

Supporting Information

Structural Insights into a Novel Esterase from the East Pacific Rise and its Improved Thermostability by Semi-rational Design

Chunhua Zhu^{†, ‡, §, ¶}, Yayu Chen[§], Michail N. Isupov[¶], Jennifer A. Littlechild[¶], Lifang Sun[§], Xiaodong Liu^{§, #}, Qianchao Wang^{†, ‡}, Hui Gong[#], Panpan Dong[§], Na Zhang[§], Yunkun Wu^{*, §}

[†] State Key Laboratory of Structural Chemistry, Fujian Institute of Research on the Structure of Matter, Chinese Academy of Sciences, Fuzhou 350002, China

[‡] University of Chinese Academy of Sciences, Beijing 100049, China

[§] Provincial University Key Laboratory of Cellular Stress Response and Metabolic Regulation, College of Life Science, Fujian Normal University, Fuzhou 350117, China

[¶] Institute of Animal Husbandry and Veterinary Medicine, Fujian Academy of Agricultural Sciences, Fuzhou 350013, China

^{||} Henry Wellcome Building for Biocatalysis, Biosciences, University of Exeter, Stocker Road, Exeter, EX4 4QD, UK

[#] Institute of Biotechnology, Fujian Academy of Agricultural Sciences, Fuzhou 350003, China

*Correspondence to: Yunkun Wu, Provincial University Key Laboratory of Cellular Stress Response and Metabolic Regulation, College of Life Science, Fujian Normal University, Fuzhou, 350117, China. Tel: 86) 591-63173176. Fax: 86) 591-63173174. E-mail: wuyk@fjnu.edu.cn

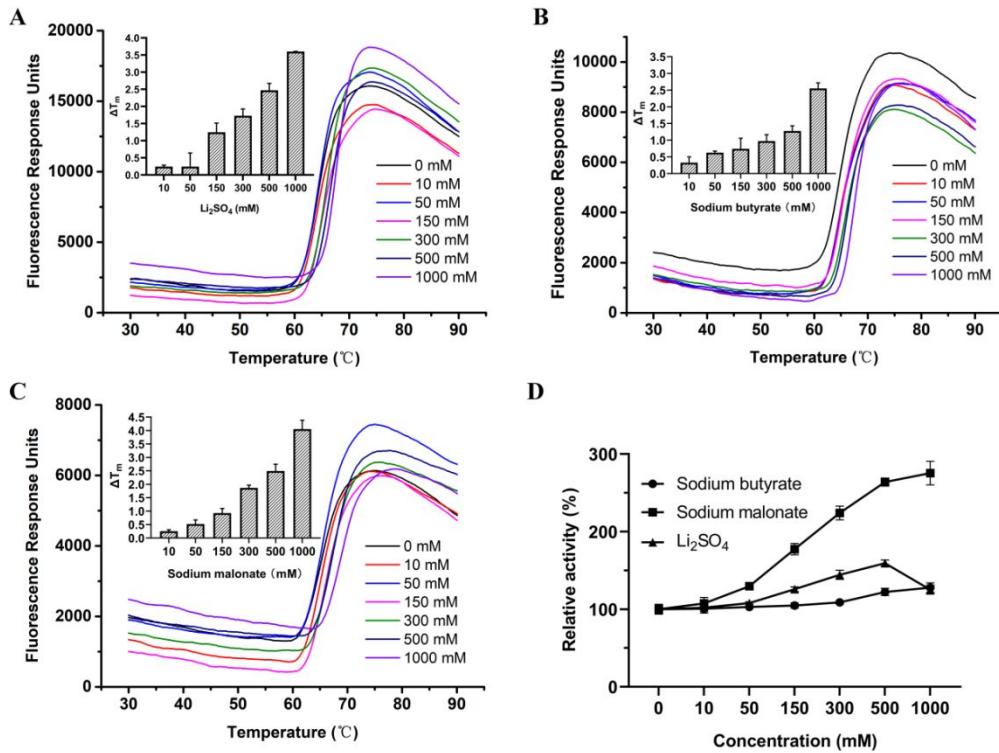


Figure S1. Influence of small molecule ligands on thermostability and activity of EprEst. The differential scanning fluorescence (DSF) was performed to screen the potential small molecules interacted with EprEst. (A) Li_2SO_4 , (B) Sodium butyrate, (C) Sodium malonate. (D) The relative activity of EprEst with added different concentrations of Li_2SO_4 , sodium butyrate or sodium malonate. The relative activity of EprEst is identified as 100%. The samples were determined in triplicate, and data are mean \pm s.d. ($n = 3$).

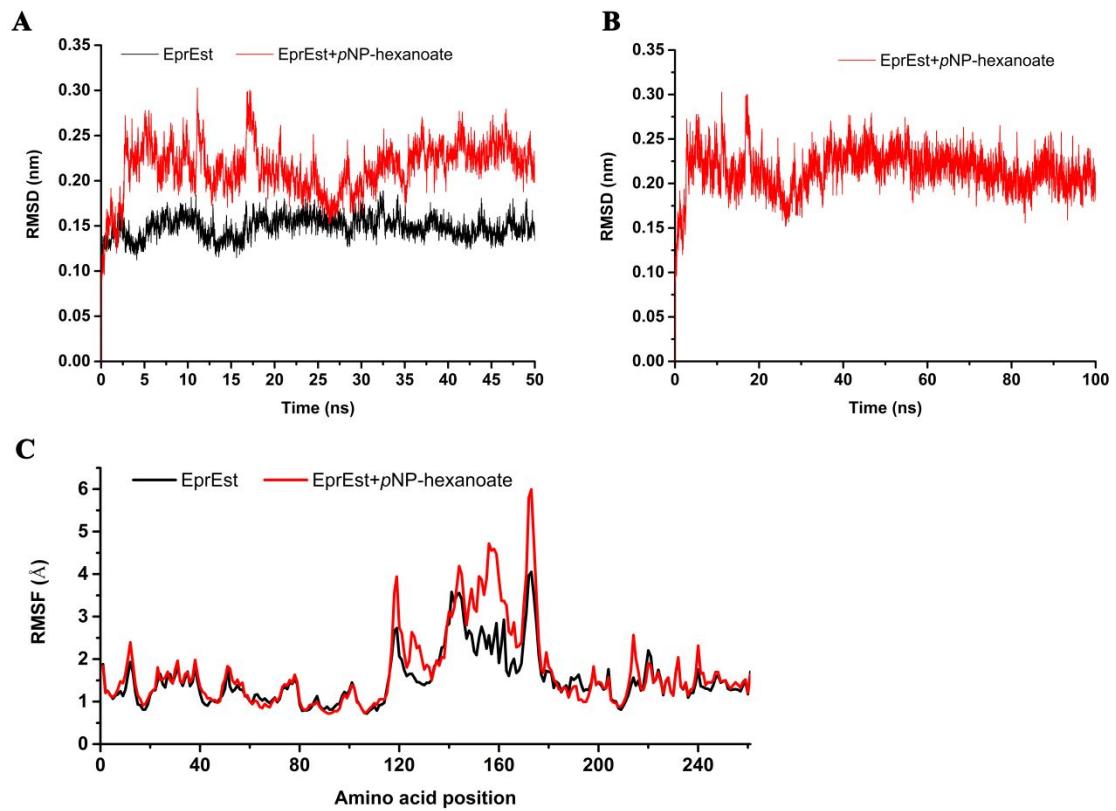


Figure S2. The RMSD and RMSF values of EprEst and its complex with *p*NP-hexanoate. (A)

The MD simulations were performed for 50 ns at 298 K. (B) 100 ns. (C) The RMSF values.

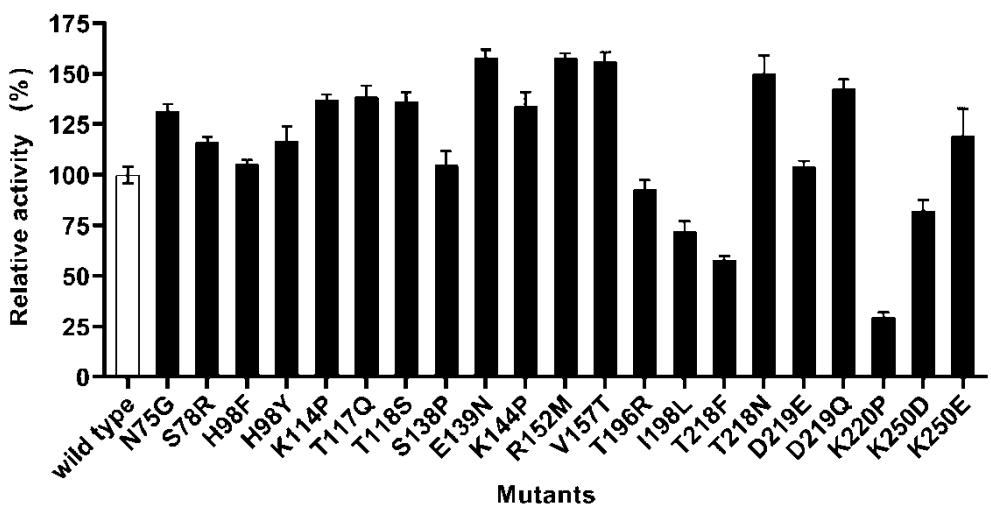


Figure S3. The relative activities of the mutants were determined through the first round of screening. All the mutants were incubated at the optimal temperature of 50 °C, the relative activity of wild type was identified as 100%.

Table S1. The ligands for molecular docking

Ligand	PubChem CID	Lowest Binding Energy (kcal mol ⁻¹)
<i>p</i> NP-butyrate ester	75834	-10.00
<i>p</i> NP-hexanoate ester	567162	-9.53
<i>p</i> NP-octanoate ester	97416	-7.23

Table S2. Mutagenic primers used in this work

Mutants	Primer	Sequence (5' to 3')
L21A	L21A -F	ATCATCCTGCACGGC <u>GCGT</u> ACGGTAGC
	L21A -R	GCGCCGTGCAGGATGATCAGCGGTTCG
Y115A	Y115A -F	ATTGCGCCGGGCAA <u>AAGCCG</u> ATACCACC
	Y115A -R	GCTTGCCCCGGCGCAATATCCGCCACG
N121A	N121A -F	GATACCACCTCTCCG <u>GCCG</u> TAAAACC
	N121A -R	GCCGGAGAGGTGGTATCGTATTGCC
H125A	H125A -F	CCGAACGTTAAAACC <u>GCCAA</u> AAAGATC
	H125A -R	GCGGTTTAACGTTGGAGAGGTGGTA
M192A	M192A -F	AACATCATCACACAT <u>CGCA</u> AGCGGCATCA
	M192A -R	TGCGATGTTGATGATGTTTCTCAATG
W243A	M192A -F	CCGGGTGCGGGCCAC <u>GCG</u> CTGCACGCG
	M192A -R	GCGTGGCCCGCACCCGGAATGGTAACC
K114P	K114P -F	GATATTGCGCCGGGC <u>CCAT</u> ACGATACC
	K114P -R	GGGCCC GGCGCAATATCCGCCACGATC
Q74N	Q74N-F	GAATTCATAAAAG <u>CAAC</u> ACCTGGAAA
	Q74N-R	GTTGCTTTGATGAATT CGTGCAGATC
N75G	N75G-F	TTCATCAAAAGCCAG <u>GGC</u> CTGGAAAGC
	N75G-R	CCCTGGCTTTGATGAATT CGTGCAG
S78R	S78R-F	AGCCAGAACCTGGA <u>ACG</u> CGTGAACA
	S78R-R	GTTCCAGGTTCTGGCTTTGATGAA
H98F	H98F-F	TGGTTCACCGCAGCG <u>TTCC</u> CGGATAA
	H98F-R	AACGCTGCGGTGAACCACATCGCGGT
H98Y	H98Y-F	TGGTTCACCGCAGCG <u>TTCC</u> CGGATA
	H98Y-R	ACGCTGCGGTGAACCACATCGCGGT
K114M	K114M-F	ATATTGCGCCGGC <u>ATG</u> TACGATACC
	K114M-R	CATGCCCGGCGCAATATCCGCCACGA
T117L	T117L-F	CCGGGCAAATACGAT <u>CTG</u> ACCTCTCCGA
	T117L-R	CAGATCGTATTGCCCGGCGCAATATC
T117Q	T117Q-F	CCGGGCAAATACGAT <u>CAG</u> ACCTCTCCGA
	T117Q-R	CTGATCGTATTGCCCGGCGCAATATC
T118S	T118S-F	GCAAATACGATACC <u>AGC</u> TCTCCGAAC
	T118S-R	CTGGTATCGTATTGCCCGGCGCAA

Mutants	Primer	Sequence (5' to 3')
S138P	S138P-F	AAAAGCATCGATCC <u>GG</u> GAAGCGAAAA
	S138P-R	CGGCGGATCGATGCTTTCAGCGCCGC
E139N	E139N-F	AGCATCGATCCGT <u>CA</u> CGCGAAACCC
	E139N-R	GTTAGACGGATCGATGCTTTCAGCGC
K144P	K144P-F	GAAGCGAAAACCGT <u>CC</u> AGAAATCGAA
	K144P-R	GGACGGGTTTCGCTTCAGACGGATC
R152L	R152L-F	AAACCCAGCTGT <u>CT</u> GTACATCGATA
	R152L-R	CAGAGACAGCTGGGTTCGATTCTT
R152M	R152M-F	GAAACCCAGCTGT <u>AT</u> GTACATCGATA
	R152M-R	CATAGACAGCTGGGTTCGATTCTT
V157T	V157T-F	CGTTACATCGATAAC <u>AC</u> TCAGCTGCGC
	V157T-R	GTGTTATCGATGTAACGAGACAGCTG
T196R	T196R-F	ATCATGAGCGGCATC <u>CG</u> GGTATCGAC
	T196R-R	CGGATGCCGCTCATGATGTTGATGAT
I198L	I198L-F	AGCGGCATCACCGG <u>CT</u> GATCGACATCC
	I198L-R	CAGACCGGTGATGCCGCTCATGATGTT
T218N	T218N-F	TGAGCGATTACAT <u>CA</u> CGATAAAGAC
	T218N-R	TTGATGTAATCGCTCAGTCACCTT
T218D	T218D-F	CTGAGCGATTACAT <u>CG</u> ATGATAAAGACA
	T218D-R	ATCGATGTAATCGCTCAGTCACCTT
T218F	T218F-F	CTGAGCGATTACAT <u>CT</u> CGATAAAGAC
	T218F-R	AAGATGTAATCGCTCAGTCACCTT
D219E	D219E-F	CGATTACATCAC <u>CC</u> AAAAAGACATCC
	D219E-R	TTCGGTGATGTAATCGCTCAGTTCA
D219Q	D219Q-F	AGCGATTACATCAC <u>CC</u> AAAAGACATCC
	D219Q-R	TTGGGTGATGTAATCGCTCAGTCACC
K220P	K220P-F	GATTACATCACCG <u>CC</u> GACATCCC
	K220P-R	CGGATCGGTGATGTAATCGCTCAGTT
K250D	K250D-F	CACGCGCAGCAGCC <u>G</u> ATATCTTCATCC
	K250D-R	ATCCGGCTGCTGCGCGTGCAGCCAGTG
K250E	K250E-F	ACGCGCAGCAGCC <u>G</u> AAATCTTCATCC
	K250E-R	TTCCGGCTGCTGCGCGTGCAGCCAGT

Note: The underline represents the mutagenic position.