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Supporting Information

Biomimetic Crystallization of $MnFe_2O_4$ Mediated by Peptide-Catalyzed Esterification at Low Temperature

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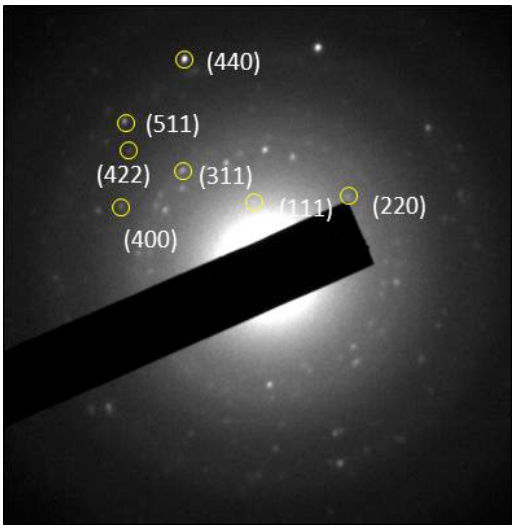
Electron diffraction

Detailed indexation of the selected area electron diffraction pattern in Figure 1-a-inlset in the main text is shown in Supplementary Figure S1.



Supplementary Figure S1. Detailed indexations of the diffraction patterns in Figure 1-a, inset in the main text.

Gas chromatograph-mass spectroscopy (GC-MS)

After 11-day incubation of the CP4 and Mn/Fe precursor solution, the reaction mixture was centrifuged to precipitate the $MnFe_2O_4$/peptide aggregation and supernatant was transferred to new tube. Twice volume of decane was added and the tube was vigorously stirred, centrifuged (18,000x*g*, 15 min) to separate decane and methanol phases, and then decane phase was collected. In this purification step, polar species (acetate ion and Mn/Fe ion) are estimated to remain in methanol/benzyl alcohol phase, and non-polar methyl acetate is expected to move to decane phase. As prepared decane fraction was applied to GC-MS (Varian 4000 GC/MS). GC conditions were set as the following, column: Varian factor four capillary column (30 m x 0.25 mm x 0.25 μm), carrier gas: helium, oven temperature: 40°C, Column Flow: 1.2 mL/min, Injector temperature: 250˚C, Split Ratio - 100:1. The detector on GC was activated from 1.25~1.75 min after the sample injection to prevent the detection of large peaks from decane and its impurities. Characteristic peak was detected at 1.55 min as retention time (Figure 2-(a) in the main text), which matched with standard methyl acetate (Sigma-Aldrich) peak (Figure 2-(b)). MS analysis further confirmed the detection of methyl acetate, supporting the $MnFe_2O_4$ synthesis *via* ester-elimination pathway.