Supplementary Materials

Supplementary Table S1 The relative activity of purified wild-type LATA and its mutants toward L-*allo*-threonine and L-threonine

Enzyme	Relative activity (%)		Specificity ratio
	L-allo-Thr	L-Thr	L-allo-Thr/L-Thr
LATA_WT	100	100	115
LATA_E90A	6.56	3.41	222
LATA_D126A	46.1	57.1	93.1

The activity of the wild-type LATA toward the each substrate is represented as 100, respectively.

The method for purification and activity assay of LATA and its mutants were described in the subsections 2.3. and 2.6., respectively. The purified LATA and its mutants were prepared and 8 mM substrates were added to the reaction mixture.

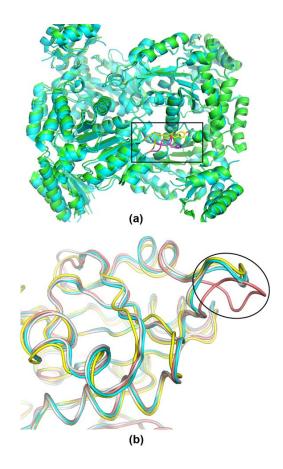
Supplementary Table S2 The relative activity of His128 saturation mutagenesis toward L-*allo*-threonine and L-threonine

Enzyme —	Relative activity (%)		Specificity ratio
	L-allo-Thr	L-Thr	L-allo-Thr/L-Thr
WT	100	100	74.6
H128A	48.5	83.6	43.3
H128C	31.3	79.3	29.4
H128D	9.01	4.90	136
H128E	9.24	13.6	50.8
H128F	140	833	12.5
H128G	27.1	46.6	43.4
H128I	48.3	199	22.7
H128K	57.6	165	32.7
H128L	95.5	476	18.7
H128M	115	297	36.1
H128N	23.7	55.1	40.2
H128P	35.4	64.1	51.8
H128Q	23.5	53.5	42.8
H128R	15.1	37.7	39.2
H128S	19.7	453	4.24
H128T	25.4	68.1	36.3
H128V	33.8	111	29.6
H128W	61.7	208	28.9
H128Y	201	844	17.8

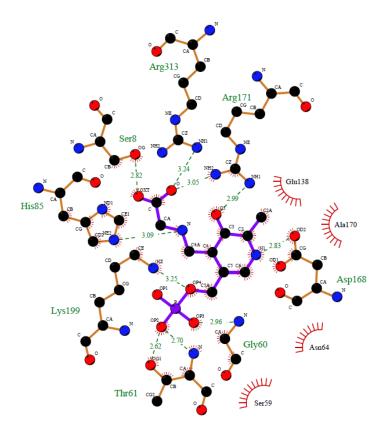
The activity of the wild-type LATA toward each substrate is taken as 100%. The method for measuring threonine aldolase activity of random mutagenesis of LATA was described in the subsection 2.1. The cell-free extracted LATA and its mutants were prepared and 4 mM substrates were added to the reaction mixture.

 $\textbf{Supplementary Fig. S1} \ \text{Proposed mechanism of the reaction catalyzed by threonine aldolases}.$

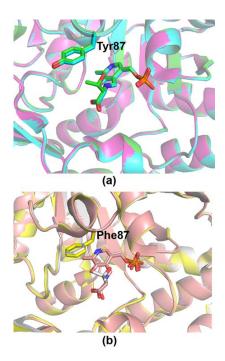
Supplementary Fig. S2 Enzymatic reaction scheme of threonine aldolases for the reversible interconversion of L-allo-threonine/L-threonine to glycine and acetaldehyde.



Supplementary Fig. S3 (a) The movable loop of Ala123-Pro131 in the tetrameric structures of LATA (green) and LATA_H128Y/S291R (cyan). (b) Superposition of the structures of LATA (cyan), LATA_H128Y/S291R (salmon), TMTA (yellow) and eTA (white). The movable loop is denoted in black cycle.



Supplementary Fig. S4 Schematic diagram of protein-ligand interactions generated by LIGPLOT. The hydrogen bonds are shown as green dashed lines. Hydrophobic contacts to the ligand are represented by red semi-circles with radiating spokes.



Supplementary Fig. S5 (a) The superposition of Tyr87 in TMTA structures (TMTA-PLP, magenta; TMTA-PLP-Gly, cyan; TMTA-PLP-Thr, green). (b) The superposition of Phe87 in eTA structures (eTA-PLP, yellow; eTA-PLP-Ser, salmon; eTA-PLP-Thr, white).