Supplementary data

Molecular drug design, synthesis and structure elucidation of new specific target peptide based metallo drug for cancer chemotherapy as topoisomerase I inhibitor†

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Figures

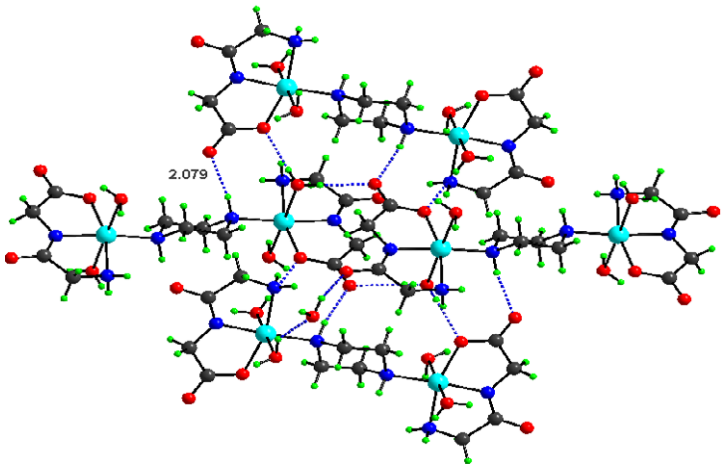

Fig. S1. The Packing diagram of $[Cu(glygly)_2(ppz)(H_2O)_4].2H_2O$, showing O–H interactions.

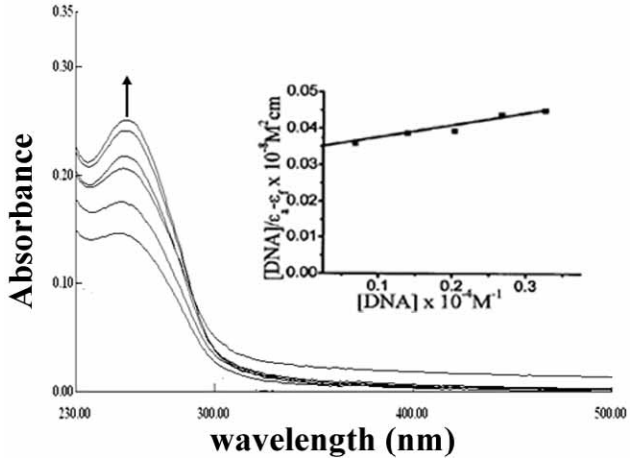

Fig. S2. Absorption spectral traces of complex **1** in 5mM Tris HCl/ 50 mM NaCl buffer at pH 7.2 upon addition of CT DNA. Inset: Plots of [DNA]/ $\varepsilon_a - \varepsilon_f$ (m^2 cm) vs [DNA] for the titration of CT DNA with complexes ■, experimental data points; full lines, linear fitting of the data. [Complex **1**] 0.67 x 10^{-4} M, [DNA] 0.067–0.33 x 10^{-4} M.

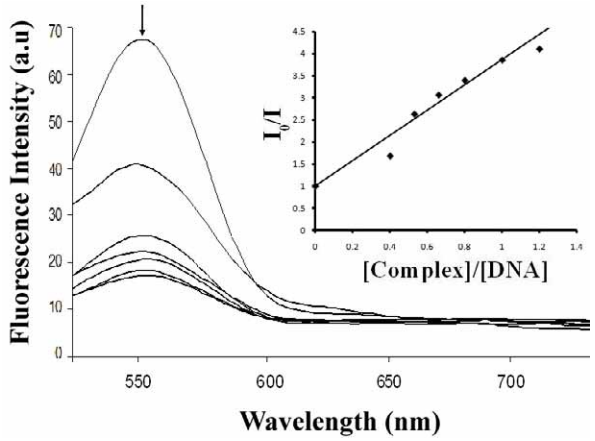

Fig. S3. Emission spectra of EB bound to DNA in the absence and presence complex **1** in 5 mM Tris–HCl/50 mM NaCl buffer. Arrows show the intensity changes upon increasing concentration of the complex **1**. Inset: Plots of I_0/I vs [complex]/[DNA]. **(■)** experimental data points; full lines, linear fitting of the data.

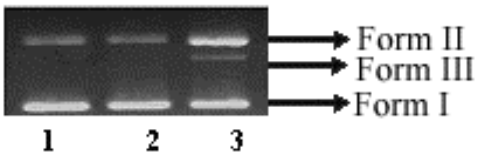

Fig. S4. Agarose Gel electrophoresis pattern for the cleavage of pBR322 supercoiled DNA (300 ng) by complex **1** in presence of DNA minor binding agent DAPI and major binding agent methyl green at 310 K after incubation for 45 min. Lane 1, DNA control; Lane 2, 25 μM of **1** + DNA + DAPI (8 μM); Lane 3, 25 μM of **1** + DNA+ methyl green (2.5 μL of a 0.01mg/ml solution).

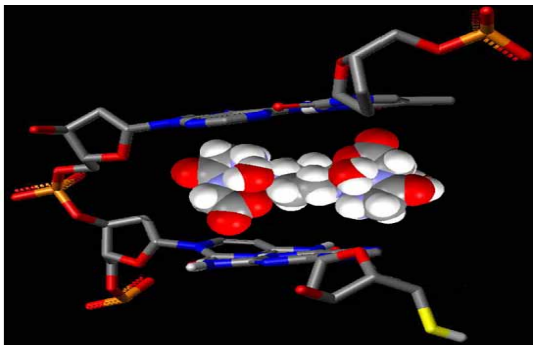

Fig. S5. View is a cut–out of sequence 5′–AAAAAGACTTsX–GAAAATTTTT–3′ showing complex **1** (space filling model) docked in DNA sequence between C112, A113 and T10, TGP11.

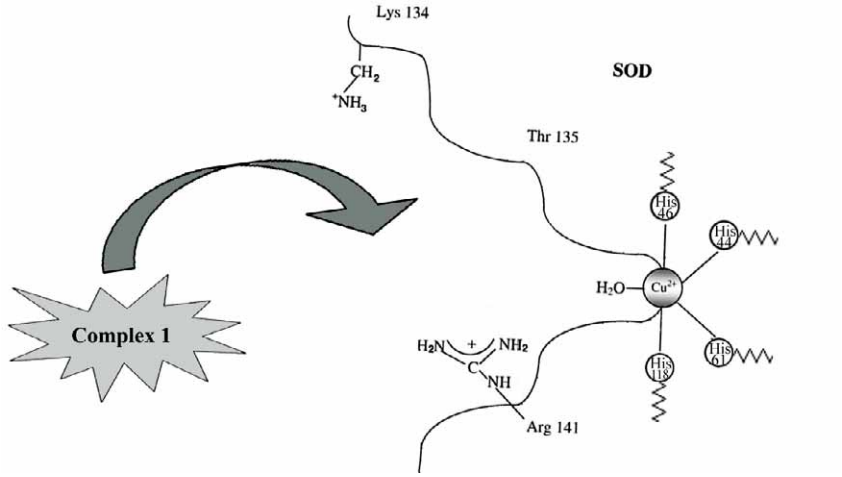

Fig. S6. Schematic representation of the key–lock interaction between the CuZnSOD enzyme (PDB ID: 1SXA) and the complex **1**.

Tables:

Table S1 : Selected bond lengths (Å) and angles (°) for complex **1**

Bond lengths	(Å)
Cu(1) – N(1)	1.897(3)
Cu(1) – N(3)	1.993(3)
Cu(1) – O(1)	2.017(3)
Cu(1) – N(2)	2.063(3)
Cu(1) – O(4)	2.381(4)

Bond Angles	(°)
N(1) – Cu(1) – N(3)	173.20(15)
N(1) – Cu(1) – O(1)	82.38(13)
N(3) – Cu(1) – O(1)	98.77(13)
N(3) – Cu(1) – N(2)	82.44(15)
N(3) – Cu(1) – N(2)	95.56(15)
O(1) – Cu(1) – N(2)	163.48(13)
N(1) – Cu(1) – O(4)	92.83(14)
N(3) – Cu(1) – O(4)	93.89(14)
O(1) – Cu(1) – O(4)	89.36(15)
N(2) – Cu(1) – O(4)	97.85(17)

Table S2: IC_{50} (μM) values of the complex **1**, some of the dipeptide–based SOD–mimicking compounds and the native Cu,ZnSOD enzyme.

Complexes	IC_{50} (μM)
$[Cu_2(glygly)_2(ppz)(H_2O)_4]$. $2H_2O$ (**1**)	0.086 (This work)
[Cu(ala–ile)]	330
[Cu(ala–thr)]	0.99
[Cu(ala–tyr)]	252
[Cu(ala–val)]	237
[Cu(ala–Phen)]	0.149
Native Cu,Zn–SOD	0.045