

Computational study of calix[4]arene derivatives and complexation with Zn^{2+}

A. Suwattanamala, A.L. Magalhães*, J.A.N.F. Gomes

REQUIMTE/Departamento de Química, Faculdade de Ciências, Universidade do Porto, Rua do Campo Alegre, 687, 4169-007 Porto, Portugal

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Abstract

High level DFT was applied to study structure and conformational equilibrium of amino and mercaptocalix[4]arenes possessing methylene groups or sulfur atoms at their four junctions. All the calculations point to *cone* and *1,3-alternate* as the most stable conformers for sulfur and methylene bridged compounds, respectively. The presence of four sulfur atoms in place of the methylene bridges can lead to novel features in the complexation with transition metals. The host–guest 1:1 complexes between Zn^{2+} and each conformer of tetraaminothiacalix[4]arene were also investigated at the same DFT level. The four nitrogens of amino groups play a dominant role in the interaction with Zn^{2+} via distorted tetrahedral coordination for *1,3-alternate*, or distorted square planar for *partial cone* and *1,2-alternate*. On the other hand, the 2:1 complexes with *cone* show that the sulfur bridges can also bind Zn^{2+} and contribute to form two sets of five-membered chelated rings with two N donor atoms.

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1. Introduction

Molecular recognition plays an extremely important role in chemistry and biochemistry, especially in the fast growing field of supramolecular host–guest chemistry [1]. One interesting class of supramolecular systems is the macrocyclic calixarenes that are widely used as effective host compounds for various guest species such as cations, anions, and neutral molecules [2–4]. The increasing interest on calixarenes is certainly due to their versatility in terms of complexation capability, conformational flexibility and reactivity, and they have been applied in a wide range of areas as catalysis, host–guest chemistry, molecular recognition, separation chemistry,

selective ion transport and sensors [2,3,5]. The most well known member of this class is calix[4]arene which comprises cyclic tetramers of phenol units linked by *ortho*-methylene bridges and reveals a basket-shaped molecular structure [6]. In addition, calix[4]arenes have been widely used as a molecular platform for the design and construction of different kinds of new excellent receptors in molecular recognition by easy chemical modifications [3,7]. By complete or partial functionalization of the lower (phenolic OH groups) and/or upper rims (the *p*-position), a wide variety of calix[4]arenes has been obtained [2,3,6,8]. The replacement of methylene junctions between the phenolic moieties by hetero atoms has been recently reported [9,10], in particular the remarkable thiacalix[4]arenes where sulfur atoms are used in place of the four methylene bridges [11–15]. NMR study has shown that thiacalix[4]arene is much more flexible in solution than parent calix[4]arene [11]. The flexibility increases with the number of

* Corresponding author. Tel.: +351 226 082804; fax: +351 226 082959.

E-mail address: almagalh@fc.up.pt (A.L. Magalhães).

additional binding sites at sulfur bridges. The complexation ability of thiacalix[4]arenes towards neutral molecules [12,13], or metal ions, especially transition metal ions [14–16], has also been investigated. A study of the extraction with transition metal ions shows that thiacalix[4]arene formed 1:1 complexes with divalent metal ions M^{2+} [Co^{2+} , Cu^{2+} , Zn^{2+}] by ligating sulfurs in addition to the adjacent two phenoxide oxygens to form two sets of five-membered chelated rings as evidenced by the NMR study of the diamagnetic Zn^{2+} complex [14c].

Theoretical calculations based on full geometry optimizations by density functional theory (DFT) methodology are now feasible and are being applied successfully to investigate the properties of calix[4]arene derivatives and, in particular, the complexation with charged species [17–22]. Structure and conformational equilibrium of thiacalix[4]arene derivatives namely tetraaminothiocalix[4]arene (**1**) and tetramercaptothiacalix[4]arene (**2**) have been the subject of a previous theoretical study in gas-phase [22]. In this work, apart from the application of new DFT functionals in gas phase, we have studied the influence of two different solvents (chloroform and dichloromethane) on the conformational equilibrium of these thiacalix[4]arenes by means of a polarizable continuum model. On the other hand, structures of the corresponding methylene bridged compounds, namely tetraaminocalix[4]arene (**3**) and tetramercaptothiacalix[4]arene (**4**) were also investigated to analyze the effect of bridges counterparts. The structures of the four main conformers of each compound are presented in Fig. 1. The main goal of this study is to understand how the presence of different substituents at the lower rim and methylene junctions modifies their conformational flexibilities and binding abilities and selectivities, which is a fundamental aspect in complexation of supramolecular compounds. The interest on the transition metal zinc in the chemical and biochemical systems grew due to its ability to coordinate with a variety of ligands in different structural patterns, and it has been used in a wide diversity of chemistry fields as catalysis, metalloenzymes, complexation of macrocyclic ligands, organometallic and bioinorganic systems [23,24]. In this study, structural and energetic data for the complexes formed between the zinc cation and each conformer of compound **1** are also reported, which may open new perspectives in host–guest supramolecular chemistry based on aniline rather than phenol. High level DFT calculations are applied for the first time to study the complexation of this thiacalix[4]arene derivative with a transition metal ion. In addition, we hope that the understanding of the complexation/recognition process from a microscopic point of view will provide a new progress for the design and development of sophisticated sensors at molecular level in future.

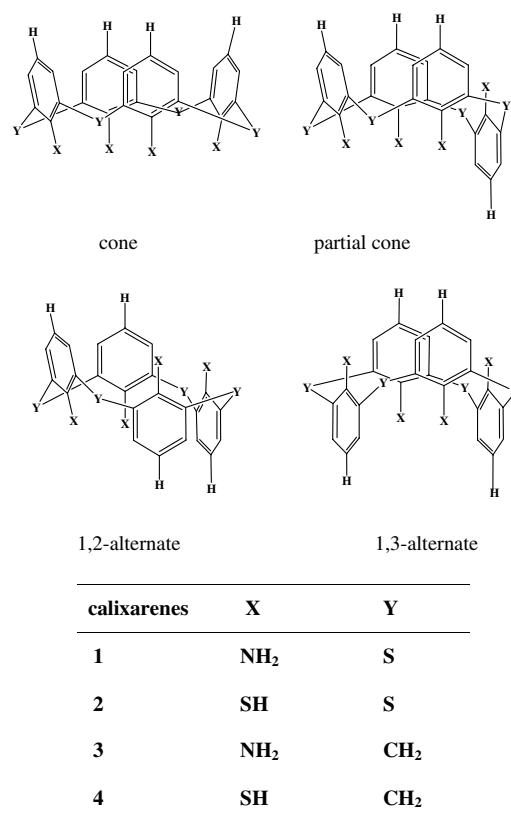


Fig. 1. Structural formula of each conformer of compounds **1–4**.

2. Computational methodology

The structures of the four main conformers of **1**, **2**, **3** and **4** were initially obtained by complete optimization without any constraints at the restricted Hartree–Fock (RHF) level with the 6-31G(d) basis set. These geometries were then used as input for final optimizations with the 6-31G(d,p) basis set at DFT level, using the Becke’s three parameter hybrid exchange functional [25] combined with the Lee, Yang and Parr correlation functional [26] (B3LYP). The electronic energies of these optimized structures were also calculated by single point calculations with the B3LYP and the Becke’s three parameter hybrid exchange functional [25] and Perdew and Wang’s 1991 correlation functional [27] (B3PW91) with the 6-311G(d,p) basis set. New exchange and correlation functionals provided by GAUSSIAN03 program [28] were also tested, namely OPTXPBE (Handy’s OPTX modification of Becke’s exchange functional and Perdew, Burke and Ernzerhof’s 1996 gradient-corrected correlation functional) [29,30] and PBEPBE (the 1996 exchange and correlation functionals of Perdew, Burke and Ernzerhof) [30] with the same 6-311G(d,p) basis set. In order to include the electrostatic influence of the solvent in liquid phase (chloroform and dichloromethane), the integral equation formalism of the polarizable continuum model (IEF-PCM) [31] was employed at B3LYP/6-31G(d,p) level.

The geometry of the complexes of each conformer of **1** with Zn^{2+} were optimized at B3LYP/DFT level. The 6-31G(d,p) basis set was used for H, C, N and S and the combination of double zeta valence basis set (DZ) and Los Alamos effective core potential, (LANL2DZ), [32] basis set was used for Zinc. The binding energy was calculated as the difference between the total energy of the complexes and the sum of the total energies of the metal ion and the most stable conformer of the isolated ligand. The basis-set superposition error (BSSE) in the binding energy was estimated with the new counterpoise correction method which automates the geometry optimization of the complexes on potential surfaces that are corrected for this error [33]. All the calculations were performed with the GAUSSIAN03 software [28].

3. Results and discussion

3.1. Structure and hydrogen bonding

The DFT optimized structures of the four conformers *cone*, *partial cone* (*paco*), *1,2-alternate* (*1,2-alt*) and *1,3-alternate* (*1,3-alt*) of all the compounds were obtained at B3LYP/6-31G(d,p) level. Unfortunately, none of them have been experimentally achieved yet, though very similar compounds with *tert*-butyl groups at *para* position were synthesized,

namely the tetraamino-*p-tert*-butylthiacalix[4]arene [34], tetramercapto-*p-tert*-butylthiacalix[4]arene [35], and tetramercapto-*p-tert*-butylcalix[4]arene [36]. Compounds **1** and **2** have been the subject of a previous theoretical analysis in gas phase [22]. In order to keep consistency in the present comparative study of the compounds **1–4**, the results for the conformational equilibrium of **1** and **2** were checked using the new features of GAUSSIAN03. The structures of *cone* conformers of all the four compounds are depicted in Fig. 2, and the values obtained at B3LYP/6-31G(d,p) level for some relevant geometrical parameters are presented in Table 1. The results indicate that sulfur bridged compounds (**1** and **2**) have a larger cavity than the corresponding methylene bridged compounds (**3** and **4**). The distances between the two distal and the two proximal sulfur atoms ($\text{S}'\text{--}\text{S}'$) are 7.9 and 5.6 Å, respectively, for **1** and **2** whereas the corresponding distances in **3** and **4** are 7.3 Å and 5.1 Å, respectively. The C–C'–C angle in methylene bridged compounds is larger than the corresponding C–S'–C angle in sulfur bridged compounds by about 10°. We observe that the majority of the bond distances and bond angles are not sensitive to the substituent groups at lower rim (SH or NH_2) in both classes of compounds. The X–X distances (see Table 1) depend on the atomic size and steric hindrance of substituent groups, but they are not affected by the bridge replacement. An interesting observation is that in

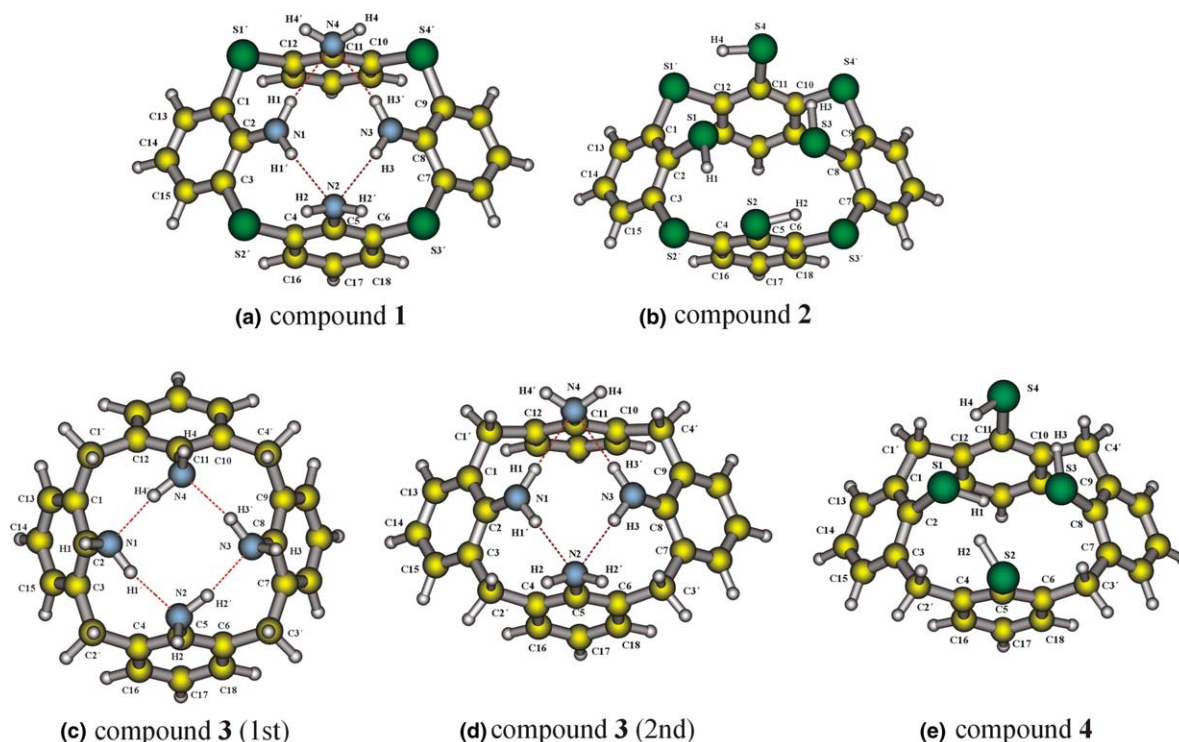


Fig. 2. Optimized structures of *cone* conformer of compounds **1–4** obtained at B3LYP/6-31G(d,p) level.

Table 1
Structural parameters for *cone* conformers at B3LYP/6-31G(d,p) level

	Compound 1 ^a	Compound 2 ^a	Compound 3 1st possibility	Compound 3 2nd possibility	Compound 4	Thiacalix[4]arene ^b
Bond distance (Å)						
Y ₁ '-C ₁	1.80	1.80	1.53	1.53	1.53	1.80
C ₁ -C ₂	1.43	1.42	1.41	1.42	1.41	1.41
C ₂ -X ₁	1.36	1.77	1.43	1.39	1.80	1.36
C ₂ -C ₃	1.43	1.42	1.41	1.42	1.41	1.41
C ₃ -Y ₂ '	1.80	1.80	1.53	1.53	1.53	1.80
Y ₂ '-C ₄	1.81	1.81	1.53	1.53	1.53	1.80
C ₄ -C ₅	1.41	1.41	1.41	1.41	1.42	1.41
C ₅ -X ₂	1.40	1.78	1.43	1.43	1.81	1.36
C ₅ -C ₆	1.41	1.42	1.41	1.41	1.42	1.41
C ₆ -Y ₃ '	1.81	1.81	1.53	1.53	1.54	1.80
Y ₃ '-C ₇	1.80	1.80	1.53	1.53	1.53	1.80
C ₇ -C ₈	1.43	1.42	1.41	1.42	1.41	1.41
C ₈ -X ₃	1.36	1.77	1.43	1.39	1.79	1.36
C ₈ -C ₉	1.43	1.42	1.41	1.42	1.41	1.41
C ₉ -Y ₄ '	1.80	1.80	1.53	1.53	1.53	1.80
Y ₄ '-C ₁₀	1.81	1.81	1.53	1.53	1.54	1.80
C ₁₀ -C ₁₁	1.41	1.41	1.41	1.41	1.42	1.41
C ₁₁ -X ₄	1.40	1.78	1.43	1.43	1.81	1.36
C ₁₁ -C ₁₂	1.41	1.42	1.41	1.41	1.42	1.41
C ₁₂ -Y ₁ '	1.81	1.81	1.53	1.53	1.53	1.80
X ₁ -X ₂	3.27	3.94	2.93	3.19	3.82	2.74
X ₂ -X ₃	3.27	3.82	2.93	3.19	3.74	2.74
X ₃ -X ₄	3.27	3.94	2.93	3.19	3.77	2.74
X ₄ -X ₁	3.27	3.82	2.93	3.19	3.75	2.74
X ₁ -X ₃	3.56	3.71	4.15	3.49	3.64	3.87
X ₂ -X ₄	5.41	6.81	4.15	5.29	6.60	3.87
Bond angle ^c (°)						
C ₁₂ -Y ₁ '-C ₁	102.8	100.2	112.3	112.5	110.5	104.3
Y ₁ '-C ₁ -C ₂	121.5	121.3	121.8	121.0	122.4	120.7
C ₁ -C ₂ -X ₁	121.5	118.0	118.1	120.3	119.1	122.2
C ₂ -C ₃ -Y ₂ '	121.5	122.5	122.7	121.0	122.2	120.7
C ₃ -Y ₂ '-C ₄	102.8	100.0	112.3	112.5	110.3	104.3
Y ₂ '-C ₄ -C ₅	119.9	120.9	121.8	123.5	124.3	120.7
C ₄ -C ₅ -X ₂	120.6	118.4	118.1	119.6	121.1	122.2
C ₅ -C ₆ -Y ₃ '	119.9	122.1	122.7	123.5	124.3	120.7
C ₆ -Y ₃ '-C ₇	102.8	100.2	112.3	112.5	110.4	104.3
Y ₃ '-C ₇ -C ₈	121.5	121.3	121.9	121.0	121.4	120.7
C ₇ -C ₈ -X ₃	121.5	118.0	118.1	120.3	116.0	122.2
C ₈ -C ₉ -Y ₄ '	121.5	122.5	122.7	121.0	123.0	120.7
C ₉ -Y ₄ '-C ₁₀	102.8	100.0	112.2	112.5	110.6	104.3
Y ₄ '-C ₁₀ -C ₁₁	119.9	120.9	121.8	123.5	124.9	120.7
C ₁₀ -C ₁₁ -X ₄	120.6	118.4	118.1	119.6	118.2	122.2
C ₁₁ -C ₁₂ -Y ₁ '	119.9	122.1	122.7	123.5	124.8	120.7
φ ^c (°)	109.1 ; 7.2	95.5 ; 26.4	57.5 ; 57.7	97.3 ; 11.2	89.4 ; 13.1	77.2 ; 77.4

X is denoted to the atom N for compounds **1** and **3**; the atom S for compounds **2** and **4** and O for thiacalix[4]arene, respectively. Y is denoted to the atom S and C for the sulfur bridged compound (compounds **1** and **2**) and the methylene bridged compound (compounds **3** and **4**), respectively.

^a Ref. [22].

^b Ref. [21].

tetraaminocalix[4]arene (**3**) the four amino groups at lower rim can adopt two different patterns of hydrogen bonds (named 1st and 2nd) with a small energy gap, which was not observed in the tetrahydroxycalix[4]arene [37]. The first pattern possesses *C*₄ symmetry and the corresponding conformer is less stable, ca. 3 kcal mol⁻¹, than the second one which shows *C*₂ symmetry. The results show that the X–X distances in the first possibility of *cone* are shorter than in

the second possibility. The *cone* conformer of **1** and **2** present *C*₂-like symmetry rather than the *C*₄ symmetry obtained for the parent thiacalix[4]arene [21], as the X₁–X₃ and X₂–X₄ distances are not identical anymore, nor the angles φ (see Table 1) formed by two opposite benzene rings are consistent. A *cone* conformer possessing *C*₂ symmetry is called *pinched cone* and seems to play a relevant role at low temperature in thiacalix[4]arene derivatives [38,39].

As expected, the optimized structures present an array of hydrogen bonds that contribute dominantly to the stabilization of the conformers. Hydrogen bonds in *cone* conformers are also shown in Fig. 2; information concerning the other conformers can be supplied upon request. The most favorable arrangement of hydrogen bonds for both *cone* and *paco* conformers of **1** shows two amino groups playing as donors and the others as acceptors (see Fig. 2(a) for *cone*). It differs from the parent thiacalix[4]arene, where each hydroxyl group acts simultaneously as a donor and as an acceptor [21]. It is interesting to note that NH–N hydrogen bond distances and N–H–N bond valence angles are 2.28 Å and 167.6°, respectively, whereas the OH–O hydrogen bond distances are 1.82 Å in parent thiacalix[4]arene [21]. The number of hydrogen bonds between amino groups is four and it decreases to two in *paco* and *1,2-alt*, and none in the *1,3-alt*. The additional NH–S' bonding between amino groups and sulfur bridges is also observed in **1**. The bond distance NH–S' and the bond angle N–H–S' of *cone* conformer at B3LYP/6-31G(d,p) level are 2.58 Å and 108.2°, respectively.

As referred above, in **3** two different arrays of hydrogen bonds with similar energies can be found in *cone* and in *paco* conformer as well. In the first pattern (see Fig. 2(c) for *cone*), the arrangement of hydrogen bonds reminds the one adopted by hydroxyl groups in parent thiacalix[4]arene and, for the second pattern (Fig. 2(d)), the array of hydrogen bonds corresponds to the one of **1**. The latter pattern is the most stable for *cone* and *paco* in **3**. The NH–N hydrogen bond distances and N–H–N bond valence angles for the first pattern are 1.93 Å and 164.0°, respectively, but 2.18 Å and 177.5° for the second pattern. This also supports the idea that hydrogen bonding is stronger in the second pattern than in the first one. The presence of the methylene bridges increases the hydrogen bond angle by about 10°. The number of such hydrogen bonds between amino groups is four in the first and second *cone* conformation, two in first and second *paco* and *1,2-alt*, and none in the *1,3-alt*.

Even though the steric hindrance and the weaker acceptor character of thiol groups (-SH) in **2** seems to form less effective hydrogen bonds, the orientation of the -SH hydrogens towards sulfur bridges may contribute to stabilize all the conformations much more than the hydrogen bonds between -SH groups as shown in Fig. 2(b). This hypothesis is supported for instance by the *cone* structure where the distances SH–S' (2.50 Å) are shorter than the distances SH–S (2.73, 3.15 Å). For comparison, the optimized *cone* structure of the corresponding methylene bridged compound **4**, obtained at same DFT level, is presented in Fig. 2(e). The hydrogen bond distances SH–S are in the range of 2.48–2.67 Å and seem to contribute to stabilize the *cone* conformer. However, the absence of the acceptor sulfur bridges

explains the relative smaller stability of *cone* when compared with *1,3-alt* (see Table 2).

3.2. Energetics and conformational equilibrium

Taking the total energy of the most stable conformer as a reference (*cone* for **1** and **2**, and *1,3-alt* for **3** and **4**), the energy differences (ΔE) of the other conformers obtained at different DFT levels are reported in Table 2. The stability ordering of **1** and **2** is predicted to be: *1,2-alt* < *1,3-alt* < *paco* < *cone*. By contrast, the stability ordering of **3** is modified to 1st *cone* < 2nd *cone* 1st *paco* < *1,2-alt* < 2nd *paco* < *1,3-alt* and for **4** is: *1,2-alt* < *paco* < *cone* < *1,3-alt*. The hydrogen bonding between the amino groups (NH–NH) and between the NH hydrogens and sulfur bridges (NH–S') seems to give a dominant contribution in stabilizing the *cone* and *paco* conformer of **1**, whereas the *1,3-alt* conformer is stabilized only by NH–S' bondings. Interestingly, previous experimental studies concluded that a similar compound, the tetraamino-*p-tert*-butylthiacalix[4]arene adopted a typical *pinched-cone* conformation upon complexation with Pd²⁺ ion [40], which contrasted with the geometry of the uncomplexed *1,3-alt* conformer obtained in the solid state [34]. The experimental results suggest, therefore, the great flexibility of the molecule. In fact, the DFT calculations indicate that the energy gap between conformers is ca. 4.0 kcal mol⁻¹. For **2**, the *cone* is predicted as the most stable conformer. By contrast, the solid state conformation adopted by a similar compound, namely tetramercapto-*p-tert*-butylthiacalix[4]arene obtained by X-ray diffraction was the *1,3-alt* conformer [35]. The DFT calculations show indeed a small energy gap of about 2 kcal mol⁻¹ between these conformers.

The same stability ordering was obtained in a previous theoretical study of the parent thiacalix[4]arene [21]. It seems that the nature of the substituent groups at lower rim does not affect the conformational equilibrium. However, we have found a reduction of ΔE for all conformers of **1** and **2**, especially for **1**, when compared with the hydroxylated thiacalix[4]arene. It may be suggested that the weaker intramolecular hydrogen bonds in both compounds reduce the relative stabilization of the conformers, as the breaking of a hydrogen bond when the molecule changes to a less stable conformer is not so energetically unfavourable.

Concerning the methylene bridged compounds, the most stable conformer is predicted to be the *1,3-alt* for both compounds, which differs from the sulfur bridged compounds. The reason for this point in **3** may be due to the absence of acceptor sulfur atoms and the favorable N–H/ π interactions between the amino hydrogens and the adjacent aromatic rings which are observed in the *paco* and *alternate* conformers. Unfortunately, no experimental data are still available

Table 2

Relative energy (ΔE , in kcal mol⁻¹) of the main conformers of compounds **1–4** at different DFT levels (the energy of the most stable conformer was taken as reference in each case)

	1st <i>cone</i>	2nd <i>cone</i>	1st <i>paco</i>	2nd <i>paco</i>	1,2- <i>alt</i>	1,3- <i>alt</i>
Tetraaminothiacalix[4]arene: compound 1						
B3LYP/6-31G(d,p) ^{a,e} <i>vacuum</i>		0.00	–	1.41	6.83	4.11
B3LYP/6-311G(d,p) ^{b,e} <i>vacuum</i>	–	0.00	–	1.37	6.70	4.36
B3PW91/6-311G(d,p) ^{b,e} <i>vacuum</i>	–	0.00	–	0.89	6.48	2.94
OPTXPBE/6-311G(d,p) ^b <i>vacuum</i>	–	0.53	–	0.00	4.06	0.50
PBEPBE/6-311G(d,p) ^b <i>vacuum</i>	–	0.00	–	0.45	5.89	1.94
B3LYP/6-31G(d,p) ^c <i>chloroform</i>	–	0.00	–	1.79	6.87	5.92
B3LYP/6-31G(d,p) ^d <i>dichloromethane</i>	–	0.00	–	1.56	6.66	6.01
Tetramercaptothiacalix[4]arene: compound 2						
B3LYP/6-31G(d,p) ^{a,e} <i>vacuum</i>	0.0	–	1.81	–	4.97	2.04
B3LYP/6-311G(d,p) ^{b,e} <i>vacuum</i>	0.0	–	2.16	–	5.15	2.10
B3PW91/6-311G(d,p) ^{b,e} <i>vacuum</i>	0.0	–	2.67	–	5.85	2.75
OPTXPBE/6-311G(d,p) ^b <i>vacuum</i>	0.0	–	2.65	–	4.78	2.36
PBEPBE/6-311G(d,p) ^b <i>vacuum</i>	0.0	–	2.91	–	5.72	2.85
B3LYP/6-31G(d,p) ^c <i>chloroform</i>	0.0	–	1.72	–	4.75	0.66
B3LYP/6-31G(d,p) ^d <i>dichloromethane</i>	0.0	–	1.54	–	4.68	0.05
Tetraaminocalix[4]arene: compound 3						
B3LYP/6-31G(d,p) ^a <i>vacuum</i>	13.22	10.49	7.63	5.24	7.12	0.0
B3LYP/6-311G(d,p) ^b <i>vacuum</i>	13.15	9.56	7.32	4.66	6.46	0.0
B3PW91/6-311G(d,p) ^b <i>vacuum</i>	15.72	11.77	8.69	5.92	7.78	0.0
OPTXPBE/6-311G(d,p) ^b <i>vacuum</i>	20.82	15.61	10.80	8.18	9.56	0.0
PBEPBE/6-311G(d,p) ^b <i>vacuum</i>	17.10	12.52	9.35	6.41	8.19	0.0
B3LYP/6-31G(d,p) ^c <i>chloroform</i>	9.96	5.71	5.06	2.14	4.30	0.0
B3LYP/6-31G(d,p) ^d <i>dichloromethane</i>	9.24	4.82	4.55	1.44	3.70	0.0
Tetramercaptoalix[4]arene: compound 4						
B3LYP/6-31G(d,p) ^a <i>vacuum</i>	1.03	–	1.20	–	2.36	0.0
B3LYP/6-311G(d,p) ^b <i>vacuum</i>	1.73	–	1.06	–	2.59	0.0
B3PW91/6-311G(d,p) ^b <i>vacuum</i>	1.58	–	1.16	–	2.58	0.0
OPTXPBE/6-311G(d,p) ^b <i>vacuum</i>	2.02	–	2.94	–	1.72	0.0
PBEPBE/6-311G(d,p) ^b <i>vacuum</i>	0.76	–	1.75	–	1.50	0.0
B3LYP/6-31G(d,p) ^c <i>chloroform</i>	0.54	–	1.67	–	1.99	0.0
B3LYP/6-31G(d,p) ^d <i>dichloromethane</i>	0.45	–	1.80	–	1.94	0.0

^a Geometries were optimized at this level of the theory.

^b Geometries were optimized at B3LYP/6-31G(d,p).

^c Free energy of solvation difference ($\Delta\Delta G_{\text{sol}}$ in kcal mol⁻¹) in chloroform.

^d Free energy of solvation difference ($\Delta\Delta G_{\text{sol}}$ in kcal mol⁻¹) in dichloromethane.

^e Ref. [22].

for comparison. In the particular case of **4**, *1,3-alt* is also the most stable conformer, which is in good agreement with a previous experimental study on a similar molecule, tetramercapto-*p-tert*-butylcalix[4]arene, where it was concluded that the *1,3-alt* conformer is favored both in solution and in solid state [36]. On the other hand, *cone* and *paco* are almost identical from the energetical point of view, the energy difference between both conformers is ca. 0.20 kcal mol⁻¹ and they lie ca. 1.0 kcal mol⁻¹ above the *1,3-alt*. These results suggest that **4** may be more flexible than **2**, and that interconversion between conformers can easily occur. This conclusion is in good agreement with previous experimental work by Hill et al. [41] who observed that a conformational conversion of the *1,3-alt* to the *cone* conformer occurred in the adsorption of the tetramercapto-*p-tert*-butylcalix[4]arene onto a rough silver surface.

Some interesting results are obtained from a variety of additional single point calculations. It may be seen in Table 2 that, in general, triple zeta basis set is able to decrease the value of ΔE when compared with the double zeta basis set. However, this is not observed with the compounds in which substituent groups at lower rim are thiol groups. The B3PW91 functional can reduce ΔE for all the conformers of **1** when compared with B3LYP functional. Single point calculations at B3LYP/6-311G(d,p) level show that the relative stability ordering of *paco* and *1,3-alt* of **2** is reversed when compared with B3LYP/6-31G(d,p) results. The stability ordering of *paco* and *cone* in **4** is also reversed for single point calculations at both B3LYP/6-311G(d,p) and B3PW91/6-311G(d,p) levels. However, all the calculations predict that there is a small ΔE between these conformers in **1**, **2** and **4**. This suggests the possibility of interconversion between conformers especially for **4**.

The new exchange and correlation functionals, namely OPTXPBE and PBEPBE, are available in the new version of GAUSSIAN program [28], and were tested for these molecular systems through additional single point calculations with the 6-311G(d,p) basis set. Compared with the B3LYP and B3PW91 functional, PBEPBE seems to give similar results except in **4**, while the results obtained with the OPTXPBE are quite different in **1** and **4**. On the other hand, these new exchange-correlation functionals are able to reduce ΔE for **1** much more than previous ones. Comparison of OPTX and PBE exchange functionals indicates that the PBE can reduce ΔE much more than OPTX in the methylene bridged compounds. From these results, we may conclude that PBEPBE can be better than OPTPBE to apply as new functional for the study in conformational analysis of this particular molecular system.

The total free energy difference ($\Delta\Delta G_{\text{sol}}$) for conformational transition in solvent was obtained with a combination of B3LYP/6-31G(d,p) level and IEF-PCM methodology [31]. This takes into account the influence of the solvent through a mean electrostatic potential. The large size of the molecular systems does not allow a geometry optimization or inclusion of individual solvent molecules in the first solvation shell. However, it is expected that molecules such as chloroform and dichloromethane do not make short interactions with the atoms of the solutes that could eventually induce a change in their geometries. Therefore, the study of the solvent effect was carried out by single-point calculations on the structures previously optimized in vacuum. The results obtained for solvents chloroform and dichloromethane, are reported in Table 2, where the total free energy in solution (ΔG_{sol}) of the most stable conformer is taken as reference. The ΔG_{sol} is the sum of the electronic energy and all the non-electrostatic terms such as cavitation, dispersion and repulsion energy. The electrostatic influence of chloroform and dichloromethane solvents does not modify the stability ordering of the compounds obtained in vacuum, except the reversion between the *paco* and *1,3-alt* in **2**. However, the ΔE values are reduced in both solvents for all the conformers, especially in **3**, but not for **1**. The values of $\Delta\Delta G_{\text{sol}}$ of all the compounds in dichloromethane are smaller than in chloroform. These results suggested that the polarity of the solvent can affect the energy difference between conformers in solution.

Many conformational studies of tetraalkoxythiacalix[4]arene using a combination of NMR spectroscopy and X-ray diffraction analysis may be found in the literature [38,42,43]. A variety of different conformations of tetraalkoxythiacalix[4]arene derivatives were reported, whereas the parent thiacalix[4]arene adopt only *cone* conformation both in solution and in solid state. The fast interconversion of the four conformers of tetramethoxythiacalix[4]arene is observed in CDCl_3 solution

[38b] whereas the presence of all the four possible conformers of tetraethoxythiacalix[4]arene was found in Cl_2 CDCl_2 solution at room temperature [38a]. Very interestingly, the lowering of temperature leads to the appearance of *pinched cone* conformer in both compounds [38a, 38b]. The introduction of propoxy groups into the lower rim could lead to the formation of four stable isomers [42]. The X-ray analysis of the tetramethoxy-*p-tert*-butylthiacalix[4]arene showed that it adopts a *1,3-alt* conformer and, by contrast, the tetramethoxythiacalix[4]arene was found to adopt an unprecedented solid-state structure where the *cone* and *1,3-alt* conformers co-exist in the crystal lattice with a 3:1 ratio [38b]. From all these points we can conclude that the enlargement of cavity in the sulfur bridged derivative compounds produces a higher conformational mobility and flexibility in comparison with the methylene bridged compounds. This suggests that interconversion between all the four conformers of the thiacalix[4]arene derivatives can easily occur. This phenomenon reflects the distinct conformational behavior of thiacalix[4]arene skeleton as compared with classical calix[4]arene. Therefore, it is not surprising that the DFT results of the sulfur bridged compounds (**1** and **2**) indicate the *cone* conformer as the most stable, which contrasts with the most stable *1,3-alt* conformer of similar molecules obtained by X-ray studies at solid state [34,35].

3.3. Charge distribution

Partial charges for the *cone* conformer of all the compounds and parent thiacalix[4]arene are reported in Table 3. The charge distribution was calculated by the Merz–Kollman–Singh (MK) scheme [44] at B3LYP/6-31G(d,p) level, which is a fitting of point charges, selected on a set of concentric spheres around each atom, to the calculated electrostatic potential. For simplicity, and owing to the C_4 -like or C_2 -like symmetry of the systems, we present only data for one benzene ring or two contiguous benzene rings, respectively. The high negative charges of donor atoms at lower rim are predicted to follow the order: $\text{NH}_2 > \text{OH} > \text{SH}$ in both the sulfur and methylene bridged compounds. However, the replacement of the four methylene bridges by the more negative sulfur atoms reduces the charges of the donor atoms. The bridging sulfurs exhibit more negative charge in **1** and **2** than in the parent thiacalix[4]arene. This may suggest a higher ability of the sulfur bridged compounds to bind metal ions. This is in good agreement with experimental information [40], which showed that the two tetraamino-*p-tert*-butylthiacalix[4]arene can bind two Pd^{2+} ions with a *trans*-square planar coordination geometry *via* two sets of sulfur and nitrogen atoms. It is interesting to note that the negative charges of N donor atoms in second pattern of **3** are higher than in the first pattern. The higher negative charges of N donor

Table 3

Atomic charges (in e) calculated by MK scheme for the *cone* conformer of compounds **1–4** and parent thiacalix[4]arene at B3LYP/6-31G(d,p) level

Atoms ^a	Compound 1 ^b	Compound 2 ^b	Compound 3		Compound 4	Thiacalix[4]arene ^c
			1st	2nd		
C1	0.13	0.41	0.08	−0.07	0.12	−0.12
C2	0.10	−0.33	0.12	0.46	0.10	0.39
C3	0.13	0.36	0.00	−0.07	0.11	−0.16
X1	−0.55	−0.19	−0.31	−0.99	−0.28	−0.42
H1	0.23	0.19	0.19	0.43	0.16	0.30
H1′	0.23		0.09	0.43		
Y1′	−0.24	−0.27	−0.17	−0.11	0.02	−0.13
C13	−0.09	−0.21	−0.21	−0.21	−0.33	0.04
C14	−0.30	−0.15	−0.16	−0.15	0.02	−0.31
C15	−0.09	−0.20	−0.14	−0.21	−0.32	0.04
C4	−0.01	0.25		0.02	−0.16	
C5	0.31	−0.03		0.16	0.16	
C6	0.01	0.17		−0.01	0.12	
X2	−0.51	−0.20		−0.95	−0.32	
H2	0.27	0.21		0.40	0.24	
H2′	0.27			0.40		
Y2′	−0.24	−0.24		−0.11	0.03	
C16	−0.18	−0.33		−0.17	−0.11	
C17	−0.09	0.03		−0.15	−0.11	
C18	−0.19	−0.27		−0.17	−0.25	

^a X is denoted to the atom N for the compounds **1** and **3**, S for the compounds **2** and **4** and O for thiacalix[4]arene, respectively (refer to Fig. 2). Y is denoted to the sulfur bridge atom in compounds **1** and **2**, and the methylene carbon atom in compounds **3** and **4**.

^b Ref. [22].

^c Ref. [21].

atoms in **3** can suggest new ligands with better binding sites for inclusion complexes with metal ions. The charge distribution of S donor atoms and C atoms in benzene rings of **4** exhibit negative charge. This suggests also that both regions can dominantly contribute to bind metal ions. A previous experimental study demonstrated that a similar compound, the tetramercapto-*p-tert*-butylcalix[4]arene, was able to form mono- and bi-nuclear mercury complexes in which calix unit adopted the *1,3-alt* conformation [36a]. The Hg²⁺ was strongly coordinated to two thiolate moieties and may have other weak interactions with two aromatic rings, thus fulfilling its ‘2p+4’ coordination model requirements. From these observations, we realized that sulfur bridged compounds have more binding sites than methylene bridged compounds, which reflects the diversity of complexation with metal ions. Interestingly, benzene ring carbons, especially those at the upper rim side (C₁₃–C₁₈), carry a reasonable negative charge. This suggests an important contribution to non covalent cation- π interactions upon complexation with metal ions.

3.4. Structure and energetic analysis of Zn²⁺ complexes with compound **1**

The optimized structures of each conformer of tetraaminothiacalix[4]arene (**1**) and the corresponding complexes with Zn²⁺ are gathered in Fig. 3. Obviously, the N atoms in the amino groups at the lower rim of compound **1** have a dominant role in the coordination of

Zn²⁺. A four coordination model may provide either tetrahedral or square-planar geometry. The electron configuration of the Zn²⁺ ion is 3d¹⁰, which corresponds to a completely fulfilled d block. The Zn²⁺ four coordination complexes seems to favor the tetrahedral geometry which is in agreement with the valence shell electron pair repulsion (VSEPR) theory. Some geometry parameters are gathered in Table 4. As shown in Fig. 3, the Zn²⁺ complex of *1,3-alt* adopts an asymmetric and slightly distorted tetrahedral structure (see Fig. 3(d)) whereas the complexes of *1,2-alt* and *paco* favor a square planar coordination (see Figs. 3(c) and (b)). The bond angles N₁–Zn–N₂, N₁–Zn–N₃, and N₁–Zn–N₄ in the *1,3-alt* complex are 104.0°, 121.1° and 103.9°, respectively. The corresponding bond angles in *1,2-alt* complex are 91.0°, 180.0° and 89.0°, respectively which are close to the standard square planar structure (90.0°, 180.0°). In *paco* complex the values of those angles are 92.0°, 146.3° and 92.0°, respectively, which correspond to a distorted square planar coordination. By contrast, only two N donor atoms are coordinated to Zn²⁺ in the *cone* complex (see Fig. 3(a)); it is interesting to refer the role of the π -electron density of two opposite benzene rings to accomplish a tetrahedral-like structure. In addition, the Zn–N bond lengths remain approximately the same, namely 2.14, 2.18 and 2.16 Å in *1,3-alt*, *1,2-alt* and *cone* complexes, respectively. In *paco* complex two different values of this bond length are observed: 2.14 Å and 2.18 Å. There is no variation of N–H and N–C distances among different complexes or isolated ligand conform-

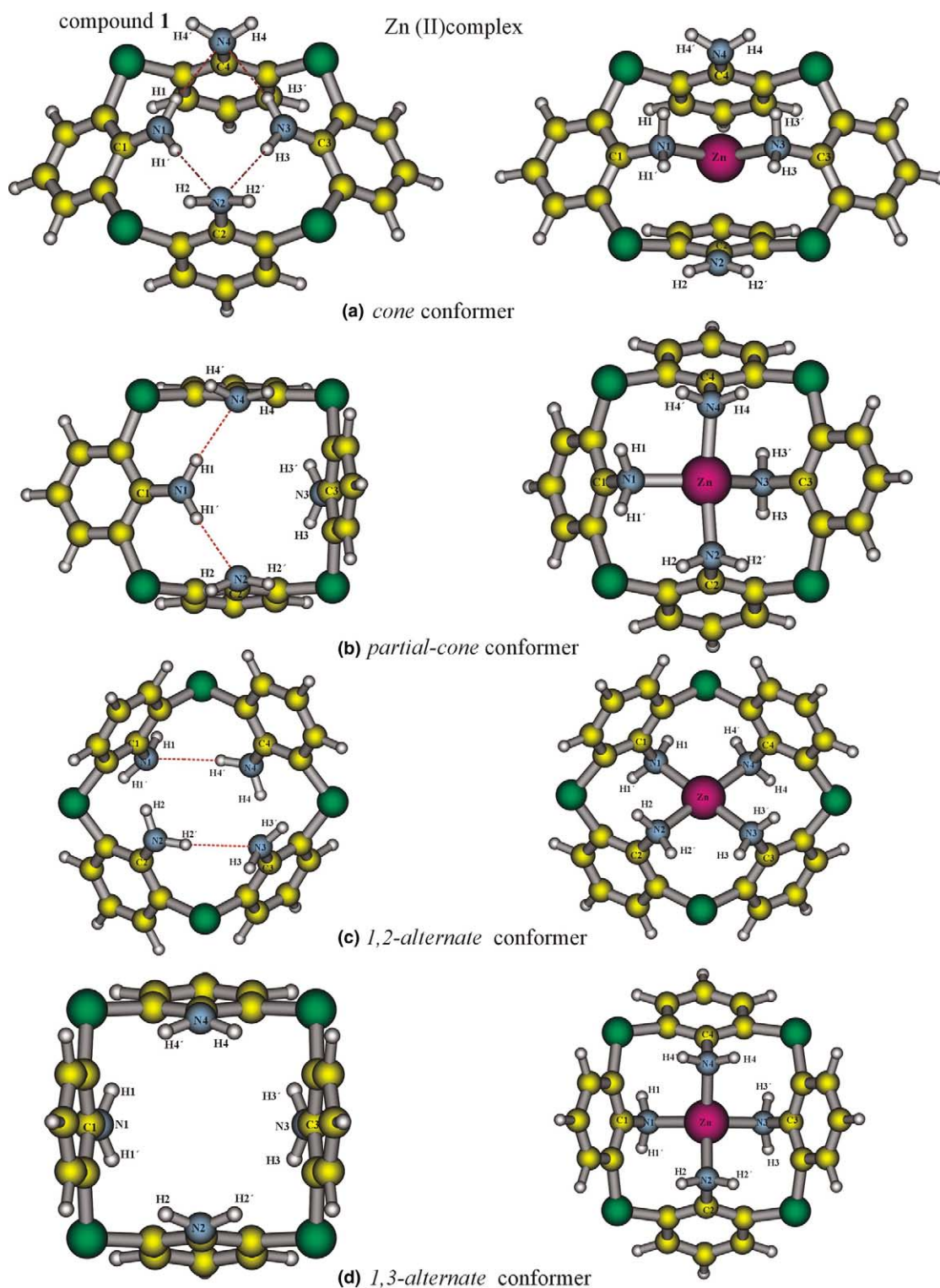


Fig. 3. Conformers of tetraaminothiacalix[4]arene (**1**) and the corresponding Zn^{2+} complexes. Optimized structures obtained at B3LYP/DFT level, using the 6-31G(d,p) basis set for free-ligand and LANL2DZ for Zn^{2+} .

ers. However, a slight increase of N–C bonds, less than 0.10 Å, is observed upon complexation, except the case of N_2 –C and N_4 –C bonds of *cone* because these nitrogens do not establish a close interaction with Zn^{2+} . By

contrast, most of the bond angles like H–N–H and H–N–C are reduced by about 4.0–7.0° in the *paco*, *1,2-alt* and *1,3-alt* complexes when compared with the corresponding isolated ligands. For the *cone* complex, a

Table 4
Structural parameters for each conformer of the compound **1** and their corresponding complex with Zn²⁺^a

parameter	<i>cone</i>	Zn- <i>cone</i>	<i>paco</i>	Zn- <i>paco</i>	<i>1,2-alt</i>	Zn- <i>1,2-alt</i>	<i>1,3-alt</i>	Zn- <i>1,3-alt</i>
Bond distance (Å)								
H ₁ –N ₁	1.008	1.025	1.010	1.023	1.012	1.020	1.008	1.022
H' ₁ –N ₁	1.008	1.024	1.010	1.023	1.012	1.021	1.008	1.022
N ₁ –C ₁	1.358	1.446	1.356	1.450	1.387	1.447	1.370	1.450
H ₂ –N ₂	1.013	1.010	1.012	1.022	1.012	1.021	1.008	1.022
H' ₂ –N ₂	1.013	1.010	1.011	1.025	1.009	1.020	1.008	1.022
N ₂ –C ₂	1.402	1.357	1.387	1.452	1.374	1.447	1.370	1.450
H ₃ –N ₃	1.008	1.024	1.008	1.020	1.012	1.020	1.008	1.022
H' ₃ –N ₃	1.008	1.025	1.008	1.020	1.012	1.021	1.008	1.022
N ₃ –C ₃	1.358	1.446	1.373	1.459	1.387	1.447	1.370	1.450
H ₄ –N ₄	1.013	1.014	1.011	1.025	1.012	1.021	1.008	1.022
H' ₄ –N ₄	1.013	1.014	1.012	1.022	1.009	1.020	1.008	1.022
N ₄ –C ₄	1.402	1.386	1.387	1.452	1.374	1.447	1.370	1.450
Zn–N ₁		2.161		2.144		2.180		2.136
Zn–N ₂		–		2.175		2.180		2.136
Zn–N ₃		2.161		2.155		2.180		2.136
Zn–N ₄		–		2.175		2.180		2.136
Bond angle (°)								
H ₁ –N ₁ –H' ₁	117.43	107.73	116.67	108.25	113.80	108.02	114.96	107.72
H ₁ –N ₁ –C ₁	120.84	109.15	121.66	108.05	114.69	110.91	117.33	110.82
H' ₁ –N ₁ –C ₁	120.84	108.61	121.66	108.05	114.35	109.21	117.33	110.73
H ₂ –N ₂ –H' ₂	113.13	115.74	114.39	107.55	113.69	108.02	114.96	107.72
H ₂ –N ₂ –C ₂	113.88	120.54	114.83	109.12	115.98	109.22	117.33	110.81
H' ₂ –N ₂ –C ₂	113.88	120.54	114.90	108.67	116.83	110.91	117.33	110.72
H ₃ –N ₃ –H' ₃	117.43	107.73	113.75	107.32	113.80	108.02	114.96	107.72
H ₃ –N ₃ –C ₃	120.84	108.61	116.72	110.75	114.69	110.91	117.33	110.82
H' ₃ –N ₃ –C ₃	120.84	109.15	116.72	110.75	114.35	109.21	117.33	110.73
H ₄ –N ₄ –H' ₄	113.13	112.82	114.39	107.55	113.69	108.02	114.96	107.72
H ₄ –N ₄ –C ₄	113.88	115.46	114.90	108.67	115.98	109.22	117.33	110.81
H' ₄ –N ₄ –C ₄	113.88	115.46	114.84	109.17	116.83	110.91	117.33	110.72
Zn–N ₁ –C ₁		114.08		111.12		99.02		96.90
Zn–N ₂ –C ₂		–		104.94		98.97		96.93
Zn–N ₃ –C ₃		114.06		99.28		99.03		96.90
Zn–N ₄ –C ₄		–		104.93		98.98		96.93
N ₁ –Zn–N ₂				91.97		90.98		104.0
N ₁ –Zn–N ₃		103.54		146.27		179.99		121.07
N ₁ –Zn–N ₄				91.98		89.03		103.93
N ₂ –Zn–N ₃				94.97		89.03		103.93
N ₂ –Zn–N ₄				155.71		179.99		121.25
N ₃ –Zn–N ₄				94.98		90.97		103.99

^a Each conformer of compound **1** was optimized at B3LYP/6-31G(d,p) level and its complex with Zn²⁺ was optimized at B3LYP/6-31G(d,p) for ligand and B3LYP/LANL2DZ for Zn²⁺.

different behavior is observed; the bond angles involving N atoms interacting directly with Zn²⁺ are reduced by *ca.* 10.0° whereas angles involving non-bonding nitrogen (N₂, N₄) are increased by about 5.0°.

The energetic analysis of all the conformers of the free compound **1** and their complexes with Zn²⁺ ion is summarized in Table 5. The results include the computation of binding energies (E_{binding}) defined as the total energy of complex minus the sum of the total energies of the metal ion and the most stable free ligand conformer, i.e., the *cone* structure. The binding energy ordering of the complexes was found to be *paco* < *1,3-alt* < *1,2-alt* < *cone*, which differs from the stability ordering of the free ligand conformers. An estimate of the basis set superposition error (BSSE) in the binding

energy was obtained from a procedure that allows automatic calculation of the counterpoise correction within the geometry optimization of complexes that are corrected for this error [33]. The effect of BSSE can improve a little the E_{binding} by reducing the values *ca.* 6.5–7.0 kcal mol⁻¹ for each complex. However, this effect does not modify the binding energy ordering. Strain energies, E_{strain} were calculated by the difference between the energies of **1** in its most stable conformation and in the complex structure. Surprisingly, the Zn²⁺ complexes with **1** prefer the *paco* and *1,3-alt* conformations. The E_{binding} of *paco* complex is smaller than *1,3-alt* complex about 1.2 kcal mol⁻¹, though both conformers must undergo a large deformation to complex the Zn²⁺ efficiently. The *cone* conformer, however, suffers only a

Table 5

Energetic information for the complexation between each conformer of the compound **1** and Zn^{2+} ^a

	<i>cone</i>	<i>partial cone</i>	<i>1,2-alternate</i>	<i>1,3-alternate</i>
Total energy (a.u.): X ^b	−2738.419859	−2738.417615	−2738.40898	−2738.413313
Total energy (a.u.): X– Zn^{2+}	−2803.484927	−2803.504513	−2803.492779	−2803.502495
	(−2803.474736) ^c	(−2803.494057)	(−2803.481890)	(−2803.491205)
E^d (binding energy; kcal mol ^{−1})	−275.32	−287.61	−280.25	−286.35
	(−268.93) ^c	(−281.05)	(−273.42)	(−279.26)
BSSE energy (kcal mol ^{−1})	6.39	6.56	6.83	7.08
E (strain; kcal mol ^{−1})	21.81	34.90	33.13	30.86

^a Each conformer of compound **1** was optimized at B3LYP/6-31G(d,p) level and its complex with Zn^{2+} was optimized at B3LYP/6-31G(d,p) for ligand and B3LYP/LANL2DZ for Zn^{2+} .

^b X is denoted to the free conformer of the compound **1**.

^c The values in parenthesis are corrected for BSSE.

^d The electronic energy of Zn^{2+} at B3LYP/LANL2DZ level is −64.62631 a.u.

little adaptation upon complexation. The observations point out that the favorable tetrahedral geometry orientation of strong Zn–N interactions can overcome the strain energy of deformation and stabilize the complex. Interestingly, the four N donors of the amino groups play a more important role than the bridging sulfurs in the coordination of the Zn^{2+} ion. This is confirmed by the longer Zn–S distances when compared with Zn–N distances. In *cone* conformation, by contrast, the Zn^{2+} binds only two N donor atoms and the E_{binding} is less than the others, as shown in Fig. 3(a) and Table 5.

A previous study on a complex of Pd^{2+} with a similar compound, tetraamino-*p-tert*-butylthiacalix[4]arene, indicated that two ligands adopting a *pinched-cone* con-

formation are fused at the lower rims to coordinate two Pd^{2+} ions with a *trans*-square planar geometry via two sets of nitrogen and sulfur bridge [40]. This may reveal an additional contribution of the sulfur bridges in the *cone* conformer to coordinate the Zn^{2+} ion. Using the same level of theoretical calculation, we have decided to study the complexation of a single Zinc ion by two calix[4]arene molecules in *cone* conformation. In order to save computing time, a simple and smaller model was used to study complexation with Zn^{2+} in the ratio 2:1. This model comprises two ligands, each one using only two aniline units linked by a sulfur atom in a conformation corresponding to a typical *cone*. The two structures resulting from a complete optimization are presented in

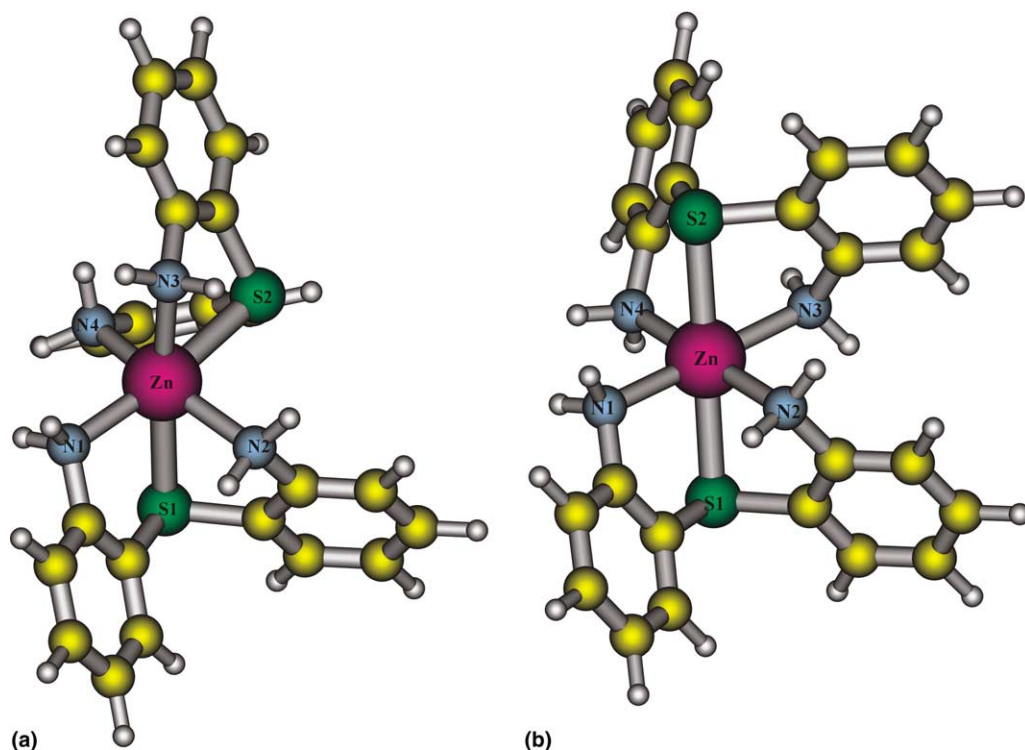


Fig. 4. Two different orientations of the Zn^{2+} complex with two *cone* conformer, obtained with the smaller model.

Table 6
Comparison of some selected bond lengths (Å) and bond angles (°) for first and second orientations of new model complex

	Zn–X (Å)		X–Zn–Y (°)		
	1st	2nd	1st	2nd	
Zn–N ₁	2.26	2.27	N ₄ –Zn–N ₁	97.1	92.2
Zn–N ₂	2.28	2.27	N ₁ –Zn–S ₁	77.3	78.4
Zn–N ₃	2.26	2.27	S ₁ –Zn–N ₂	75.5	76.6
Zn–N ₄	2.28	2.27	N ₂ –Zn–S ₂	92.3	N ₃ –Zn–S ₂ 76.6
Zn–S ₁	2.64	2.61	S ₂ –Zn–N ₃	77.3	S ₂ –Zn–N ₄ 78.3
Zn–S ₂	2.64	2.61	N ₃ –Zn–N ₄	95.5	N ₂ –Zn–N ₃ 82.2
			N ₃ –Zn–S ₁	172.2	N ₁ –Zn–N ₃ 175.9
			N ₁ –Zn–S ₂	172.2	S ₁ –Zn–S ₂ 179.6
			N ₂ –Zn–N ₄	160.1	N ₂ –Zn–N ₄ 175.9

Numbering of each atoms as shown in Fig. 4.

Fig. 4, and some relevant geometry parameters are summarized in Table 6. The structures reveal two different octahedral orientations of sulfur and nitrogen atoms. In the first orientation (Fig. 4(a)), one sulfur atom lies in axial position and the other one is equatorial, whereas for the second orientation (Fig. 4(b)), both sulfur atoms lie in axial position. All the Zn–N and Zn–S bond distances are almost the same in both structures. The second orientation is more stable by about 0.53 kcal mol⁻¹ and the bond angles (X–Zn–Y) are closer to the standard octahedral geometry (90°, 180°) than the first one. The structure previously obtained for the 1:1 complex (see Fig. 3(a)) was also analyzed with the small model. For that, two opposite sulfur bridges of the complex structure were replaced by hydrogens, and a single point calculation was performed at the same DFT level. The energy obtained this way lies above the two possible octahedral orientations. This energetic behavior gives us an idea of how favorable the octahedral orientation of the 2:1 complex is. From these points, the simultaneous binding of two *cone* conformers to Zn²⁺ can be ascribed to the presence of the sulfide linkage. The lone pair electrons of sulfur can contribute to coordinate the cationic center. In addition, the two N donor atoms of the amino groups are able to form a set two of five-membered chelated rings per ligand (Fig. 4). The results seem to agree with previous studies on the Zn²⁺ complex with *cone p-tert-butylthiacalix[4]arene*, in which it is notorious the role of the bridging sulfurs in binding the Zn²⁺ with two adjacent phenoxide groups, forming two five membered rings [14a, 14c]. In the particular case of tetraaminothiacalix[4]arene (1), no experimental study has been carried out yet, but the present study opens good perspectives in that direction.

4. Conclusion

The four main conformers of the sulfur bridged compounds, namely tetraaminothiacalix[4]arene (1) and tetramercaptothiacalix[4]arene (2), and the correspond-

ing methylene bridged compounds, namely tetraamino-calix[4]arene (3) and tetramercapto-calix[4]arene (4) have been studied by a DFT methodology. Our results predict the *cone* to be the most stable conformer for both sulfur bridged derivatives, which is in a good agreement with a previous theoretical work on parent thiacaalix[4]arene. On the other hand, the conformer adopts *1,3-alternate* as the most stable conformation for both methylene bridged derivatives. Interestingly, different substituents at the lower rim do not affect the stability ordering. Owing to a small difference in the relative energies of the conformers, especially in 4, the interconversion between conformers is expected to occur easily. For both sulfur bridged compounds, the intramolecular bonding between hydrogen atoms and sulfur bridges seems to be a dominant factor in the stabilization of all the conformers rather than the hydrogen bonds between substituent groups at the lower rim. By contrast, the favorable NH–π interactions between the amino hydrogens and adjacent aromatic rings is a dominant stabilization in 3. The free energy difference for conformational transition in chloroform and dichloromethane solvents was also obtained with a combination of DFT level and IEF-PCM model. It is concluded that both solvents do not affect the stability ordering of the compounds. However, the values of the free energy difference in chloroform are higher than in dichloromethane, which is explained by the different polarity of the solvents.

The structures and energetic of 1:1 Zn²⁺ complexes of each conformer of 1 were analyzed in detail at B3LYP/6-31G(d,p) for ligand and B3LYP/LANL2DZ for Zn²⁺. An estimate of the basis set superposition error in the binding energy was obtained from a procedure that allows automatic calculation of the counterpoise correction within the geometry optimization of complexes that are corrected for this error. The new sulfur bridged compound 1 can bind Zn²⁺ in different coordination environments, which depend on the conformation of the ligand. It is interesting to note that close interactions with the central Zinc ion are only established by the N

atoms of the amino groups. In addition, a smaller and new model was successfully applied to study the 2:1 complex with Zn^{2+} via two units composed each by only two anilines linked by one sulfur atom. Our results suggest that for the *cone* conformer an asymmetric distorted octahedral coordination is more favorable than the distorted tetrahedral structure observed in the 1:1 complex. In this case, the sulfur atoms interact directly with the Zinc ion, and they both prefer the axial orientation of an octahedral coordination. In addition, they contribute with the N atoms to form a pair of five-membered chelated rings per ligand, which can be another factor for the complex stabilization. This is in good agreement with a previous study on the Zn^{2+} complex with *cone p-tert-butylthiacalix[4] arene*, where it is shown the important role of the bridging sulfurs in binding the Zn^{2+} with two adjacent phenoxide groups and the formation of two five membered rings.

In conclusion, the new sulfur bridged compound **1** shows a good binding capability to form complexes with Zn^{2+} , owing to the coordination sites of sulfur atoms and amino groups. This work opens a new strategy in the study of host–guest properties in metal-binding for transition metal complexes. The study of specific selectivity of this compound towards several transition metals is an interesting topic, which is now being investigated.

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