

Table A-10: Gene rank produced by amss scoring function (anaerobic mixed-acid fermentation)

The rank position, rank fraction (in *pct*), cluster of orthologous groups (COG), and the loci of the prioritised rank by *amss* scoring function in the EC-K12 genome.

Rank	<i>pct</i>	Score	COG	Gene	Locus	Function
1	0.02	0.806	F	<i>nrdD</i>	b4238	anaerobic ribonucleoside-triphosphate reductase
2	0.05	0.806	C	<i>tdcE</i>	b3114	pyruvate formate-lyase 4/2-ketobutyrate formate-lyase
3	0.07	0.805	O	<i>ybiY</i>	b0824	predicted pyruvate formate lyase activating enzyme
3	0.07	0.805	O	<i>pflC</i>	b3952	pyruvate formate lyase II activase
3	0.07	0.805	O	<i>yjyW</i>	b4379	predicted pyruvate formate lyase activating enzyme
6	0.15	0.803	C	<i>pflB</i>	b0903	pyruvate formate lyase I
7	0.17	0.802	C	<i>pflD</i>	b3951	predicted formate acetyltransferase 2 (pyruvate formate lyase II)
8	0.19	0.797	O	<i>pflA</i>	b0902	pyruvate formate lyase activating enzyme 1
9	0.22	0.787	C	<i>ybiW</i>	b0823	predicted pyruvate formate lyase
10	0.24	0.781	O	<i>nrdG</i>	b4237	anaerobic ribonucleotide reductase activating protein
11	0.27	0.781	R	<i>yfiD</i>	b2579	pyruvate formate lyase subunit
12	0.29	0.774	R	<i>yhcC</i>	b3211	predicted Fe-S oxidoreductase
13	0.31	0.765	R	<i>ybhA</i>	b0766	predicted hydrolase
14	0.34	0.757	E	<i>pepT</i>	b1127	peptidase T
15	0.36	0.748	G	<i>nagE</i>	b0679	fused <i>N</i> -acetyl glucosamine specific PTS enzyme: IIC, IIB , and IIA components
15	0.36	0.748		<i>crr</i>	b2417	glucose-specific enzyme IIA component of PTS
15	0.36	0.748	G	<i>bglF</i>	b3722	fused beta-glucoside-specific PTS enzymes: IIA component/IIB component/IIC component
18	0.44	0.746	G	<i>treB</i>	b4240	fused trehalose(maltose)-specific PTS enzyme: IIB component/IIC component
19	0.46	0.744	G	<i>murP</i>	b2429	fused predicted PTS enzymes: IIB component/IIC component
20	0.48	0.737	G	<i>ascF</i>	b2715	fused cellobiose/arbutin/salicin-specific PTS enzymes: IIB component/IC component

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Rank	<i>pct</i>	Score	COG	Gene	Locus	Function
21	0.51	0.734	P	<i>thiI</i>	b0423	sulfurtransferase required for thiamine and 4-thiouridine biosynthesis
22	0.53	0.733	G	<i>ptsH</i>	b2415	phosphohistidinoprotein-hexose phosphotransferase component of PTS system (Hpr)
23	0.56	0.732	E	<i>brnQ</i>	b0401	predicted branched chain amino acid transporter (LIV-II)
24	0.58	0.725	F	<i>deoD</i>	b4384	purine-nucleoside phosphorylase
25	0.61	0.721	R	<i>ybiV</i>	b0822	predicted hydrolase
26	0.63	0.721	G	<i>nagB</i>	b0678	glucosamine-6-phosphate deaminase
27	0.65	0.718	P	<i>nirC</i>	b3367	nitrite transporter
28	0.68	0.715	G	<i>chbC</i>	b1737	<i>N,N'</i> -diacetylchitobiose-specific enzyme IIC component of PTS
29	0.70	0.714		<i>manZ</i>	b1819	mannose-specific enzyme IID component of PTS
29	0.70	0.714		<i>agaV</i>	b3133	<i>N</i> -acetylgalactosamine-specific enzyme IIB component of PTS
31	0.75	0.713	R	<i>cof</i>	b0446	thiamin pyrimidine pyrophosphate hydrolase
32	0.77	0.711	S	<i>yjjP</i>	b4364	predicted inner membrane protein
33	0.80	0.710	P	<i>focB</i>	b2492	predicted formate transporter
34	0.82	0.710		<i>luxS</i>	b2687	S-ribosylhomocysteinase
35	0.85	0.709		<i>agaD</i>	b3140	<i>N</i> -acetylgalactosamine-specific enzyme IID component of PTS
36	0.87	0.708	G	<i>agaI</i>	b3141	galactosamine-6-phosphate isomerase
37	0.90	0.707		<i>manY</i>	b1818	mannose-specific enzyme IIC component of PTS
38	0.92	0.707	GT	<i>ulaC</i>	b4195	L-ascorbate-specific enzyme IIA component of PTS
39	0.94	0.707		<i>ulaA</i>	b4193	L-ascorbate-specific enzyme IIC component of PTS
40	0.97	0.706		<i>agaB</i>	b3138	<i>N</i> -acetylgalactosamine-specific enzyme IIB component of PTS

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