

Synthesis, X-ray Crystal Structure and Antimicrobial activity of unexpected trinuclear Cu(II) complex from *s*-triazine-Based Di-compartmental Ligand *via* self-assembly

Saied M. Soliman^a, Jamal Lasri^b, Matti Haukka, Essam N. Sholkamy, Hessa H. Al-Rasheed^c, Ayman El-Faham^d

Table of Content

S1	X-ray Structure Determination
Figure S1	Growth inhibition images of target pathogenic microbes with the Cu(II) complex (1) and H ₂ L (2), negative control DMSO alone (C), positive control, Gentamicin
Figure S2	Photography images of inhibition of pathogenic microbe's growth at different concentrations of synthetic compounds to determine their MIC and MBC; the Cu(II) complex (1) and H ₂ L (2).
Table S1	AIM Topological parameters (a.u.) of the Cu-N, Cu-Cl and Cu-O interactions.

S1- X-ray Structure Determination

The crystal of $[\text{Cu}_3(\text{HL})(\text{Cl})_2(\text{NO}_3)(\text{H}_2\text{O})_5](\text{NO}_3)_2$ (**1**) was immersed in cryo-oil, mounted in a MiTeGen loop and measured at 120 K on a Rigaku Oxford Diffraction Supernova diffractometer using Mo $K\alpha$ ($\lambda = 0.71073 \text{ \AA}$) radiation. The CrysAlisPro [16] program package was used for cell refinement and data reduction. Multi-scan absorption correction (*CrysAlisPro* [16]) was applied to the intensities before structure solution. The structure was solved by intrinsic phasing method using the *SHELXT* [17] software. Structural refinement was carried out using *SHELXL-2017* [17] program and *Olex2* [18] graphical user interface. The NH hydrogen atom was located from the difference Fourier map and refined isotropically. The H₂O hydrogen atoms were also located from the difference Fourier map but constrained to ride on their parent oxygen with $U_{\text{iso}} = 1.5 U_{\text{eq}}(\text{parent atom})$. Other hydrogen atoms were positioned geometrically and constrained to ride on their parent atoms, with C-H = 0.95-0.98 \AA and $U_{\text{iso}} = 1.2-1.5 U_{\text{eq}}(\text{parent atom})$. The crystallographic details are summarized in Table 1.

Figure S1 Growth inhibition images of target pathogenic microbes with the Cu(II) complex (1) and H₂L (2), negative control DMSO alone (C), positive control, Gentamicin.

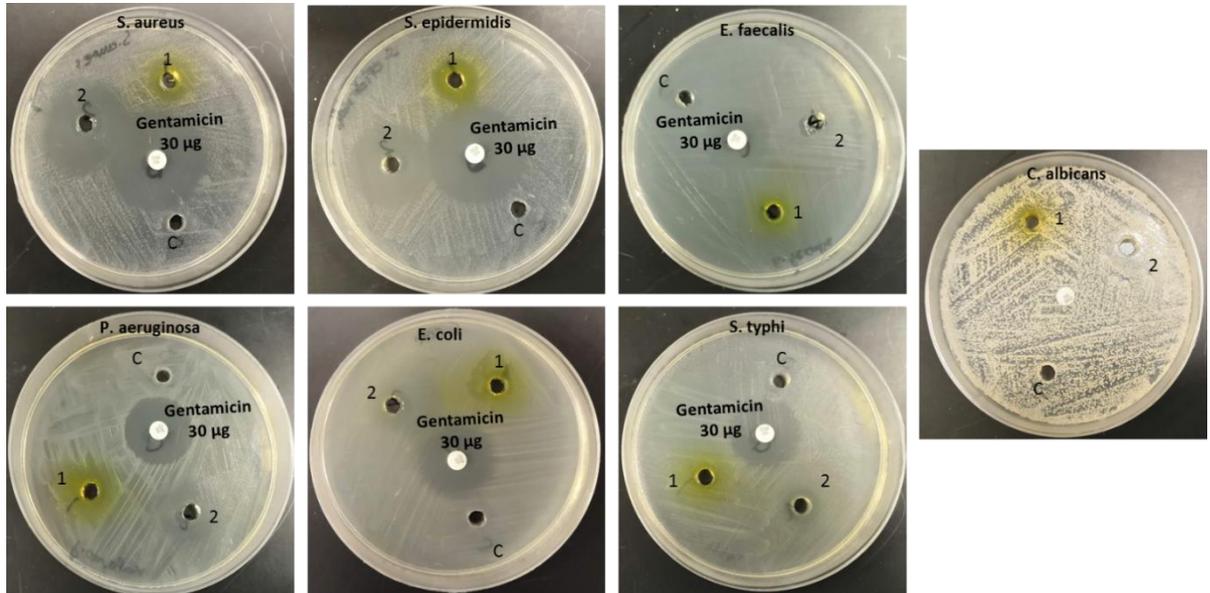


Figure S2 Photography images of inhibition of pathogenic microbe's growth at different concentrations of synthetic compounds to determine their MIC and MBC; the Cu(II) complex (1) and H₂L (2).

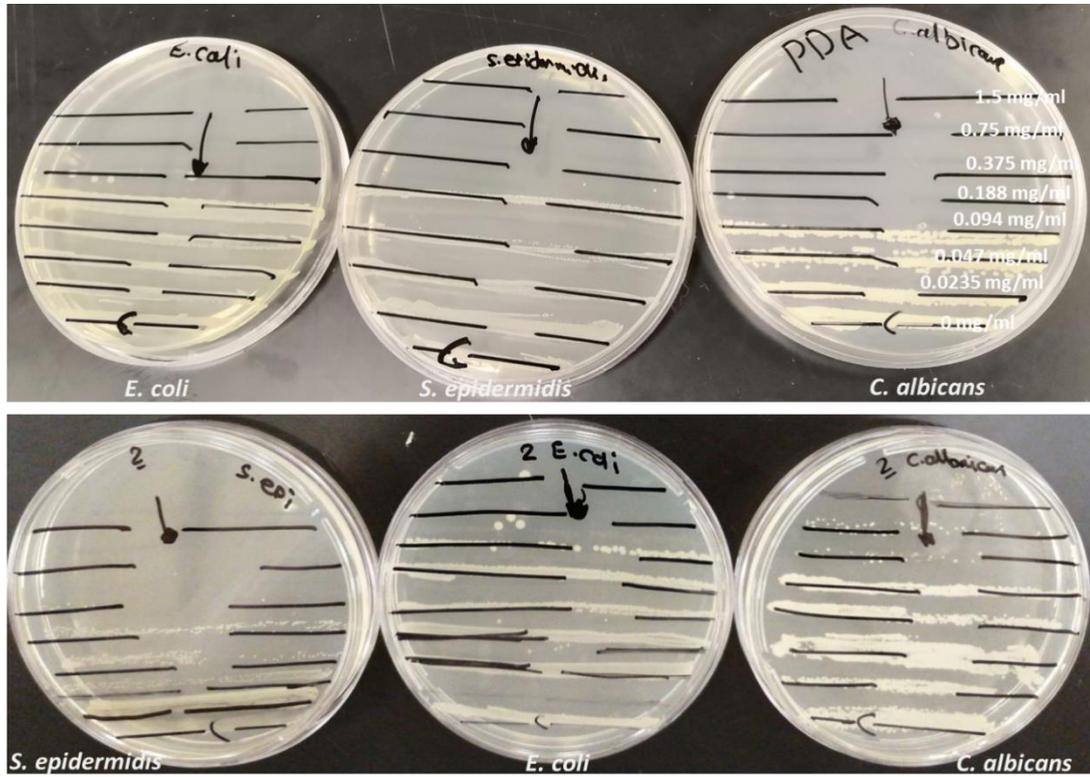


Table S1 AIM Topological parameters (a.u.) of the Cu-N, Cu-Cl and Cu-O interactions.

Bond	$\rho(\mathbf{r})$	$G(\mathbf{r})$	$V(\mathbf{r})$	$H(\mathbf{r})$	$V(\mathbf{r})/G(\mathbf{r})$	$E_{\text{int}}^{\text{a}}$
Cu1-Cl1	0.0773	0.0745	-0.0979	-0.0234	1.31	30.70
Cu1-O1	0.0373	0.0469	-0.0476	-0.0008	1.02	14.95
Cu1-N1	0.0789	0.0989	-0.1194	-0.0205	1.21	37.46
Cu1-N2	0.0927	0.1310	-0.1582	-0.0272	1.21	49.64
Cu1-N6	0.0739	0.0917	-0.1096	-0.0179	1.20	34.37
Cu2-Cl2	0.0774	0.0822	-0.1058	-0.0236	1.29	33.20
Cu2-O3	0.0317	0.0369	-0.0366	0.0003	0.99	11.49
Cu2-N9	0.0863	0.1087	-0.1333	-0.0246	1.23	41.82
Cu2-N8	0.0954	0.1264	-0.1563	-0.0299	1.24	49.04
Cu2-N4	0.0785	0.1029	-0.1229	-0.0200	1.19	38.56
Cu3-N7	0.0841	0.1106	-0.1337	-0.0231	1.21	41.95
Cu3-O7	0.0398	0.0470	-0.0492	-0.0022	1.05	15.42
Cu3-O6	0.0804	0.1234	-0.1424	-0.0190	1.15	44.67
Cu3-O5	0.0796	0.1302	-0.1478	-0.0176	1.13	46.38
Cu3-O4	0.0858	0.1247	-0.1466	-0.0219	1.18	45.99

^akcal/mol