

Electronic Supplementary Information

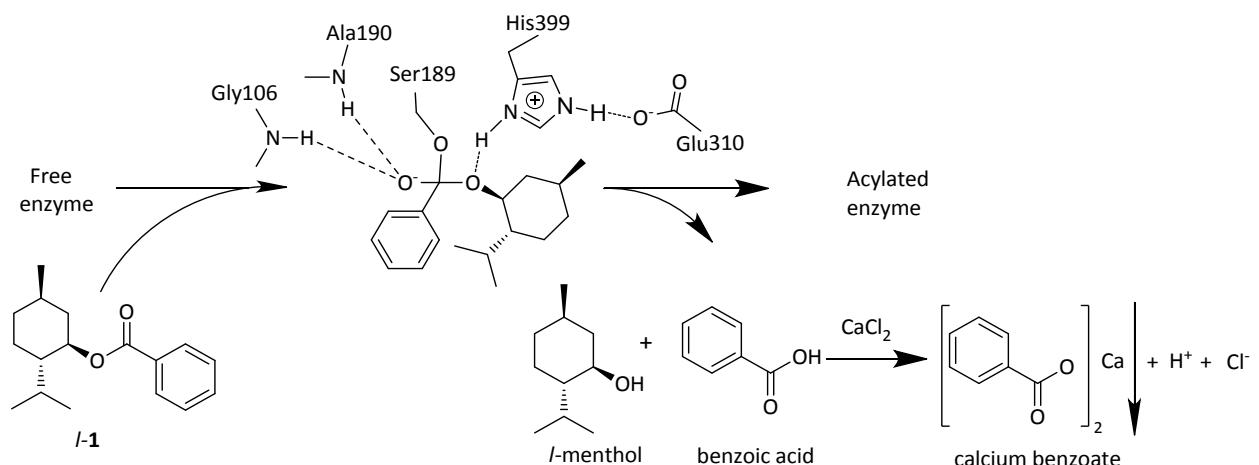
Iterative Multitarget Evolution Dramatically Enhances Enantioselectivity and Catalytic Efficiency of *Bacillus subtilis* Esterase towards Bulky Benzoate Ester of *dl*-Menthol

Yi Gong, Guo-Chao Xu, Qi Chen, Jin-gang Yin, Chun-Xiu Li* and Jian-He Xu*

Laboratory of Biocatalysis and Synthetic Biotechnology, State Key Laboratory of Bioreactor Engineering, Shanghai Collaborative Innovation Center for Biomanufacturing, East China University of Science and Technology, Shanghai 200237, China. E-mails: chunxiuli@ecust.edu.cn; jianhexu@ecust.edu.cn.

Table of Contents

1. **Scheme S1.** An abbreviated reaction mechanism for the formation of a tetrahedral intermediate of *l*-**1**.
2. **Table S1.** Primers designed for mutation.
3. **Table S2.** Substitutions observed over multiple rounds of evolutions.
4. **Table S3.** Docking analysis.
5. **Table S4.** T_m values (°C) of BSE variants measured with purified proteins.
6. **Table S5.** Effects with different cosolvents and surfactants.
7. **Figure S1.** Rescreening results of the random mutagenesis library.
8. **Figure S2.** Thermodynamic analysis of deconvolved BSE_{V7} variants in *dl*-**1** hydrolysis.
9. **Figure S3.** Asymmetric preparation of *l*-menthol from 0.5 M *dl*-**1** employing BSE_{V11} 0.5 g_{CFE} L⁻¹.



Scheme S1. An abbreviated reaction mechanism for the formation of a tetrahedral intermediate of *I*-1. The model used for selection of the amino acid residues for CASTing has docked this intermediate into the active site. The formation of benzoic acid was detected by phenol red with the addition of CaCl_2 .

Table S1. Primers designed for mutation (all are written 5'–3'). The respective mutant codons are indicated in red, and the restriction sites are underlined. Degenerate nucleotide designation: n = a, t, c, g; k = t, g; m = a, c. Primers were ordered from Sangon, Shanghai.

Primer	Sequence of primer
107/109/110-f	attcacggaggcnkttnnknk ⁿ ggagcggc ^{gg} cgtgagcc
107/109/110-r	cactgccc ^{gt} ccmnmnnaamnnngc ^{tc} ccgtgaatccac
362/363-f	atgactgattannknk ⁿ tggcgcc ^c ctgccgtcgc
362/363-r	ggcagg ^{gg} gc ^{cc} camnnmnntaaatcagtcatcatat
400-f	aaagcg ^{ttt} cacnnk ^t tagagcttc ^{ttt} tg ^t c
400-r	aggaagctctaamnnngt ^{gaa} acgc ^{ttt} tattgt ^a
68/71-f	ccgtctgattgnnk ^t cactnnktatactgagctgccc
68/71-r	cagctc ^{agt} tatamnnnaagtgamnncaa ^{at} cagacggctg
188-f	aacagtatttg ^g annk ^t ccgc ^{gg} gg ^g ga
188-r	ccgccc ^{gg} cg ^g amnn ^t ccaaatactgttac
217/218-f	atggaaagcg ^{gc} cnknnk ^c gaacgatgac ^{aaa}
217/218-r	cgtcatcg ^t cgmn ^m nnngcc ^{gtt} ccat ^{gat}
401/403-f	cgttca ^t ctgcnnkgagnnkc ^{ttt} gtt ^g ga
401/403-r	aagaca ^{aa} aggmn ⁿ ctcmnnngc ^{ag} t ^{gaa} acgc ^{ttt} a
A107G-f	tggattcacggaggcg ^{gttt} atctaggagc ^g
A107G-r	cgc ^t c ^c tagataaaaaaccgc ^c ccgtgaatcca
Y109E-f	tcacggaggcg ^c tttgagctaggagc ^{ggg} c ^a g
Y109E-r	ctgccc ^c c ^t ctagct ^{aaa} acgc ^c c ^t ccgt ^g a
L110V-f	cacggaggcg ^c tttatgttaggagc ^{gg} g
L110V-r	ccgc ^t c ^c tacataaaaaaggc ^c c ^t ccgt ^g
A400C-f	aaagcg ^{ttt} c ^t actgc ^t tagagcttc ^{ttt} tg ^t c
A400C-r	aggaagctcta ^{ag} c ^{gt} gaaacgc ^{ttt} tattgt ^a
A107G/Y109E-f	tggattcacggaggcg ^{gttt} gagctaggagc ^{ggg} c ^a gt ^g
A107G/Y109E-r	cactgccc ^c c ^t ctagct ^{aaa} acgc ^c c ^t ccgt ^g aatcca
A107G/L110V-f	gattcacggaggcg ^c tttatgttaggagc ^{ggg} c ^a gt ^g

A107G/L110V-r actgcccgtcctacataaaaaaccgcctccgtgaatc
Y109E/L110V-f gtggattcacggaggcgctttgaggtaggagcggca
Y109E/L110V-r tgcccgtcctacctaaaagcgcctccgtgaatccac
ep-f cgcggatccatgactcatcaaatacgtaacg
ep-r cccaagctttatttcctttgaaggaa

Table S2. Substitutions observed over multiple rounds of evolution. The substitution was showed in bold when it was the first time introduced.

Variants	BSE _{V4}	BSE _{V5}	BSE _{V6}	BSE _{V7}	BSE _{V8}	BSE _{V9}	BSE _{V10}	BSE _{V11}	
Evolutional target	—	Enantioselectivity			Activity				
14	R	R	R	R	R	R	R	R	
34	I	I	I	I	I	I	I	I	
68	L	L	L	L	L	L	I	L	
73	T	T	T	T	T	T	T	S	
75	L	L	L	L	L	L	L	P	
107	A	A	G	G	G	G	G	G	
109	Y	Y	E	E	E	E	E	V	
110	L	L	V	V	V	V	V	V	
270	I	I	I	I	H	I	I	I	
327	L	L	L	L	L	L	L	H	
391	E	E	E	E	E	E	E	E	
400	A	C	A	C	C	C	C	C	
401	L	L	L	L	L	M	M	M	
465	F	F	F	F	F	F	F	F	
Total	4	5	7	8	9	9	10	12	

Table S3. Docking analysis.

Mutant	<i>I-1</i>			<i>d-1</i>		
	<i>r</i> (O-C) [Å]	<i>r</i> (N-O) [Å]	Binding affinity [kcal/mol] ^a	<i>r</i> (O-C) [Å]	<i>r</i> (N-O) [Å]	Binding affinity [kcal/mol] ^a
BSE _{V4}	3.2	3.4	-7.0	3.6	4.8	-6.9
BSE _{V7}	3.8	3.3	-7.1	4.3	4.4	-6.3
BSE _{V11}	3.1	3.4	-7.1	3.7	4.4	-6.3

^a The binding affinity is caculated by AutoDock.

Table S4. T_m value (°C) of BSE mutants measured with purified proteins.

Entry	Mutant	T_m (°C)
1	BSE _{V4}	55.2
2	BSE _{V5}	51.0
3	BSE _{V6}	54.2
4	BSE _{V7}	53.3
5	BSE _{V9}	52.9
6	BSE _{V11}	52.6

Table S5. Effects of different cosolvents and surfactants. BSE_{V4} was applied to hydrolyze 50 mM *d,l*-menthyl benzoate in 10-mL scale.

Cosolvent	LogP	Time (h)	Conv. (%)	ee _p (%)
DMSO	-1.49	5	6.1	69.3
DMF	-0.60	5	10.1	64.3
Methanol	-0.27	5	6.6	70.6
Ethanol	0.07	5	12.5	72.7
Isopropanol	0.38	5	9.9	64.9
<i>n</i> -Butanol	0.97	5	6.6	93.5
Triton X-100	–	0.5	35.7	92.1
Tween 80	–	0.5	47.1	90.2

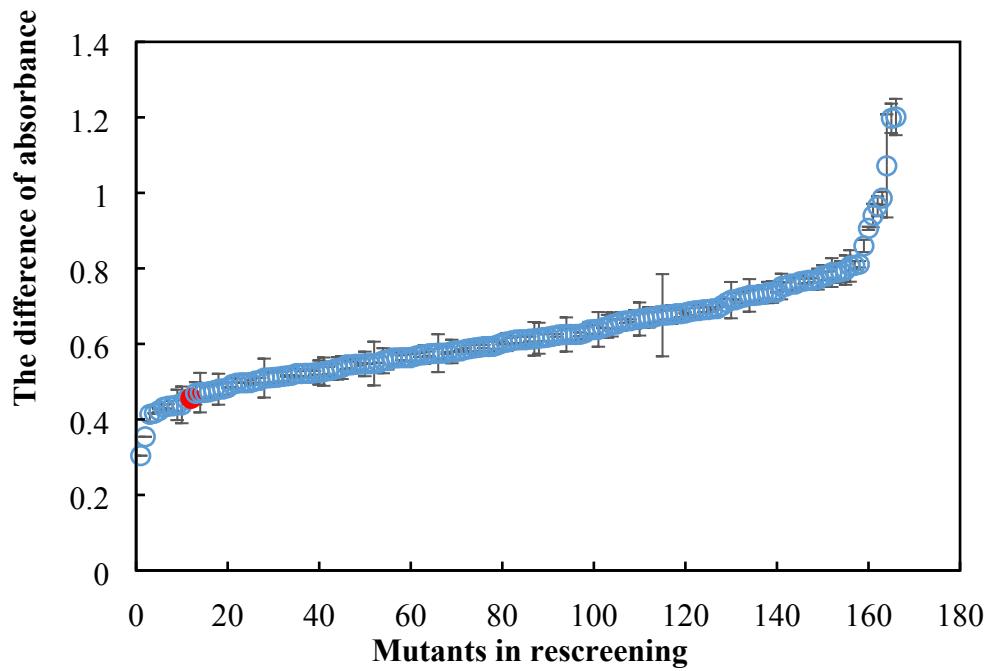


Figure S1. Rescreening results of the random mutagenesis library. The parent enzyme BSE_{V9} was displayed in red point.

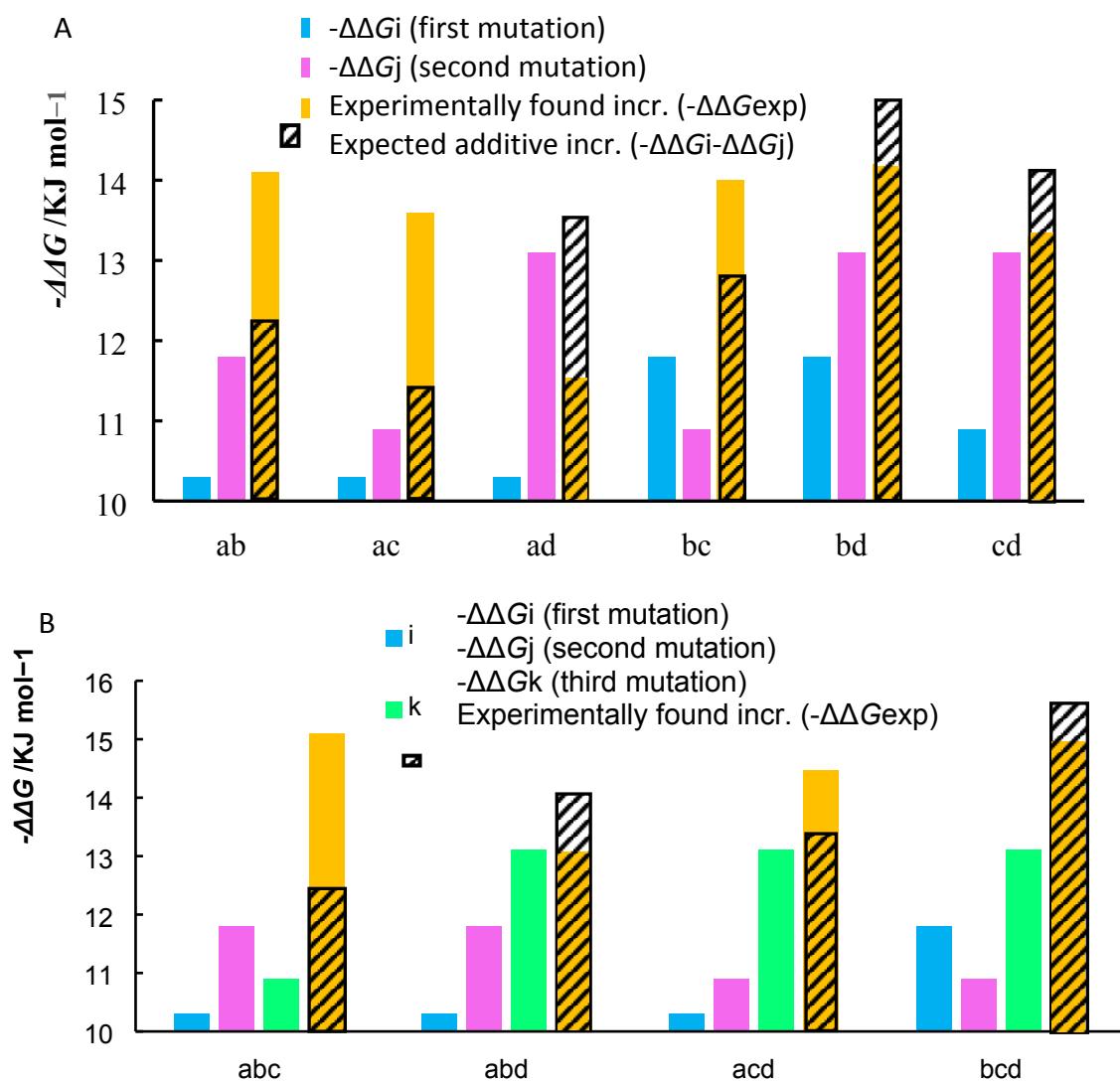


Figure S2. Thermodynamic analysis of deconvolved BSE_{V7} variants in the hydrolysis of substrate *dl-1*.

A) The double mutants: ab, ac, ad, bc, bd and cd; **B)** The triple mutants: abc, abd, acd and bcd.

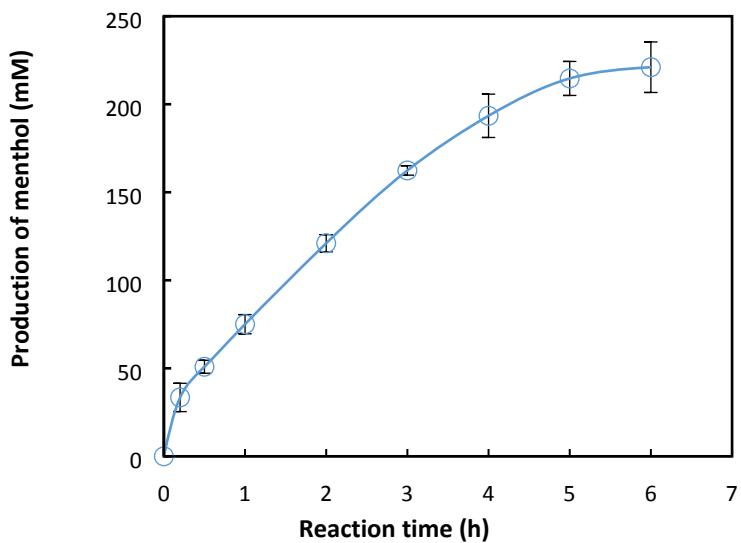


Figure S3. Asymmetric preparation of *l*-menthol from substrate *dl*-**1** at 0.5 M employing BSE_{V11} with a catalyst loading of 0.5 g_{CFE} L⁻¹ in 0.1-L scale.