

Genes

WID	Name
<u>MG_001</u>	<u>DNA polymerase III, beta subunit</u>
<u>MG_002</u>	<u>DnaJ domain protein</u>
<u>MG_003</u>	<u>DNA gyrase, B subunit</u>
<u>MG_004</u>	<u>DNA gyrase, A subunit</u>
<u>MG_005</u>	<u>seryl-tRNA synthetase</u>
<u>MG_006</u>	<u>thymidylate kinase</u>
<u>MG_007</u>	<u>DNA polymerase III delta prime subunit, putative</u>
<u>MG_008</u>	<u>tRNA modification GTPase TrmE</u>
<u>MG_009</u>	<u>deoxyribonuclease</u>
<u>MG_010</u>	<u>DNA primase-related protein</u>
<u>MG_011</u>	
<u>MG_012</u>	<u>alpha-L-glutamate ligase</u>
<u>MG_013</u>	<u>methylenetetrahydrofolate dehydrogenase/methylenetetrahydrofolate cyclohydrolase</u>
<u>MG_014</u>	<u>multidrug ABC transporter, ATP-binding/permease protein</u>
<u>MG_015</u>	<u>multidrug ABC transporter, ATP-binding/permease protein</u>
<u>MG_018</u>	<u>SNF2 family helicase putative</u>
<u>MG_019</u>	<u>chaperone protein DnaJ</u>
<u>MG_020</u>	<u>proline iminopeptidase</u>
<u>MG_021</u>	<u>methionyl-tRNA synthetase</u>
<u>MG_022</u>	<u>DNA-directed RNA polymerase, delta subunit</u>
<u>MG_023</u>	<u>fructose-1,6-bisphosphate aldolase, class II</u>
<u>MG_024</u>	<u>GTP-binding protein YchF</u>
<u>MG_025</u>	<u>Beta-glycosyl transferase</u>
<u>MG_026</u>	<u>translation elongation factor P</u>
<u>MG_027</u>	<u>transcription termination/antitermination protein NusB</u>

<u>MG_028</u>	
<u>MG_029</u>	<u>DJ-1/Pfpl family protein</u>
<u>MG_030</u>	<u>uracil phosphoribosyltransferase</u>
<u>MG_031</u>	<u>DNA polymerase III, alpha subunit, Gram-positive type</u>
<u>MG_032</u>	
<u>MG_033</u>	<u>glycerol uptake facilitator</u>
<u>MG_034</u>	<u>thymidine kinase</u>
<u>MG_035</u>	<u>histidyl-tRNA synthetase</u>
<u>MG_036</u>	<u>aspartyl-tRNA synthetase</u>
<u>MG_037</u>	<u>nicotinate phosphoribosyltransferase</u>
<u>MG_038</u>	<u>glycerol kinase</u>
<u>MG_039</u>	<u>FAD-dependent glycerol-3-phosphate dehydrogenase, putative</u>
<u>MG_040</u>	<u>Monosaccharide (riboside/galactoside) ABC transporter, substrate binding protein</u>
<u>MG_041</u>	<u>PTS system, HPr</u>
<u>MG_042</u>	<u>spermidine/putrescine (polyamine) ABC transporter, ATP-binding protein, putative</u>
<u>MG_043</u>	<u>spermidine/putrescine (polyamine) ABC transporter, permease protein, putative</u>
<u>MG_044</u>	<u>spermidine/putrescine (polyamine) ABC transporter, permease protein, putative</u>
<u>MG_045</u>	<u>spermidine/putrescine (polyamine) ABC transporter, spermidine/putrescine bind...</u>
<u>MG_046</u>	<u>metalloendopeptidase</u>
<u>MG_047</u>	<u>S-adenosylmethionine synthetase</u>
<u>MG_048</u>	<u>signal recognition particle protein</u>
<u>MG_049</u>	<u>purine nucleoside phosphorylase</u>
<u>MG_050</u>	<u>deoxyribose-phosphate aldolase</u>
<u>MG_051</u>	<u>pyrimidine-nucleoside phosphorylase</u>
<u>MG_052</u>	<u>cytidine deaminase</u>
<u>MG_053</u>	<u>phosphoglucomutase/phosphomannomutase, putative</u>
<u>MG_054</u>	<u>transcription antitermination protein NusG, putative</u>
<u>MG_055</u>	<u>preprotein translocase, SecE subunit</u>
<u>MG_056</u>	<u>tetrapyrrole (corrin/porphyrin) methylase protein</u>

<u>MG_057</u>	<u>small primase-like protein</u>
<u>MG_058</u>	<u>ribose-phosphate pyrophosphokinase</u>
<u>MG_059</u>	<u>SsrA-binding protein</u>
<u>MG_060</u>	<u>glycosyl transferase</u>
<u>MG_061</u>	<u>Mycoplasma MFS transporter</u>
<u>MG_062</u>	<u>PTS system, fructose-specific IIABC component</u>
<u>MG_063</u>	<u>1-phosphofruktokinase, putative</u>
<u>MG_064</u>	<u>ABC transporter, permease protein, putative</u>
<u>MG_065</u>	<u>ABC transporter, ATP-binding protein</u>
<u>MG_066</u>	<u>transketolase</u>
<u>MG_067</u>	<u>lipoprotein, putative</u>
<u>MG_068</u>	<u>lipoprotein, putative</u>
<u>MG_069</u>	<u>PTS system, glucose-specific IIABC component</u>
<u>MG_070</u>	<u>ribosomal protein S2</u>
<u>MG_071</u>	<u>ATPase, P-type (transporting), HAD superfamily, subfamily IC</u>
<u>MG_072</u>	<u>preprotein translocase, SecA subunit</u>
<u>MG_073</u>	<u>excinuclease ABC, B subunit</u>
<u>MG_074</u>	
<u>MG_075</u>	<u>116 kDa surface antigen</u>
<u>MG_076</u>	
<u>MG_077</u>	<u>oligopeptide ABC transporter, permease protein</u>
<u>MG_078</u>	<u>oligopeptide ABC transporter, permease protein</u>
<u>MG_079</u>	<u>oligopeptide ABC transporter, ATP-binding protein</u>
<u>MG_080</u>	<u>oligopeptide ABC transporter, ATP-binding protein</u>
<u>MG_081</u>	<u>ribosomal protein L11</u>
<u>MG_082</u>	<u>ribosomal protein L1</u>
<u>MG_083</u>	<u>peptidyl-tRNA hydrolase</u>
<u>MG_084</u>	<u>tRNA(Ile)-lysidine synthetase</u>
<u>MG_085</u>	<u>HPr(Ser) kinase/phosphatase</u>
<u>MG_086</u>	<u>prolipoprotein diacylglyceryl transferase</u>
<u>MG_087</u>	<u>ribosomal protein S12</u>
<u>MG_088</u>	<u>ribosomal protein S7</u>

<u>MG_089</u>	<u>translation elongation factor G</u>
<u>MG_090</u>	<u>ribosomal protein S6</u>
<u>MG_091</u>	<u>single-strand binding protein family</u>
<u>MG_092</u>	<u>ribosomal protein S18</u>
<u>MG_093</u>	<u>ribosomal protein L9</u>
<u>MG_094</u>	<u>replicative DNA helicase</u>
<u>MG_095</u>	<u>lipoprotein, putative</u>
<u>MG_096</u>	
<u>MG_097</u>	<u>uracil-DNA glycosylase, putative</u>
<u>MG_098</u>	<u>glutamyl-tRNA(Gln) and/or aspartyl-tRNA(Asn) amidotransferase, C subunit</u>
<u>MG_099</u>	<u>glutamyl-tRNA(Gln) and/or aspartyl-tRNA(Asn) amidotransferase, A subunit</u>
<u>MG_100</u>	<u>glutamyl-tRNA(Gln) and/or aspartyl-tRNA(Asn) amidotransferase, B subunit</u>
<u>MG_101</u>	<u>Uncharacterized HTH-type transcriptional regulator</u>
<u>MG_102</u>	<u>thioredoxin-disulfide reductase</u>
<u>MG_103</u>	
<u>MG_104</u>	<u>ribonuclease R</u>
<u>MG_105</u>	<u>putative DNA integrity scanning protein</u>
<u>MG_106</u>	<u>peptide deformylase</u>
<u>MG_107</u>	<u>guanylate kinase</u>
<u>MG_108</u>	<u>Ser/Thr protein phosphatase 2C, putative</u>
<u>MG_109</u>	<u>serine/threonine protein kinase, putative</u>
<u>MG_110</u>	<u>ribosome small subunit-dependent GTPase A</u>
<u>MG_111</u>	<u>glucose-6-phosphate isomerase</u>
<u>MG_112</u>	<u>ribulose-phosphate 3-epimerase</u>
<u>MG_113</u>	<u>asparaginyl-tRNA synthetase</u>
<u>MG_114</u>	<u>CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase</u>
<u>MG_115</u>	<u>competence/damage-inducible protein CinA domain protein</u>
<u>MG_116</u>	
<u>MG_117</u>	

<u>MG_118</u>	<u>UDP-glucose 4-epimerase</u>
<u>MG_119</u>	<u>Monosaccharide (riboside/galactoside) ABC transporter, ATP-binding protein</u>
<u>MG_120</u>	<u>Monosaccharide (riboside/galactoside) ABC transporter, permease protein</u>
<u>MG_121</u>	<u>Monosaccharide (riboside/galactoside) ABC transporter, permease protein</u>
<u>MG_122</u>	<u>DNA topoisomerase I</u>
<u>MG_123</u>	<u>arginine deaminase</u>
<u>MG_124</u>	<u>thioredoxin</u>
<u>MG_125</u>	<u>Cof-like hydrolase, putative</u>
<u>MG_126</u>	<u>tryptophanyl-tRNA synthetase</u>
<u>MG_127</u>	<u>Spx subfamily protein</u>
<u>MG_128</u>	<u>inorganic polyphosphate/ATP-NAD kinase, probable</u>
<u>MG_129</u>	<u>Putative phosphotransferase enzyme glucose-specific IIB component</u>
<u>MG_130</u>	
<u>MG_131</u>	<u>hypothetical protein</u>
<u>MG_132</u>	<u>purine nucleoside phosphoramidase</u>
<u>MG_133</u>	<u>membrane protein, putative</u>
<u>MG_134</u>	
<u>MG_135</u>	<u>membrane protein, putative</u>
<u>MG_136</u>	<u>lysyl-tRNA synthetase</u>
<u>MG_137</u>	<u>UDP-galactopyranose mutase</u>
<u>MG_138</u>	<u>Translation elongation factor 4</u>
<u>MG_139</u>	<u>ribonuclease J</u>
<u>MG_140</u>	<u>putative ATP-dependent helicase</u>
<u>MG_141</u>	<u>transcription termination factor NusA</u>
<u>MG_142</u>	<u>translation initiation factor IF-2</u>
<u>MG_143</u>	<u>ribosome-binding factor A</u>
<u>MG_144</u>	
<u>MG_145</u>	<u>riboflavin biosynthesis protein RibF</u>
<u>MG_146</u>	<u>UPF0053 protein</u>
<u>MG_147</u>	<u>membrane protein, putative</u>

<u>MG_148</u>	
<u>MG_149</u>	<u>lipoprotein, putative</u>
<u>MG_150</u>	<u>ribosomal protein S10</u>
<u>MG_151</u>	<u>ribosomal protein L3</u>
<u>MG_152</u>	<u>ribosomal protein L4/L1 family</u>
<u>MG_153</u>	<u>ribosomal protein L23</u>
<u>MG_154</u>	<u>ribosomal protein L2</u>
<u>MG_155</u>	<u>ribosomal protein S19</u>
<u>MG_156</u>	<u>ribosomal protein L22</u>
<u>MG_157</u>	<u>ribosomal protein S3</u>
<u>MG_158</u>	<u>ribosomal protein L16</u>
<u>MG_159</u>	<u>ribosomal protein L29</u>
<u>MG_160</u>	<u>ribosomal protein S17</u>
<u>MG_161</u>	<u>ribosomal protein L14</u>
<u>MG_162</u>	<u>ribosomal protein L24</u>
<u>MG_163</u>	<u>ribosomal protein L5</u>
<u>MG_164</u>	<u>ribosomal protein S14</u>
<u>MG_165</u>	<u>ribosomal protein S8</u>
<u>MG_166</u>	<u>ribosomal protein L6</u>
<u>MG_167</u>	<u>ribosomal protein L18</u>
<u>MG_168</u>	<u>ribosomal protein S5</u>
<u>MG_169</u>	<u>ribosomal protein L15</u>
<u>MG_170</u>	<u>preprotein translocase, SecY subunit</u>
<u>MG_171</u>	<u>adenylate kinase</u>
<u>MG_172</u>	<u>methionine aminopeptidase, type I</u>
<u>MG_173</u>	<u>translation initiation factor IF-1</u>
<u>MG_174</u>	<u>ribosomal protein L36</u>
<u>MG_175</u>	<u>ribosomal protein S13</u>
<u>MG_176</u>	
<u>MG_177</u>	<u>DNA-directed RNA polymerase, alpha subunit</u>
<u>MG_178</u>	<u>ribosomal protein L17</u>
<u>MG_179</u>	<u>metal ion (cobalt) ABC transporter, ATP-binding protein, putative</u>

<u>MG_180</u>	<u>metal ion (cobalt) ABC transporter, ATP-binding protein, putative</u>
<u>MG_181</u>	<u>metal ion (cobalt) ABC transporter, permease protein</u>
<u>MG_182</u>	<u>tRNA pseudouridine synthase A</u>
<u>MG_183</u>	<u>oligoendopeptidase F</u>
<u>MG_184</u>	<u>adenine-specific DNA modification methylase</u>
<u>MG_185</u>	<u>lipoprotein, putative</u>
<u>MG_186</u>	<u>Oligosaccharide or polyol ABC transporter, substrate binding protein</u>
<u>MG_187</u>	<u>Oligosaccharide or polyol ABC transporter, ATP-binding protein</u>
<u>MG_188</u>	<u>Oligosaccharide or polyol ABC transporter, permease protein</u>
<u>MG_189</u>	<u>Oligosaccharide or polyol ABC transporter, permease protein</u>
<u>MG_190</u>	<u>phosphoesterase</u>
<u>MG_191</u>	<u>MgPa adhesin</u>
<u>MG_192</u>	<u>P110 protein</u>
<u>MG_194</u>	<u>phenylalanyl-tRNA synthetase, alpha subunit</u>
<u>MG_195</u>	<u>phenylalanyl-tRNA synthetase, beta subunit</u>
<u>MG_196</u>	<u>translation initiation factor IF-3</u>
<u>MG_197</u>	<u>ribosomal protein L35</u>
<u>MG_198</u>	<u>ribosomal protein L20</u>
<u>MG_199</u>	<u>ribonuclease HIII, putative, frameshift</u>
<u>MG_200</u>	<u>DnaJ domain protein</u>
<u>MG_201</u>	<u>co-chaperone GrpE</u>
<u>MG_202</u>	
<u>MG_203</u>	<u>DNA topoisomerase IV, B subunit</u>
<u>MG_204</u>	<u>DNA topoisomerase IV, A subunit</u>
<u>MG_205</u>	<u>heat-inducible transcription repressor HrcA, putative</u>
<u>MG_206</u>	<u>excinuclease ABC, C subunit</u>
<u>MG_207</u>	<u>Ser/Thr protein phosphatase 2A</u>
<u>MG_208</u>	<u>glycoprotease</u>
<u>MG_209</u>	<u>23S rRNA pseudouridine synthase; U955, U2504, U2580</u>

<u>MG_210</u>	<u>prolipoprotein signal peptidase, signal peptidase II</u>
<u>MG_211</u>	
<u>MG_212</u>	<u>1-acyl-sn-glycerol-3-phosphate acyltransferase, putative</u>
<u>MG_213</u>	<u>segregation and condensation protein A</u>
<u>MG_214</u>	<u>segregation and condensation protein B</u>
<u>MG_215</u>	<u>6-phosphofructokinase</u>
<u>MG_216</u>	<u>pyruvate kinase</u>
<u>MG_217</u>	<u>P65 adhesin</u>
<u>MG_218</u>	<u>high molecular weight cytodherence accessory protein 2</u>
<u>MG_219</u>	
<u>MG_220</u>	
<u>MG_221</u>	<u>mraZ protein</u>
<u>MG_222</u>	<u>S-adenosyl-methyltransferase MraW</u>
<u>MG_223</u>	
<u>MG_224</u>	<u>cell division protein FtsZ</u>
<u>MG_225</u>	<u>amino acid-polyamine-organocation (APC) permease</u>
<u>MG_226</u>	<u>amino acid-polyamine-organocation (APC) permease</u>
<u>MG_227</u>	<u>thymidylate synthase</u>
<u>MG_228</u>	<u>dihydrofolate reductase</u>
<u>MG_229</u>	<u>ribonucleoside-diphosphate reductase, beta chain</u>
<u>MG_230</u>	<u>ribonucleotide reductase stimulatory protein</u>
<u>MG_231</u>	<u>ribonucleoside-diphosphate reductase, alpha chain</u>
<u>MG_232</u>	<u>ribosomal protein L21</u>
<u>MG_233</u>	
<u>MG_234</u>	<u>ribosomal protein L27</u>
<u>MG_235</u>	<u>apurinic endonuclease</u>
<u>MG_236</u>	<u>ferric uptake repressor</u>
<u>MG_237</u>	
<u>MG_238</u>	<u>trigger factor</u>
<u>MG_239</u>	<u>ATP-dependent protease La</u>
<u>MG_240</u>	<u>nicotinamide-nucleotide adenyltransferase/conserved hypothetical protein</u>
<u>MG_241</u>	

<u>MG_242</u>	
<u>MG_243</u>	<u>conserved hypothetical protein, authentic frameshift</u>
<u>MG_244</u>	<u>3-5' helicase</u>
<u>MG_245</u>	<u>5-formyltetrahydrofolate cyclo-ligase, putative</u>
<u>MG_246</u>	<u>Ser/Thr protein phosphatase 2A</u>
<u>MG_247</u>	<u>membrane protein, putative</u>
<u>MG_248</u>	
<u>MG_249</u>	<u>RNA polymerase sigma factor RpoD</u>
<u>MG_250</u>	<u>DNA primase</u>
<u>MG_251</u>	<u>glycyl-tRNA synthetase</u>
<u>MG_252</u>	<u>23S rRNA methyltransferase; G2251</u>
<u>MG_253</u>	<u>cysteinyl-tRNA synthetase</u>
<u>MG_254</u>	<u>DNA ligase, NAD-dependent</u>
<u>MG_255</u>	
<u>MG_256</u>	
<u>MG_257</u>	<u>ribosomal protein L31</u>
<u>MG_258</u>	<u>peptide chain release factor 1</u>
<u>MG_259</u>	<u>modification methylase</u>
<u>MG_260</u>	<u>lipoprotein, putative</u>
<u>MG_261</u>	<u>DNA polymerase III, alpha subunit</u>
<u>MG_262</u>	<u>poll-like 5'-3' exonuclease, putative</u>
<u>MG_263</u>	<u>Cof-like hydrolase</u>
<u>MG_264</u>	<u>dephospho-CoA kinase</u>
<u>MG_265</u>	<u>sugar phosphatase</u>
<u>MG_266</u>	<u>leucyl-tRNA synthetase</u>
<u>MG_267</u>	
<u>MG_268</u>	
<u>MG_269</u>	
<u>MG_270</u>	<u>lipoyltransferase/lipoate-protein ligase, putative</u>
<u>MG_271</u>	<u>dihydrolipoamide dehydrogenase</u>
<u>MG_272</u>	<u>dihydrolipoamide acetyltransferase</u>
<u>MG_273</u>	<u>pyruvate dehydrogenase component E1, beta subunit</u>
<u>MG_274</u>	<u>pyruvate dehydrogenase component E1, alpha subunit</u>

<u>MG_275</u>	<u>NADH oxidase</u>
<u>MG_276</u>	<u>adenine phosphoribosyltransferase</u>
<u>MG_277</u>	<u>Protein-export membrane protein secDF</u>
<u>MG_278</u>	<u>GTP diphosphokinase</u>
<u>MG_279</u>	
<u>MG_280</u>	<u>sensory rhodopsin II transducer motif</u>
<u>MG_281</u>	
<u>MG_282</u>	<u>transcription elongation factor GreA</u>
<u>MG_283</u>	<u>prolyl-tRNA synthetase</u>
<u>MG_284</u>	
<u>MG_285</u>	
<u>MG_286</u>	
<u>MG_287</u>	<u>acyl carrier protein</u>
<u>MG_288</u>	<u>protein L</u>
<u>MG_289</u>	<u>phosphonate ABC transporter, substrate binding protein (P37), putative</u>
<u>MG_290</u>	<u>phosphonate ABC transporter, ATP-binding protein, putative</u>
<u>MG_291</u>	<u>phosphonate ABC transporter, permease protein (P69), putative</u>
<u>MG_292</u>	<u>alanyl-tRNA synthetase</u>
<u>MG_293</u>	<u>glycerophosphoryl diester phosphodiesterase</u>
<u>MG_294</u>	<u>major facilitator superfamily (MFS) protein</u>
<u>MG_295</u>	<u>tRNA U34 sulfurtransferase</u>
<u>MG_296</u>	
<u>MG_297</u>	<u>signal recognition particle receptor</u>
<u>MG_298</u>	<u>chromosome segregation protein SMC</u>
<u>MG_299</u>	<u>phosphate acetyltransferase</u>
<u>MG_300</u>	<u>phosphoglycerate kinase</u>
<u>MG_301</u>	<u>glyceraldehyde-3-phosphate dehydrogenase, type I</u>
<u>MG_302</u>	<u>metal ion (cobalt) ABC transporter, permease protein, putative</u>
<u>MG_303</u>	<u>metal ion (cobalt) ABC transporter, ATP-binding protein, putative</u>

<u>MG_304</u>	<u>metal ion (cobalt) ABC transporter, ATP-binding protein, putative</u>
<u>MG_305</u>	<u>chaperone</u>
<u>MG_306</u>	<u>membrane protein, putative</u>
<u>MG_307</u>	<u>lipoprotein, putative</u>
<u>MG_308</u>	<u>ATP-dependent RNA helicase</u>
<u>MG_309</u>	<u>lipoprotein, putative</u>
<u>MG_310</u>	<u>hydrolase, Putative esterase/lipase 1</u>
<u>MG_311</u>	<u>ribosomal protein S4</u>
<u>MG_312</u>	<u>high molecular weight cytodherence accessory protein 1</u>
<u>MG_313</u>	<u>membrane protein, putative</u>
<u>MG_314</u>	
<u>MG_315</u>	<u>DNA polymerase III, delta subunit, putative</u>
<u>MG_316</u>	<u>DNA internalization-related competence protein ComEC/Rec2</u>
<u>MG_317</u>	<u>high molecular weight cytodherence accessory protein 3</u>
<u>MG_318</u>	<u>P32 adhesin</u>
<u>MG_319</u>	
<u>MG_320</u>	<u>membrane protein, putative</u>
<u>MG_321</u>	<u>oligopeptide ABC transporter, substrate binding protein</u>
<u>MG_322</u>	<u>potassium uptake protein</u>
<u>MG_323</u>	<u>potassium uptake protein</u>
<u>MG_324</u>	<u>aminopeptidase</u>
<u>MG_325</u>	<u>ribosomal protein L33</u>
<u>MG_326</u>	<u>degV family protein</u>
<u>MG_327</u>	<u>hydrolase, Putative esterase/lipase 2</u>
<u>MG_328</u>	<u>coiled coil putative structural protein involved in cytoskeleton</u>
<u>MG_329</u>	<u>GTP-binding protein engA</u>
<u>MG_330</u>	<u>cytidylate kinase</u>
<u>MG_331</u>	
<u>MG_332</u>	
<u>MG_333</u>	<u>FMN-dependent NADH-azoreductase, putative</u>
<u>MG_334</u>	<u>valyl-tRNA synthetase</u>

<u>MG_335</u>	<u>GTP-binding protein engB, putative</u>
<u>MG_336</u>	<u>cysteine desulfurase</u>
<u>MG_337</u>	
<u>MG_338</u>	<u>lipoprotein, putative</u>
<u>MG_339</u>	<u>recombination protein, strand exchange</u>
<u>MG_340</u>	<u>DNA-directed RNA polymerase, beta subunit</u>
<u>MG_341</u>	<u>DNA-directed RNA polymerase, beta subunit</u>
<u>MG_342</u>	<u>NADPH-dependent FMN reductase domain protein</u>
<u>MG_343</u>	
<u>MG_344</u>	<u>hydrolase, Putative esterase/lipase 3</u>
<u>MG_345</u>	<u>isoleucyl-tRNA synthetase</u>
<u>MG_346</u>	<u>23S rRNA methyltransferase; U2552</u>
<u>MG_347</u>	<u>tRNA (guanine-N(7)-)-methyltransferase</u>
<u>MG_348</u>	<u>lipoprotein, putative</u>
<u>MG_349</u>	<u>Replication initiation/membrane attachment protein</u>
<u>MG_350</u>	
<u>MG_351</u>	<u>inorganic pyrophosphatase</u>
<u>MG_352</u>	<u>Holliday junction endonuclease</u>
<u>MG_353</u>	<u>DNA-binding protein HU, putative</u>
<u>MG_354</u>	
<u>MG_355</u>	<u>ATP-dependent Clp protease, ATPase subunit</u>
<u>MG_356</u>	<u>choline/ethanolamine kinase, putative</u>
<u>MG_357</u>	<u>acetate kinase</u>
<u>MG_358</u>	<u>Holliday junction DNA helicase</u>
<u>MG_359</u>	<u>Holliday junction DNA helicase RuvB</u>
<u>MG_360</u>	<u>ImpB/MucB/SamB family protein</u>
<u>MG_361</u>	<u>ribosomal protein L10</u>
<u>MG_362</u>	<u>ribosomal protein L7/L12</u>
<u>MG_363</u>	<u>ribosomal protein L32</u>
<u>MG_364</u>	<u>Replication initiation/membrane attachment protein</u>
<u>MG_365</u>	<u>methionyl-tRNA formyltransferase</u>
<u>MG_366</u>	
<u>MG_367</u>	<u>ribonuclease III</u>

<u>MG_368</u>	<u>fatty acid/phospholipid synthesis protein PlsX</u>
<u>MG_369</u>	<u>DAK2 phosphatase domain protein</u>
<u>MG_370</u>	<u>23S rRNA pseudouridine synthase; U1911, U1915, U1917</u>
<u>MG_371</u>	<u>DHH family protein</u>
<u>MG_372</u>	<u>thiamine biosynthesis/tRNA modification protein Thil</u>
<u>MG_373</u>	
<u>MG_374</u>	
<u>MG_375</u>	<u>threonyl-tRNA synthetase</u>
<u>MG_376</u>	
<u>MG_377</u>	
<u>MG_378</u>	<u>arginyl-tRNA synthetase</u>
<u>MG_379</u>	<u>tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA</u>
<u>MG_380</u>	<u>methyltransferase GidB</u>
<u>MG_381</u>	
<u>MG_382</u>	<u>uridine kinase</u>
<u>MG_383</u>	<u>NH(3)-dependent NAD+ synthetase, putative</u>
<u>MG_384</u>	<u>GTPase1 Obg</u>
<u>MG_385</u>	<u>glycerophosphoryl diester phosphodiesterase family protein</u>
<u>MG_386</u>	<u>P200 protein</u>
<u>MG_387</u>	<u>GTP-binding protein Era</u>
<u>MG_388</u>	<u>Putative metalloprotease</u>
<u>MG_389</u>	
<u>MG_390</u>	<u>toxin ABC transporter, ATP-binding/permease protein</u>
<u>MG_391</u>	<u>cytosol aminopeptidase</u>
<u>MG_392</u>	<u>chaperonin</u>
<u>MG_393</u>	<u>chaperonin, 10 kDa</u>
<u>MG_394</u>	<u>serine hydroxymethyltransferase</u>
<u>MG_395</u>	<u>lipoprotein, putative</u>
<u>MG_396</u>	<u>ribose 5-phosphate isomerase B</u>
<u>MG_397</u>	
<u>MG_398</u>	<u>ATP synthase F1, epsilon subunit</u>

<u>MG_399</u>	<u>ATP synthase F1, beta subunit</u>
<u>MG_400</u>	<u>ATP synthase F1, gamma subunit</u>
<u>MG_401</u>	<u>ATP synthase F1, alpha subunit</u>
<u>MG_402</u>	<u>ATP synthase F1, delta subunit</u>
<u>MG_403</u>	<u>ATP synthase F0, B subunit</u>
<u>MG_404</u>	<u>ATP synthase F0, C subunit</u>
<u>MG_405</u>	<u>ATP synthase F0, A subunit</u>
<u>MG_406</u>	
<u>MG_407</u>	<u>enolase</u>
<u>MG_408</u>	<u>methionine-S-sulfoxide reductase</u>
<u>MG_409</u>	<u>phosphate transport system regulatory protein PhoU, putative</u>
<u>MG_410</u>	<u>phosphate ABC transporter, ATP-binding protein</u>
<u>MG_411</u>	<u>phosphate ABC transporter, permease protein PstA</u>
<u>MG_412</u>	<u>phosphate ABC transporter, substrate-binding protein</u>
<u>MG_414</u>	
<u>MG_417</u>	<u>ribosomal protein S9</u>
<u>MG_418</u>	<u>ribosomal protein L13</u>
<u>MG_419</u>	<u>DNA polymerase III, subunit gamma and tau</u>
<u>MG_421</u>	<u>excinuclease ABC, A subunit</u>
<u>MG_422</u>	
<u>MG_423</u>	<u>metallo-beta-lactamase superfamily protein</u>
<u>MG_424</u>	<u>ribosomal protein S15</u>
<u>MG_425</u>	<u>ATP-dependent RNA helicase</u>
<u>MG_426</u>	<u>ribosomal protein L28</u>
<u>MG_427</u>	<u>osmotically inducible peroxidase</u>
<u>MG_428</u>	<u>LuxR bacterial regulatory protein, putative</u>
<u>MG_429</u>	<u>PTS system, E1</u>
<u>MG_430</u>	<u>2,3-bisphosphoglycerate-independent phosphoglycerate mutase</u>
<u>MG_431</u>	<u>triosephosphate isomerase</u>
<u>MG_432</u>	<u>membrane protein, putative</u>
<u>MG_433</u>	<u>translation elongation factor Ts</u>

<u>MG_434</u>	<u>uridylate kinase</u>
<u>MG_435</u>	<u>ribosome recycling factor</u>
<u>MG_437</u>	<u>phosphatidate cytidyltransferase</u>
<u>MG_438</u>	<u>type I restriction modification DNA specificity domain protein</u>
<u>MG_439</u>	<u>lipoprotein, putative</u>
<u>MG_440</u>	<u>lipoprotein, putative</u>
<u>MG_441</u>	
<u>MG_442</u>	<u>ribosomal biogenesis GTPase</u>
<u>MG_443</u>	<u>membrane protein, putative</u>
<u>MG_444</u>	<u>ribosomal protein L19</u>
<u>MG_445</u>	<u>tRNA (guanine-N1)-methyltransferase</u>
<u>MG_446</u>	<u>ribosomal protein S16</u>
<u>MG_447</u>	<u>multidrug efflux pump</u>
<u>MG_448</u>	<u>methionine-R-sulfoxide reductase</u>
<u>MG_449</u>	<u>conserved hypothetical protein, authentic frameshift</u>
<u>MG_450</u>	<u>degV family protein</u>
<u>MG_451</u>	<u>translation elongation factor Tu</u>
<u>MG_452</u>	<u>membrane protein, putative</u>
<u>MG_453</u>	<u>UTP-glucose-1-phosphate uridylyltransferase</u>
<u>MG_454</u>	<u>thiol-dependent peroxidase</u>
<u>MG_455</u>	<u>tyrosyl-tRNA synthetase</u>
<u>MG_456</u>	
<u>MG_457</u>	<u>ATP-dependent metalloprotease FtsH</u>
<u>MG_458</u>	<u>hypoxanthine phosphoribosyltransferase</u>
<u>MG_459</u>	<u>putative 2-C-methyl-D-erythritol-2,4-cyclodiphosphate synthase</u>
<u>MG_460</u>	<u>L-lactate dehydrogenase/malate dehydrogenase</u>
<u>MG_461</u>	<u>HD domain protein</u>
<u>MG_462</u>	<u>glutamyl-tRNA synthetase</u>
<u>MG_463</u>	<u>dimethyladenosine transferase</u>
<u>MG_464</u>	<u>inner-membrane protein insertion factor</u>
<u>MG_465</u>	<u>ribonuclease P protein component</u>

<u>MG_466</u>	<u>ribosomal protein L34</u>
<u>MG_467</u>	<u>salivaricin A ABC transporter, ATP-binding protein</u>
<u>MG_468</u>	<u>salivaricin A ABC transporter, permease protein</u>
<u>MG_469</u>	<u>chromosomal replication initiator protein DnaA</u>
<u>MG_470</u>	<u>CobQ/CobB/MinD/ParA nucleotide binding domain</u>
<u>MG_473</u>	<u>ribosomal protein L33 type 2</u>
<u>MG_474</u>	
<u>MG_476</u>	<u>preprotein translocase, SecG subunit</u>
<u>MG_477</u>	
<u>MG_478</u>	
<u>MG_480</u>	
<u>MG_481</u>	<u>30S ribosomal protein S21</u>
<u>MG_482</u>	<u>holo-(acyl-carrier-protein) synthase</u>
<u>MG_491</u>	
<u>MG_494</u>	
<u>MG_498</u>	<u>formamidopyrimidine-DNA glycosylase</u>
<u>MG_505</u>	<u>putative holliday junction resolvase</u>
<u>MG_515</u>	
<u>MG_516</u>	
<u>MG_517</u>	<u>glycosyl transferase, group 2 family protein</u>
<u>MG_521</u>	<u>membrane protein, putative</u>
<u>MG_522</u>	<u>ribosomal protein S20</u>
<u>MG_524</u>	
<u>MG_525</u>	
<u>MG_526</u>	<u>salivaricin A ABC transporter, ATP-binding protein</u>