

**SupplementalTable S2.** Complete information of amino acid biosynthesis enzymes in this study.

<i>GENE<sub>i</sub></i>	ORF	PDB entry <sup>a</sup>	E.C. <sup>b</sup>	Cofactor <sup>c</sup>	Protein domains <sup>d</sup>	Cellular Component <sup>e</sup>	Biological Process <sup>f</sup>
<i>ALT1</i>	YLR089C	3ihj (45%)	2.6.1.2	PLP	1 (PLP-dependent transferases)	Mitochondrion	Alanine biosynthetic process; alanine catabolic process; chronological cell aging
<i>ARG3</i>	YJL088W	1oth (40%)	2.1.3.3		1 (Aspartate/ornithine carbamoyltransferase)	Cytoplasm	Arginine biosynthetic process
<i>ARG4*</i>	YHR018C	1c3c (23%)	4.3.2.1		1 (L-aspartase-like)	Cytoplasm	Arginine biosynthetic process via ornithine
<i>ARO3</i>	YDR035W	1q3n (16%)	2.5.1.54		1 (Aldolase)	Cytoplasm, mitochondrion, nucleus	Chorismate biosynthetic process
<i>ARO4</i>	YBR249C	1q3n (15%)	2.5.1.54		1 (Aldolase)	Cytoplasm, nucleus	Chorismate biosynthetic process
<i>ARO7</i>	YPR060C	4csm (100%)	5.4.99.5		1 (Chorismate mutase II)	Cytoplasm, nucleus	Phenylalanine and tyrosine biosynthetic processes
<i>ASN1</i>	YPR145W	1ct9 (48%)	6.3.5.4	ATP	2 (Adenine nucleotide alpha hydrolases-like; Nucleophile aminohydrolases)	Cytoplasm	Asparagine biosynthetic process
<i>ASN2</i>	YGR124W	1ct9 (49%)	6.3.5.4	ATP	2 (Adenine nucleotide alpha hydrolases-like; Nucleophile aminohydrolases)	Cytoplasm	Asparagine biosynthetic process
<i>BAT2</i>	YJR148W	2coi (50%)	2.6.1.42	PLP	1 (PLP-dependent enzymes)	Cytoplasm, nucleus	Branched-chain amino acid biosynthetic and catabolic processes
<i>HOM2</i>	YDR158W	2qz9 (30%)	1.2.1.11	NADP	2 (GAPDH-like; Rossmann-fold)	Cytoplasm, nucleus, plasma membrane	Homoserine, methionine and threonine biosynthetic processes

<i>HOM6</i>	YJR139C	1ebf (100%)	1.1.1.3	NADP	2 (GAPDH -like; NAD(P)-binding Rossmann-fold)	Cytoplasm, nucleus	Homoserine, methionine and threonine biosynthetic processes
<i>ILV1</i>	YER086W	1pwh (29%)	4.3.1.19	PLP	2 (PLP-dependent enzymes; ACT-like)	Mitochondrion	Isoleucine biosynthetic process; threonine catabolic process
<i>ILV2</i>	YMR108W	1n0h (100%)	2.2.16	TPP; FAD	3 (2 ThDP binding; 1 DHS-like NAD/FAD-binding)	Acetolactate synthase complex, mitochondrion	Branched-chain amino acid biosynthetic process
<i>MET2</i> *	YNL277W	2vat (42%)	2.3.1.31		1 (alpha/beta-Hydrolases)	Cytoplasm	Homoserine and sulfur amino acid metabolic processes; methionine biosynthetic process
<i>THR4</i>	YCR053W	1kl7 (100%)	4.2.3.1	PLP	1 (PLP-dependent enzymes)	Cytoplasm, nucleus	Threonine biosynthetic process
<i>TKL1</i>	YPR074C	1trk (100%)	2.2.1.1	TPP	3 (2 ThDP binding; 1 TK C-like)	Cytoplasm	Pentose-phosphate shunt
<i>TKL2</i> *	YBR117C	1trk (71%)	2.2.1.1	TPP	3 (2 ThDP binding; 1 TK C-like)	Cytoplasm, nucleus	Pentose-phosphate shunt
<i>TRP1</i> *	YDR007W	1nsj (33%)	5.3.1.24		(1) Ribulose-phosphate binding barrel	Cytoplasm	Tryptophan biosynthetic process

<sup>a</sup> PDB ID used as entry in Catalytic Site Atlas (Furnham *et al.*, 2014) or the MACiE Database (Holliday *et al.*, 2014). In parenthesis is shown the % identity of alignments between protein sequences of *Gene<sub>i</sub>* and the PDB. Alignments were obtained from SGD (WU-BLAST), or for 1q3n, made in EMBOSS Needle Pairwise Sequence Alignment.

<sup>b</sup> E.C. numbers shown are the Enzyme Commission number of *GENE<sub>i</sub>* enzymes. PDB entries 1q3n, 1pwh and 2vat have different E.C. to the represented *GENE<sub>i</sub>*.

<sup>c</sup> PLP, Pyridoxal phosphate; ATP, adenosine triphosphate; NADP, Nicotinamide adenine dinucleotide phosphate; TPP, Thiamine pyrophosphate; FAD, flavin adenine dinucleotide (Uniprot).

<sup>d</sup> Number and domain names of *GENE<sub>i</sub>* proteins (superfamily).

<sup>e</sup> *GENE<sub>i</sub>* protein localization either by manual curation or high-throughput experiments (SGD).

<sup>f</sup> Biological process annotation for *Gene<sub>i</sub>* from different evidence sources (SGD).

\* *GENE<sub>i</sub>* with overlapping sequences: *ARG4* overlaps with an autonomously-replicating sequence; *MET2*, *TKL2* and *TRP1* overlap with a dubious open reading frame.