

Supplementary Materials

Genomic characterization and probiotic potential assessment of an exopolysaccharide-producing strain *Pediococcus pentosaceus* LL-07 isolated from fermented meat

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Supplementary Table 1 Prediction of tRNA in *P. pentosaceus* LL-07

tRNA ID	Startbp	Endbp	tRNA Type	Anti Codon	Score
<i>LL-07.tRNA01</i>	244262	244335	Thr	GGT	75.24
<i>LL-07.tRNA02</i>	645925	645999	Ile	GAT	91.61
<i>LL-07.tRNA03</i>	646005	646077	Ala	TGC	84.82
<i>LL-07.tRNA04</i>	649404	649476	Val	TAC	88.44
<i>LL-07.tRNA05</i>	649486	649558	Lys	TTT	85.34
<i>LL-07.tRNA06</i>	649618	649690	Thr	TGT	86.9
<i>LL-07.tRNA07</i>	649701	649772	Gly	GCC	79.21
<i>LL-07.tRNA08</i>	649805	649890	Leu	TAA	65.63
<i>LL-07.tRNA09</i>	649899	649972	Arg	ACG	67.59
<i>LL-07.tRNA10</i>	649982	650055	Pro	TGG	88.17
<i>LL-07.tRNA11</i>	650095	650168	Met	CAT	77.61
<i>LL-07.tRNA12</i>	650189	650262	Met	CAT	90.44
<i>LL-07.tRNA13</i>	650309	650398	Ser	TGA	63.3
<i>LL-07.tRNA14</i>	650408	650481	Met	CAT	77.81
<i>LL-07.tRNA15</i>	650486	650559	Asp	GTC	76.71
<i>LL-07.tRNA16</i>	650565	650637	Phe	GAA	73.75
<i>LL-07.tRNA17</i>	650662	650732	Gly	TCC	71.75
<i>LL-07.tRNA18</i>	650751	650825	Ile	GAT	91.61
<i>LL-07.tRNA19</i>	650829	650916	Ser	GCT	63.03
<i>LL-07.tRNA20</i>	650940	651011	Glu	TTC	66.65
<i>LL-07.tRNA21</i>	651045	651118	Met	CAT	77.81
<i>LL-07.tRNA22</i>	651123	651196	Asp	GTC	76.71
<i>LL-07.tRNA23</i>	667965	668048	Leu	CAG	60.3
<i>LL-07.tRNA24</i>	677769	677839	Gly	CCC	65.08
<i>LL-07.tRNA25</i>	817680	817753	Asn	GTT	80.23
<i>LL-07.tRNA26</i>	1065580	1065667	Ser	CGA	70.45
<i>LL-07.tRNA27</i>	1268928	1269000	Glu	CTC	59.24
<i>LL-07.tRNA28</i>	1269009	1269081	Gln	CTG	68
<i>LL-07.tRNA29</i>	1708262	1708334	Lys	CTT	84.99
<i>LL-07.tRNA30</i>	1443949	1443875	Ile	GAT	91.61
<i>LL-07.tRNA31</i>	1443869	1443797	Ala	TGC	84.82
<i>LL-07.tRNA32</i>	1440469	1440397	Asn	GTT	79.59
<i>LL-07.tRNA33</i>	1440348	1440276	Thr	CGT	74.08
<i>LL-07.tRNA34</i>	1437207	1437122	Tyr	GTA	75.5
<i>LL-07.tRNA35</i>	1437118	1437047	Gln	TTG	64.93
<i>LL-07.tRNA36</i>	1424809	1424724	Leu	AAG	58.01
<i>LL-07.tRNA37</i>	1348046	1347974	Val	TAC	87.25
<i>LL-07.tRNA38</i>	1347931	1347850	Leu	TAG	63.26
<i>LL-07.tRNA39</i>	1347837	1347765	Thr	TGT	86.05
<i>LL-07.tRNA40</i>	1347760	1347689	Gly	GCC	79.21
<i>LL-07.tRNA41</i>	1347667	1347594	Arg	ACG	69.22
<i>LL-07.tRNA42</i>	1347503	1347430	Pro	CGG	70.99
<i>LL-07.tRNA43</i>	1148771	1148699	Asn	GTT	79.59
<i>LL-07.tRNA44</i>	1148686	1148595	Ser	GGA	58.11
<i>LL-07.tRNA45</i>	1148576	1148505	Glu	TTC	66.65
<i>LL-07.tRNA46</i>	1148497	1148425	Val	TAC	87.25
<i>LL-07.tRNA47</i>	1148406	1148333	Asp	GTC	76.71
<i>LL-07.tRNA48</i>	1148310	1148238	Phe	GAA	73.75
<i>LL-07.tRNA49</i>	1148193	1148120	Trp	CCA	64.7
<i>LL-07.tRNA50</i>	1148114	1148042	His	GTG	64.51

<i>LL-07.tRNA51</i>	1147994	1147911	Leu	CAA	62.57
<i>LL-07.tRNA52</i>	1147826	1147756	Cys	GCA	71.31
<i>LL-07.tRNA53</i>	753385	753312	Arg	TCT	81.51
<i>LL-07.tRNA54</i>	621983	621910	Arg	CCT	75.06
<i>LL-07.tRNA55</i>	468377	468306	Arg	CCG	49.87
<i>LL-07.tRNA56</i>	94149	94077	Ala	CGC	79.98

Supplementary Table 2 Prediction of rRNA in *P. pentosaceus* LL-07

rRNA ID	Location	Startbp	Endbp	Strand	rRNA Type
<i>LL-07.rRNA01</i>	Chromosome	103431	105002	+	16S_rRNA
<i>LL-07.rRNA02</i>	Chromosome	105234	108153	+	23S_rRNA
<i>LL-07.rRNA03</i>	Chromosome	108253	108364	+	5S_rRNA
<i>LL-07.rRNA04</i>	Chromosome	239210	240781	+	16S_rRNA
<i>LL-07.rRNA05</i>	Chromosome	241013	243932	+	23S_rRNA
<i>LL-07.rRNA06</i>	Chromosome	244032	244143	+	5S_rRNA
<i>LL-07.rRNA07</i>	Chromosome	644274	645845	+	16S_rRNA
<i>LL-07.rRNA08</i>	Chromosome	646266	649185	+	23S_rRNA
<i>LL-07.rRNA09</i>	Chromosome	649285	649396	+	5S_rRNA
<i>LL-07.rRNA10</i>	Chromosome	1148891	1148780	-	5S_rRNA
<i>LL-07.rRNA11</i>	Chromosome	1151910	1148991	-	23S_rRNA
<i>LL-07.rRNA12</i>	Chromosome	1153713	1152142	-	16S_rRNA
<i>LL-07.rRNA13</i>	Chromosome	1440589	1440478	-	5S_rRNA
<i>LL-07.rRNA14</i>	Chromosome	1443608	1440689	-	23S_rRNA
<i>LL-07.rRNA15</i>	Chromosome	1445600	1444029	-	16S_rRNA

Supplementary Table 3 Prediction of sRNA in *P. pentosaceus* LL-07

sRNA ID	Location	Startbp	Endbp	sRNA Lengthbp	Strand	Rfam ID	Score
<i>LL-07.sRNA01</i>	Chromosome	133913	134093	181	+	RF00168	104.3
<i>LL-07.sRNA02</i>	Chromosome	341499	341388	112	-	RF00059	57.6
<i>LL-07.sRNA03</i>	Chromosome	364820	364947	128	+	RF02840	90.4
<i>LL-07.sRNA04</i>	Chromosome	528421	528487	67	+	RF01734	38.8
<i>LL-07.sRNA05</i>	Chromosome	579842	580081	240	+	RF00230	114.8
<i>LL-07.sRNA06</i>	Chromosome	589593	589698	106	+	RF00059	68.1
<i>LL-07.sRNA07</i>	Chromosome	654097	654177	81	+	RF01767	60.2
<i>LL-07.sRNA08</i>	Chromosome	658224	658428	205	+	RF00230	104.2
<i>LL-07.sRNA09</i>	Chromosome	714084	714211	128	+	RF00558	65.5
<i>LL-07.sRNA10</i>	Chromosome	755115	755182	68	+	RF00559	53.9
<i>LL-07.sRNA11</i>	Chromosome	914528	914900	373	+	RF00011	319.9
<i>LL-07.sRNA12</i>	Chromosome	1118582	1118368	215	-	RF00230	114.1
<i>LL-07.sRNA13</i>	Chromosome	1216025	1215795	231	-	RF00230	111.5
<i>LL-07.sRNA14</i>	Chromosome	1222550	1222339	212	-	RF00230	94.7
<i>LL-07.sRNA15</i>	Chromosome	1241476	1241234	243	-	RF00230	96.7
<i>LL-07.sRNA16</i>	Chromosome	1313944	1313884	61	-	RF00555	48.7
<i>LL-07.sRNA17</i>	Chromosome	1317350	1317294	57	-	RF01708	37.3
<i>LL-07.sRNA18</i>	Chromosome	1352288	1352111	178	-	RF00168	95.7
<i>LL-07.sRNA19</i>	Chromosome	1357962	1357578	385	-	RF01766	86.2
<i>LL-07.sRNA20</i>	Chromosome	1362688	1362783	96	+	RF01831	82.6
<i>LL-07.sRNA21</i>	Chromosome	1380157	1380406	250	+	RF00230	96.9
<i>LL-07.sRNA22</i>	Chromosome	1393715	1393629	87	-	RF00169	59.1
<i>LL-07.sRNA23</i>	Chromosome	1399757	1399631	127	-	RF00557	58.1
<i>LL-07.sRNA24</i>	Chromosome	1500055	1499931	125	-	RF00050	97.1
<i>LL-07.sRNA25</i>	Chromosome	1731784	1731652	133	-	RF00050	113.2
<i>LL-07.sRNA26</i>	Chromosome	1750605	1750702	98	+	RF00167	61.8

Supplementary Table 4 Carbohydrate metabolism in *P. pentosaceus* LL-07

Gene ID	KO ID	KO Name	KO Description
<i>gene0023</i>	K02761	<i>celB</i>	cellobiose PTS system EIIC component
<i>gene0220</i>	K02761	<i>celB</i>	cellobiose PTS system EIIC component
<i>gene1716</i>	K02761	<i>celB</i>	cellobiose PTS system EIIC component
<i>gene0025</i>	K23257	<i>yvgN</i>	methylglyoxal/glyoxal reductase [EC:1.1.1.283 1.1.1.-]
<i>gene0060</i>	K00034	<i>gdh</i>	glucose 1-dehydrogenase [EC:1.1.1.47]
<i>gene0109</i>	K01223	<i>bglA</i>	6-phospho-beta-glucosidase [EC:3.2.1.86]
<i>gene0268</i>	K01223	<i>bglA</i>	6-phospho-beta-glucosidase [EC:3.2.1.86]
<i>gene1717</i>	K01223	<i>bglA</i>	6-phospho-beta-glucosidase [EC:3.2.1.86]
<i>gene0116</i>	K00849	<i>galK</i>	galactokinase [EC:2.7.1.6]
<i>gene0195</i>	K00849	<i>galK</i>	galactokinase [EC:2.7.1.6]
<i>gene0141</i>	K00882	<i>fruK</i>	1-phosphofructokinase [EC:2.7.1.56]
<i>gene1119</i>	K00882	<i>fruK</i>	1-phosphofructokinase [EC:2.7.1.56]
<i>gene0143</i>	K01635	<i>lacD</i>	tagatose 1,6-diphosphate aldolase [EC:4.1.2.40]
<i>gene0144</i>	K04041	-	fructose-1,6-bisphosphatase III [EC:3.1.3.11]
<i>gene0152</i>	K01788	<i>nanE</i>	N-acetylglucosamine-6-phosphate 2-epimerase [EC:5.1.3.9]
<i>gene0160</i>	K03077	<i>araD</i>	L-ribulose-5-phosphate 4-epimerase [EC:5.1.3.4]
<i>gene0161</i>	K01804	<i>araA</i>	L-arabinose isomerase [EC:5.3.1.4]
<i>gene0170</i>	K00848	<i>rhaB</i>	rhamnulokinase [EC:2.7.1.5]
<i>gene0172</i>	K01813	<i>rhaA</i>	L-rhamnose isomerase [EC:5.3.1.14]
<i>gene0173</i>	K01629	<i>rhaD</i>	rhamnulose-1-phosphate aldolase [EC:4.1.2.19]
<i>gene0182</i>	K01805	<i>xylA</i>	xylose isomerase [EC:5.3.1.5]
<i>gene0183</i>	K00854	<i>xylB</i>	xylulokinase [EC:2.7.1.17]
<i>gene0191</i>	K01785	<i>galM</i>	aldose 1-epimerase [EC:5.1.3.3]
<i>gene0210</i>	K01785	<i>galM</i>	aldose 1-epimerase [EC:5.1.3.3]
<i>gene1010</i>	K01785	<i>galM</i>	aldose 1-epimerase [EC:5.1.3.3]
<i>gene0193</i>	K01190	<i>lacZ</i>	beta-galactosidase [EC:3.2.1.23]
<i>gene0194</i>	K01190	<i>lacZ</i>	beta-galactosidase [EC:3.2.1.23]
<i>gene0196</i>	K01784	<i>galE</i>	UDP-glucose 4-epimerase [EC:5.1.3.2]
<i>gene1424</i>	K01784	<i>galE</i>	UDP-glucose 4-epimerase [EC:5.1.3.2]
<i>gene0197</i>	K00965	<i>galT</i>	UDPglucose--hexose-1-phosphate uridylyltransferase [EC:2.7.7.12]
<i>gene0198</i>	K01679	<i>fumC</i>	fumarate hydratase, class II [EC:4.2.1.2]
<i>gene0207</i>	K00016	<i>ldh</i>	L-lactate dehydrogenase [EC:1.1.1.27]
<i>gene1503</i>	K00016	<i>ldh</i>	L-lactate dehydrogenase [EC:1.1.1.27]
<i>gene0235</i>	K01958	<i>pyc</i>	pyruvate carboxylase [EC:6.4.1.1]
<i>gene0261</i>	K00086	<i>dhaT</i>	1,3-propanediol dehydrogenase [EC:1.1.1.202]
<i>gene0266</i>	K02760	<i>celA</i>	cellobiose PTS system EIIB component [EC:2.7.1.196 2.7.1.205]
<i>gene0267</i>	K02759	<i>celC</i>	cellobiose PTS system EIIC component [EC:2.7.1.196 2.7.1.205]
<i>gene0271</i>	K03366	<i>butA</i>	meso-butanediol dehydrogenase / (S,S)-butanediol dehydrogenase / diacetyl reductase [EC:1.1.1.-1.1.1.76 1.1.1.304]
<i>gene0278</i>	K04042	<i>glmU</i>	bifunctional UDP-N-acetylglucosamine pyrophosphorylase / Glucosamine-1-phosphate N-acetyltransferase [EC:2.7.7.23 2.3.1.157]
<i>gene0280</i>	K00948	<i>prsA</i>	ribose-phosphate pyrophosphokinase [EC:2.7.6.1]
<i>gene1122</i>	K00948	<i>prsA</i>	ribose-phosphate pyrophosphokinase [EC:2.7.6.1]
<i>gene0303</i>	K00244	<i>frdA</i>	fumarate reductase flavoprotein subunit [EC:1.3.5.4]
<i>gene0320</i>	K02564	<i>nagB</i>	glucosamine-6-phosphate deaminase [EC:3.5.99.6]
<i>gene0321</i>	K00925	<i>ackA</i>	acetate kinase [EC:2.7.2.1]
<i>gene1761</i>	K00925	<i>ackA</i>	acetate kinase [EC:2.7.2.1]
<i>gene0322</i>	K00625	<i>pta</i>	phosphate acetyltransferase [EC:2.3.1.8]
<i>gene0338</i>	K01621	<i>xfp</i>	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase [EC:4.1.2.9 4.1.2.22]
<i>gene0390</i>	K01652	<i>ilvB</i>	acetolactate synthase I/II/III large subunit [EC:2.2.1.6]
<i>gene0965</i>	K01652	<i>ilvB</i>	acetolactate synthase I/II/III large subunit [EC:2.2.1.6]

<i>gene0391</i>	K01575	<i>alsD</i>	acetolactate decarboxylase [EC:4.1.1.5]
<i>gene0429</i>	K00963	<i>galU</i>	UTP--glucose-1-phosphate uridylyltransferase [EC:2.7.7.9]
<i>gene0431</i>	K01835	<i>manB</i>	phosphoglucomutase [EC:5.4.2.2]
<i>gene0444</i>	K00134	<i>gapA</i>	glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]
<i>gene0445</i>	K00927	<i>pgk</i>	phosphoglycerate kinase [EC:2.7.2.3]
<i>gene0446</i>	K01803	<i>tpiA</i>	triosephosphate isomerase (TIM) [EC:5.3.1.1]
<i>gene0447</i>	K01689	<i>eno</i>	enolase [EC:4.2.1.11]
<i>gene0504</i>	K01689	<i>eno</i>	enolase [EC:4.2.1.11]
<i>gene0459</i>	K00075	<i>murB</i>	UDP-N-acetylmuramate dehydrogenase [EC:1.3.1.98]
<i>gene0462</i>	K03431	<i>glmM</i>	phosphoglucosamine mutase [EC:5.4.2.10]
<i>gene0463</i>	K00820	<i>glmS</i>	glutamine---fructose-6-phosphate transaminase (isomerizing) [EC:2.6.1.16]
<i>gene0508</i>	K00874	<i>kdgK</i>	2-dehydro-3-deoxygluconokinase [EC:2.7.1.45]
<i>gene0512</i>	K00158	<i>poxL</i>	pyruvate oxidase [EC:1.2.3.3]
<i>gene0650</i>	K00158	<i>poxL</i>	pyruvate oxidase [EC:1.2.3.3]
<i>gene1205</i>	K00158	<i>poxL</i>	pyruvate oxidase [EC:1.2.3.3]
<i>gene0588</i>	K01854	<i>glf</i>	UDP-galactopyranose mutase [EC:5.4.99.9]
<i>gene0608</i>	K01791	<i>wecB</i>	UDP-N-acetylglucosamine 2-epimerase (non-hydrolysing) [EC:5.1.3.14]
<i>gene0723</i>	K00033	<i>gntZ</i>	6-phosphogluconate dehydrogenase [EC:1.1.1.44 1.1.1.343]
<i>gene1314</i>	K00033	<i>gntZ</i>	6-phosphogluconate dehydrogenase [EC:1.1.1.44 1.1.1.343]
<i>gene0727</i>	K01512	<i>acyP</i>	acylphosphatase [EC:3.6.1.7]
<i>gene0742</i>	K00845	<i>glk</i>	glucokinase [EC:2.7.1.2]
<i>gene0749</i>	K01915	<i>glnA</i>	glutamine synthetase [EC:6.3.1.2]
<i>gene0781</i>	K01783	<i>rpe</i>	ribulose-phosphate 3-epimerase [EC:5.1.3.1]
<i>gene0806</i>	K02160	<i>accB</i>	acetyl-CoA carboxylase biotin carboxyl carrier protein
<i>gene0808</i>	K01961	<i>accC</i>	acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2 6.3.4.14]
<i>gene0809</i>	K01963	<i>accD</i>	acetyl-CoA carboxylase carboxyl transferase subunit beta [EC:6.4.1.2 2.1.3.15]
<i>gene0810</i>	K01962	<i>accA</i>	acetyl-CoA carboxylase carboxyl transferase subunit alpha [EC:6.4.1.2 2.1.3.15]
<i>gene0875</i>	K01641	-	hydroxymethylglutaryl-CoA synthase [EC:2.3.3.10]
<i>gene0883</i>	K03778	<i>ldhA</i>	D-lactate dehydrogenase [EC:1.1.1.28]
<i>gene0969</i>	K00865	<i>glxK</i>	glycerate 2-kinase [EC:2.7.1.165]
<i>gene0980</i>	K01838	<i>pgmB</i>	beta-phosphoglucomutase [EC:5.4.2.6]
<i>gene0981</i>	K00691	<i>mapA</i>	maltose phosphorylase [EC:2.4.1.8]
<i>gene0996</i>	K07106	<i>murQ</i>	N-acetylmuramic acid 6-phosphate etherase [EC:4.2.1.126]
<i>gene1045</i>	K00873	<i>pyk</i>	pyruvate kinase [EC:2.7.1.40]
<i>gene1046</i>	K00850	<i>pfkA</i>	6-phosphofructokinase 1 [EC:2.7.1.11]
<i>gene1111</i>	K01092	<i>suhB</i>	myo-inositol-1(or 4)-monophosphatase [EC:3.1.3.25]
<i>gene1118</i>	K02768	<i>fruB</i>	fructose PTS system EIIA component [EC:2.7.1.202]
<i>gene1150</i>	K02781	<i>srlB</i>	glucitol/sorbitol PTS system EIIA component [EC:2.7.1.198]
<i>gene1151</i>	K07404	<i>pgl</i>	6-phosphogluconolactonase [EC:3.1.1.31]
<i>gene1192</i>	K00852	<i>rbsK</i>	ribokinase [EC:2.7.1.15]
<i>gene1641</i>	K00852	<i>rbsK</i>	ribokinase [EC:2.7.1.15]
<i>gene1220</i>	K00036	<i>zwf</i>	glucose-6-phosphate 1-dehydrogenase [EC:1.1.1.49 1.1.1.363]
<i>gene1280</i>	K00600	<i>glyA</i>	glycine hydroxymethyltransferase [EC:2.1.2.1]
<i>gene1287</i>	K01809	<i>manA</i>	mannose-6-phosphate isomerase [EC:5.3.1.8]
<i>gene1302</i>	K01810	<i>pgi</i>	glucose-6-phosphate isomerase [EC:5.3.1.9]
<i>gene1304</i>	K01624	<i>fbaA</i>	fructose-bisphosphate aldolase, class II [EC:4.1.2.13]
<i>gene1313</i>	K00851	<i>gntK</i>	gluconokinase [EC:2.7.1.12]
<i>gene1391</i>	K00847	<i>scrK</i>	fructokinase [EC:2.7.1.4]
<i>gene1455</i>	K01807	<i>rpiA</i>	ribose 5-phosphate isomerase A [EC:5.3.1.6]
<i>gene1459</i>	K01834	<i>gpmA</i>	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase [EC:5.4.2.11]
<i>gene1652</i>	K01834	<i>gpmA</i>	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase [EC:5.4.2.11]

<i>gene1462</i>	K02769	<i>fruAb</i>	fructose PTS system EIIB component [EC:2.7.1.202]
<i>gene1465</i>	K02796	<i>manZ</i>	mannose PTS system EIID component
<i>gene1699</i>	K02796	<i>manZ</i>	mannose PTS system EIID component
<i>gene1466</i>	K02795	<i>manY</i>	mannose PTS system EIIC component
<i>gene1700</i>	K02795	<i>manY</i>	mannose PTS system EIIC component
<i>gene1467</i>	K02793	<i>manXa</i>	mannose PTS system EIIA component [EC:2.7.1.191]
<i>gene1703</i>	K02793	<i>manXa</i>	mannose PTS system EIIA component [EC:2.7.1.191]
<i>gene1477</i>	K01443	<i>nagA</i>	N-acetylglucosamine-6-phosphate deacetylase [EC:3.5.1.25]
<i>gene1696</i>	K01443	<i>nagA</i>	N-acetylglucosamine-6-phosphate deacetylase [EC:3.5.1.25]
<i>gene1519</i>	K00790	<i>murA</i>	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [EC:2.5.1.7]
<i>gene1560</i>	K22212	<i>mleA</i>	malolactic enzyme [EC:4.1.1.101]
<i>gene1636</i>	K22373	<i>larA</i>	lactate racemase [EC:5.1.2.1]
<i>gene1701</i>	K02794	<i>manX</i>	mannose PTS system EIAB component [EC:2.7.1.191]
<i>gene1711</i>	K00382	<i>pdhD</i>	dihydrolipoamide dehydrogenase [EC:1.8.1.4]
<i>gene1712</i>	K00627	<i>aceF</i>	pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]
<i>gene1713</i>	K00162	<i>pdhB</i>	pyruvate dehydrogenase E1 component beta subunit [EC:1.2.4.1]
<i>gene1714</i>	K00161	<i>pdhA</i>	pyruvate dehydrogenase E1 component alpha subunit [EC:1.2.4.1]
<i>gene1746</i>	K01226	<i>treC</i>	trehalose-6-phosphate hydrolase [EC:3.2.1.93]

Supplementary Table 5 Gene details of prophage in *P. pentosaceus* LL-07

Prophage ID	Gene ID	Strand	Start (bp)	End (bp)	Description
Ph01	<i>gene0817</i>	-	805991	806881	hypothetical protein
	<i>gene0818</i>	-	806957	807349	ImmA/IrrE family metallo-endopeptidase
	<i>gene0819</i>	-	807356	807679	helix-turn-helix domain-containing protein
	<i>gene0820</i>	+	807822	808043	helix-turn-helix transcriptional regulator
	<i>gene0821</i>	+	808040	808291	hypothetical protein
	<i>gene0822</i>	-	808272	808463	hypothetical protein
	<i>gene0823</i>	+	808527	808769	hypothetical protein
	<i>gene0824</i>	+	808843	809301	helix-turn-helix domain-containing protein
	<i>gene0825</i>	+	809302	809577	helix-turn-helix domain-containing protein
	<i>gene0826</i>	+	809591	809722	hypothetical protein
	<i>gene0827</i>	+	809815	810096	hypothetical protein
	<i>gene0828</i>	+	810089	810940	recombinase RecT
	<i>gene0829</i>	+	810900	811727	PD-(D/E)XK nuclease-like domain-containing protein
	<i>gene0837</i>	+	815195	815545	DUF1642 domain-containing protein
	<i>gene0838</i>	+	815538	815735	hypothetical protein
	<i>gene0839</i>	+	815779	816069	hypothetical protein
	<i>gene0840</i>	+	816137	816442	hypothetical protein
	<i>gene0841</i>	+	816445	816639	hypothetical protein
	<i>gene0842</i>	+	816642	816842	hypothetical protein
	<i>gene0843</i>	+	816839	817012	hypothetical protein
	<i>gene0844</i>	+	817082	817522	hypothetical protein
	<i>gene0846</i>	+	817847	819043	hypothetical protein
	<i>gene0847</i>	+	819236	819805	terminase small subunit
	<i>gene0848</i>	+	819802	821175	PBSX family phage terminase large subunit
	<i>gene0849</i>	+	821229	822725	phage portal protein
	<i>gene0850</i>	+	822722	823855	capsid protein
	<i>gene0851</i>	+	823955	824509	phage scaffolding protein
	<i>gene0852</i>	+	824522	825412	hypothetical protein
	<i>gene0853</i>	+	825490	825957	Ig-like domain-containing protein
	<i>gene0854</i>	+	825969	826385	hypothetical protein
Ph02	<i>gene0855</i>	+	826382	826729	capsid protein
	<i>gene0856</i>	+	826729	827079	minor capsid protein
	<i>gene0857</i>	+	827066	827461	minor capsid protein
	<i>gene0858</i>	+	827465	828010	hypothetical protein
	<i>gene0859</i>	+	828084	828521	hypothetical protein
	<i>gene0860</i>	+	828528	829160	Gp15 family bacteriophage protein
	<i>gene0861</i>	+	829164	834437	tape measure protein
	<i>gene0862</i>	+	834490	835287	phage tail family protein
	<i>gene0863</i>	+	835296	836432	phage tail protein
	<i>gene0864</i>	+	836422	836748	hypothetical protein
	<i>gene0865</i>	+	836738	837013	hypothetical protein
	<i>gene0866</i>	+	837013	838833	metallophosphoesterase
	<i>gene0867</i>	+	838846	839601	hypothetical protein
	<i>gene0868</i>	+	839612	839932	DUF2977 domain-containing protein
	<i>gene0869</i>	+	839934	840077	XkdX family protein
	<i>gene0870</i>	+	840111	840245	-
	<i>gene0871</i>	+	840279	840680	phage holin family protein
	<i>gene0872</i>	+	840664	841989	Lysozyme M1 (1,4-beta-N-acetylmuramidase)
	<i>gene0873</i>	+	842659	842979	acetyl-CoA carboxylase

Supplementary Table 6 Prediction of CRISPR/Cas in *P. pentosaceus* LL-07

Element	Start (bp)	End (bp)	DR Length (bp)	Orientation
Cas3-1	434,183	435,502	-	+
Cas3-2	1,188,788	1,190,149	-	-
Cas3-3	1,466,831	1,468,411	-	-
CRISPR-1	649,410	649,515	24	-
CRISPR-2	1,686,878	1,686,990	29	+

Supplementary Table 7 Prediction of Transposon in *P. pentosaceus* LL-07

Transposon ID	Location	Start	End	Transposon families	Match Start	Match End	Evalue
chain00001	Chromosome	308858	309301	LINE	913	1033	1.00E-08
chain00002	Chromosome	767731	767937	helitronORF	859	924	1.00E-06
chain00003	Chromosome	1519704	1520369	LINE	6	205	4.00E-06

Supplementary Table 8 Detailed table of virulence gene prediction in *P. pentosaceus* LL-07

Gene ID	VFDB ID	Level 1	Level 2	Identity (%)
<i>gene0016</i>	VFG002176(gb AAM75252)	Offensive virulence factors	Toxin	28.20
<i>gene0019</i>	VFG000344(gb NP_438273)	Nonspecific virulence factor	Iron uptake system	30.60
<i>gene0026</i>	VFG038840(gb YP_008043465)	Offensive virulence factors	Adherence	28.70
<i>gene0049</i>	VFG001306(gb NP_644948)	Defensive virulence factors	Antiphagocytosis	35.70
<i>gene0053</i>	VFG010862(gb YP_094891)	Nonspecific virulence factor	Iron uptake system	29.60
<i>gene0060</i>	VFG005767(gb NP_687682)	Offensive virulence factors	Toxin	34.60
<i>gene0068</i>	VFG000574(gb NP_462662)	Nonspecific virulence factor	Magnesium uptake system	25.70
<i>gene0072</i>	VFG000574(gb NP_462662)	Nonspecific virulence factor	Magnesium uptake system	29.80
<i>gene0080</i>	VFG001341(gb NP_688173)	Defensive virulence factors;Defensive virulence factors	Antiphagocytosis;Serum resistance	33.90
<i>gene0108</i>	VFG001285(gb NP_647403)	Offensive virulence factors	Adherence	31.70
<i>gene0146</i>	VFG038840(gb YP_008043465)	Offensive virulence factors	Adherence	29.10
<i>gene0150</i>	VFG000575(gb NP_462663)	Nonspecific virulence factor	Magnesium uptake system	40.90
<i>gene0190</i>	VFG002197(gb NP_814691)	-	-	25.60
<i>gene0196</i>	VFG002361(gb YP_001007253)	-	-	39.30
<i>gene0200</i>	VFG041304(gb YP_095978)	Offensive virulence factors	Secretion system	39.60
<i>gene0205</i>	VFG013260(gb NP_438427)	-	-	27.60
<i>gene0214</i>	VFG013496(gb NP_439840)	-	-	22.60
<i>gene0232</i>	VFG000344(gb NP_438273)	Nonspecific virulence factor	Iron uptake system	35.10
<i>gene0239</i>	VFG002548(gb YP_109384)	-	Antiphagocytosis	33.00
<i>gene0262</i>	VFG001267(gb NP_252913)	Nonspecific virulence factor	Iron uptake system	27.40
<i>gene0271</i>	VFG005767(gb NP_687682)	Offensive virulence factors	Toxin	34.80
<i>gene0275</i>	VFG002176(gb AAM75252)	Offensive virulence factors	Toxin	28.00
<i>gene0278</i>	VFG047256(gb YP_169432.1)	-	-	41.60
<i>gene0300</i>	VFG047726(gb YP_170570.1)	-	-	41.20
<i>gene0301</i>	VFG047708(gb YP_170571.1)	-	-	46.80
<i>gene0307</i>	VFG001285(gb NP_647403)	Offensive virulence factors	Adherence	27.60
<i>gene0316</i>	VFG001206(gb NP_273675)	Nonspecific virulence factor	Iron uptake system	37.80
<i>gene0331</i>	VFG040705(gb YP_067664)	-	-	23.00
<i>gene0362</i>	VFG002176(gb AAM75252)	Offensive virulence factors	Toxin	26.60
<i>gene0374</i>	VFG000344(gb NP_438273)	Nonspecific virulence factor	Iron uptake system	28.90
<i>gene0375</i>	VFG001983(gb NP_282073)	Offensive virulence factors	Adherence	31.30
<i>gene0384</i>	VFG000344(gb NP_438273)	Nonspecific virulence factor	Iron uptake system	31.80
<i>gene0385</i>	VFG007023(gb NP_231091)	Offensive virulence factors	Toxin	32.60
<i>gene0397</i>	VFG000574(gb NP_462662)	Nonspecific virulence factor	Magnesium uptake system	28.10
<i>gene0407</i>	VFG001855(gb YP_094724)	Offensive virulence factors	Adherence	56.40
<i>gene0416</i>	VFG038219(gb YP_001845364)	Regulation of virulence-associated genes	Regulation	38.80
<i>gene0417</i>	VFG009810(gb NP_215272)	Regulation of virulence-associated genes	Regulation	31.90
<i>gene0421</i>	VFG007023(gb NP_231091)	Offensive virulence factors	Toxin	32.70
<i>gene0422</i>	VFG000344(gb NP_438273)	Nonspecific virulence factor	Iron uptake system	30.10
<i>gene0429</i>	VFG000964(gb NP_270109)	Defensive virulence factors;Offensive virulence factors	Antiphagocytosis;Adherence	69.90
<i>gene0431</i>	VFG013327(gb NP_438900)	-	-	31.50
<i>gene0440</i>	VFG000077(gb NP_465991)	Defensive virulence factors	Stress protein	71.10
<i>gene0442</i>	VFG043396(gb YP_002344093)	-	-	27.50
<i>gene0459</i>	VFG002184(gb NP_816135)	Defensive virulence factors	Antiphagocytosis	39.00
<i>gene0462</i>	VFG013327(gb NP_438900)	-	-	22.90
<i>gene0471</i>	VFG037386(gb YP_001847242)	Nonspecific virulence factor	Iron uptake system	26.30
<i>gene0488</i>	VFG005776(gb NP_687685)	Offensive virulence factors	Toxin	29.90
<i>gene0493</i>	VFG049114(gb YP_002918199.1)	-	-	37.10

<i>gene0525</i>	VFG043504(gb NP_357669)	Offensive virulence factors	Adherence	48.60
<i>gene0526</i>	VFG001386(gb NP_215271)	Regulation of virulence-associated genes	Regulation	36.40
<i>gene0527</i>	VFG009810(gb NP_215272)	Regulation of virulence-associated genes	Regulation	24.90
<i>gene0528</i>	VFG037100(gb NP_273110)	Defensive virulence factors	Stress protein	35.50
<i>gene0558</i>	VFG000329(gb NP_439689)	-	-	28.50
<i>gene0560</i>	VFG038840(gb YP_008043465)	Offensive virulence factors	Adherence	26.00
<i>gene0578</i>	VFG001297(gb NP_644939)	Defensive virulence factors	Antiphagocytosis	33.10
<i>gene0579</i>	VFG001298(gb NP_644940)	Defensive virulence factors	Antiphagocytosis	44.70
<i>gene0580</i>	VFG001299(gb NP_644941)	Defensive virulence factors	Antiphagocytosis	35.70
<i>gene0581</i>	VFG013365(gb NP_439033)	-	-	43.90
<i>gene0582</i>	VFG049073(gb YP_002920346.1)	Defensive virulence factors	Serum resistance	31.30
<i>gene0583</i>	VFG002188(gb NP_816139)	Defensive virulence factors	Antiphagocytosis	33.60
<i>gene0584</i>	VFG001341(gb NP_688173)	Defensive virulence factors;Defensive virulence factors	Antiphagocytosis;Serum resistance	34.20
<i>gene0588</i>	VFG002182(gb NP_816133)	Defensive virulence factors	Antiphagocytosis	60.90
<i>gene0590</i>	VFG046732(gb YP_169804.1)	-	-	28.10
<i>gene0608</i>	VFG001373(gb NP_344890)	Defensive virulence factors	Antiphagocytosis	58.90
<i>gene0618</i>	VFG000080(gb NP_464522)	Defensive virulence factors	Stress protein	59.90
<i>gene0669</i>	VFG015551(gb NP_248741)	-	-	29.40
<i>gene0687</i>	VFG032878(gb NP_465743)	-	-	36.90
<i>gene0690</i>	VFG000344(gb NP_438273)	Nonspecific virulence factor	Iron uptake system	26.90
<i>gene0695</i>	VFG002409(gb NP_645079)	Offensive virulence factors	Secretion system	29.40
<i>gene0705</i>	VFG000120(gb NP_253949)	Defensive virulence factors;Defensive virulence factors	Antiphagocytosis;Serum resistance	29.10
<i>gene0706</i>	VFG000119(gb NP_253948)	Defensive virulence factors;Defensive virulence factors	Antiphagocytosis;Serum resistance	31.40
<i>gene0723</i>	VFG048830(gb YP_002920353.1)	Defensive virulence factors	Antiphagocytosis	67.90
<i>gene0724</i>	VFG038219(gb YP_001845364)	Regulation of virulence-associated genes	Regulation	40.10
<i>gene0725</i>	VFG009810(gb NP_215272)	Regulation of virulence-associated genes	Regulation	27.80
<i>gene0770</i>	VFG037118(gb NP_273782)	Defensive virulence factors	Stress protein	32.30
<i>gene0779</i>	VFG002060(gb NP_248764)	Offensive virulence factors	Secretion system	36.30
<i>gene0781</i>	VFG046610(gb YP_169796.1)	-	-	41.90
<i>gene0788</i>	VFG011430(gb NP_540392)	-	-	40.30
<i>gene0800</i>	VFG011399(gb NP_539749)	-	-	41.00
<i>gene0803</i>	VFG049155(gb YP_006635481.1)	Offensive virulence factors	Toxin	27.80
<i>gene0804</i>	VFG038840(gb YP_008043465)	Offensive virulence factors	Adherence	43.40
<i>gene0888</i>	VFG002190(gb NP_816141)	Defensive virulence factors	Antiphagocytosis	61.90
<i>gene0889</i>	VFG002189(gb NP_816140)	Defensive virulence factors	Antiphagocytosis	50.00
<i>gene0890</i>	VFG015000(gb NP_252339)	Defensive virulence factors	Antiphagocytosis	33.20
<i>gene0893</i>	VFG039491(gb NP_820417)	Offensive virulence factors	Secretion system	40.60
<i>gene0909</i>	VFG038839(gb YP_858598)	Offensive virulence factors	Adherence	36.00
<i>gene0913</i>	VFG000969(gb NP_269989)	Nonspecific virulence factor	Exoenzyme	32.50
<i>gene0928</i>	VFG047055(gb YP_170389.1)	-	-	39.00
<i>gene0949</i>	VFG002161(gb NP_465369)	-	-	40.80
<i>gene0952</i>	VFG047726(gb YP_170570.1)	-	-	34.30
<i>gene0953</i>	VFG047708(gb YP_170571.1)	-	-	31.10
<i>gene0954</i>	VFG002160(gb NP_465354)	Offensive virulence factors	Adherence	45.30
<i>gene0967</i>	VFG037100(gb NP_273110)	Defensive virulence factors	Stress protein	38.20
<i>gene0968</i>	VFG037100(gb NP_273110)	Defensive virulence factors	Stress protein	63.50
<i>gene0983</i>	VFG002197(gb NP_814691)	-	-	34.70
<i>gene0987</i>	VFG000080(gb NP_464522)	Defensive virulence factors	Stress protein	46.00

<i>gene1018</i>	VFG001206(gb NP_273675)	Nonspecific virulence factor	Iron uptake system	32.90
<i>gene1022</i>	VFG000344(gb NP_438273)	Nonspecific virulence factor	Iron uptake system	25.70
<i>gene1049</i>	VFG002076(gb NP_248780)	Offensive virulence factors	Secretion system	39.20
<i>gene1061</i>	VFG045566(gb YP_096368)	Offensive virulence factors	Secretion system	42.20
<i>gene1065</i>	VFG002188(gb NP_816139)	Defensive virulence factors	Antiphagocytosis	41.10
<i>gene1073</i>	VFG001826(gb NP_217099)	Regulation of virulence-associated genes	Regulation	40.30
<i>gene1089</i>	VFG001206(gb NP_273675)	Nonspecific virulence factor	Iron uptake system	35.80
<i>gene1096</i>	VFG046465(gb YP_169203.1)	Offensive virulence factors	Adherence	69.20
<i>gene1106</i>	VFG000320(gb NP_208266)	Offensive virulence factors	Adherence	36.20
<i>gene1147</i>	VFG002409(gb NP_645079)	Offensive virulence factors	Secretion system	26.60
<i>gene1191</i>	VFG001876(gb YP_095349)	Offensive virulence factors	Secretion system	31.60
<i>gene1193</i>	VFG039536(gb NP_820549)	Offensive virulence factors	Secretion system	46.50
<i>gene1203</i>	VFG002197(gb NP_814691)	-	-	28.10
<i>gene1209</i>	VFG013265(gb NP_438428)	-	-	44.80
<i>gene1233</i>	VFG038840(gb YP_008043465)	Offensive virulence factors	Adherence	30.20
<i>gene1238</i>	VFG000344(gb NP_438273)	Nonspecific virulence factor	Iron uptake system	39.20
<i>gene1264</i>	VFG005776(gb NP_687685)	Offensive virulence factors	Toxin	34.30
<i>gene1270</i>	VFG001254(gb NP_249795)	Offensive virulence factors	Adherence	32.70
<i>gene1272</i>	VFG007158(gb NP_798047)	Offensive virulence factors	Secretion system	29.90
<i>gene1278</i>	VFG000344(gb NP_438273)	Nonspecific virulence factor	Iron uptake system	33.80
<i>gene1289</i>	VFG013248(gb NP_438233)	-	-	32.90
<i>gene1290</i>	VFG013248(gb NP_438233)	-	-	27.70
<i>gene1305</i>	VFG009810(gb NP_215272)	Regulation of virulence-associated genes	Regulation	28.00
<i>gene1306</i>	VFG038219(gb YP_001845364)	Regulation of virulence-associated genes	Regulation	37.80
<i>gene1314</i>	VFG048830(gb YP_002920353.1)	Defensive virulence factors	Antiphagocytosis	35.30
<i>gene1339</i>	VFG001206(gb NP_273675)	Nonspecific virulence factor	Iron uptake system	30.90
<i>gene1340</i>	VFG037386(gb YP_001847242)	Nonspecific virulence factor	Iron uptake system	29.20
<i>gene1377</i>	VFG000079(gb NP_463763)	Defensive virulence factors	Stress protein	55.80
<i>gene1407</i>	VFG047582(gb YP_169891.1)	-	-	32.40
<i>gene1410</i>	VFG047564(gb YP_169890.1)	-	-	38.80
<i>gene1411</i>	VFG015551(gb NP_248741)	-	-	29.20
<i>gene1424</i>	VFG002361(gb YP_001007253)	-	-	44.80
<i>gene1463</i>	VFG002085(gb NP_232518)	Offensive virulence factors	Secretion system	32.00
<i>gene1472</i>	VFG000574(gb NP_462662)	Nonspecific virulence factor	Magnesium uptake system	29.50
<i>gene1518</i>	VFG000812(gb NP_290268)	Offensive virulence factors	Secretion system	29.70
<i>gene1538</i>	VFG000130(gb NP_252238)	Defensive virulence factors;Defensive virulence factors	Antiphagocytosis;Serum resistance	33.30
<i>gene1539</i>	VFG016058(gb NP_251114)	Nonspecific virulence factor	Iron uptake system	28.50
<i>gene1546</i>	VFG002188(gb NP_816139)	Defensive virulence factors	Antiphagocytosis	44.90
<i>gene1549</i>	VFG002181(gb NP_816132)	Defensive virulence factors	Antiphagocytosis	49.90
<i>gene1550</i>	VFG002180(gb NP_816131)	Defensive virulence factors	Antiphagocytosis	41.10
<i>gene1551</i>	VFG002188(gb NP_816139)	Defensive virulence factors	Antiphagocytosis	41.90
<i>gene1553</i>	VFG000670(gb NP_706258)	-	-	41.10
<i>gene1570</i>	VFG047654(gb YP_169518.1)	-	-	22.30
<i>gene1571</i>	VFG047654(gb YP_169518.1)	-	-	22.50
<i>gene1583</i>	VFG001306(gb NP_644948)	Defensive virulence factors	Antiphagocytosis	51.60
<i>gene1588</i>	VFG000574(gb NP_462662)	Nonspecific virulence factor	Magnesium uptake system	28.60
<i>gene1592</i>	VFG002176(gb AAM75252)	Offensive virulence factors	Toxin	25.30
<i>gene1593</i>	VFG001206(gb NP_273675)	Nonspecific virulence factor	Iron uptake system	32.70
<i>gene1594</i>	VFG000574(gb NP_462662)	Nonspecific virulence factor	Magnesium uptake system	30.20
<i>gene1598</i>	VFG000344(gb NP_438273)	Nonspecific virulence factor	Iron uptake system	33.10

<i>gene1601</i>	VFG013248(gb NP_438233)	-	-	27.50
<i>gene1624</i>	VFG005776(gb NP_687685)	Offensive virulence factors	Toxin	28.90
<i>gene1628</i>	VFG044083(gb NP_250948)	Nonspecific virulence factor	Iron uptake system	26.40
<i>gene1642</i>	VFG002197(gb NP_814691)	-	-	28.50
<i>gene1658</i>	VFG009810(gb NP_215272)	Regulation of virulence-associated genes	Regulation	28.30
<i>gene1659</i>	VFG038219(gb YP_001845364)	Regulation of virulence-associated genes	Regulation	38.80
<i>gene1675</i>	VFG000119(gb NP_253948)	Defensive virulence factors;Defensive virulence factors	Antiphagocytosis;Serum resistance	32.40
<i>gene1678</i>	VFG001206(gb NP_273675)	Nonspecific virulence factor	Iron uptake system	29.30
<i>gene1685</i>	VFG005776(gb NP_687685)	Offensive virulence factors	Toxin	36.10
<i>gene1715</i>	VFG002158(gb NP_464456)	-	-	37.30
<i>gene1721</i>	VFG002437(gb YP_108306)	Offensive virulence factors	Adherence	24.70
<i>gene1732</i>	VFG014950(gb NP_249457)	Defensive virulence factors	Antiphagocytosis	38.80
<i>gene1736</i>	VFG009810(gb NP_215272)	Regulation of virulence-associated genes	Regulation	32.40
<i>gene1737</i>	VFG038219(gb YP_001845364)	Regulation of virulence-associated genes	Regulation	40.90
<i>gene1740</i>	VFG044083(gb NP_250948)	Nonspecific virulence factor	Iron uptake system	26.50
<i>gene1748</i>	VFG002197(gb NP_814691)	-	-	24.60
<i>gene1752</i>	VFG001206(gb NP_273675)	Nonspecific virulence factor	Iron uptake system	33.20

Supplementary Table 9 Statistical table of prediction and classification of antibiotic resistance genes in *P. pentosaceus* LL-07

Drug Class	Gene No.	Drug Class	Gene No.
Macrolide antibiotic	26	Peptide antibiotic	5
Tetracycline antibiotic	16	Penam	5
Fluoroquinolone antibiotic	10	Mupirocin	4
Lincosamide antibiotic	10	Diaminopyrimidine antibiotic	3
Phenicol antibiotic	9	Nitroimidazole antibiotic	3
Streptogramin antibiotic	8	Cephalosporin	2
Oxazolidinone antibiotic	7	Isoniazid	2
Pleuromutilin antibiotic	6	Fosfomycin	2
Aminoglycoside antibiotic	6	Carbapenem	1
Glycopeptide antibiotic	6	Monobactam	1
Aminocoumarin antibiotic	6	Penem	1
Acridine dye	6	Cephamycin	1
Rifamycin antibiotic	5		

Supplementary Table 10 The probiotic-related genes in *P. pentosaceus* LL-07

Characterization	Gene ID	Length (bp)	Gene Description
Bile tolerance	<i>gene0057</i>	1,026	Choloylglycine hydrolase family protein
Acid tolerance	<i>gene1269</i>	420	F0F1 ATP synthase subunit epsilon
	<i>gene1270</i>	1,410	F0F1 ATP synthase subunit beta
	<i>gene1271</i>	921	F0F1 ATP synthase subunit gamma
	<i>gene1272</i>	1,518	F0F1 ATP synthase subunit alpha
	<i>gene1273</i>	543	F0F1 ATP synthase subunit delta
	<i>gene1274</i>	522	F0F1 ATP synthase subunit B
	<i>gene1275</i>	213	F0F1 ATP synthase subunit C
	<i>gene1276</i>	717	F0F1 ATP synthase subunit A
Universal stress resistance	<i>gene0046</i>	432	Universal stress protein
	<i>gene0258</i>	474	Universal stress protein
	<i>gene0259</i>	450	Universal stress protein
	<i>gene0340</i>	453	Universal stress protein
	<i>gene0660</i>	453	Universal stress protein
	<i>gene1253</i>	456	Universal stress protein
Adhesion	<i>gene0406</i>	284	Co chaperone GroES
	<i>gene0407</i>	1,619	Chaperonin GroEL
	<i>gene0903</i>	1,859	Molecular chaperone DnaK
	<i>gene1002</i>	761	LPXTG cell wall anchor domain containing protein
	<i>gene1003</i>	2,435	LPXTG cell wall anchor domain containing protein
	<i>gene1096</i>	1,187	Elongation factor Tu
	<i>gene1191</i>	962	Flp pilus assembly complex ATPase component TadA
	<i>gene1267</i>	257	Membrane protein insertion efficiency factor YidD
	<i>gene1515</i>	689	Class A sortase
	<i>gene1783</i>	839	Membrane protein insertase YidC
Antioxidant	<i>gene0132</i>	764	4-hydroxy-tetrahydrodipicolinate reductase
	<i>gene0133</i>	899	4-hydroxy-tetrahydrodipicolinate reductase
	<i>gene1049</i>	2,591	ATP-dependent chaperone ClpB
	<i>gene0618</i>	2,219	ATP-dependent Clp protease ATP-binding subunit
	<i>gene1377</i>	2,465	ATP-dependent Clp protease ATP-binding subunit
	<i>gene1094</i>	1,256	ATP-dependent Clp protease ATP-binding subunit ClpX
	<i>gene0045</i>	1,601	Divalent metal cation transporter MntH
	<i>gene1436</i>	230	Glutaredoxin-like protein NrdH
	<i>gene0027</i>	794	NAD(P)H-dependent oxidoreductase
	<i>gene0961</i>	668	NAD(P)H-dependent oxidoreductase
	<i>gene1001</i>	599	NAD(P)H-dependent oxidoreductase
	<i>gene1300</i>	545	NAD(P)H-dependent oxidoreductase
	<i>gene1607</i>	683	NAD(P)H-dependent oxidoreductase
	<i>gene1600</i>	1,040	Oxidoreductase
	<i>gene0968</i>	443	Peptide-methionine (R)-S-oxide reductase MsrB
	<i>gene0528</i>	512	Peptide-methionine (S)-S-oxide reductase MsrA
	<i>gene0967</i>	515	Peptide-methionine (S)-S-oxide reductase MsrA
	<i>gene0026</i>	794	SDR family oxidoreductase
	<i>gene0050</i>	749	SDR family oxidoreductase
	<i>gene0060</i>	785	SDR family oxidoreductase

	<i>gene0146</i>	893	SDR family oxidoreductase
	<i>gene0222</i>	638	SDR family oxidoreductase
	<i>gene0497</i>	743	SDR family oxidoreductase
	<i>gene0524</i>	107	SDR family oxidoreductase
	<i>gene1233</i>	725	SDR family oxidoreductase
	<i>gene1650</i>	632	SDR family oxidoreductase
	<i>gene1710</i>	851	SDR family oxidoreductase
	<i>gene0358</i>	329	Thioredoxin
	<i>gene1211</i>	311	Thioredoxin
	<i>gene0430</i>	926	Thioredoxin-disulfide reductase
	<i>gene0440</i>	593	Thioredoxin-disulfide reductase
Folic acid synthesis	<i>Gene1243</i>	1,275	Bifunctional folylpolyglutamate synthase/dihydrofolate synthase
