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Table S1. Primers used for site-directed mutagenesis of Cbotu_EstA gene. The inserted mutations are underlined.

Zn-coordination	
	5'-ACC GTT GGT CCG GTT AGC AGC AAT TGG CTG CGT GCA TGT
Chotu EstA D130L F	GAA CTG ATG CAT ATA TTG T-3'
	5'-ACA ATA TAT GCA TAC AGT TCA CAT GCA CGC AGC CAA
Chotu EstA D130L R	TTG CTG CTA ACC GGA CCA ACG GT-3'
<u>coota_bar_bisol_</u> it	
Cbotu EstA H150F F	5′-GAT TAT GGT GAA GCA TTT GCC AAA AAA TTC-3′
Cbotu EstA H150F R	5′-GAA TTT TTT GGC AAA TGC TTC ACC ATA ATC-3′
Cbotu_EstA_H156F_F	5′-CCA AAA AAT TCA AA <u>T T</u> TA ATC GTT ACG GTC G-3′
Cbotu_EstA_H156F_R	5′-CGA CCG TAA CGA TTA <u>AA</u> T TTG AAT TTT TTG G-3′
Cbotu_EstA_D302L_F	5'-ACA GCA CCA AA <u>C TG</u> A TTG CAA CCT ATG-3'
Cbotu_EstA_D302L_R	5'-CAT AGG TTG CAA T <u>CA G</u> TT TGG TGC TGT-3'
Zn-cavity	
	5'-CCT ATA CCG CAA CCG TTG GTC CGG TTA GC <u>G CC</u> A ATT
Cbotu_EstA_S127A_F	GGG ATC GTG CAT GTG AAC TGT ATG CA-3'
	5'-TGC ATA CAG TTC ACA TGC ACG ATC CCA ATT <u>GGC</u> GCT
Cbotu_EstA_S127A_R	AAC CGG ACC AAC GGT TGC GGT ATA GG -3'
	5'-CAC CGT TGA TTA TGG TGA AGC ACA TGC CAA AAA A <u>TA</u>
Cbotu_EstA_F154Y_F	CAA ACA TAA TCG TTA CGG TCG TAC CTA TCC-3
	5'-GGA TAG GTA CGA CCG TAA CGA TTA TGT TT <u>G TA</u> T TTT TTG
Cbotu_EstA_F154Y_R	GCA TGT GCT TCA CCA TAA TCA ACG GTG-3
	5 -AGC AGC ATC TAT GAT CIG AAA CIG GAT CAG <u>CAC</u> GGT
Cbotu_EstA_W274H_F	CIG AAA AAA CAG AAI GGI GAA AGC-3
Chat Frid W274H D	5 -GCT TTC ACC ATT CTG TTT TTT CAG ACC <u>GTG</u> CTG ATC CAG
Cbotu_EstA_W2/4H_K	ITT CAG ATC ATA GAT GCT GCT-3
Constant and the second	
Cavity entrance	
Choty EstA W120A E	$\beta = COC AAC COT TOO TCC OOT TAO CAO CAA TOC OOA TCOTGC ATG TGA ACT GTA TGC ATA TAT TGT TGG T3'$
CDOIU_ESIA_W129A_F	5' ACC AAC AAT ATA TGC ATA CAG TTC ACA TGC ACG ATC
Choty EstA W120A P	CGC ATT GCT GCT AAC CGG ACC AAC GGT TGC G_3'
COORT_ESTA_W127A_K	5'_ATT OGT ACC CTG ACC CAG CTG CTG AGC GAA GGT GCC
Chotu EstA \$1994 F	GAA GAA GAA ATT AAC TGC GGT CAA GAA AAC AT-3'
Coold_Lour_DIPPA_I	5'- ATG TTT TCT TGA CCG CAG TTA ATT TCT TCT TCG GCA CCT
Cbotu EstA S199A R	TCG CTC AGC AGC TGG GTC AGG GTA CGA AT -3'



Figure S1. SDS-PAGE (4-15%) of Cbotu_EstA wild-type and zinc-binding variants expressed in *E. coli* BL21-Gold(DE3). Samples were withdrawn after 20 h of induction, lysed and centrifuged to test the lysate and the pellet for soluble proteins and inclusion bodies, respectively. Lane 1: Cbotu_EstA wild-type; lane 2-5: D130L, H150F, H156F, and D302L variant.



Figure S2. SDS-PAGE (4-15%) of Cbotu_EstA wild-type and zinc cavity variants expressed in *E. coli* BL21-Gold(DE3). Samples were withdrawn after 20 h of induction, lysed and centrifuged to test the lysate and the pellet for soluble proteins and inclusion bodies, respectively. Lane 1: Cbotu_EstA wild-type; lane 2-6: S127A, W129A, F154Y, S199A, and W274H variant.



Figure S3. SDS-PAGE analysis (4-15%) of Cbotu_EstA wild-type and variants expressed in *E. coli* BL21-Gold(DE3) with 0.05 mM IPTG and purified by IMAC. M: protein marker IV; lane 1: Cbotu_EstA Wild-type; lane 2: D130L; lane 3: H150F; lane 4: H156F; lane 5: D302L; lane 6: S127A; lane 7: W129A; lane 8: F154Y; lane 9: S199A; lane 10: W274H.



Figure S4. Michaelis-Menten plot of Cbotu_EstA wild-type and variants kinetics with the substrate *para*nitrophenyl butyrate (*p*NPB) in a concentration range 0.3 - 15 mM. (**A**) Cbotu_EstA wild-type and variants from the zinc cavity and the entrance to the cavity: Cbotu_EstA (+); S127A (×); W129A (*); F154Y (\Box); S199A (**•**); W274H (\circ). (**B**) Cbotu_EstA variants from the zinc-coordination site: D130L (+); H150F (×); H156F (*); D302L (\Box).



Figure S5. Possible PBAT hydrolysis patterns. Products terephthalic acid (Ta) and mono(4-

hydroxybutyl) terephthalate (BTa) were detected by HPLC ⁴³.



Figure S6. Enzyme inhibition of Cbotu_EstA wild-type and variants by terephthalic acid in a range of concentration of 0 - 0.75 mM.