Supplementary information, Table S1 Data collection and refinement statistics

	MOF$_{HAT}$-MSL1$_{MBM}$
Data collection	
Space group	$P2_1$
Cell dimensions	
-a, b, c (Å)	64.801, 111.518, 66.751
-α, β, γ (°)	90.00, 111.05, 90.00
Resolution (Å) (high-resolution shell)	50-2.05 (2.12-2.05)
R_{merge} (%) (high-resolution shell)	6.2 (30.6)
I/σ (high-resolution shell)	21.52 (3.13)
Completeness (%) (high-resolution shell)	97.9 (87.1)
Redundancy (high-resolution shell)	4.3 (3.1)
Refinement	
Resolution (Å)	50-2.05
Number of reflections	54319
R_{work} / R_{free} (%)	20.82/24.82
Number of atoms	
-Proteins	5299
-Water	150
-Zn	2
B-factors	
-protein	40.169
-water	34.783
-Zn	38.605
Rms deviations	
-Bond lengths (Å)	0.009
-Bond angles (°)	1.290