# **Supporting Information**

# New Small-Molecule Alcohol Synthesis by Breaking the Space

Limitation of "Aromatic Cage" in Pseudomonas sp. AK1 BBOX

Zhiqin Xu<sup>a</sup>, Yaling Mo<sup>a</sup>, Zhengwen Li<sup>a</sup>, Shurong Ban<sup>a\*</sup>, Heng song<sup>b,c\*</sup>.

<sup>a</sup>School of Pharmacy, Shanxi Medical University, Taiyuan, Shanxi Province 030001, China

<sup>b</sup>College of Chemistry & Molecular Science, Wuhan University, Wuhan, Hubei Province 430072, China

<sup>c</sup>Wuhan University Shenzhen Research Institute, Shenzhen, Guangdong Province 518000, China

\*Email: hengsong@whu.edu.cn; <a href="mailto:sknu.edu.cn">shurongban@sxmu.edu.cn</a>

# Contents

SDS-PAGE analysis of WT-psBBOX	2
Sequence alignment <sup>1</sup>	3
Homology modelling	4
Molecular docking	5
Construction of psBBOX mutants	6
SDS-PAGE analysis of mutants	7
Analysis of psBBOX-188A activity	7
kinetic analysis	
Synthesis of γ-BB analogues	10
Stereoselective synthesis of two configurations of 4a, 7a, 8a	11
NMR spectra	
References	28

# SDS-PAGE analysis of WT-psBBOX



Figure S1 SDS-PAGE analysis of the WT-psBBOX (45.3 KD).

#### Sequence alignment<sup>1</sup>



**Figure S2** Sequence alignment of *Pseudomonas* sp. AK1 BBOX (psBBOX gi|231642) and human BBOX (hBBOX gi|158261239).

Homology modelling



Figure S3 hBBOX template (PDB: 3O2G) (left) and psBBOX model (right).

#### **Molecular docking**



Figure S4 Catalytic center of psBBOX is composed of His-350, His-209, Asp211 and Metal ion.



Figure S5 2D graphic of interaction between  $\gamma$ -BB and amino acid residues.

# Construction of psBBOX mutants

Table S1 Primers used in this study						
Primers	Sequence					
184A-F	5'-CGAAAGCAACGCAGGCGTGCTGTTTGATGTGCG-3'					
184A-R	5'-CAGCACGCCTGCGTTGCTTTCGCGAATAAAGC-3'					
188A-F	5'-GGCGTGCTGGCAGATGTGCGCAGCAAAGCGG-3'					
188A-R	5'-GCGCACATCTGCCAGCACGCCAAAGTTGCTTTCG-3'					
201A-F	5'-GATAGCAACGCGGCAACCGCGTTTAACCTGCCGCTG-3'					
201A-R	5'-GTTAAACGCGGTTGCCGCGTTGCTATCCGCATCC-3'					
184Y-F	5'-GCAACTATGGCGTGCTGTTTGATGTGCG-3'					
184Y-R	5'-GCACGCCATAGTTGCTTTCGCGAATAAAGC-3'					
188Y-F	5'-CGTGCTGTATGATGTGCGCAGCAAAGCGGATG-3'					
188Y-R	5'-GCACATCATACAGCACGCCAAAGTTGCTTTCGC-3'					
201F-F	5'-CAACGCGTTTACCGCGTTTAACCTGCCGC-3'					
201F-R	5'-GCGGTAAACGCGTTGCTATCCGCATCCG-3'					
368A-F	5'-GCTGCGCAGTGGATCGCGATGAACTGC-3'					
368A-R	5'-CGATCCACTGCGCAGCCTTGAAAATGGC-3'					
184W-F	5'-GCAACTGGGGGCGTGCTGTTTGATG-3'					
184W-R	5'-CGCCCCAGTTGCTTTCGCGAATAAAG-3'					
188W-F	5'-GCTGTGGGATGTGCGCAGCAAAGC-3'					
188W-R	5'-CATCCCACAGCACGCCAAAGTTGC-3'					
188G-F	5'-GCTGGGTGATGTGCGCAGCAAAG-3'					
188G-R	5'-CATCACCCAGCACGCCAAAGTTGC-3'					
188V-F	5'-GCTGGTTGATGTGCGCAGCAAAG-3'					
188V-R	5'-CATCAACCAGCACGCCAAAGTTGC-3'					

### Table S2 Construction of mutants based on PCR methods

#### For 184A, 188A, 201A:

	Reaction mixtures (20 µL)		PCR conditions
	0.6 µL	template DNA	95°C and 3 min,
	1µL	forward primer	95°C and 30 s
	1 µL	reverse primer	55°C and 30 s
	7.4 μL	H <sub>2</sub> O	72°C and 4 min 30 s
	10 µL	Gloria Nova HS 2×	72°C and 5 min.
For the other n	nutants:		
	Reaction mixtures (20 µL)		PCR conditions
	0.6 uL	template DNA	95°C and 3 min,

0.6 µL	template DNA	95°C and 3 min,	
1 µL	forward primer	95°C and 30 s	
1 µL	reverse primer	52°C and 30 s $\times 30$ cycles	
7.4 μL	H <sub>2</sub> O	72°C and 4 min	
10 µL	Gloria Nova HS 2×	72°C and 5 min.	

#### **SDS-PAGE** analysis of mutants



Figure S6 SDS-PAGE analysis of psBBOX mutants.



Analysis of psBBOX-188A activity

**Figure S7** Comparison of conversion of quaternary ammonium analogs 4-6 catalyzed by WT and 188A.

7



Figure S8 Dependence of reaction rates on  $\gamma$ -BB, 4 and 7 concentration for wt-psBBOX.



Figure S9 Dependence of reaction rates on 7 and 8 concentration for 188A mutant.



Figure S10 Ratio of oxygen consumption to product formation.

#### Synthesis of **γ-BB** analogues



Figure S11 Synthetic routes of quaternary ammonium analogues 4~8.

#### Procedure a<sup>2</sup>

Ethyl 4-bromobutyrate (1.2equiv.); tertiary amine (1.0equiv. For (4), N,N-Dimethylethylamine; for(5), N,N-Dimethylisopropylamine; for (6), N,N-Diethylmethylamine; for (7), 1-Methylpyrrolidine; for (8), N-Methylpiperidine.) and acetone (10ml) was added to round-bottom flask, room temperature stirred for 12h. Solvents were evaporated in vacuo. Without purification, it can be directly used in the next reaction.

#### Procedure b<sup>2</sup>

3M hydrochloric acid was added until pH1, overnight at room temperature, the product was purified by cationic exchange resin.



#### Stereoselective synthesis of two configurations of 4a, 7a, 8a.

Figure S12 Synthetic routes of 4a-S, 7a-S, 8a-S.



Figure S13 Synthetic routes of 4a-R, 7a-R, 8a-R.

**Procedure a<sup>3</sup>:** Adding 193mg sodium hydroxide into 3.5ml water, stir to dissolve it, cool down in the ice bath, add 2.5mmol corresponding tertiary amine and 3mmol Ethyl (R)-(+)-4-chloro-3-hydroxybutyrate or Ethyl (S)-4-chloro-3-hydroxybutyrate successively, react in the ice bath for 1h, and temperature rise to room temperature for 12h.

Procedure b<sup>3</sup>: Adding 3M hydrochloric acid to pH 6, purification using cationic resin.

#### NMR spectra







Figure S17 <sup>13</sup>CNMR spectra of 5.



Figure S19 <sup>13</sup>CNMR spectra of 6.



Figure S21 <sup>13</sup>CNMR spectra of 7.



Figure S23 <sup>13</sup>CNMR spectra of 8.



Figure S25 <sup>13</sup>CNMR spectra of 4a.



Figure S27 <sup>13</sup>CNMR spectra of 7a.



Figure S29 <sup>13</sup>CNMR spectra of 8a.



Figure S31 <sup>13</sup>CNMR spectra of 4a-R.



Figure S33 <sup>13</sup>CNMR spectra of 4a-S.



Figure S35 <sup>13</sup>CNMR spectra of 7a-R.



Figure S37 <sup>13</sup>CNMR spectra of 7a-S.



Figure S39 <sup>13</sup>CNMR spectra of 8a-R.



Figure S41 <sup>13</sup>CNMR spectra of 8a-S.



3.5 3.4 3.3 3.2 3.1 3.0 2.9 2.8 2.7 2.6 2.5 2.4 2.3 2.9 2.1 2.0 1.9 1.8 1.7 1.6 1.5 1.4 1.3 1.2 1.1 1.0 0.9 0.8 f1 (spen)

Figure S42 <sup>1</sup>H NMR monitoring of the 2 hydroxylation by psBBOX.



Figure S43 <sup>1</sup>H NMR monitoring of the 2 hydroxylation by psBBOX.



Figure S44 The inhibitory effect of (5), (6), (8) on the transformation of original substrate (1).

#### References

1. Robert, X.; Gouet, P., Deciphering key features in protein structures with the new ENDscript server. *Nucleic acids research* **2014**, *42* (W1), W320-W324.

2. Rydzik, A. M.; Chowdhury, R.; Kochan, G. T.; Williams, S. T.; McDonough, M. A.;

Kawamura, A.; Schofield, C. J., Modulating carnitine levels by targeting its biosynthesis – selective inhibition of  $\gamma$ -butyrobetaine hydroxylase. *Chemical Science* **2014**, *5* (5), 1765–1771.

3. 吴静; 刘九知; 白洁; 孙德夫 一种左卡尼汀化合物的制备方法. CN104030934B, 2016-06-15.