Supplementary Table S1. Primers used in this study.

Primers	Sequences [a]
Cloning of C14ofr149 gene into pETDuet-1	
P1 (BamHI)	5′-catggatccgGAGAGCGCGCTGGCGGTGCCCCGGC-3′
P2 (PstI)	5′-tggctgcagTCACTTGAGAAGAAATCCATCCCTC-3′
Cloning of PaLhpD genes into pETDuet-1	
P3 (BamHI)	5′-catggatccgATCCGAATGACGCTGGACGAGGTCCGCG-3′
P4 (HindIII)	5′-attaagctTCACTCCAGCAACGCCAGCAGCTCCCGG-3′
Cloning of AbLhpH gene into pETDuet-1	
P5 (BamHI)	5′-catggatccgAAAATTACCCGATCCCTTTCCACCGTCG-3′
P6 (HindIII)	5′-aattaagctTCAGGCGATGTTTTGCTCGGCCGACCAGCTGGC-3′
Cloning of CpLhpH gene into pETDuet-1	
P7 (BamHI)	5′-catggatccgACAAAAAATATAGCGCAAGCAGCTG-3′
P8 (PstI)	5′-tggctgcagTTATCTTAATAAAAAACCATATTTC-3′
Cloning of AbLhpI into pETDuet-1	
P9 (BamHI)	5′-catggatccgACCGCTCTTTCCCCGATTCCCGTTTTCG-3′
P10 (HindIII)	5′-attaagctTCAGCCGGCCCGGCGTGCGGCCAGCG-3′
Cloning of CpLhpI into pETDuet-1	
P11 (BamHI)	5′-catggatccgAAAATTATTAGCGCCGAACAAGTCCACC-3′
P12 (HindIII)	5′-tggctgcagTTAATCTGCTAACTTTTCTACTACGCTATG-3′
Disruptant construction of AbLhpI	
P13 (SacII)	5′-catccgcggGTCACGACGTTGTAAAACGACGGCC-3′
P14 (SacII)	5′-tggccgcggTTTCACACAGGAAACAGCTATGACC-3′
P15 (MfeI)	5′-catcaattgACCGCTCTTTCCCCGATTCCCGTTTTCG-3′
P16 (MfeI)	5′-attcaattgCAGCCGGCCCGGCGTGCGGCCAGCG-3′

[a] Small letters indicate additional bases for introducing digestion sites of restriction enzymes in parentheses.

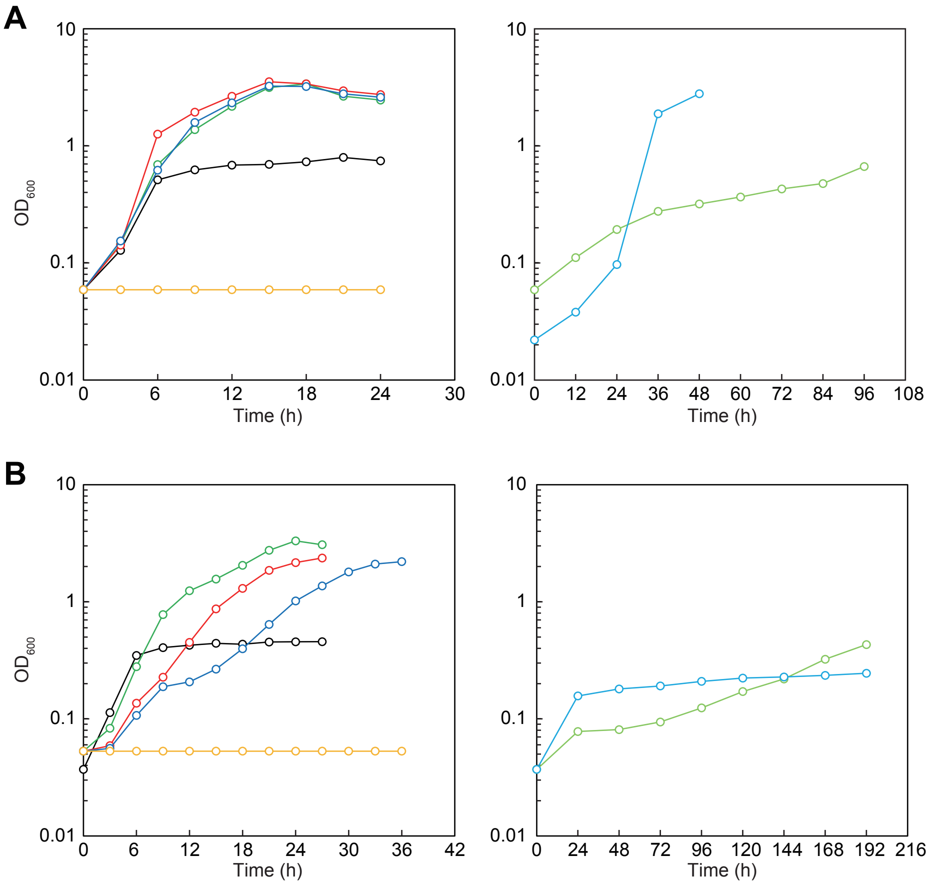


FIGURE S1. Growth curves of *P. putida* (A) and *P. aeruginosa* (B) on glucose (*black*), L-proline (*green*), D-proline (*light-green*), T4LHyp (*red*), C4DHyp (*blue*), T3LHyp (*yellow*) and D-lysine (*aqua*) as a sole carbon source (30 mM).

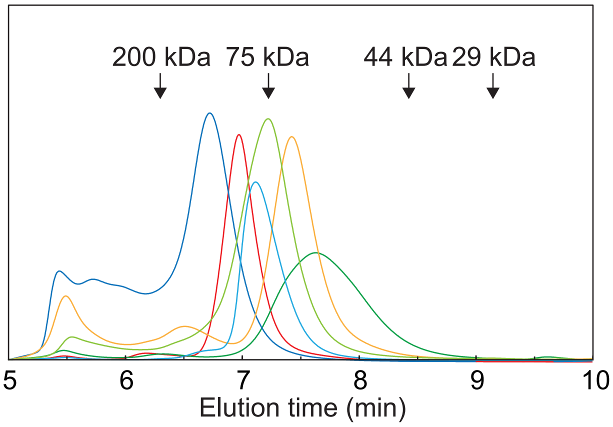
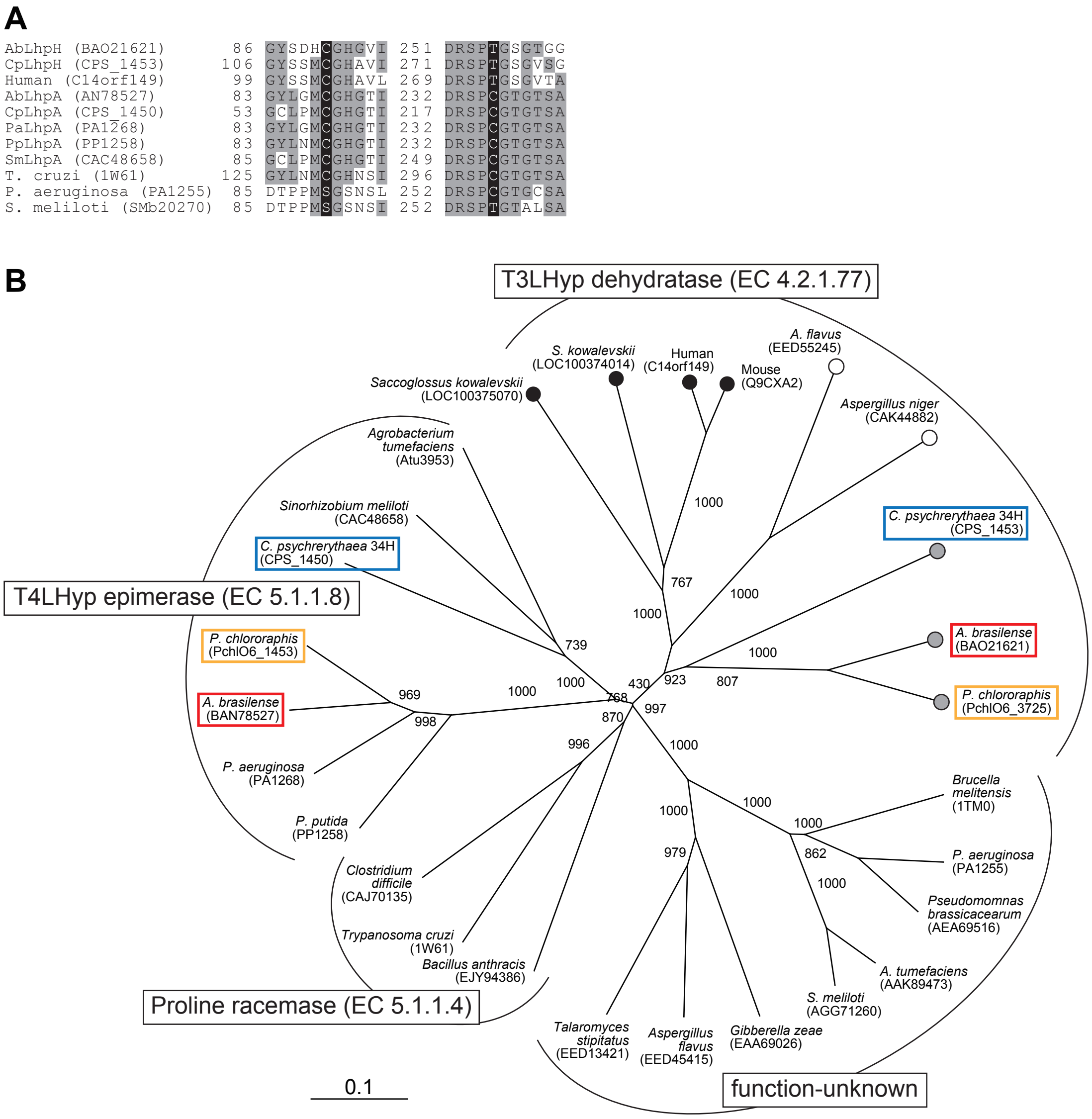


FIGURE S2. Elution profile of purified recombinant proteins during gel filtration. AbLhpH, *red;* CpLhpH, *blue*; C14orf149, *orange*; PaLhpD, *green*; AbLhpI, *light-green*; CpLhpI, *aqua*.



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AbLhpH (BAO21621)       86 GYSDHCGHGVI 251 DRSPTGSGTGG
CpLhpH (CPS_1453)      106 GYSSMCGHAVI 271 DRSPTGSGVSG
Human (C14orf149)       99 GYSSMCGHAVL 269 DRSPTGSGVTA
AbLhpA (AN78527)        83 GYLGMCGHGTI 232 DRSPCGTGTSA
CpLhpA (CPS_1450)       53 GCLPMCGHGTI 217 DRSPCGTGTSA
PaLhpA (PA1268)         83 GYLGMCGHGTI 232 DRSPCGTGTSA
PpLhpA (PP1258)         83 GYLNMCGHGTI 232 DRSPCGTGTSA
SmLhpA (CAC48658)       85 GCLPMCGHGTI 249 DRSPCGTGTSA
T. cruzi (1W61)        125 GYLNMCGHNSI 296 DRSPCGTGTSA
P. aeruginosa (PA1255)  85 DTPPMSGSNSL 252 DRSPCGTGCSA
S. meliloti (SMb20270)  85 DTPPMSGSNSI 252 DRSPTGTALSA
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FIGURE S3. Phylogenetic analysis of T3LHyp dehydratase. (A) Phylogenetic tree of proline racemase superfamily. The *number* on each *branch* indicates the bootstrap value. T3LHyp dehydratases and T4LHyp epimerases from the same organisms are in the colored box. Proteins with *black*, *white* and *gray-colored circles* in T3LHyp dehydratase subfamily are from mammalian, fungi and bacteria (discovered in this study), respectively. (B) Partial multiple sequence alignment of deduced amino acid sequences. Catalytic cysteine and/or threonine residues are shown as *white letters in black boxes*. *Gray-shaded letters* indicate highly conserved amino acid residues.

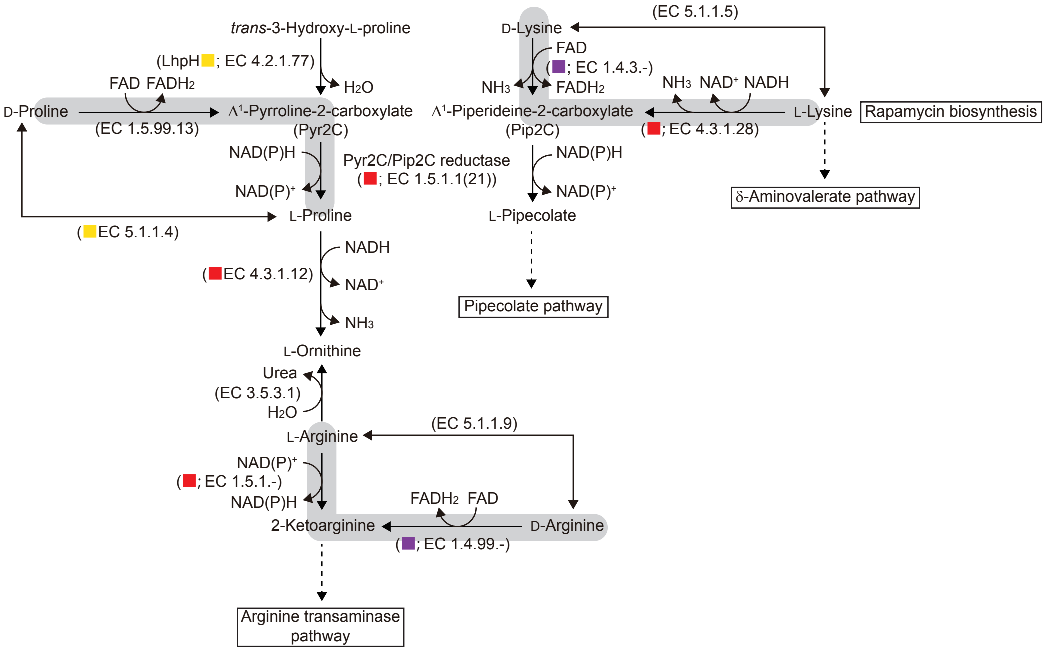

FIGURE S4. Metabolic pathways around Pyr2C/Pip2C reductase. Homologous genes are indicated in the same color, and correspond to Fig. 1ABD. *Gray-colored routes* indicate L- to D-epimerization (racemization) of amino acid consisting of two distinct FAD- and NAD(P)$^+$-dependent dehydrogenase (oxidase).