

Electronic Supplementary Information

Two-dimensional (6,3) networks obtained with the $\{\text{Cu}_3(\text{Hmesox})_3\}^{3-}$ secondary building unit. (H_4mesox = mesoxalic acid)

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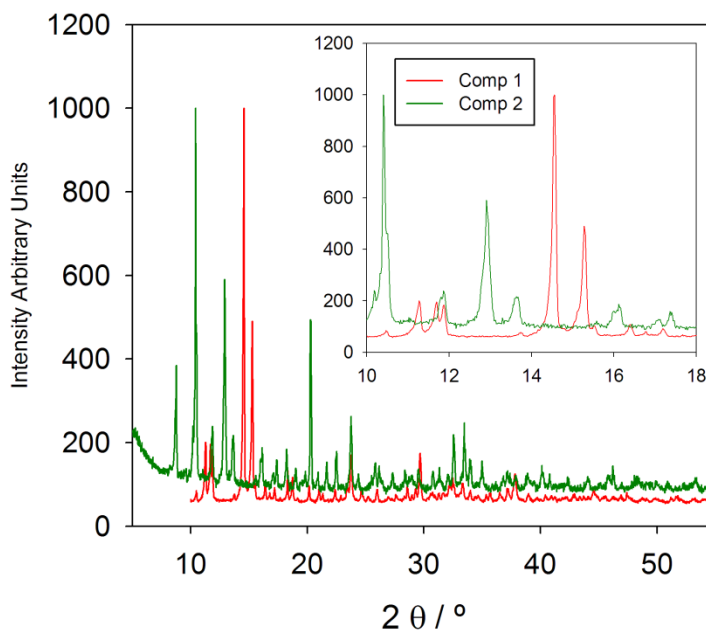


Fig. S1 X-Ray powder diffraction patterns of polycrystalline samples of compounds **1** and **2**. The insert show the same patterns but in the 10° to 18° range.

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Purity of the compounds

The X-Ray powder diffraction patterns of polycrystalline samples of compounds $[\text{La}(\text{H}_2\text{O})_3\text{Cu}_3(\text{Hmesox})_3(\text{H}_2\text{O})_5] \cdot 8\text{H}_2\text{O}$ (**1**) and $[\text{La}(\text{H}_2\text{O})_2\text{Cu}_3(\text{Hmesox})_3(\text{H}_2\text{O})_3] \cdot 7\text{H}_2\text{O}$ (**2**) are shown in Fig S1. Both compounds display very different patterns. The insert shows the spectra between 10° and 18° , it can be seen that the spectra of both compounds do not display coincidences, thus the intense peak shown by compound **2** at 13° is not observed in the polycrystalline sample of **1** and the intense peak observed at 14.5° for a polycrystalline sample of **1** is not observed in the pattern of that of **2**, so we can conclude that the samples are not contaminated one by the other.

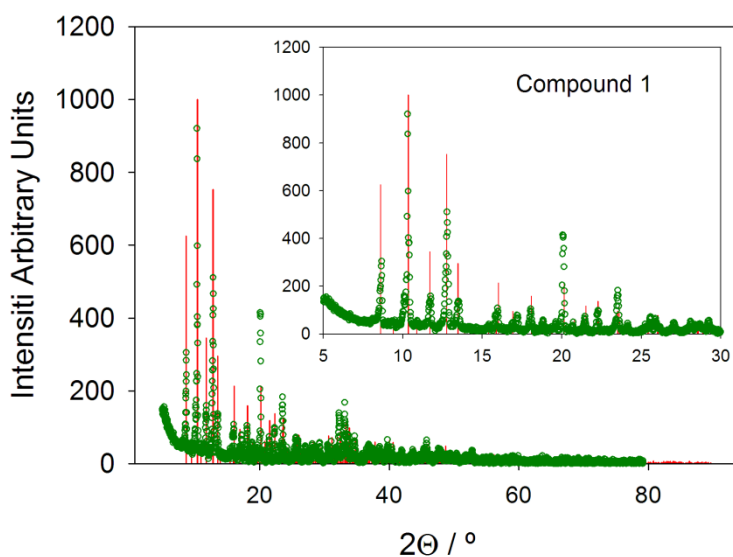


Fig. S2 Simulated (red lines) and the experimental (green dots) powder diffraction patterns for compound **1**. The simulation is performed with the DIAMOND¹ program from the .cif file obtained by the X-ray diffraction of a single crystal of **1**.

Figure S2 shows the simulated and the experimental powder diffraction patterns for compound **1**. The simulated spectrum has been generated with the Diamond program from the .cif file. It can be observed that the experimental spectrum matches very well the simulation. Similarly the simulated and the experimental powder diffraction patterns for compound **2** are shown in **Figure S3**. Also the simulated and the experimental spectra have a very good matching. So the polycrystalline samples correspond to the single crystals.

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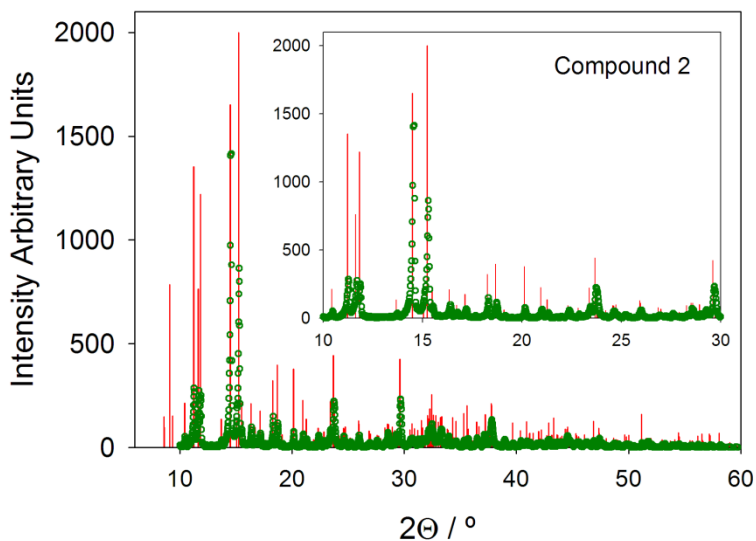


Fig. S3 Simulated (red lines) and the experimental (green dots) powder diffraction patterns for compound **2**. The simulation is performed with the DIAMOND¹ program from the .cif file obtained by the X-ray diffraction of a single crystal of **2**.

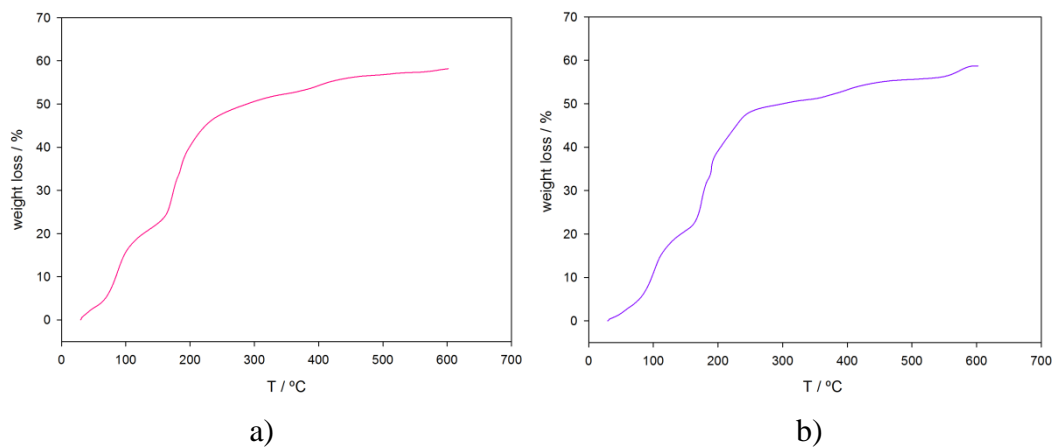


Fig. S4 TGA curves for **1** (a) and **2** (b). The sample were heated to 600 °C at the heating rate of 5 °C /min

TG measurements

Compound **1** in a first step, from room temperature to 140°C, exhibits a weight loss of a ca. 23.3% consistent with the loss of thirteen crystallization water molecules, the eight crystallization water molecules and five weakly bound coordination water molecules. Then at temperatures above 180°C the degradation of the organic ligand takes place.

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In a first step, from room temperature to 120°C, compound **2** shows a weight loss of a ca. 19.1%, consistent with the loss of ten water molecules which correspond to the seven crystallization water molecules and three weakly bound coordination water molecules. Then at temperatures above 180°C the degradation of the organic ligand takes place.

References

1. K. Brandenburg, in *Diamond (Version 3.2c), Crystal and Molecular Structure Visualization*, Crystal Impact - K. Brandenburg & H. Putz Gbr Bonn (Germany); <http://www.Crystalimpact.com/diamond>, 2009.