

**Table S6 Strain variable enzymes**

Process	EC Number	Functions
<b>409-05 only<sup>1</sup></b>		
Amino acid metabolism	2.3.1.46	Homoserine O-succinyltransferase (HMPREF0424_0141)
	2.5.1.49	O-acetylhomoserine aminocarboxypropyltransferase (HMPREF0424_0640)
	4.2.1.20	Tryptophan synthase, beta subunit (HMPREF0424_1349)
	5.1.1.13	Aspartate racemase (HMPREF0424_0465)
Amino acid metabolism / Nitrogen metabolism	6.3.5.4	Asparagine synthase (glutamine-hydrolyzing) (HMPREF0424_0474)
Folate biosynthesis	2.5.1.15	Dihydropteroate synthase (HMPREF0424_0665)
	2.7.6.3	2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphokinase (HMPREF0424_0619)
PTS transport	2.7.3.9	Phosphoenolpyruvate phosphotransferase system enzyme I (HMPREF0424_1268)
Nucleic acid metabolism	3.1.21.-	LlaJI-family restriction endonuclease (HMPREF0424_0537)
	3.5.2.5	Allantoinase (HMPREF0424_0775)
	3.5.3.9	Allantoate amidohydrolase (HMPREF0424_0773)
	3.5.4.-	Cytidine/deoxycytidylate deaminase (HMPREF0424_0498)
Glycosylase	3.2.2.24	ADP-ribosylglycohydrolase (HMPREF0424_0289)
<b>317 only<sup>1</sup></b>		
Protein regulation	2.7.11.-	Serine/threonine protein kinase (HMPREF0421_20141)
Nucleic acid metabolism	3.1.4.-	Rne/Rng family ribonuclease (HMPREF0421_20320)
Glycan degradation	3.2.1.18	Sialidase (HMPREF0421_20186)
Toluene and xylene degradation	5.1.2.2	Mandelate racemase/muconate lactonizing enzyme C-terminal domain protein (HMPREF0421_20695)
Glycolysis / Gluconeogenesis	5.1.3.3	Aldose 1-epimerase (HMPREF0421_21170)
<b>594 only</b>		
Aminosugar metabolism	2.7.7.23	N-acetylglucosamine diphosphorylase (ORF 865)
Glycogen/starch metabolism	5.4.99.16	Trehalose synthase (ORF 883)
Nucleic acid metabolism	5.99.1.-	Topoisomerase IV subunit B (ORF 1053)
<b>409-05 and 317<sup>1</sup></b>		
Lipid metabolism	2.3.1.157	UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase (HMPREF0424_1013 & HMPREF0421_20975)
Fatty acid biosynthesis	2.3.1.85	Fatty acid synthase (HMPREF0424_1197 & HMPREF0421_21228)
Amino acid metabolism	2.6.1.1	Aspartate transaminase (HMPREF0424_1220 & HMPREF0421_20325)
Amino acid metabolism / Drug metabolism	2.4.2.3	Pnp/Udp-family phosphorylase (HMPREF0424_0551 & HMPREF0421_21030)
Nicotinate & Nicotinamide metabolism	2.7.1.23	NAD(+)/NADH kinase (HMPREF0424_0680 & HMPREF0421_20594)
Vitamin metabolism	3.6.1.9	Type I phosphodiesterase/nucleotide pyrophosphatase (HMPREF0424_0700 & HMPREF0421_20620)
Protein modification	3.4.24.71	Endothelin-converting enzyme (HMPREF0424_1076 & HMPREF0421_20934)
Amino acid metabolism	3.5.1.4	Amidohydrolase (HMPREF0424_0452 & HMPREF0421_20509)
Lipid metabolism	3.1.1.3	Triacylglycerol lipase (HMPREF0424_0004 & HMPREF0421_20172)
Glycolysis / Gluconeogenesis	4.1.2.13	Fructose-bisphosphate aldolase class II (HMPREF0424_0114 & HMPREF0421_20056)
	4.2.1.11	Enolase (HMPREF0424_0662 & HMPREF0421_20718)
<b>317 and 594</b>		
Amino acid metabolism	2.3.1.3	Serine acetyltransferase (HMPREF0421_21032 & ORF 878)
	2.7.2.4	Aspartate kinase (HMPREF0421_20041 & ORF 446)
	2.7.2.4	Aspartate kinase (HMPREF0421_20042 & ORF 447)
	3.3.1.1	S-adenosyl-L-homocysteine hydrolase (HMPREF0421_20382 & ORF 512)
	3.5.99.2	TENA/THI-4 protein (HMPREF0421_21010 & ORF 986)
	4.2.1.52	Dihydrodipicolinate synthase (HMPREF0421_20180 & ORF 1097)
	4.2.1.52	Dihydrodipicolinate synthase (HMPREF0421_20691 & ORF 1012)
	Carbohydrate metabolism	3.2.1.135
3.2.1.2		Glycoside hydrolase family 31 (HMPREF0421_20452 & ORF 423)
5.1.3.13		Fused dTDP-4-keto-L-rhamnose reductase and dTDP-4-keto-6-deoxyglucose-3,5-epimerase enzyme (HMPREF0421_20400 & ORF 530)
2.4.1.230		Kojibiose phosphorylase (HMPREF0421_21250 & ORF 1088)
5.1.3.4		L-Ribulose-5-phosphate 4-epimerase (HMPREF0421_20373 & ORF 1154)
5.3.1.4		L-Arabinose isomerase (HMPREF0421_20374 & ORF 1155)
2.7.1.6		Galactokinase (HMPREF0421_21182 & ORF 1193)
3.2.1.23		Beta-galactosidase (HMPREF0421_20100 & ORF 1134)
3.2.1.23		Beta-galactosidase (HMPREF0421_21246 & ORF 1092)
2.7.1.2		Glucokinase (HMPREF0421_20174 & ORF 900)
2.7.1.2		Glucokinase (HMPREF0421_20897 & ORF 830)
Glycan degradation	3.2.1.51	$\alpha$ -L-fucosidase (HMPREF0421_20101 & ORF 1135)
Glycogen/starch metabolism	5.4.2.6	$\beta$ -phosphoglucomutase (HMPREF0421_21248 & ORF 1090)
N-acetylglucosamine metabolism	3.5.1.25	N-acetylglucosamine-6-phosphate deacetylase (HMPREF0421_20182 & ORF 1099)
	3.5.99.6	Glucosamine-6-phosphate deaminase (HMPREF0421_20181 & ORF 1098)
	5.1.3.8	N-acyl-D-glucosamine 2-epimerase (HMPREF0421_20908 & ORF 1042)
	5.1.3.9	N-acylglucosamine-6-phosphate 2-epimerase (HMPREF0421_20175 & ORF 899)
Xylose metabolism	2.7.1.16	Ribulokinase (HMPREF0421_20372 & ORF 1153)
Pentose phosphate pathway	2.7.1.12	Gluconokinase (HMPREF0421_20297 & ORF 1005)
Nucleic acid metabolism	3.5.4.28	S-adenosylhomocysteine deaminase (HMPREF0421_20381 & ORF 511)
Ascorbate biosynthesis	1.1.1.274	2,5-didehydrogluconate reductase (HMPREF0421_20375 & ORF 1156)
Nicotinate & Nicotinamide metabolism	2.7.7.1	Galactose-1-phosphate uridylyltransferase (HMPREF0421_21097 & ORF 765)
	2.7.7.1	Galactose-1-phosphate uridylyltransferase (HMPREF0421_21183 & ORF 93)
Protein modification	2.7.1.95	Aminoglycoside phosphotransferase (HMPREF0421_20507 & ORF 1079)
Bile acid metabolism	3.5.1.24	Choloylglycine hydrolase (HMPREF0421_21234 & ORF 145)
Glyoxylate & dicarboxylate metabolism	1.1.1.77	Lactaldehyde reductase (HMPREF0421_20697 & ORF 18)
Terpenoid biosynthesis	2.5.1.-	1,4-dihydroxy-2-naphthoate octaprenyltransferase (HMPREF0421_20560 & ORF 622)
	2.7.7.24	Glucose-1-phosphate thymidyltransferase (HMPREF0421_20399 & ORF 529)

<sup>1</sup> These enzymes may also be present in the missing segments of the strain 594 genome. Enzymes with ambiguous EC numbers are not reported