

Table A-9: Anaerobic mixed-acid fermentation genes ranked by *amss* scoring functionThe rank fraction (in *pct*) and the gene loci of the prioritised rank by *amss* scoring function in the EC-K12 genome.

Gene	Gene product	Locus	<i>pct</i>
Genes specific to mixed-acid fermentation			
Pyruvate formate-lyase complex			
<i>pflA</i>	pyruvate formate-lyase activating enzyme [E.C. 1.97.1.4]	b0902	0.19
<i>pflB</i>	pyruvate formate lyase I [E.C. 2.3.1.54]	b0903	0.15
<i>pflD</i>	formate C-acetyltransferase [E.C. 2.3.1.54]	b3951	0.17
<i>tdcE</i>	pyruvate formate-lyase 4/2-ketobutyrate formate-lyase	b3114	0.05
<i>pflC</i>	pyruvate formate lyase II activase	b3952	0.07
<i>ybiY</i>	predicted pyruvate formate lyase activating enzyme	b0824	0.07
<i>yijW</i>	predicted pyruvate formate lyase activating enzyme	b4379	0.07
<i>ybiW</i>	predicted pyruvate formate lyase	b0823	0.22
<i>yfiD</i>	pyruvate formate lyase subunit	b2579	0.27
Acetate formation			
<i>pta</i>	phosphate acetyltransferase [E.C. 2.3.1.8]	b2297	12.03
<i>ackA</i>	acetate kinase [E.C. 3.6.1.7]	b2296	2.08
Ethanol and lactate formation			
<i>adhE</i>	alcohol / acetaldehyde dehydrogenase [E.C. 1.1.1.1 and 1.2.1.10]	b1241	2.06
<i>ldhA</i>	D-lactate dehydrogenase (NAD dependent) [E.C. 1.1.1.28]	b1380	66.28
Formate hydrogenlyase complex			
<i>hycA</i>	regulator of the transcriptional regulator FhlA	b2725	30.19
<i>hycB</i>	hydrogenase 3, Fe-S subunit	b2724	10.34
<i>hycC</i>	hydrogenase 3, membrane subunit	b2723	99.27
<i>hycD</i>	hydrogenase 3, membrane subunit	b2722	99.71
<i>hycE</i>	hydrogenase 3, large subunit	b2721	99.83
<i>hycF</i>	formate hydrogenlyase complex iron-sulfur protein	b2720	99.69
<i>hycG</i>	hydrogenase 3 and formate hydrogenase complex, HycG subunit	b2719	99.93

(Continue on next page)

Gene	Gene product	Locus	<i>pct</i>
<i>hycH</i>	protein required for maturation of hydrogenase 3	b2718	21.98
<i>hycI</i>	protease involved in processing C-terminal end of HycE	b2717	23.00
<i>fdhD</i>	formate dehydrogenase formation protein	b3895	70.61
<i>fdhE</i>	formate dehydrogenase formation protein	b3891	15.47
<i>fdhF</i>	formate dehydrogenase-H, selenopolypeptide subunit	b4079	88.31
Fumarate/Succinate formation			
<i>frdA</i>	fumarate reductase (anaerobic) catalytic and NAD/ flavoprotein subunit	b4154	93.00
<i>frdB</i>	fumarate reductase (anaerobic), Fe-S subunit	b4153	99.15
<i>frdC</i>	fumarate reductase (anaerobic), membrane anchor subunit	b4152	10.38
<i>frdD</i>	fumarate reductase (anaerobic), membrane anchor subunit	b4151	7.84
Genes that also share with other pathways			
Pyruvate kinases			
<i>pykF</i>	pyruvate kinase I	b1676	41.06
<i>pykA</i>	pyruvate kinase II	b1854	41.06
<i>ppc</i>	phosphoenolpyruvate carboxylase	b3956	57.15
Fumarate/Succinate formation			
<i>mdh</i>	malate dehydrogenase, NAD(P)-binding	b3236	2.35
<i>fumA</i>	fumarate hydratase (fumarase A), aerobic Class I	b1612	61.49
<i>fumB</i>	anaerobic class I fumarate hydratase (fumarase B)	b4122	61.49
<i>fumC</i>	fumarate hydratase (fumarase C), aerobic Class II	b1611	95.59
Ethanol and Lactate formation			
<i>lldD</i>	FMN- linked L-lactate dehydrogenase	b3605	91.77
<i>adhP</i>	ethanol-active dehydrogenase/acetaldehyde-active reductase	b1478	87.9

(End of table)