Supporting Information

Figure S1. Le Bail fit (R_{wp} = 9.98%) between the reflection PXRD data of **1** with a model consisting of the cell parameters derived from the single crystal structure (a = 9.5670, b = 20.5293, c = 17.6775 Å). Black dots indicate raw data, while the red line indicates the calculated model. Tick marks (green) are the 2θ positions for the *hkl* reflections. The difference pattern is shown at the bottom.

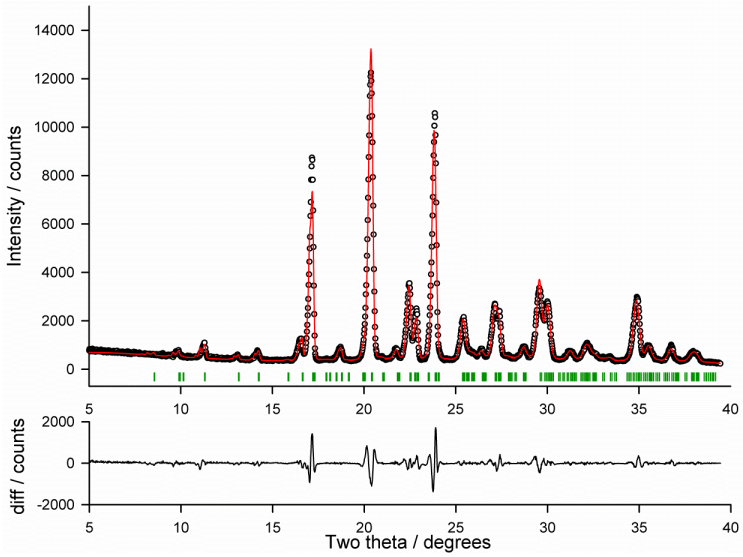

Figure S2. Le Bail fit (R_{wp} = 16.24%) between the reflection PXRD data of **3b** with a model consisting of the cell parameters derived from the single crystal structure (a = 16.0291, b = 7.5748, c = 11.5224 Å). Black dots indicate raw data, while the red line indicates the calculated model. Tick marks (green) are the 2θ positions for the *hkl* reflections. The difference pattern is shown at the bottom.