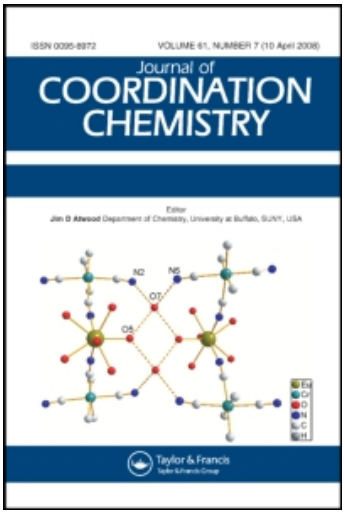


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# Ternary copper(II) complex of 1,10-phenanthroline and L-glycine: crystal structure and interaction with DNA

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# Ternary copper(II) complex of 1,10-phenanthroline and L-glycine: crystal structure and interaction with DNA

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A ternary copper(II) complex, $[Cu(phen)(L\text{-}Gly)(H_2O)] \cdot NO_3 \cdot 1.5H_2O$ (phen = 1,10-phenanthroline, L-Gly = L-glycine), has been synthesized and structurally characterized. The complex crystallized in a monoclinic system with space group $C2/c$, $a = 20.572(3)$ Å, $b = 6.9987(10)$ Å, $c = 23.561(3)$ Å, $\beta = 98.776(5)^\circ$. The five-coordinate copper(II) center is a distorted square pyramid. Absorption spectra, fluorescence spectra and viscosity measurements showed interaction between the copper complex and DNA through an intercalative mode. The complex exhibited efficient DNA cleavage activity at micromolar concentration in the presence of ascorbate with hydroxyl radicals as the active species.

*Keywords*: Copper complex; DNA binding; DNA cleavage; 1,10-Phenanthroline; L-glycine

## 1. Introduction

The interaction between transition metal complexes and nucleic acids has been examined for several decades. Considerable investigation has concentrated on the design and synthesis of novel transition metal complexes which bind to, and cleave, duplex DNA with high sequence or structure selectivity [1–5]. Transition metal complexes, especially copper, not only bind to DNA by intercalation or partial intercalation, but also exhibit excellent nuclease activity [6, 7]. Especially, efforts have been devoted to using copper complexes of phenanthroline as intercalating agents of DNA and as artificial nucleases [8–11]. *Bis*(1,10-phenanthroline)copper(II) shows efficient DNA cleavage activity in the presence of thiol and hydrogen peroxide [12], binding to DNA non-covalently in the minor groove and reacting with $H_2O_2$ to generate species that leads to DNA strand scission [13–15]. Meunier *et al*. exploited a new type of ligand with two phenanthrolines bridged on their C2 or C3 carbon by a short flexible arm, namely Clip-phen, and found that the copper complexes of Clip-phen cleaved DNA more efficiently than $[Cu(phen)_2]$ in the presence of reductants and air [16, 17]. Moremore, some ternary copper(II) complexes having heterocyclic bases, such as 1,10-phenanthroline and its derivatives capable of DNA-intercalation/binding in the presence of auxiliary ligands were reported. These complexes bind to

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and cleave DNA efficiently under physiological conditions in the presence of a reductant or on irradiation with UV or visible light [18–20].

Some copper complexes of amino acids were reported to exhibit potent antitumor and artificial nuclease activity [21–23]. We focused our interests on the development of ternary copper(II) complexes of phenanthroline with amino acids, and investigated the interaction with DNA [24]. The selection of amino acid as a second ligand in the ternary copper(II) complex enhances affinity of the complex towards DNA and the DNA cleavage activities. We report here the preparation and crystal structure of a ternary copper(II) complexes of 1,10-phenanthroline and L-glycine, $[Cu(phen)(L\text{-}Gly)(H_2O)]\cdot NO_3\cdot 1.5H_2O$. The binding of the complex to DNA and nuclease activity are also discussed.

## 2. Experimental

### 2.1. *Chemicals and physical measurements*



Common reagents such as $Cu(NO_3)_2\cdot 3H_2O$, 1,10-phenanthroline monohydrate, ethanol, anhydrous ether and NaOH are all analytical grade and used as received. L-glycine was purchased from Aldrich. Plasmid pBR322 was purchased from MBI Fermentas. Disodium salt of calf thymus DNA (CT-DNA), ascorbic acid, *tris*(hydroxymethyl) aminomethane (*Tris*) and ethidium bromide (EB) were purchased from Sigma. Infrared spectra were recorded on a Bruker VECTOR22 spectrometer as KBr pellets (4000–500 $cm^{-1}$), and elemental analysis was performed on a Perkin-Elmer 240°C analytical instrument. Fluorescence spectra were recorded on an AMINCO Bowman Series 2 Luminescence Spectrometer.

### 2.2. *Synthesis of $[Cu(phen)(L\text{-}Gly)(H_2O)]\cdot NO_3\cdot 1\cdot 5H_2O$*

To the mixture of L-glycine (150 mg, 2 mmol) and NaOH (80 mg, 2 mmol) in water, an aqueous solution of $Cu(NO_3)_2\cdot 3H_2O$ (483.0 mg, 2 mmol) was added with stirring. Several minutes later, ethanolic solution (5 mL) of 1,10-phenanthroline monohydrate (396.4 mg, 2 mmol) was added and then the solution was stirred for about 3 h at 60°C. On cooling the solution to ambient temperature, large amount of blue precipitate was produced, which was filtered and washed with ethanol and ether. Blue blocky single crystals suitable for X-ray diffraction were obtained on slow evaporation of an aqueous ethanol solution of the complex. Anal. Calcd for $C_{14}H_{17}CuN_4O_{7.50}$ (%): C, 39.5; H, 4.00; N, 13.2%. Found: C, 39.0; H, 4.07; N, 13.5%. IR/(KBr, $\nu/cm^{-1}$): 3450s $\nu_{as}$(N–H), 3079s $\nu_s$(N–H), 1648s $\nu_{as}(CO_2)$, 1385m $\nu_s(CO_2)$, 860m $\delta$(C–C, phen), 724m $\delta$(C–N, phen).

### 2.3. *X-ray crystallography*

Details of the crystal parameters, data collection and refinements are listed in table 1. The structure was determined on a Simens P4 four-circle diffractometer. Cell constants and an orientation matrix for data collection were obtained by least-squares refinement

Table 1. Crystal data and structure refinement for $[Cu(phen)(L\text{-}Gly)(H_2O)] \cdot NO_3 \cdot 1.5H_2O$.

| | |
|---|---|
| Empirical formula | $C_{14}H_{17}CuN_4O_{7.50}$ |
| Formula weight | 424.86 |
| $T$ (K) | 293(2) |
| Crystal size ($mm^3$) | $0.30 \times 0.25 \times 0.15$ |
| Crystal habit, color | Block, blue |
| Crystal system | Monoclinic |
| Space group | $C2/c$ |
| $a$ (Å) | 20.572(3) |
| $b$ (Å) | 6.9987(10) |
| $c$ (Å) | 23.561(3) |
| $\beta$ (°) | 98.776(5) |
| $V$ ($Å^3$) | 3352.5(8) |
| $Z$ | 8 |
| Calculated density ($Mg\,m^{-3}$) | 1.684 |
| Absorption coeffcient ($mm^{-1}$) | 1.354 |
| $F(000)$ | 1744 |
| $\theta$ range for data collection (°) | 1.75–28.07 |
| Limiting indices | $-26 \le h \le 22$<br>$-9 \le h \le 9$<br>$-30 \le l \le 28$ |
| Reflections collected/unique | 9709/3867 ($R_{int} = 0.0729$) |
| Absorption corrections | Empirical |
| Data/restraints/parameters | 3867/0/240 |
| Goodness-of-fit on $F^2$ | 0.968 |
| Final $R$ indices $[I > 2\sigma(I)]$[a] | $R_1 = 0.0637$, $wR_2 = 0.1264$ |
| $R$ indices (all data)[a] | $R_1 = 0.1096$, $wR_2 = 0.1422$ |
| Largest diff. peak, hole (e $Å^{-3}$) | 0.599, −0.448 |

[a] $R_1 = \sum ||F_o| - |F_c|| / \sum |F_o|$; $wR_2 = \left[\left(F_o^2 - F_c^2\right)^2 / \sum w\left(F_o^2\right)^2\right]^{1/2}$.



of diffraction data from 34 reflections in the range $1.84 < \theta < 24.97$. Data were collected at 293 K using monochromated Mo-K$\alpha$ radiation and the $\omega$–$2\theta$ scan technique with a variable scan speed of 5.0–50.0 $min^{-1}$ in $\omega$ and corrected for Lorentz and polarization effects. An empirical absorption correction was made ($\psi$-scan). The structure was solved by Patterson methods and completed by iterative cycles of least-squares refinement and $\Delta F$-syntheses. H-atoms were located in their calculated positions and treated as riding on the atoms to which they are attached. All non-hydrogen atoms were refined anisotropically. All calculations were carried out using the SHELXTL program [25].

### 2.4. *Interaction between $[Cu(phen)(L\text{-}Gly)(H_2O)] \cdot NO_3 \cdot 1.5H_2O$ with DNA*

**2.4.1. Absorption spectra.** The UV absorbances at 260 and 280 nm of the CT DNA solution in 50 mM NaCl/5 mM *Tris*-HCl buffer (pH 7.4) give a ratio of ~1.9, indicating that the DNA was sufficiently free of protein [26]. The DNA concentration was determined by measuring the UV absorption at 260 nm, taking the molar absorption coefficient ($\varepsilon_{260}$) of CT-DNA as 6600 $M^{-1}\,cm^{-1}$ [27]. Electronic spectra of $[Cu(phen)(L\text{-}Gly)(H_2O)] \cdot NO_3 \cdot 1.5H_2O$ ($5.0 \times 10^{-5}$ M) were recorded before and after addition of CT-DNA ($r = 0.0$, 0.2, 0.4, 0.7, 1.0, where $r$ is the molar ratio of DNA and complex) in the 5 mM *Tris*-HCl/50 mM NaCl

buffer, pH 7.4. The intrinsic binding constant $K_b$ for the interaction of the studied complex with CT-DNA was calculated by absorption spectral titration data using the following equation [28]:

$$[\mathrm{DNA}]/(\varepsilon_a - \varepsilon_f) = [\mathrm{DNA}]/(\varepsilon_b - \varepsilon_f) + 1/K_b(\varepsilon_b - \varepsilon_f)$$

where $\varepsilon_a$, $\varepsilon_f$ and $\varepsilon_b$ correspond to $A_{obsd}/[Cu]$, the extinction coefficient for the free copper complex, and the extinction coefficient for the copper complex in the fully bound form, respectively. In the plot of $[DNA]/(\varepsilon_a - \varepsilon_f)$ *versus* [DNA], $K_b$ is then given by the ratio of the slope to intercept.

**2.4.2. Fluorescence spectra.** The fluorescence spectra were recorded at room temperature with excitation at 520 nm and emission at 600 nm. The experiment was carried out by titrating $[Cu(phen)(L\text{-}Gly)(H_2O)] \cdot NO_3 \cdot 1.5H_2O$ ($1.2 \times 10^{-3}$ M in 5 mM *Tris*-HCl/50 mM NaCl buffer) into samples containing $1.0 \times 10^{-4}$ M DNA and $1.0 \times 10^{-5}$ M ethidium bromide (EB).



**2.4.3. Viscosity studies.** Viscosity experiments were carried out using an Ubbelodhe viscometer maintained at $30.0 \pm 0.1^{\circ}C$ in a thermostatic water-bath. Calf thymus DNA samples, approximately 200 base pairs in average length, were prepared by sonicating in order to minimize complexities arising from DNA flexibility [29]. Flow time was measured with a digital stopwatch, and each sample was measured three times, and an average flow time was calculated. Data were presented as $(\eta/\eta_0)^{1/3}$ *versus* binding ratio [30], where $\eta$ is the viscosity of CT DNA in the presence of complex, and $\eta_0$ is the viscosity of CT DNA alone.

**2.4.4. DNA cleavage.** A typical reaction was carried out by mixing 1 μL of pBR322 DNA (0.335 μg μL$^{-1}$, 0.1185 μM), 4.5 μL of *Tris*-HCl/NaCl buffer (pH 7.4) and 8.5 μL $[Cu(phen)(L\text{-}Gly)(H_2O)] \cdot NO_3 \cdot 1.5H_2O$ solution (20 μM) in 40 mM *Tris*-HCl/NaCl buffer (pH 7.4, 4% DMF) with 3 μL of ascorbic acid ($H_2A$) at a 50-fold molar excess relative to the complex to yield a total volume of 17 μL. After mixing, the sample was incubated at 310 K. The reactions were quenched at appropriate time by the addition of sodium diethydithiocarbamate trihydrate (DDTC) and loading buffer (0.25% bromphenol blue, 50% glycerol). Then, the solution was subjected to electrophoresis on 0.7% agarose gel in TAE buffer (40 mM *Tris* acetate/1 mM EDTA) at 100 V and visualized by ethidium bromide staining. The Gel Imaging and Documentation DigiDoc-It$^{TM}$ System (Version 1.1.23, UVP, Inc. Unpland, CA) was assessed using labworks Imaging and Analysis Software (UVP, Inc. Unpland, CA).

In the inhibition reactions, DMSO (4 μL) was added initially to pBR322 DNA (300 ng) in the *Tris*-HCl/NaCl buffer, and incubated for 15 min at 310 K prior to the addition of $[Cu(phen)(L\text{-}Gly)(H_2O)] \cdot NO_3 \cdot 1.5H_2O$ (7.5 μM) and $H_2A$ (750 μM). The mixture was diluted with the buffer to a total volume of 20 μL. After a further incubation of 3 h at 310 K, the sample was subjected to gel electrophoresis using the described procedures.

## 3. Results and discussion

### 3.1. *Crystal structure*

The perspective view of $[Cu(phen)(L\text{-}Gly)(H_2O)] \cdot NO_3 \cdot 1.5H_2O$ is shown in figure 1 and key bond lengths and angles are summarized in table 2. In this complex, the copper(II) is coordinated in a distorted square pyramidal geometry through the carboxylate oxygen O(2) and the amino nitrogen N(3) atoms of L-glycine and two N atoms of the 1,10-phenanthroline in the basal plane, and a water molecule in the apical position. The Cu–N(phen) bond lengths of 2.000(6) Å and 1.997(6) Å and the bite angle N(1)–Cu–N(2) of 82.9(2)° are close to the corresponding values for some copper-phenanthroline complexes [31–33]. The bond lengths of Cu(1)–O(2) (1.920(5) Å) and Cu(1)–N(3) (1.984(6) Å) are similar to those of related copper-amino acid complexes [34–37]. The Cu(1)–O(2) bond length is shorter than Cu(1)–O(1W)

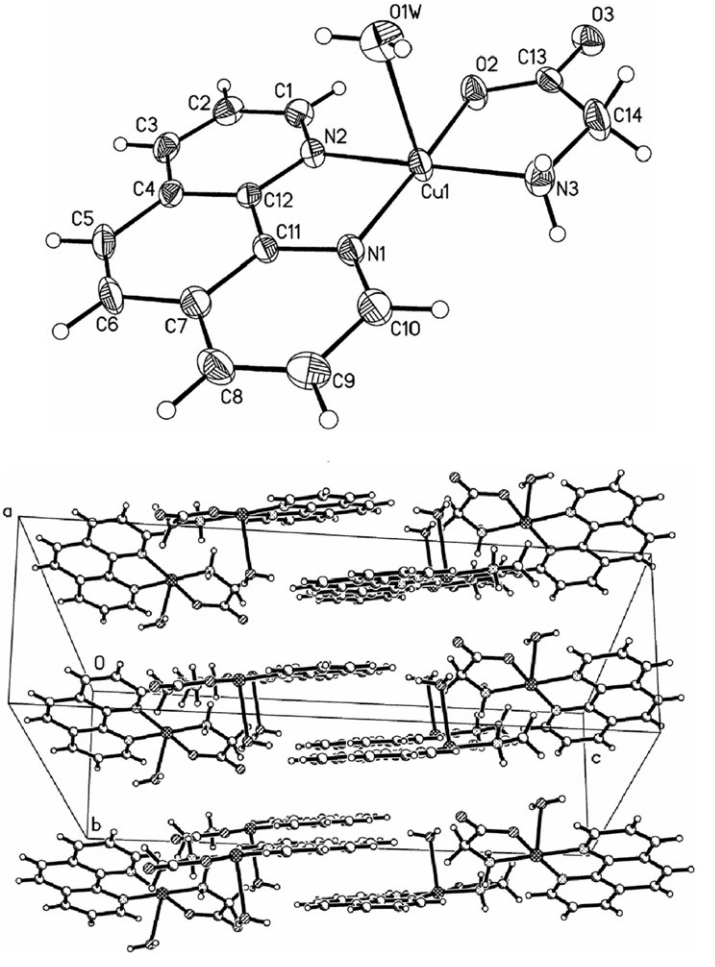


Figure 1. ORTEP diagram (top) and packing structure along the b-axis (bottom) for $[Cu(phen)(L\text{-}Gly)(H_2O)] \cdot NO_3 \cdot 1.5H_2O$.

bond length, indicating that the coordination ability of carboxylate oxygen of glycine is stronger than that of water. The bond angles of N(1)–Cu(1)–O(2) (173.7(3)°) and N(2)–Cu(1)–N(3) (163.5(3)°) are contracted from the ideal value of 180° for a regular square-planar structure, indicating distortion in the basal plane. There is a stacking interaction between the phenanthroline rings of two adjacent molecules in the unit cell shown in figure 1 (bottom). Such a stacking between the aromatic rings has also been found in other copper(II) complexes, such as $[Cu(L\text{-}Asp)(bpy)(H_2O)]\cdot 3H_2O$ (L-Asp = L-aspartate ion) and $[Cu(L\text{-}Glu)(phen)(H_2O)]\cdot 3H_2O$ (L-Glu = L-glutamate ion) [38].

### 3.2. *Interaction between $[Cu(phen)(L\text{-}Gly)(H_2O)]\cdot NO_3\cdot 1.5H_2O$ and DNA*

**3.2.1. Absorption spectra.** The application of electronic absorption spectroscopy in DNA-binding studies is most useful. The absorption spectra of $[Cu(phen)(L\text{-}Gly)(H_2O)]\cdot NO_3\cdot 1.5H_2O$ in the absence and presence of CT-DNA are shown in figure 2. In the UV region, the complex has three bands at 223 ($\varepsilon = 2.58\times 10^4\,M^{-1}cm^{-1}$), 271 ($\varepsilon = 2.54\times 10^4\,M^{-1}cm^{-1}$) and 293 nm ($\varepsilon = 0.87\times 10^4\,M^{-1}cm^{-1}$), which can be attributed to $\pi\rightarrow\pi^*$ transitions of the coordinated phenanthroline ligand.



Table 2. Selected bond lengths (Å) and angles (°).

| | | | |
|---|---|---|---|
| Cu(1)–N(1) | 2.000(6) | Cu(1)–O(2) | 1.920(5) |
| Cu(1)–N(2) | 1.997(6) | Cu(1)–O(1W) | 2.280(7) |
| Cu(1)–N(3) | 1.984(6) | | |
| N(1)–Cu(1)–N(3) | 98.3(2) | N(2)–Cu(1)–N(3) | 163.5(3) |
| N(1)–Cu(1)–N(2) | 82.9(2) | N(2)–Cu(1)–O(2) | 93.4(2) |
| N(1)–Cu(1)–O(1W) | 92.1(3) | N(2)–Cu(1)–O(1W) | 97.7(3) |
| N(1)–Cu(1)–O(2) | 173.7(3) | N(3)–Cu(1)–O(1W) | 98.8(3) |
| O(2)–Cu(1)–O(1W) | 93.4(3) | N(3)–Cu(1)–O(2) | 83.8(2) |

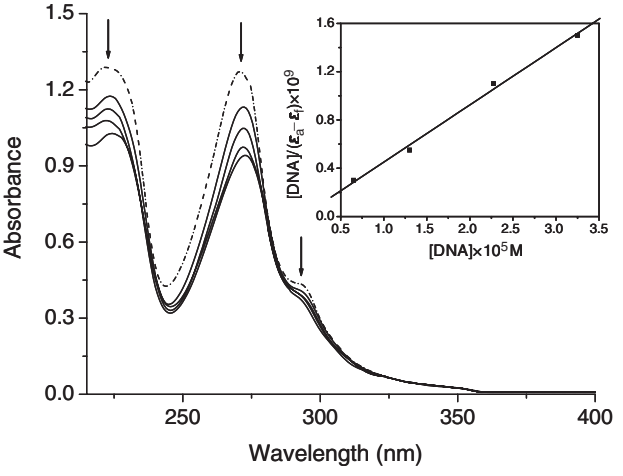


Figure 2. Absorption spectra of $5.0\times 10^{-5}$ M $[Cu(phen)(L\text{-}Gly)(H_2O)]\cdot NO_3\cdot 1.5H_2O$ in the absence (- - -) and presence (—) of increasing amounts of CT DNA at the ratio $r = 0.2, 0.4, 0.7, 1.0$.

In the presence of DNA, a decrease in absorption intensity (hypochromism) and a slight increase in wavelength (bathochromism) were observed. Both hypochromism and bathochromism suggested that there were interactions between DNA and the complex. In general, complex binding with DNA through intercalation results in hypochromism and bathochromism due to the intercalative mode involving a strong stacking interaction of the planar aromatic chromophore of the complex with the base pairs of DNA [39]. The intrinsic binding constant $K_b$ of $4.68 \times 10^3\,M^{-1}$ was determined from a plot of [DNA]/($\varepsilon_a - \varepsilon_f$) *versus* [DNA] (inset of figure 2) using the absorption at 271 nm. The $K_b$ value was comparable to those observed for other copper complexes with phenanthroline [24, 40] but lower than that of classical intercalator EB [41], which indicated the complex has a low binding affinity to DNA.

**3.2.2. Fluorescence spectra.** Fluorescence spectra were also used to study the interaction between [Cu(phen)(L-Gly)($H_2O$)] · $NO_3$ · 1.5$H_2O$ and DNA by measuring the emission intensity of EB bound to CT-DNA. EB is weakly fluorescent, and it can emit intense fluorescent light in the presence of DNA due to its intercalative binding to DNA. However, this enhanced fluorescence could be quenched or partly quenched by the addition of a second molecule that can replace the bound EB or break the secondary structure of DNA [42]. So, EB can be used as a probe for determination of DNA structure. In this study, the emission spectra of EB bound to DNA in the absence and presence of [Cu(phen)(L-Gly)($H_2O$)] · $NO_3$ · 1.5$H_2O$ are shown in figure 3. The results show that the fluorescence intensity of CT-DNA-EB decreased remarkably with the addition of the copper complex, suggesting that the complex binds to DNA by intercalation or partial intercalation replacing EB from the DNA structure.



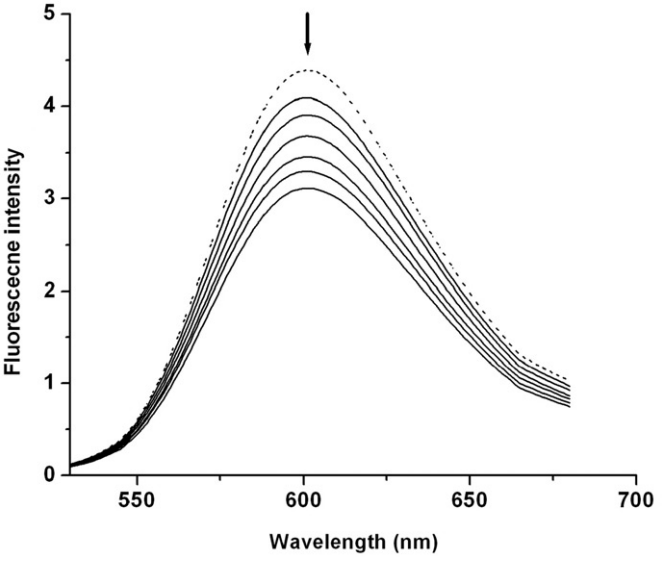


Figure 3. Fluorescence emission spectra (excited at 520 nm) of the CT DNA-EB system ($1.0 \times 10^{-5}$ mol $L^{-1}$ EB, $1.0 \times 10^{-4}$ mol $L^{-1}$ CT DNA) in the absence (- - -) and presence (—) of $1.2 \times 10^{-3}$ mol $L^{-1}$ [Cu(phen)(L-Gly)($H_2O$)] · $NO_3$ · 1.5$H_2O$ (20 μL per scan).

**3.2.3. Viscosity studies.** Optical photophysical probes provide necessary, but not sufficient evidence to support the binding of metal complexes with DNA. Further clarification of the interaction between $[Cu(phen)(L\text{-}Gly)(H_2O)] \cdot NO_3 \cdot 1.5H_2O$ and DNA was carried out by viscosity measurements (figure 4). The relative viscosity of DNA increased steadily with increasing the amounts of the copper complex, which was similar to the behavior of the proven intercalator EB [43]. The results suggested that the copper complex intercalated between the base pairs of DNA, consistent with the results obtained from absorption spectra and fluorescence spectra.

**3.2.4. DNA cleavage activity.** The capacity of $[Cu(phen)(L\text{-}Gly)(H_2O)] \cdot NO_3 \cdot 1.5H_2O$ to cleave DNA by gel electrophoresis using plasmid pBR322 DNA was also studied. The naturally occurring supercoiled form (Form I), when nicked, gives rise to an open circular relaxed form (Form II) and upon further cleavage, results in the linear form (Form III). When subjected to gel electrophoresis, relatively fast migration is observed for Form I. Form II migrates slowly and Form III migrates between Forms I and II. The addition of $[Cu(phen)(L\text{-}Gly)(H_2O)] \cdot NO_3 \cdot 1.5H_2O$ to pBR322 DNA in the presence of a 50-fold excess of ascorbic acid ($H_2A$) converted Form I to both Form II and Form III products. Figure 5 shows the cleavage of DNA at different concentrations of the complex for 30 min reaction time (pH 7.4, 310 K). Control experiments using only ascorbic acid ($H_2A$) or copper complex failed to show any apparent cleavage of DNA (figure 5, lanes 2, 3). With the increase of complex concentration, the supercoiled DNA decreased and was finally converted completely to nicked and linear DNA. The cleavage efficiency of $[Cu(phen)(L\text{-}Gly)(H_2O)] \cdot NO_3 \cdot 1.5H_2O$ reached 92% at a concentration of 7.5 μM (figure 5, lane 6) in converting Form I to Form II. When the concentration of the complex was 10.0 μM or above, Form I was degraded completely to Form II and Form III (figure 5, lines 7 and 8). The amount of Form III reached 22% at a complex concentration of 12.5 μM, which indicated that $[Cu(phen)(L\text{-}Gly)(H_2O)] \cdot NO_3 \cdot 1.5H_2O$ was a potent DNA cleavage agent in the presence of ascorbate as a reductant under the experimental conditions.



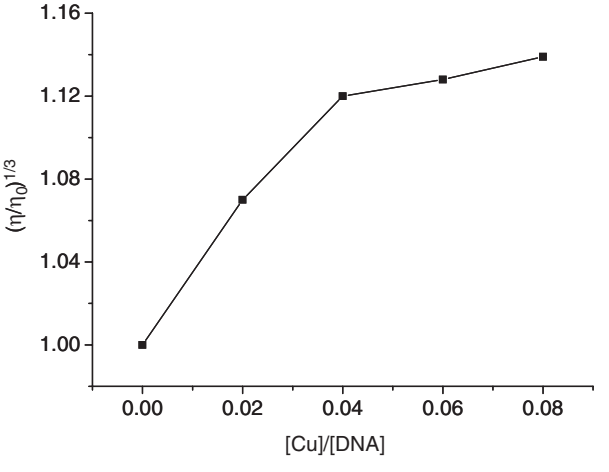


Figure 4. Effect of increasing concentration of $[Cu(phen)(L\text{-}Gly)(H_2O)] \cdot NO_3 \cdot 1.5H_2O$ on the relative viscosity of CT DNA at $30.0 \pm 0.1$°C. [DNA] = 0.5 mM.

The preliminary mechanism of pBR 322 DNA cleavage by [Cu(phen)(L-Gly)($H_2O$)] · $NO_3$ · 1.5$H_2O$ was also studied by using inhibiting reagent DMSO (figure 6). It is evident that the hydroxyl radical scavenger DMSO diminished significantly the nuclease activity of the complex, which is indicative of the involvement of the radical in the cleavage process. [Cu(phen)(L-Gly)($H_2O$)] · $NO_3$ · 1.5$H_2O$ may first

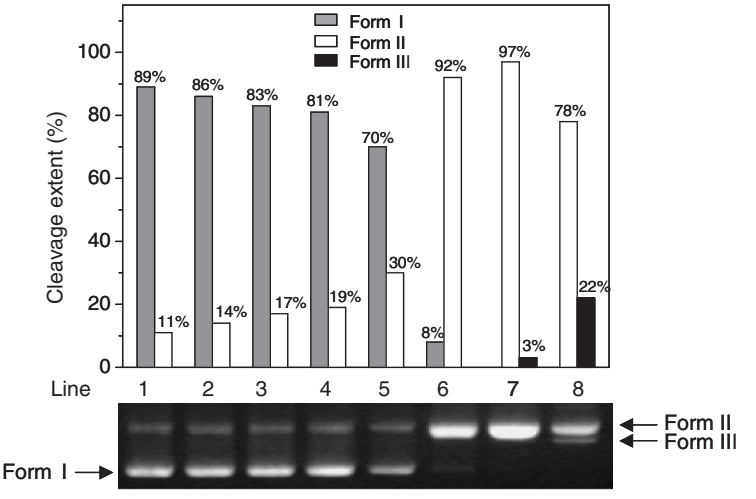


Figure 5. The cleavage patterns of the gel electrophoresis and the corresponding cleavage extent (%) for supercoiled pBR322 DNA by [Cu(phen)(L-Gly)($H_2O$)] · $NO_3$ · 1.5$H_2O$ in buffer (5 mM *Tris*-HCl/50 mM NaCl, pH 7.4) at 310 K. Lane 1, DNA control; lane 2, DNA + $H_2A$; lane 3, DNA + [Cu(phen)(L-Gly)($H_2O$)] · $NO_3$ · 1.5$H_2O$ (7.5 μM); lanes 4-8 represent the DNA cleavage status at 2.5, 5.0, 7.5, 10.0 and 12.5 μM of [Cu(phen)(L-Gly)($H_2O$)] · $NO_3$ · 1.5$H_2O$ in the presence of 50-fold excess of $H_2A$, respectively.

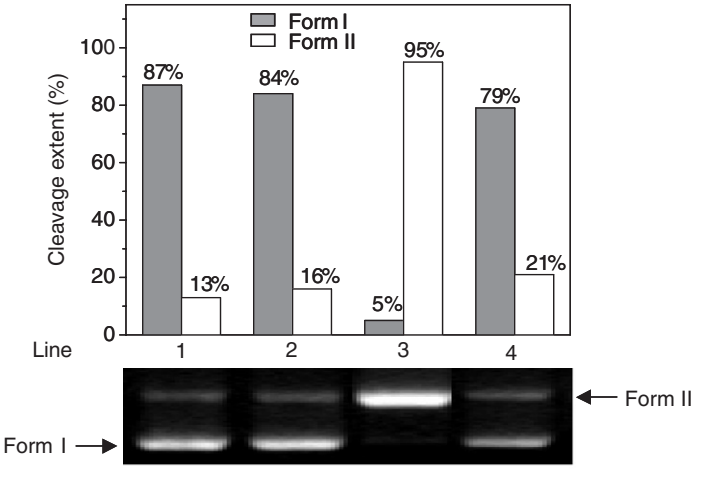


Figure 6. Gel electrophoresis patterns and histogram representation for the cleavage of plasmid pBR322 DNA by [Cu(phen)(L-Gly)($H_2O$)] · $NO_3$ · 1.5$H_2O$ (7.5 μM) in the presence of standard radical scavenger DMSO in 5 mM *Tris*-HCl/50 mM NaCl buffer (pH 7.4) at 310 K. Lane 1, DNA control; Lane 2, DNA + DMSO; Lane 3, DNA + $H_2A$ + [Cu(phen)(L-Gly)($H_2O$)] · $NO_3$ · 1.5$H_2O$ (7.5 μM); line4, DNA + $H_2A$ + [Cu(phen)(L-Gly)($H_2O$)] · $NO_3$ · 1.5$H_2O$ (7.5 μM) + DMSO.

interact with DNA by intercalation to form Cu(II)-DNA species, which then is reduced to Cu(I)-DNA by reductant with the generation of hydroxyl radicals. The hydroxyl radicals attack DNA and thus cause the DNA strand scission.

## Supplementary material

Crystallographic data of $[Cu(phen)(L\text{-}Gly)(H_2O)] \cdot NO_3 \cdot 1.5H_2O$ have been deposited at the Cambridge Crystallographic Data Centre with CCDC No. 227570. Copies of this information may be obtained free of charge from The Director, CCDC, 12 Union Road, Cambridge, CB2 1EZ, UK (Fax: +44-1223-336033; Email: deposit@ccdc.cam.ac.uk or http://www.ccdc.cam.ac.uk).

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