

# Computational insights on the adsorption of glycine, methionine, tyrosine and phenylalanine on the zinc oxide nanocluster $Zn_{12}O_{12}$

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## Abstract

The current work investigated the interaction of ZnO nanoparticles (NPs) with glycine, tyrosine, methionine and phenylalanine.  $(ZnO)_{12}$  cage-like cluster was modeled using the density functional theory to determine the adsorption energy, the preferred sites for adsorption of amino acids, and the electronic structure of the formed complexes. The findings suggest that pure amino acids interact with  $(ZnO)_{12}$  via a chemisorption process. The thermodynamic parameters computed showed that the complexation is an exothermic process and enthalpy-driven. The oxygen atoms in the carboxyl groups of the four studied amino acids are involved in the adsorption process. PHE- $Zn_{12}O_{12}$  exhibits the highest adsorption energy (–207.50 kJ/mol) due to its interaction with the  $Zn_{12}O_{12}$  nanocluster through two different adsorption sites. The electronic and sensing properties were examined by analyzing the HOMO and LUMO energies and the HOMO–LUMO energy gap ( $\Delta E_{gl}$ ). The sensitivity of  $Zn_{12}O_{12}$  nanocluster toward the studied amino acids was examined by comparing the percentage variation of the gap after the adsorption, which can reach the value of 38%, suggesting the potential of  $Zn_{12}O_{12}$  nanocluster as a promising sensor for the detection of amino acids. Interaction region indicator (IRI) analysis was performed for a visual understanding of the different interactions occurring between the amino acids and the  $Zn_{12}O_{12}$  nanocluster. The results of this study can shed some light on the possible application of ZnO-based nanobiosensors for detecting protein tyrosine/tryptophan nitration as an early symptom of several serious chronic diseases.

**Keywords** Zinc oxide · Amino acids · Density functional theory · Nanobiosensors

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## 1 Introduction

Nanotechnology has served as a platform for the development of innovative devices and processes for a wide variety of applications [1–3], ranging from high-tech electronics and communication to the intricate and sensitive realm of forensic inquiry. In this respect, medicine was without a doubt one of the first scientific disciplines to utilize nanodevices and nanomaterials in order to improve illness prevention, diagnostic, and treatment approaches [4, 5]. Nanostructured materials have attracted a great deal of attention due to the unique features they possess and the intriguing uses that can be found for them in a wide variety of innovative new products [6, 7]. They have been placed into the categories of rods, shells, dots, sheets, and composites [8–10], depending on the overarching shape they take. While nanoparticles have already revolutionized industries like paint and solar cells, their full potential in medicine, bio-imaging [11, 12], biomarkers [13, 14], biosensing [15–17], drug delivery [18,

19] and various nano-based-targeted therapies [20, 21]) applications have been realized.

Nanoscale zinc oxide ZnO is a semiconducting metal oxide that has great potential for use in the medical field due to the high excitation binding energy that it possesses [22]. Because ZnO nanoparticles are biocompatible and exhibit bioactivity [23], they have the potential to be an interesting option for use in biological applications. Making use of this versatile compound's electrochemical activity, luminescence, and piezoelectricity can result in the production of biosensors [24]. ZnO has potential for use in theranostic systems due to the fact that it eliminates microorganisms and reduces the risk of cancer [25, 26].

- Various  $(\text{ZnO})_n$  nanostructures, such as nanoclusters, nanohorns, nanotubes, and nanowires, have been the subject of medical research [27]. Meanwhile, the zinc oxide-like cages  $(\text{ZnO})_{12}$  have been explored conceptually and empirically [28, 29].  $(\text{ZnO})_{12}$  nanoclusters have been explored as potential biosensors for amino acids due to their advantageous morphological, microstructural, and electrical properties [30–32]. Amino acids are zwitterionic compounds that can be employed as promising components of devices for clinical use [33–36]. Amino acids, which are smaller building blocks, are used to assemble proteins, and the interactions between amino acids and the zinc oxide could be of use in the development of new bioconjugates. Glycine is the smallest and simplest amino acid, simultaneously exhibits both carboxylate/carboxylic and amine/ammonium moieties and thus represents a good reference object for other more complex biological molecules [37, 38]. Glycine, which has the chemical formula  $\text{NH}_2\text{CH}_2\text{COOH}$ , is the tiniest and most straightforward of all the naturally occurring amino acids. As a side chain, it merely contains a single hydrogen atom. As a direct result, glycine is capable of adopting conformations that are normally disallowed in the case of other amino acids and can offer a high level of local flexibility to both polypeptides and proteins. In the literature, A number of studies can be found in the published research that demonstrate how glycine reacts with oxide metals. Indeed, P. Chaudhuri and colleagues looked at the adsorption of glycine molecules on single-walled zigzag and armchair boron-nitrogen nanotubes. Because the hydroxyl group of the glycine binds with the SBNNT surface, this configuration is the one with the highest degree of stability [39]. In the same way, S. Irrera et al. performed an exhaustive study of glycine adsorption on the Zn–ZnO surface, from the limit of the isolated molecule to the full layer and bilayer glycine formation at the surface [40]. They found that the adsorption through both functions (carboxylate and amine) is more favorable than the adsorption through one function only [40]. Other

amino acid molecules, such as tyrosine, methionine and phenylalanine, have been studied in complexation with metal oxide [41–43].

To the best of our knowledge, no attempt has been made as of yet to investigate the way in which these four amino acids interact with the zinc oxide-like cages  $(\text{ZnO})_{12}$ .

It is essential to use computational molecular modeling as a tool for elaborating the mechanisms of molecular recognition between host–guest compounds [24–47]. This type of knowledge can be essential to the comprehension and development of new medicinal products for the treatment of a variety of disorders [48, 49]. The vast majority of *ab initio* investigations of amino acid adsorption were carried out without the presence of any solvent; hence, these studies are relevant to adsorption that occurs in the gas phase. On ZnO, the preferred pathways for amino acid adsorption are ones that require coordination, also known as the creation of covalent bonds.

Evidently, gaining an understanding of the nature of the interactions that biomolecules have with the zinc oxide-like cages  $(\text{ZnO})_{12}$  on an atomic level would provide extremely useful information for the design and manufacture of nanodevices that are meant to be employed for biomedical reasons.

In this context, the current research is aimed to investigate the binding properties between  $\text{Zn}_{12}\text{O}_{12}$  nanocluster and four amino acids, namely, glycine (GLY), tyrosine (TYR), methionine (MET) and phenylalanine (PHE). Structural, energetic and electronic properties of the aminoacids\_  $\text{Zn}_{12}\text{O}_{12}$  complexes were determined.

## 2 Computational details

In computational investigations of bio-conjugated systems, the most essential thing is to discover the proper simulation units that are huge enough to match the behavior of the real sample but tiny enough to keep the cost of computing down. In other words, finding the right simulation units that are big enough to match the behavior of the real sample but small enough to keep the cost of computing down. In relation to these aspects, rather than working with a massive system containing tens of thousands of atoms, the  $(\text{ZnO})_{12}$  cluster, which contains only 24 atoms, was selected to mimic zinc oxide nanoparticles [50]. This was due to the fact that it was the most stable cage and symmetrical small ZnO cluster. The structures of  $\text{Zn}_{12}\text{O}_{12}$  nanocluster and the amino acids methionine, glycine, tyrosine and phenylalanine, as well as the complexes of amino acid\_  $\text{Zn}_{12}\text{O}_{12}$  were fully optimized by ORCA program (version 5.0.0) [51–53] using the B3LYP functional [54, 55] associated

with def2-TZVP basis set [56] and D4 atomic-charge dependent London dispersion correction model [57], the use of the recently developed D4 dispersion correction scheme is important to improve the accurate description of chemical systems. The resolution of the identity approximation (RIJCOSX) [58] was employed to speed up the DFT calculations. A geometrical counterpoise-type correction scheme (GCP) [59] was utilized to account for the basis set superposition error (BSSE). All geometry optimization calculations were carried out using default SCF convergence criteria in ORCA program. All real 3N-6 vibrational frequencies are obtained for the optimized geometries using B3LYP-D4/ def2-TZVP level to ensure that the obtained structures have no imaginary frequencies. The adsorption energies were calculated for the most stable configurations as follows:

$$E_{\text{ads}} = E_{(\text{amino acid}_{\text{Zn12O12}})} - (E_{\text{Zn12O12}} + E_{\text{amino acid}}) \quad (1)$$

where  $E_{(\text{amino acid}_{\text{Zn12O12}})}$  represents the adsorption energy for each amino acid on the  $\text{Zn}_{12}\text{O}_{12}$  nanocluster;  $E_{\text{Zn12O12}}$  and  $E_{\text{amino acid}}$  represent the energies of  $\text{Zn}_{12}\text{O}_{12}$  nanocluster and free amino acids, respectively. Negative values of adsorption energy correspond to an exothermic process, indicating that the formed complexes are stable, while positive values of adsorption energy indicate an unfavorable process. All the studied systems were verified as minima on the potential energy surface through frequency calculations.

## 3 Results and discussion

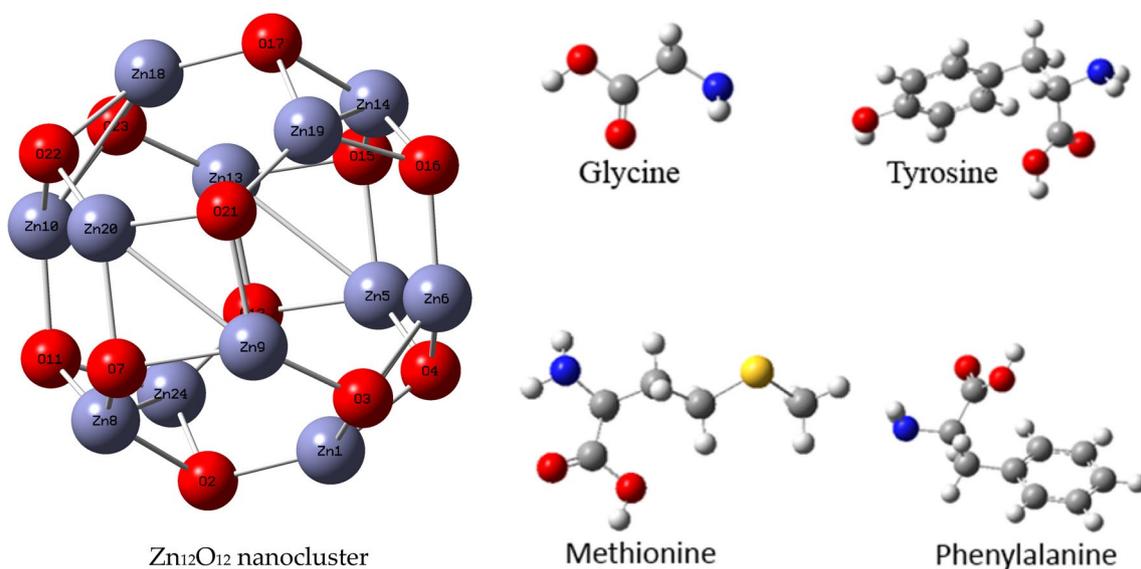
### 3.1 Geometric parameters of $\text{Zn}_{12}\text{O}_{12}$ nanocage

The molecular structure of  $\text{Zn}_{12}\text{O}_{12}$  nanocage represented in Fig. 1 may be described as constructed from eight hexagon rings ( $\text{Zn}_3\text{O}_3$ ) and six tetragon rings ( $\text{Zn}_2\text{O}_2$ ), which are connected by sharing all their Zn and O atoms. The Zn–O bond lengths values range from 1.867 to 1.963 Å and are in accord with those reported in the literature [60, 61].

The shortest Zn–O distances ranging from 1.868 to 1.869 Å are observed for three alternating Zn–O bonds in the hexagons, while the longest ones in the interval (1.959–1.963 Å) correspond to all Zn–O bonds in the tetragons and the remaining three alternating Zn–O bonds in the hexagons shared with the tetragons. The bonds angles of the Zn–O–Zn and O–Zn–O in the tetragons are in the range of 87.32–91.08°, whereas those of the hexagons range from 110.73 to 127.99° with the O–Zn–O bond angles being wider than 127°. Selected bond lengths and bond angles calculated at B3LYP-D4/def2-TZVP-gCP level for  $\text{Zn}_{12}\text{O}_{12}$  nanocluster are listed in Table 1.

### 3.2 Adsorption energies

The initial geometries with different adsorption orientations for the interaction of amino acids with the  $\text{Zn}_{12}\text{O}_{12}$  nanocluster considered in this work are shown in Supplementary Data (Figure S1). The most stable complexes for each amino acid



**Fig. 1** Molecular structure of optimized  $\text{Zn}_{12}\text{O}_{12}$  nanocluster, glycine, tyrosine, methionine and phenylalanine. Atomic color code: carbon (gray), hydrogen (white), oxygen (red), blue (nitrogen), sulfur (yellow), zinc (Corsican purple)

**Table 1** Selected bond lengths (Å) and angles (°) for Zn<sub>12</sub>O<sub>12</sub> nanocluster

Bond length (Å)		Bond angle (°)	
Zn1-O2	1.869	Zn9-O7-Zn20	87.32
Zn1-O3	1.960	Zn1-O4-Zn6	87.49
Zn1-O4	1.961	O4-Zn1-O3	90.97
Zn6-O3	1.963	O2-Zn8-O11	91.00
Zn6-O4	1.959	O16-Zn19-O17	91.08
Zn6-O16	1.868	O7-Zn20-O21	91.11
Zn9-O3	1.868	Zn1-O2-Zn8	110.73
Zn9-O7	1.962	Zn19-O21-Zn20	111.05
Zn9-O21	1.961	Zn8-O7-Zn9	111.23
Zn19-O16	1.963	O22-Zn18-O17	127.47
Zn19-O17	1.959	O12-Zn24-O11	127.75
Zn18-O17	1.869	O2-Zn1-O3	127.99

adsorbed on the Zn<sub>12</sub>O<sub>12</sub> nanocluster are depicted in Fig. 2 using Gaussview 5.0 program [62].

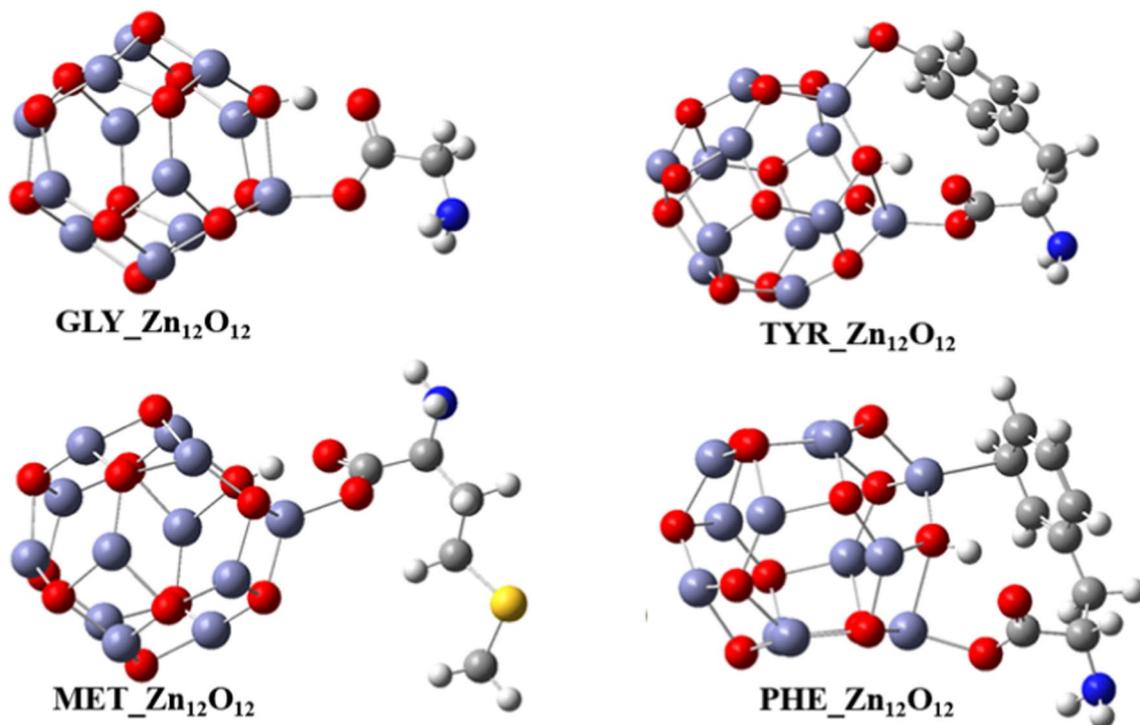
The adsorption energy values ( $E_{\text{ads}}$ ) of GLY\_Zn<sub>12</sub>O<sub>12</sub>, TYR\_Zn<sub>12</sub>O<sub>12</sub>, MET\_Zn<sub>12</sub>O<sub>12</sub> and PHE\_Zn<sub>12</sub>O<sub>12</sub> complexes calculated in vacuum at B3LYP-D4/def2-TZVP-gCP level of theory are respectively,  $-147.83$ ,  $-207.50$ ,  $-161.72$  and  $-193.51$  kJ/mol. The complexes TYR\_Zn<sub>12</sub>O<sub>12</sub> and PHE\_Zn<sub>12</sub>O<sub>12</sub> exhibit the highest adsorption energies due

to their interaction with the Zn<sub>12</sub>O<sub>12</sub> nanocluster through two different adsorption sites, as shown in Fig. 2.

The adsorption process involves the oxygen atoms of the carboxyl groups of all the amino acids. Indeed, the relaxed geometries showed that carbonyl moiety of the carboxyl groups of glycine, tyrosine, methionine and phenylalanine move toward the Zn atoms of Zn<sub>12</sub>O<sub>12</sub> with which they establish short Zn–O bonds (1.944–1.956 Å), thus leading to the chemisorption of the amino acids on Zn<sub>12</sub>O<sub>12</sub> nanocluster. The carboxyl groups are found more favorable to interact with the Zn atoms of the Zn<sub>12</sub>O<sub>12</sub> nanocluster than the amino groups. In addition, tyrosine and phenylalanine are also bound to the adsorbent through the oxygen atom of the hydroxyl group of tyrosine and a carbon atom from the benzene ring of phenylalanine.

### 3.3 Thermodynamic analysis

Thermodynamic parameters such as the changes of Gibbs energy, enthalpy and entropy were calculated at 298.15 K and 1 atm using B3LYP-D4/def2-TZVP-gCP level of theory in a vacuum. The zero-point energy (ZPE) correction was applied in the energy calculations. The values of Gibbs free energy, enthalpy and entropy changes of the adsorption process of the amino acids on Zn<sub>12</sub>O<sub>12</sub> nanocluster were computed at standard temperature and pressure values (298.15 K

**Fig. 2** Full optimized geometries in vacuum of amino acids glycine, tyrosine, methionine and phenylalanine adsorbed on Zn<sub>12</sub>O<sub>12</sub> nanocluster. Atomic color code: carbon (gray), hydrogen (white), oxygen (red), blue (nitrogen), sulfur (yellow), zinc (Corsican purple)

and 1 atm) and listed in Table 2. Negative Gibbs energy changes for all complexes ( $\Delta G < 0$ ), indicating that the reaction process proceeds spontaneously. The Gibbs energy of TYR\_Zn<sub>12</sub>O<sub>12</sub> and PHE\_Zn<sub>12</sub>O<sub>12</sub> are.

more negative than that of GLY\_Zn<sub>12</sub>O<sub>12</sub> and MET\_Zn<sub>12</sub>O<sub>12</sub>. Moreover, the computed values of energy changes of enthalpy and entropy are also negative, showing that the complexation is an exothermic process and enthalpy-driven.

### 3.4 Electronic properties

The electronic properties such as the HOMO, LUMO, HOMO–LUMO gap and the percentage variation of the HOMO–LUMO gap of Zn<sub>12</sub>O<sub>12</sub> nanocluster and the formed complexes are summarized in Table 3. As can be seen from Table 3, the HOMO energy values of the complexes are above (less negative) that of the pristine Zn<sub>12</sub>O<sub>12</sub>; the HOMO of MET\_Zn<sub>12</sub>O<sub>12</sub> has increased considerably. However, the LUMO levels were similar to the pristine Zn<sub>12</sub>O<sub>12</sub> once the complexes were formed. The HOMO–LUMO gap value of Zn<sub>12</sub>O<sub>12</sub> calculated at B3LYP-D4/def2-TZVP-gCP level of theory (4.25 eV) is consistent with the value reported in similar studies [28, 63, 64]. The  $\Delta E_g$  of the complexes is significantly reduced in comparison to that of pristine Zn<sub>12</sub>O<sub>12</sub> and follows the decreasing order:  $\Delta E_g$  (PHE\_Zn<sub>12</sub>O<sub>12</sub>) >  $\Delta E_g$  (TYR\_Zn<sub>12</sub>O<sub>12</sub>) >  $\Delta E_g$  (GLY\_Zn<sub>12</sub>O<sub>12</sub>) >  $\Delta E_g$  (MET\_Zn<sub>12</sub>O<sub>12</sub>). By comparing the percentage change in the gap following the adsorption, we were able to investigate the degree to which the Zn<sub>12</sub>O<sub>12</sub> nanocluster reacts to the amino acids that were under investigation. From Table 3, the percentage variation of  $E_g$  during the adsorption of glycine, tyrosine, methionine and phenylalanine is respectively 20.94%, 19.06%, 38.12% and 12.00%, suggesting the potential of Zn<sub>12</sub>O<sub>12</sub> nanocluster as a promising sensor for the detection of amino acids.

Useful information can be provided on the electronic properties of the obtained complexes through the analysis of frontier molecular orbitals isosurfaces. The frontier molecular orbitals of the studied complexes were generated with Multiwfn [65] and visualized with IboView program [66, 67]. As shown in Fig. 3, the HOMO's are almost entirely localized on the amino acids, whereas the LUMO's are predominantly localized on Zn<sub>12</sub>O<sub>12</sub> nanocluster with some contributions from the amino acids. Before the adsorption of the amino acids, the HOMO and LUMO energies of pristine Zn<sub>12</sub>O<sub>12</sub> nanocluster were  $-7.24$  and  $-2.99$  eV, respectively. After their chemisorption, a quite significant changes were observed in HOMO and LUMO energies; the HOMO levels of PHE\_Zn<sub>12</sub>O<sub>12</sub>, GLY\_Zn<sub>12</sub>O<sub>12</sub>, TYR\_Zn<sub>12</sub>O<sub>12</sub> and MET\_Zn<sub>12</sub>O<sub>12</sub> complexes shift up to higher energies from  $-6.44$  to  $-5.75$  eV ( $-6.44$ ,  $-6.41$ ,  $-6.31$  and  $-5.75$  eV, respectively). The LUMO energies of TYR\_Zn<sub>12</sub>O<sub>12</sub> and PHE\_Zn<sub>12</sub>O<sub>12</sub> are shifted up ( $-2.87$  and  $-2.70$  eV) whereas those of GLY\_Zn<sub>12</sub>O<sub>12</sub> and MET\_Zn<sub>12</sub>O<sub>12</sub> are shifted down ( $-3.05$  and  $-3.12$  eV).

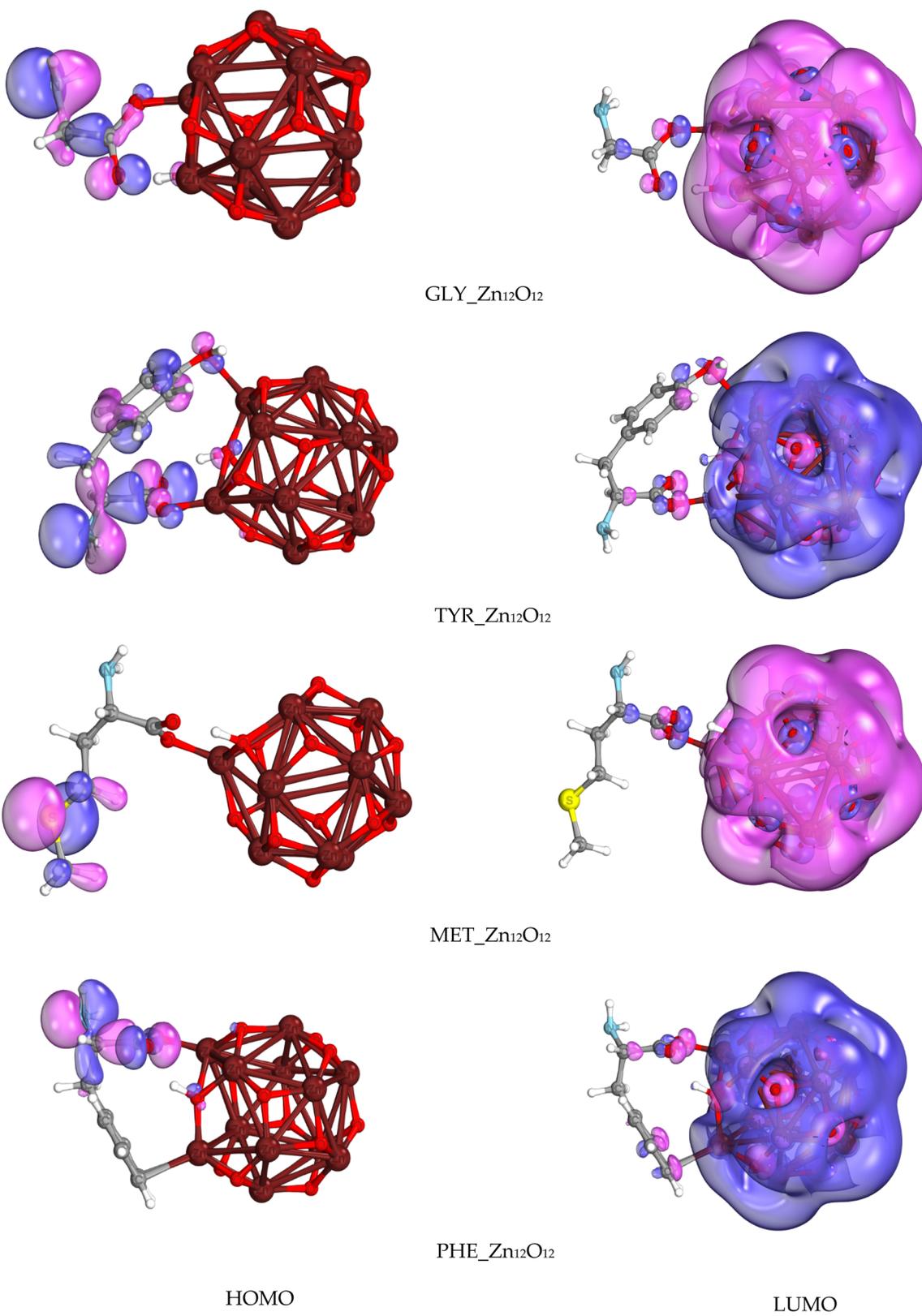
The orbital composition analysis shows that the HOMO of GLY\_Zn<sub>12</sub>O<sub>12</sub> comes mainly from the orbitals of nitrogen atom (64.8%), oxygen atoms (16.6%) and carbon atoms (12.6%); the HOMO of MET\_Zn<sub>12</sub>O<sub>12</sub> is localized mainly on the sulfur atom (86.4%), with a contribution of 8.8 and 4.6% from the hydrogen and carbon atoms, respectively. The HOMO of PHE\_Zn<sub>12</sub>O<sub>12</sub> is distributed on nitrogen atom (47.2%), oxygen atoms (30%) and carbon atoms (18%), while the HOMO of TYR\_Zn<sub>12</sub>O<sub>12</sub> complex is mainly composed of 41.8% (N), 30.2% (C) and 22.6% (O). The LUMO of all complexes is mainly localized on the Zn atoms of the Zn<sub>12</sub>O<sub>12</sub> nanocluster.

**Table 2** Thermodynamic parameters of the adsorption of amino acids on Zn<sub>12</sub>O<sub>12</sub> nanocluster computed at B3LYP-D4/def2-TZVP in vacuum

Thermodynamic parameters	GLY_Zn <sub>12</sub> O <sub>12</sub>	TYR_Zn <sub>12</sub> O <sub>12</sub>	MET_Zn <sub>12</sub> O <sub>12</sub>	PHE_Zn <sub>12</sub> O <sub>12</sub>
$\Delta H^\circ$ (kJ/mol)	-156.08	-213.92	-158.78	-201.89
$\Delta G^\circ$ (kJ/mol)	-102.84	-148.06	-100.92	-133.59
$\Delta S^\circ$ (kJ/mol)	-53.26	-65.90	-57.91	-68.32

**Table 3** HOMO, LUMO, HOMO–LUMO gap ( $\Delta E_g$ ) and HOMO–LUMO gap variation ( $\Delta E_g$  %) for Zn<sub>12</sub>O<sub>12</sub>, GLY\_Zn<sub>12</sub>O<sub>12</sub>, TYR\_Zn<sub>12</sub>O<sub>12</sub>, MET\_Zn<sub>12</sub>O<sub>12</sub> and PHE\_Zn<sub>12</sub>O<sub>12</sub> complexes

Electronic Parameters	Zn <sub>12</sub> O <sub>12</sub>	GLY_Zn <sub>12</sub> O <sub>12</sub>	TYR_Zn <sub>12</sub> O <sub>12</sub>	MET_Zn <sub>12</sub> O <sub>12</sub>	PHE_Zn <sub>12</sub> O <sub>12</sub>
$E_{\text{HOMO}}$ (eV)	-7.24	-6.41	-6.31	-5.75	-6.44
$E_{\text{LUMO}}$ (eV)	-2.99	-3.05	-2.87	-3.12	-2.70
$ \Delta E_g $ (eV)	4.25	3.36	3.44	2.63	3.74
$\Delta E_g$ %	-	20.94	19.06	38.12	12.00



**Fig. 3** Frontier molecular orbital isosurfaces for GLY\_Zn<sub>12</sub>O<sub>12</sub>, MET\_Zn<sub>12</sub>O<sub>12</sub>, TYR\_Zn<sub>12</sub>O<sub>12</sub> and PHE\_Zn<sub>12</sub>O<sub>12</sub> complexes

### 3.5 Charge transfer analysis

Multiwfn program was utilized to quantify the charge transfer based on the Mulliken method through the charge decomposition analysis (CDA) [65, 68] and its extended version (ECDA) [69]. ECDA analysis provides theoretical insight into the charge transfer process between two fragments, which can be characterized in the framework of ECDA approach by excluding the electronic polarization (PL). The CDA and ECDA results of the studied complexes are reported in Table 4. According to the CDA results, the number of donated electrons from  $Zn_{12}O_{12}$  to the amino acids is in the range [0.236–0.305] a.u., while electrons back-donated from amino acids to  $Zn_{12}O_{12}$  range from 0.226 to 0.396 a.u., indicating that both donation and back-donation are significantly involved in the electron transfer process. ECDA analysis shows that the net electrons obtained by glycine and methionine from  $Zn_{12}O_{12}$  are 0.046 a.u. For TYR\_ $Zn_{12}O_{12}$  and PHE\_ $Zn_{12}O_{12}$  complexes, the net number of electrons obtained by  $Zn_{12}O_{12}$  from tyrosine and phenylalanine is, respectively, 0.030 and 0.111.

### 3.6 Interaction region indicator (IRI) analysis

The optimized structures at B3LYP-D4/def2-TZVP-gCP level of theory were subjected to the interaction region indicator (IRI) analysis [70, 71] to explore the nature of the interaction regions occurring in each complex. The IRI approach is based on the charge density and its gradient to determine the intra- and intermolecular interactions in molecular systems in which both chemical bonding and weak interactions regions can be investigated. The IRI function is formulated as:

$$IRI(\mathbf{r}) = \frac{|\nabla\rho(\mathbf{r})|}{[\rho(\mathbf{r})]^a}$$

where a parameter is set to the recommended value of 1.1 [71]. According to the values of sign of  $(\lambda_2)\rho$ , the color mapping of IRI isosurfaces can reveal the nature of the

interaction regions of interest. The isosurfaces are filled with the blue, green and red (BGR) color model, which correspond, respectively, to notable attractive forces, weak attractive interactions, and a notable repulsion. The covalent bonding regions are depicted by the blue circular disc-shaped isosurfaces. Figure 4 shows the IRI isosurfaces of GLY\_ $Zn_{12}O_{12}$ , TYR\_ $Zn_{12}O_{12}$ , MET\_ $Zn_{12}O_{12}$  and PHE\_ $Zn_{12}O_{12}$  complexes.

The IRI generated isosurfaces with an isovalue of 1.0 a.u confirm the presence of hydrogen bonds represented by the blue disc-shaped surfaces between O–H groups of the aminoacids and oxygen atoms of  $Zn_{12}O_{12}$  nanocluster. The red spots observed in  $Zn_{12}O_{12}$  and inside the aromatic rings of TYR\_ $Zn_{12}O_{12}$  and PHE\_ $Zn_{12}O_{12}$  complexes indicate a steric repulsion. The chemical bond regions in glycine, tyrosine, methionine and phenylalanine are revealed by the blue dumbbell-shaped discs as shown in Fig. 4. The green areas are attributed to the van der Waals interactions that are more significant for TYR\_ $Zn_{12}O_{12}$  and PHE\_ $Zn_{12}O_{12}$  than for GLY\_ $Zn_{12}O_{12}$  and MET\_ $Zn_{12}O_{12}$  complexes. It is important to point out that TYR\_ $Zn_{12}O_{12}$  and PHE\_ $Zn_{12}O_{12}$  complexes are associated with the highest complexation energies, suggesting that van der Waals interactions account for the stabilization of the formed complexes, and therefore, play a key role in the complexation process.

### 3.7 Molecular electrostatic potential

The molecular electrostatic potential, often known as MEP, is an extremely useful tool for the investigation of electron density clouds as well as the prediction of electrostatic effects and hydrogen bonding in molecular systems. These effects can be seen in nucleophilic or electrophilic regions. The molecular electrostatic potential maps calculated in vacuum at B3LYP-D4/def2-TZVP-gCP level of theory for GLY\_ $Zn_{12}O_{12}$ , TYR\_ $Zn_{12}O_{12}$ , MET\_ $Zn_{12}O_{12}$  and PHE\_ $Zn_{12}O_{12}$  complexes are plotted in Fig. 5 with Jmol program [72]. Coloring scheme is used to represent different levels of electron density in the range [-0.1, +0.1 a.u.]: red color corresponds to high electron density (negative potential),

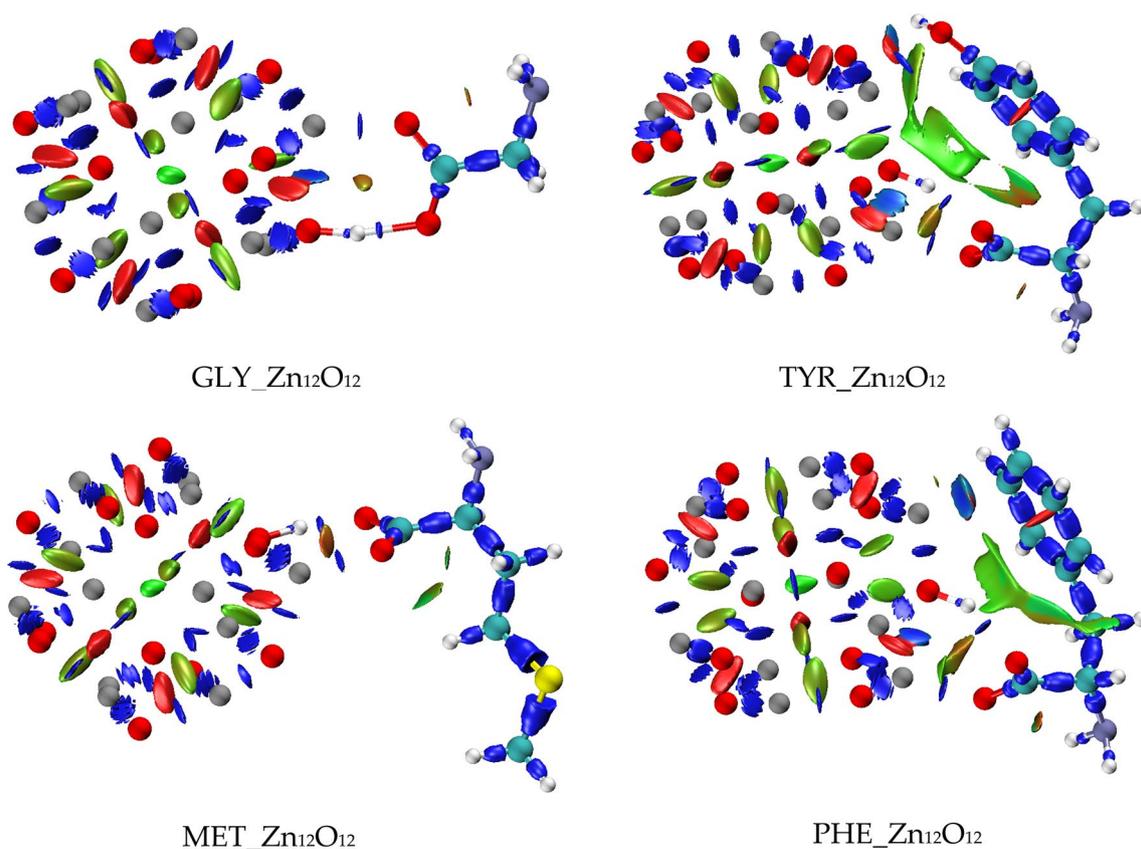
**Table 4** Computed terms of donation (d), back-donation (b), (d-b), repulsive polarization (r) and the net electrons transferred from CDA and ECDA analysis

Complex	CDA analysis				ECDA analysis
	d	b	d-b	r	Net electrons obtained by amino acid
GLY_ $Zn_{12}O_{12}$	0.236	0.235	0.001	-0.283	0.046
MET_ $Zn_{12}O_{12}$	0.236	0.226	0.010	-0.306	0.046
					Net electrons obtained by $Zn_{12}O_{12}$
TYR_ $Zn_{12}O_{12}$	0.305	0.380	-0.075	-0.359	0.030
PHE_ $Zn_{12}O_{12}$	0.241	0.396	-0.155	-0.307	0.111

d: the number of electrons donated from  $Zn_{12}O_{12}$  to amino acid

b: the number of electrons back-donated from amino acid to  $Zn_{12}O_{12}$

r: the number of electrons involved in repulsive polarization



**Fig. 4** Interaction region indicator isosurfaces (isovalue 1.0 a.u) for GLY\_Zn<sub>12</sub>O<sub>12</sub>, MET\_Zn<sub>12</sub>O<sub>12</sub>, TYR\_Zn<sub>12</sub>O<sub>12</sub> and PHE\_Zn<sub>12</sub>O<sub>12</sub> complexes

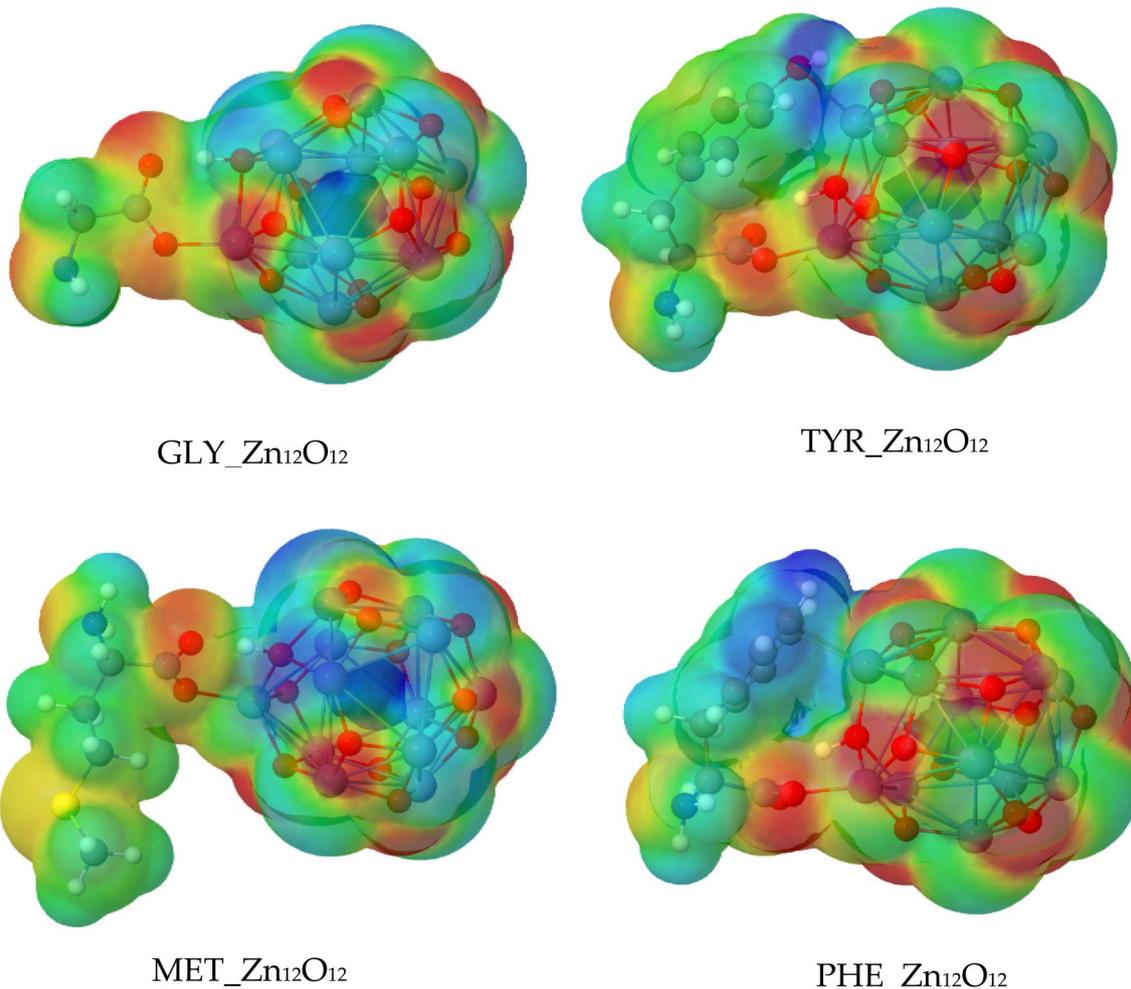
blue indicates low electron density (positive potential) and yellow and green represent respectively, moderate and neutral potentials.

Figure 5 reveals that the majority of the electron density is localized on the negatively charged oxygen atoms, which are indicated by the red color and represent the regions of most negative electrostatic potential. On the other hand, the regions of most positive electrostatic potential are localized on the positively charged zinc atoms of the Zn<sub>12</sub>O<sub>12</sub> nanocluster, which are depicted by the blue color.

## 4 Conclusions

The current work investigated the interaction of ZnO nanocluster with the amino acids glycine, tyrosine, methionine and phenylalanine using the DFT-D4 approach. We were able to characterize the nature of the happening interactions by analyzing the structural, energetic and electronic features utilizing the thermodynamic parameters, the analysis of frontier molecular orbitals isosurfaces, and the charge decomposition analysis (CDA). Results indicated that the four amino acids interact with (ZnO)<sub>12</sub>

via a chemisorption process, with adsorption energy values equal to  $-147.83$ ,  $-207.50$ ,  $-161.72$  and  $-193.51$  kJ/mol for GLY\_Zn<sub>12</sub>O<sub>12</sub>, TYR\_Zn<sub>12</sub>O<sub>12</sub>, MET\_Zn<sub>12</sub>O<sub>12</sub> and PHE\_Zn<sub>12</sub>O<sub>12</sub> complexes, respectively. Therefore, the interaction between the tyrosine and the (ZnO)<sub>12</sub> is the most favorable among the studied amino acids. The thermodynamic parameters such as the changes of Gibbs energy, enthalpy and entropy showed that the complexation is an exothermic process and driven by changes in enthalpy. The four complexes have a lower  $\Delta E_g$  (HOMO–LUMO gap) than isolated Zn<sub>12</sub>O<sub>12</sub> and follow the decreasing order: PHE\_Zn<sub>12</sub>O<sub>12</sub> > TYR\_Zn<sub>12</sub>O<sub>12</sub> > GLY\_Zn<sub>12</sub>O<sub>12</sub> > MET\_Zn<sub>12</sub>O<sub>12</sub>. The charge decomposition analysis results show that donation and back-donation are important in the electronic charge transfer. The results show also that hydrogen bonding and van der Waals interactions contribute to the complexation process, with the latter being more important for TYR\_Zn<sub>12</sub>O<sub>12</sub> and PHE\_Zn<sub>12</sub>O<sub>12</sub> complexes, therefore, ZnO nanoparticles can be considered as attractive nanobiosensors for amino acids and in particular for aromatic amino acids. These findings can be used as a guide to support the experimental works in the field of sensing applications.



**Fig. 5** Molecular electrostatic potential maps of GLY\_Zn<sub>12</sub>O<sub>12</sub>, TYR\_Zn<sub>12</sub>O<sub>12</sub>, MET\_Zn<sub>12</sub>O<sub>12</sub> and PHE\_Zn<sub>12</sub>O<sub>12</sub> complexes plotted using Jmol program

**Author contributions** SR, YB, MS contributed to conceptualization and methodology; MD, YB, MD done software; SR, YB, NS, MS done validation; SR, MD, YB performed formal analysis; SR, MD, MD done investigation; YB and MS helped in resources; SR and YB helped in data curation; SR, MD, YB, NS, MD, MS helped in writing—original draft preparation; SR, MD, YB, NS, MD, MS helped in writing—review and editing; SR done visualization; YB contributed to supervision. All authors have read and agreed to the published version of the manuscript.

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## Declarations

**Conflicts of interest** The authors declare no conflict of interest.

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