Probing Interactions between Metal−Organic Frameworks and Freestanding Enzymes in a Hollow Structure

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Abstract

It has been reported that the biological functions of enzymes could be altered when they are encapsulated in metal-organic frameworks (MOFs) due to the interfacial interactions between them. Herein, we compared the interfacial interactions of catalase in solid and hollow ZIF-8 microcrystals. The solid sample with confined catalase is prepared through a reported method and the hollow sample is generated by hollowing the MOFs crystal, sealing freestanding enzymes in the central cavities of hollow ZIF-8. The samples were characterized by electron microscopy, powder X-ray diffraction (PXRD), and nitrogen sorption. The hollowing process was monitored by small angle X-ray scattering (SAXS) spectroscopy.[1] The interfacial interactions of the two samples were studied by infrared (IR) and fluorescence spectroscopy. IR study shows that freestanding catalase has less chemical interaction with ZIF-8 than confined catalase, and fluorescence study indicates that the freestanding catalase has lower structural confinement. We have then compared the hydrogen peroxide degradation activities of confined and freestanding catalase and revealed that the freestanding catalase in hollow ZIF-8 has higher activity. This discovery implies that reducing interfacial interactions could lead to a higher biological activity.[2]

Keywords: metal-organic frameworks, hollowing process, small angle X-ray scattering, freestanding protein

References

[1]H.-C. Yang *et al.*, "Homology Modeling and Molecular Dynamics Simulation Combined with X-ray Solution Scattering Defining Protein Structures of Thromboxane and Prostacyclin Synthases," *The Journal of Physical Chemistry B,* vol. 121, no. 50, pp. 11229-11240, December 2017.

[2]S.-Y. Chen *et al.*, "Probing Interactions between Metal–Organic Frameworks and Freestanding Enzymes in a Hollow Structure," *Nano Letters,* vol. 20, no. 9, pp. 6630-6635, September 2020.