Electronic Supplementary Material (ESI) for

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pH-modulated luminescence switching in a Eu-MOF: rapid detention of acidic amino acids

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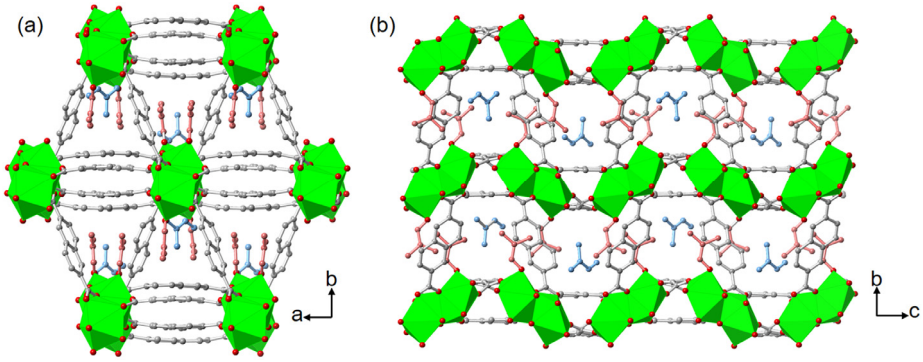

Fig. S1 3D structures of Eu-MOF (**1**) along *c* axis (a) and *a* axis (b) of the as-synthesized framework. The red balls represent the coordinated DMF molecules and the blue ones are the non-coordinated DMF molecules.

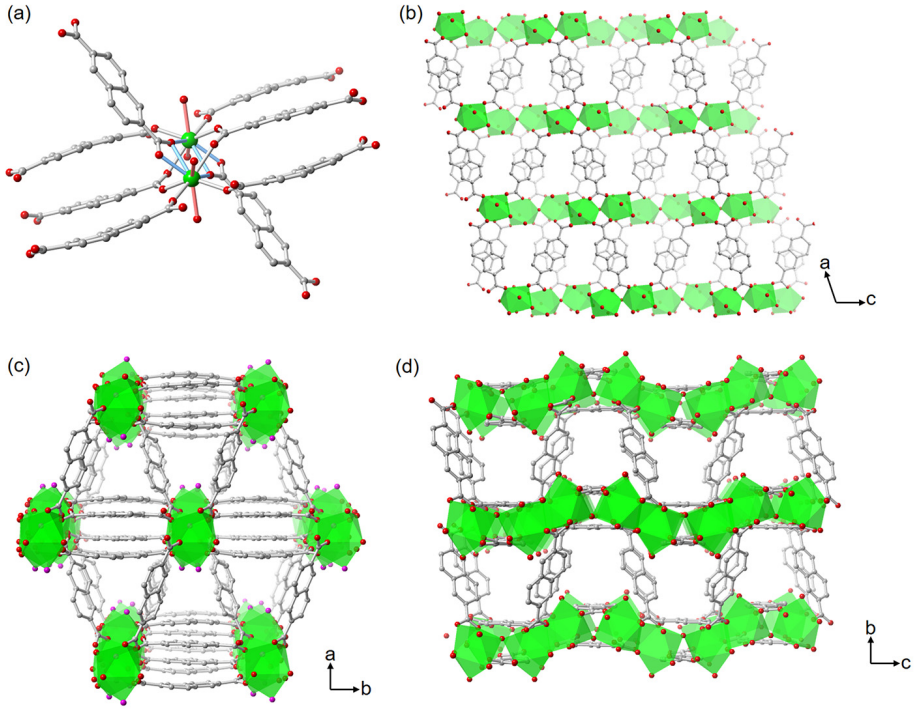

Fig. S2 (a) Coordination environments of a pair of Eu ions; (b) a packed 2D layers along *b* axis; and perspective view of the channels along *c* axis (c) and *a* axis (d) of **2** after the detection experiment. The hydrogen atoms are omitted for clarity. The red balls represent the bridging and terminal water molecules.

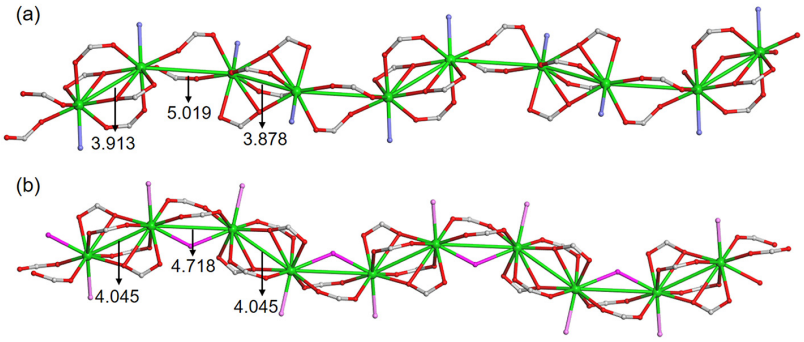

Fig. S3 The Eu chains along *c* axis before (a) and after (b) detection experiment. The numbers represent the distances between Eu ions in Å.

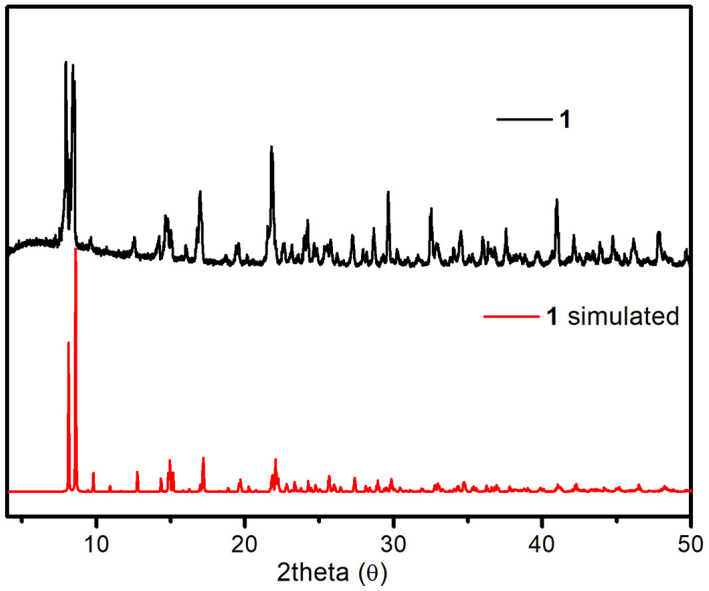

Fig. S4 Simulated and experimental powder X-ray diffraction patterns (PXRD) of the as-synthesized **1**.

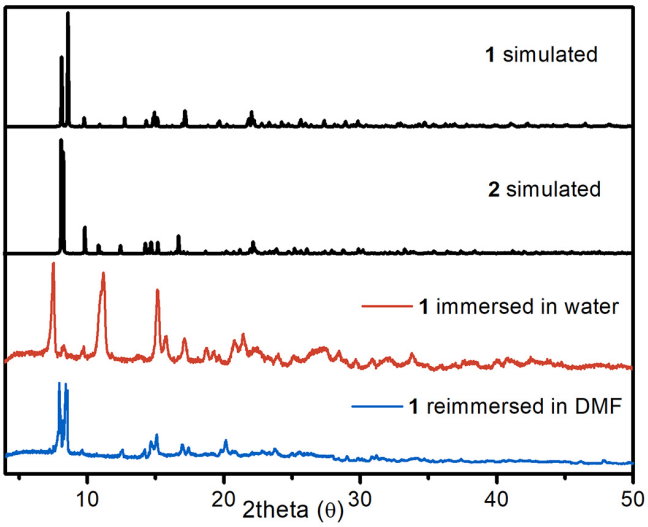

Fig. S5 PXRD patterns of the simulated patterns of **1** and **2**, **1** immersed in water, and **1** reimmersed in DMF solvents.

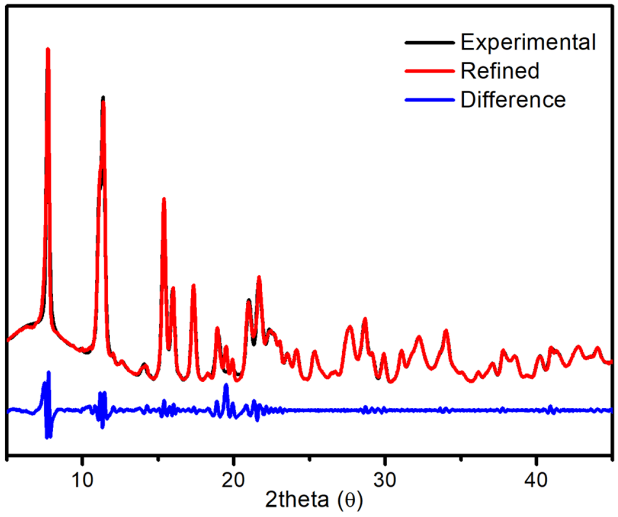

Fig. S6 Pawley refinement of PXRD patterns of **1** immersed in water. Experimental (balck line), refined (red line) and the difference (below) patterns of **1** immersed in water.

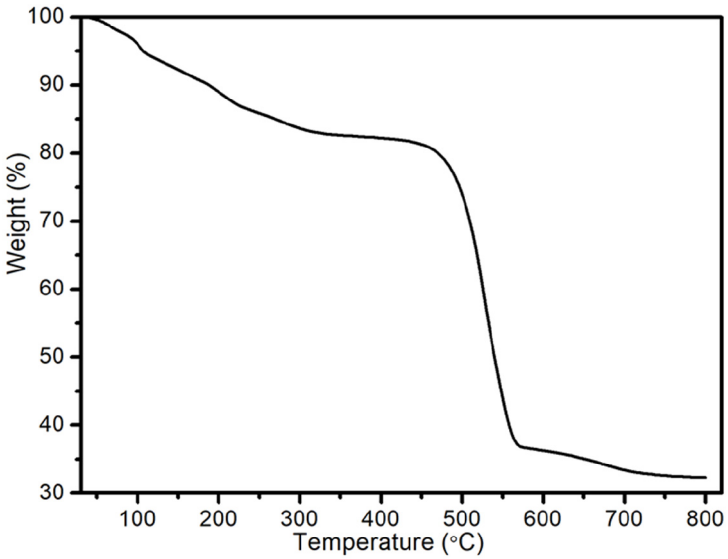

Fig. S7 The TG curve of **1** in a N_2 flow from 40 °C to 800 °C.

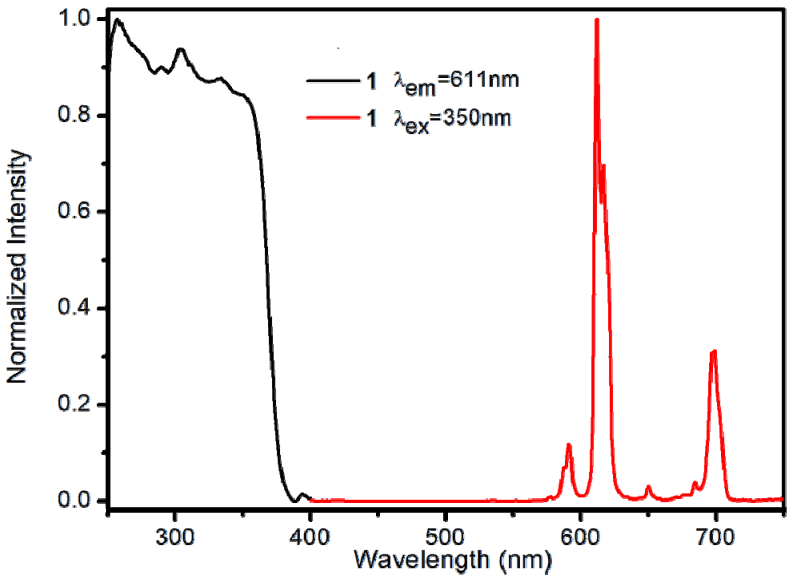

Fig. S8 The excitation (black line) and emission spectra (red line) of **1** in the solid state.

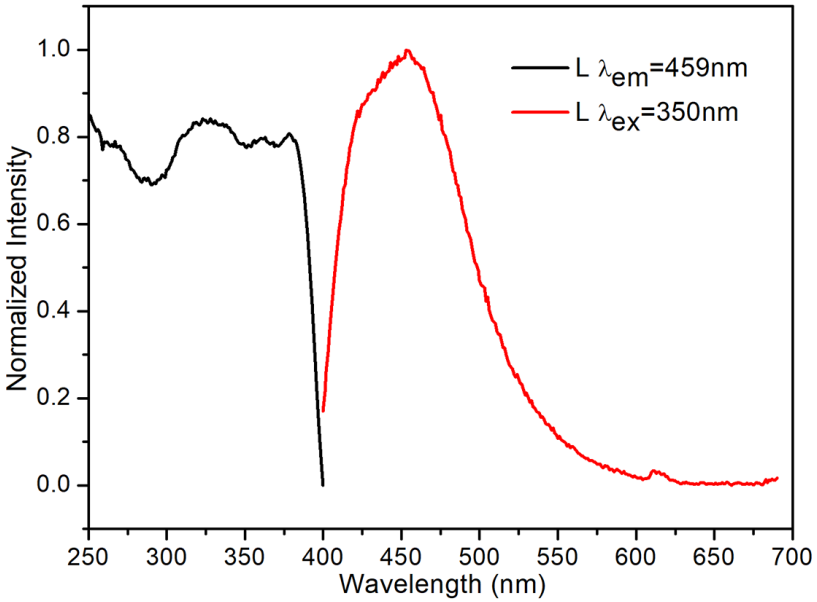

Fig. S9 The excitation (black line) and emission spectra (red line) of ligands H_2NDC in the solid state.

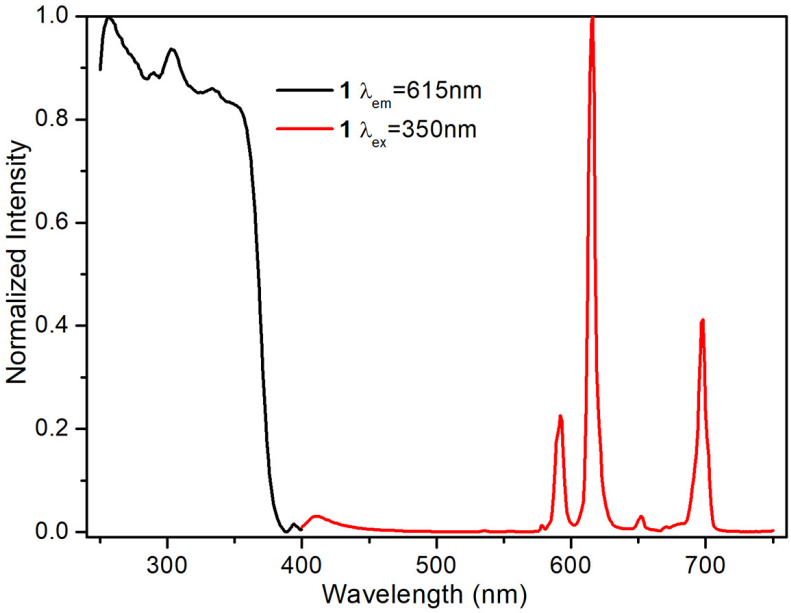

Fig. S10 The excitation (black line) and emission spectra (red line) of **1** dispersed in water (pH 7).

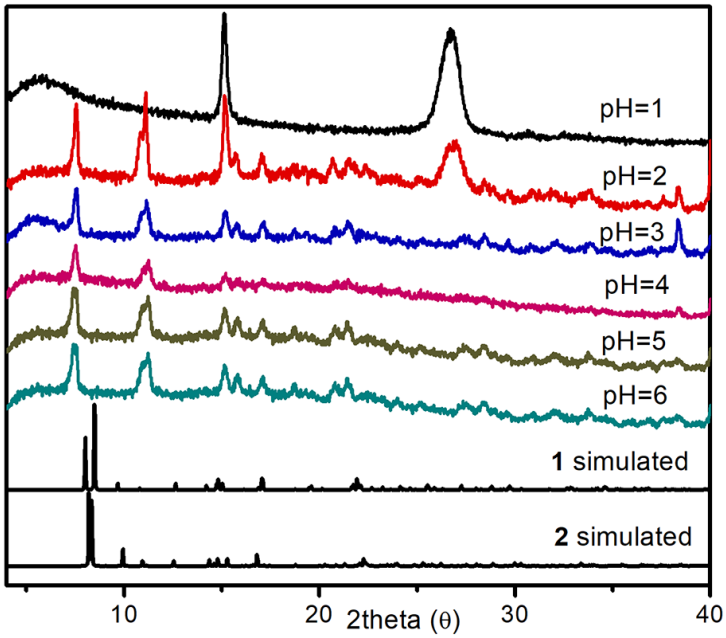

Fig. S11 PXRD patterns of **1** after treated with HCl solutions at different pH (1 to 6) for 24 hrs and the simulated patterns of **1** and **2**.

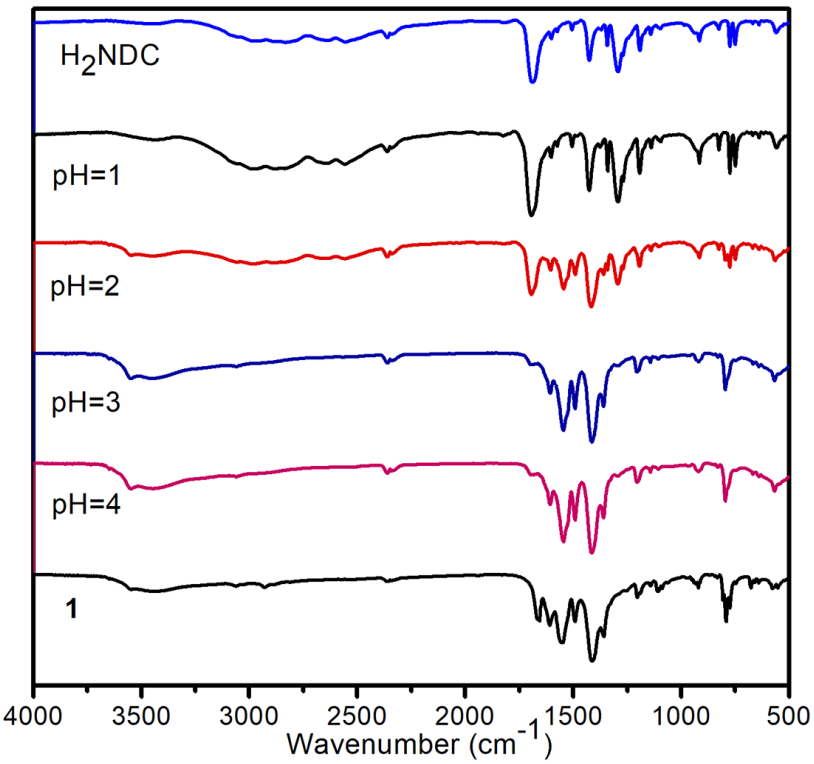

Fig. S12 IR spectra of **1**, the HCl-treated **1** (immersed in HCl solutions with pH from 1 to 4) and the ligand.

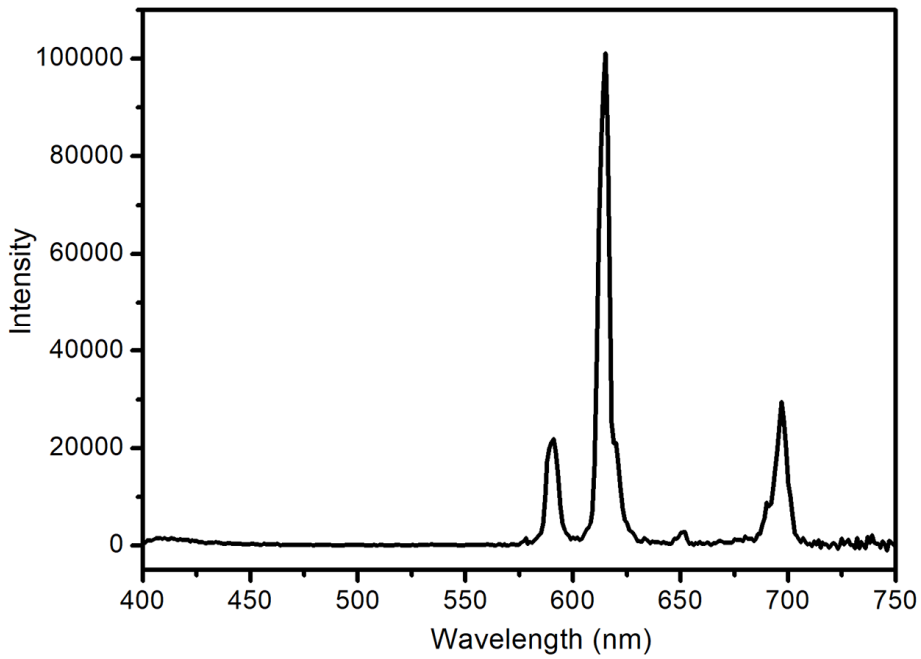

Fig. S13 Emission spectra of **1** after immersed in water for half a year.

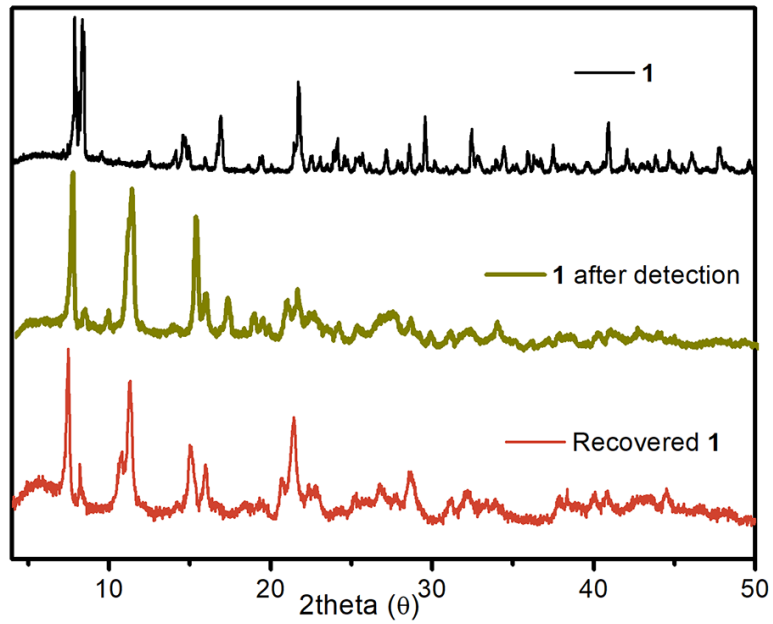

Fig. S14 PXRD patterns of as-synthesized 1, 1 after detection experiment, and 1 immersed in ethanol.

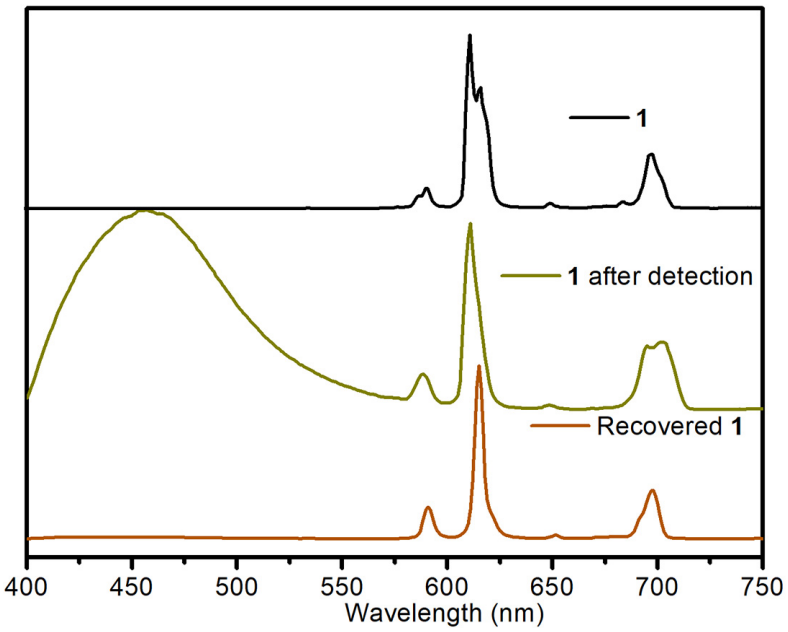

Fig. S15 Solid state emission spectra of **1**, **1** after detection experiment, and recovered **1** (immersed into ethanol and filtered).

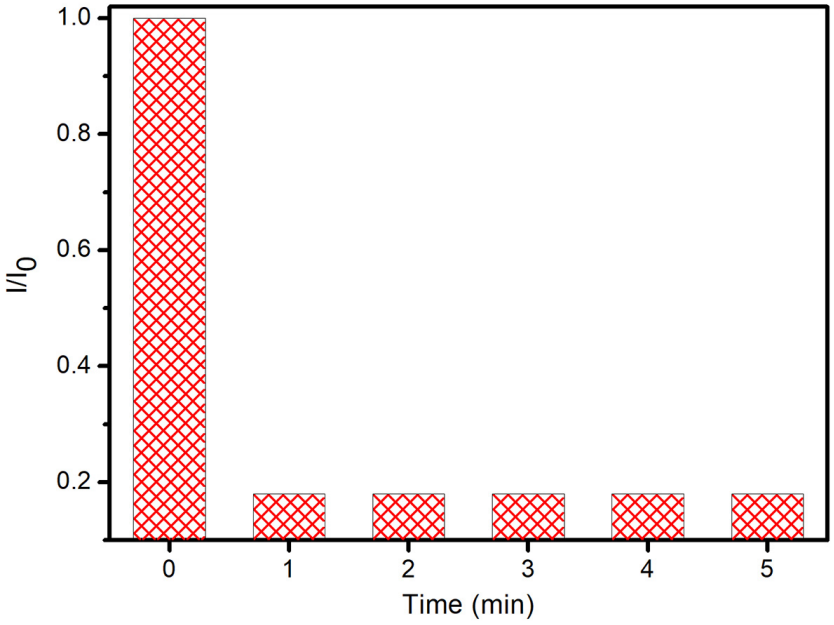

Fig. S16 Quenching efficiency of emission at 615 nm for **1** as a function of time when immersed in HCl solution (pH = 3.2).

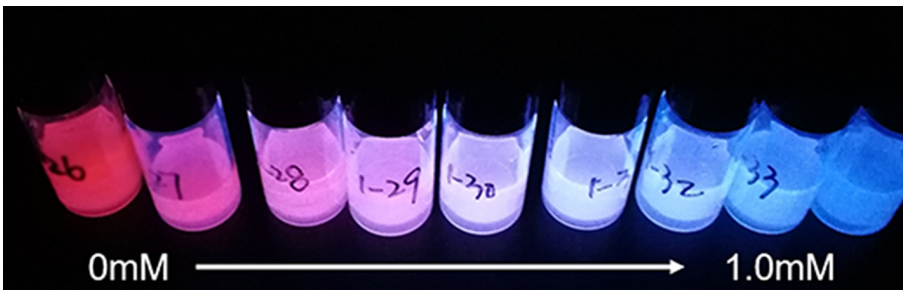

Fig. S17 The photographs of **1** in aqueous Asp solutions with different concentrations under the irradiation of 365 nm UV light.

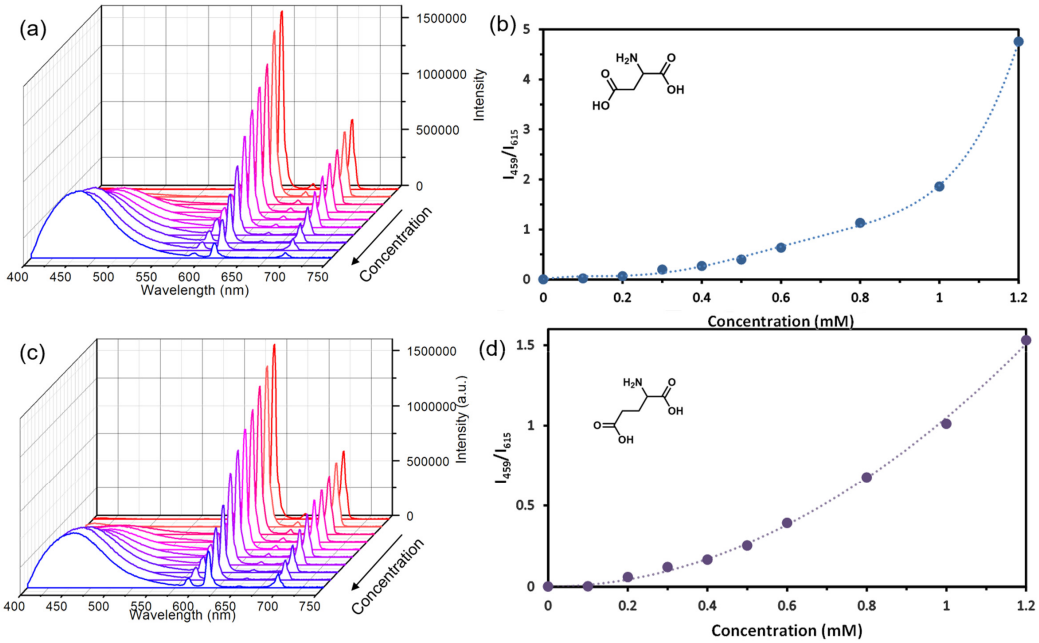

Fig. S18 The emission spectra of **1** in aqueous Asp solutions at different concentrations (a, b) and Glu (c, d) and the corresponding plots of the relative intensity I_{459}/I_{615} and the concentration.

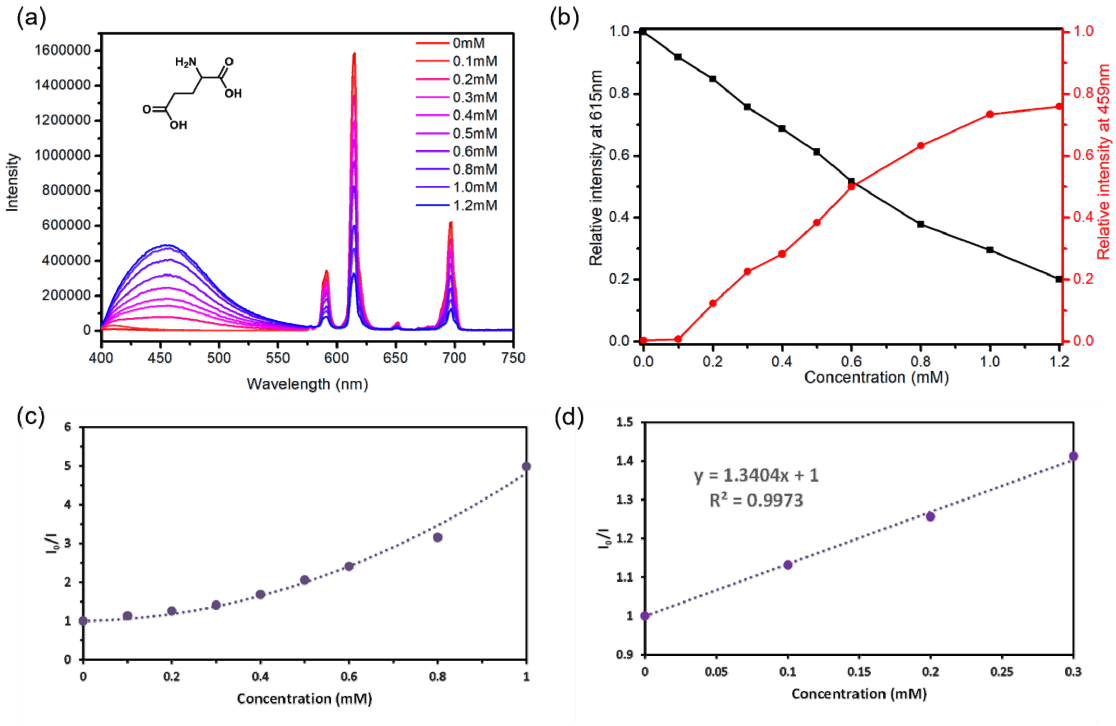

Fig. S19 Emission spectra of **1** in aqueous solutions of Glu at different concentrations; (b) the corresponding plot of the relative intensity at 615 nm and 459 nm as a function of concentrations. The relative intensity at 615 nm is calculated by I/I_0 (I_0 is the peak intensity at 615 nm of the as-synthesized sample). The relative intensity at 459 nm is calculated by $I/I_{3.00}$ ($I_{3.00}$ is the peak intensity at 459 nm of the HCl-treated samples at pH 3.00). (c) S-V plot of **1** in Glu and (d) the corresponding linear fitting at low concentrations.

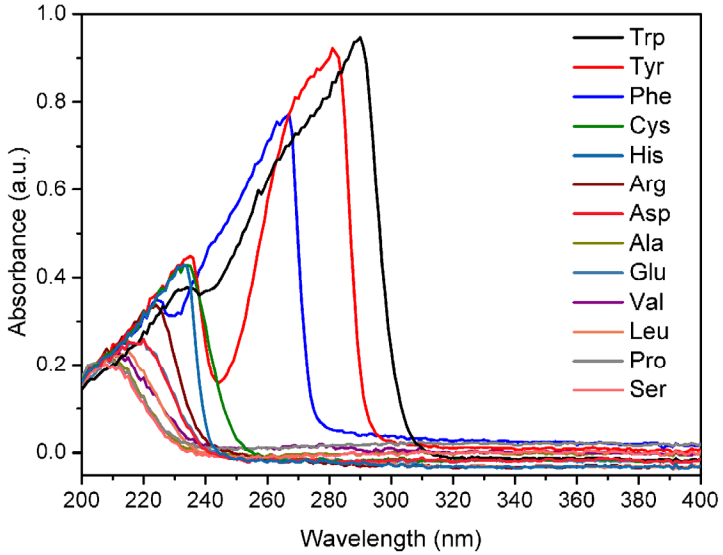

Fig. S20 UV-vis absorption spectra of various amino acids.

Table S1. Crystal data and structure refinement parameters for **1** and **2**.

Compound	**Eu-MOF (1)**	**Eu-MOF-H_2O (2)**
Empirical fomula	$[Eu_2(NDC)_3(DMF)_2]\cdot DMF$	$[Eu(H_2O)_{0.5}(NDC)_{1.5}(H_2O)]$
***M*$_r$**	1165.73	998.45
Temperature(K)	149.99(10)	150.01(10)
Crystal size(mm)	0.08×0.06×0.02	0.08×0.05×0.02
Crystal system	Monoclinic	Monoclinic
Space group	$P2_1/n$	$C2/c$
a/Å	11.93700(10)	12.4096(5)
b/Å	21.89300(10)	21.3850(8)
c/Å	16.57120(10)	16.2060(6)
***α*/°**	90	90
***β*/°**	100.5340(10)	103.343(4)
***γ*/°**	90	90
***V*/Å^3**	4257.68(5)	4184.6(3)
Z	4	4
***F*(000)**	2304.0	1936.0
Reflection collected	8885	3450
Independent reflections	7963	4115
GOF on F^2	1.103	1.051
Final R indexes [I>=4σ (I)]	0.0310	0.0509
Final R indexes [all data]	0.0323	0.0575
***w*R$_2$**	0.0932	0.1318
Largest diff. peak and hole (e.Å^{-3})	0.89/-0.95	1.26/-0.77

Table S2. Bond lengths of Eu ions in **1.**

Eu(00)-O(004)	2.2627(17)	Eu(00)-O(003)	2.3329(16)	Eu(00)-O(00C)	2.3680(18)
Eu(00)-O(008)#1	2.3680(17)	Eu(00)-O(00B)#2	2.3798(17)	Eu(00)-O(00G)	2.4319(18)
Eu(00)-O(006)#1	2.4496(18)	Eu(00)-O(003)#1	2.7518(18)		
Eu(1)-O(00A)	2.2636(16)	Eu(1)-O(005)#3	2.3442(16)	Eu(1)-O(007)#4	2.3600(19)
Eu(1)-O(00F)#5	2.3774(16)	Eu(1)-O(009)#6	2.3873(17)	Eu(1)-O(00D)#3	2.4605(18)
Eu(1)-O(00E)	2.4769(18)	Eu(1)-O(005)#7	2.6836(17)		
Eu(00)-Eu(00)#3	3.9127(2)	Eu(00)-Eu(1)#8	5.0192(2)	Eu(1)-Eu(1)#3	3.8776(2)

Symmetry transformations used to generate equivalent atoms:

#1 -x,-y+1,-z+1 #2 x-1,y,z #3 -x+1/2,y+1/2,-z+1/2 #4 x,y,z-1 #5 x+1,y,z

#6 –x+2.-y+1,-z+1 #7 x+1/2,-y+1/2,z-1/2 #8 x-1,y,z

Table S3. Bond lengths of Eu ions in **2**.

Eu(01)-O(6)	2.310(5)	Eu(01)-O(2)	2.350(5)	Eu(01)-O(3)	2.366(5)
Eu(01)-O(7)#1	2.367(5)	Eu(01)-O(5)#2	2.428(5)	Eu(01)-O(4)#2	2.471(5)
Eu(01)-O(8)	2.508(7)	Eu(01)-O(1)	2.592 (3)	Eu(01)-O(2)#2	2.750 (5)
Eu(01)-Eu(01)#2	4.0447(7)	Eu(01)-Eu(01)#1	4.7181(7)		

Symmetry transformations used to generate equivalent atoms:

#1 –x+1,y,-z+1/2 #2 –x+1,-y+1,-z+1

Table S4. Crystal data and Pawley refinement parameters for **1** immersed in water.

Compound	**1 immersed in water**
Temperature(K)	293
Space group	$P2_1/n$
a/Å	11.08325(7)
b/Å	22.61446(6)
c/Å	16.47657(9)
***α*/°**	90
***β*/°**	95.255(01)
***γ*/°**	90
***V*/Å^3**	4112.20(5)
R_{wp}	0.0378
R_{wp}(w/o bck)	0.0677
R_p	0.021

Table S5. The pH values of different concentration of amino acid solution tested by pH meter.

C (mM)	**pH value of Asp solution**	**pH value of Glu solution**
0.05	4.07	4.50
0.1	3.91	4.26
0.2	3.80	4.05
0.3	3.71	3.96
0.4	3.67	3.88
0.5	3.60	3.81
0.6	3.52	3.79
0.8	3.48	3.75
1.0	3.40	3.69
10.0	3.09	3.35