

1 **Supporting Information**

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3 A chemo-enzymatic strategy for efficient synthesis of
4 amphenicol antibiotic chloramphenicol mediated by an
5 engineered L-threonine transaldolase with high activity and
6 stereoselectivity

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14

15 Running title: Chemo-enzymatic strategy for synthesis of chloramphenicol

16 **Table S1.** Primers used for site-directed mutagenesis of PsLTTA.

Primer	Sequence (5'-3')
N35A F ^a	GACCGCAgcaGAAAATTATCCGAGCGC
N35A R	AATTTTCtgcTGCGGTCAGGCTCAGGC
N35S F	GACCGCAagcGAAAATTATCCGAGCGC
N35S R	AATTTTCgctTGCGGTCAGGCTCAGGC
N35C F	GACCGCAtgtGAAAATTATCCGAGCGC
N35C R	AATTTTCacaTGCGGTCAGGCTCAGGC
N35V F	GACCGCAgttGAAAATTATCCGAGCGC
N35V R	AATTTTCaacTGCGGTCAGGCTCAGGC
N35I F	GACCGCAattGAAAATTATCCGAGCGC
N35I R	AATTTTCaatTGCGGTCAGGCTCAGGC
N35G F	GACCGCAggcGAAAATTATCCGAGCGC
N35G R	AATTTTCgccTGCGGTCAGGCTCAGGC
Y55N F	GCATTTaatCATTGTAGCTTTCCGTTT
Y55N R	ACAATGattAAATGCGCCTGCGGTGCT
Y55L F	GCATTTctgCATTGTAGCTTTCCGTTT
Y55L R	ACAATGcagAAATGCGCCTGCGGTGCT
Y55T F	GCATTTaccCATTGTAGCTTTCCGTTT
Y55T R	ACAATGggtAAATGCGCCTGCGGTGCT
Y55S F	GCATTTagcCATTGTAGCTTTCCGTTT
Y55S R	ACAATGgctAAATGCGCCTGCGGTGCT
Y55A F	GCATTTgcaCATTGTAGCTTTCCGTTT
Y55A R	ACAATGtgcAAATGCGCCTGCGGTGCT
C57I F	TTATCATattAGCTTTCCGTTTGAAGTTCC
C57I R	GAAAGCTaatATGATAAAATGCGCCTGC
C57M F	TTATCATatgAGCTTTCCGTTTGAAGTTCC
C57M R	GAAAGCTcatATGATAAAATGCGCCTGC
C57V F	TTATCATgttAGCTTTCCGTTTGAAGTTCC
C57V R	GAAAGCTaacATGATAAAATGCGCCTGC
C57A F	TTATCATgcaAGCTTTCCGTTTGAAGTTCC
C57A R	GAAAGCTtgcATGATAAAATGCGCCTGC
F59A F	TGTAGCgcaCCGTTTGAAGTTCCGGCA
F59A R	AAACGGtgcGCTACAATGATAAAATGC
F59I F	TGTAGCattCCGTTTGAAGTTCCGGCA
F59I R	AAACGGaatGCTACAATGATAAAATGC
F59V F	TGTAGCggtCCGTTTGAAGTTCCGGCA
F59V R	AAACGGaacGCTACAATGATAAAATGC
F59S F	TGTAGCagcCCGTTTGAAGTTCCGGCA
F59S R	AAACGGgctGCTACAATGATAAAATGC
F59L F	TGTAGCctgCCGTTTGAAGTTCCGGCA
F59L R	AAACGGcagGCTACAATGATAAAATGC
C57I-F59A F	TATCATattAGCgcaCCGTTTGAAGTTCCGGCA
C57I-F59A R	AAACGGtgcGCTaatATGATAAAATGCGCCTGC
F61A F	TTTCCGgcaGAAGTTCCGGCAGGCGAA
F61A R	AACTTCtgcCGGAAAGCTACAATGATA
F61I F	TTTCCGgattGAAGTTCCGGCAGGCGAA
F61I R	AACTTCaatCGGAAAGCTACAATGATA
F61V F	TTTCCGggtGAAGTTCCGGCAGGCGAA
F61V R	AACTTCaacCGGAAAGCTACAATGATA
F61S F	TTTCCGgagGAAGTTCCGGCAGGCGAA
F61S R	AACTTCgctCGGAAAGCTACAATGATA
F61L F	TTTCCGctgGAAGTTCCGGCAGGCGAA
F61L R	AACTTCcagCGGAAAGCTACAATGATA
P64A F	GAAGTTagcGCAGGCGAATGGCATT
P64A R	GCCTGCgctAACTTCAAACGGAAAGCT

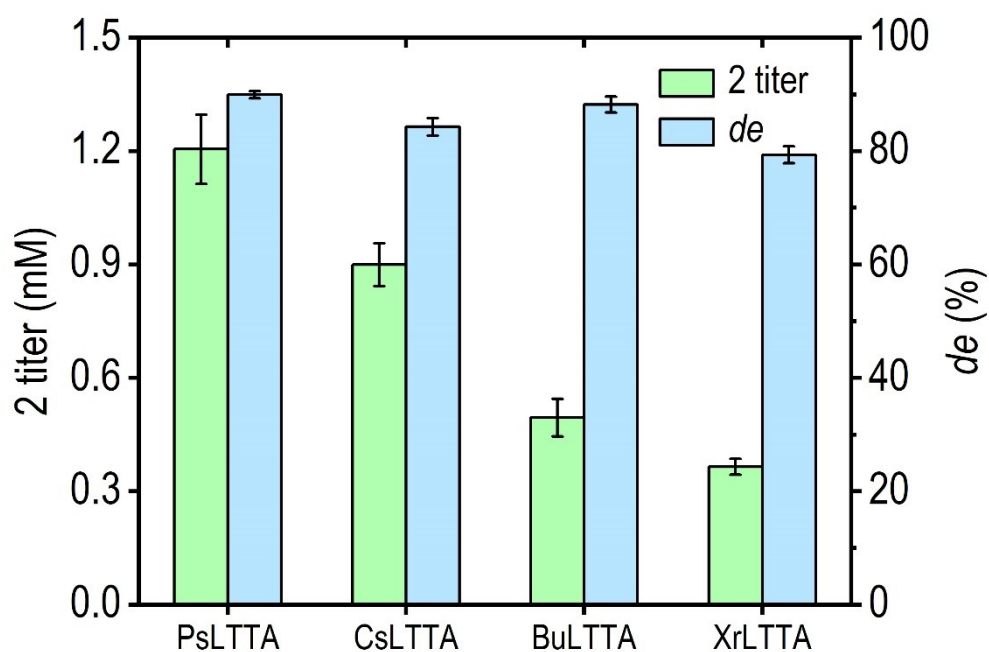
P64A F	GAAGTT	agc	GCAGGCGAATGGC	ATTTT
P64A R	GCCTGC	gct	AACTTCAAACGGAAAGCT	
P64G F	GAAGTT	ggt	GCAGGCGAATGGC	ATTTT
P64G R	GCCTGC	cacc	AACTTCAAACGGAAAGCT	
P64V F	GAAGTT	gtt	GCAGGCGAATGGC	ATTTT
P64V R	GCCTGC	caac	AACTTCAAACGGAAAGCT	
W68A F	GGCGAA	agca	CATTTTCCGGAACCGGGT	
W68A R	AAAATG	tgc	TTCGCCTGCCGGA	ACTTCAAA
W68F F	GGCGAA	attt	CATTTTCCGGAACCGGGT	
W68F R	AAAATG	aaa	TTCGCCTGCCGGA	ACTTCAAA
W68L F	GGCGAA	actg	CATTTTCCGGAACCGGGT	
W68L R	AAAATG	cag	TTCGCCTGCCGGA	ACTTCAAA
W68Q F	GGCGAA	acag	CATTTTCCGGAACCGGGT	
W68Q R	AAAATG	ctg	TTCGCCTGCCGGA	ACTTCAAA
W68S F	GGCGAA	agc	CATTTTCCGGAACCGGGT	
W68S R	AAAATG	gct	TTCGCCTGCCGGA	ACTTCAAA
H69F F	GAATGG	ttt	TTCGGAACCGGGT	CAT
H69F R	CGGAAA	aaa	CCATTTCGCCTGCCGGAAC	
H69Y F	GAATGG	tat	TTCGGAACCGGGT	CAT
H69Y R	CGGAAA	ata	CCATTTCGCCTGCCGGAAC	
H69V F	GAATGG	gtt	TTCGGAACCGGGT	CAT
H69V R	CGGAAA	aac	CCATTTCGCCTGCCGGAAC	
H69L F	GAATGG	ctg	TTCGGAACCGGGT	CAT
H69L R	CGGAAA	acag	CCATTTCGCCTGCCGGAAC	
H69A F	GAATGG	gca	TTCGGAACCGGGT	CAT
H69A R	CGGAAA	atg	CCATTTCGCCTGCCGGAAC	
H69I F	GAATGG	att	TTCGGAACCGGGT	CAT
H69I R	CGGAAA	aat	CCATTTCGCCTGCCGGAAC	
H126A F	TTTGCA	agca	CGTGATGGTGGT	CATTTTGCC
H126A R	ATCACG	tgc	TGCAAAATGAACAAAACCTTC	
H126T F	TTTGCA	aacc	CGTGATGGTGGT	CATTTTGCC
H126T R	ATCACG	ggt	TGCAAAATGAACAAAACCTTC	
H126S F	TTTGCA	aage	CGTGATGGTGGT	CATTTTGCC
H126S R	ATCACG	gct	TGCAAAATGAACAAAACCTTC	
H126L F	TTTGCA	actg	CGTGATGGTGGT	CATTTTGCC
H126L R	ATCACG	cag	TGCAAAATGAACAAAACCTTC	
H132A F	GGTCAT	gca	GCCCTGGAAAGCCTGGCA	
H132A R	CAGGGC	ctgc	ATGACCACCATCACGATG	
H132V F	GGTCAT	gtt	GCCCTGGAAAGCCTGGCA	
H132V R	CAGGGC	caac	ATGACCACCATCACGATG	
H132L F	GGTCAT	ctg	GCCCTGGAAAGCCTGGCA	
H132L R	CAGGGC	cag	ATGACCACCATCACGATG	
H132N F	GGTCAT	aat	GCCCTGGAAAGCCTGGCA	
H132N R	CAGGGC	att	ATGACCACCATCACGATG	
S180V F	GACCAG	ggt	TTTAAACTGCGTTGGCAG	
S180V R	TTTAAA	aac	CTGGTCCAGAATAACAATACGAAT	
S180I F	GACCAG	att	TTTAAACTGCGTTGGCAG	
S180I R	TTTAAA	aat	CTGGTCCAGAATAACAATACGAAT	
S180A F	GACCAG	gca	TTTAAACTGCGTTGGCAG	
S180A R	TTTAAA	atg	CTGGTCCAGAATAACAATACGAAT	
S180G F	GACCAG	ggc	TTTAAACTGCGTTGGCAG	
S180G R	TTTAAA	agc	CTGGTCCAGAATAACAATACGAAT	
S180V F	GACCAG	ggt	TTTAAACTGCGTTGGCAG	
S180V R	TTTAAA	aac	CTGGTCCAGAATAACAATACGAAT	
C262A F	TGGGTT	gca	CCGCATCTGCAGAGCAAT	
C262A R	ATGCGG	tgc	AACCCACAGGCTGGTATC	
C262I F	TGGGTT	att	CCGCATCTGCAGAGCAAT	

C262I R	ATGCGGaatAACCCACAGGCTGGTATC
C262V F	TGGGTTgttCCGCATCTGCAGAGCAAT
C262V R	ATGCGGaacAACCCACAGGCTGGTATC
C262L F	TGGGTTctgCCGCATCTGCAGAGCAAT
C262L R	ATGCGGcagAACCCACAGGCTGGTATC
P263A F	GTTTGTgcaCATCTGCAGAGCAATTGT
P263A R	CAGATGtgcACAAACCCACAGGCTGGT
P263G F	GTTTGTggcCATCTGCAGAGCAATTGT
P263G R	CAGATGgccACAAACCCACAGGCTGGT
P263V F	GTTTGTgttCATCTGCAGAGCAATTGT
P263V R	CAGATGaacACAAACCCACAGGCTGGT
S267A F	TGCAGgcaAATTGTCATGCCGAACAGCTGC
S267A R	CAATTtgcGATGCGGACAAACCCACAGG
S267V F	TGCAGgttAATTGTCATGCCGAACAGCTGC
S267V R	CAATTaacGATGCGGACAAACCCACAGG
S267G F	TGCAGggcAATTGTCATGCCGAACAGCTGC
S267G R	CAATTgccGATGCGGACAAACCCACAGG
S267I F	TGCAGattAATTGTCATGCCGAACAGCTGC
S267I R	CAATTaatGATGCGGACAAACCCACAGG

17 ^a: the replacement nucleotide sequences were shown in lower case text.

18

19 **Figure S1.**

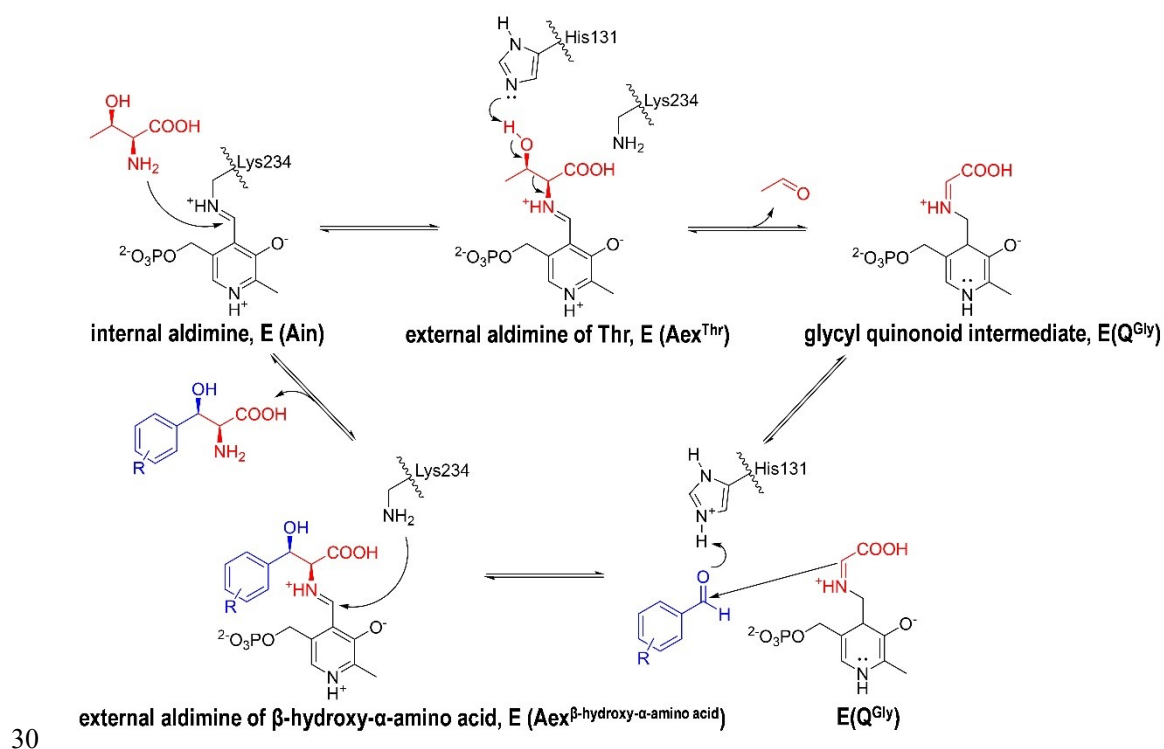


20

21 **Figure S1.** Four L-threonine transaldolase (PsLTTA, CsLTTA, BuLTTA and
22 XrLTTA) were screened for synthesizing of **2**. Transaldol reaction was performed in a
23 1 ml volume comprising 6 mM of L-threonine, 5 mM of **1**, 0.1 mM of PLP and 25 mg
24 of whole-cell catalyst in Tris-HCl buffer (50 mM, pH 7.5) and incubated at 30°C with
25 shaking for 2 h. After reaction, the pellets were removed by centrifugation and the
26 supernatant was submitted for evaluating the conversion and stereoselectivity of **2** by
27 chromatography analysis.

28

29 **Figure S2.**



31 **Figure S2.** Based on the crystal structure of ObiH (PDB code: 7K34), the catalytic

32 mode of L-threonine transaldolase was a multi-stage reaction following a Ping-Pong

33 mechanism. The reaction is initiated by the binding of L-threonine to

34 phosphopyridoxal (PLP) to form an external aldimine of L-threonine ($E(Aex^{Thr})$) and a

35 re-aldol cleavage is followed to produce a highly basic glycyl quinonoid intermediate

36 Q^{Gly} and acetaldehyde. Then Q^{Gly} attacks on substrate aldehyde to form an external

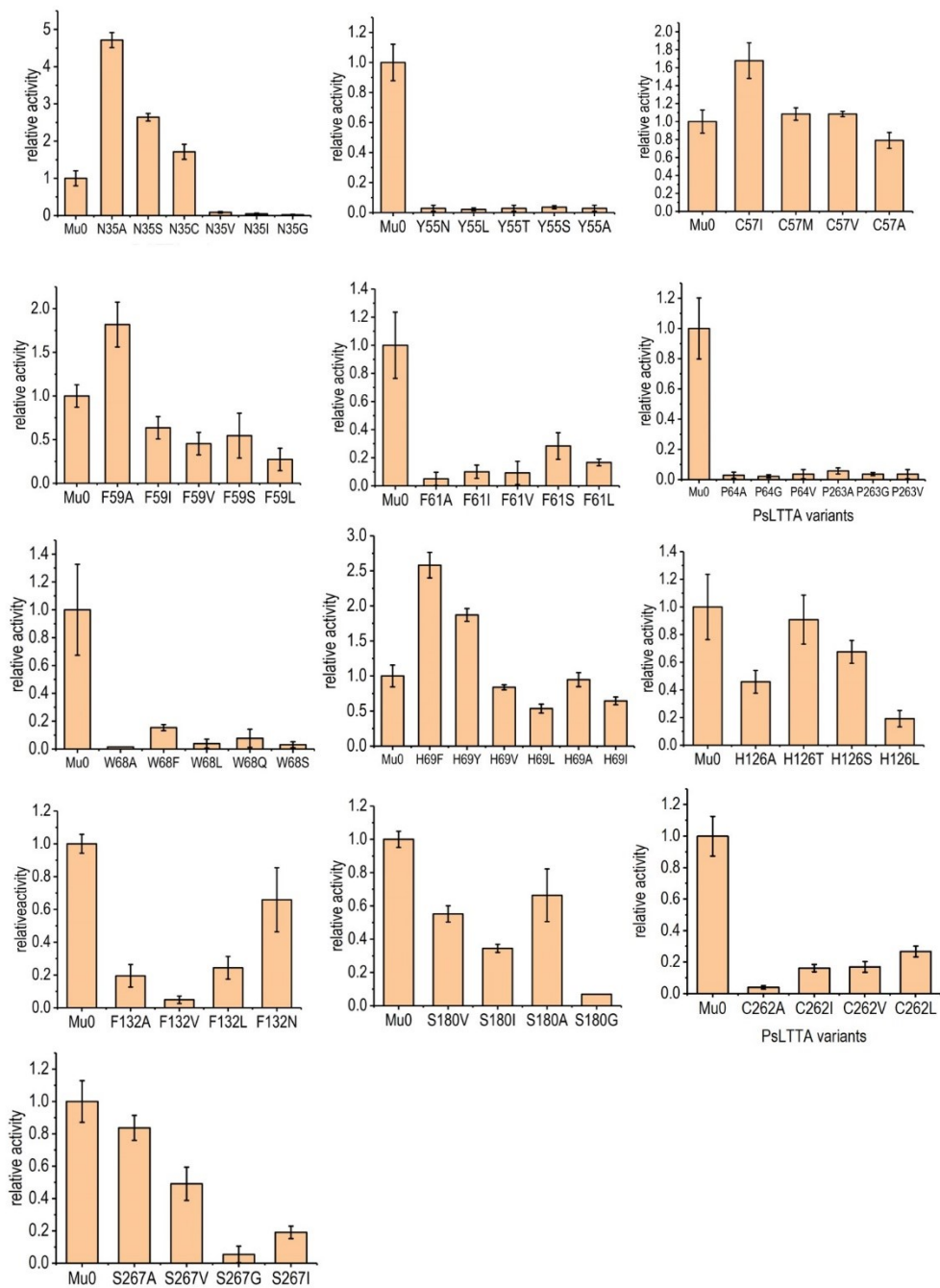
37 aldimine of β -hydroxy- α -amino acid ($E(Aex^{\beta\text{-hydroxy-}\alpha\text{-amino acid}})$) and the reintegration of

38 catalytic residue K234 with PLP is occurred to form an internal aldimine (Ain),

39 leading to the release of β -hydroxy- α -amino acids.

40

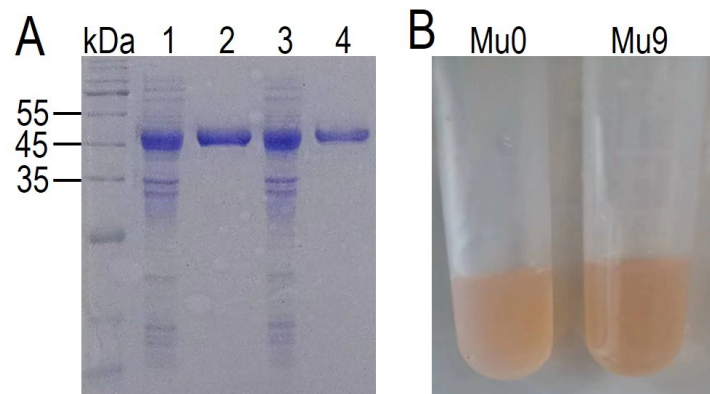
41 **Figure S3.**



42

43 **Figure S3.** The activities of PsLTTA variants were screened by high-throughput
 44 screening method. The reaction catalyzed by wild-type PsLTTA (Mu0) was used as a
 45 control. All experiments were conducted in triplicate and the results were represented
 46 as the mean \pm standard deviation.

48 **Figure S4.**



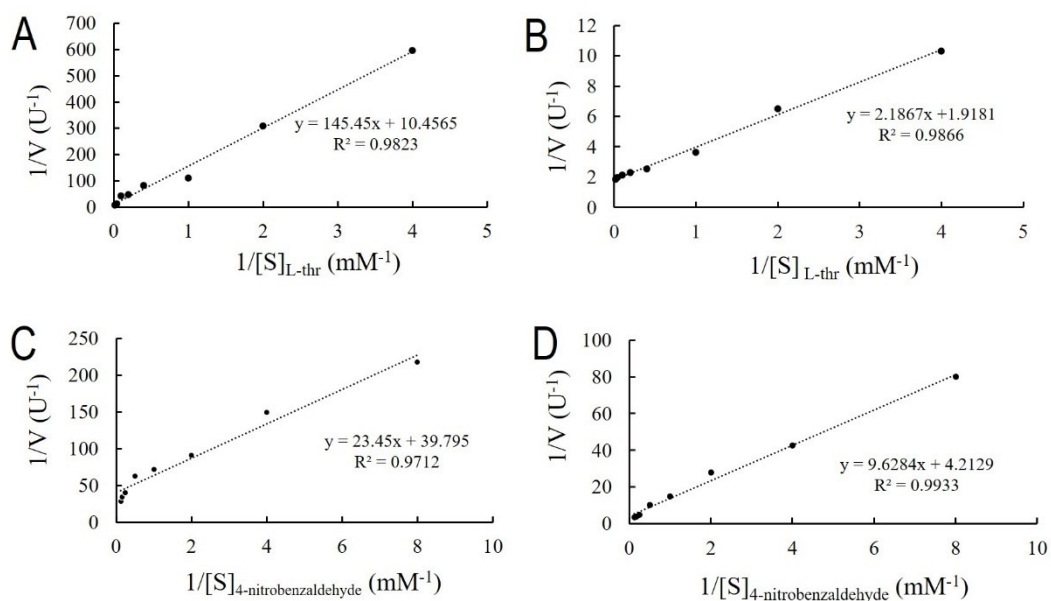
49

50 **Figure S4.** (A) SDS-PAGE analysis of PsLTTA-Mu0 and PsLTTA-Mu9. Lane 1,
51 whole cell extract of PsLTTA-Mu0; Lane 2, purified PsLTTA-Mu0; Lane 3, whole
52 cell extract of PsLTTA-Mu9; Lane 4, purified PsLTTA-Mu9. (B) The purified
53 PsLTTA-Mu0 and PsLTTA-Mu9 were pink in solution.

54

55

56 **Figure S5.**



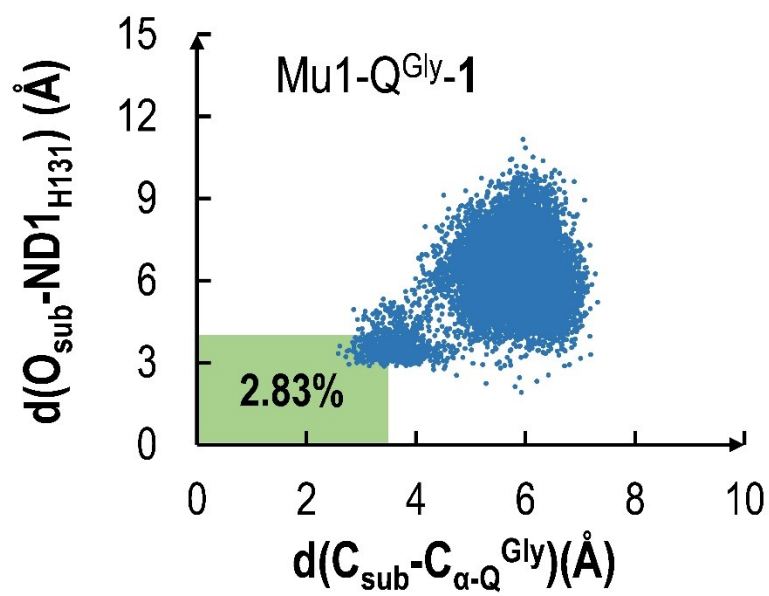
57

58 **Figure S5.** The kinetic plots of PsLTTA-Mu0 and PsLTTA-Mu9 toward substrates **1**

59 and L-threonine. V : reaction rate; $[S]$: substrate concentration.

60

61 **Figure S6.**



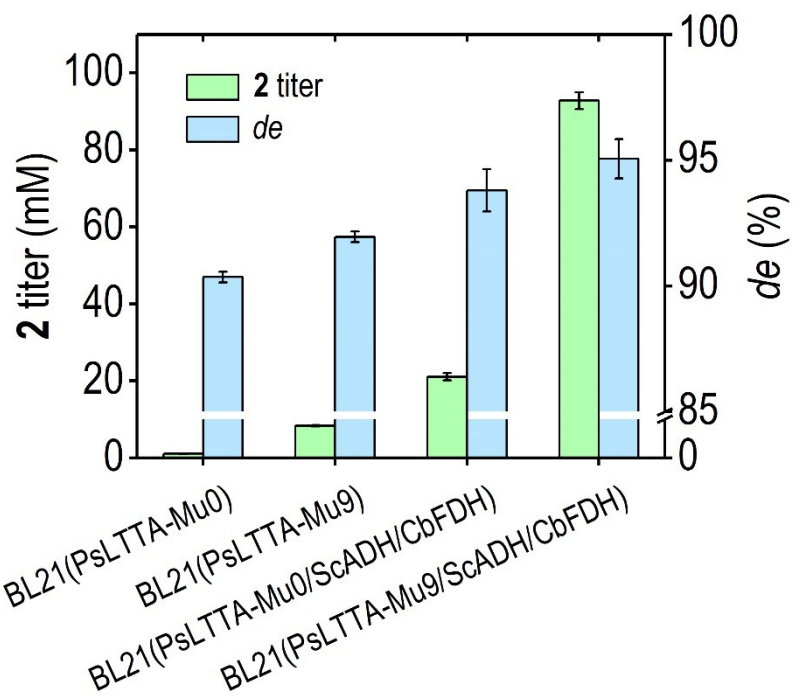
62

63 **Figure S6.** Conformation maps of Mu1-Q^{Gly}-1. The limit of “catalytic distance”

64 $d(\text{O}_{\text{sub}}-\text{ND1}_{\text{H131}}) < 4.0$ Å and $d(\text{C}_{\text{sub}}-\text{C}_{\alpha\text{-Q}}^{\text{Gly}}) < 3.5$ Å are colored by green.

65

66 **Figure S7.**



67

68 **Figure S7.** The yield and *de* of **2** synthesized by whole-cell catalyst BL21(PsLTTA-

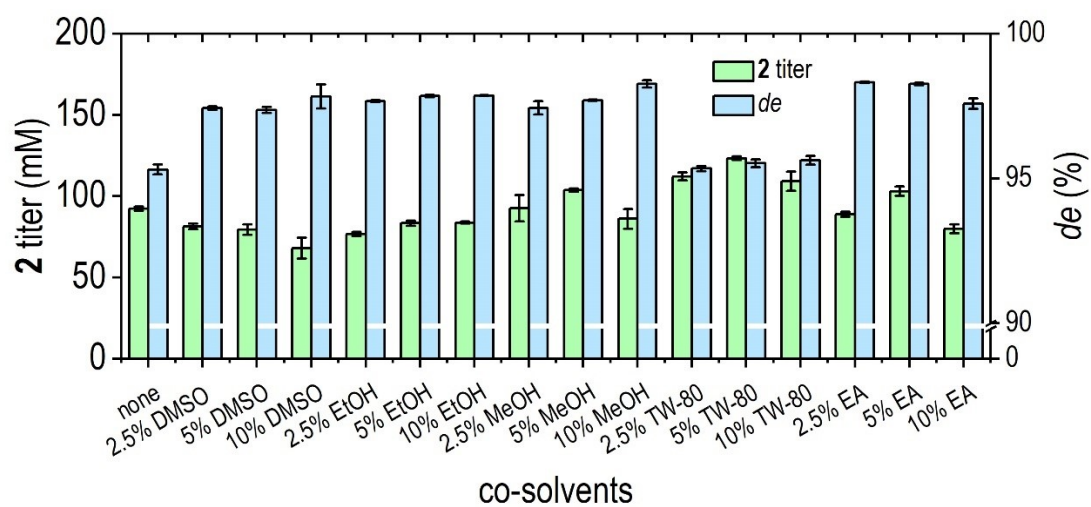
69 Mu0), BL21(PsLTTA-Mu9), BL21(PsLTTA-Mu0/ScADH/CbFDH) and

70 BL21(PsLTTA-Mu9/ScADH/CbFDH).

71

72

73 **Figure S8.**

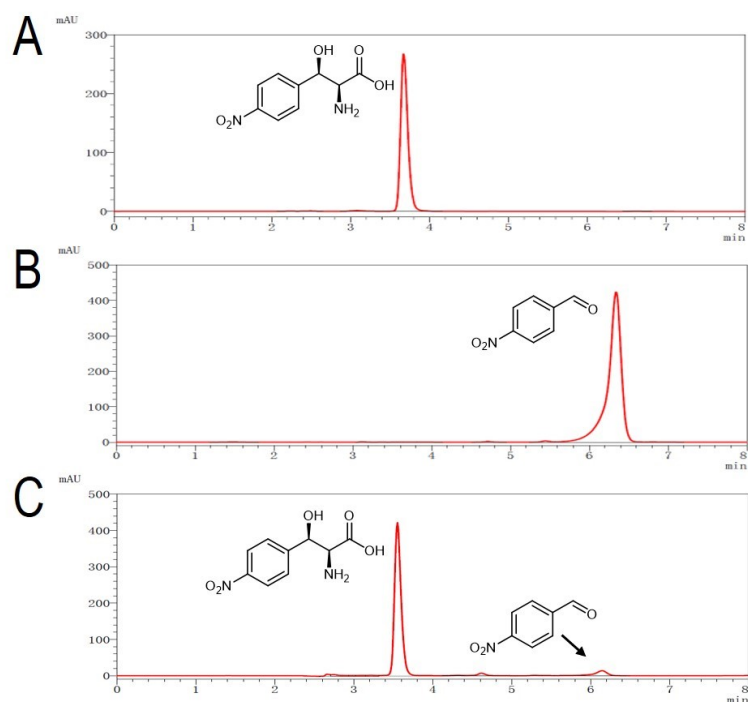


74

75 **Figure S8.** The optimization of co-solvents addition on the synthesis of **2**. Transaldol
76 reaction was performed at 30 °C and 200 rpm for 2 h, in 1 mL of Tris-HCl buffer (50
77 mM, pH 7.5) containing 50 mg/mL of whole-cell catalyst, 200 mM **1**, 220 mM L-
78 threonine, 250 mM sodium formate, 0.1 mM PLP and 0.3 mM NAD⁺. The conversion
79 and stereospecificity of **2** were detected by chromatography analysis.

80

81 **Figure S9.**

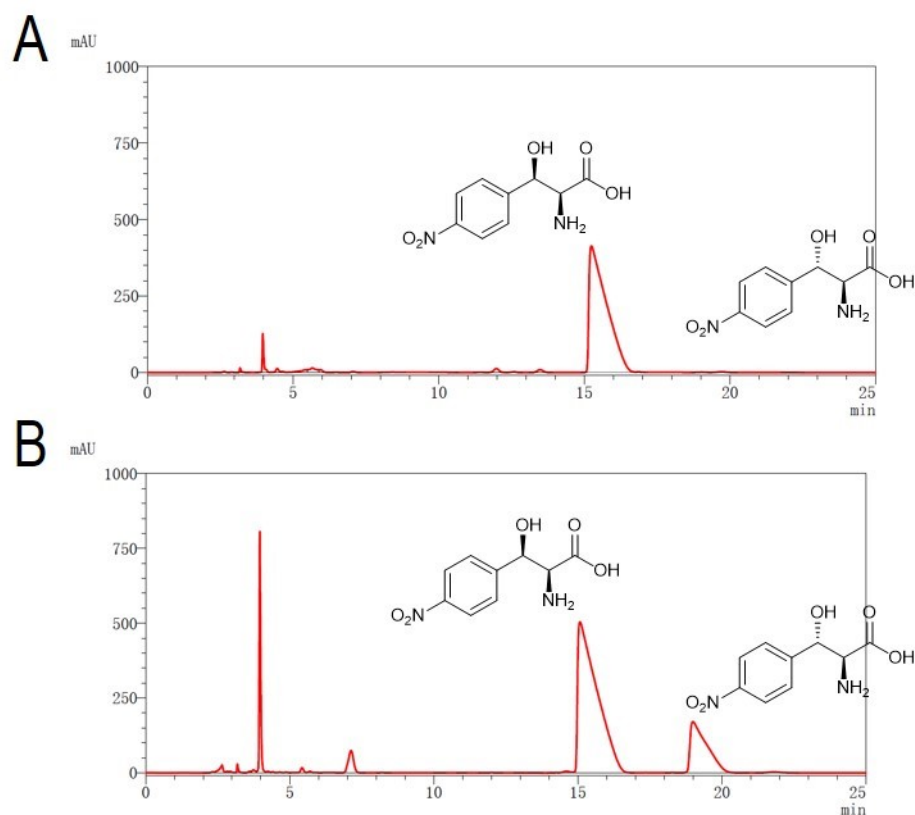


82

83 **Figure S9.** HPLC chromatogram of sample from bio-catalysis of **1** to **2** with whole
84 cell catalyst BL21(PsLTTA-Mu9/ScADH/CbFDH). (A) HPLC chromatogram of **2**
85 standard (t=3.6 min). (B) HPLC chromatogram of **1** standard (t=6.1 min). (C) HPLC
86 chromatogram of sample catalyzed by whole cell catalyst BL21(PsLTTA-
87 Mu9/ScADH/CbFDH).

88

89 **Figure S10.**

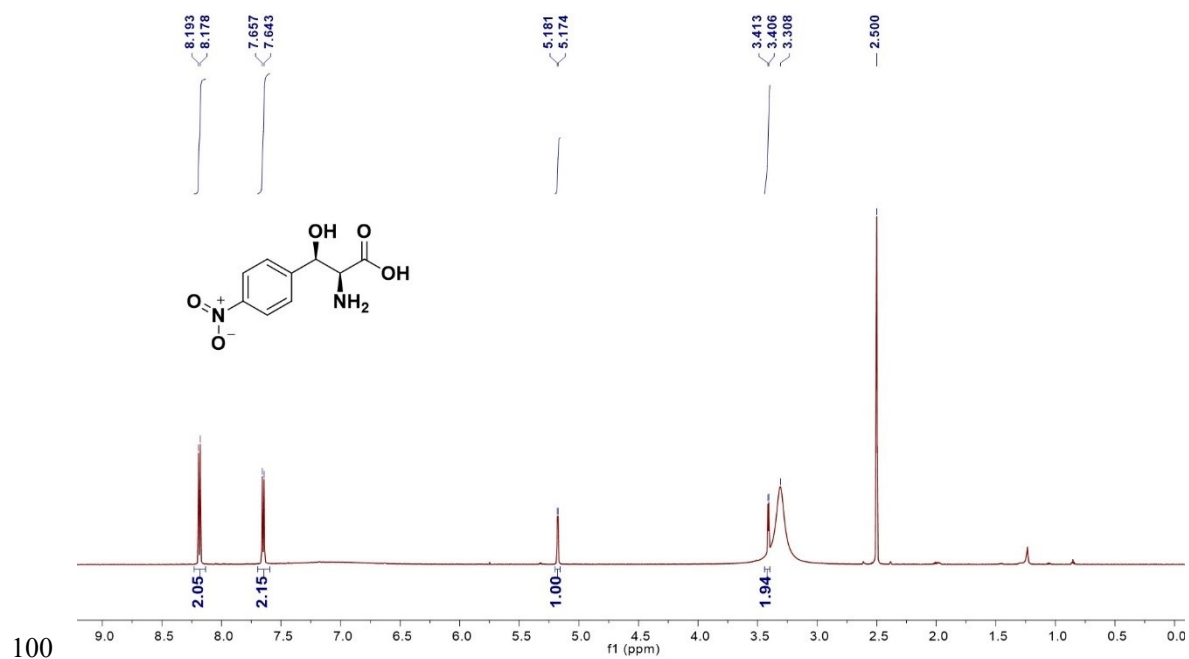


90

91 **Figure S10.** Chiral HPLC chromatograms of 2-amino-3-hydroxy-3-(4-
92 nitrophenyl)propanoic acid. (A) Transaldol reaction catalyzed by whole cell catalyst
93 BL21(PsLTTA-Mu9/ScADH/CbFDH) with 98.9% *de*. 2-amino-3-hydroxy-3-(4-
94 nitrophenyl)propanoic acid ($t_{(2S, 3R)}=15.3$ min, $t_{(2S, 3S)}=19.2$ min). (B) Transaldol
95 reaction catalyzed L-Threonine aldolase with 62% *de* was selected as a control. 2-
96 amino-3-hydroxy-3-(4-nitrophenyl)propanoic acid ($t_{(2S, 3R)}=15.2$ min, $t_{(2S, 3S)}=19.1$
97 min).

98

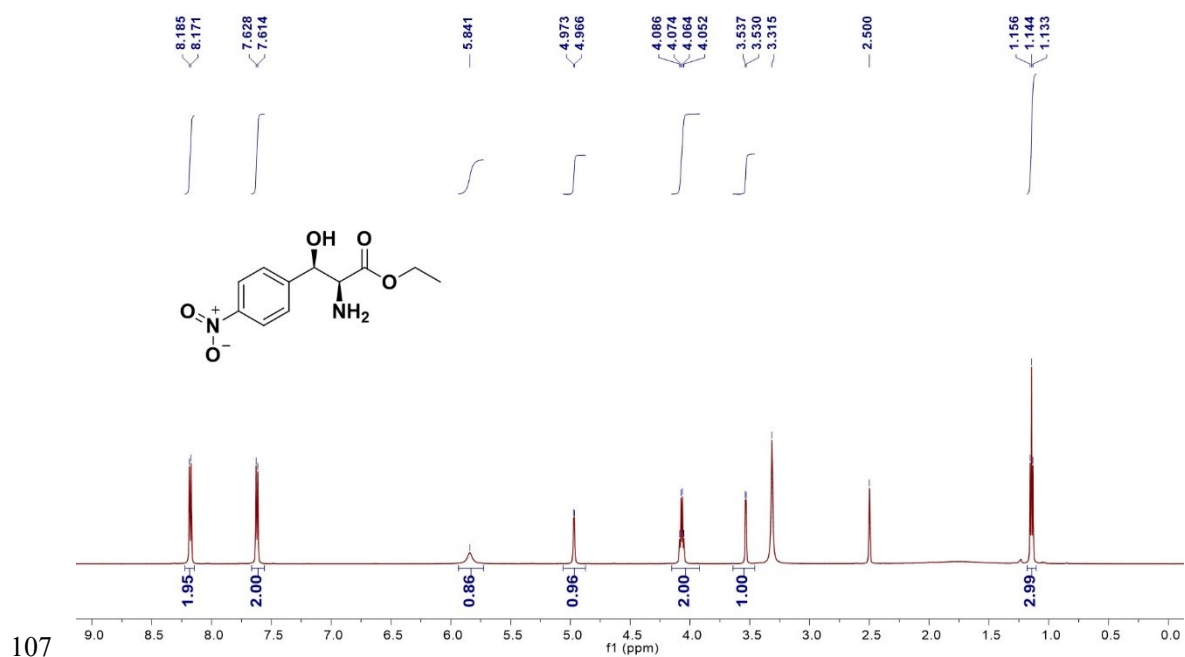
99 **Figure S11.**



101 **Figure S11.** ¹H- NMR spectra of (2*S*,3*R*)-2-amino-3-hydroxy-3-(4-
102 nitrophenyl)propanoic acid (**2**). ¹H NMR (600 MHz, DMSO-*d*₆) δ (ppm) = 8.18 (d, *J*
103 = 9.0 Hz, 2H), 7.62 (d, *J* = 8.4 Hz, 1H), 5.18 (d, *J* = 4.2 Hz, 1H), 3.41 (d, *J* = 4.2 Hz,
104 1H).

105

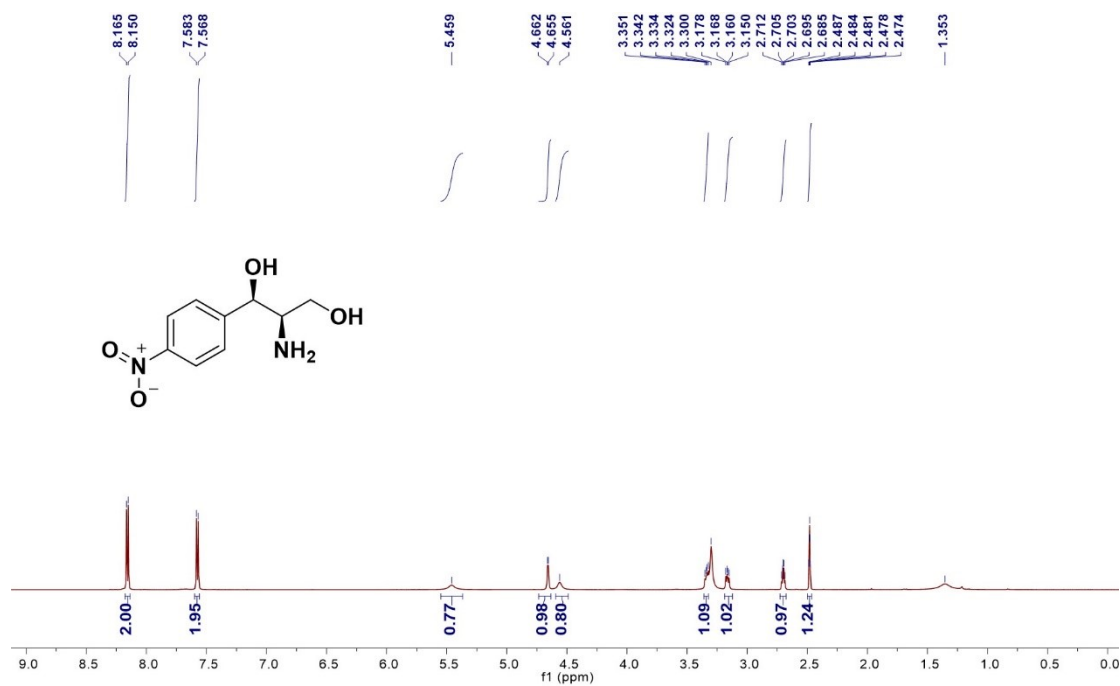
106 **Figure S12.**



107
 108 **Figure S12.** ¹H- NMR spectra of ethyl (2*S*,3*R*)-2-amino-3-hydroxy-3-(4-
 109 nitrophenyl)propanoate (**3**). ¹H NMR (600 MHz, DMSO-*d*₆) δ (ppm) = 8.18 (d, *J* =
 110 8.6 Hz, 2H), 7.62 (d, *J* = 8.4 Hz, 2H), 5.84 (s, 1H), 4.97 (d, *J* = 4.2 Hz, 1H), 4.07 (q, *J*
 111 = 7.2 Hz, 2H), 3.53 (d, *J* = 4.2 Hz, 1H), 1.14 (t, *J* = 7.2 Hz, 3H).

112

113 **Figure S13.**



114

115 **Figure S13.** ¹H- NMR spectra of (1*R*,2*R*)-2-amino-1-(4-nitrophenyl)propane-1,3-diol

116 (4). ¹H NMR (600 MHz, DMSO-*d*₆) δ (ppm) = 8.16 (d, *J* = 9.0 Hz, 2H), 7.58 (d, *J* =

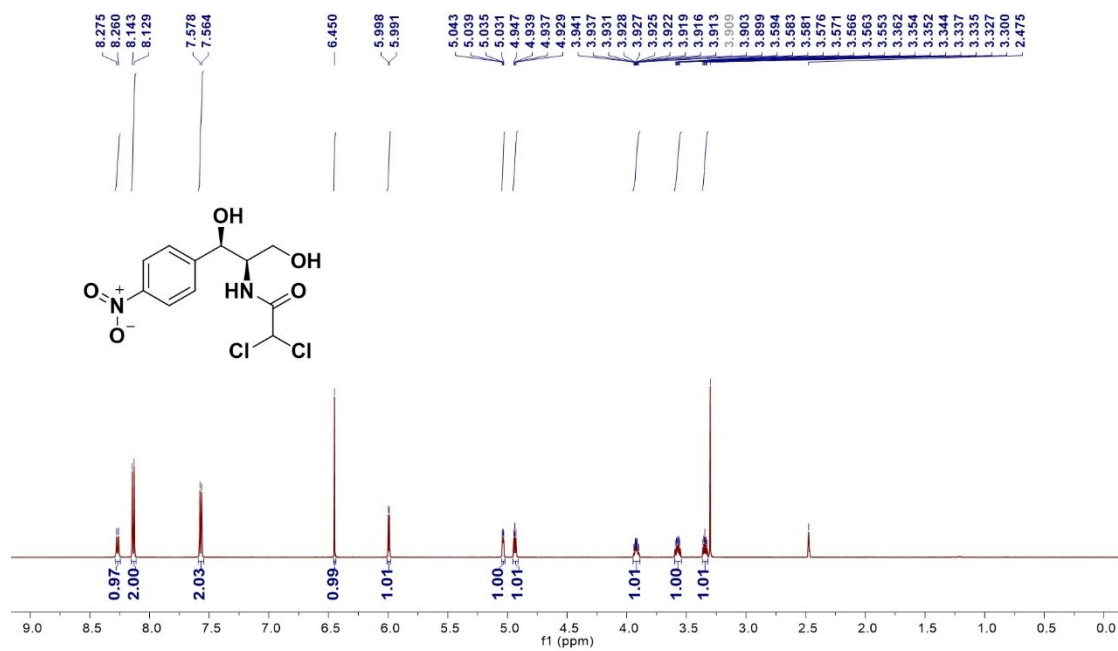
117 9.0 Hz, 2H), 5.46 (s, 1H), 4.66 (d, *J* = 4.2 Hz, 1H), 4.56 (s, 1H), 3.34 (dd, *J* = 10.2,

118 5.4 Hz, 1H), 3.16 (dd, *J* = 10.2, 6.0 Hz, 1H), 2.70 (q, *J* = 5.4 Hz, 1H), 2.48-2.47 (m,

119 2H).

120

121 **Figure S14.**



122

123 **Figure S14.** ¹H- NMR spectra of 2,2-dichloro-N-((1R,2R)-1,3-dihydroxy-1-(4-
 124 nitrophenyl)propan-2-yl)acetamide (**5**). ¹H NMR (600 MHz, DMSO-*d*₆) δ (ppm) =
 125 8.27 (d, *J* = 9.0 Hz, 1H), 8.14 (d, *J* = 8.4 Hz, 2H), 7.57 (d, *J* = 8.4 Hz, 2H), 6.45 (s,
 126 1H), 5.99 (d, *J* = 4.2 Hz, 1H), 5.04 (dd, *J* = 4.8, 2.4 Hz, 1H), 4.94 (dd, *J* = 6.0, 4.8 Hz,
 127 1H), 4.11-3.88 (m, 1H), 3.59-3.55 (m, 1H), 3.36-3.33 (m, 1H).