

## ***Electronic supplementary information for:***

### ***A new Cu(II) complex derived from the reaction between tris(2-aminoethyl)amine, and Cu(I)-activated acetonitrile; Potent anticancer activity against some cell lines and high affinity for the essential proteins of SARS-CoV-2***

Farshid Hajibabaei<sup>a</sup>, Sadegh Salehzadeh<sup>a\*</sup>, Katayoun Derakhshandeh<sup>b, c\*</sup>, Robert William Gable<sup>d</sup>

<sup>a</sup> Faculty of Chemistry and Petroleum of Sciences, Bu-Ali Sina University, Hamedan, Iran

<sup>b</sup> Department of Pharmaceutics, School of Pharmacy, Hamadan University of Medical Sciences, Hamadan, Iran

<sup>c</sup> Medicinal Plants and Natural Products Research Center, Hamadan University of Medical Sciences, Hamadan, Iran

<sup>d</sup> School of Chemistry, University of Melbourne, Victoria 3010, Australia

\*Corresponding authors. E-mail addresses: saleh@basu.ac.ir (S. Salehzadeh), [k.derakhshandeh@umsha.ac.ir](mailto:k.derakhshandeh@umsha.ac.ir)

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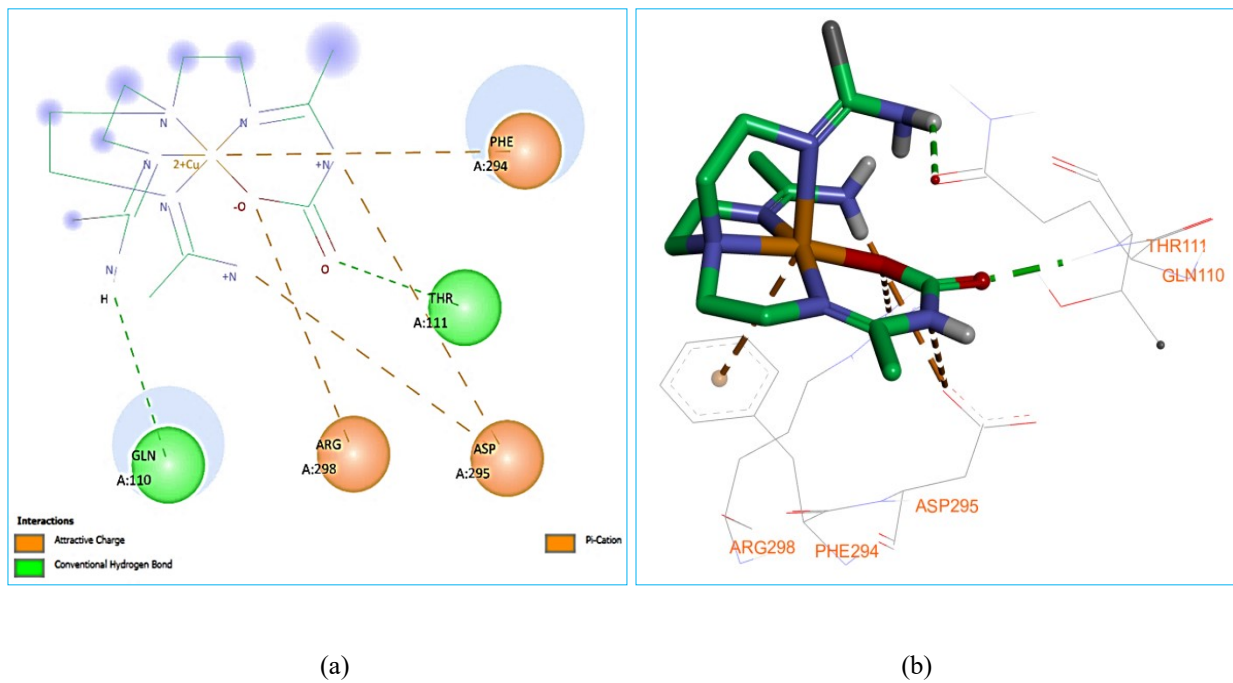
**Figure S2.** Molecular docking 2D (a) and 3D (b) models of CuL–M<sup>pro</sup> interaction (PDB ID: 6LU7) which show the binding sites of the CuL with selected amino acids residues of M<sup>pro</sup>.....3

**Table S1.** Crystal data and structure refinement for CuL, CCDC: 2223417

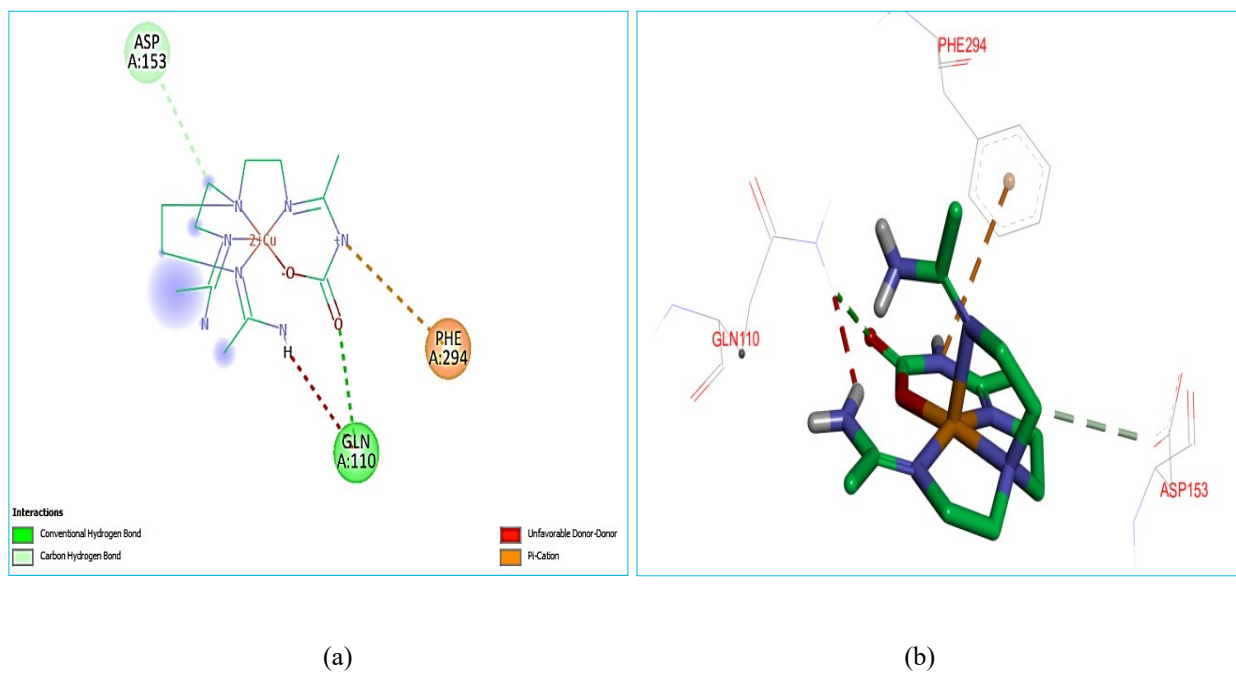
Empirical formula	C <sub>13</sub> H <sub>28</sub> ClCuN <sub>7</sub> O <sub>3</sub>
Formula weight	429.41
Temperature/K	100(1)
Crystal system	triclinic
Space group	P-1
a/Å	8.3648(4)
b/Å	11.0439(6)
c/Å	11.5384(8)
α/°	107.679(6)
β/°	103.872(5)
γ/°	106.779(5)
Volume/Å <sup>3</sup>	907.55(10)
Z	2
ρ <sub>calc</sub> /g/cm <sup>3</sup>	1.571
μ/mm <sup>-1</sup>	1.379
F(000)	450.0
Crystal size/mm <sup>3</sup>	0.335 × 0.226 × 0.038
Radiation	Mo Kα (λ = 0.71073)
2θ range for data collection/°	5.43 to 59.674
Index ranges	-11 ≤ h ≤ 11, -15 ≤ k ≤ 11, -11 ≤ l ≤ 15
Reflections collected	7277
Independent reflections	4481 [Rint = 0.0202, Rsigma = 0.0365]
Data/restraints/parameters	4481/0/233
Goodness-of-fit on F <sup>2</sup>	1.048
Final R indexes [I ≥ 2σ (I)]	R1 = 0.0317, wR2 = 0.0798
Final R indexes [all data]	R1 = 0.0362, wR2 = 0.0826
Largest diff. peak/hole / e Å <sup>-3</sup>	0.56/-0.50

**Table S2.** Selected bond Angles (°) and bond Lengths (Å) of CuL

Bond angles		Bond lengths	
O1—Cu1—N1	172.05(6)	Cu1—O1	1.9525(14)
O1—Cu1—N2	89.69(6)	Cu1—N1	2.0205(16)
O1—Cu1—N3	98.00(6)	Cu1—N2	1.9609(17)
O1—Cu1—N4	103.89(6)	Cu1—N3	2.0033(17)
N1—Cu1—N4	83.44(6)	Cu1—N4	2.2605(17)
N2—Cu1—N1	85.54(7)		
N2—Cu1—N3	161.17(7)		
N2—Cu1—N4	103.75(7)		
N3—Cu1—N1	84.75(7)		
N3—Cu1—N4	91.11(7)		



**Fig. S1.** Molecular docking 2D (a) and 3D (b) models of CuL–M<sup>pro</sup> interaction (PDB ID: 7C8U) which show the binding sites of the CuL with selected amino acids residues of M<sup>pro</sup>.



**Fig. S2.** Molecular docking 2D (a) and 3D (b) models of CuL–M<sup>pro</sup> interaction (PDB ID: 6LU7) which show the binding sites of the CuL with selected amino acids residues of M<sup>pro</sup>.