

Supporting Information for

**Bilirubin oxidase adsorption onto charged self-assembled  
monolayers: Insights from multiscale simulations**

Shengjiang Yang<sup>a</sup>, Jie Liu<sup>b</sup>, Xuebo Quan<sup>a</sup>, Jian Zhou<sup>a\*</sup>

<sup>a</sup> School of Chemistry and Chemical Engineering, Guangdong Provincial Key Lab for  
Green Chemical Product Technology, South China University of Technology,  
Guangzhou 510640, P. R. China

<sup>b</sup> Key Laboratory for Green Chemical Process of Ministry of Education, School of  
Chemical Engineering and Pharmacy, Wuhan Institute of Technology, Wuhan 430073,  
P. R. China

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\* Corresponding author

Tel./fax: +86 20 87114069

E-mail address: jianzhou@scut.edu.cn

**Table S1.** The key adsorption residues of MvBOx adsorbed on charged surfaces.

system	The main adsorption residues
MvBOx on HOOC-SAM (7%)	Thr348, Gln351, Arg353, Arg356, Thr357, Gly358, Gly365, Asn394, Gly415, Asn416, Arg437
MvBOx on HOOC-SAM (25%)	Arg353, Arg356, Thr357, Gly358, Asn364, Gly365, Val366, Asp370, Gln372, Asn373, Asn394, Arg437
MvBOx on NH <sub>2</sub> -SAM (7%)	Val13, Pro14, Gln22, Thr47, Gln49, Pro52, Asp53, Gly55, Ser56, Phe213, Asn215, Asp322, Asp323, Thr325, Gln505, Ala506, Gln507, Ser508, Val513, Gln514
MvBOx on NH <sub>2</sub> -SAM (25%)	Pro14, Gln22, Pro52, Asp53, Phe172, Asp322, Asp323, Thr324, Thr325, Gln505, Ala506, Gln507

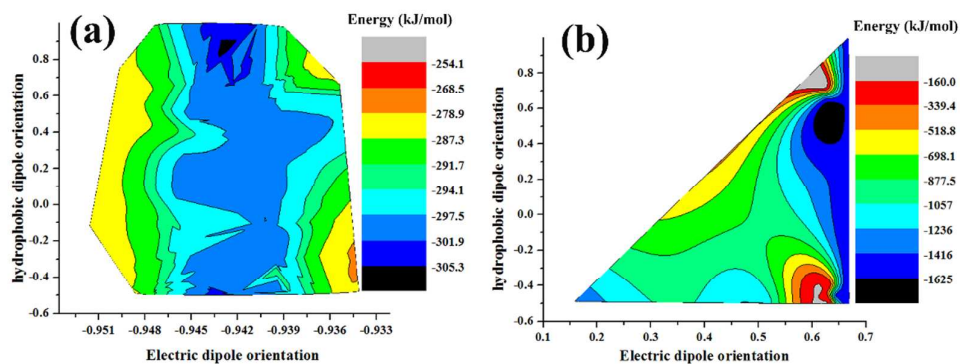
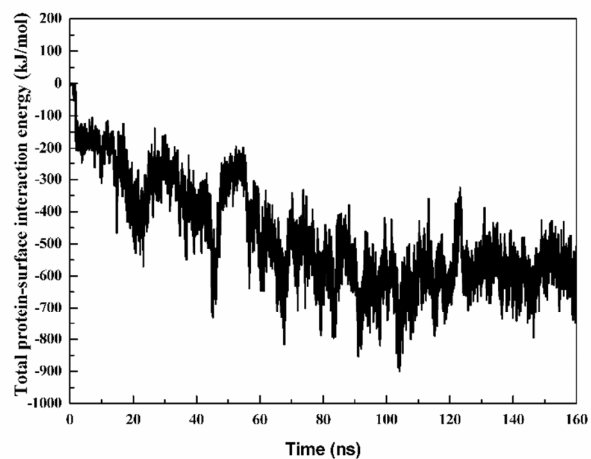
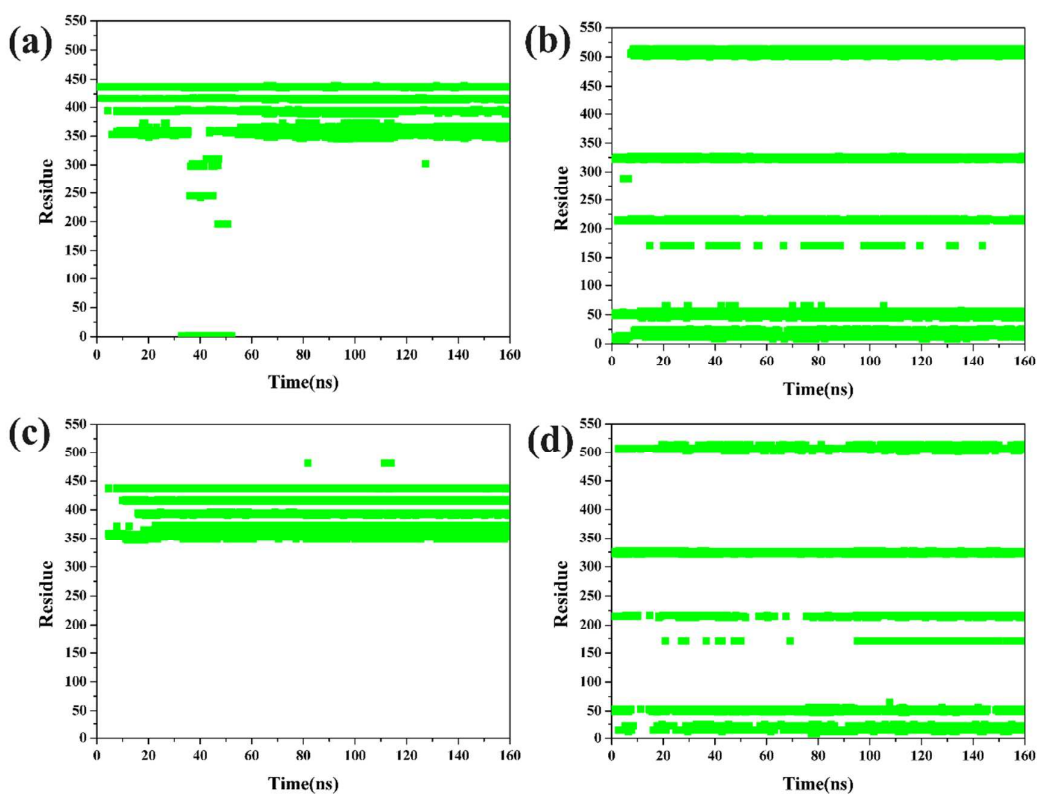


Figure S1 Interaction energies versus electric dipole and hydrophobic dipole of MvBOx in PTMC sampling. (a) MvBOx on the positively charged surface; (b) MvBOx on the negatively charged surface.

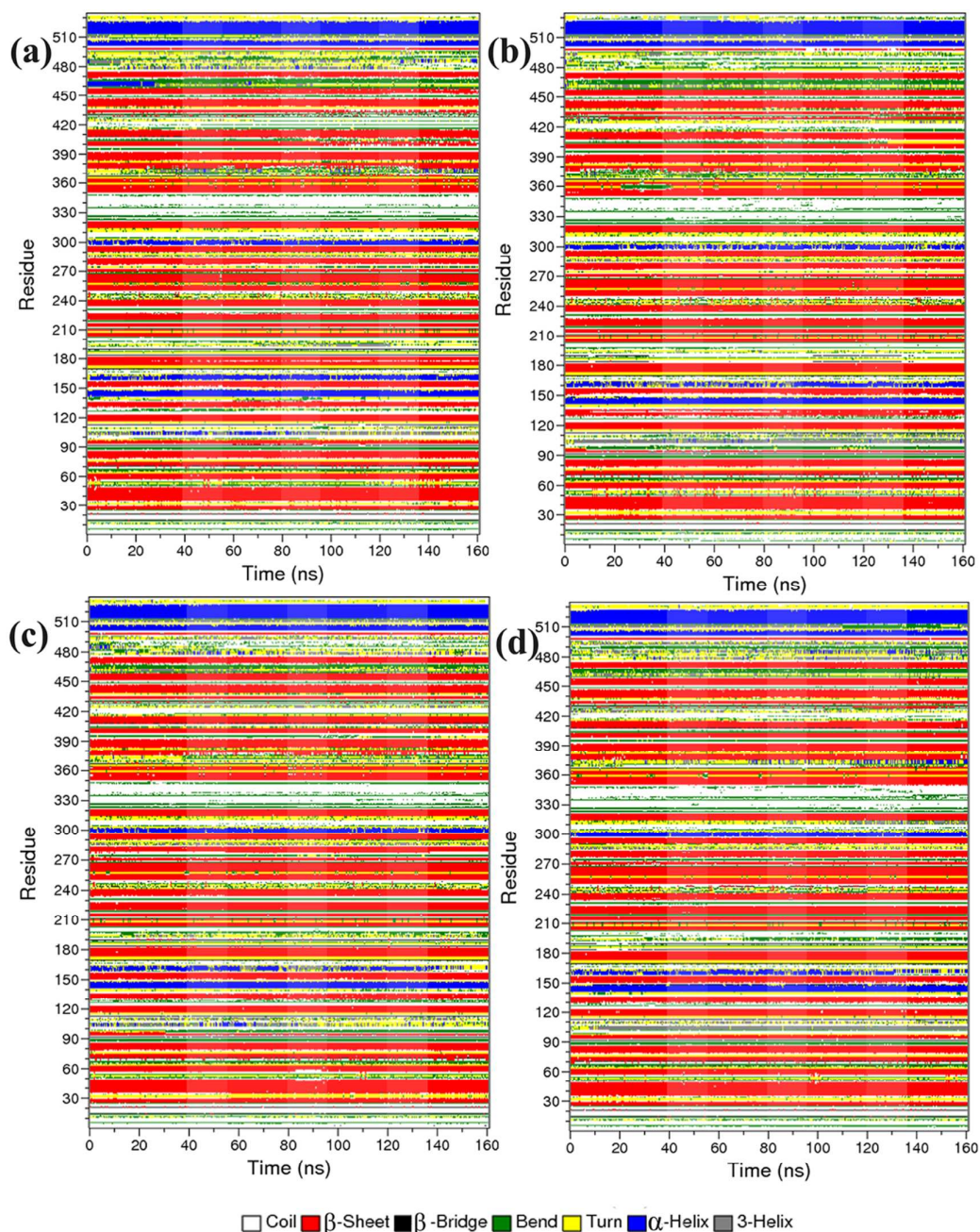


**Figure S2.** The time evolution of total protein-surface interaction energy during the MD simulation



**Figure S3.** Contact maps between MvBOx and charged SAMs during simulations: (a) 7% dissociated COOH-SAM; (b) 7% dissociated  $\text{NH}_2$ -SAM; (c) 25% dissociated COOH-SAM; (d) 25%

dissociated  $\text{NH}_2$ -SAM.



**Figure S4.** Time evolution of the secondary structures of MvBOx adsorbed on different charged surfaces: (a) on 7% dissociated  $\text{COOH}$ -SAM; (b) on 7% dissociated  $\text{NH}_2$ -SAM; (c) on 25% dissociated  $\text{COOH}$ -SAM; (d) on 25% dissociated  $\text{NH}_2$ -SAM.

