

# An Analysis of Iron Oxide Nanoclusters as Antifungal Agents and *In Silico* Model with Lanosterol 14 $\alpha$ -Demethylase in *Candida albicans*

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## Abstract

The burden on human health has risen with the infections of *Candida sp.*, and looking for therapy is becoming difficult. Because of its different medical applications, metallic iron oxide NPs attract interest. Therefore, five spherical iron oxide nanoclusters were tested in silico for binding of *Candida sp.* For the purpose of predicting the binding mechanism and energy, each iron oxide nanocluster was docked in the active position of the lanosterol 14  $\alpha$ -demethylase enzyme (CYP51), which is crucial for *Candida sp.* growth. The binding energy range for all test iron oxide nanoclusters was  $-8.17$  to  $-9.75$  Kcal/mol. In general, the molecular docking analysis revealed that increasing the size of the sphere nanoclusters (0.5-1 nm) increases the binding energy within 5TZ. Experimentally, the inhibition zone ranged from 16mm to 13mm. High inhibition zones were received from 50% of *Candida albicans* isolates, and the minimum inhibition concentrations were  $256\mu\text{g/ml}$  for all *Candida albicans* isolates. The current findings suggest that iron oxide nanoclusters can be used as potential antifungal medications.

## Keywords

*Candida* infections, Metallic iron oxide NPs, Lanosterol 14 $\alpha$ -demethylase enzyme (CYP51)

## Introduction

Fungal infections have become a rising health concern, leading to substantial economic losses in hospitals [1, 2]. About 200 species of *Candida* exist in the world, but only a few are capable of infecting humans if the immune system is compromised [3]. One of the most common kinds of fungal infections that *Candida* species are responsible for is mucocutaneous candidiasis and invasive candidiasis [4, 5].

A standard treatment for invasive or mucocutaneous candidiasis is the application of antifungal drug classes, such as azoles, polyene, echino-candines and flucytosine. Due to the incorrect use of antifungals, fungi evolved resistant mechanisms against antifungal drugs. Hence, new antifungal alternative methods for better treatment are required [6-8].

Nanoparticles are currently of considerable significance for their biological use, such as metal oxide nanoparticles, as an *antimicrobial* agent. Abo-zeid and Williams have been reported in 2019 for antimicrobial activity of metal oxide NPs [9]. Mainly, metal oxide NPs have been shown to be effective in combating nosocomial bacterial infections in hospitals and overcoming bacterial resistance [10-12]. More recently, abbas et al. (2020 a, b) specifically found the pronounced antifungal efficacy of  $\alpha$ -Fe<sub>2</sub>O<sub>3</sub> against *C. albicans*, which is due to the excessive production of Reactive Oxygen Species (ROS), and it destroys the cellular con-

stituents and deoxyribonucleic acid damage [13-14].

A docking model study is presented here to understand and investigate the interactions of iron oxide nanoclusters with the lanosterol 14 $\alpha$ -demethylase (CYP51) enzyme, which is produced by the (CYP51/ERG11) gene and is necessary to support candida growth. Moreover, the antifungal activity was studied *in vitro* against *Candida albicans*. The heme group of CYP51 proteins in the active site is involved in cytochrome P450, which is a key enzyme in the sterol's production and a vital component of the fungal membrane [15]. The docking model was also applied to determine the potential application of iron oxide nanoclusters in the treatment and controlling candida infections.

## Materials and Methodology

### Ligand preparation

Using material studio software, the crystal structure of Fe<sub>2</sub>O<sub>3</sub> was converted into a three-dimensional form using the American mineralogist's crystal structure database, [http://www.minsocam.org/MSA/Crystal\\_Database.html](http://www.minsocam.org/MSA/Crystal_Database.html). We selected five Sphere Fe<sub>2</sub>O<sub>3</sub> nanoclusters as a model of Fe<sub>2</sub>O<sub>3</sub> to study their inhibitory effect against CYP51 by molecular docking analysis. This optimized structure was used to construct the sphere nanoclusters using the built-in tools in the material studio program, as follow: Sphere, 0.5 nm (radius = 2.5 Å, Fe = 7, and O=7 atoms), 0.6 nm (radius = 3.0 Å, Fe = 14, and O = 17 atoms), 0.7 nm (radius = 3.5 Å, Fe = 16, and O = 21 atoms), 0.8 nm (radius = 4.0 Å, Fe = 28, and O = 36 atoms), 0.9 nm (radius = 4.5 Å, Fe = 38, and O = 46 atoms), and 1 nm (radius = 5.0 Å, Fe = 42, and O = 56 atoms). The structural optimization of all studied compounds was implemented using the Molecular Mechanics 2 (MM2) force field. After that, using Auto DockTools 1.5.6 software, the structures were transformed to pdbqt format.

### Protein preparation

The crystal structure of CYP51 with a potent ligand (VT1161) (PDB code: 5TZ1) was obtained from the Protein Data Bank ([www.rcsb.org](http://www.rcsb.org)). The BIOVA Discovery Studio software was used to eliminate small molecules from the crystal structures of 5TZ1 [15].

### Molecular docking

The protein was given polar hydrogen and Kollman charges, and a pdbqt format file was created using AutoDock Tools 1.5.6 software. The protein was made with AutoDock Tools 1.5.6's protein preparation wizard. The protein was given polar hydrogen and Kollman charges, and a pdbqt format file was created with AutoDock Tools. 5TZ1 was stripped of all water molecules. The ligands' torsions were determined by first detecting the roots in AutoDock Tools 1.5.6, then setting aromaticity criteria of 7.5. For 5TZ1, we set a grid size of 80Å x80Å x80 Å and used the Lamarckian Genetic Algorithm (LGA) to carry out the molecular docking procedure, as outlined in this paper [16-17].

### Size measurement of SIONs

Spherical iron oxide nanoparticles (SIONs) were prepared previously by Dr Heba S Abbas in Microbiology Laboratory (C), Egyptian Drug Authority (previously, National Organization for Drug Control and Research), the size of tested SIONs was characterized by High-Resolution Transmission Electron Microscope (HRTEM).

### Antifungal assay of SIONs

The antifungal activity of SIONs was assessed against three clinical strains of *C. albicans*, and *C. albicans* ATCC 10231. The isolates were plated on Sabroud dextrose agar plates for the test. A sterile cork-borer was used to cut the wells into the plates, and 50  $\mu$ l of SIONs (two-fold serial dilution method (512, 265,128 $\mu$ g/ml)) in DMSO solutions were dispensed in each well. For 24 hours, the plates were kept at 27°C. The inhibitory zone's diameter was measured in millimetres [18]. The minimum inhibitory concentration (MIC) of SIONs was examined [19].

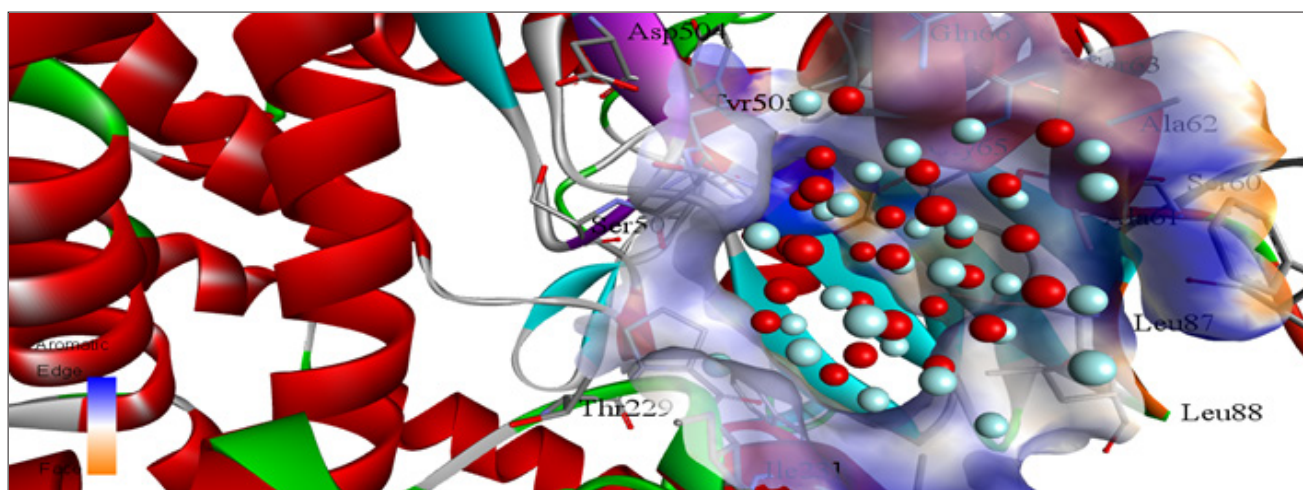
## Results and Discussion

### Molecular docking

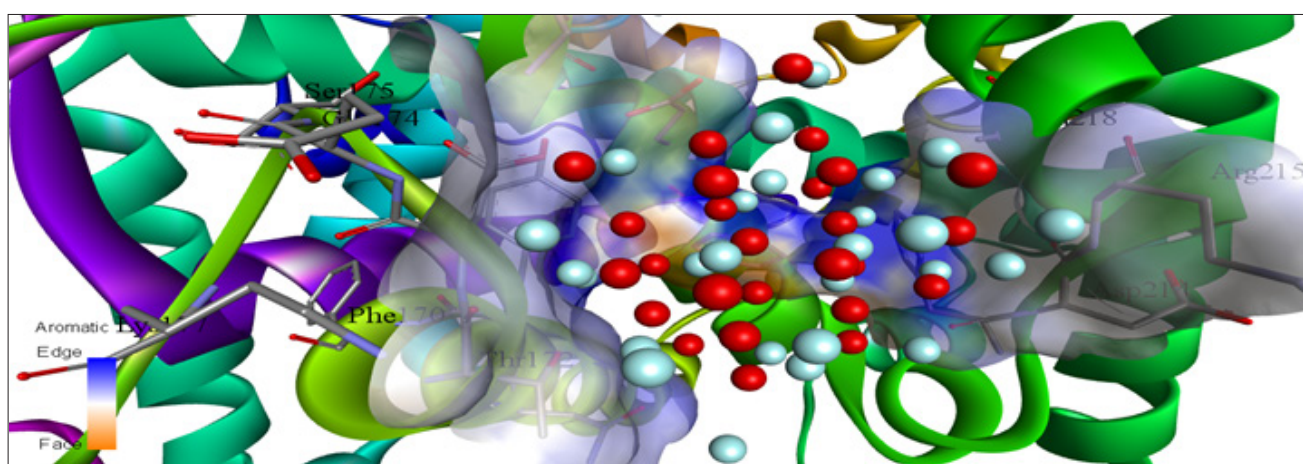
Figure 1 depicts the interactions of all nanoclusters investigated inside 5TZ1. The results of the molecular docking analysis for all Fe<sub>2</sub>O<sub>3</sub> sphere nanoclusters examined against 5TZ1 are shown in table 1. The binding energy inside 5TZ1 increased as the size of the sphere nanoclusters grew larger, according to the molecular docking study. So, 1nm Fe<sub>2</sub>O<sub>3</sub> nanoclusters exhibited the highest binding energy (-9.17 k. cal/mol) inside 5TZ1, as displayed in Table 1 in the case of 5TZ1. Also, 1nm nanoclusters which revealed the maximum binding energy interact with GLU 473, PHE 463, TYR 353 and LYS 358 amino acid residuals of 5TZ1 through hydrogen bond interaction at distances 2.41, 2.38, 2.32, and 2.18 Å, respectively and with LYS 433, SER 436, and THR 152 through van der walls interactions as shown in figure 1. In case of 0.9 nm Fe<sub>2</sub>O<sub>3</sub> nanoclusters, they interact with THR 172, PHE 170, ASP 214 and GLU 174 amino acid residuals of 5TZ1 through hydrogen bond interaction at distances 2.49, 2.42, 2.16, and 2.10 Å, respectively and with SER 175, and ARG 215 through van der walls interactions as shown in figure 1. However, 0.8 nm Fe<sub>2</sub>O<sub>3</sub> nanoclusters interact with LEU 87, SER 507, ALA 62 and GLN 65 amino acid residuals of

**Table 1:** Molecular docking study of Fe<sub>2</sub>O<sub>3</sub> nanoclusters against 5TZ1.

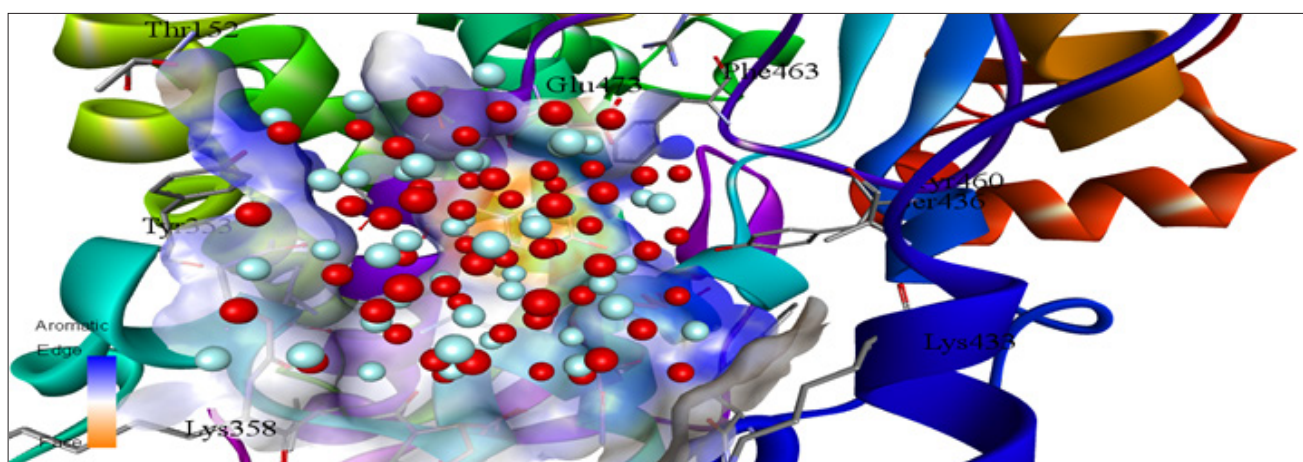
Ligand	Binding Energy ( $\Delta$ G) k.cal/mol
0.5 nm Fe <sub>2</sub> O <sub>3</sub> nanoclusters	-8.17
0.6 nm Fe <sub>2</sub> O <sub>3</sub> nanoclusters	-8.36
0.7 nm Fe <sub>2</sub> O <sub>3</sub> nanoclusters	-8.68
0.8 nm Fe <sub>2</sub> O <sub>3</sub> nanoclusters	-8.87
0.9 nm Fe <sub>2</sub> O <sub>3</sub> nanoclusters	-9.22
1 nm Fe <sub>2</sub> O <sub>3</sub> nanoclusters	-9.75



0.8 nm Fe<sub>2</sub>O<sub>3</sub> nanoclusters inside 5TZ1 receptor



0.9 nm Fe<sub>2</sub>O<sub>3</sub> nanoclusters inside 5TZ1 receptor

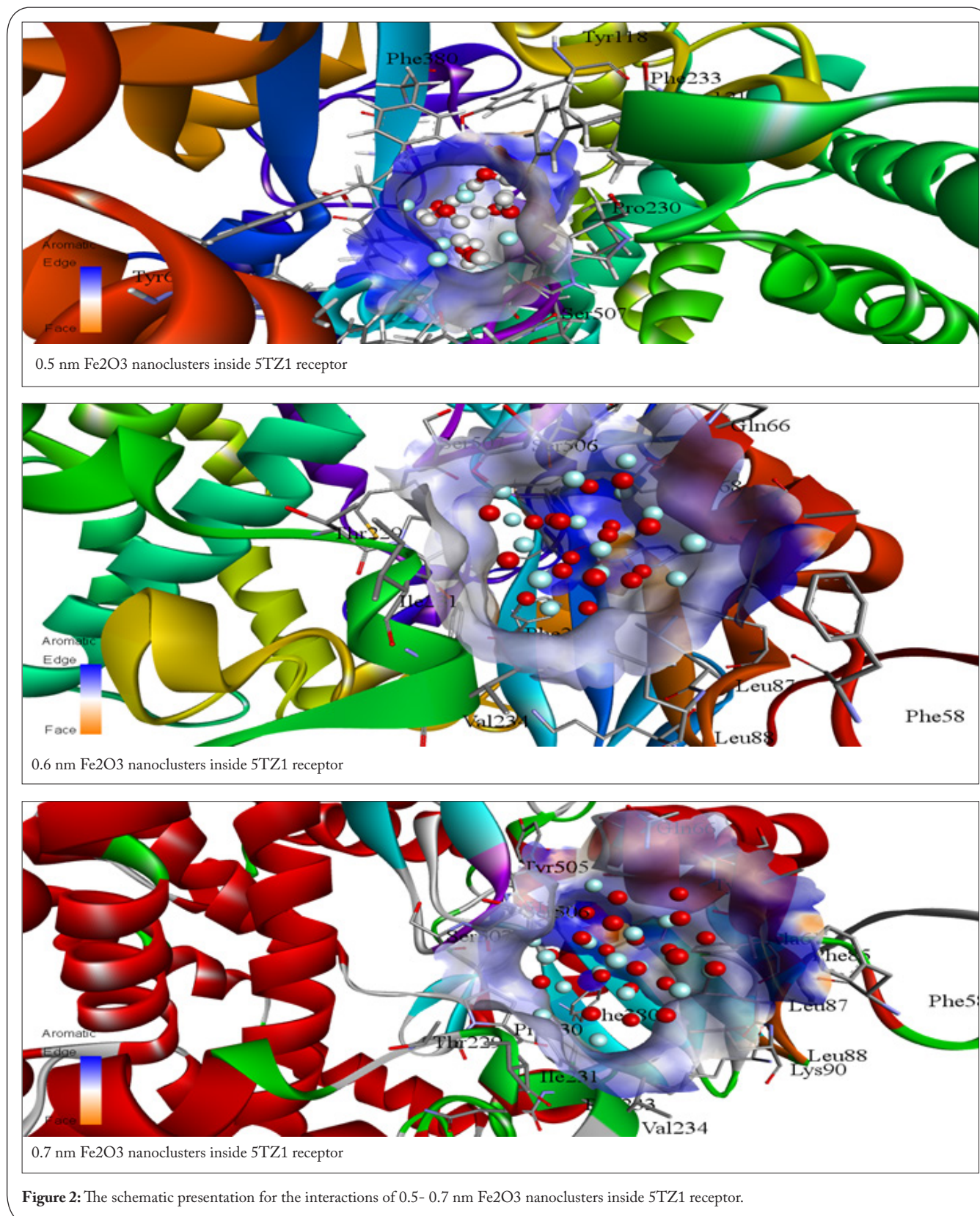


1 nm Fe<sub>2</sub>O<sub>3</sub> nanoclusters inside 5TZ1 receptor

**Figure 1:** The schematic presentation for the interactions of 0.8- 1 nm Fe<sub>2</sub>O<sub>3</sub> nanoclusters inside 5TZ1 receptor.

5TZ1 through hydrogen bond interaction at distances 2.34, 2.31, 2.33, and 2.11 Å, respectively and with LEU 88, SER 60, and THR 229 through van der Waals interactions as shown in [figure 1](#). In addition, 0.7 nm Fe<sub>2</sub>O<sub>3</sub> nanoclusters interact with GLN 66, PHE 280, TYR 505 and SER 507 amino acid

residuals of 5TZ1 through hydrogen bond interaction at distances 2.47, 2.39, 2.29, and 2.22 Å, respectively and with LEU 87, LYS 90, and ILE 231 through van der Waals interactions as shown in [figure 2](#). Also, 0.6 nm Fe<sub>2</sub>O<sub>3</sub> nanoclusters interact with SER 506, THR 229, and GLN 66 amino acid residuals



of 5TZ1 through hydrogen bond interaction at distances 2.33, 2.26, and 2.30 Å, respectively and with ILE 231, VAL 234, LEU 88 and PHE 280 through van der Waals interactions as shown in Figure 2. Furthermore, 0.5 nm Fe<sub>2</sub>O<sub>3</sub> nanoclusters interact with PHE 380, PRO 230, and SER 507 amino acid residues of 5TZ1 through hydrogen bond interaction at dis-

tances 2.45, 2.40 and 2.29 Å, respectively and with PHE 233, and TYR 118 through van der Waals interactions as shown in figure 2. We can deduce that all studied nanoclusters with different sizes can act as 5TZ1 inhibitors from all the previous discussions. Also, increasing the size of the nanoclusters can lead to an increase in the inhibitory of Fe<sub>2</sub>O<sub>3</sub> nanoclusters

against 5TZ1 inhibitors. Finally, a molecular docking study suggested that Fe<sub>2</sub>O<sub>3</sub> nanoclusters could be used as inhibitors against CYP51.

### HRTEM of SIONS

The shape of iron oxide nanoparticles was found to be spherical with approximately an average diameter of 5.74 ± 0.87 nm. The diameter was in the range 6.79, 4.62 nm as shown in figure 3.

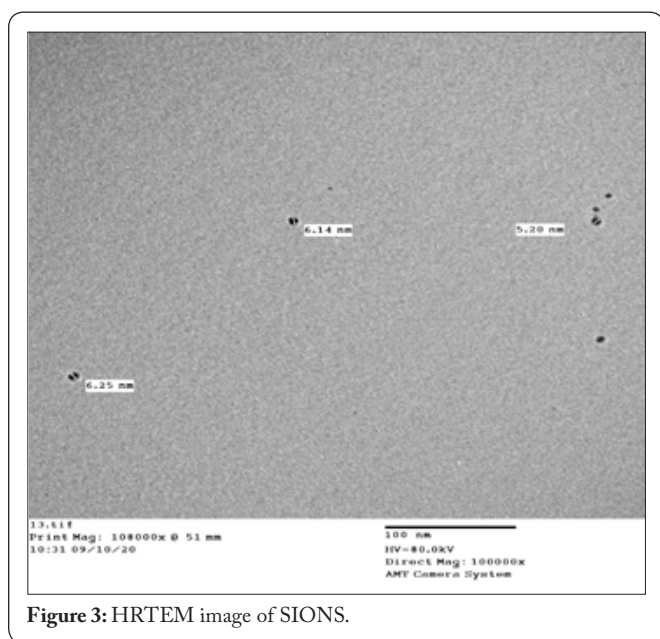


Figure 3: HRTEM image of SIONS.

### In vitro evaluation of antifungal activity

The antifungal activity of SIONS has been evaluated using the agar well diffusion method. The SIONS showed antifungal activity compared to negative control (DMSO). The inhibition zone ranged from 16 mm to 13 mm. High inhibition zones were received from 50% of *Candida albicans* isolates, and the minimum inhibition concentrations were 256 µg/ml for all *Candida albicans* isolates (Table 2). Increasing the size of the spherical nanoclusters increased the binding energy within 5TZ1, which is the explanation for SION's antifungal activity, according to the molecular docking study.

According to other research papers, metal oxide NPs, such as ZnO NPs or CuO NPs, have been discovered to exhibit

Table 2: Antifungal activity of SIONS.

<i>Candida albicans</i> strains	Diameter of Inhibition Zone (mm)	Minimum Inhibitory Concentration (MIC)
<i>Candida albicans</i> (1)	13	256 µg/ml
<i>Candida albicans</i> (2)	16	256 µg/ml
<i>Candida albicans</i> (3)	16	256 µg/ml
<i>Candida albicans</i> ATCC 10231	14	256 µg/ml
Negative Control	NIL	

antimicrobial activities compared to iron oxide nanoparticles [20]. However, Abbas et al. 2020 a & b demonstrated the high antibacterial and anti-candidal activities of iron oxide NPs. The following is how the authors explained the ROS production in candida cells by iron oxide nanoparticles: overproduction of reactive oxygen species (ROS) promotes organelle malfunction and apoptosis [12, 13].

### Conclusions

*Candida* infections are a serious health problem. These infections can be superficial, resulting in mucocutaneous candidiasis, or they can spread to the bloodstream and internal organs, resulting in life-threatening invasive illnesses. There are antifungal drugs, but due to the development of fungal resistance, they have drawbacks. As a result, there is a high demand for new antifungal strategies that can control or limit the spread of *Candida* infections. Herein, a series of spherical iron oxide nanoclusters was tested in silico. The binding mechanism and binding energy of the test iron oxide nanoclusters could be anticipated in each case by docking them in the active site of fungal CYP51. The docking results show that for each iron oxide nanoclusters, the binding mode of each test interacts with at least four amino acid residues in the active site of fungal CYP51. We found that increasing the size of the sphere nanoclusters improved the binding energy. Also, in vitro antifungal activity of 5.74 ± 0.87 nm of the sphere iron oxide nanoparticles were assessed. The minimum inhibitory concentrations were 256 µg/ml against *C. albicans*. In the future, we recommend iron oxide nanoclusters to proceed with in vivo study for the treatment of *Candida* infections.

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### Ethical Approval

There is no Ethical approval needed for this article.

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None.

### Conflict of Interest

None.

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