Electronic Supplementary Material (ESI) for Physical Chemistry Chemical Physics.

Supporting Information

Atomistic insight into the binding mode and self-regulation mechanism of *Is*PETase towards PET substrates with different polymerization degree

Linyu Chen,[a] Fangfang Fan,[*ab] Meiyuan Yang,[a] Linquan Wang,[a] Yushuo Bai, [a] Shuai Qiu,[a] Changjiang Lyu,[a] Jun Huang[*a]

[a]Key Laboratory of Chemical and Biological Processing Technology for Farm Products of Zhejiang Province, Zhejiang Provincial Collaborative Innovation Center of Agricultural Biological Resources Biochemical Manufacturing, School of Biological and Chemical Engineering, Zhejiang University of Science and Technology, Hangzhou 310023, People's Republic of China

[b]State Key Laboratory of Physical Chemistry of Solid Surfaces and Fujian Provincial Key Laboratory of Theoretical and Computational Chemistry, College of Chemistry and Chemical Engineering, Xiamen University, Xiamen 360015, People's Republic of China.

Email: huangjun@zust.edu.cn **(**Jun Huang**),** fffan@zust.edu.cn (Fangfang Fan)

Table S1. The distance of center distance between benzene rings from the first MHET unit of substrate and W185/Y87 during the 100 ns simulation. (unit:Å)

Model	B	C	D	E	F
Y87	5.75±0.36	5.82±0.48	6.02±0.49	5.81±0.54	5.71±0.37
W185$_1$	5.47±0.32	5.16±0.39	5.28±0.36	5.26±0.38	5.20±0.34
W185$_2$	5.26±0.35	5.22±0.47	5.18±0.38	5.35±0.34	5.07±0.40

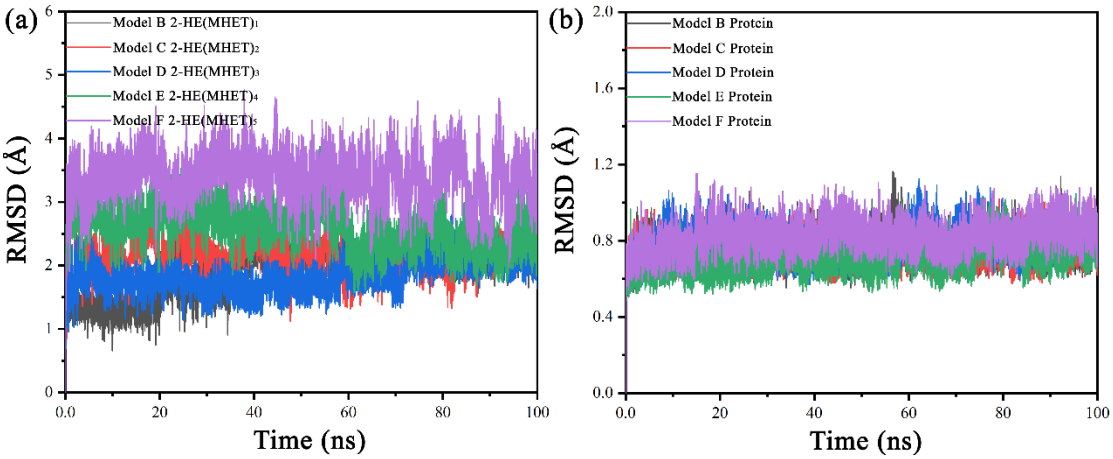

Fig. S1 RMSD results of the substrate and protein (Model B-F) during 100 ns of MD simulation, respectively.

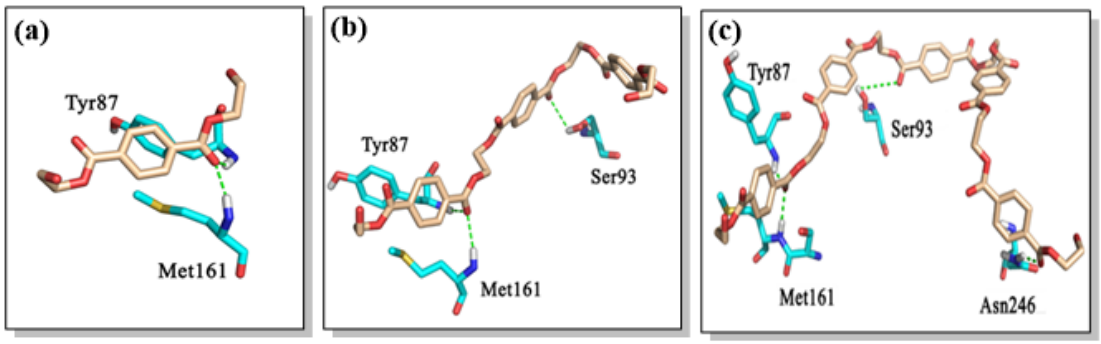

Fig. S2 Schematic diagram of restraint forces applied between a monomer $(MHET)_1$ (a), trimer $(MHET)_3$ (b), pentamer $(MHET)_5$ (c) and *Is*PETase during the MD simulation.

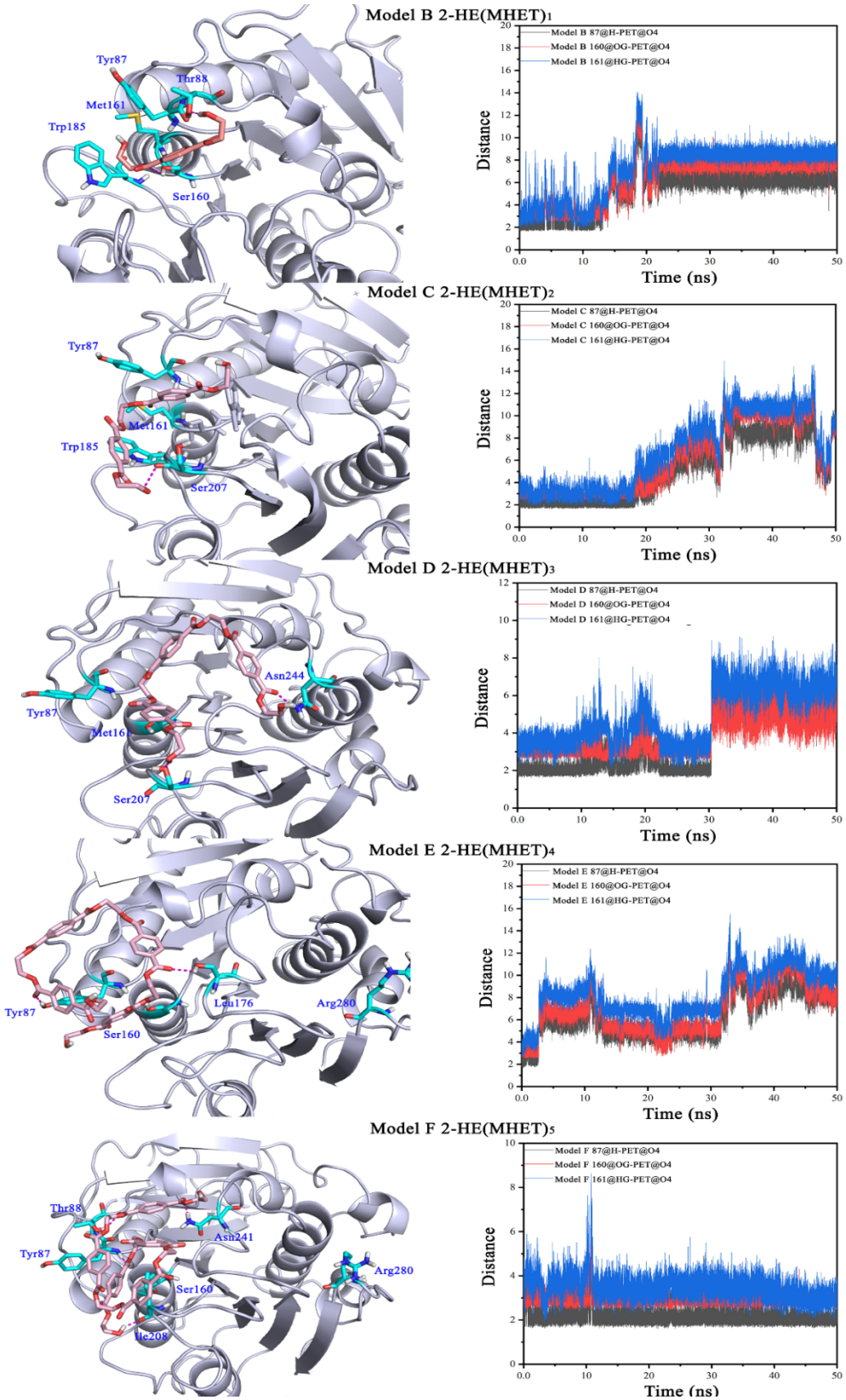

Fig. S3 The structure diagram that represents each model and the time evolution of protein and substrates (Y87/M161/S160) distances along MD simulations.

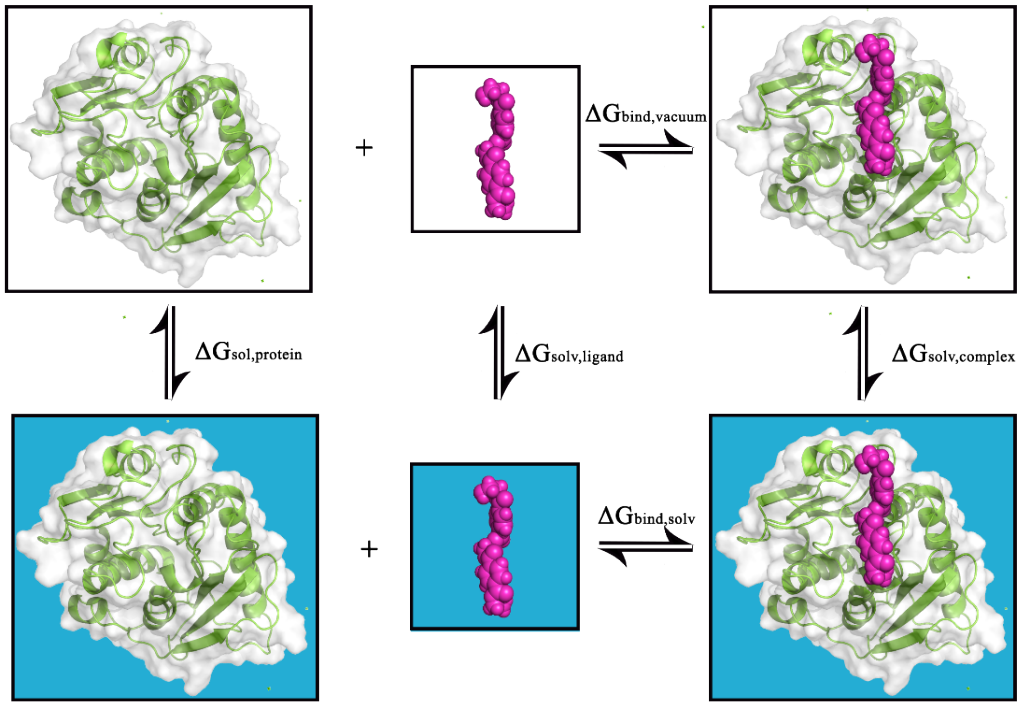

Fig. S4 The calculation process diagram of MM-GBSA. $^{\Delta G_{sol,protein}}$, $^{\Delta G_{sol,ligand}}$ and $^{\Delta G_{sol,complex}}$ represent the Gibbs free energy required for the protein, ligand and complex to transition from vacuum to the solvated state, respectively. $^{\Delta G_{bind,vacuum}}$ and $^{\Delta G_{bind,solv}}$ represent the Gibbs energy required for ligand and protein binding in vacuum and solution, respectively.

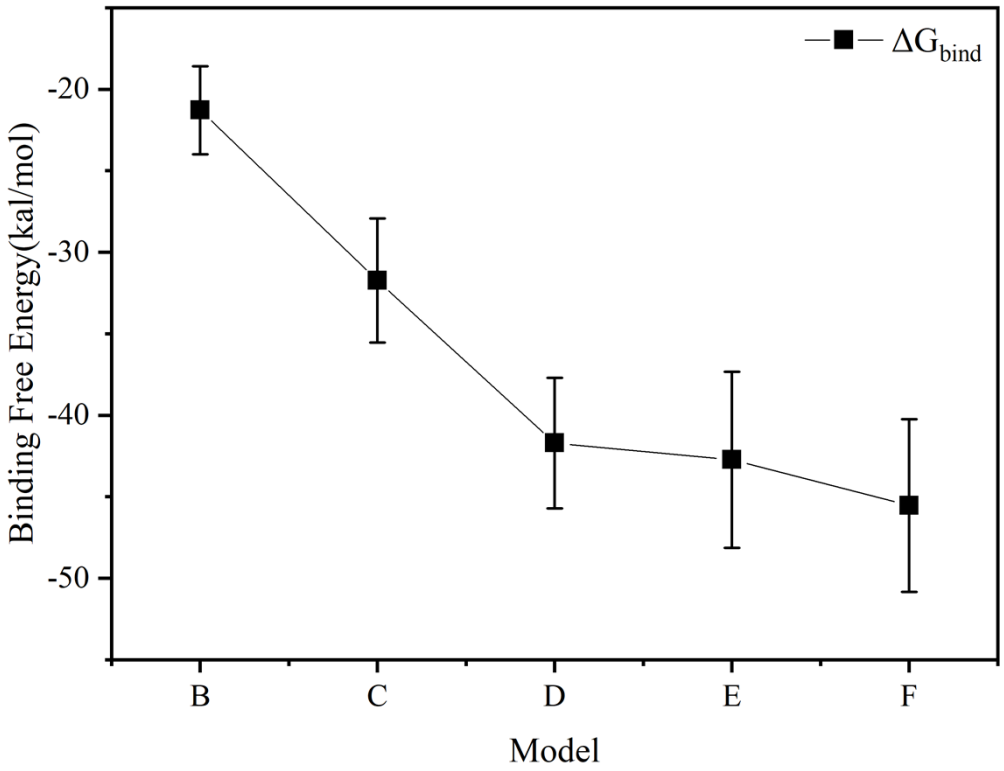

Fig. S5 The binding free energy of the five models (Model B-F)).

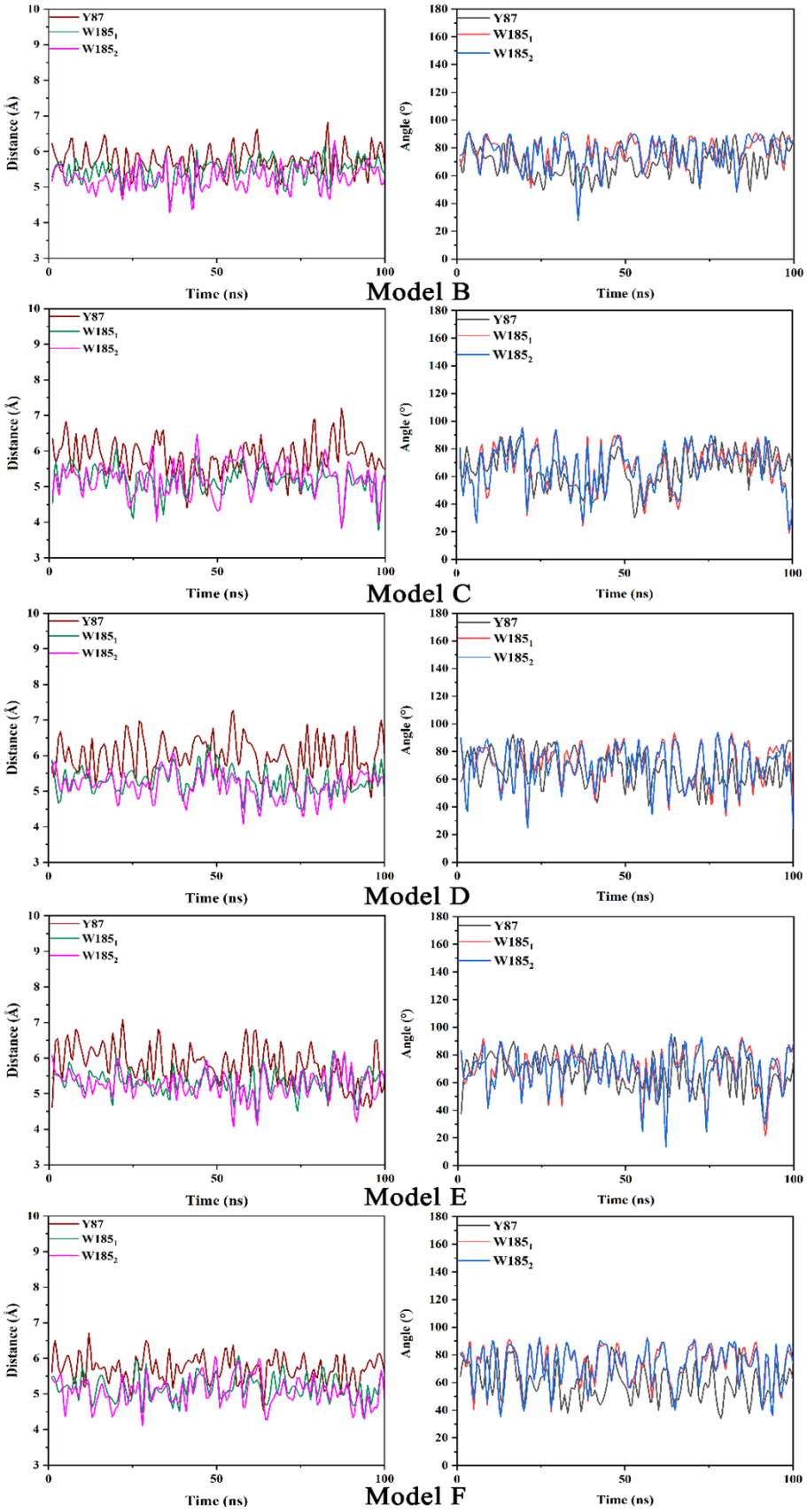

Fig. S6 The change of center distance and the included angle between benzene rings from the first MHET unit of substrate and W185/Y87 during the 100 ns simulation.