



Density functional theory study of π -aromatic interaction of benzene, phenol, catechol, dopamine isolated dimers and adsorbed on graphene surface

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Abstract

We analyze the influence of different groups on the intermolecular energy of aromatic homodimers and on the interaction between a single aromatic molecule and a graphene surface. The analysis is performed for benzene, phenol, catechol, and dopamine. For calculating the energies, we employ density functional theory within the local density approximation (LDA-DFT). Our results show that the lowest intermolecular energies between the aromatic molecules are related to the T-shaped configurations. This lower energy results from the quadrupole interaction. In the case of the interaction between the graphene sheet and the aromatic molecules, the lowest energy configuration is the face to face. The adsorption energy of a molecule on a graphene surface involves $\pi - \pi$ interactions that explain the face to face arrangement. These results provide insight into the manner by which substituents can be utilized in crystal engineering, supramolecular chemistry, bioinspired materials, formation of various molecular clusters, parameterization of force fields suitable for classical simulations, and design of novel sensing, drug delivery, and filters based on graphene.

Keywords Graphene · Aromatic homodimers · Density functional theory · Parameterization of force fields suitable for classical simulations

Introduction

Carbon is a very versatile and important chemical element, not only because when combined with other elements it becomes the building block of organic compounds but also because of its ability to form a variety of allotropic forms [1–3]. Moreover, depending on the arrangement of

the atoms in the different allotropic forms, the resulting molecule presents different physical properties. One of the last allotropes to be obtained experimentally was the graphene (GR) [4].

Graphene has attracted interest from the scientific community due to its electronic and structural characteristic [5, 6]. This crystalline allotrope of carbon has one layer of atoms arranged in a honeycomb lattice in which the electrons are free in two directions and confined in one that gives strength to the structure. This monolayer has a huge and flexible surface area and huge electric and thermal conductivity which enables a variety of applications from sensors to drug delivery [7–9]. The idea is that the interaction between the graphene and other materials can be activated or suppressed by the environment. Therefore, it is relevant to understand the interaction between graphene and other materials, particularly the aromatic molecules [10–17].

Aromatic compounds are candidates for drug delivery due to their presence in a number of biological processes. In order to understand how the graphene might capture and release the molecules, it is relevant to obtain which is the orientation of the molecules close to the graphene surface. In very dilute systems and at very low temperatures,

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in which only the interaction between the molecule and the graphene is taken into account, the lowest energy configurations are the aromatic ring parallel or perpendicular to the confining surface [18]. However, other orientations become relevant between molecule-molecule and molecule-graphene systems if temperature is taken into account [19–22].

A good parametrization method to account for the molecule-graphene interaction is still missing. While the atomistic approaches fit the interaction parameters with experimental results at a certain temperature, the first principle calculations focus on the zero temperature configurations what captures the minimum energy configurations. The idea here is to combine both approaches by selecting representative low energy intermolecular geometries to parametrize an atomistic interaction [23–26] which is adequate to capture essential trends of the structural properties in a large range of the temperatures and pressures for a mixture.

In the bulk, the aromatic molecule intermolecular interactions are responsible for the formation of clusters [27–30], the supramolecular assembly phenomena, [31] the formation of structures [32], the crystal packaging [33], and the engineering of nanomaterials [34]. These structures result from the competition between the interactions H- π [35, 36], π - π stacking, and H-H [37–41]. Thus, investigating the bulk system in classical simulations, so that the classic force fields provide information on the most probable configurations at zero temperature, gives an understanding of the origin of the molecular structure computed by the radial distribution function for aromatic molecules which depend on the competitions between the interactions in each configuration of the system.

In this paper, we address two questions which are relevant for the interaction of molecules and the graphene. We compare the molecule-molecule and molecule-graphene energies when the orientations and distance are changed. The idea is to identify the lowest energy molecule-molecule and molecule-graphene configurations. The other question is the impact of the competition between the π - π and the H- π interactions in the definition of the optimal molecule-molecule and molecule-graphene configurations. In order to answer these two issues, we evaluate the interaction between two molecules of benzene (BZ), phenol, catechol or dopamine (DA) in different configurations. Then we compare this intermolecular energy with the energy of the same molecule when interacting with a GR sheet. We focus on the influence of the interactions X- π (X = CH, OH, NH₂), π - π , and X-X in the molecule-molecule and molecule-graphene interactions to identify the more relevant configurations in both cases. This allows us to understand the effect of these groups in the adsorption of these molecules in graphene. The remaining of the paper

goes as follows. In the “**Model and methods**” section, the models and methods are presented; in the “**Results and discussion**” section, the results are discussed; and in the “**Conclusions**” section, we present our conclusions.

Model and methods

We studied the influence of the interactions X-X, X- π (X = CH, OH, two OH, NH₂), and π - π on the aromatic ring in the interaction of molecule-molecule (homodimers) and molecule-graphene versus distance through density functional theory (DFT) [42, 43], implemented in the SIESTA (Spanish Initiative for the Electronic Simulations of Thousands of Atoms) code [44]. The electronic, energetic, and structural properties were analyzed solving the self-consistent Kohn-Sham equations. In all calculations, a double ζ plus a polarized function (DZP) was used for the numerical basis set. In order to describe the exchange and correlation potential (V_{xc}), we investigated the performance of the three functional implemented in the SIESTA: (i) the LDA with the Perdew and Zunger (PZ) parametrization [45] the correction to basis set superposition error (BSSE corrected) [46], (ii) the generalized gradient approximation (GGA) with the Perdew, Burke, and Ernzerhof (PBE) version [47], and (iii) GGA dispersion correction [48] with the Perdew, Burke, and Ernzerhof (PBE) version.

In this work, we adopted the LDA functional with the correction to basis for two complementary reasons. First, when compared with the other two options above, it gives a better agreement with the literature [23, 24, 49, 50] for the minimum energies configuration. The second reason is that since we want to compare the energies between the molecule-molecule and the molecule-graphene cases, the energy has to go to zero at very large distances. This constraint is important because our proposal is to construct a force field from first principles.

In order to represent the electronic charge in real space, a grid cutoff of 200 Ry was used. All of the studied systems present a neutral charge in the initial electronic configuration. The isolated molecules and graphene structures were relaxed until the residual forces were less than 0.05 eV Å⁻¹ in all atomic coordinates. Additionally, graphene studied shows 144 carbon atoms to carry out the simulations of molecule-graphene we used periodic boundary conditions, the cell had dimensions of 25.94 × 40.00 × 14.98 Å³, also called supercell method. In the case of the molecule-molecule interaction, we use a super cell of 40 × 40 × 40 Å³. The isolated molecules are relaxed residual lower forces than 0.05 eV/Å and then kept frozen upon adsorption on the graphene, and in the interactions of the homodimers. The distance (r) between the homodimers and the molecule-graphene refers

to the minimum atom–atom distance of each configuration studied.

The relative numerical accuracy on the interaction energy versus distance, computed with the correction to the basis set superposition error (BSSE corrected) is estimated to be of the order of around 0.96 kJ/mol.

For the interaction energy calculations, we used the following equation through BSSE (basis set superposition error) corrected for all calculations with the counterpoise method [46]:

$$E = E(A + B) - E(A + B_{\text{ghost}}) - E(B + A_{\text{ghost}}). \quad (1)$$

This correction is performed starting from the initial geometry of the AB system and calculating the total energy of system A, considering the whole set of base functions, where the set of base functions B is in the position corresponding to system B, without the explicit presence of the atoms. The same occurs in the calculation of system B. The system with negative binding energies implies attractive interaction.

Results and discussion

First, we selected representative parallel and T-shaped intermolecular configurations for benzene (BZ), phenol, catechol, or dopamine (DA). Thereafter, we calculated the potential-energy curves of these configurations as a function of the distance r between the molecule–molecule and molecule–graphene via DFT formalism with the correction to basis as indicated in the Eq. 1.

Intermolecular interactions

For the benzene–benzene interaction, we considered five basic configurations: (a) face to face (BZ-BZ_FF), (b) slipped parallel (BZ-BZ_SP), (c) side by side (BZ-BZ_SS), (d) T-shaped (BZ-BZ_TS₁), and (e) T-shaped displaced (BZ-BZ_TSD). The interaction energy curves calculated between the benzene dimers are illustrated in Fig. 1, in units kJ/mol.

The side by side configuration showed in Fig. 1c is the least attractive since its energy major configuration is the H–H repulsion. The T-shaped and the T-shaped displaced configurations illustrated in Fig. 1d and e exhibit the lowest energies when compared with other configurations. The attractive behavior at very low distances in this case can be explained in terms of the favorable electrostatic interaction between the negatively charged π -cloud located in the center of the lower ring and the positively charged hydrogen atom of the other subsequent. The most stable configuration is the BZ-BZ_TS₁ which optimizes the distance between the H– π interactions. The total energy for the BZ-BZ_TS₁

is -9.0 kJ/mol at $r = 2.5$ Å, while for BZ-BZ_TSD configuration the energy is about -7.2 kJ/mol at $r = 2.5$ Å.

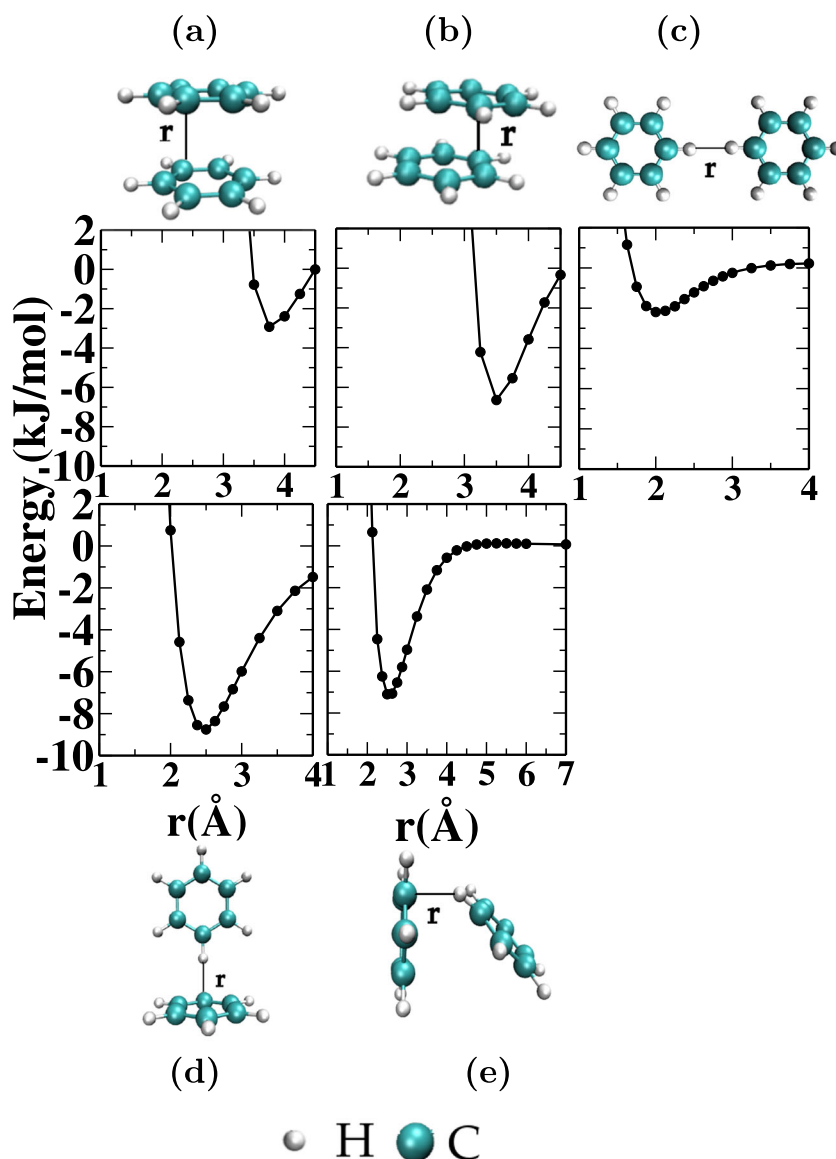
The face to face configurations BZ-BZ_FF and BZ-BZ_SP (Fig. 1a and b) show the minimum energies at -2.92 kJ/mol at ($r = 3.75$ Å) and -6.63 kJ/mol at ($r = 3.5$ Å), respectively. These energies result to the attractive π – π stacking. The difference between the two parallel configurations occurs because the displacement decreases the quadrupolar repulsion between benzene dimer and adds an electrostatic attraction between the positive H and the negative π -cloud [51, 52].

In order to confirm that the configurations with lowest energies are the TS, TSD, and the SP, we compared our results with the energies obtained using other functionals. Cacelli et al. [23, 49] found that the interacting energy of the BZ-BZ_SP, BZ-BZ_TS₁, and BZ-BZ_FF configurations for benzene were around -7.0 , -9.8 , and -4.0 kJ/mol, respectively. These values were computed by the MP2/6-31G (BZ-BZ_TS₁) and MP2/CAM-B3LYP-D3 (BZ-BZ_FF and BZ-BZ_SP) theory. The same behavior is observed in other theoretical approaches [52–54]. Comparison with the results of Cacelli et al. [23, 49] shows energy differences that are less than 0.8 [49], 1.08 [23], 1.37 [23] kJ/mol, respectively. Grover et al. [25] reported that the experimental binding energy TS of the benzene dimer was -10.05 ± 1.67 kJ/mol. Tsuzuki et al. [55] reported that the minimum value for the interacting energy of the BZ-BZ_FF is around -6.19 (-3.59) kJ/mol computed by CCSD(T)/6-31G (MP2/6-31G*) theory gives similar behavior as our results. In general, chemical bonding and electron transfer can be described well within the LDA functional.

When compared with more sophisticated theories, for instance, high-level quantum calculation MP2, CCSD(T) and vdW-DF methods [52–54], the energies computed by the LDA functional, show some differences for the minimum values for the BZ-BZ_FF settings. These differences are due to the dispersion, and van der Waals (vdW) forces are not represented with accuracy in the LDA functional. However, the DFT-LDA for parallel and TS configuration results are in quite good agreement with high level quantum calculation proposed at work [52–54]. Even in this case, the T-shaped and the SP are the preferential configurations.

For the phenol–phenol interaction, we also considered five basic configurations: (a) the face to face with parallel OH groups (phenol–phenol_FF), (b) the face to face with antiparallel OH groups (phenol–phenol_AFF), (c) the side by side (phenol–phenol_SS), (d) the T-shaped with opposing OH groups (phenol–phenol_TS₁), and (e) the T-shaped with confronting OH groups (phenol–phenol_TS₂). The interaction energy curves calculated between the phenol dimers are illustrated in Fig. 2, in units kJ/mol.

Fig. 1 Structural configurations and interaction energy curves computed for the benzene. **a** Face to face (BZ-BZ_FF). **b** Slipped parallel (BZ-BZ_SP). **c** Side by side (BZ-BZ_SS). **d** T-shaped (BZ-BZ_TS₁). **e** T-shaped displaced (BZ-BZ_TSD)

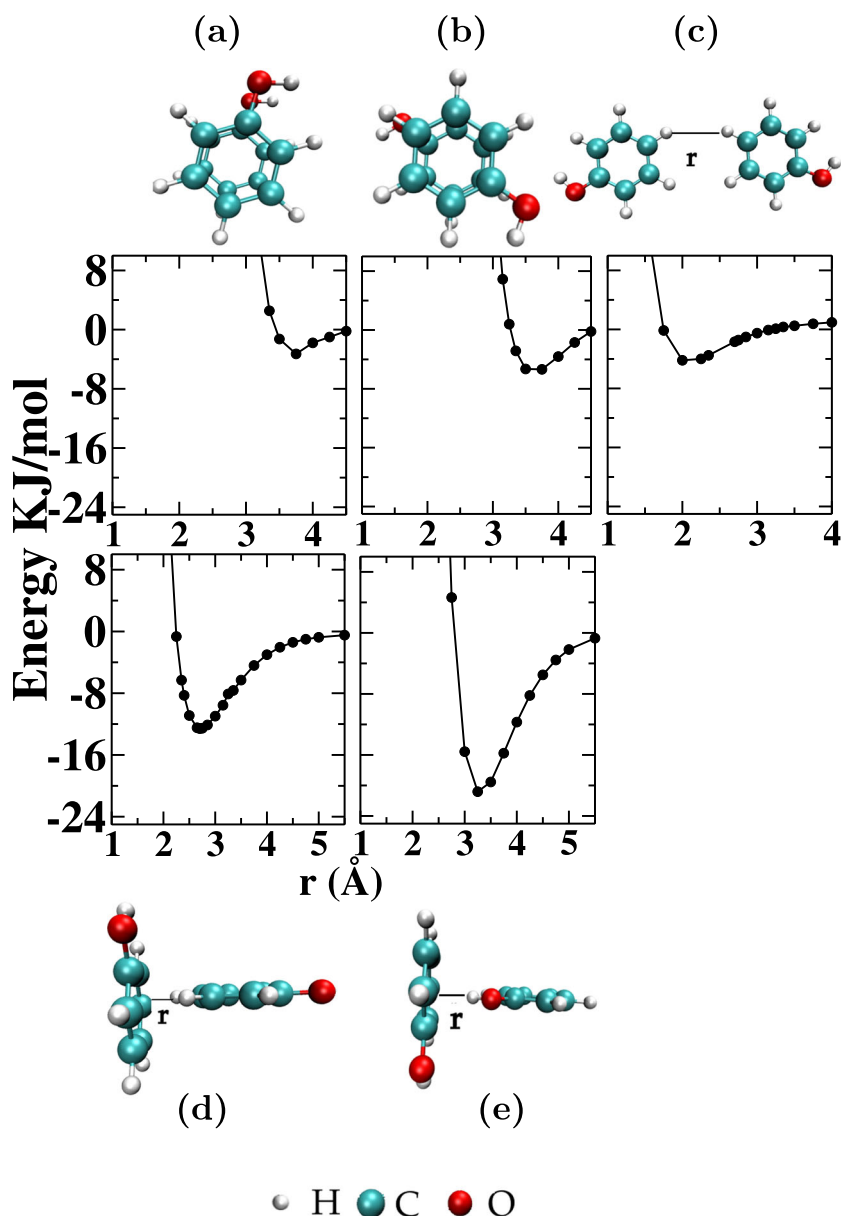


Between the two stacked conformations, FF and AFF, depicted in Fig. 2a and b, the second is the more stable. The phenol-phenol_AFF has its minimum energy of -5.35 kJ/mol at $r = 2.75$ Å, while the phenol-phenol_FF around -3.28 kJ/mol at $r = 3.8$ form. The energy arises from the competition between the H- π , OH- π , and π - π interactions. The difference between the two stacked configurations is due to the additional OH-OH repulsion present in the phenol-phenol_FF case. The side by side (phenol-phenol_SS) showed in the Fig. 2c is the least stable configuration since its energetics is dominated by the H-H repulsion [55–57]. The more stable structures as illustrated in the Fig. 2d and e are the phenol-phenol_TS₁ conformation which has its minimum at $r = 2.7$ Å, with energy -12.58 kJ/mol and the phenol-phenol_TS₂ with energy

around -20.8 kJ/mol at $r = 3.25$ Å. These low energies arise from the H- π and OH- π electrostatic attraction.

In order to confirm that the configurations with lower energies are the T-shaped, we compared our results with the energies obtained by other functionals. Kolaski et al. [41] evaluated the interactions of the configurations the phenol-phenol employing different functionals and ab initio calculations. They obtained the binding energies between the two phenol molecules in the T-shaped configurations around -17.2 and -51 kJ/mol by optimizing the levels with MP2/CAM-B3LYP theory. According to the author, the geometry of the minimum energy is directed by the hydrogen bond formed by two hydroxyl groups and the H- π interaction between two aromatic rings as in our case. Our results for the minimum of the T-shaped configurations are

Fig. 2 Structural configurations and interaction energy curves of phenol dimer, for the five configurations. **a** Phenol-phenol_FF. **b** Phenol-phenol_AFF. **c** Phenol-phenol_SS. **d** Phenol-phenol_TS1. **e** Phenol-phenol_TS2



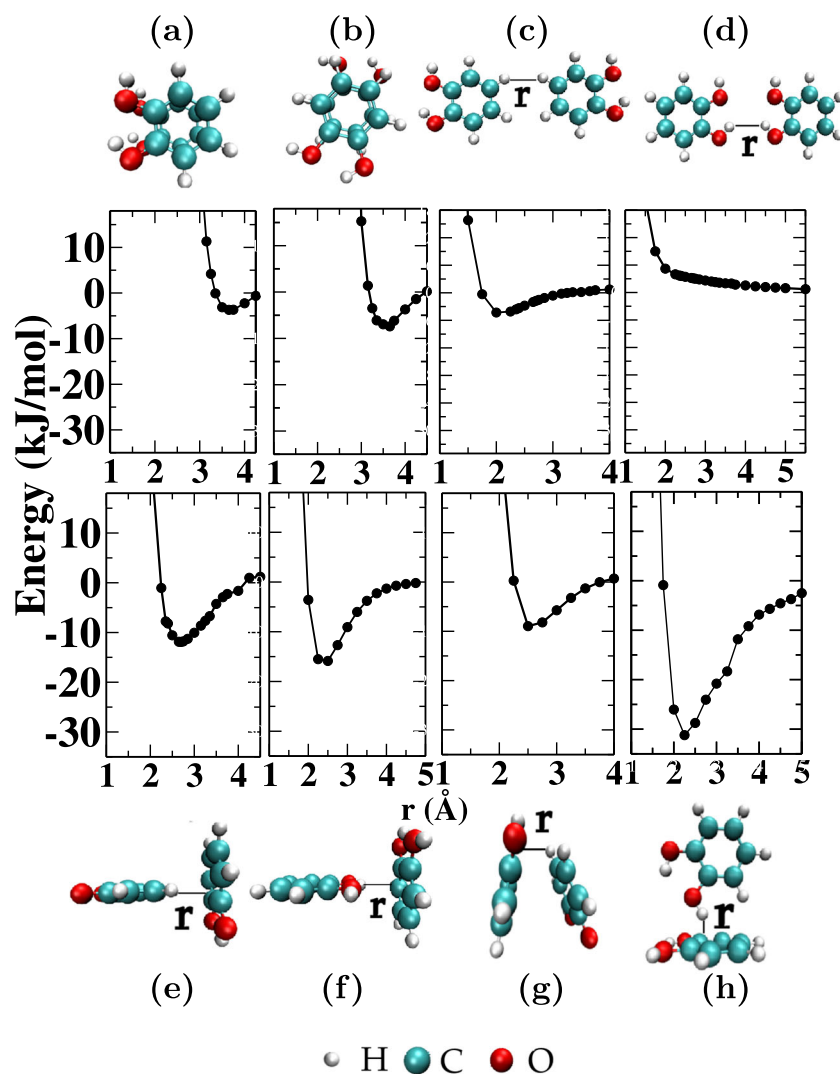
in the range of values computed by their work and provide energies for different distances as well.

In the case of the catechol-catechol interaction energy, the two OH groups expand the configurational space and we computed the energy for different distances of eight different configurations: (a) face to face (catechol-catechol_FF), (b) antiparallel face to face (catechol-catechol_AFF), (c) side by side with opposing OH groups (catechol-catechol_SS1), (d) side by side with confronting OH groups (catechol-catechol_SS2), (e) T-shaped with opposing OH group (catechol-catechol_TS1), (f) T-shaped with confronting OH groups (catechol-catechol_TS2), (g) T-shaped displaced (catechol-catechol_TSD), and (h) T-shaped with OH groups displaced (catechol-catechol_TS3).

The comparison between the interaction energies curves of the eight configurations the catechol dimers is illustrated in Fig. 3. In these systems, a strong electrostatic attraction between the π cloud and the OH and H is present. The configuration which combines a small distance between the OH- π is the T-shaped. Within the three TS cases, the most stable configuration is the catechol-catechol_TS3 with an energy minimum of -31.2 kJ/mol at $r = 2.25$ Å. This value is smaller than the similar catechol-catechol_TS2, with energy value of -15.8 kJ/mol at $r = 2.5$ Å. A comparable behavior was observed in the work of Barone et al. [58].

Among the two parallel configurations catechol-catechol_FF and catechol-catechol_AFF, the second is more stable with interaction energy value of -7.41 kJ/mol

Fig. 3 Structural configurations and interaction energy curves of catechol dimer, for eight configuration. **a** Face to face . **b** Antiparallel face to face (catechol-catechol_AFF). Side by side (SS) dimers **c** catechol-catechol_SS₁ and **d** catechol-catechol_SS₂. T-shaped (TS) dimers **e** catechol-catechol_TS₁, **f** catechol-catechol_TS₂, and **g** catechol-catechol_TS₃. **h** Catechol-catechol_TS₃



at $r = 3.65 \text{ \AA}$, in agreement with the repulsive interaction between the OH dipoles, present in the catechol-catechol_FF value of -3.69 kJ/mol at $r = 3.65 \text{ \AA}$ form; the same behavior is observed in the study [58]. The system side by side, the catechol-catechol_SS₁, is more stable with interaction energy of -4.31 kJ/mol at $r = 2 \text{ \AA}$, in agreement with the strong repulsive interaction between the four OH dipoles in the catechol-catechol_SS₂ configuration. The catechol-catechol_FF has larger interaction energy than the benzene-benzene_FF and phenol-phenol_FF dimer. The two hydroxyl groups are electron-donating substituent, leading to the decrease of electrostatic repulsion between aromatic rings. The substituent effects are additive for these FF homodimers.

In a recent study, Barone et al. [58] investigated the energy of interaction between the catechol dimers using MP2_{mod} and CCSD(T)/CBS methods, through four distinct configurations, similar to the investigated in our work. In

the catechol-catechol_FF, catechol-catechol_AFF, catechol-catechol_TS₂, and catechol-catechol_TS₃ configurations, the energies for configurations correspond -9.62 , -15.9 , -17 , and -21 kJ/mol , respectively. The binding energy values found in our study are below the values found in the study proposed by Barone et al. [58]. This difference is attributed to the methodology, exchange-correlation functional, and the basis sets used in each work. The neglecting flexibility of dimers catechol does not allow the OH group which can rotate and displace the H atom out of the aromatic plane to form a hydrogen bond with the other monomer, hence stabilizing the complex. As a matter of fact, Barone et al. [58] work shows the importance of such mechanism in the stability of catechol dimers. However, this is not a problem for the parameterization of force fields suitable for classical simulations.

For the calculation of the dopamine–dopamine (DA-DA) interaction energy, we selected six different configurations:

(a) face to face with parallel rings (DA-DA_FF₁), (b) face to face with dislocated rings (DA-DA_FF₂), (c) side by side (DA-DA_SS), (d) T-shaped (TS) with opposing hydroxyls (DA-DA_TS₁), (e) T-shaped with two *NH*₂ groups pointing towards the other ring (DA-DA_TS₂), and (f) T-shaped with one *NH*₂ group pointing towards the other ring (DA-DA_TS₃). The interaction energy curves calculated between the dopamine dimers are illustrated in Fig. 4, in units kJ/mol. The most attractive configurations are T-shaped DA-DA_TS₂ (energy of -24.76 kJ/mol at $r = 2.7$ Å), DA-DA_TS₃ (energy -14.75 kJ/mol at $r = 2.7$ Å), DA-DA_TS₁ (energy of -10.28 kJ/mol at $r = 2.5$ Å), respectively. The stability of the configurations is dominated by the *NH*₂ interaction with the aromatic ring, which differs from the benzene–benzene, phenol–phenol, and catechol–catechol interactions dominated by the OH– π and H– π interactions. This behavior is due to the influences of the amine groups and the by ethyl interactions, which is not in the same plane

as the catechol of the molecule, similar to the study of L-tyrosine dimers [59].

Table 1 shows the values of the interaction energy between the homodimers for the FF, SP, and TS configurations. Even though the benzene, phenol, catechol, and dopamine exhibit different electronic structures, our study suggest that these systems share similar configurations of minimum energy T-shaped and parallel dimers. The relevant interactions in all cases are the negatively charged π -electron cloud above the ring center, where the FF (TS) configuration interaction of the electronic cloud is parallel (90°) increasing (decreasing) repulsion between the dimers. Electron-withdrawing substituents should reduce the negative π charge and lead to decreased $\pi - \pi$ electrostatic repulsion, and vice versa for electron-donating substituents [55–57, 60]. Indeed, this occurs for phenol–phenol, catechol–catechol, and dopamine–dopamine interactions. The hydroxyl group is electron-donating sub-

Fig. 4 Structural configurations and interaction energy curves computed for the dopamine dimer in **a** DA-DA_FF₁ and **b** DA-DA_FF₂; **c** Side by side (DA-DA_SS); and T-shaped (DA-DA_TS) dimers **d** DA-DA_TS₁, **e** DA-DA_TS₂, and **f** DA-DA_TS₃ configurations

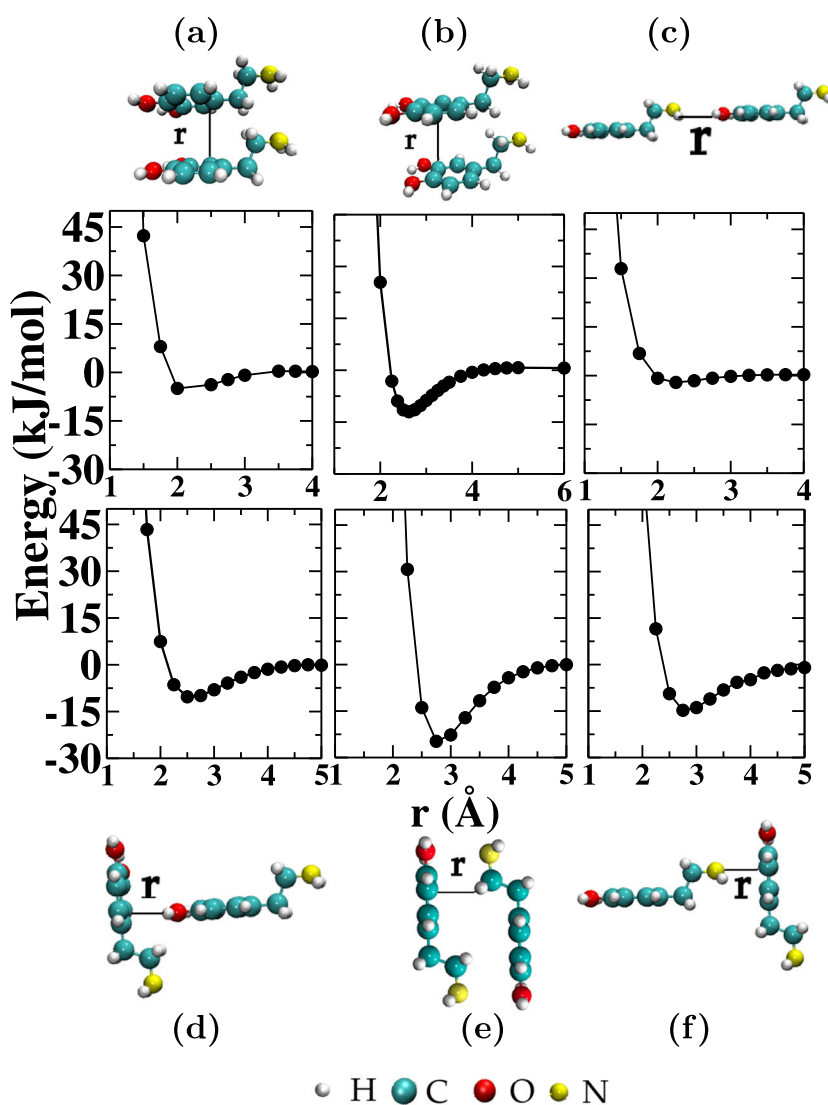


Table 1 Configurations, interaction energies, and distances for benzene, phenol, catechol, and dopamine homodimers

Configurations	Energy (kJ/mol)	Distance (Å)
Face to face		
Benzene	−2.97	3.75
Phenol	−3.28	3.8
Catechol	−3.69	3.65
Dopamine	−4.2	2.0
Slipped parallel		
Benzene	−6.63	3.5
Phenol	−5.35	2.75
Catechol	−7.41	3.65
Dopamine	−6.25	2.5
T-shaped		
Benzene_TS ₁	−9.0	2.5
Benzene_TSD	−7.2	2.5
Phenol_TS ₁	−12.58	2.7
Phenol_TS ₂	−20.8	3.25
Catechol_TS ₁	−12.65	2.75
Catechol_TS ₃	−21.0	2.25
Dopamine_TS ₃	−14.75	2.7
Dopamine_TS ₂	−24.76	2.7

stituent, leading to the decrease of electrostatic repulsion between molecule and molecule. The substituents in benzene ring have an additive effect (decreasing repulsion) on the interacting energy of face to face dimers, in the case catechol-catechol_FF when substituents are two hydroxyls. This behavior is attributed to repulsion between the dipoles of four OH group. The energetics of substituted TS configurations are more stable than benzene-benzene_TS. Among all TS configurations studied, the catechol-catechol_TS₃ arrangement is more stable than other molecule–molecule configurations, due to the contribution of the π – π and OH– π in this arrangement.

The benzene–benzene, phenol–phenol, catechol–catechol, and dopamine–dopamine dimers are ideal candidates to test the capability of new computational approaches to accurately represent the different kinds of interactions of dimers, occurring in the presence of π – π and X– π , and charge transfer interactions between these species are also an important role in the parameterization of force fields derived from calculations suitable for classical simulations [23, 26, 49, 61]. In this case, it is very important that each system has several configurations and that for

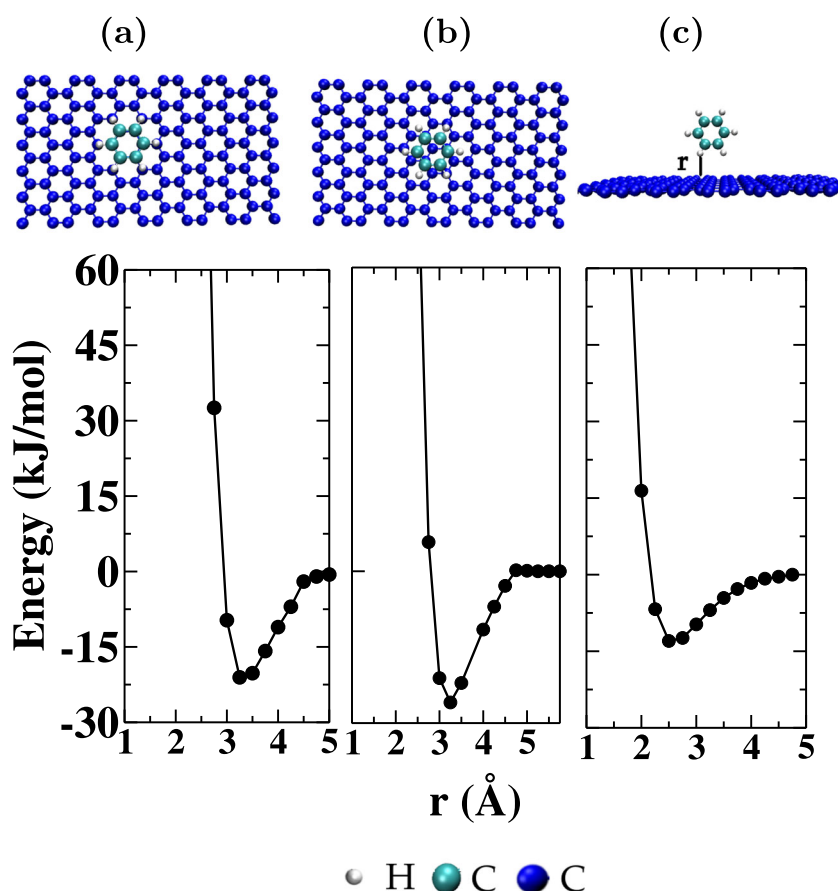
a long distance (at a range 4 – 6 Å) the quantum interaction energy tends to zero. The dimers studied have some important characteristics for modeling process: they are small, have OH and NH₂ groups, and dissociate in water [62, 63]. The presence of these two groups produces an electrostatic interaction and hydrogen bonds with water and graphene. Our results are therefore expected to support the crystal engineering, supramolecular chemistry, bioinspired materials, and parameterization of force fields derived from calculations suitable for classical simulations.

Molecule-graphene interaction

First, we examine the energy interaction between graphene and benzene. Among many possible configurations, we concentrate on three: two face to face (BZ-BZ_FF₁ and BZ-BZ_FF₂) and one perpendicular (BZ-BZ_CR). The interaction energy curves calculated between the benzene and the graphene are illustrated in Fig. 5, in units kJ/mol. In the BZ-BZ_FF₁ stacking case, illustrated in the Fig. 5a, the aromatic ring of the adsorbate faces the graphene hexagons, and the hydrogen atom binding to the benzene group is on top of a graphene carbon atom. In the BZ-BZ_FF₂ stacking configuration, showed in the Fig. 5b, the center of the aromatic ring of the molecule is on top of a graphene carbon atom which is similar to the configuration studies by Chakarova et al. [64]. Both BZ-GR_FF₁ and BZ-GR_FF₂ stacking configurations have very similar electronic structures with minima energies at −22 kJ/mol and −27 kJ/mol and at the equilibrium separation $r = 3.5$ Å, respectively. The BZ-GR_FF₁ configuration optimizes the π – π stacking. The adsorption energy of BZ-GR_FF₂ in graphene was confirmed to be more stable by Tournus et al. [24], which obtained −22.9 kJ/mol obtained using the LDA of the DFT/BSSE with the SIESTA code and by Alzahrani [65] which computed −28.95 kJ/mol using the LDA of the DFT with a plane wave basis set as implemented in the Quantum ESPRESSO [66]. In the BZ-BZ_CR arrangement, depicted in Fig. 5c, the benzene is perpendicular to the graphene sheet. This configuration has a binding energy of −13 kJ/mol at $r = 2.5$ Å which is larger than the energy of the face to face case. The π – π stacking, in this particular arrangement, is more attractive than the H– π cloud case probably due to the lower number of π bonds in the graphene when compared with the benzene. This generates a smaller charge distribution in the center of the ring that makes the interaction with H less attractive [24, 50, 65, 67].

Then, we evaluated the energy between a phenol and graphene sheet. The following configurations were

Fig. 5 Structural configurations and interaction energy curves for the benzene molecule above the graphene layer. **a** BZ-GR_FF₁. **b** BZ-GR_FF₂. **c** BZ-GR_CR. The distance (r) is measured from the benzene molecule to the graphene layer



considered: one face to face (phenol-GR_FF) and two perpendicular configurations (phenol-GR_CR₁ and phenol-GR_CR₂). The interaction energy curves calculated between the phenol and the graphene are illustrated in Fig. 6, in units kJ/mol. In the phenol-GR_FF case, the aromatic ring of the phenol faces the graphene hexagons directly as showed in the Fig. 6a. In one of the perpendicular orientations, the phenol-GR_CR₁, the group OH of the phenol points to the graphene ring as shown in Fig. 6b while in the other perpendicular orientation phenol-GR_CR₂, the H group points to the graphene ring, as indicated in the Fig. 6c.

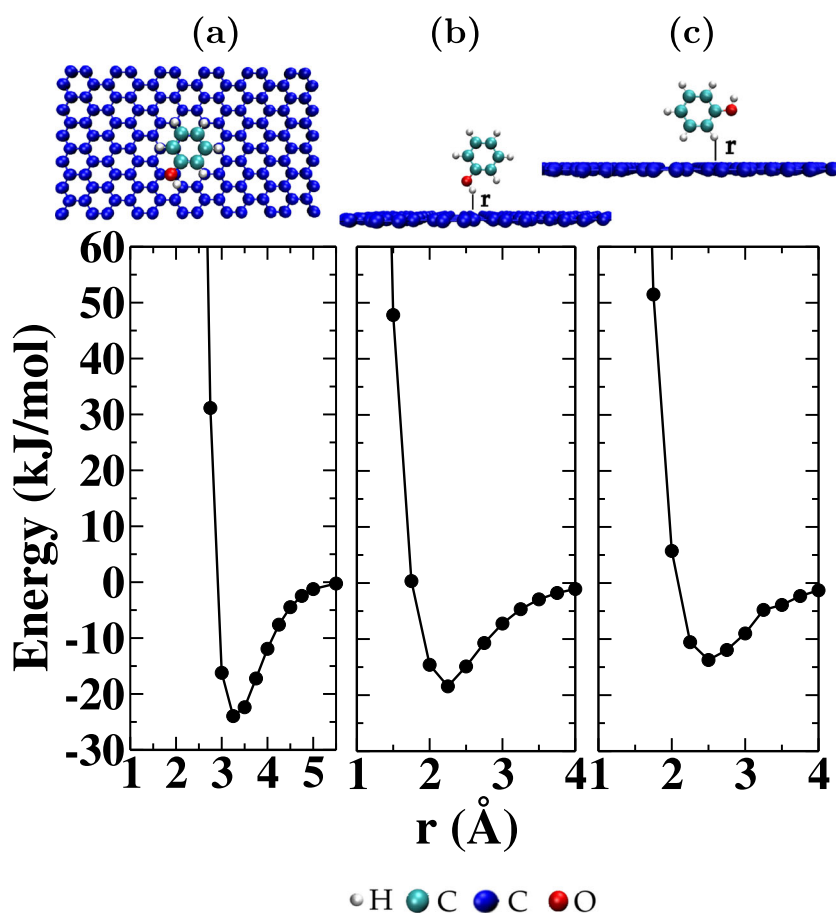
The minimum of the phenol-graphene interaction in the face to face configuration is -24 kJ/mol at $r=3.25$ Å, while for the phenol-GR_CR₁ and phenol-GR_CR₂ correspond to -18.43 kJ/mol (2.25 Å) and -12 kJ/mol (2.75 Å), respectively. Comparing all the configurations analyzed, the lowest energy is the face to face due to the π - π stacking. Within the two perpendicular configurations, the phenol-GR_CR₁ exhibits the lower minimum since the electrostatic attraction between the OH and the negative cloud in the

center of the graphene ring is stronger than the attraction between the H and the π cloud.

Computational simulation by Hernandez et al. [68] reveals that the pristine phenol-graphene interaction has a minimum of -8.104 kJ/mol. The author evaluated six different configurations, using a different methodology compared with this work, analyzed through the Quantum ESPRESSO package [66] and used GGA [47], which tends to underestimate the binding energy values [69]. As the most stable configuration was obtained with phenol parallel to graphene (π - π type interaction) at a distance of $r = 4.07$ Å. Using similar methodology, Avila et al. [70] who evaluated the interaction of phenol with pristine graphene in three configurations observed that the most stable one is FF similar to that we evaluated phenol-graphene_FF, the adsorption energy values of -4.650 kJ/mol and vdW-DF adsorption energy of about -75.14 kJ/mol; however, no BSSE was performed.

Next, we calculated the catechol-graphene energy as a function of the distance between them. We studied four configurations: one face to face (catechol-GR_FF) and three

Fig. 6 Structural configurations and interaction energy curves for the phenol molecule above the graphene layer. **a** phenol-GR_FF. **b** phenol-GR_CR₁. **c** Phenol-GR_CR₂. The distance (r) is measured from the phenol molecule to the graphene layer

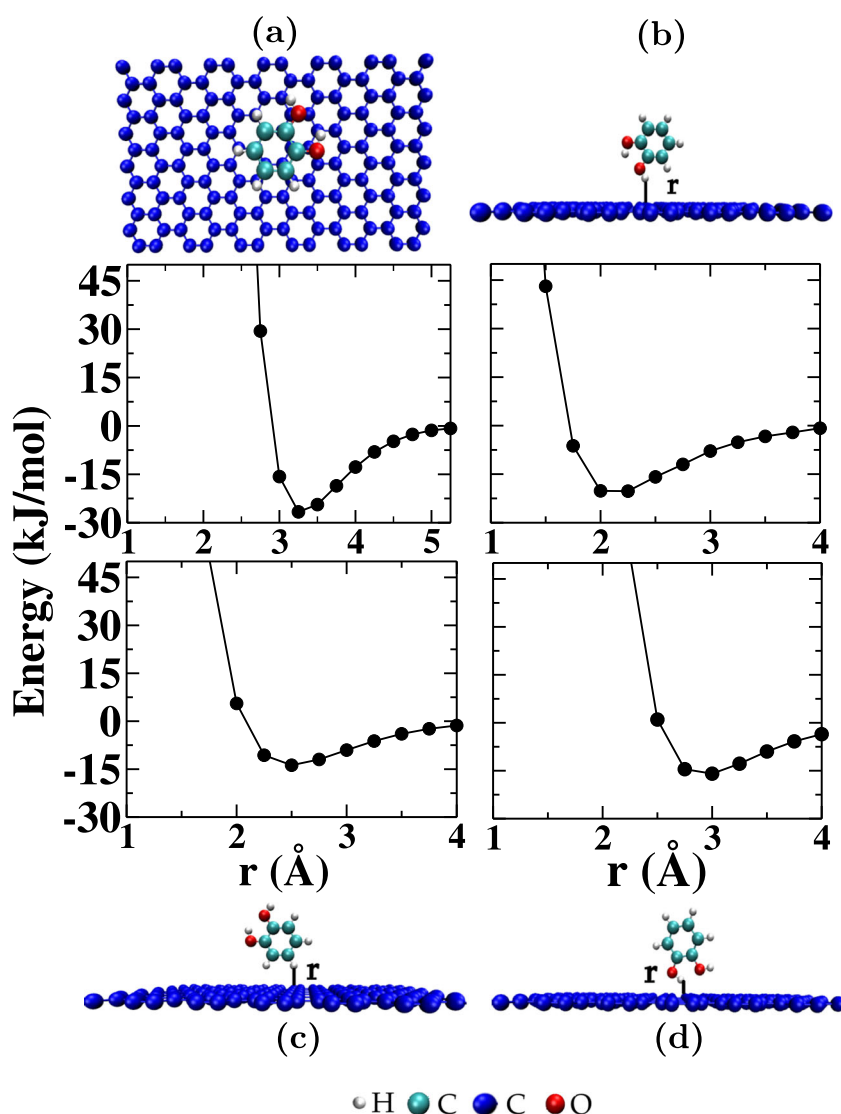


perpendicular configurations (catechol-GR_CR₁, catechol-GR_CR₂, and catechol-GR_CR₃). Figure 7 shows the calculated interaction energies as a function of the distance in units kJ/mol. For the minimum energy for the catechol-GR_FF, illustrated in Fig. 7a, we found -26.7 kJ/mol at the equilibrium separation $r = 3.25$ Å. As in the previous cases, this behavior is attributed to the attractive interaction $\pi - \pi$. The perpendicular orientations, catechol-GR_CR₁, catechol-GR_CR₂, and catechol-GR_CR₃ shown in Fig. 7b, c, and d present energies of -20.25 , -13.75 , and -16 kJ/mol at 2.25, 2.5, and 2.75 Å, respectively. The catechol-GR_CR₁ is the most attractive configuration between the perpendicular orientations. The H and the OH are electrostatically attracted to the electronic charges at the center of the graphene ring. However, since the hydrogen in the OH linked to the C is more polarized than the H covalent linked to the C, the configuration in which the OH points towards the center of the graphene ring is the lower in energy.

Our results can be qualitatively compared with other methods. The case of the binding energy of a catechol interaction energy was approximate molecule absorbed on a silica surface analyzed using DFT/BSSE functionals with the SIESTA code [71, 72], show that the catechol in the face to face configuration adhered stronger to the silica surface than other configurations with energy of -96.2 kJ/mol. They also observed the presence of catechol adhesion arising from both the OH groups interacting with the aromatic ring and the $\pi - \pi$ stacking [72].

Finally, we evaluated the graphene dopamine interaction in four different configurations: two face to face (DA-GR_FF₁ and DA-GR_FF₂) and two perpendicular (DA-GR_CR₁ and DA-GR_CR₂). Figure 8 shows the calculated interaction energies as a function of the distance in units kJ/mol. The most stable system was the DA-GR_FF₁ (approaching the $-\text{NH}_2$ group and the parallel aromatic ring) in the distance of 2.75 Å and the interaction energy was approximately -35 kJ/mol. In this configuration, the

Fig. 7 Structural configurations and interaction energy curves for a catechol molecule on graphene sheet. **a** Catechol-GR_FF. **b** Catechol-GR_CR₁. **c** Catechol-GR_CR₂. **d** Catechol-GR_CR₃. The distance (r) is measured from the catechol molecule to the graphene layer



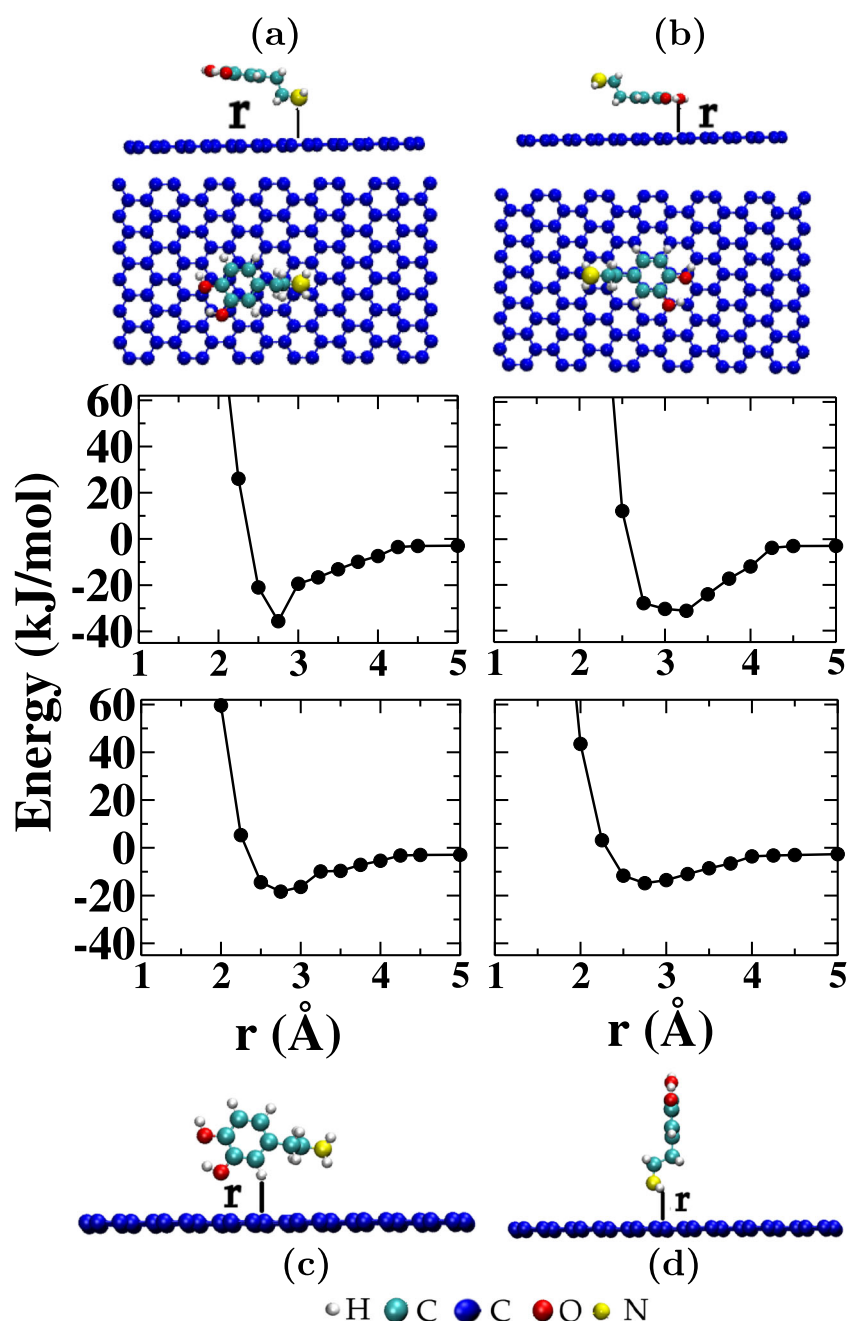
aromatic ring of dopamine is dislocated with reference to the graphene allowing both a $\pi - \pi$ and a $-\text{NH}_2-\pi$ -cloud interaction. The minimum of the DA-GR_FF₂ configuration is -31.3 kJ/mol at $r = 3.25$ Å. In the perpendicular configurations, the DA-GR_CR₁ shows minimum energy is around -30 kJ/mol at 3.25 Å.

Using similar methodology Rossi et al. [73] evaluated the interaction of dopamine with pristine graphene in six configurations, observed that in the aromatic ring can be the most stable was two face to face arrangements. The face to face configurations similar to that we evaluated DA-GR_FF₂, the DFT-D2 adsorption energy of about -67.54 kJ/mol; however, no BSSE was performed. The

distance between the dopamine ring and graphene was almost $3.18-3.30$ Å. Furthermore, in a DFT/6-31G** studies [74] on an DA-GR_FF₁ system performed without BSSE, the calculated adsorption energy was approximately -145.69 kJ/mol and distance between DA-GR was about 3.4 Å. Other studies [75] with aromatic molecules as in the case of nucleobases in graphene show that the distance with greater stability between the aromatic ring and the graphene is around 3.2 Å.

Li et al. [76] investigated the adsorption of aromatic molecules on graphene. They observed, via MD simulations, that the effect of substituent groups on the aromatic ring increases the adsorption on graphene and have the

Fig. 8 Structural configurations and interaction energy curves for the dopamine molecule above the graphene layer. **a** DA-Gr_FF₁. **b** DA-Gr_FF₂. **c** DA-Gr_CR₁. **d** DA-Gr_CR₂. The distance (r) is measured from the dopamine to the graphene layer



following order: nitrobenzene (-27.8 kJ/mol) > anisole (-23.7 kJ/mol) > chlorobenzene (-22.9 kJ/mol) > phenol (-22.1 kJ/mol) > aniline (-17.6 kJ/mol) > benzene (-16.7 kJ/mol). In addition, the authors show through the rupture forces of molecule–graphene that there may be a strong resonance effect between the aromatic ring and the hydroxyl group.

Table 2 shows the values of the adsorption energy of a molecule on graphene. The adsorption energy has the following order: dopamine > catechol > phenol > benzene.

The hydroxyl group has a strong effect for aromatic ring adsorption on graphene [76]. The FF configurations are the stable for molecule–graphene systems, due to the favoring of π – π interactions in these arrangements. The dopamine binding energy to graphene (FF and CR arrangements) is more stable than other molecules, due to the contribution of the π – π , OH– π , and $-\text{NH}_2$ interactions.

Our results suggest that in the interaction between the graphene and the molecules, the face to face arrangements are the most stable structures. The dopamine binds to

Table 2 Configurations, interaction energies, and distances for benzene-GR, phenol-GR, catechol-GR, and dopamine-GR

Configurations	Energy (kJ/mol)	Distance (Å)
FF		
Benzene-GR	-22.0	3.5
Phenol-GR	-24.0	3.25
Catechol-GR	-26.7	3.25
Dopamine-GR_FF ₁	-35.0	2.75
CR		
Benzene-GR	-13.0	2.5
Phenol-GR_CR ₁	-18.43	2.25
Catechol-GR_CR ₁	-20.25	2.25
Dopamine-GR_CR ₁	-30.0	3.25

graphene more stable when compared with other molecules, due to the contribution of the $\pi - \pi$, OH- π , and -NH₂ interactions. This indicates that this molecule would be interesting for drug delivery and filters based in graphene.

Conclusions

We applied DFT with the LDA functional to evaluate the interaction energies between benzene-benzene, phenol-phenol, catechol-catechol, dopamine-dopamine, benzene-graphene, phenol-graphene, catechol-graphene, and dopamine-graphene systems. The interaction energy between dimers is determined mainly by the directionality of $\pi - \pi$ and X- π interactions in these systems.

The T-shaped configurations are the most stable among the molecule-molecule interaction configurations, due to the fact of favoring the multipoles in this arrangement, decreasing repulsion between π -electron from the electronic cloud of the dimers. The energetics of substituted T-shaped configurations are more stable than benzene-benzene_TS₁. Among all T-shaped configurations studied, the catechol-catechol_TS₃ arrangement is more stable than other molecule-molecule configurations, due to the contribution of the π - π and OH- π in this arrangement. The substituent effects of -OH, two OH, or -NH₂ groups on the aromatic ring in face to face arrangement decrease the repulsion between molecule-molecule interacting. These results provide insight into the manner by which substituents X- π in the aromatic ring can be utilized in the supramolecular design.

The adsorption energy of a molecule on graphene involves weak $\pi - \pi$ interactions. The face to face configurations are the most stable for molecule-graphene systems, due to the favoring of π - π interactions in these arrangements. The substituent groups effect can strengthen

the FF interaction when compared with the unsubstituted benzene dimer. The dopamine binding energy to graphene is more stable than other molecules, due to the contribution of the $\pi - \pi$, OH- π , and -NH₂ interactions. The molecule-graphene_FF distance around 3.2 Å is of the same order as the usual separation between two sp^2 systems, interplanar distance in graphite.

Consequently, in a three-body configuration, the lowest energy is not the additive combination of the lowest energy of the molecule-molecule and the molecule-graphene interaction, but is a combination of all the presented configurations in some balance. Therefore, in the modeling of a proper carrier, all the presented configurations have to be taken into account with an appropriated thermal balance. This analysis is relevant for parameterization of force fields derived from calculations suitable for classical simulations.

Our results are therefore expected to support the design of novel sensing, drug delivery, and filters based in graphene. The substituent effects of aromatic ring provide insight into the manner by which substituents X- π on the aromatic ring can be utilized in the supramolecular design and crystal engineering, bioinspired materials, formation of various molecular agglomerates, and parameterization of force fields suitable for classical simulations.

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