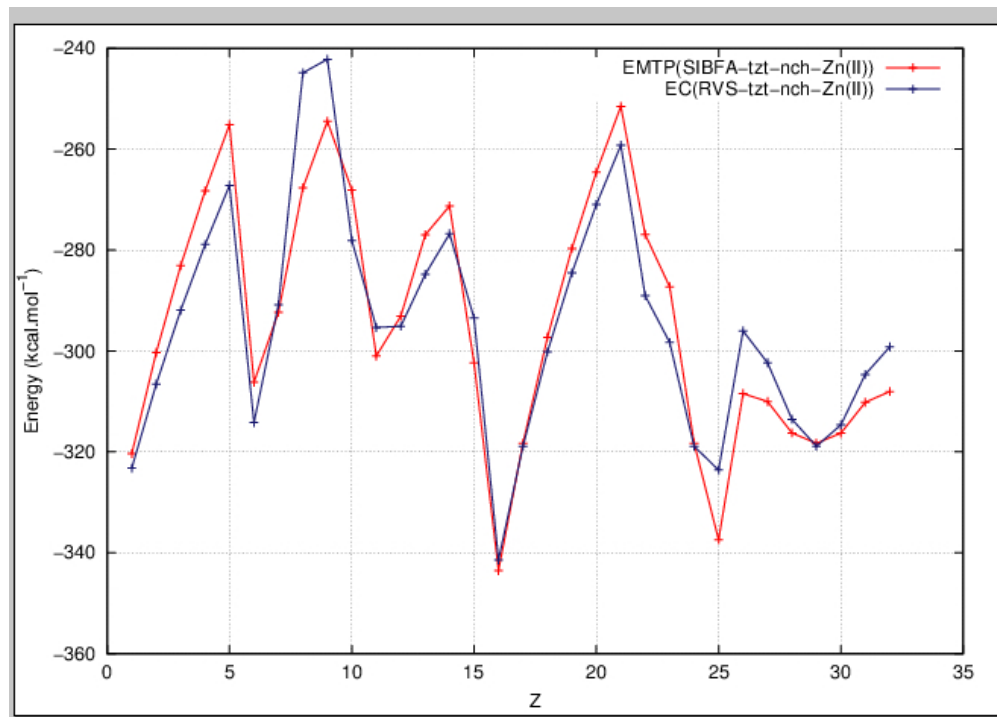


Figure 4 a.

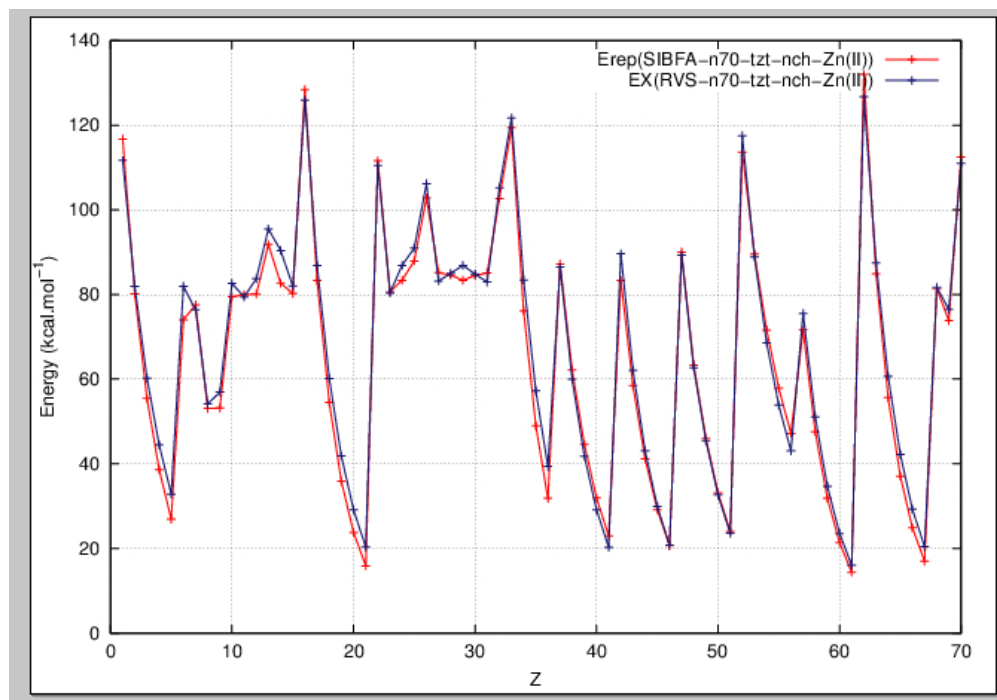


Figure 4b.

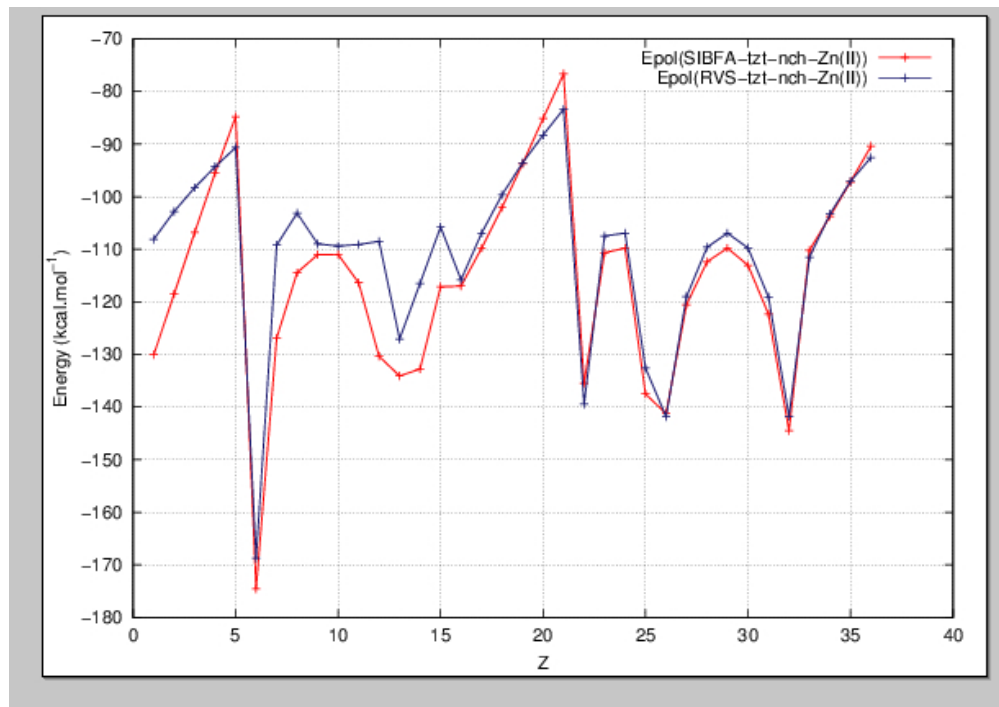


Figure 4c

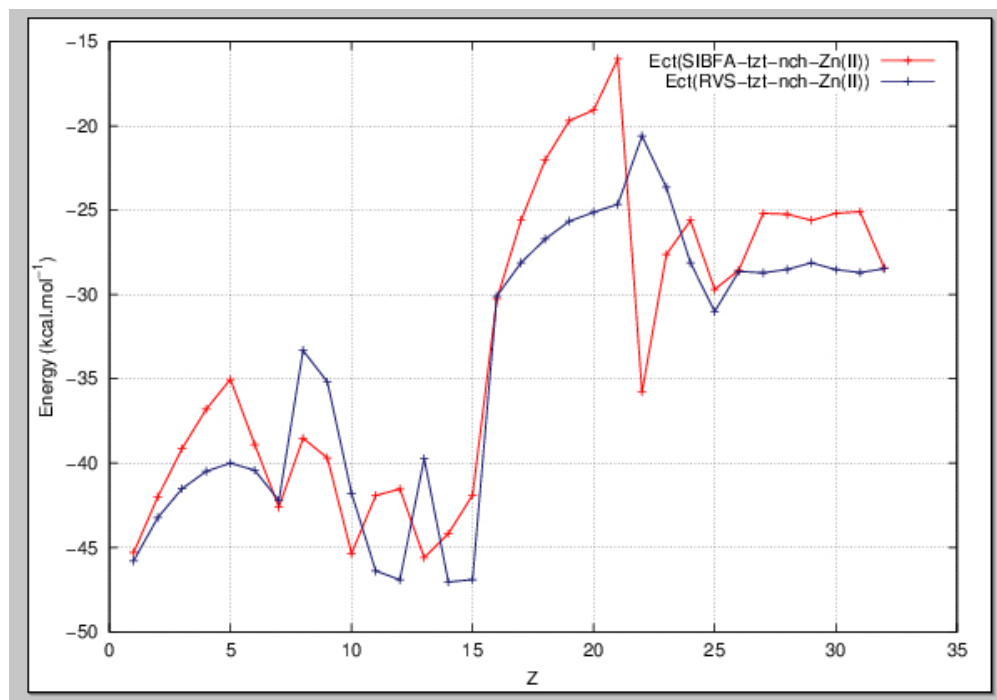


Figure 4d

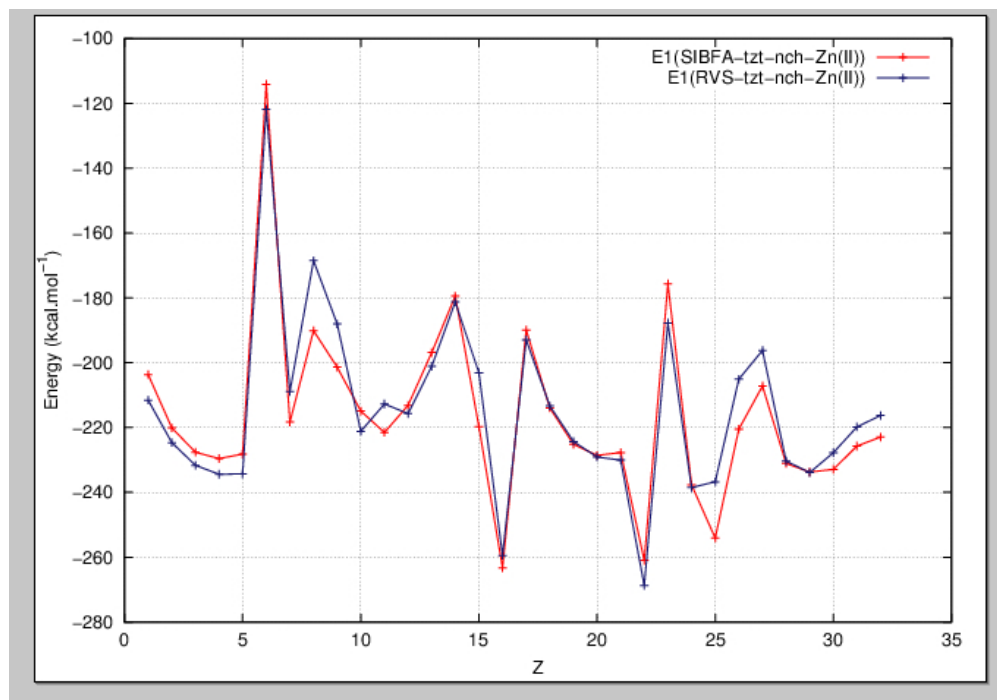


Figure 4e.

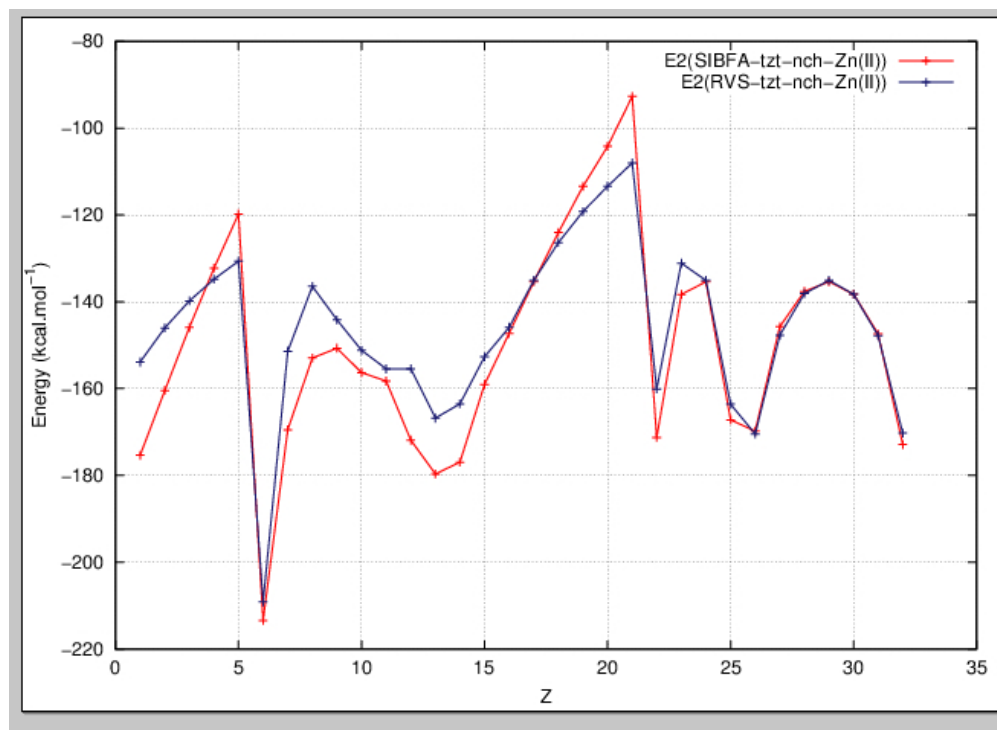


Figure 4f

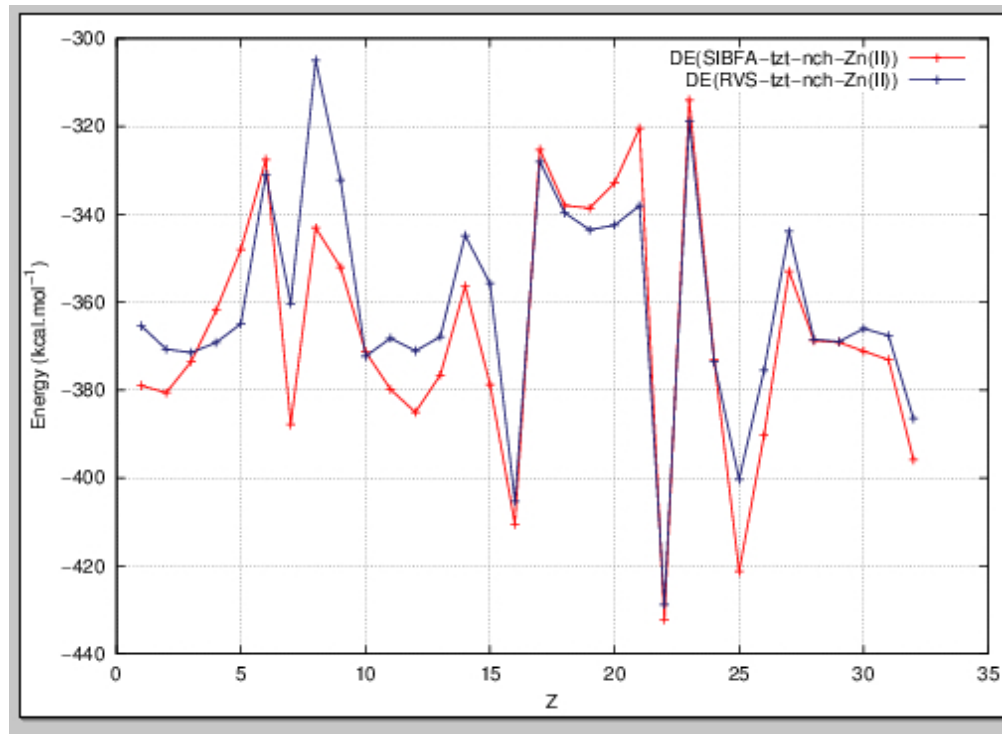


Figure 4g

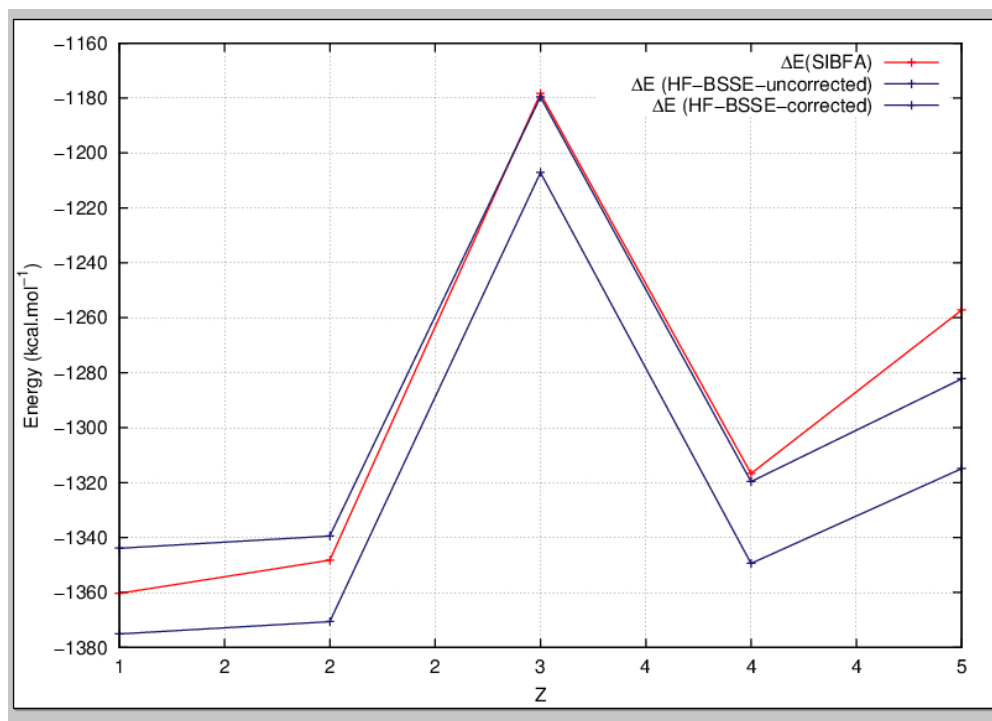


Figure 5a

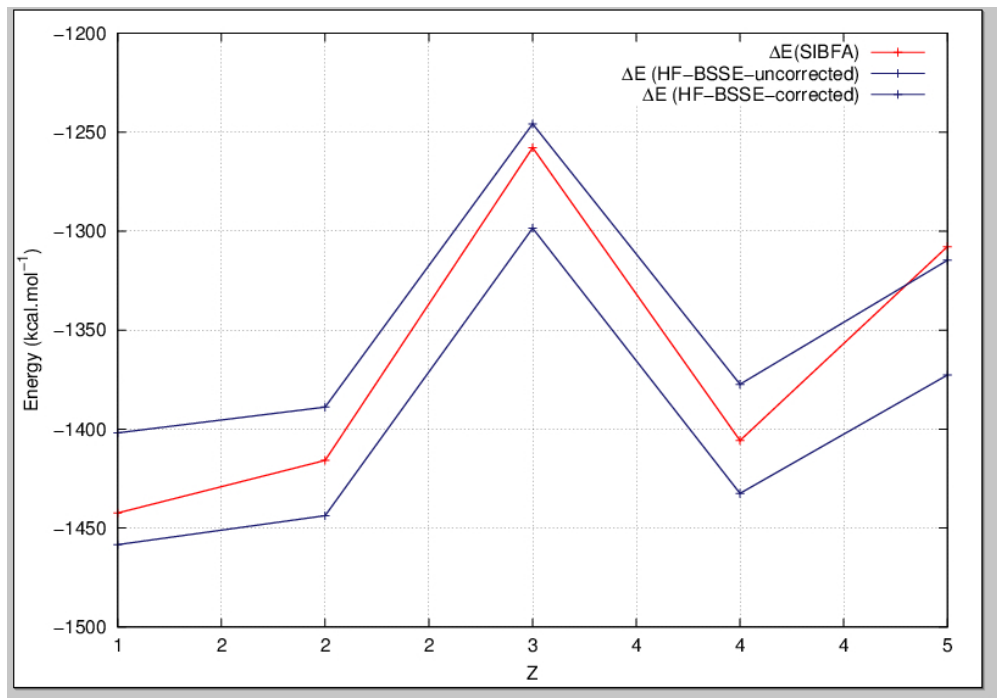


Figure 5b

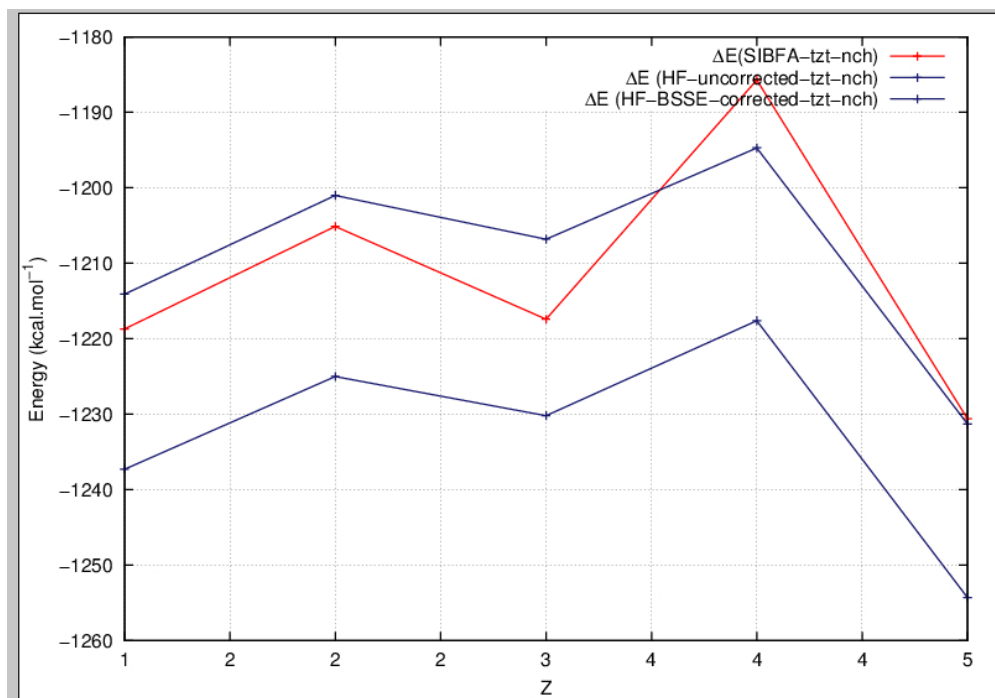


Figure 5-c

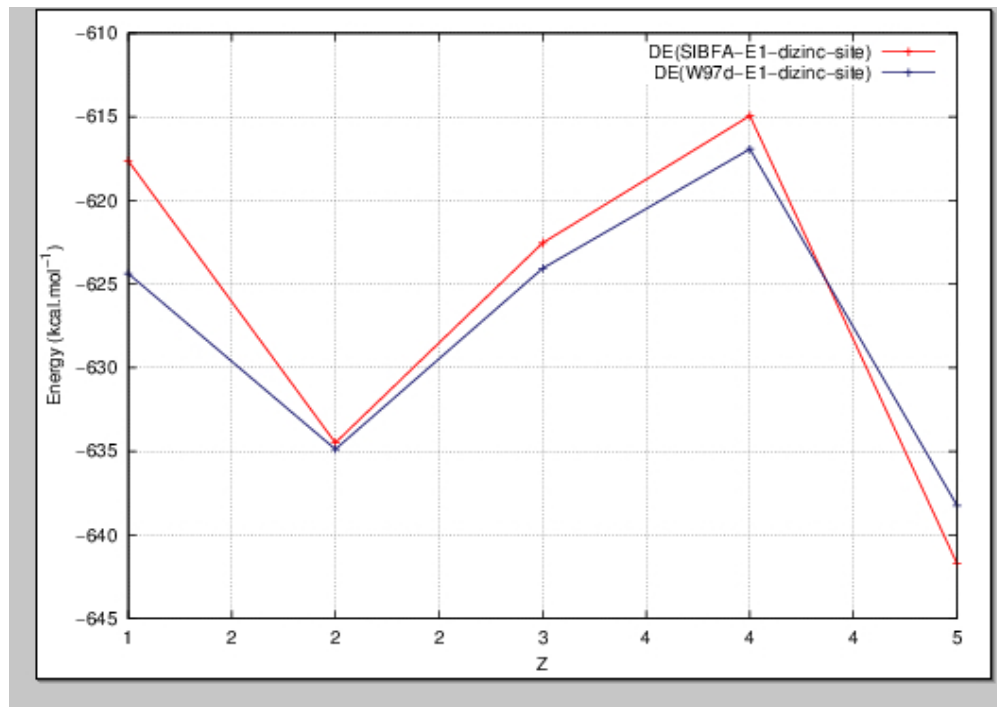


Figure 6-a

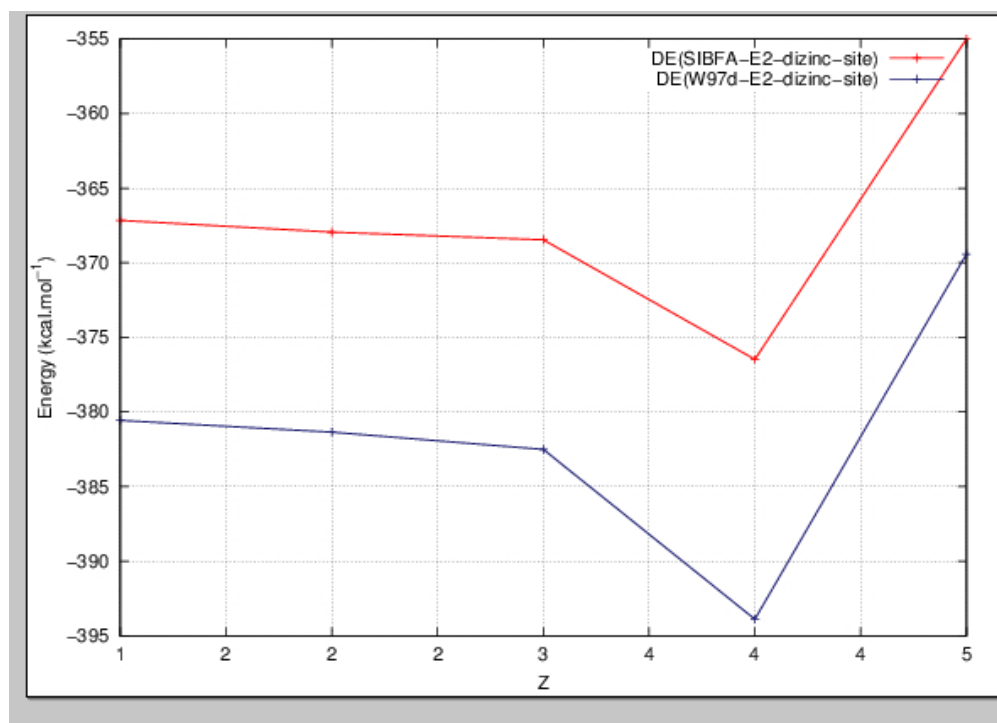


Figure 6-b

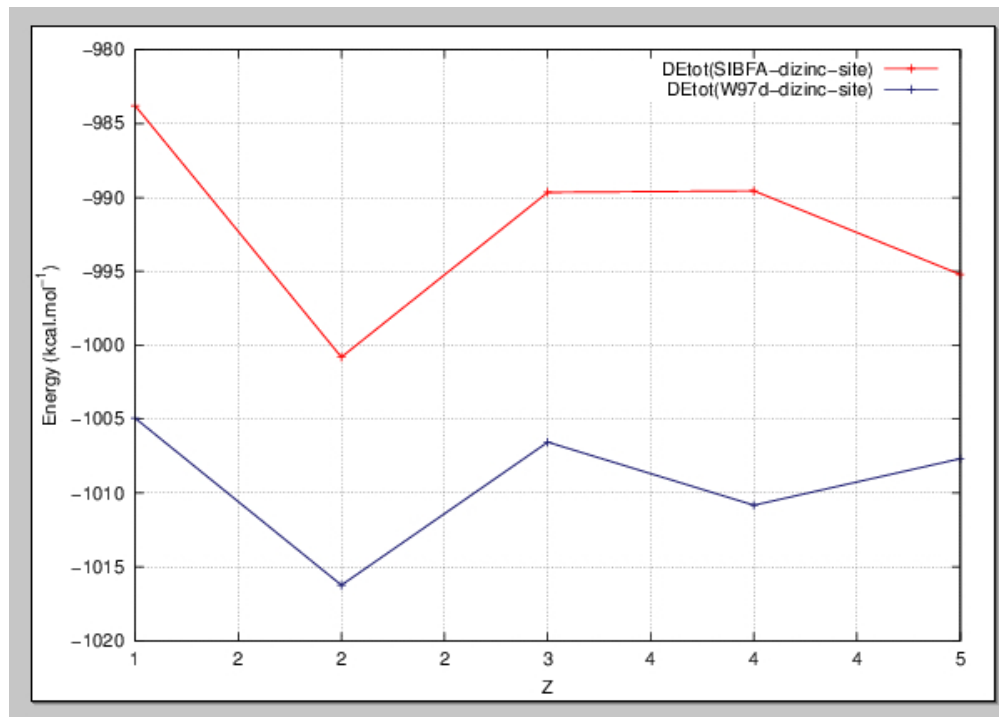


Figure 6-c

Table I. Complexes of the extended recognition site of VIM-2 with ligands I-V. Compared $\Delta E(\text{SIBFA})$ and $\Delta E(\text{QC}/\text{HF})$ on the following:

a) intermolecular interactions prior to ligand binding and without the 'discrete' water molecules; b) intermolecular interactions prior to ligand binding and with the 'discrete' water molecules; c) intermolecular interactions with the Tzt anchor and without the waters; d) intermolecular interactions with the entire ligands and without the waters; e) intermolecular interactions with the entire ligands and with the waters. Energies in kcal/mol. The $\Delta E(\text{QC})$ BSSE-corrected values are given in bold. Energies in kcal/mol.

	a) Nolig-nowats		b) Nolig		c) Tzt		d) Lig-nowats		e) Lig-wats	
	SIBFA	QC	SIBFA	QC	SIBFA	QC	SIBFA	QC	SIBFA	QC
Lig-4690	-997.9	1013.5/ -995.9	-1076.7	-1095.1/ -1055.3	-1233.0	-1237.3/ -1214.1	-1374.3	-1375.2/ -1343.9	-1459.2	-1458.4/ -1401.9
Lig-4390	-1000.2	-1011.6/ -993.1	-1066.5	-1081.8/ -1041.4	-1220.8	-1225.0/ -1201.0	-1372.4	-1370.6/ -1339.4	-1447.4	-1443.8/ -1388.9
Lig-4684	-990.5	-1008.8/ -991.1	-1085.8	-1108.7/ -1068.6	-1225.4	-1230.2/ -1206.8	-1207.3	-1207.1/ -1179.6	-1298.2	-1298.5/ -1245.8
Lig-5064	-993.0	-1004.2/ -986.6	-1069.3	-1085.9/ -1045.3	-1205.0	-1217.6/ -1194.7	-1307.0	-1349.4/ -1319.6	-1411.5	-1432.5/ -1377.4
Lig-5069	-996.3	-1022.6/ -1004.8	-1055.6	-1085.2/ -1044.3	-1234.9	-1254.3/ -1231.3	-1283.3	-1314.9/ -1282.9	-1341.4	-1372.7/ -1314.7

Table II. Mono-zinc binding sites of VIM-2 in their complexes with the five inhibitors. QC (HF/RVS) and SIBFA intermolecular interaction energies and their contributions. Energies in kcal/mol.

Blue core unbound										
	I. Lig-4690		II. Lig-4390		III. Lig-4684		IV. Lig-5064		V. Lig-5069	
	QC	SIBFA	QC	SIBFA	QC	SIBFA`	QC	SIBFA	QC	SIBFA
EC/EMTP	-271.6	-278.4	-290.2	-297.5	-284.8	-292.6	-304.1	-311.8	-275.5	-282.3
EX/Erep	118.0	125.5	145.6	153.0	138.0	145.8	166.5	173.0	131.8	139.2
E1	-153.5	-152.9	-144.6	-144.6	-146.8	-146.8	-137.5	-138.8	-143.9	-143.1
Epol	-125.2	-123.9	-130.3	-126.4	-129.9	-126.8	-137.8	-130.4	-126.3	-123.0
Ect	-33.4	-30.7	-35.3	-33.5	-35.0	-32.9	-37.6	-34.2	-33.8	-32.1
E2	-158.6	-154.7	-165.7	-159.9	-164.9	-159.7	-175.4	-164.5	-160.1	-155.1
ΔE	-312.1	-308.2	-310.3	-305.3	-311.7	-307.3	-313.0	-305.4	-303.9	-299.7

Colored core unbound										
	I. Lig-4690		II. Lig-4390		III. Lig-4684		IV. Lig-5064		V. Lig-5069	
	QC	SIBFA	QC	SIBFA	QC	SIBFA`	QC	SIBFA	QC	SIBFA
EC/EMTP	-559.9	-549.6	-568.6	-561.6	-553.8	-545.3	-563.3	-556.0	-568.6	-559.5
EX/Erep	99.8	88.0	107.7	95.9	94.9	84.2	104.6	93.2	116.4	107.5
E1	-458.1	-461.6	-460.9	-465.6	-459.0	-461.2	-458.7	-462.8	-452.3	-452.0
Epol	-89.7	-94.5	-92.3	-96.0	-89.9	-99.3	-91.1	-95.5	-96.1	-99.0
Ect	-40.0	-34.8	-40.5	-35.6	-39.0	-34.2	-40.2	-35.5	-40.1	-35.0
E2	-129.8	-129.3	-132.8	-131.6	-128.9	-130.0	-131.3	-131.0	-136.2	-134.0
ΔE	-587.9	-594.8	-594.7	-600.8	-587.9	-594.8	-590.0	-598.1	-588.5	-588.9

Blue core bound										
	I. Lig-4690		II. Lig-4390		III. Lig-4684		IV. Lig-5064		V. Lig-5069	
	QC	SIBFA	QC	SIBFA	QC	SIBFA`	QC	SIBFA	QC	SIBFA
EC/EMTP	-547.3	-555.7	-557.2	-562.9	-566.0	-574.9	-579.3	-583.4	-532.3	-533.9
EX/Erep	198.3	200.5	214.3	217.5	227.8	230.6	256.2	260.8	189.8	193.4
E1	-349.3	-355.3	-342.9	-345.4	-338.2	-344.3	-323.0	-322.6	-342.4	-340.4
Epol	-131.1	-130.6	-133.9	-130.5	-135.4	-131.9	-141.2	-133.7	-128.7	-128.4
Ect	-37.7	-31.6	-39.5	-33.4	-40.6	-33.7	-43.2	-35.3	-38.9	-32.1
E2	-168.9	-162.2	-173.4	-163.9	-176.0	-165.5	-184.3	-169.0	-167.5	-160.5
ΔE	-518.1	-520.6	-516.3	-511.7	-514.2	-513.2	-507.4	-492.7	-510.0	-503.3

Colored core bound										
	I. Lig-4690		II. Lig-4390		III. Lig-4684		IV. Lig-5064		V. Lig-5069	
	QC	SIBFA	QC	SIBFA	QC	SIBFA`	QC	SIBFA	QC	SIBFA
EC/EMTP	-690.4	-704.5	-693.9	-709.8	-683.9	-699.9	-687.5	-700.8	-655.6	-658.1
EX/Erep	231.3	232.4	240.0	244.2	226.5	224.5	226.2	227.0	179.0	171.8
E1	-459.2	-472.2	-453.9	-465.5	-457.4	-475.4	-461.3	-473.8	-476.6	-486.2
Epol	-99.3	-96.4	-101.6	-97.0	-99.1	-99.3	-98.9	-94.3	-94.6	-93.6
Ect	-48.4	-43.0	-48.0	-42.8	-47.9	-42.3	-47.5	-42.4	-43.6	-38.0
E2	-147.7	-139.4	-149.7	-139.7	-147.0	-141.6	-146.4	-136.7	-138.2	-131.7
ΔE	-606.8	-613.3	-603.5	-606.1	-604.4	-618.3	-607.7	-612.3	-614.7	-618.8

Table III. Di-zinc cores of Vim-2 in their complexes with the five inhibitors. QC (HF/RVS) and SIBFA intermolecular interaction energies. Energies in kcal/mol. (a) and (b): QC results with the ccp-pVTZ and augcc-pVTZ basis sets, respectively.

Dizinc core unbound										
	I. Lig-4690		II. Lig-4390		III. Lig-4684		IV. Lig-5064		V. Lig-5069	
	QC	SIBFA	QC	SIBFA	QC	SIBFA`	QC	SIBFA	QC	SIBFA
ΔE (a)	-915.6	-912.7	-914.9	-921.8	-916.6	-913.7	-919.2	-914.7	-921.4	-908.1
ΔE (b)	-914.0	-912.7	-921.6	-921.8	-912.3	-913.7	-914.8	-914.7	-917.2	-908.1

Dizinc core bound										
	I. Lig-4690		II. Lig-4390		III. Lig-4684		IV. Lig-5064		V. Lig-5069	
	QC	SIBFA	QC	SIBFA	QC	SIBFA	QC	SIBFA	QC	SIBFA
ΔE (a)	-1116.8	-1113.1	-1117.0	-1109.0	-1113.6	-1118.5	-1111.3	-1096.7	-1131.0	-1124.3
ΔE (b)	-1116.8	-1113.1	-1117.7	-1109.0	-1111.2	-1118.5	-1109.5	-1096.7	-1128.5	-1124.3

Table IV. Complexes of the extended recognition site of VIM-2 with ligands I-V. Compared $\Delta E(\text{SIBFA})$ and $\Delta E(\text{QC}/\text{HF})$ at the outcome of the recalibration procedure on the following:

a) intermolecular interactions prior to ligand binding and without the 'discrete' water molecules; b) intermolecular interactions prior to ligand binding and with the 'discrete' water molecules; c) intermolecular interactions with the Tzt anchor and without the waters; d) intermolecular interactions with the entire ligands and without the waters; e) intermolecular interactions with the entire ligands and with the waters. The BSSE-corrected $\Delta E(\text{QC})$ values are given in bold. Energies in kcal/mol.

	a) Nolig-nowats		b) Nolig		c) Tzt-nch		d) Lig-nowats		e) Lig-wats	
	SIBFA	QC	SIBFA	QC	SIBFA	QC	SIBFA	QC	SIBFA	QC
Lig-4690	-1002.4	1013.5/ -995.9	-1073.4	-1095.1/ -1055.3	-1217.1	-1237.3/ -1214.1	-1346.1	-1375.2/ -1343.9	-1426.1	-1458.4/ -1401.9
Lig-4390	-1001.4	-1011.6/ -993.1	-1060.2	-1081.8/ -1041.4	-1204.8	-1225.0/ -1201.0	-1336.9	-1370.6/ -1339.4	-1405.5	-1443.8/ -1388.9
Lig-4684	-992.4	-1008.8/ -991.1	-1080.5	-1108.7/ -1068.6	-1217.1	-1230.2/ -1206.8	-1182.0	-1207.1/ -1179.6	-1261.3	-1298.5/ -1245.8
Lig-5064	-985.4	-1004.2/ -986.6	-1060.4	-1085.9/ -1045.3	-1188.3	-1217.6/ -1194.7	-1303.9	-1349.4/ -1319.6	-1391.9	-1432.5/ -1377.4
Lig-5069	-995.4	-1022.6/ -1004.8	-1045.0	-1085.2/ -1044.3	-1231.4	-1254.3/ -1231.3	-1270.7	-1314.9/ -1282.9	-1328.4	-1372.7/ -1314.7

Table Va.

Lig-4690. Compared $\Delta E(\text{RVS})$ and $\Delta E(\text{SIBFA})$ values for the binding of the R2 benzocarboxylate arm with the Tyr67, Arg228, and His263 side-chains.

	Benzocarboxylate-Tyr67		Benzocarboxylate-Arg228		Benzocarboxylate-His263	
	RVS	SIBFA	RVS	SIBFA	RVS	SIBFA
E_C/E_{MTP}	1.4	1.7	-57.5	-56.4	-0.8	-4.2
$E_{\text{exch}}/E_{\text{rep}}$	1.9	2.0	4.7	4.6	13.6	12.0
E_1	3.2	3.7	-52.8	-51.9	12.8	8.2
E_{pol}	-0.7	-0.7	-4.1	-3.4	-2.7	-2.0
E_{ct}	0.0	0.0	-0.1	-0.2	-0.4	-0.1
E_2	-0.7	-0.7	-4.2	-3.9	-3.1	-2.1
ΔE	2.5	3.0	-57.0	-55.5	10.5	5.6

Lig-4690. Compared $\Delta E(\text{RVS})$ and $\Delta E(\text{SIBFA})$ values for the binding of the R2 benzocarboxylate arm with the main-chain of Asn233.

	Asn233	
	RVS	SIBFA
E_C/E_{MTP}	-24.1	-30.3
$E_{\text{exch}}/E_{\text{rep}}$	15.7	14.3
E_1	-8.5	-13.8
E_{pol}	-7.7	-6.3
E_{ct}	-1.7	-1.9
E_2	-9.4	-8.2
ΔE	-17.9	-24.8

Lig-4690. Compared $\Delta E(\text{RVS})$ and $\Delta E(\text{SIBFA})$ values for the binding of the R1 arm with the Phe61 and Trp87 side-chains.

	o-methoxy—Phe61		o-methoxy—Trp87	
	RVS	SIBFA	RVS	SIBFA
E_C/E_{MTP}	-2.7	-5.1	-3.9	-5.0
$E_{\text{exch}}/E_{\text{rep}}$	6.1	6.7	7.6	6.7
E_1	3.3	1.5	3.8	2.9
E_{pol}	-0.8	-0.2	-1.4	-0.7
E_{ct}	-0.2	-0.1	-0.2	-0.4
E_2	-1.0	-0.3	-1.6	-1.1
ΔE	2.3	1.3	2.2	1.3

Table Vb.

Lig-4390. Compared $\Delta E(\text{RVS})$ and $\Delta E(\text{SIBFA})$ values for the binding of the R2 benzocarboxylate side-chain with the Arg228 and His263 side-chains.

	Benzocarboxylate-Arg228		Benzocarboxylate-His263	
	RVS	SIBFA	RVS	SIBFA
E_C/E_{MTP}	-55.9	-55.0	2.5	0.0
$E_{\text{exch}}/E_{\text{rep}}$	4.2	4.3	5.5	5.9
E_1	-51.7	-50.7	8.0	5.9
E_{pol}	-3.7	-3.1	-2.7	-1.7
E_{ct}	-0.1	-0.2	-0.1	-0.1
E_2	-3.8	-3.3	-2.8	-1.8
ΔE	-55.5	-54.0	5.2	4.1

Lig-4390. Compared ΔE (RVS) and ΔE (SIBFA) values for the binding of the R2 benzocarboxylate arm with the main-chain of Asn233.

	Asn233	
	RVS	SIBFA
E_C/E_{MTP}	-28.2	-36.6
E_{exch}/E_{rep}	22.7	24.9
E_1	-5.5	-11.7
E_{pol}	-9.7	-7.3
E_{ct}	-3.3	-3.0
E_2	-13.0	-10.4
ΔE	-18.5	-22.1

Lig-4390. Compared ΔE (RVS) and ΔE (SIBFA) values for the binding of the R1 benzene side-chain with the Phe61 and Trp87 side-chains.

	Benzene-Phe61		Benzene-Trp87	
	RVS	SIBFA	RVS	SIBFA
E_C/E_{MTP}	-1.4	-3.1	-1.4	-2.8
E_{exch}/E_{rep}	2.9	3.7	4.8	4.5
E_1	1.5	0.6	3.4	1.7
E_{pol}	-0.5	-0.1	-0.8	-0.4
E_{ct}	-0.0	-0.0	-0.2	-0.2
E_2	-0.5	-0.1	-1.0	-0.6
ΔE	1.1	0.4	2.4	1.1

Table Vc.

Lig-4684. Compared ΔE (RVS) and ΔE (SIBFA) values for the binding of the R2 N-hydrazone-connected dihydroxy-phenyl arm with the Arg228, and His263 and Tyr67 side-chains.

	Dihydroxy-phenyl-Arg228		Dihydroxy-phenyl-His263		Dihydroxy-phenyl-Tyr67	
	RVS	RVS	RVS	SIBFA	RVS	SIBFA
E_C/E_{MTP}	-7.2	-7.5	-2.3	-4.5	-3.1	-4.2
$E_{\text{exch}}/E_{\text{rep}}$	3.6	4.3	5.6	8.3	8.3	8.4
E_1	-3.6	-3.2	3.3	3.7	5.2	4.2
E_{pol}	-3.8	-2.5	-0.7	-0.4	-1.3	-0.6
E_{ct}	-0.2	-0.1	-0.1	-0.2	-0.5	-0.4
E_2	-4.0	-2.7	-0.8	-0.6	-1.8	-1.0
ΔE	-7.6	-5.9	2.5	3.2	3.4	3.2

Lig-4684. Compared ΔE (RVS) and ΔE (SIBFA) values for the binding of the R1 dihydroxy-phenyl arm with the Phe61 and Trp87 side-chains.

	Dihydroxy-phenyl-Phe61		Dihydroxy-phenyl-Trp87	
	RVS	SIBFA	RVS	SIBFA
E_C/E_{MTP}	-1.3	-3.2	-9.3	-8.9
$E_{\text{exch}}/E_{\text{rep}}$	3.2	3.8	15.8	15.8
E_1	1.9	0.6	6.5	6.9
E_{pol}	-0.5	-0.1	-2.4	-0.9
E_{ct}	-0.1	-0.1	-1.1	-1.4
E_2	-0.6	-0.2	-3.5	-2.3
ΔE	1.3	0.4	3.0	4.6

Table Vd.

Lig-5064. Compared $\Delta E(\text{RVS})$ and $\Delta E(\text{SIBFA})$ values for the binding of the R2 benzocarboxylate arm with the Arg228 and His263 side-chains.

	Benzocarboxylate-Arg228		Benzocarboxylate-His263	
	RVS	RVS	RVS	SIBFA
E_C/E_{MTP}	-55.1	-53.4	3.9	2.4
$E_{\text{exch}}/E_{\text{rep}}$	3.2	3.4	1.9	2.7
E_1	-51.9	-50.0	5.8	5.1
E_{pol}	-3.3	-3.1	-1.3	-1.5
E_{ct}	-0.2	-0.1	0.0	-0.1
E_2	-3.5	-3.2	-1.3	-1.6
ΔE	-55.5	-53.2	4.5	3.5

Lig-5064. Compared ΔE (RVS) and ΔE (SIBFA) values for the binding of the R2 benzocarboxylate arm with the central backbone of Arg228.

	Benzocarboxylate-Arg228	
	RVS	SIBFA
E_C/E_{MTP}	-31.1	-41.9
E_{exch}/E_{rep}	30.4	32.7
E_1	-0.7	-9.3
E_{pol}	-11.7	-8.3
E_{ct}	-4.8	-3.5
E_2	-16.5	-11.8
ΔE	-17.2	-21.0

Lig-5064. Compared ΔE (RVS) and ΔE (SIBFA) values for the binding of the R1 dichlorophenyl arm with the Phe61, Trp87, and Asp119 side-chains.

	Dichlorophenyl-Phe61		Dichlorophenyl-Trp87		Dichlorophenyl-Asp119	
	RVS	SIBFA	RVS	SIBFA	RVS	SIBFA
E_C/E_{MTP}	-6.6	-11.8	-3.1	-3.6	-2.6	-6.7
E_{exch}/E_{rep}	17.9	19.2	7.9	11.7	9.9	12.0
E_1	11.3	8.0	4.9	8.1	7.3	5.3
E_{pol}	-0.9	-0.2	-1.1	-0.5	-5.2	-5.5
E_{ct}	-0.8	-0.0	-0.3	-0.4	-0.7	-0.0
E_2	-1.7	-0.2	-1.4	-0.9	-5.9	-5.5
ΔE	9.6	7.8	3.5	7.3	1.4	-0.2

Table Ve.

Lig-5069. Compared ΔE (RVS) and ΔE (SIBFA) values for the binding of the N-hydrazone substituting benzene of arm R2 with Tyr 67 and Arg228 side-chains.

	Benzene-Tyr67		Benzene-Arg228	
	RVS	RVS	RVS	SIBFA
E_C/E_{MTP}	-3.6	-5.2	-1.9	-3.4
E_{exch}/E_{rep}	10.1	13.4	3.0	2.9
E_1	6.5	8.2	1.1	-0.5
E_{pol}	-1.0	-0.4	-3.5	-2.1
E_{ct}	-0.4	-0.1	-0.3	-0.1
E_2	-1.4	-0.5	-3.3	-2.2
ΔE	5.1	7.7	-2.2	-2.7

Lig-5069. Compared ΔE (RVS) and ΔE (SIBFA) values for the binding of the benzocarboxylate of the R2 arm with the Arg228 and His263 side-chains.

	Benzocarboxylate-Arg228		Benzocarboxylate-His263	
	RVS	SIBFA	RVS	SIBFA
E_C/E_{MTP}	-62.1	-59.0	-24.0	-28.0
E_{exch}/E_{rep}	14.4	15.4	54.3	47.7
E_1	-47.7	-43.6	30.2	19.7
E_{pol}	-8.8	-6.8	-8.1	-6.3
E_{ct}	-2.1	-1.0	-3.5	-2.1
E_2	-10.9	-7.8	-11.6	-8.4
ΔE	-58.6	-51.4	18.6	11.4

Lig-5069. Compared ΔE (RVS) and ΔE (SIBFA) values for the binding of the benzocarboxylate of the R2 arm with the Glu225 main-chain.

	Benzocarboxylate- Glu225 backbone	
	RVS	SIBFA
E_C/E_{MTP}	-7.8	-10.9
E_{exch}/E_{rep}	0.7	1.7
E_1	-7.1	-9.2
E_{pol}	-2.2	-1.9
E_{ct}	-0.0	-0.4
E_2	-2.2	-2.3
ΔE	-9.3	-11.5

Lig-5069. Compared ΔE (RVS) and ΔE (SIBFA) values for the binding of the R1 dihydroxyphenyl group with the Trp87 side-chain.

	Dihydroxyphenyl- Trp87	
	RVS	SIBFA
E_C/E_{MTP}	-5.7	-6.1
E_{exch}/E_{rep}	6.8	6.9
E_1	1.1	0.8
E_{pol}	-1.4	-0.7
E_{ct}	-0.4	-0.7
E_2	-1.8	-1.4
ΔE	-0.7	-0.7

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Table VI. Mono-zinc binding sites of Vim-2 in their complexes with the five inhibitors. ALMOEDA DFT, HF, and SIBFA intermolecular interaction energies and their contributions. Energies in kcal/mol.

Blue core unbound					
	I. Lig-4690	II. Lig-4390	III. Lig-4684	IV. Lig-5064	V. Lig-5069
E1(B3LYP)	-159.8	-152.5	-154.5	-146.2	-151.2
E1(ωB97X-D)	-166.6	-159.7	-161.6	-153.0	-157.7
E1(SIBFA)	-167.7	-161.1	-163.6	-156.4	-158.6
E1(HF)	-158.1	-149.7	-151.9	-142.6	-148.6
For Peer Review					
Epol(B3LYP)	-138.5	-144.1	-143.7	-151.9	-138.9
Ect(B3LYP)	-52.5	-53.4	-53.1	-55.7	-53.9
E2(B3LYP)	-192.0	-177.5	-196.8	-207.7	-192.8
Epol(ω B97X-D)	-137.8	-143.5	-143.1	-151.6	-138.1
Ect(ω B97X-D)	-48.9	-50.2	-49.8	-52.7	-50.4
E2(ωB97X-D)	-186.6	-193.7	-192.8	-204.3	-188.5
Epol(SIBFA)	-127.8	-128.1	-130.0	-131.7	-128.5
Ect(SIBFA)	-28.8	-31.2	-30.3	-32.7	-29.6
E2(SIBFA)	-154.5	-159.2	-160.3	-164.4	-156.9
Edisp(SIBFA)	-18.3	-21.1	-20.2	-23.2	-19.2
E2+Edisp	-172.9	-180.3	-180.5	-187.6	-176.0
Epol(HF)	-123.5	-128.5	-128.1	-136.0	-123.7
Ect(HF)	-32.4	-34.1	-33.7	-36.5	-33.5

E2(HF)	-155.9	-162.6	-161.8	-172.5	-157.2
$\Delta E(\text{B3LYP})$	-350.8	-350.0	-351.3	-353.9	-344.0
$\Delta E(\omega\text{B97X-D})$	-353.2	-353.4	-354/4	-357.3	-346.1
$\Delta E_{\text{tot}}(\text{SIBFA})$	-341.8	-340.1	-342.9	-342.4	-334.8
$\Delta E(\text{HF})$	-314.0	-312.3	-313.7	-315.1	-305.8

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	Colored core unbound				
	I. Lig-4690	II. Lig-4390	III. Lig-4684	IV. Lig-5064	V. Lig-5069
E1(B3LYP)	-471.8	-475.5	-472.0	-472.6	-466.3
E1(ωB97X-D)	-472.8	-476.6	-473.2	-473.7	-467.4
E1(SIBFA)	-469.2	-478.4	-472.2	-471.0	-473.9
E1(HF)	-471.1	-473.7	-470.7	-470.9	-464.2
Epol(B3LYP)	-93.6	-97.7	-94.6	-96.0	-102.7
Ect(B3LYP)	-67.3	-65.3	-66.3	-66.6	-63.9
E2(B3 LYP)	-160.9	-163.0	-160.9	-162.6	-166.6
Epol(W97-D)	-93.1	-97.6	-94.3	-95.8	-102.6
Ect(W97-D)	-62.5	-61.2	-61.4	-62.0	-59.8
E2(ωB97X-D)	-155.6	-158.7	-155.7	-157.8	-162.4
Epol(SIBFA)	-104.2	-105.5	-105.2	-102.3	-102.6
Ect(SIBFA)	-32.2	-33.0	-31.6	-33.0	-33.2
E2(SIBFA)	-136.4	-136.7	-136.8	-138.0	-140.0
Edisp(SIBFA)	-14.0	-14.9	-13.4	-14.3	-16.0
E2+Edisp	-150.4	-151.5	-150.2	-152.3	-156.0
Epol(HF)	-81.8	-85.5	-82.7	-84.0	-89.9
Ect(HF)	-39.3	-39.0	-38.8	-39.5	-38.6
E2(HF)	-121.1	-124.5	-121,5	-123.5	-128.5

$\Delta E(\text{B3LYP})$	-632.7	-638.5	-632.9	-635.2	-632.8
$\Delta E(\omega\text{B97X-D})$	-628.4	-635.3	-628.9	-631.5	-629.8
$\Delta E_{\text{tot}}(\text{SIBFA})$	-619.4	-631.4	-622.2	-623.0	-631.0
$\Delta E(\text{HF})$	-592.2	-598.1	-592.3	-594.5	-592.7

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Table VII. Dizinc cores of VIM-2 in their complexes with the five inhibitors. ALMOEDA DFT, HF, and SIBFA intermolecular interaction energies and their contributions. Energies in kcal/mol.

Dizinc core					
	I. Lig-4690	II. Lig-4390	III. Lig-4684	IV. Lig-5064	V. Lig-5069
E1(B3LYP)	-609.3	-619.7	-609.3	-602.5	-625.1
E1(ωB97X-D)	-624.4	-634.9	-624.1	-616.9	-638.3
E1(SIBFA)	-617.6	-634.5	-622.5	-614.9	-641.7
E1(HF)	-607.8	-616.5	-606.6	-598.4	-622.6
For Peer Review					
Epol(B3LYP)	-262.7	-265.6	-265.7	-273.8	-257.7
Ect(B3LYP)	-129.2	-125.2	-127.3	-129.2	-121.5
E2(B3LYP)	-391.9	-390.8	-392.9	-403.1	-379.2
Epol(ω B97X-D)	-261.0	-264.3	-264.1	-272.8	-256.2
Ect(ω B97X-D)	-119.6	-117.1	-118.4	-121.1	-113.2
E2(ωB97X-D)	-380.6	-381.4	-382.5	-393.9	-369.4
Epol(SIBFA)	-271.3	-265.4	-270.6	-270.8	-255.6
Ect(SIBFA)	-60.0	-62.9	-60.7	-64.7	-61.5
E2(SIBFA)	-331.3	-328.3	-331.3	-335.5	-317.0
Edisp(SIBFA)	-35.9	-39.6	-37.1	-41.0	-38.0
E2+Edisp	-367.2	-368.0	-368.5	-376.5	-355.0
Epol(HF)	-233.8	-236.0	-236.2	-244.0	-228.3
Ect(HF)	-77.8	-77.3	-77.7	-80.7	-74.5
E2(HF)	-311.5	-313.3	-313.9	-324.7	-302.8

$\Delta E(\text{B3LYP})$	-1001.2	-1010.5	-1002.2	-1005.5	-1004.3
$\Delta E(\omega\text{B97X-D})$	-1004.9	-1016.2	-1006.6	-1010.8	-1007.7
$\Delta E_{\text{tot}}(\text{SIBFA})$	-983.8	-1000.8	-989.7	-989.6	-995.2
$\Delta E(\text{HF})$	-919.4	-929.8	-920.5	-923.1	-925.4

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Colored core unbound					
	I. Lig-4690	II. Lig-4390	III. Lig-4684	IV. Lig-5064	V. Lig-5069
E1(B3LYP)	-471.8	-475.5	-472.0	-472.6	-466.3
E1(ωB97X-D)	-472.8	-476.6	-473.2	-473.7	-467.4
E1(SIBFA)	-469.2	-478.4	-472.2	-471.0	-473.9
E1(HF)	-471.1	-473.7	-470.7	-470.9	-464.2
Epol(B3LYP)	-93.6	-97.7	-94.6	-96.0	-102.7
Ect(B3LYP)	-67.3	-65.3	-66.3	-66.6	-63.9
E2(B3 LYP)	-160.9	-163.0	-160.9	-162.6	-166.6
Epol(ωB97X-D)	-93.1	-97.6	-94.3	-95.8	-102.6
Ect(ωB97X-D)	-62.5	-61.2	-61.4	-62.0	-59.8
E2(ωB97X-D)	-155.6	-158.7	-155.7	-157.8	-162.4
Epol(SIBFA)	-104.2	-105.5	-105.2	-102.3	-102.6
Ect(SIBFA)	-32.2	-33.0	-31.6	-33.0	-33.2
E2(SIBFA)	-136.4	-136.7	-136.8	-138.0	-140.0
Edisp(SIBFA)	-14.0	-14.9	-13.4	-14.3	-16.0
E2+Edisp	-150.4	-151.5	-150.2	-152.3	-156.0
Epol(HF)	-81.8	-85.5	-82.7	-84.0	-89.9
Ect(HF)	-39.3	-39.0	-38.8	-39.5	-38.6
E2(HF)	-121.1	-124.5	-121,5	-123.5	-128.5
ΔE(B3LYP)	-632.7	-638.5	-632.9	-635.2	-632.8

$\Delta E(\omega B97X-D)$	-628.4	-635.3	-628.9	-631.5	-629.8
$\Delta E_{tot}(SIBFA)$	-619.4	-631.4	-622.2	-623.0	-631.0
$\Delta E(HF)$	-592.2	-598.1	-592.3	-594.5	-592.7

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Supp-Info-SI. LSQF-optimized parameters on the triazole-thione fragment.

The atoms of TZT are defined in the following succession:

C2: C atom bearing the R1 substituent;
 N3: unsubstituted N atom ortho to it;
 N4: unsubstituted N atom meta to C2, which binds to Zn(II) in the Zn1 ('blue') site;
 C5: C atom bearing the extracyclic S atom;
 N6: N atom ortho to C2 and substituted by the hydrazone group;
 S7: extracyclic S atom, which binds to Zn(II) in the Zn2 ('colored') site.

The hydrazone atoms are defined with first the nitrogen, N2, then the carbon, C3.
 The first atom on each fragment is always an H atom, denoted as H1.

1. Values of the effective radii for EMTP*, Erep, Epol, Ect, and Edisp.

	EMTP*	Erep	Epol	Ect	Edisp
C2	1.605	1.785	1.700	1.758	1.785
N3	1.536	1.700	1.827	1.850	1.800
N4	1.536	1.700	1.827	1.850	1.800
C5	1.605	1.785	1.700	1.758	1.785
N6	1.601	1.802	1.844	1.580	1.729
S7	1.678	1.340	3.117	2.535	1.340
N2	1.800	1.700	1.529	2.080	1.720
C3	1.499	1.786	1.700	1.758	1.786

2. Internal coordinates of the lone pairs of the triazole-thione and hydrazone fragments.

'popul' denotes the electronic population of the lone pair, incre and increb denote the increment of the effective radii of the lone pair bearer along the lone pair direction for the short-range repulsion and for the charge-transfer, respectively.

fragment TZT

	theta	phi	R	popul	incre	increb
C2	124.957	91.340	0.385	0.438	-1.114	0.081
C2	124.957	-88.659	0.385	0.438	-1.114	0.081
N3	140.776	0.039	1.064	1.501	-0.287	-1.209
N3	94.395	48.015	1.146	0.174	-1.526	-0.084
N3	94.395	-47.984	1.146	0.174	-1.526	-0.084

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3	N3	85.856	133.385	-0.167	0.612	1.189	0.789
4	N3	85.856	226.385	-0.167	0.612	1.189	0.789
5	N4	107.901	180.172	1.548	1.490	-0.838	-1.002
6	N4	120.353	227.916	0.887	0.863	0.040	-0.585
7	N4	120.353	131.916	0.887	0.863	0.040	-0.585
8	N4	73.595	46.407	-0.410	0.660	-0.101	-0.089
9	N4	73.595	-46.772	-0.410	0.660	-0.101	-0.089
10	C5	83.855	108.924	0.665	0.435	0.289	-0.134
11	C5	83.855	250.924	0.665	0.435	0.289	-0.134
12	N6	28.157	-89.979	-0.035	0.935	-0.312	0.066
13	N6	28.157	90.020	-0.035	0.935	-0.312	0.066
14	S7	108.386	180.041	0.931	0.800	0.939	-0.159
15	S7	108.386	120.041	0.931	0.800	0.939	-0.159
16	S7	108.386	60.041	0.931	0.800	0.939	-0.159
17	S7	108.386	0.041	0.931	0.800	0.939	-0.159
18	S7	108.386	-59.958	0.931	0.800	0.939	-0.159
19	S7	108.386	240.041	0.931	0.800	0.939	-0.159
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fragment HN=CH2

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	theta	phi	R	popul	incra	incrb	
24							
25							
26							
27							
28	N2	127.540	180.000	0.727	2.000	-0.200	0.200
29	N2	45.000	90.000	0.750	0.500	0.350	0.200
30	N2	45.000	-90.000	0.750	0.500	0.350	0.200
31	C3	90.000	90.000	0.750	0.500	0.500	-0.225
32	C3	90.000	-90.000	0.750	0.500	0.500	-0.225
33							
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3. Lone-pair and bond polarizabilities.

Ea, Eb, Ec, and Ed denote the multiplicative factors used in the Gaussian screening of the field, for, respectively the bond and the lone pair polarizabilities prior to iterating with the induced dipoles, and for the bond and lone pair polarizabilities upon iterating.

Fa, Fb, Fc, and Fd denote the corresponding Gaussian exponents.

TZT:

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52								
53	Ea	Eb	Ec	Ed	Fa	Fb	Fc	Fd
54	0.851	0.871	0.885	1.279	2.039	1.057	1.623	3.332
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57								
58								
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3 hydrazone:
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6 Ea Eb Ec Ed Fa Fb Fc Fd
7 0.851 1.129 0.818 0.705 2.039 1.620 2.048 2.311
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10 Values of the polarizabilities in Angstrom ** 3
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13 TZT. There is one lone-pair polarizability on atoms N3, N4, and N6, and three ones on atom S7.
14 The numbering of the bond polarizabilities is as follows:
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17 9: H1-C2
18 10: C2-N3
19 11: C2-N3
20 12: C2-N6
21 13: N3-N4
22 14: N4-C5
23 15: N4-C5
24 16: N5-N6
25 17: N5-N6
26 18: C5-S7
27 19: N6-H8
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31 Values of the lone-pair polarizabilities

32 3 3.813
33 4 4.101
34 6 1.658
35 7 11.836
36 7 4.862
37 7 6.872
38
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40 Values of the bond polarizabilities

41 9 0.000
42 10 11.132
43 11 6.579
44 12 2.179
45 13 2.629
46 14 3.229
47 15 3.161
48 16 1.849
49 17 1.915
50 18 1.593
51 19 2.141
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Hydrazone. There is one lone-pair polarizability on atom N2.
The numbering of the bond polarizabilities is as follows:

6: H1-N2

7: N2-C3

8: C3-H4

9: C3-H5

Value of the lone-pair polarizability

2 12.804

Value of the bond polarizabilities

6 0.000

7 2.534

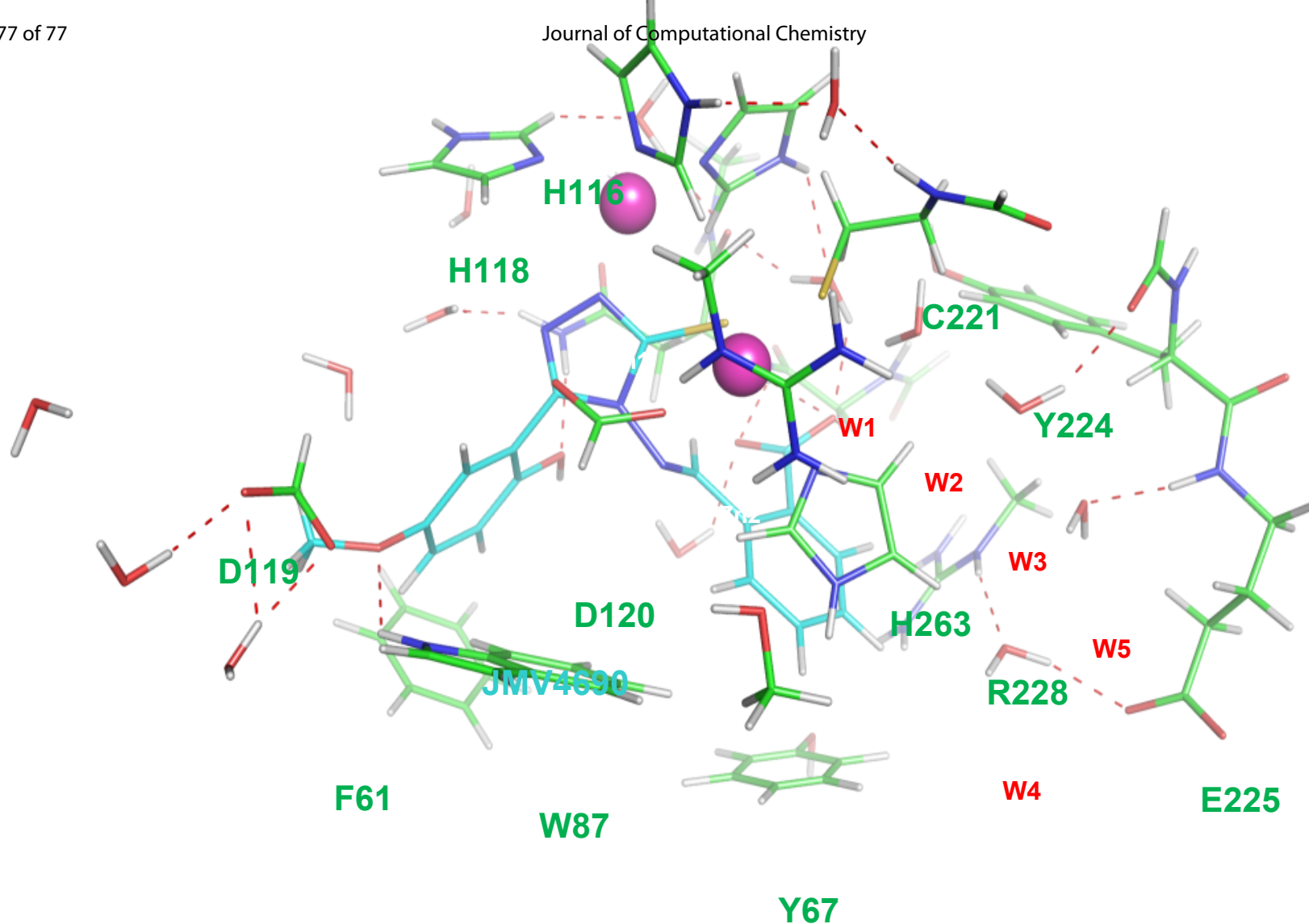
8 0.727

9 3.450

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Supp. Info S2. Distances (in Angstrom units) between Zn(II) and its ligands in the dizinc core. Values in parentheses in the Lig-4690 column correspond to the ones determined by X-ray crystallography.

	I. Lig-4690	II. Lig-4390	III. Lig-4684	IV. Lig-5064	V. Lig-5069
Zn1-H116	2.01 (2.02)	1.92	1.99	1.87	2.02
Zn1-H118	2.16 (1.90)	2.13	1.96	2.12	2.18
Zn1-H196	1.97 (2.08)	1.94	2.03	1.88	1.94
Zn1-N(TZT)	1.92 (1.91)	1.93	2.28	1.88	1.98
Zn2-D120	1.97 (2.08)	1.99	1.93	1.96	2.08
Zn2-C221	2.30 (2.16)	2.23	2.32	2.27	2.33
Zn2--H263	2.48 (2.31)	2.30	2.48	2.46	2.00
Zn2-S(TZT)	2.06 (2.25)	2.07	2.07	2.08	2.35



VIM-2 is a bacterial Zn-metallo-beta-lactamase, responsible for nosocomial infections. We consider its complexes with five novel inhibitors sharing a triazole-thione anchoring group. For each of these, we validate a polarizable molecular mechanics/dynamics potential against ab initio QC computations. The test cases embody the interactions in the two mono-zinc sites and in the di-zinc site, up to the entirety of the extended recognition site, which totals up to 280 atoms.