

1 **SUPPLEMENTARY INFORMATION**

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34 **Supplementary Texts**

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36 **Supplementary Text 1**

37 **Reason for using a continuous-flow bioreactor system to enrich deep marine**  
38 **sedimentary microorganisms and deep-sea methane seep sediment as an inoculum**  
39 **source.** Culture-independent molecular studies showed that deep marine sediment  
40 harbors phylogenetically diverse microorganisms, most of which belong to uncultured  
41 taxa and are distinct from those living on the Earth's surface<sup>1-4</sup>. Hence, their physiology  
42 and metabolic functions still remain largely unknown<sup>5,6</sup>. To gain insight into deep marine  
43 sedimentary microbes, they need to be cultivated, and this has been a significant challenge.  
44 However, only a small fraction of indigenous deep seafloor microbes has been  
45 successfully isolated and characterized<sup>7,8</sup>. It is unclear why the cultivation of deep marine  
46 sedimentary microbes is difficult, but the batch-type cultivation techniques commonly  
47 used in previous studies may have been inadequate for this purpose. Therefore, the  
48 development of a new cultivation technique is needed. We have, therefore, employed a  
49 continuous-flow bioreactor technique for the cultivation of deep marine sedimentary  
50 microbes since 2006. The bioreactor is called a down-flow hanging sponge (DHS) reactor,  
51 which was originally developed to treat municipal sewage at a low cost in developing  
52 countries<sup>9-11</sup>. Specifically, a polyurethane sponge packed in the DHS reactor column  
53 provides a large surface area for microbial colonization and a longer cell residence time.  
54 As such, this type of continuous-flow reactor cultivation can provide substrates at low  
55 concentrations, similarly to those found in the natural environment. In addition,  
56 continuous-flow bioreactors allow the outflow of metabolic products that may inhibit  
57 microbial growth if accumulated. These continuous-flow reactors thereby might increase  
58 the culturability of deep marine sedimentary microorganisms in a controlled manner and  
59 serve as better sources (incubators) for microbial isolation than the original samples<sup>12</sup>. In  
60 fact, using DHS reactors, we have successfully enriched phylogenetically diverse  
61 microorganisms from deep marine sediments<sup>12-15</sup> and isolated and characterized various  
62 microorganisms using enriched microbial community from the bioreactors<sup>16-20</sup>.

63 In this study, we used deep-sea methane-seep sediments collected off Kumano area,  
64 Japan. In deep-sea methane seep sediments, anaerobic oxidation of methane (AOM)  
65 reaction is the major microbial process and is mediated by a syntrophic association of  
66 euryarchaeal anaerobic methanotrophs (ANMEs) and deltaproteobacterial sulfate-

67 deducing bacteria (SRB)<sup>21</sup>. In addition to ANMEs and SRB, abundant and diverse  
68 microorganisms, most of which are affiliated with uncultured microbial groups of high  
69 taxonomic ranks, such as phylum, class, and order, live in methane-seep sediments<sup>22-24</sup>.  
70 Therefore, deep-sea methane-seep sediment can be regard as a hot spot for uncultured  
71 microorganisms. As such, cultivation and characterization of these uncultured  
72 microorganisms can greatly expand our knowledge regarding microbial physiology,  
73 genetics, and ecology. This was our rationale for using deep-sea methane seep sediment  
74 as an inoculum source for uncultured microorganism cultivation. However, in 2006, when  
75 we started the DHS bioreactor cultivation, there was extremely limited information about  
76 the metabolism of uncultured microorganisms because the metagenomic approach was  
77 not a common technique. We, therefore, could not predict the appropriate carbon and  
78 energy sources to culture uncultured microorganisms. However, we were aware that  
79 methane-seep microbial communities were sustained by methane released below the sea  
80 floor. Thus, we expected that if we provided methane as a major energy source in the  
81 DHS reactor system, the uncultured microorganisms could be cultivated from the  
82 methane-seep sediment under laboratory conditions, along with ANMEs and SRB. Indeed,  
83 using a combination of the DHS bioreactor “pre-enrichment” and subsequent *in vitro*  
84 cultivation, we have successfully cultured and isolated microorganisms representing  
85 predominant uncultured taxa. The “*Candidatus* Prometheoarchaeum syntrophicum”  
86 strain MK-D1 reported in this study is an example of cultured microorganism using our  
87 deep-sea methane seep-derived bioreactor enrichment.

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100 **Supplementary Text 2**

101 **Reason for use of the four antibiotics to isolate the Lokiarchaeota.** In parallel to the  
102 attempted the cultivation of microorganisms from methane-seep sediment, we tried to  
103 isolate anaerobic microorganisms from the enriched methanogenic microbial community  
104 in another DHS reactor, which was established from deep marine sediments collected off  
105 the Shimokita Peninsula, Japan<sup>15</sup>. During the isolation attempt, we detected few  
106 Lokiarchaeota sequences in a propionate-fed culture (Supplementary Table S8 in Imachi  
107 et al. [2011]<sup>15</sup>). However, the Lokiarchaeota sequences became undetectable after five  
108 successive transfers. After this, we could not revive the culture any longer. However, we  
109 detected some Lokiarchaeota sequences in several anaerobic enrichment cultures  
110 supplemented with four antibiotics (i.e., ampicillin, vancomycin, kanamycin, and  
111 streptomycin, each at a final concentration of 50 µg/ml), via archaeal 16S rRNA gene-  
112 based clone analysis (data not shown). This finding suggested that Lokiarchaeota  
113 members can tolerate these antibiotics. Therefore, we added these four antibiotics into the  
114 media to serve as selective agents for the isolation of Lokiarchaeota members from the  
115 enriched AOM microbial community in the DHS reactor.

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## 133 **Supplementary Methods**

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135 **Culturing.** The purity of *Ca. P. syntrophicum* strain MK-D1 was routinely examined by  
136 microscopy and iTAG analysis. In addition, the purity was verified by the whole genome  
137 shotgun sequencing, which only detected the sequences of MK-D1 and *Methanogenium*  
138 genomes. We also confirmed the culture purity based on failure to amplify the bacterial  
139 16S rRNA gene through PCR using the bacterial primer pairs 27F/907R<sup>24</sup> and  
140 EUB338F\*/1492R<sup>25-27</sup>. Moreover, we evaluated the culture purity based on the failure of  
141 microbial growth in the following media at 10°C, 20°C, 30°C, 37°C, and 55°C: (i)  
142 thioglycolate medium (Difco); (ii) basal medium supplemented with 1 mM sucrose, 1  
143 mM glucose, 1 mM fructose, 1 mM xylose, and 0.01% (w/v) yeast extract; and (iii) basal  
144 medium containing 5 mM lactate, 10 mM sulfate, 0.05% (w/v) CA, and 0.01% (w/v)  
145 yeast extract.

146 To confirm *Halodesulfobivrio* has ability to use H<sub>2</sub> and formate, we isolated the  
147 bacterium from the Lokiarchaeum enrichment culture using a roll-tube technique, with  
148 lactate (10 mM) and sulfate (10 mM), acting as an electron donor and acceptor,  
149 respectively. After isolation, we confirmed that the *Halodesulfobivrio*, designated strain  
150 MK-HDV, could grow on a hydrogen- or formate-fed medium supplemented with sulfate  
151 at 20°C.

152 *Methanobacterium* sp. strain MO-MB1 was previously isolated from subseafloor  
153 sediment in our laboratory as a hydrogen- and formate-utilizing methanogenic archaea<sup>15</sup>.  
154 *Methanogenium cariaci* strain JR1 was obtained from the Japan Collection of  
155 Microorganisms (Tsukuba, Japan) and cultured the basal medium supplemented with H<sub>2</sub>  
156 (ca. 150 kPa in head space of culture bottle) and acetate (1 mM) and yeast extract (0.01%)  
157 at 20°C

158 Cultures of *Halodesulfobivrio* sp. strain MK-HDV and *Methanobacterium* sp.  
159 strain MO-MB1 have been deposited in Japan Collection for Microorganisms (JCM  
160 32479 and JCM 18473, respectively).

161 **Growth monitoring using qPCR.** The reaction mixture for qPCR was prepared  
162 according to the manufacturer's protocol. To construct a template standard for the primer  
163 set, we used a dilution series of the 16S rRNA gene amplicon of MK-D1, which was  
164 obtained via clone analysis using an archaeal primer pair Arch21F/1492R<sup>28,29</sup>. The  
165 dilution series of the PCR product was used in each qPCR analysis to calculate the 16S

166 rRNA gene copy number. Template DNA was quantified using a Quant-iT dsDNA High-  
167 Sensitivity Assay Kit (Life Technologies). The PCR condition was as follows: initial  
168 denaturation at 95°C for 30 s, followed by 40 cycles of denaturation at 95°C for 10 s,  
169 annealing at 58°C for 30 s, and extension at 72°C for 31 s. The annealing temperature  
170 was optimized empirically through the amplification of the 16S rRNA gene of MK-D1.  
171 To verify the specificity of the qPCR assay, we performed two types of experiments. First,  
172 a melting-curve analysis was performed for every qPCR assay. Second, the PCR product  
173 size was confirmed by gel electrophoresis and subsequent clone library analysis. The  
174 clone library experiment was performed only for three DNA samples, which were  
175 obtained from two- and three-successive transferred Lokiarchaeota enrichment cultures  
176 and the DHS bioreactor enrichment. We confirmed that all the PCR products showed the  
177 expected PCR amplicon size (i.e., about 390 bp) and all retrieved clones were identical  
178 to MK-D1 or were affiliated with the candidate phylum Lokiarchaeota (16 clones were  
179 randomly collected from each library).

180 **FISH.** MK-D1-specific probes were designed using the probe design tool of the ARB  
181 program<sup>30</sup>. The specificity of the probes was confirmed using the BLAST and the ARB-  
182 SILVA databases<sup>31</sup>. The  $\Delta G^0_{\text{overall}}$  values of the probes and target MK-D1 16S rRNA  
183 sequence were calculated using the mathFISH web server<sup>32</sup>. Both probes exhibited high  
184 hybridization efficiencies (-15.5 kcal/mol for DSAG-Gr2-1142, -14.4 kcal/mol for  
185 DSAG-Gr2-1432).

186 **Growth test using multiple substrates.** A highly purified culture of MK-D1 was  
187 inoculated in the medium (15% inoculum, v/v). Then, 1 ml of the culture liquid was  
188 immediately taken from each culture to examine the initial 16S rRNA gene copy numbers  
189 of MK-D1 using the qPCR technique. The liquid culture samples for qPCR analysis were  
190 stored at -80°C until further processing. After the sampling, all the cultures were  
191 incubated at 20°C for 120 days in the dark without shaking. After 120 days of incubation,  
192 1 ml of liquid culture was sampled from each culture vial to quantify the final 16S rRNA  
193 gene copy numbers of MK-D1. DNA extraction and qPCR analysis were performed, as  
194 the methods mentioned in the Methods section. In the qPCR assay, samples taken from  
195 the same culture vial (e.g., 0-day and 120-day samples of H2-1 culture) were applied to  
196 the same PCR plate for accurate quantification. To confirm microbial community  
197 structure after incubation, iTAG analysis was performed on the samples, which showed  
198 an increase of about 10-fold or more in the 16S rRNA gene copy numbers of MK-D1

199 after incubation, as observed by the qPCR assay.

200 **Stable isotope probing incubation and NanoSIMS analysis.** During incubation, 5 ml  
201 of culture liquid was taken from the vials once every 30 days, 1 ml of which was used for  
202 qPCR and iTAG analyses, and the remaining 4 ml was processed for NanoSIMS analysis.  
203 The samples for NanoSIMS analysis were fixed in 2% PFA under anaerobic condition for  
204 approximately 2 h. The fixed cells were washed twice in PBS and stored in a 1:1 mixture  
205 of PBS and ethanol at -20°C until further processing.

206 Due to the low-biomass sample, the fixed cells were concentrated in a small analysis  
207 area (0.5–1 mm<sup>2</sup>) of indium tin oxide-coated polycarbonate membranes using a  
208 fluorescence-activated cell sorting<sup>33</sup>. Microbial cells on membranes were stained with  
209 SYBR Green I and observed with an epifluorescence microscope (BX-51, Olympus) prior  
210 to NanoSIMS analysis.

211 Samples were analyzed by raster ion imaging with a CAMECA NanoSIMS 50L at  
212 the Kochi Institute for Core Sample Research, JAMSTEC. A focused primary Cs<sup>+</sup> beam  
213 of ~1 pA for carbon and nitrogen isotopic analysis was rastered over 30 × 30 μm<sup>2</sup> areas  
214 on the samples. Negative secondary ions of <sup>12</sup>C (EM#1), <sup>13</sup>C (EM#2), <sup>16</sup>O (EM#4), <sup>12</sup>C<sup>14</sup>N  
215 (EM#5), <sup>12</sup>C<sup>15</sup>N (EM#6), and <sup>32</sup>S (EM#7) were measured using six electron multipliers  
216 (EMs) in a multi-detection mode at a high mass resolving power of ~7,000 (CAMECA  
217 NanoSIMS definition), which is sufficient to separate all relevant isobaric interferences  
218 (i.e., <sup>13</sup>C on <sup>12</sup>C<sup>1</sup>H, <sup>12</sup>C<sup>14</sup>N on <sup>13</sup>C<sup>++</sup>, and <sup>12</sup>C<sup>14</sup>N<sup>1</sup>H). Each run was initiated after the  
219 stabilization of the secondary ion beam intensity following a pre-sputtering of  
220 approximately 2 min with a strong primary ion beam current. The same area was  
221 repeatedly scanned (20–30 times) in each run, with individual images consisting of 256  
222 × 256 pixels and with a dwell time of 2,000 μs. The total acquisition time was  
223 approximately 1 h.

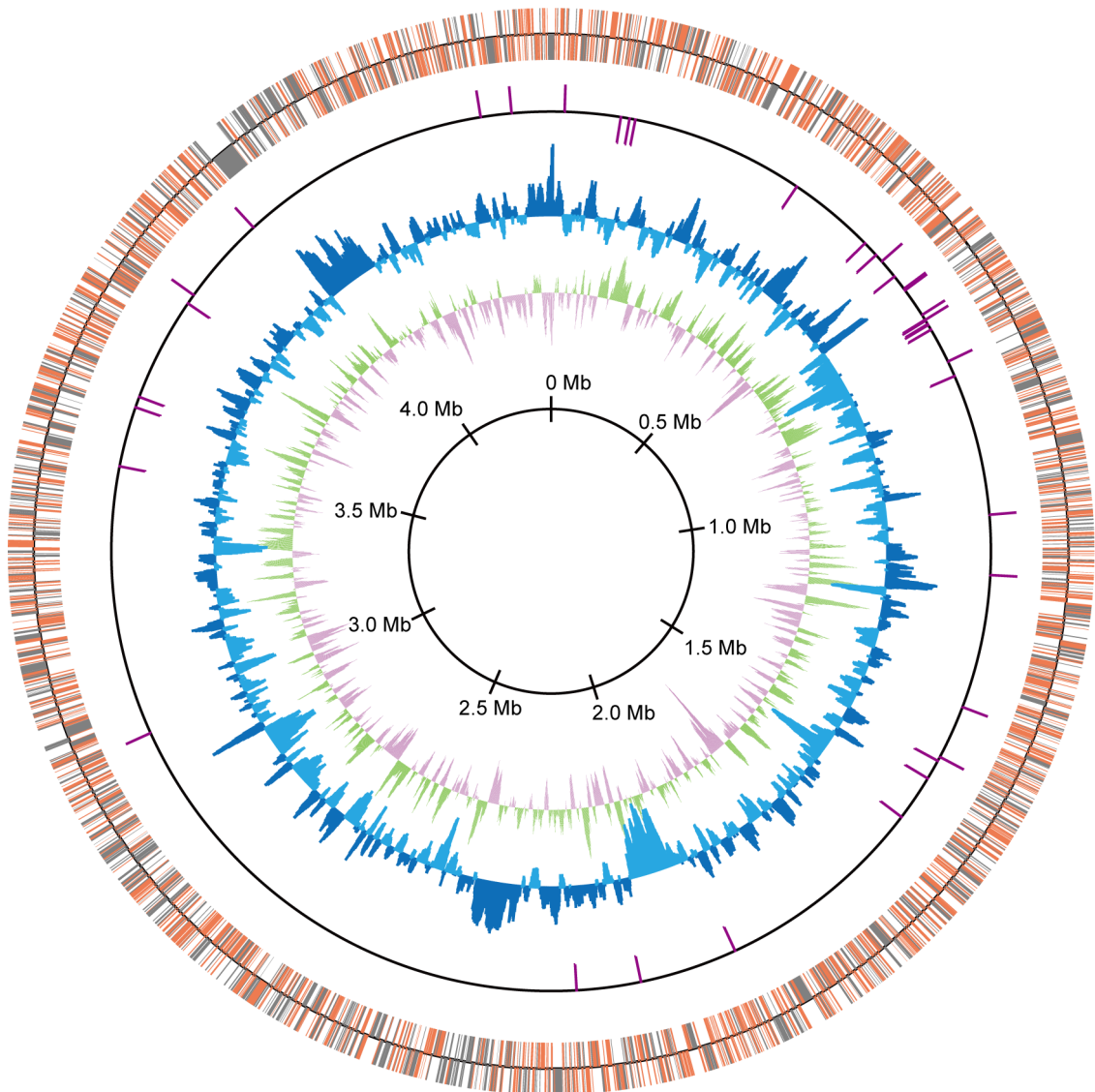
224 The recorded images and data were analyzed using IDL based NASA JSC imaging  
225 software for NanoSIMS<sup>34</sup>, OpenMIMS (<https://github.com/BWHCNI/OpenMIMS>) and  
226 Look@NanoSIMS<sup>35</sup>. The images were corrected for quasi-simultaneous arrival effect and  
227 detector dead time. Different scans of each image were aligned to correct image drift  
228 during acquisition. The final images were generated by adding the secondary ion counts  
229 of each recorded secondary ion from each pixel for all scans.

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232 **Supplementary Figures**

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235 **Supplementary Figure S1 | Circular representation of the *Ca. Prometheoarchaeum***

236 ***syntrophicum* strain MK-D1 genome.** From the outside to the center: the distribution

237 of the CDSs based on the conserved (orange) or non-conserved (gray) genes in the first

238 circle, non-coding RNAs in the second circle, GC content showing deviation from

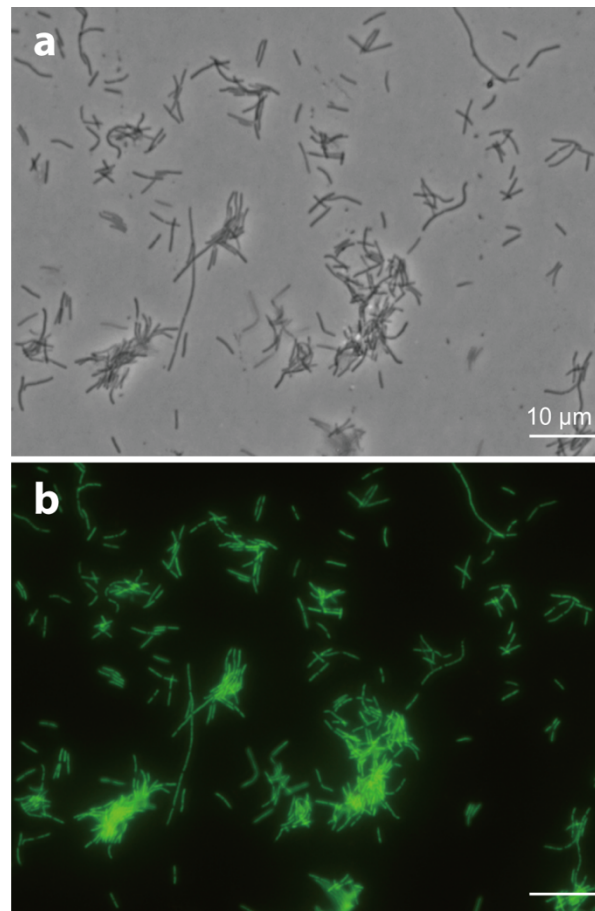
239 average (40.7%) in the third circle, and GC skew in the fourth circle. The GC content and

240 GC skew were calculated using a sliding window of 2 kb in step of 10 kb. The CDS and

241 RNA genes illustrate the findings for plus and minus strands.

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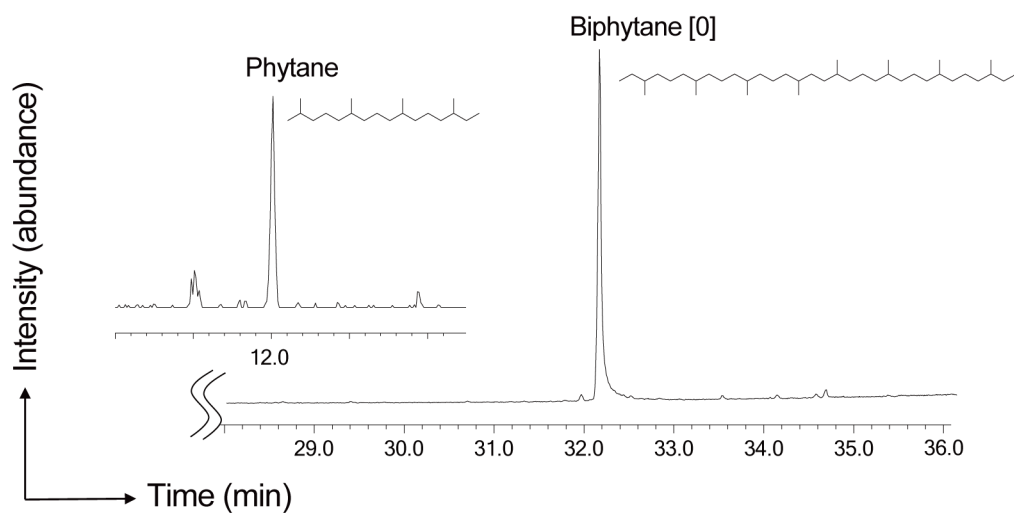




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245 **Supplementary Figure S2 | Photomicrographs of *Methanobacterium* sp. strain MO-**  
246 **MB1 cells stained with SYBR Green I.** Phase-contrast (a) and fluorescence (b)  
247 micrographs of the same field are shown. Cells of strain MO-MB1 were fixed with 2%  
248 PFA after culturing with the basal medium under the optimal cultivation condition (i.e.,  
249 supplementation with H<sub>2</sub> [ca. 150 kPa in head space of culture bottle] and acetate [1 mM]  
250 and yeast extract [0.01%], and incubation temperature 30°C). All the *Methanobacterium*  
251 cells were stained well with SYBR Green I. The weak fluorescence intensities of some  
252 *Methanobacterium* cells in Fig. 2b were likely due to increased rigidity and reduced  
253 permeability of their membranes incurred from growth under low hydrogen  
254 concentrations (*c.f.*, Nakamura et al. [2006]<sup>36</sup>). Bars, 10 µm.

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257 **Supplementary Figure S3** | A total ion chromatogram of gas chromatography/mass  
 258 spectrometry (GC/MS) for lipid obtained from *Methanogenium cariaci* strain JR1 (JCM  
 259 10550). The chemical structures of isoprenoid lipids are also shown.

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Supplementary Figure S4 | Ribosomal protein-(left) and 16S rRNA gene-(right) based phylogeny of MK-D1. (see next page)

263 **Supplementary Figure S4 (cont.) | Ribosomal protein- (left) and 16S ribosomal RNA**  
264 **gene- (right) based phylogeny of MK-D1.** Phylogenomic tree of MK-D1 and select  
265 cultured archaea, eukaryotes, and bacteria based on 31 ribosomal proteins conserved  
266 across the three domains (Supplementary Table S4). Ribosomal protein sequences were  
267 collected from MK-D1, the organisms shown in the tree, and metagenome-assembled  
268 genomes (MAGs) of uncultured archaeal lineages (Supplementary Table S5) and aligned  
269 individually using MAFFT (--linsi). MAG-derived sequences were included to generate  
270 an alignment that maximizes the archaeal diversity taken into account, but removed for  
271 subsequent tree construction to avoid any influence of contamination (*i.e.*, concatenation  
272 of sequences that do not belong to the same organism). *Ca. Korarchaeum* sequences were  
273 kept due to its critical phylogenetic position in TACK phylogeny. After removing all-gap  
274 positions and concatenation, the maximum likelihood tree was constructed using  
275 RAxML-NG (fixed empirical substitution matrix [LG], 4 discrete GAMMA categories,  
276 empirical AA frequencies, and 100 bootstrap replicates). Bootstrap values around critical  
277 branching points are also shown. Phylogenetic tree of MK-D1 and related archaea based  
278 on 16S rRNA genes. 16S rRNA gene sequences were aligned using SINA<sup>37</sup> against the  
279 Silva v132 alignment<sup>31</sup>. The maximum likelihood tree was calculated using RAxML<sup>38</sup>  
280 using the generalized time reversible (GTR) model, 4 discrete GAMMA categories,  
281 generalized time reversible model, and 100 bootstrap replicates.  
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**Supplementary Figure S5 | Eukaryotic signature proteins and anaerobic metabolism of select Asgard archaea.** Asgard archaea candidate phyla are abbreviated as follows: Lokiarchaeota (La), Thorarchaeota (Ta), Odinarchaeota (Oa), and Heimdallarchaeota (Ha).

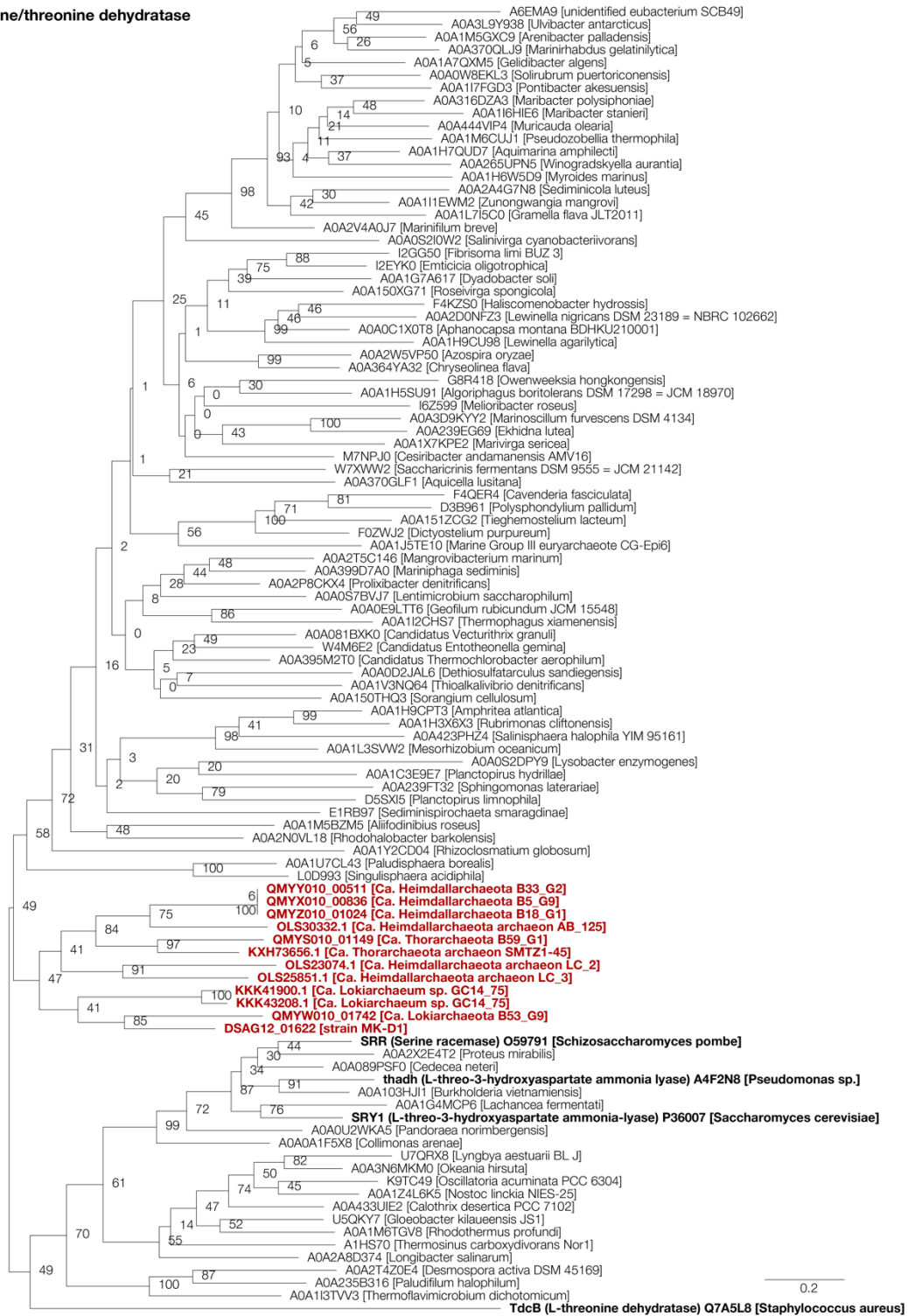
**Urocanate hydratase**



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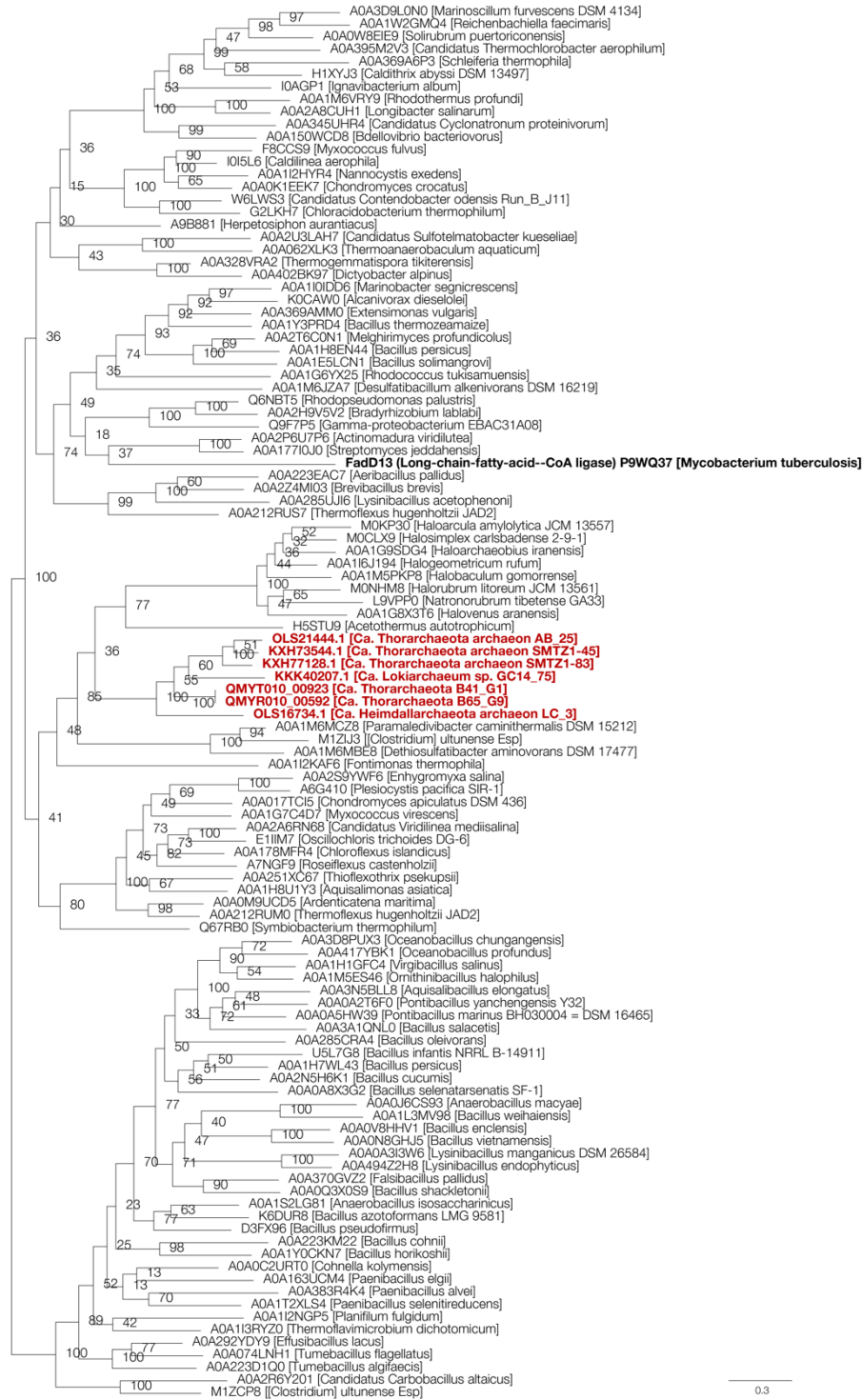
**Supplementary Figure S6 | Maximum likelihood tree of Asgard archaea urocanate hydratase (HutU).** HutU homologs were collected through BLASTp analysis of the Asgard archaea sequences against the UniProt database (release 2019\_06). Of homologs with sequence similarity  $\geq 40\%$  and overlap  $\geq 70\%$ , representative sequences were selected using CD-HIT with a clustering cutoff of 70% similarity (default settings otherwise). Additional homologs with verified biochemical activity, sequence similarity  $\geq 30\%$ , and overlap  $\geq 70\%$  were collected through BLASTp analysis of the Asgard archaea sequences against the UniProt/SwissProt database. Sequences were aligned using MAFFT v7<sup>39</sup> with default settings and trimmed using trimA1<sup>40</sup> with default settings. The phylogenetic tree was constructed using RAXML-NG<sup>38</sup> using fixed empirical substitution matrix (LG), 4 discrete GAMMA categories, empirical amino acid frequencies from the alignment, and 100 bootstrap replicates.

Serine/threonine dehydratase



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Supplementary Figure S7 | Maximum likelihood tree of Asgard archaea L-threonine/L-serine dehydratase (TdcB). See Fig S4 caption for details.

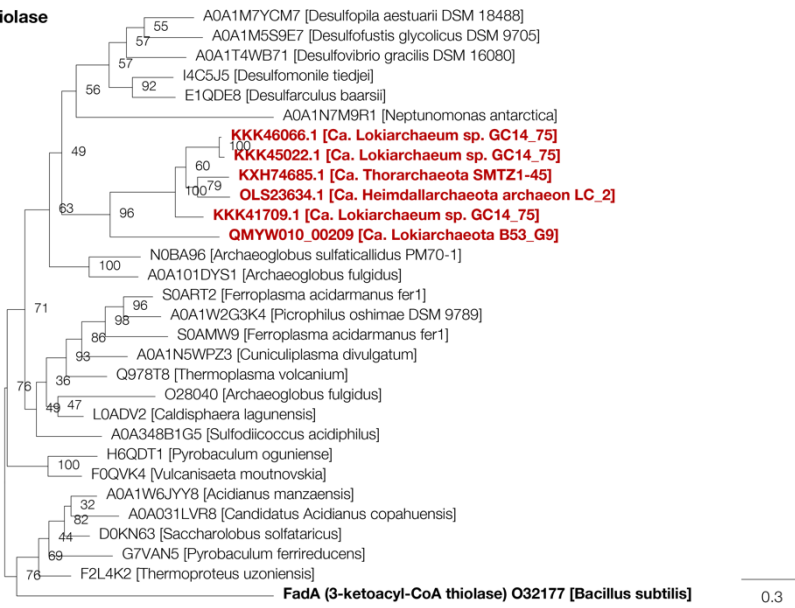


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**Supplementary Figure S8 | Maximum likelihood tree of Asgard archaea fatty-acid--CoA ligase.** Although the closest characterized relative of the Asgard archaea genes is a long-chain-fatty-acid--CoA ligase, the preferred substrate remains unclear as fatty-acid--CoA ligases have broad/diverse substrate specificities. See Fig S4 caption for details.



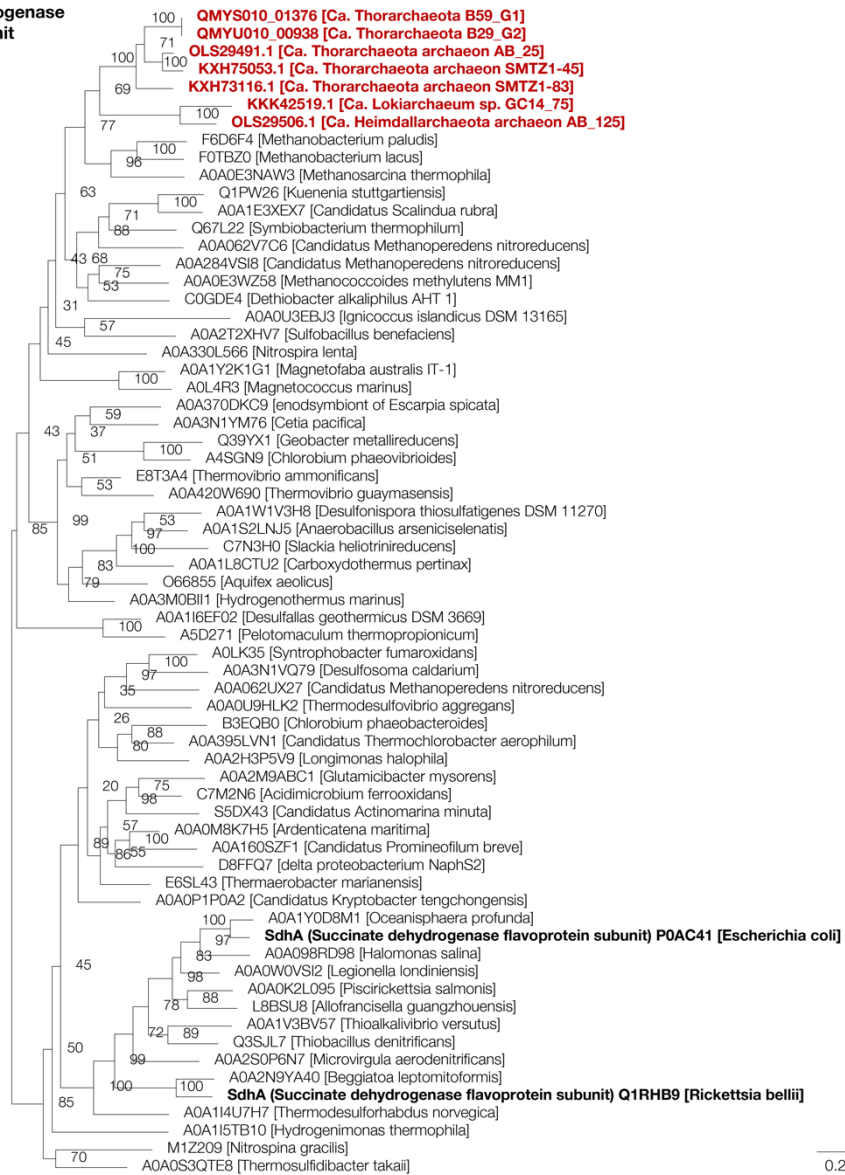
**3-ketoacyl-CoA thiolase**



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**Supplementary Figure S9 | Maximum likelihood tree of Asgard archaea 3-ketoacyl-CoA thiolase (FadA).** See Fig S4 caption for details.

Succinate dehydrogenase flavoprotein subunit

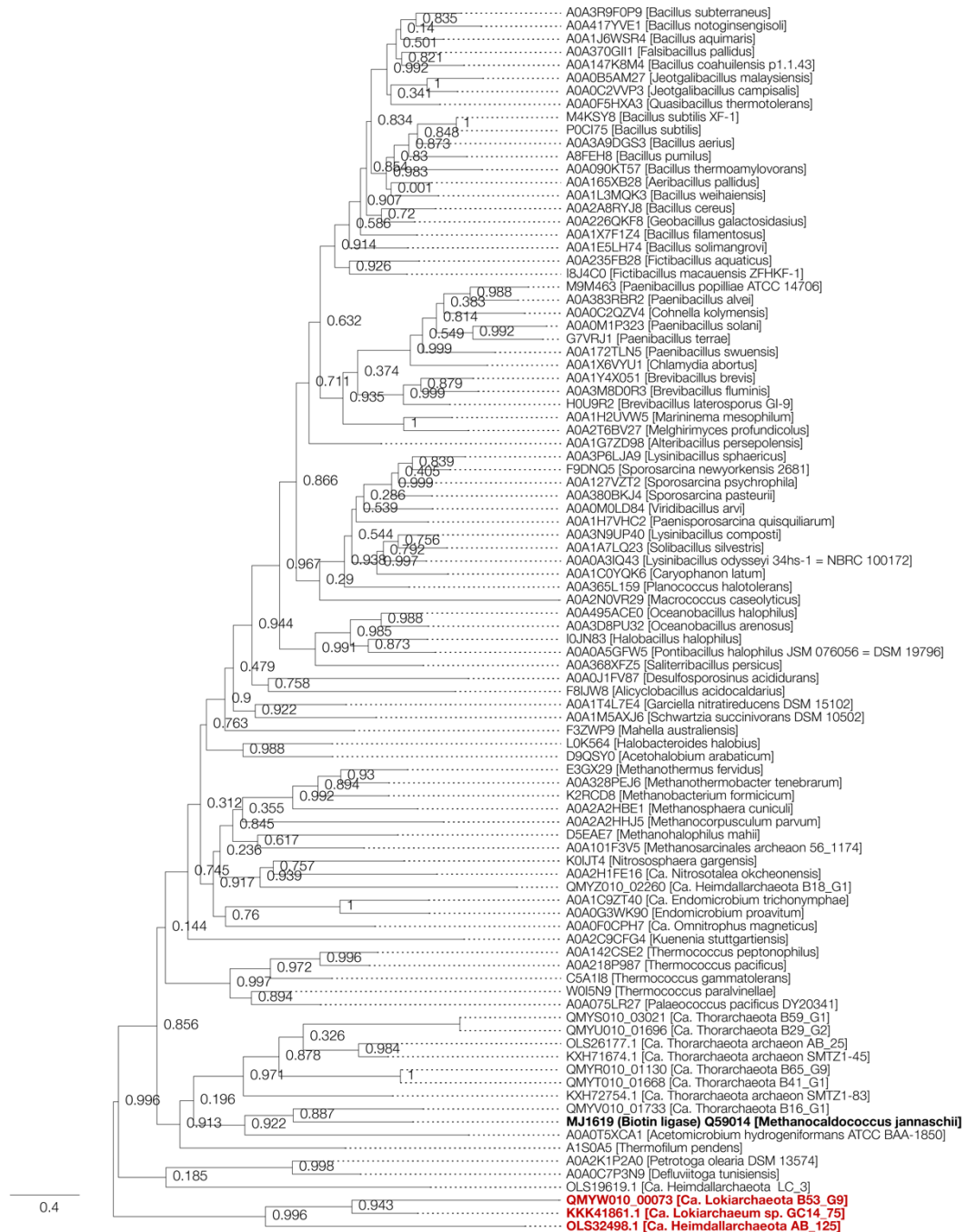


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312 **Supplementary Figure S10 | Maximum likelihood tree of Asgard archaea succinate**  
 313 **dehydrogenase flavoprotein subunit (SdhA).** See Fig S4 caption for details.

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**Supplementary Figure S11 | Maximum likelihood tree of Asgard archaea biotin ligase (BirA).** BirA homologs were collected through BLASTp analysis of the Asgard archaea sequences against the UniProt database (release 2019\_06). Of homologs with sequence similarity  $\geq 40\%$  and overlap  $\geq 70\%$ , representative sequences were selected using CD-HIT with a clustering cutoff of 70% similarity (default settings otherwise). Additional homologs with verified biochemical activity, sequence similarity  $\geq 30\%$ , and overlap  $\geq 70\%$  were collected through BLASTp analysis of the Asgard archaea sequences against the UniProt/SwissProt database. Sequences were aligned using MAFFT v7<sup>39</sup> with default settings and trimmed using trimAl<sup>40</sup> with default settings. The phylogenetic tree

326 was constructed using FastTree<sup>41</sup> using fixed empirical substitution matrix (LG) and 1000  
327 bootstrap replicates.  
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**Supplementary Table S1 | Genome information of *Ca. P. syntrophicum*, *Halodesulfovibrio* and *Methanogenium* cultured in this study.**

	<i>Ca. P. syntrophicum</i> MK-D1	<i>Halodesulfovibrio</i> MK-HDV	<i>Methanogenium</i> MK-MG
Size (bp)	4,427,796	4,171,812	2,331,727
Contigs	1	3	13
Coverage (times)	52	189	66
G+C content (%)	31.1	44.28	49.59
Number of ORF	3946	3594	2294
rRNAs	2	7	16
tRNAs	24	100	49
Genome completeness (%) <sup>a</sup>	100	99.38	98.37
Contamination (%) <sup>a</sup>	0	0.59	1.96

<sup>a</sup>Genome completeness and contamination were estimated using CheckM (Parks, D. H., Imelfort, M., Skennerton, C. T., Hugenholtz, P. & Tyson, G. W. CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. *Genome Res.* **25**, 1043–1055 [2015]).

**Supplementary Table 2 | iTAG analysis of cultures used for characterization of MK-D1.**

Sequencing was performed on a MiSeq platform using universal primer pair 530F and 907R. OTUs that have only two or fewer tag-sequences were not included in the microbial community analysis of the MK-D1 cultures.

**<Fig. 1b, and Extended Data Fig. 2a (FISH image for a tri-culture)>**

Accession number: DRR184081

Phylogenetic group	Sequence read number	Relative abundance (%)
Bacteria, Halodesulfobivrio	66871	76.9
Archaea, Lokiarchaeota ( <i>Ca. P. syntrophicum</i> )	12502	14.4
Archaea, Methanogenium	7398	8.5
Archaea, Methanococcoides	179	0.2
Bacteria, Dehalococcoidia GIF9 group	12	0.01
Total	86962	

**<Fig. 1c, d, and Extended Data Fig. 2b, c (FISH image for a co-culture)>**

Accession number: DRR184082

Phylogenetic group	Sequence read number	Relative abundance (%)
Archaea, Lokiarchaeota ( <i>Ca. P. syntrophicum</i> )	112611	87.5
Archaea, Methanogenium	15458	12.0
Archaea, Methanobacterium	612	0.5
Total	128681	

**<Fig. 1e>**

Accession number: DRR184083

Phylogenetic group	Sequence read number	Relative abundance (%)
Archaea, Lokiarchaeota ( <i>Ca. P. syntrophicum</i> )	72338	75.8
Archaea, Methanogenium	23120	24.2
Bacteria, Sphingomonas	16	0.02
Bacteria, Atribacteria	15	0.02
Bacteria, Lactobacillus	5	0.01
Total	95494	

**<Fig. 2b–c, and Extended Data Table 2 (NanoSIMS analysis, co-culture with *Methanobacterium*)>**

Accession number: DRR184084

Phylogenetic group	Sequence read number	Relative abundance (%)
Archaea, Lokiarchaeota ( <i>Ca. P. syntrophicum</i> )	87664	98.9
Archaea, Methanobacterium	954	1.1
Archaea, Methanococcoides	14	0.02
Bacteria, Halodesulfobivrio	10	0.01
Bacteria, Dehalococcoidia GIF9 group	9	0.01
Total	88651	

**<Extended Data Table 2 (tri-culture with *Halodesulfobivrio* and *Methanogenium*)>**

Accession number: DRR184085

Phylogenetic group	Sequence read number	Relative abundance (%)
Bacteria, Halodesulfobivrio	67531	77.7
Archaea, Methanogenium	20972	24.1
Archaea, Lokiarchaeota ( <i>Ca. P. syntrophicum</i> )	15774	18.1
Archaea, Methanococcoides	705	0.8
Archaea, Methanobacterium	13	0.01
Total	104995	

**<Fig. 3a, b, and Extended Data Fig. 2d (SEM images)>**

Accession number: DRR184086

Phylogenetic group	Sequence read number	Relative abundance (%)
Archaea, Lokiarchaeota ( <i>Ca. P. syntrophicum</i> )	115119	89.26
Archaea, Methanogenium	13846	10.74
Total	128965	

**<Fig. 3c, f, i and Extended Data Fig. 2e, h, i, l (SEM and TEM images)>**

Accession number: DRR184087

Phylogenetic group	Sequence read number	Relative abundance (%)
Archaea, Lokiarchaeota ( <i>Ca. P. syntrophicum</i> )	130923	87.0
Archaea, Methanogenium	19496	13.0
Bacteria, Phenyllobacterium	14	0.01
Total	150433	

**<Fig. 3d, e, and Extended Data Fig. 2f, g (Cryo-EM images)>**

Accession number: DRR184088

Phylogenetic group	Sequence read number	Relative abundance (%)
Archaea, Lokiarchaeota ( <i>Ca. P. syntrophicum</i> )	86292	84.6
Archaea, Methanogenium	15647	15.3
Archaea, Methanobacterium	82	0.1
Bacteria, Dehalococcoidia GIF9 group	19	0.02
Bacteria, Halodesulfobivrio	8	0.01
Bacteria, Lysinibacillus	7	0.01
Total	102055	

**<Fig. 3g, h and Extended Data Fig. 2j, k (SEM images)>**

Accession number: DRR184089

Phylogenetic group	Sequence read number	Relative abundance (%)
Archaea, Lokiarchaeota ( <i>Ca. P. syntrophicum</i> )	104002	90.0
Archaea, Methanogenium	11610	10.0
Total	115612	

**<Fig. 3j (Lipid analysis)>**

Accession number: DRR184090

Phylogenetic group	Sequence read number	Relative abundance (%)
Archaea, Lokiarchaeota ( <i>Ca. P. syntrophicum</i> )	163886	91.5
Archaea, Methanogenium	15257	8.5
Bacteria, Sphingomonas	22	0.01
Total	179165	

**<Extended Data Fig. 3a (Amino acids concentrations at 90 days)>**

Accession number: DRR184091

Phylogenetic group	Sequence read number	Relative abundance (%)
Archaea, Lokiarchaeota ( <i>Ca. P. syntrophicum</i> )	109046	86.8
Archaea, Methanogenium	16580	13.2
Total	125626	

<Extended Data Fig. 3b (Amino acids concentrations at 90 days)>

Accession number: DRR184092

Phylogenetic group	Sequence read number	Relative abundance (%)
Archaea, Lokiarchaeota ( <i>Ca. P. syntrophicum</i> )	126553	91.0
Archaea, Methanogenium	12539	9.0
Total	139092	

<Extended Data Table 3 (Inoculum)>

Accession number: DRR184093

Phylogenetic group	Sequence read number	Relative abundance (%)
Archaea, Lokiarchaeota ( <i>Ca. P. syntrophicum</i> )	78508	39.8
Archaea, Methanogenium	72659	36.8
Archaea, Methanobacterium	46017	23.3
Bacteria, Massilia	10	0.005
Bacteria, Bacillus	4	0.002
Bacteria, Paenibacillus	3	0.002
Bacteria, Pseudomonas	3	0.002
Total	197204	

<Extended Data Table 3 (Control-1)>

Accession number: DRR184094

Phylogenetic group	Sequence read number	Relative abundance (%)
Archaea, Lokiarchaeota ( <i>Ca. P. syntrophicum</i> )	140431	76.7
Archaea, Methanogenium	39929	21.8
Archaea, Methanobacterium	2655	1.4
Bacteria, Veillonellaceae	60	0.03
Total	183075	

<Extended Data Table 3 (Control-2)>

Accession number: DRR184095

Phylogenetic group	Sequence read number	Relative abundance (%)
Archaea, Lokiarchaeota ( <i>Ca. P. syntrophicum</i> )	70273	60.3
Archaea, Methanogenium	44282	38.0
Archaea, Methanobacterium	1906	1.6
Bacteria, Hydrogenophilus	25	0.02
Bacteria, Deinococcus	19	0.02
Bacteria, Propionibacterium	4	0.003
Archaea, Thaumarchaeota	3	0.003
Total	116512	

<Extended Data Table 3 (Sulfate-1)>

Accession number: DRR184096

Phylogenetic group	Sequence read number	Relative abundance (%)
Archaea, Lokiarchaeota ( <i>Ca. P. syntrophicum</i> )	84925	79.5
Archaea, Methanogenium	20854	19.5
Archaea, Methanobacterium	1017	1.0
Archaea, Thaumarchaeota	14	0.01
Bacteria, Oceanospirillales	7	0.01
Archaea, Marine Group II	5	0.005
Bacteria, Veillonellaceae	5	0.005
Total	106827	

<Extended Data Table 3 (Glucose-1)>

Accession number: DRR184097

Phylogenetic group	Sequence read number	Relative abundance (%)
Archaea, Lokiarchaeota ( <i>Ca. P. syntrophicum</i> )	118208	73.8
Archaea, Methanogenium	38864	24.3
Archaea, Methanobacterium	2998	1.9
Bacteria, Sedimentibacter	30	0.02
Archaea, Thaumarchaeota	9	0.01
Total	160109	

<Extended Data Table 3 (Glucose-2)>

Accession number: DRR184098

Phylogenetic group	Sequence read number	Relative abundance (%)
Archaea, Lokiarchaeota ( <i>Ca. P. syntrophicum</i> )	85521	70.3
Archaea, Methanogenium	34100	28.0
Archaea, Methanobacterium	2010	1.7
Total	121631	

<Extended Data Table 3 (Xylose-2)>

Accession number: DRR184099

Phylogenetic group	Sequence read number	Relative abundance (%)
Archaea, Lokiarchaeota ( <i>Ca. P. syntrophicum</i> )	92052	61.4
Archaea, Methanogenium	54674	36.5
Archaea, Methanobacterium	3128	2.1
Bacteria, Sphingomonas	15	0.01
Total	149869	

<Extended Data Table 3 (Archaeal cell-1)>

Accession number: DRR184100

Phylogenetic group	Sequence read number	Relative abundance (%)
Archaea, Lokiarchaeota ( <i>Ca. P. syntrophicum</i> )	115040	81.5
Archaea, Methanogenium	24713	17.5
Archaea, Methanobacterium	1064	0.8
Bacteria, Afipia	391	0.3
Total	141208	

<Pure co-culture>

Accession number: DRR184101

Phylogenetic group	Sequence read number	Relative abundance (%)
Archaea, Lokiarchaeota ( <i>Ca. P. syntrophicum</i> )	95965	91.4
Archaea, Methanogenium	9049	8.6
Total	105014	

No bacterial PCR amplicons and no bacterial growth were observed from the culture. The purity check of culture is described in the Supplementary Methods.



**Supplementary Table S3 | DNA probes used in this study.**

Probe	Target group	Probe sequence (5' to 3') <sup>a</sup>	Labeling	%FA <sup>b</sup>	Reference
<b>Standard-FISH</b>					
DSAG-Gr2-1142 <sup>c</sup>	<i>Ca. P. syntrophicum</i> strain MK-D1 and its relatives	CAGTCCGCTTAGCGTTCC	Alexa Fluor 488	35	This study
MBGB-525 <sup>c,d</sup>	Almost all members of Lokiarchaeota	AGAGCTGGTTTTACCGCG	Alexa Fluor 488	10	Knittel <i>et al.</i> , 2005
EUB338	Most <i>Bacteria</i>	GCTGCCCTCCCGTAGGAGT	Alexa Fluor 555	20	Amann <i>et al.</i> , 1990
ARC915	Most <i>Archaea</i>	GTGCTCCCCGCCAATTCCT	Alexa Fluor 555	35	Stahl <i>et al.</i> , 1991
<b>in situ DNA-HCR-FISH</b>					
DSAG-Gr2-1142-initiatorH	<i>Ca. P. syntrophicum</i> strain MK-D1 and its relatives	<u>CCGAATACAAAGCATCAACGACTAGA</u> AAAAACAGTCCGCTTAGCGTTCC	—	35	This study
DSAG-Gr2-1432-initiatorH <sup>e</sup>	<i>Ca. P. syntrophicum</i> strain MK-D1	<u>CCGAATACAAAGCATCAACGACTAGA</u> AAAAACGACCCTTAGGACCGTTTTTC	—	30	This study
EUB338-initiatorC	Most <i>Bacteria</i>	<u>CCAGTTATCAGTAGTCCGTCCTTCAT</u> TTTTTGTGCTCCCGTAGGAGT	—	20	Yamaguchi <i>et al.</i> , 2015
MG1200-initiatorC	most <i>Methanomicrobiales</i> (including <i>Methanogenium</i> )	<u>CCAGTTATCAGTAGTCCGTCCTTCAT</u> TTTTTTCGGATAATTCGGGGCATGCTG	—	10 <sup>f</sup>	Raskin <i>et al.</i> , 1994.
ARC915-initiatorC	Most <i>Archaea</i>	<u>CCAGTTATCAGTAGTCCGTCCTTCAT</u> TTTTTGTGCTCCCCGCCAATTCCT	—	35	Yamaguchi <i>et al.</i> , 2015
<b>Amplifier probes</b>					
H1	—	<u>TCTAGTCGTTgatgettgtattcgg</u> CGACAGATAAccgaatacaagcatc	Alexa Fluor 488	—	Choi <i>et al.</i> , 2010 <sup>g</sup>
H2	—	ccgaatacaagcatcAACGACTAGAgatgctttgtattcggTTATCTGTCG	Alexa Fluor 488	—	Choi <i>et al.</i> , 2010 <sup>g</sup>
C1	—	<u>ATGAAGGACGgactactgataactgg</u> GACTTCCATAccagttatcagtagtc	Alexa Fluor 555	—	Choi <i>et al.</i> , 2010 <sup>g</sup>
C2	—	ccagttatcagtagtcCGTCCATCgactactgataactggTATGGAAGTC	Alexa Fluor 555	—	Choi <i>et al.</i> , 2010 <sup>g</sup>

<sup>a</sup>Double underlined sequences are the initiator sequence. Lowercase letters represent stem structures of amplifier probe. Underlined sequence of amplifier probes are complementary to the initiator sequences.

<sup>b</sup>%FA represent formamide concentration (v/v). For *Ca. P. syntrophicum*-specific probes, FA concentrations were determined by Clone-FISH method (Schramm *et al.*, 2002). The Clone-FISH sample inserted a nearly full 16S rRNA gene sequence of MK-D1 was prepared as described in Kubota *et al.* (2006).

<sup>c</sup>For the probes, both of 5'-singly fluorescence labeled and 5'-,3'-doubly fluorescence labeled probes (Stoecker *et al.*, 2010) were applied to detect *Ca. P. syntrophicum* strain MK-D1 cells.

<sup>d</sup>The probe also targets sequences of the some Thorarchaeota, some Bathyarchaeota and many Marine Hydrothermal Vent Group.

<sup>e</sup>When HCR-FISH detection using DSAG-Gr2-1142 probe, we obtained clear fluorescence signals of MK-D1 cells from the tri-culture, but not from the co-cultures. Therefore, we designed a new probe DSAG-Gr2-1432 and mixed with DSAG-Gr2-1142 probe for clear detection of the cells in the co-cultures. FA concentration was 30% when we used two probes simultaneously.

<sup>f</sup>FA concentration for the MG1200 probe was re-evaluated using a pure culture of *Methanogenium cariaci* strain JR1 (JCM 10550).

<sup>g</sup>Amplifier probe sequences were changed to DNA probe from RNA probe.

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**Supplementary Table S4 | Ribosomal proteins used for phylogenomic tree construction.**

<b>COG</b>	<b>Ribosomal protein</b>
COG00081	Ribosomal protein L1
COG00090	Ribosomal protein L2
COG00087	Ribosomal protein L3
COG00088	Ribosomal protein L4
COG00094	Ribosomal protein L5
COG00097	Ribosomal protein L6P/L9E
COG00080	Ribosomal protein L11
COG00102	Ribosomal protein L13
COG00093	Ribosomal protein L14
COG00200	Ribosomal protein L15
COG00256	Ribosomal protein L18
COG00091	Ribosomal protein L22
COG00089	Ribosomal protein L23
COG00198	Ribosomal protein L24
COG00255	Ribosomal protein L29
COG01841	Ribosomal protein L30/L7E
COG00052	Ribosomal protein S2
COG00092	Ribosomal protein S3
COG00522	Ribosomal protein S4 and related proteins
COG00098	Ribosomal protein S5
COG00049	Ribosomal protein S7
COG00096	Ribosomal protein S8
COG00103	Ribosomal protein S9
COG00051	Ribosomal protein S10
COG00100	Ribosomal protein S11
COG00048	Ribosomal protein S12
COG00099	Ribosomal protein S13
COG00184	Ribosomal protein S15P/S13E
COG00186	Ribosomal protein S17
COG00185	Ribosomal protein S19



**Supplementary Table S6 | MK-D1 gene expression data.** For each gene, the locus tag, predicted product, KEGG annotation (if available), and gene expression level (reads per kilobase of transcript per million mapped reads; RPKM).

Locus Tag	Product	KEGG	RPKM	ESPs
DSAG12_00001	hypothetical protein	--	204	
DSAG12_00002	hypothetical protein	--	213	
DSAG12_00003		K00837	204	
DSAG12_00004	hypothetical protein	--	1148	
DSAG12_00005	hypothetical protein	--	529	
DSAG12_00006	HSP20 family protein	K13993	283	
DSAG12_00007	hypothetical protein	--	170	
DSAG12_00008	hypothetical protein	--	162	
DSAG12_00009	hypothetical protein	--	314	
DSAG12_00010	urocanate hydratase	K01712	238	
DSAG12_00011	histidine ammonia-lyase	K01745	259	
DSAG12_00012	imidazolonepropionase	K01468	236	
DSAG12_00013	formate--tetrahydrofolate ligase	K01938	161	
DSAG12_00014	hypothetical protein	--	276	
DSAG12_00015	ferredoxin hydrogenase large subunit	K00533	132	
DSAG12_00016	NADH-quinone oxidoreductase subunit E	K00334	189	
DSAG12_00017	putative transposase	K07496	0	
DSAG12_00018	tRNA-Trp		187	
DSAG12_00019	O-methyltransferase	K15471	155	
DSAG12_00020	hypothetical protein	--	224	
DSAG12_00021	polar amino acid transport system ATP-binding protein	K02028	223	
DSAG12_00022	arginine/lysine/histidine/glutamine transport system substrate-binding and permease protein	K17062	309	
DSAG12_00023	polar amino acid transport system substrate-binding protein	K02030	182	
DSAG12_00024	uncharacterized protein	K06864	0	
DSAG12_00025	hypothetical protein	--	157	
DSAG12_00026	Lrp/AsnC family transcriptional regulator, leucine-responsive regulatory protein	K03719	174	
DSAG12_00027	Ras-related protein Rab-43	K07930	130	small GTP-binding domain protein
DSAG12_00028	hypothetical protein	--	175	
DSAG12_00029	hypothetical protein	--	105	
DSAG12_00030	hypothetical protein	--	172	
DSAG12_00031	proteasome beta subunit	K03433	239	
DSAG12_00032	hypothetical protein	--	158	
DSAG12_00033	glutamyl-tRNA synthetase	K01885	250	
DSAG12_00034	hypothetical protein	--	112	
DSAG12_00035	hypothetical protein	--	164	
DSAG12_00036	hypothetical protein	--	83	
DSAG12_00037	tRNA pseudouridine38-40 synthase	K06173	158	
DSAG12_00038	hypothetical protein	--	223	
DSAG12_00039	replication factor C small subunit	K04801	211	
DSAG12_00040	hypothetical protein	--	164	
DSAG12_00041	hypothetical protein	--	167	
DSAG12_00042	hypothetical protein	--	181	
DSAG12_00043	UDP-2,3-diacetylglucosamine hydrolase	K03269	197	
DSAG12_00044	hypothetical protein	--	263	
DSAG12_00045	hypothetical protein	--	166	
DSAG12_00046	hypothetical protein	--	221	
DSAG12_00047	hypothetical protein	--	96	
DSAG12_00048	hypothetical protein	--	32	
DSAG12_00049		K06889	0	
DSAG12_00050	dihydrodiol dehydrogenase / D-xylose 1-dehydrogenase (NADP)	K00078	169	
DSAG12_00051	MFS transporter, SP family, sugar:H+ symporter	K08139	228	
DSAG12_00052	peptide methionine sulfoxide reductase msrA/msrB	K12267	234	
DSAG12_00053	phosphohistidine phosphatase	K08296	188	
DSAG12_00054	hypothetical protein	--	171	
DSAG12_00055	hypothetical protein	K09164	194	
DSAG12_00056	hypothetical protein	--	166	
DSAG12_00057	hypothetical protein	--	171	
DSAG12_00058	ADP-ribosylation factor-like protein 5B	K07950	172	
DSAG12_00059	hypothetical protein	--	302	
DSAG12_00060	hypothetical protein	--	420	
DSAG12_00061	internalin A	K13730	115	
DSAG12_00062	hypothetical protein	--	224	
DSAG12_00063	peptide-methionine (R)-S-oxide reductase	K07305	155	
DSAG12_00064	aminopeptidase N	K01256	178	
DSAG12_00065	hypothetical protein	K09120	228	
DSAG12_00066	hypothetical protein	--	128	
DSAG12_00067	hypothetical protein	--	152	
DSAG12_00068	hypothetical protein	--	147	
DSAG12_00069	exosome complex component CSL4	K07573	59	
DSAG12_00070	putative methylase	K07579	160	
DSAG12_00071	hypothetical protein	--	169	
DSAG12_00072	Trp repressor binding protein	K03809	19	
DSAG12_00073	hypothetical protein	--	213	
DSAG12_00074	enolase	K01689	333	
DSAG12_00075	serine/threonine-protein phosphatase 4 catalytic subunit	K15423	236	

DSAG12_00076	hypothetical protein	--	189
DSAG12_00077	alanine dehydrogenase	K00259	147
DSAG12_00078	acetyl-CoA C-acetyltransferase	K00626	274
DSAG12_00079	hypothetical protein	--	304
DSAG12_00080	butyryl-CoA dehydrogenase	K00248	205
DSAG12_00081	3-hydroxybutyryl-CoA dehydratase	K17865	284
DSAG12_00082	hypothetical protein	--	175
DSAG12_00083	3-oxoacid CoA-transferase subunit B	K01029	223
DSAG12_00084	3-oxoacid CoA-transferase subunit A	K01028	272
DSAG12_00085	putative membrane protein	K08981	273
DSAG12_00086	hypothetical protein	--	90
DSAG12_00087	hypothetical protein	--	174
DSAG12_00088		K00936	164
DSAG12_00089	hypothetical protein	--	238
DSAG12_00090	hypothetical protein	--	201
DSAG12_00091	elongation factor 1-alpha	K03231	146
DSAG12_00092	magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase	K04035	289
DSAG12_00093	hypothetical protein	--	200
DSAG12_00094	archaea-specific DNA-binding protein	K03622	42
DSAG12_00095		K06883	138
DSAG12_00096	2-isopropylmalate synthase	K01649	218
DSAG12_00097	hypothetical protein	--	231
DSAG12_00098	small nuclear ribonucleoprotein D2	K11096	216
DSAG12_00099	hypothetical protein	--	51
DSAG12_00100	hypothetical protein	--	163
DSAG12_00101	hypothetical protein	--	114
DSAG12_00102	hypothetical protein	--	150
DSAG12_00103	hypothetical protein	--	145
DSAG12_00104	hypothetical protein	--	65
DSAG12_00105		K07051	225
DSAG12_00106	hypothetical protein	K09125	245
DSAG12_00107	tocopherol O-methyltransferase	K05928	209
DSAG12_00108	tRNA-Ser		0
DSAG12_00109	large subunit ribosomal protein L14e	K02875	98
DSAG12_00110	cytidylate kinase	K00945	207
DSAG12_00111	large subunit ribosomal protein L34e	K02915	105
DSAG12_00112	hypothetical protein	--	0
DSAG12_00113	hypothetical protein	--	229
DSAG12_00114	hypothetical protein	--	151
DSAG12_00115	hypothetical protein	--	221
DSAG12_00116	hypothetical protein	--	156
DSAG12_00117	RNA 3'-terminal phosphate cyclase (ATP)	K01974	173
DSAG12_00118	nicotinamide-nucleotide amidase	K03742	348
DSAG12_00119	hypothetical protein	--	129
DSAG12_00120	hypothetical protein	K09134	156
DSAG12_00121	hypothetical protein	--	195
DSAG12_00122	hypothetical protein	--	109
DSAG12_00123	hypothetical protein	--	162
DSAG12_00124	hypothetical protein	--	162
DSAG12_00125	hypothetical protein	--	180
DSAG12_00126	tRNA-Ile	Intron(12645	169
DSAG12_00127	hypothetical protein	--	254
DSAG12_00128	valyl-tRNA synthetase	K01873	131
DSAG12_00129	hypothetical protein	--	205
DSAG12_00130	hypothetical protein	--	129
DSAG12_00131	hypothetical protein	--	0
DSAG12_00132	tRNA-Ala		207
DSAG12_00133	hypothetical protein	--	212
DSAG12_00134	4-hydroxybutyryl-CoA synthetase (ADP-forming)	K18593	0
DSAG12_00135	glucosamine--fructose-6-phosphate aminotransferase (isomerizing)	K00820	272
DSAG12_00136	hypothetical protein	--	120
DSAG12_00137	pyruvate, water dikinase	K01007	216
DSAG12_00138	MFS transporter, DHA1 family, tetracycline resistance protein	K08151	179
DSAG12_00139	hypothetical protein	--	213
DSAG12_00140	hypothetical protein	--	0
DSAG12_00141	hypothetical protein	--	206
DSAG12_00142	leucyl-tRNA synthetase	K01869	27
DSAG12_00143	hypothetical protein	--	250
DSAG12_00144	hypothetical protein	--	173
DSAG12_00145	meiotic recombination protein SPO11	K10878	162
DSAG12_00146	hypothetical protein	--	214
DSAG12_00147	phosphopantothencysteine decarboxylase / phosphopantothenate--cysteine ligase	K13038	224
DSAG12_00148	hypothetical protein	--	207
DSAG12_00149	archaea-specific RecJ-like exonuclease	K07463	127
DSAG12_00150	hypothetical protein	--	198
DSAG12_00151	O-phospho-L-seryl-tRNA <sup>Sec</sup> :L-selenocysteinyl-tRNA synthase	K03341	196
DSAG12_00152	hypothetical protein	--	220
DSAG12_00153	nucleolar GTP-binding protein	K06943	196

DSAG12_00154	hypothetical protein	--	156
DSAG12_00155	hypothetical protein	--	211
DSAG12_00156	hypothetical protein	--	250
DSAG12_00157		K00837	168
DSAG12_00158	D-3-phosphoglycerate dehydrogenase	K00058	271
DSAG12_00159	hypothetical protein	--	260
DSAG12_00160	retinol dehydrogenase 13	K11161	236
DSAG12_00161	TldD protein	K03568	218
DSAG12_00162	PmbA protein	K03592	272
DSAG12_00163	acetyltransferase	K09181	238
DSAG12_00164		K06873	339
DSAG12_00165	hypothetical protein	--	266
DSAG12_00166	hypothetical protein	--	131
DSAG12_00167	putative protease	K08303	197
DSAG12_00168	hypothetical protein	--	235
DSAG12_00169	hypothetical protein	--	191
DSAG12_00170	presenilin 1	K04505	116
DSAG12_00171	hypothetical protein	--	232
DSAG12_00172	starch synthase (maltosyl-transferring)	K16147	276
DSAG12_00173	nitrogen fixation protein NifU and related proteins	K04488	220
DSAG12_00174	putative ABC transport system permease protein	K02004	175
DSAG12_00175	putative ABC transport system permease protein	K02004	171
DSAG12_00176	putative ABC transport system ATP-binding protein	K02003	138
DSAG12_00177	hypothetical protein	--	188
DSAG12_00178	hypothetical protein	--	270
DSAG12_00179	hypothetical protein	K09732	128
DSAG12_00180	hypothetical protein	--	65
DSAG12_00181	hypothetical protein	--	51
DSAG12_00182	beta-phosphoglucosyltransferase	K01838	283
DSAG12_00183	hypothetical protein	--	165
DSAG12_00184	glycerophosphoryl diester phosphodiesterase	K01126	161
DSAG12_00185	hypothetical protein	--	186
DSAG12_00186	lipoprotein-releasing system ATP-binding protein	K09810	219
DSAG12_00187	hypothetical protein	--	202
DSAG12_00188	hypothetical protein	--	190
DSAG12_00189	centriolar protein POC1	K16482	116
DSAG12_00190	hypothetical protein	--	165
DSAG12_00191	Xaa-Pro aminopeptidase	K01262	133
DSAG12_00192	hypothetical protein	--	219
DSAG12_00193	hypothetical protein	--	187
DSAG12_00194		K06933	192
DSAG12_00195	hypothetical protein	--	150
DSAG12_00196	Lrp/AsnC family transcriptional regulator, leucine-responsive regulatory protein	K03719	255
DSAG12_00197	hypothetical protein	--	180
DSAG12_00198	MFS transporter, DHA1 family, tetracycline resistance protein	K08151	233
DSAG12_00199	DNA mismatch repair protein MutL	K03572	171
DSAG12_00200	elongation factor 1-beta	K03232	192
DSAG12_00201	hypothetical protein	--	100
DSAG12_00202	hypothetical protein	--	137
DSAG12_00203	long-chain acyl-CoA synthetase	K01897	153
DSAG12_00204	hypothetical protein	--	270
DSAG12_00205	carboxypeptidase T	K05996	169
DSAG12_00206	DNA adenine methylase	K06223	187
DSAG12_00207	phosphate transport system protein	K02039	113
DSAG12_00208	hypothetical protein	--	179
DSAG12_00209	hypothetical protein	--	173
DSAG12_00210	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase	K08680	181
DSAG12_00211	hypothetical protein	--	173
DSAG12_00212	ArsR family transcriptional regulator	K03892	52
DSAG12_00213	hypothetical protein	--	132
DSAG12_00214		K07089	113
DSAG12_00215	hypothetical protein	--	210
DSAG12_00216	hypothetical protein	--	175
DSAG12_00217	hypothetical protein	--	197
DSAG12_00218	hypothetical protein	--	140
DSAG12_00219	hypothetical protein	--	142
DSAG12_00220	hypothetical protein	--	118
DSAG12_00221	hypothetical protein	--	264
DSAG12_00222	ethanolamine utilization protein EutA	K04019	241
DSAG12_00223	hypothetical protein	--	258
DSAG12_00224	hypothetical protein	--	205
DSAG12_00225	HSP20 family protein	K13993	0
DSAG12_00226	hypothetical protein	--	309
DSAG12_00227	HSP20 family protein	K13993	269
DSAG12_00228	hypothetical protein	--	361
DSAG12_00229	DNA mismatch repair protein MutS	K03555	216
DSAG12_00230	hypothetical protein	--	218
DSAG12_00231	hypothetical protein	--	226

DSAG12_00232	hypothetical protein	--	182
DSAG12_00233	hypothetical protein	--	206
DSAG12_00234	hypothetical protein	--	164
DSAG12_00235	hypothetical protein	--	60
DSAG12_00236	hypothetical protein	--	477
DSAG12_00237		K07052	203
DSAG12_00238	hypothetical protein	--	238
DSAG12_00239		K07138	185
DSAG12_00240	hypothetical protein	--	246
DSAG12_00241	hypothetical protein	--	233
DSAG12_00242	archaea-specific RecJ-like exonuclease	K07463	175
DSAG12_00243	hypothetical protein	--	226
DSAG12_00244	ABC-2 type transport system ATP-binding protein	K01990	256
DSAG12_00245	ABC-2 type transport system permease protein	K01992	258
DSAG12_00246	hypothetical protein	--	195
DSAG12_00247	hypothetical protein	--	167
DSAG12_00248	hypothetical protein	--	113
DSAG12_00249	proteasome regulatory subunit	K03420	175
DSAG12_00250	hypothetical protein	--	329
DSAG12_00251	2-oxoisovalerate ferredoxin oxidoreductase, beta subunit	K00187	57
DSAG12_00252	2-oxoisovalerate ferredoxin oxidoreductase, alpha subunit	K00186	343
DSAG12_00253	pyruvate ferredoxin oxidoreductase, delta subunit	K00171	278
DSAG12_00254	2-oxoisovalerate ferredoxin oxidoreductase, gamma subunit	K00189	171
DSAG12_00255	transcription initiation factor TFIIIB	K03124	209
DSAG12_00256	hypothetical protein	--	307
DSAG12_00257	hypothetical protein	--	68
DSAG12_00258		K01567	277
DSAG12_00259	transcription initiation factor TFIIIB	K03124	227
DSAG12_00260	hypothetical protein	--	246
DSAG12_00261	hypothetical protein	--	175
DSAG12_00262		K07073	186
DSAG12_00263		K07129	242
DSAG12_00264	hypothetical protein	--	223
DSAG12_00265	hypothetical protein	--	212
DSAG12_00266	GMP synthase (glutamine-hydrolysing)	K01951	231
DSAG12_00267		K06935	218
DSAG12_00268	protein pelota	K06965	163
DSAG12_00269	hypothetical protein	--	194
DSAG12_00270	xanthine phosphoribosyltransferase	K00769	155
DSAG12_00271	energy-coupling factor transport system permease protein	K16785	136
DSAG12_00272	energy-coupling factor transport system ATP-binding protein / energy-coupling factor transport system ATP-binding protein	K16786 K16	180
DSAG12_00273	phosphoesterase RecJ domain-containing protein	K06881	207
DSAG12_00274	prefoldin beta subunit	K04798	178
DSAG12_00275	hypothetical protein	--	142
DSAG12_00276	putative transcriptional regulator	K07728	153
DSAG12_00277	ribonuclease HII	K03470	179
DSAG12_00278	gluconate 5-dehydrogenase	K00046	222
DSAG12_00279	acyl-CoA thioesterase	K02614	202
DSAG12_00280	hypothetical protein	--	198
DSAG12_00281	3-phenylpropionate/trans-cinnamate dioxygenase ferredoxin subunit	K05710	203
DSAG12_00282	fibrillar-like pre-rRNA processing protein	K04795	132
DSAG12_00283	nucleolar protein 56	K14564	186
DSAG12_00284	dihydroorotate dehydrogenase (NAD+) catalytic subunit	K17828	207
DSAG12_00285	dihydroorotate dehydrogenase electron transfer subunit	K02823	218
DSAG12_00286	elongator complex protein 3	K07739	225
DSAG12_00287	hypothetical protein	--	298
DSAG12_00288	hypothetical protein	--	218
DSAG12_00289	hypothetical protein	--	193
DSAG12_00290	hypothetical protein	--	59
DSAG12_00291	hypothetical protein	--	274
DSAG12_00292	hypothetical protein	--	126
DSAG12_00293	hypothetical protein	--	253
DSAG12_00294		K01529	163
DSAG12_00295	hypothetical protein	--	256
DSAG12_00296	hypothetical protein	--	144
DSAG12_00297	hypothetical protein	--	128
DSAG12_00298	hypothetical protein	--	191
DSAG12_00299	hypothetical protein	--	149
DSAG12_00300	hypothetical protein	--	179
DSAG12_00301	serine/threonine protein kinase, bacterial	K08884	225
DSAG12_00302	hypothetical protein	--	160
DSAG12_00303	putative ATP-dependent endonuclease of the OLD family	K07459	162
DSAG12_00304	putative adenine-specific DNA-methyltransferase	K07319	177
DSAG12_00305	hypothetical protein	--	107
DSAG12_00306	radical S-adenosyl methionine domain-containing protein 2	K15045	138
DSAG12_00307	hypothetical protein	--	118
DSAG12_00308	hypothetical protein	--	0

DSAG12_00309	hypothetical protein	--	187
DSAG12_00310	hypothetical protein	--	187
DSAG12_00311	hypothetical protein	--	242
DSAG12_00312	hypothetical protein	--	223
DSAG12_00313	hypothetical protein	--	204
DSAG12_00314	hypothetical protein	--	189
DSAG12_00315	hypothetical protein	--	48
DSAG12_00316	hypothetical protein	--	20
DSAG12_00317	elongator complex protein 3	K07739	141
DSAG12_00318	GMP synthase (glutamine-hydrolysing)	K01951	133
DSAG12_00319	hypothetical protein	--	0
DSAG12_00320	putative DNA methylase	K07445	207
DSAG12_00321	hypothetical protein	--	192
DSAG12_00322	serine/threonine protein kinase, bacterial	K08884	101
DSAG12_00323	hypothetical protein	--	207
DSAG12_00324	hypothetical protein	--	181
DSAG12_00325	hypothetical protein	--	203
DSAG12_00326	hypothetical protein	--	226
DSAG12_00327	TetR/AcrR family transcriptional regulator, transcriptional repressor for nem operon	K16137	136
DSAG12_00328	glutamyl-tRNA(Gln) amidotransferase subunit D	K09482	139
DSAG12_00329	glutamyl-tRNA(Gln) amidotransferase subunit E	K03330	265
DSAG12_00330	hypothetical protein	--	223
DSAG12_00331	hypothetical protein	--	114
DSAG12_00332	hypothetical protein	--	157
DSAG12_00333	hypothetical protein	--	208
DSAG12_00334	molybdopterin synthase sulfur carrier subunit	K03636	145
DSAG12_00335	hypothetical protein	--	84
DSAG12_00336	aldehyde:ferredoxin oxidoreductase	K03738	179
DSAG12_00337	glutamyl-tRNA(Gln) amidotransferase subunit E	K03330	266
DSAG12_00338	glutamyl-tRNA(Gln) amidotransferase subunit D	K09482	206
DSAG12_00339	hypothetical protein	--	256
DSAG12_00340	hypothetical protein	--	62
DSAG12_00341	hypothetical protein	--	265
DSAG12_00342	hypothetical protein	--	201
DSAG12_00343	hypothetical protein	--	411
DSAG12_00344	hypothetical protein	--	337
DSAG12_00345	hypothetical protein	--	188
DSAG12_00346	hypothetical protein	--	219
DSAG12_00347	hypothetical protein	--	191
DSAG12_00348	ribosome biogenesis ATPase	K14571	193
DSAG12_00349	hypothetical protein	--	195
DSAG12_00350	hypothetical protein	--	129
DSAG12_00351	hypothetical protein	--	131
DSAG12_00352	galactokinase	K00849	168
DSAG12_00353	hypothetical protein	--	260
DSAG12_00354	hypothetical protein	--	245
DSAG12_00355	hypothetical protein	K07059	145
DSAG12_00356	hypothetical protein	--	165
DSAG12_00357	peptide/nickel transport system substrate-binding protein	K02035	215
DSAG12_00358	alanyl-tRNA synthetase	K01872	215
DSAG12_00359	hypothetical protein	--	118
DSAG12_00360	hypothetical protein	K07050	235
DSAG12_00361	ATP-binding cassette, subfamily B, bacterial	K06147	199
DSAG12_00362	ATP-binding cassette, subfamily B, bacterial MsbA	K11085	231
DSAG12_00363	hypothetical protein	--	262
DSAG12_00364	hypothetical protein	--	0
DSAG12_00365	hypothetical protein	--	263
DSAG12_00366	tRNA 2-thiouridine synthesizing protein D	K07235	50
DSAG12_00367	tRNA 2-thiouridine synthesizing protein A	K04085	213
DSAG12_00368	tRNA-Lys	Intron(41766	134
DSAG12_00369	hypothetical protein	--	48
DSAG12_00370	hypothetical protein	--	154
DSAG12_00371	hypothetical protein	--	132
DSAG12_00372	hypothetical protein	--	150
DSAG12_00373	hypothetical protein	--	141
DSAG12_00374	hypothetical protein	--	146
DSAG12_00375	hypothetical protein	--	143
DSAG12_00376	H/ACA ribonucleoprotein complex subunit 4	K11131	238 small GTP-binding domain protein
DSAG12_00377	16S rRNA (guanine1207-N2)-methyltransferase	K00564	246
DSAG12_00378	MFS transporter, DHA1 family, multidrug resistance protein	K08153	189
DSAG12_00379	DNA-directed RNA polymerase subunit H	K03053	190
DSAG12_00380	DNA-directed RNA polymerase subunit B	K13798	109
DSAG12_00381	hypothetical protein	--	311
DSAG12_00382	hypothetical protein	--	176
DSAG12_00383	aminoglycoside N6'-acetyltransferase	K00663	44
DSAG12_00384	tRNA/rRNA methyltransferase	K02533	172
DSAG12_00385	hypothetical protein	--	209
DSAG12_00386	hypothetical protein	--	186



DSAG12_00387	hypothetical protein	--	64	
DSAG12_00388	hypothetical protein	--	196	
DSAG12_00389	transcription initiation factor TFIIIE subunit alpha	K03136	182	
DSAG12_00390	hypothetical protein	--	180	
DSAG12_00391	peptidyl-prolyl cis-trans isomerase A (cyclophilin A)	K03767	129	
DSAG12_00392	RIO kinase 2	K07179	156	
DSAG12_00393	guanine nucleotidyl transferase / 2-methoxy-6-polypropenyl-1,4-benzoquinone methylase	K03183	221	
DSAG12_00394	small nuclear ribonucleoprotein	K04796	140	
DSAG12_00395	hypothetical protein	--	69	
DSAG12_00396	ArsR family transcriptional regulator	K07721	103	
DSAG12_00397	hypothetical protein	--	127	
DSAG12_00398	choloylglycine hydrolase	K01442	157	
DSAG12_00399	hypothetical protein	--	202	
DSAG12_00400	hypothetical protein	--	213	
DSAG12_00401	hypothetical protein	--	247	
DSAG12_00402	ABC-2 type transport system ATP-binding protein	K01990	228	
DSAG12_00403	ribosome-dependent ATPase	K13926	259	
DSAG12_00404	NADPH2:quinone reductase	K00344	238	
DSAG12_00405	hypothetical protein	--	242	
DSAG12_00406	hypothetical protein	--	111	
DSAG12_00407	opine dehydrogenase	K04940	91	
DSAG12_00408	hypothetical protein	--	204	
DSAG12_00409	hypothetical protein	--	197	
DSAG12_00410	hypothetical protein	--	101	
DSAG12_00411	adenine-specific DNA-methyltransferase	K07316	178	
DSAG12_00412	protein phosphatase	K01090	200	
DSAG12_00413		K06933	226	
DSAG12_00414	ArsR family transcriptional regulator	K03892	158	
DSAG12_00415	hypothetical protein	--	178	
DSAG12_00416	hypothetical protein	--	269	
DSAG12_00417	hypothetical protein	--	267	
DSAG12_00418	hypothetical protein	--	245	
DSAG12_00419	hypothetical protein	--	327	
DSAG12_00420	hypothetical protein	--	567	
DSAG12_00421	UDP-N-acetylglucosamine 3-dehydrogenase	K18855	216	
DSAG12_00422	hypothetical protein	--	218	
DSAG12_00423	hypothetical protein	--	144	
DSAG12_00424	RIO kinase 1	K07178	133	hypothetical protein with ubiquitin-like domain
DSAG12_00425	hypothetical protein	--	215	
DSAG12_00426	hypothetical protein	--	54	
DSAG12_00427	hypothetical protein	--	200	
DSAG12_00428	hypothetical protein	--	199	
DSAG12_00429	hypothetical protein	--	118	
DSAG12_00430	hypothetical protein	--	164	
DSAG12_00431	hypothetical protein	--	165	
DSAG12_00432	putative pyruvate formate lyase activating enzyme	K04070	107	
DSAG12_00433	hypothetical protein	--	204	
DSAG12_00434		K07068	9541	
DSAG12_00435	acetyl-CoA C-acetyltransferase	K00626	199	
DSAG12_00436	hypothetical protein	--	297	
DSAG12_00437	hypothetical protein	--	186	
DSAG12_00438	UDPglucose--hexose-1-phosphate uridylyltransferase	K00965	283	
DSAG12_00439	hypothetical protein	--	221	
DSAG12_00440	long-chain acyl-CoA synthetase	K01897	222	
DSAG12_00441	aldehyde:ferredoxin oxidoreductase	K03738	248	
DSAG12_00442	hypothetical protein	--	293	
DSAG12_00443	acetaldehyde dehydrogenase / alcohol dehydrogenase	K04072	143	
DSAG12_00444	hypothetical protein	--	249	
DSAG12_00445	hypothetical protein	--	210	
DSAG12_00446	hypothetical protein	--	232	
DSAG12_00447	hypothetical protein	--	254	
DSAG12_00448	MoxR-like ATPase	K03924	251	
DSAG12_00449	hypothetical protein	--	225	
DSAG12_00450	large conductance mechanosensitive channel	K03282	219	
DSAG12_00451	hypothetical protein	--	205	
DSAG12_00452	hypothetical protein	--	249	
DSAG12_00453	zinc finger protein	K06874	50	
DSAG12_00454	2-oxoisovalerate ferredoxin oxidoreductase, gamma subunit	K00189	218	
DSAG12_00455	2-oxoisovalerate ferredoxin oxidoreductase, delta subunit	K00188	233	
DSAG12_00456	pyruvate ferredoxin oxidoreductase, alpha subunit	K00169	169	
DSAG12_00457	pyruvate ferredoxin oxidoreductase, beta subunit	K00170	334	
DSAG12_00458	tRNA acetyltransferase TAN1	K06963	322	
DSAG12_00459	6-phosphofructokinase 1	K00850	174	
DSAG12_00460	hypothetical protein	--	263	
DSAG12_00461	hypothetical protein	--	10	
DSAG12_00462	transposase	K07486	46	
DSAG12_00463	hypothetical protein	--	184	

DSAG12_00464	hypothetical protein	--	157
DSAG12_00465	hypothetical protein	--	237
DSAG12_00466	5-methyltetrahydrofolate--homocysteine methyltransferase	K00548	233
DSAG12_00467	5-methyltetrahydrofolate--homocysteine methyltransferase	K00548	173
DSAG12_00468	methylenetetrahydrofolate reductase (NADPH)	K00297	219
DSAG12_00469		K01076	172
DSAG12_00470	propionyl-CoA synthetase	K01908	236
DSAG12_00471	hypothetical protein	--	221
DSAG12_00472	hypothetical protein	--	223
DSAG12_00473	hypothetical protein	--	173
DSAG12_00474	aminomethyltransferase	K00605	226
DSAG12_00475	glycine cleavage system H protein	K02437	167
DSAG12_00476	glycine dehydrogenase subunit 1	K00282	221
DSAG12_00477	glycine dehydrogenase subunit 2	K00283	285
DSAG12_00478	hypothetical protein	--	188
DSAG12_00479	hypothetical protein	--	135
DSAG12_00480	hypothetical protein	--	171
DSAG12_00481	hypothetical protein	--	201
DSAG12_00482	hypothetical protein	--	78
DSAG12_00483	hypothetical protein	K09707	118
DSAG12_00484	hypothetical protein	--	46
DSAG12_00485	aminotransferase	K10907	197
DSAG12_00486	hypothetical protein	--	63
DSAG12_00487	Ca <sup>2+</sup> -transporting ATPase	K01537	244
DSAG12_00488	hypothetical protein	--	57
DSAG12_00489	proteasome beta subunit	K03433	0
DSAG12_00490	hypothetical protein	--	0
DSAG12_00491	hypothetical protein	--	0
DSAG12_00492	4-alpha-glucanotransferase	K00705	186
DSAG12_00493	hypothetical protein	--	194
DSAG12_00494	structural maintenance of chromosome 4	K06675	215
DSAG12_00495	hypothetical protein	--	229
DSAG12_00496	hypothetical protein	--	108
DSAG12_00497	hypothetical protein	--	156
DSAG12_00498	hypothetical protein	--	140
DSAG12_00499	cold shock protein (beta-ribbon, CspA family)	K03704	134
DSAG12_00500	hypothetical protein	--	89
DSAG12_00501	hypothetical protein	--	123
DSAG12_00502	hypothetical protein	--	155
DSAG12_00503	transcription initiation factor TFIIIB	K03124	211
DSAG12_00504	hypothetical protein	--	158
DSAG12_00505	tRNA-Thr		102
DSAG12_00506	aminopeptidase	K01269	314
DSAG12_00507	tRNA-splicing ligase RtcB	K14415	0
DSAG12_00508	hypothetical protein	--	265
DSAG12_00509	3,4-dihydroxy 2-butanone 4-phosphate synthase / GTP cyclohydrolase II	K14652	270
DSAG12_00510	basic amino acid/polyamine antiporter, APA family	K03294	133
DSAG12_00511	hypothetical protein	--	258
DSAG12_00512	hypothetical protein	--	212
DSAG12_00513	hypothetical protein	--	136
DSAG12_00514	hypothetical protein	--	206
DSAG12_00515	glucosamine--fructose-6-phosphate aminotransferase (isomerizing)	K00820	191
DSAG12_00516	glucosamine--fructose-6-phosphate aminotransferase (isomerizing)	K00820	256
DSAG12_00517	hypothetical protein	--	171
DSAG12_00518	archaeal cell division control protein 6	K10725	186
DSAG12_00519	hypothetical protein	--	150
DSAG12_00520	DNA polymerase II small subunit	K02323	217
DSAG12_00521	DNA polymerase II large subunit	K02322	142
DSAG12_00522	serine/threonine protein kinase, bacterial	K08884	218
DSAG12_00523	hypothetical protein	--	235
DSAG12_00524	putative hydrolase of the HAD superfamily	K07025	0
DSAG12_00525	threonyl-tRNA synthetase	K01868	237
DSAG12_00526	tRNA (guanine10-N2)-dimethyltransferase	K07446	176
DSAG12_00527	tRNA-Lys		128
DSAG12_00528	large subunit ribosomal protein L2	K02886	103
DSAG12_00529	S-adenosylmethionine synthetase	K00789	229
DSAG12_00530	hypothetical protein	--	0
DSAG12_00531	hypothetical protein	--	273
DSAG12_00532	hypothetical protein	--	236
DSAG12_00533	hypothetical protein	--	85
DSAG12_00534	hypothetical protein	K09741	161
DSAG12_00535	large subunit ribosomal protein L37Ae	K02921	255
DSAG12_00536	exosome complex component RRP42	K12589	205
DSAG12_00537	exosome complex component RRP41	K11600	95
DSAG12_00538	exosome complex component RRP4	K03679	195
DSAG12_00539	ribosome maturation protein SDO1	K14574	280
DSAG12_00540	proteasome alpha subunit	K03432	282
DSAG12_00541	hypothetical protein	--	192

DSAG12_00542	hypothetical protein	--	194	
DSAG12_00543	ribosomal-protein-alanine N-acetyltransferase	K03789	236	
DSAG12_00544	hypothetical protein	--	204	
DSAG12_00545	hypothetical protein	--	134	
DSAG12_00546	tRNA-Val		216	
DSAG12_00547	tricorn protease interacting factor F2/3	K13722	181	profilin-like domain protein
DSAG12_00548	hypothetical protein	--	227	
DSAG12_00549	Ca2+-transporting ATPase	K01537	226	
DSAG12_00550	beta-lysine 5,6-aminomutase beta subunit	K18011	50	
DSAG12_00551	beta-lysine 5,6-aminomutase alpha subunit	K01844	237	
DSAG12_00552	hypothetical protein	--	204	
DSAG12_00553	hypothetical protein	--	267	
DSAG12_00554	lysine 2,3-aminomutase	K01843	173	
DSAG12_00555	L-erythro-3,5-diaminohexanoate dehydrogenase	K18012	180	
DSAG12_00556	hypothetical protein	--	251	
DSAG12_00557	hypothetical protein	--	297	
DSAG12_00558	alpha-aminoacidic semialdehyde synthase	K14157	0	
DSAG12_00559	saccharopine dehydrogenase (NADP+, L-glutamate forming)	K00293	309	
DSAG12_00560	hypothetical protein	--	197	
DSAG12_00561	hypothetical protein	--	249	
DSAG12_00562	23S rRNA (adenine2503-C2)-methyltransferase	K06941	136	
DSAG12_00563	L-serine dehydratase	K01752	561	
DSAG12_00564	L-serine dehydratase	K01752	0	
DSAG12_00565	3-keto-5-aminohexanoate cleavage enzyme	K18013	247	
DSAG12_00566	3-aminobutyryl-CoA ammonia-lyase	K18014	205	
DSAG12_00567	hypothetical protein	--	264	
DSAG12_00568	diamine N-acetyltransferase	K00657	267	
DSAG12_00569	tRNA-Ser		184	
DSAG12_00570	GTP-binding protein HflX	K03665	0	
DSAG12_00571	putative transcription factor	K03627	149	
DSAG12_00572	hypothetical protein	--	151	
DSAG12_00573	hypothetical protein	--	0	
DSAG12_00574	tyrosine decarboxylase / aspartate 1-decarboxylase	K18933	230	
DSAG12_00575	3-methyl-2-oxobutanoate hydroxymethyltransferase	K00606	194	
DSAG12_00576	hypothetical protein	--	21	
DSAG12_00577	2-dehydropantoate 2-reductase	K00077	160	
DSAG12_00578	hypothetical protein	--	275	
DSAG12_00579	hypothetical protein	--	726	
DSAG12_00580	hypothetical protein	--	229	
DSAG12_00581	hypothetical protein	--	165	
DSAG12_00582	transcription initiation factor TFIIB	K03124	205	
DSAG12_00583	hypothetical protein	--	151	
DSAG12_00584	translation initiation factor 1	K03113	274	
DSAG12_00585		K06885	131	
DSAG12_00586	phosphoadenosine phosphosulfate reductase	K00390	221	
DSAG12_00587	Rab family, other	K07976	0	
DSAG12_00588	hypothetical protein	--	127	
DSAG12_00589	hypothetical protein	--	217	
DSAG12_00590	hypothetical protein	--	225	
DSAG12_00591	uridylyate kinase	K09903	236	
DSAG12_00592	pantoate kinase	K06982	239	small GTP-binding domain protein
DSAG12_00593	peptide chain release factor subunit 1	K03265	116	
DSAG12_00594	4-phosphopantoate--beta-alanine ligase	K09722	72	
DSAG12_00595	peptide alpha-N-acetyltransferase	K00670	159	
DSAG12_00596	Ras-related GTP-binding protein A/B	K16185	221	
DSAG12_00597	23S ribosomal RNA	--	186	
DSAG12_00598	hypothetical protein	--	202	
DSAG12_00599	internalin A	K13730	197	
DSAG12_00600	internalin A	K13730	196	
DSAG12_00601	hypothetical protein	--	190	small GTP-binding domain protein
DSAG12_00602	hypothetical protein	--	0	
DSAG12_00603	hypothetical protein	--	0	
DSAG12_00604	hypothetical protein	--	166	
DSAG12_00605	hypothetical protein	--	244	
DSAG12_00606	hypothetical protein	--	0	
DSAG12_00607	hypothetical protein	--	184	
DSAG12_00608		K06885	99	
DSAG12_00609	hypothetical protein	--	199	
DSAG12_00610	hypothetical protein	--	217	
DSAG12_00611	hypothetical protein	--	119	
DSAG12_00612	hypothetical protein	--	182	
DSAG12_00613	hypothetical protein	--	151	
DSAG12_00614	aspartate racemase	K01779	160	
DSAG12_00615	hypothetical protein	--	183	
DSAG12_00616	hypothetical protein	--	289	
DSAG12_00617	hypothetical protein	--	0	
DSAG12_00618	aminoglycoside N6'-acetyltransferase	K00663	164	
DSAG12_00619	hypothetical protein	--	0	

DSAG12_00620	hypothetical protein	--	128	
DSAG12_00621	hypothetical protein	--	130	
DSAG12_00622	hypothetical protein	--	190	
DSAG12_00623	hypothetical protein	--	225	
DSAG12_00624	hypothetical protein	--	186	
DSAG12_00625	hypothetical protein	--	132	
DSAG12_00626	hypothetical protein	--	187	
DSAG12_00627	proteasome regulatory subunit	K03420	166	
DSAG12_00628	conserved protein with predicted RNA binding PUA domain	K07398	152	
DSAG12_00629	nascent polypeptide-associated complex subunit alpha	K03626	162	
DSAG12_00630	hypothetical protein	--	78	
DSAG12_00631	hypothetical protein	--	145	
DSAG12_00632	hypothetical protein	--	106	hypothetical protein with vacuolar fusion domain MON1
DSAG12_00633	hypothetical protein	--	25	
DSAG12_00634	hypothetical protein	--	161	
DSAG12_00635	hypothetical protein	--	298	
DSAG12_00636	hypothetical protein	--	140	
DSAG12_00637	hypothetical protein	--	190	
DSAG12_00638	diaminopimelate decarboxylase	K01586	116	
DSAG12_00639	cell division protein FtsZ	K03531	86	
DSAG12_00640	ribosomal RNA assembly protein	K06961	155	
DSAG12_00641	RIO kinase 1	K07178	238	
DSAG12_00642	nonsense-mediated mRNA decay protein 3	K07562	85	
DSAG12_00643	hypothetical protein	K09148	0	
DSAG12_00644	translation initiation factor 2 subunit 2	K03238	112	
DSAG12_00645	replication factor A2	K10739	87	
DSAG12_00646	tRNA-Met	Intron(70709	145	
DSAG12_00647	hypothetical protein	--	148	
DSAG12_00648	hypothetical protein	--	255	
DSAG12_00649	hypothetical protein	--	147	
DSAG12_00650	replication factor A1	K07466	146	
DSAG12_00651	fructokinase	K00847	132	
DSAG12_00652	protein-L-isoaspartate(D-aspartate) O-methyltransferase	K00573	83	
DSAG12_00653	thiamine biosynthesis protein Thil	K03151	137	
DSAG12_00654		K07159	173	
DSAG12_00655	tRNA-Asn		161	
DSAG12_00656	hypothetical protein	--	163	
DSAG12_00657	tRNA-Glu	Intron(71654	144	domain
DSAG12_00658	hypothetical protein	--	161	
DSAG12_00659	tRNA-Leu		196	
DSAG12_00660	pre-rRNA-processing protein TSR3	K09140	213	
DSAG12_00661	hypothetical protein	--	129	
DSAG12_00662	hypothetical protein	--	189	
DSAG12_00663		K06942	0	
DSAG12_00664	tRNA-Ala		26	
DSAG12_00665	16S ribosomal RNA		212	
DSAG12_00666	hypothetical protein	--	153	
DSAG12_00667	hypothetical protein	--	207	
DSAG12_00668		K06883	125	
DSAG12_00669	hypothetical protein	--	169	
DSAG12_00670	hypothetical protein	--	0	
DSAG12_00671	hypothetical protein	--	0	
DSAG12_00672	hypothetical protein	--	126	
DSAG12_00673	transcription initiation factor TFIIIB	K03124	118	
DSAG12_00674	threonylcarbamoyladenine tRNA methyltransferase CDKAL1	K15865	126	small GTP-binding domain protein
DSAG12_00675	tRNA-Glu		76	
DSAG12_00676	UPF0148 protein	K07143	97	
DSAG12_00677	small subunit ribosomal protein S17e	K02962	84	
DSAG12_00678	hypothetical protein	--	64	
DSAG12_00679	hypothetical protein	--	119	
DSAG12_00680	archaeal cell division control protein 6	K10725	124	
DSAG12_00681	hypothetical protein	--	0	
DSAG12_00682	hypothetical protein	--	106	
DSAG12_00683	archaeal flagellar protein FlaI	K07332	62	
DSAG12_00684	hypothetical protein	--	120	
DSAG12_00685	hypothetical protein	--	16	
DSAG12_00686	large subunit ribosomal protein L23	K02892	100	
DSAG12_00687	large subunit ribosomal protein L4e	K02930	32	
DSAG12_00688	large subunit ribosomal protein L3	K02906	48	
DSAG12_00689	ATP-binding cassette, sub-family E, member 1	K06174	107	
DSAG12_00690	lysyl-tRNA synthetase, class I	K04566	61	
DSAG12_00691	hypothetical protein	--	98	
DSAG12_00692	hypothetical protein	--	87	
DSAG12_00693		K06940	349	
DSAG12_00694	hypothetical protein	--	263	
DSAG12_00695	aspartate carbamoyltransferase regulatory subunit	K00610	204	
DSAG12_00696	hypothetical protein	--	189	

DSAG12_00697	hypothetical protein	--	95
DSAG12_00698	hypothetical protein	K07746	179
DSAG12_00699	hypothetical protein	--	0
DSAG12_00700	hypothetical protein	--	71
DSAG12_00701	hypothetical protein	K07746	115
DSAG12_00702	hypothetical protein	--	119
DSAG12_00703	hypothetical protein	--	187
DSAG12_00704	thymidylate synthase (FAD)	K03465	161
DSAG12_00705	hypothetical protein	--	18
DSAG12_00706	hypothetical protein	--	126
DSAG12_00707	hypothetical protein	--	179
DSAG12_00708	phosphomethylpyrimidine synthase	K03147	22
DSAG12_00709	histidine triad (HIT) family protein	K02503	133
DSAG12_00710	hypothetical protein	--	128
DSAG12_00711	DNA polymerase II	K02336	186
DSAG12_00712	DNA repair protein RadA	K04483	179
DSAG12_00713	3-dehydroquinate synthase	K01735	141
DSAG12_00714	hypothetical protein	--	188
DSAG12_00715	hypothetical protein	--	224
DSAG12_00716	hypothetical protein	--	181
DSAG12_00717		K07131	63
DSAG12_00718	elongation factor 1-alpha	K03231	259
DSAG12_00719	hypothetical protein	--	217
DSAG12_00720	hypothetical protein	--	121
DSAG12_00721	peroxisomal coenzyme A diphosphatase NUDT7	K17879	160
DSAG12_00722	putative mRNA 3-end processing factor	K07577	181
DSAG12_00723	5'-methylthioadenosine phosphorylase	K00772	122
DSAG12_00724	hypoxanthine phosphoribosyltransferase	K00760	139
DSAG12_00725	carbonic anhydrase	K01673	178
DSAG12_00726	adenine deaminase	K01486	158
DSAG12_00727	Ca-activated chloride channel homolog	K07114	0
DSAG12_00728	thiamine transport system permease protein	K02063	98
DSAG12_00729	spermidine/putrescine transport system ATP-binding protein	K11072	150
DSAG12_00730	inositol-phosphate transport system ATP-binding protein	K17240	226
DSAG12_00731	hypothetical protein	K07220	245
DSAG12_00732	tRNA-Ile		162
DSAG12_00733	sulfoxide reductase catalytic subunit YedY	K07147	144
DSAG12_00734	hypothetical protein	--	202
DSAG12_00735	hypothetical protein	--	192
DSAG12_00736	hypothetical protein	--	231
DSAG12_00737	secernin	K14358	207
DSAG12_00738	hypothetical protein	--	234
DSAG12_00739	hypothetical protein	--	235
DSAG12_00740	adenylate kinase	K18532	0
DSAG12_00741	phenylacetic acid degradation protein	K02617	198
DSAG12_00742	Ca-activated chloride channel homolog	K07114	280
DSAG12_00743	hypothetical protein	--	157
DSAG12_00744	hypothetical protein	--	165
DSAG12_00745	hypothetical protein	--	243
DSAG12_00746	hypothetical protein	--	196
DSAG12_00747	serine/threonine protein kinase, bacterial	K08884	161
DSAG12_00748	protein phosphatase	K01090	134
DSAG12_00749	serine/threonine-protein phosphatase 5	K04460	175
DSAG12_00750	serine/threonine-protein phosphatase PP1 catalytic subunit	K06269	220
DSAG12_00751	7-cyano-7-deazaguanine tRNA-ribosyltransferase	K18779	243
DSAG12_00752	hypothetical protein	K09738	135
DSAG12_00753	tRNA (guanine37-N1)-methyltransferase	K15429	181
DSAG12_00754	hypothetical protein	--	154
DSAG12_00755	hypothetical protein	--	244
DSAG12_00756	hypothetical protein	--	216
DSAG12_00757	tRNA-Arg		165
DSAG12_00758	hypothetical protein	--	135
DSAG12_00759	phenylacetic acid degradation protein	K02617	193
DSAG12_00760	transcription initiation factor TFIIIB	K03124	111
DSAG12_00761	Ras-related GTP-binding protein A/B	K16185	148
DSAG12_00762	foldase protein PrsA	K07533	221
DSAG12_00763	putative hydrolase of the HAD superfamily	K07025	201
DSAG12_00764	hypothetical protein	--	183
DSAG12_00765	myo-inositol-1-phosphate synthase	K01858	0
DSAG12_00766	hypothetical protein	--	132
DSAG12_00767	hypothetical protein	--	249
DSAG12_00768	hypothetical protein	--	297
DSAG12_00769	ribonuclease P/MRP protein subunit POP5	K03537	128
DSAG12_00770	ribonuclease P/MRP protein subunit RPP1	K03539	132
DSAG12_00771	hypothetical protein	K07581	121
DSAG12_00772	large subunit ribosomal protein L15e	K02877	186
DSAG12_00773		K06883	209
DSAG12_00774	hypothetical protein	--	146

DSAG12_00775	enoyl-CoA hydratase	K01715	0
DSAG12_00776	seryl-tRNA synthetase	K01875	114
DSAG12_00777	hypothetical protein	--	98
DSAG12_00778	phytol kinase	K18678	142
DSAG12_00779	geranylgeranyl-glycerol-phosphate geranylgeranyltransferase	K17105	186
DSAG12_00780	hypothetical protein	--	135
DSAG12_00781	L-threonylcarbamoyladenylyl synthase	K07566	184
DSAG12_00782	hypothetical protein	--	232
DSAG12_00783	hypothetical protein	--	122
DSAG12_00784	hypothetical protein	--	161
DSAG12_00785	hypothetical protein	--	217
DSAG12_00786	hypothetical protein	--	202
DSAG12_00787	hypothetical protein	--	180
DSAG12_00788	MFS transporter, DHA1 family, multidrug resistance protein	K08153	184
DSAG12_00789	hypothetical protein	--	254
DSAG12_00790	hypothetical protein	--	217
DSAG12_00791	hypothetical protein	--	49
DSAG12_00792	hypothetical protein	--	0
DSAG12_00793	hypothetical protein	--	191
DSAG12_00794	hypothetical protein	--	309
DSAG12_00795	hypothetical protein	--	151
DSAG12_00796	pyruvate ferredoxin oxidoreductase, beta subunit	K00170	124
DSAG12_00797	pyruvate ferredoxin oxidoreductase, alpha subunit	K00169	0
DSAG12_00798	pyruvate ferredoxin oxidoreductase, gamma subunit	K00172	12
DSAG12_00799	hypothetical protein	--	174
DSAG12_00800	hypothetical protein	--	141
DSAG12_00801	hypothetical protein	--	185
DSAG12_00802	Ras-related protein Rab-22	K07891	77
DSAG12_00803	glutamate formiminotransferase / formiminotetrahydrofolate cyclodeaminase	K13990	145
DSAG12_00804	hypothetical protein	--	144
DSAG12_00805	UDP-N-acetylglucosamine 3-dehydrogenase	K18855	140
DSAG12_00806	segregation and condensation protein B	K06024	93
DSAG12_00807	hypothetical protein	--	242
DSAG12_00808	chromosome segregation protein	K03529	326
DSAG12_00809	hypothetical protein	--	266
DSAG12_00810	hypothetical protein	--	121
DSAG12_00811	hypothetical protein	--	90
DSAG12_00812	hypothetical protein	--	175
DSAG12_00813	hypothetical protein	--	143
DSAG12_00814	hypothetical protein	--	281
DSAG12_00815	hypothetical protein	--	202
DSAG12_00816	hypothetical protein	--	249
DSAG12_00817	erbB2-interacting protein	K12796	255
DSAG12_00818	internalin A	K13730	282
DSAG12_00819	hypothetical protein	--	317
DSAG12_00820	citronellol/citronellal dehydrogenase	K13775	201
DSAG12_00821	hypothetical protein	--	71
DSAG12_00822	hypothetical protein	--	216
DSAG12_00823	oligogalacturonide transporter	K16210	226
DSAG12_00824	hypothetical protein	--	245
DSAG12_00825	hypothetical protein	K06889	0
DSAG12_00826	hypothetical protein	--	253
DSAG12_00827	hypothetical protein	--	175
DSAG12_00828	hypothetical protein	--	138
DSAG12_00829	hypothetical protein	--	64
DSAG12_00830	hypothetical protein	--	131
DSAG12_00831	inorganic pyrophosphatase	K01507	170
DSAG12_00832	hypothetical protein	--	291
DSAG12_00833	DNA replication factor GINS	K09723	244
DSAG12_00834	hypothetical protein	--	220
DSAG12_00835	hypothetical protein	--	0
DSAG12_00836	hypothetical protein	--	302
DSAG12_00837	alpha-mannosidase	K01191	166
DSAG12_00838	pyruvate formate lyase activating enzyme	K04069	235
DSAG12_00839	hypothetical protein	--	63
DSAG12_00840	hypothetical protein	--	66
DSAG12_00841	2-haloacid dehalogenase	K01560	144
DSAG12_00842	hypothetical protein	--	234
DSAG12_00843	Ras-related GTP-binding protein A/B	K16185	140
DSAG12_00844	hypothetical protein	--	165
DSAG12_00845	hypothetical protein	--	193
DSAG12_00846	hypothetical protein	--	186
DSAG12_00847	hypothetical protein	--	179
DSAG12_00848	1-acyl-sn-glycerol-3-phosphate acyltransferase	K00655	157
DSAG12_00849	hypothetical protein	--	142
DSAG12_00850	hypothetical protein	--	150
DSAG12_00851	hypothetical protein	--	224
DSAG12_00852	2-hydroxy-3-oxopropionate reductase	K00042	196

DSAG12_00853	hypothetical protein	--	204
DSAG12_00854	glycoside/pentoside/hexuronide:cation symporter, GPH family	K03292	160
DSAG12_00855	hypothetical protein	--	175
DSAG12_00856		K00540	200
DSAG12_00857	beta-galactosidase	K01190	22
DSAG12_00858	hypothetical protein	--	227
DSAG12_00859	zinc transport system ATP-binding protein	K09817	228
DSAG12_00860	manganese/iron transport system permease protein	K09819	191
DSAG12_00861	zinc/manganese transport system substrate-binding protein	K02077	217
DSAG12_00862	DtxR family transcriptional regulator, Mn-dependent transcriptional regulator	K03709	175
DSAG12_00863	molybdopterin synthase sulfur carrier subunit	K03636	169
DSAG12_00864	hypothetical protein	--	42
DSAG12_00865	hypothetical protein	--	239
DSAG12_00866	hypothetical protein	--	250
DSAG12_00867	hypothetical protein	--	181
DSAG12_00868	hypothetical protein	--	224
DSAG12_00869	methionyl-tRNA synthetase	K01874	209
DSAG12_00870	ribonucleoside-diphosphate reductase alpha chain	K00525	214
DSAG12_00871	Fe-S cluster assembly ATP-binding protein	K09013	135
DSAG12_00872		K07033	190
DSAG12_00873	hypothetical protein	--	221
DSAG12_00874	release factor glutamine methyltransferase	K02493	210
DSAG12_00875	16S rRNA (adenine1518-N6/adenine1519-N6)-dimethyltransferase	K02528	131
DSAG12_00876	putative nucleotide binding protein	K07572	106
DSAG12_00877	DNA-directed RNA polymerase subunit F	K03051	122
DSAG12_00878	large subunit ribosomal protein L21e	K02889	233
DSAG12_00879	endoglucanase	K01179	142
DSAG12_00880	hypothetical protein	--	156
DSAG12_00881	hypothetical protein	--	162
DSAG12_00882	hypothetical protein	--	127
DSAG12_00883	flotillin	K07192	260
DSAG12_00884	hypothetical protein	--	193
DSAG12_00885		K07047	255
DSAG12_00886	hypothetical protein	--	142
DSAG12_00887	hypothetical protein	--	173
DSAG12_00888	hypothetical protein	--	172
DSAG12_00889	tRNA pseudouridine synthase 10	K07583	202
DSAG12_00890	adenylyltransferase and sulfurtransferase	K11996	149
DSAG12_00891	hypothetical protein	--	199
DSAG12_00892	hypothetical protein	--	269
DSAG12_00893	excinuclease ABC subunit C	K03703	171
DSAG12_00894	hypothetical protein	--	196
DSAG12_00895	hypothetical protein	--	274
DSAG12_00896	Xaa-Pro aminopeptidase	K01262	258
DSAG12_00897	hypothetical protein	--	145
DSAG12_00898	hypothetical protein	--	233
DSAG12_00899	hypothetical protein	--	156
DSAG12_00900	hypothetical protein	--	212
DSAG12_00901	hypothetical protein	--	34
DSAG12_00902	hypothetical protein	--	210
DSAG12_00903	tryptophanyl-tRNA synthetase	K01867	193
DSAG12_00904	protein transport protein SEC61 subunit alpha	K10956	44
DSAG12_00905	hypothetical protein	--	233
DSAG12_00906	hypothetical protein	--	222
DSAG12_00907	hypothetical protein	--	191
DSAG12_00908		K01554	245
DSAG12_00909	hypothetical protein	--	258
DSAG12_00910	hypothetical protein	--	84
DSAG12_00911	hypothetical protein	--	176
DSAG12_00912		K06937	119
DSAG12_00913	hypothetical protein	--	104
DSAG12_00914	hypothetical protein	--	156
DSAG12_00915	proteasome alpha subunit	K03432	163
DSAG12_00916	hypothetical protein	--	239
DSAG12_00917	hypothetical protein	--	304
DSAG12_00918	hypothetical protein	--	197
DSAG12_00919	hypothetical protein	--	124
DSAG12_00920	sphingosine-1-phosphate phosphatase 1	K04716	194
DSAG12_00921	hypothetical protein	--	213
DSAG12_00922	hypothetical protein	--	112
DSAG12_00923	hypothetical protein	--	165
DSAG12_00924	hypothetical protein	--	275
DSAG12_00925	hypothetical protein	--	322
DSAG12_00926	hypothetical protein	--	213
DSAG12_00927	hypothetical protein	--	230
DSAG12_00928	hypothetical protein	--	266
DSAG12_00929		K06915	212 small GTP-binding domain protein
DSAG12_00930	hypothetical protein	--	182

DSAG12_00931	hypothetical protein	--	116	
DSAG12_00932	ATP-binding protein involved in chromosome partitioning	K03593	185	
DSAG12_00933		K07096	253	
DSAG12_00934	hypothetical protein	--	197	
DSAG12_00935		K00924	175	
DSAG12_00936	hypothetical protein	--	56	
DSAG12_00937	hypothetical protein	--	206	
DSAG12_00938	glycerophosphoryl diester phosphodiesterase	K01126	182	
DSAG12_00939	hypothetical protein	--	177	
DSAG12_00940	hypothetical protein	--	185	
DSAG12_00941	hypothetical protein	--	227	
DSAG12_00942	adenylyltransferase and sulfurtransferase	K11996	163	
DSAG12_00943	hypothetical protein	--	299	
DSAG12_00944	actin beta/gamma 1	K05692	213	
DSAG12_00945	hypothetical protein	--	285	
DSAG12_00946		K01175	244	
DSAG12_00947	hypothetical protein	--	133	
DSAG12_00948	hypothetical protein	--	65	
DSAG12_00949	hypothetical protein	--	160	
DSAG12_00950	NAD+ synthase	K01916	211	
DSAG12_00951	hypothetical protein	--	173	
DSAG12_00952	hypothetical protein	--	180	
DSAG12_00953	hypothetical protein	--	207	
DSAG12_00954	hypothetical protein	--	145	
DSAG12_00955	hypothetical protein	--	436	Lokiactin
DSAG12_00956	3-hydroxypropionyl-coenzyme A dehydratase	K15019	89	
DSAG12_00957	septum formation protein	K06287	192	
DSAG12_00958	hypothetical protein	--	174	
DSAG12_00959	hypothetical protein	--	199	
DSAG12_00960	tRNA-Pro		191	
DSAG12_00961	hypothetical protein	--	197	
DSAG12_00962	ADP-ribose pyrophosphatase	K01515	152	
DSAG12_00963	membrane dipeptidase	K01273	175	
DSAG12_00964	Ras-related protein Rab-5C	K07889	142	
DSAG12_00965	hypothetical protein	--	175	
DSAG12_00966	hypothetical protein	--	125	
DSAG12_00967	adenine-specific DNA-methyltransferase	K07316	201	
DSAG12_00968	magnesium transporter	K03284	216	
DSAG12_00969	elongation factor 1-alpha	K03231	157	
DSAG12_00970	hypothetical protein	--	241	
DSAG12_00971	hypothetical protein	--	0	
DSAG12_00972	hypothetical protein	--	163	
DSAG12_00973	2-iminobutanoate/2-iminopropanoate deaminase	K09022	214	
DSAG12_00974	hypothetical protein	--	247	
DSAG12_00975	phosphoglycolate phosphatase	K01091	209	small GTP-binding domain protein
DSAG12_00976	ATP-dependent RNA helicase DeaD	K05592	212	
DSAG12_00977	hypothetical protein	--	184	
DSAG12_00978	hypothetical protein	K09131	165	
DSAG12_00979	hypothetical protein	K09717	239	
DSAG12_00980	archaea-specific RecJ-like exonuclease	K07463	201	
DSAG12_00981	hypothetical protein	--	269	
DSAG12_00982	hypothetical protein	--	180	
DSAG12_00983	hypothetical protein	--	114	
DSAG12_00984	1,3-propanediol dehydrogenase	K00086	198	
DSAG12_00985	ubiquitin-conjugating enzyme E2 H	K10576	163	
DSAG12_00986	hypothetical protein	--	267	
DSAG12_00987	chlorophyll(ide) b reductase	K13606	233	
DSAG12_00988	hypothetical protein	--	90	
DSAG12_00989	hypothetical protein	--	168	
DSAG12_00990	hypothetical protein	--	177	
DSAG12_00991	hypothetical protein	--	191	
DSAG12_00992	hypothetical protein	--	82	
DSAG12_00993	dihydroflavonol-4-reductase	K00091	118	
DSAG12_00994	3-oxo-5-alpha-steroid 4-dehydrogenase 1	K12343	237	
DSAG12_00995	thiamine biosynthesis protein Thil	K03151	232	hypothetical protein with ubiquitin-conjugating domain
DSAG12_00996	hypothetical protein	--	171	
DSAG12_00997	hypothetical protein	--	208	
DSAG12_00998	hypothetical protein	--	200	
DSAG12_00999	hypothetical protein	--	133	
DSAG12_01000	hypothetical protein	--	197	
DSAG12_01001	hypothetical protein	--	118	
DSAG12_01002	nicotinamidase/pyrazinamidase	K08281	62	
DSAG12_01003	cyclic pyranopterin phosphate synthase	K03639	222	
DSAG12_01004	hypothetical protein	--	220	
DSAG12_01005	sulfate permease, SulP family	K03321	163	
DSAG12_01006	putative membrane protein	K08981	242	
DSAG12_01007	hypothetical protein	--	192	



DSAG12_01008	hypothetical protein	--	206
DSAG12_01009	hypothetical protein	--	159
DSAG12_01010	acyl-CoA thioester hydrolase	K07107	0
DSAG12_01011		K01362	208
DSAG12_01012	hypothetical protein	--	188
DSAG12_01013	hypothetical protein	--	231
DSAG12_01014	acetone/methylglyoxal methyltransferase / 2-methoxy-6-polypropenyl-1,4-benzoquinone methylase	K03183	217
DSAG12_01015		K07124	0
DSAG12_01016	hypothetical protein	--	68
DSAG12_01017	hypothetical protein	--	188
DSAG12_01018	hypothetical protein	--	270
DSAG12_01019	hypothetical protein	--	133
DSAG12_01020	hypothetical protein	K09116	152
DSAG12_01021	oligo-1,6-glucosidase	K01182	215
DSAG12_01022	hypothetical protein	--	183
DSAG12_01023	hypothetical protein	--	329
DSAG12_01024	hypothetical protein	--	244
DSAG12_01025	hypothetical protein	--	99
DSAG12_01026	hypothetical protein	--	136
DSAG12_01027	hypothetical protein	--	220
DSAG12_01028	hypothetical protein	--	315
DSAG12_01029	hypothetical protein	--	230
DSAG12_01030	long-chain acyl-CoA synthetase	K01897	238
DSAG12_01031	hypothetical protein	K09157	190
DSAG12_01032	hypothetical protein	--	230
DSAG12_01033	Lrp/AsnC family transcriptional regulator	K05800	269
DSAG12_01034	asparaginyl-tRNA synthetase	K01893	190
DSAG12_01035	threonine aldolase	K01620	234
DSAG12_01036	hypothetical protein	--	336
DSAG12_01037	beta-galactosidase	K12308	266
DSAG12_01038	adenosine kinase	K00856	151
DSAG12_01039	glycoside/pentoside/hexuronide:cation symporter, GPH family	K03292	67
DSAG12_01040	MFS transporter, DHA3 family, macrolide efflux protein	K08217	271
DSAG12_01041	molybdopterin synthase sulfur carrier subunit	K03636	340
DSAG12_01042	hypothetical protein	--	228
DSAG12_01043	hypothetical protein	--	177
DSAG12_01044	hypothetical protein	--	128
DSAG12_01045	NTE family protein	K07001	383
DSAG12_01046	hypothetical protein	--	237
DSAG12_01047	hypothetical protein	--	113
DSAG12_01048	hypothetical protein	--	166
DSAG12_01049	hypothetical protein	--	210
DSAG12_01050	tRNA-Cys		224
DSAG12_01051	hypothetical protein	--	207
DSAG12_01052	hypothetical protein	--	109
DSAG12_01053	hypothetical protein	--	502
DSAG12_01054	cysteinyl-tRNA synthetase	K01883	283
DSAG12_01055	voltage-gated potassium channel	K10716	639
DSAG12_01056	hypothetical protein	--	244
DSAG12_01057	hypothetical protein	--	283
DSAG12_01058	transposase	K07486	831
DSAG12_01059	hypothetical protein	--	379
DSAG12_01060	hypothetical protein	--	209
DSAG12_01061	MFS transporter, UMF1 family	K06902	0
DSAG12_01062	hypothetical protein	--	202
DSAG12_01063	hypothetical protein	--	239
DSAG12_01064	hypothetical protein	--	120
DSAG12_01065	glycerol-3-phosphate dehydrogenase (NAD(P)+)	K00057	192
DSAG12_01066	Cu+-exporting ATPase	K17686	191
DSAG12_01067	hypothetical protein	K09155	132
DSAG12_01068	hypothetical protein	--	49
DSAG12_01069	hypothetical protein	--	473
DSAG12_01070	ABC-2 type transport system ATP-binding protein	K01990	22
DSAG12_01071	hypothetical protein	--	271
DSAG12_01072	dihydrolipoamide dehydrogenase	K00382	160
DSAG12_01073	MarR family transcriptional regulator, transcriptional regulator for hemolysin	K06075	167
DSAG12_01074	putative ABC transport system ATP-binding protein	K02003	142
DSAG12_01075	putative ABC transport system permease protein	K02004	223
DSAG12_01076	acetolactate synthase I/II/III large subunit	K01652	244
DSAG12_01077	hypothetical protein	--	376
DSAG12_01078	hypothetical protein	--	200
DSAG12_01079	hypothetical protein	--	180
DSAG12_01080	ferritin	K02217	209
DSAG12_01081	tRNA 2-thiouridine synthesizing protein A	K04085	138
DSAG12_01082		K07092	244
DSAG12_01083	cysteine desulfurase	K04487	170
DSAG12_01084	hypothetical protein	--	225
DSAG12_01085	hypothetical protein	--	258

DSAG12_01086	cold shock protein (beta-ribbon, CspA family)	K03704	321
DSAG12_01087	hypothetical protein	--	271
DSAG12_01088	hypothetical protein	--	267
DSAG12_01089	hypothetical protein	--	527
DSAG12_01090	hypothetical protein	--	470
DSAG12_01091	hypothetical protein	--	108
DSAG12_01092	hypothetical protein	--	191
DSAG12_01093	hypothetical protein	--	323
DSAG12_01094		K00680	230
DSAG12_01095	hypothetical protein	--	322
DSAG12_01096		K00519	154
DSAG12_01097	hypothetical protein	--	150
DSAG12_01098	hypothetical protein	--	154
DSAG12_01099		K06883	155
DSAG12_01100	2-oxoglutarate ferredoxin oxidoreductase subunit beta	K00175	107
DSAG12_01101	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	K00174	145
DSAG12_01102	rubredoxin-NAD+ reductase	K05297	96
DSAG12_01103	hypothetical protein	--	0
DSAG12_01104	hypothetical protein	--	117
DSAG12_01105	hypothetical protein	--	166
DSAG12_01106	hypothetical protein	--	222
DSAG12_01107		K06888	325
DSAG12_01108	hypothetical protein	--	220
DSAG12_01109	hypothetical protein	--	133
DSAG12_01110		K07066	179
DSAG12_01111	acyl-CoA dehydrogenase	K00249	263
DSAG12_01112	heterodisulfide reductase subunit D	K08264	275
DSAG12_01113	glycolate oxidase	K00104	24
DSAG12_01114	hypothetical protein	--	201
DSAG12_01115	hypothetical protein	--	127
DSAG12_01116	hypothetical protein	--	268
DSAG12_01117	hypothetical protein	--	208
DSAG12_01118	hypothetical protein	--	176
DSAG12_01119	glutaredoxin-like protein NrdH	K06191	132
DSAG12_01120	nitrite reductase (NADH) large subunit	K00362	111
DSAG12_01121	hypothetical protein	--	307
DSAG12_01122	hypothetical protein	--	235
DSAG12_01123	4Fe-4S ferredoxin	K00205	252
DSAG12_01124	F420-non-reducing hydrogenase iron-sulfur subunit	K14127	183
DSAG12_01125	heterodisulfide reductase subunit A	K03388	263
DSAG12_01126	heterodisulfide reductase subunit B	K03389	180
DSAG12_01127	heterodisulfide reductase subunit C	K03390	282
DSAG12_01128	tRNA 2-thiouridine synthesizing protein A	K04085	141
DSAG12_01129	tRNA 2-thiouridine synthesizing protein D	K07235	90
DSAG12_01130	tRNA 2-thiouridine synthesizing protein C	K07236	198
DSAG12_01131	hypothetical protein	--	157
DSAG12_01132	hypothetical protein	--	252
DSAG12_01133	Lrp/AsnC family transcriptional regulator, regulator for asnA, asnC and gidA	K03718	189
DSAG12_01134	heterodisulfide reductase subunit C	K03390	190
DSAG12_01135	heterodisulfide reductase subunit B	K03389	267
DSAG12_01136	heterodisulfide reductase subunit A	K03388	210
DSAG12_01137	heterodisulfide reductase subunit A	K03388	245
DSAG12_01138	hypothetical protein	--	97
DSAG12_01139	hypothetical protein	--	155
DSAG12_01140	tRNA 2-thiouridine synthesizing protein A	K04085	150
DSAG12_01141	hypothetical protein	--	105
DSAG12_01142	glucose-1-phosphate thymidyltransferase	K00973	264
DSAG12_01143	hypothetical protein	--	132
DSAG12_01144	hypothetical protein	--	218
DSAG12_01145	hypothetical protein	--	248
DSAG12_01146	3-isopropylmalate dehydrogenase	K00052	281
DSAG12_01147	hypothetical protein	--	172
DSAG12_01148	hypothetical protein	--	222
DSAG12_01149	heterodisulfide reductase subunit B	K03389	275
DSAG12_01150	heterodisulfide reductase subunit C	K03390	65
DSAG12_01151	Ras-related protein Rab-8A	K07901	196
DSAG12_01152	hypothetical protein	--	171
DSAG12_01153	hypothetical protein	--	168
DSAG12_01154	hypothetical protein	--	230
DSAG12_01155	hypothetical protein	--	70
DSAG12_01156	superkiller protein 3	K12600	223
DSAG12_01157	large subunit ribosomal protein L15	K02876	972
DSAG12_01158	large subunit ribosomal protein L30	K02907	212
DSAG12_01159	small subunit ribosomal protein S5	K02988	0
DSAG12_01160	large subunit ribosomal protein L18	K02881	239
DSAG12_01161	large subunit ribosomal protein L19e	K02885	241
DSAG12_01162	large subunit ribosomal protein L32e	K02912	152
DSAG12_01163	large subunit ribosomal protein L6	K02933	224

DSAG12_01164	small subunit ribosomal protein S8	K02994	203	
DSAG12_01165	large subunit ribosomal protein L5	K02931	198	
DSAG12_01166	small subunit ribosomal protein S4e	K02987	294	Putative oligosaccharyl transferase STT3 subunit
DSAG12_01167	large subunit ribosomal protein L24	K02895	220	
DSAG12_01168	large subunit ribosomal protein L14	K02874	163	
DSAG12_01169	small subunit ribosomal protein S17	K02961	189	
DSAG12_01170	hypothetical protein	--	192	
DSAG12_01171	large subunit ribosomal protein L29	K02904	203	
DSAG12_01172	small subunit ribosomal protein S3	K02982	165	
DSAG12_01173	large subunit ribosomal protein L22	K02890	282	
DSAG12_01174	hypothetical protein	--	202	
DSAG12_01175	small subunit ribosomal protein S19	K02965	194	
DSAG12_01176	hypothetical protein	--	0	
DSAG12_01177	hypothetical protein	--	159	
DSAG12_01178	acyl-CoA dehydrogenase	K00249	218	
DSAG12_01179	hypothetical protein	--	142	
DSAG12_01180	hypothetical protein	--	149	
DSAG12_01181		K07142	193	
DSAG12_01182	hypothetical protein	--	231	
DSAG12_01183	hypothetical protein	--	41	
DSAG12_01184	DNA repair protein RadA	K04483	250	
DSAG12_01185	hypothetical protein	--	204	
DSAG12_01186	23S rRNA (uridine2552-2'-O)-methyltransferase	K02427	21	
DSAG12_01187	tRNA (guanine26-N2/guanine27-N2)-dimethyltransferase	K00555	195	
DSAG12_01188	DNA repair protein RadB	K04484	156	
DSAG12_01189	hypothetical protein	--	182	
DSAG12_01190	hypothetical protein	--	280	
DSAG12_01191	hypothetical protein	--	201	
DSAG12_01192	hypothetical protein	--	125	
DSAG12_01193	trans,trans-polyisoprenyl-diphosphate synthase [geranylgeranyl-diphosphate specific]	K15888	170	
DSAG12_01194	geranylgeranyl reductase	K10960	219	
DSAG12_01195	geranylgeranyl diphosphate synthase, type I	K13787	181	Putative oligosaccharyltransferase complex subunit
DSAG12_01196	isopentenyl-diphosphate delta-isomerase	K01823	168	
DSAG12_01197	isopentenyl phosphate kinase	K06981	132	
DSAG12_01198	mevalonate kinase	K00869	186	
DSAG12_01199	hydroxymethylglutaryl-CoA reductase	K00054	188	
DSAG12_01200	diphosphomevalonate decarboxylase	K01597	143	
DSAG12_01201	hydroxymethylglutaryl-CoA synthase	K01641	133	
DSAG12_01202	perosamine synthetase	K13010	214	
DSAG12_01203	hypothetical protein	--	153	
DSAG12_01204	hypothetical protein	--	207	
DSAG12_01205	3-hydroxybutyryl-CoA dehydratase	K17865	145	
DSAG12_01206		K00680	190	
DSAG12_01207	hypothetical protein	K09726	173	
DSAG12_01208	4'-phosphopantetheinyl transferase	K06133	195	
DSAG12_01209	proline iminopeptidase	K01259	103	
DSAG12_01210	hypothetical protein	--	161	
DSAG12_01211	hypothetical protein	--	198	
DSAG12_01212	acetaldehyde dehydrogenase / alcohol dehydrogenase	K04072	191	
DSAG12_01213	long-chain acyl-CoA synthetase	K01897	232	
DSAG12_01214	acyl carrier protein	K02078	228	
DSAG12_01215	UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminophosphotransferase	K01001	104	
DSAG12_01216	hypothetical protein	--	0	
DSAG12_01217	3-oxoadipate enol-lactonase	K01055	0	
DSAG12_01218	endonuclease III related protein	K07457	0	
DSAG12_01219	hypothetical protein	--	139	
DSAG12_01220	Ras-related protein Rab-11A	K07904	141	
DSAG12_01221		K07158	226	
DSAG12_01222	hypothetical protein	--	220	
DSAG12_01223	hypothetical protein	--	93	
DSAG12_01224	hypothetical protein	--	138	
DSAG12_01225	hypothetical protein	--	173	
DSAG12_01226	hypothetical protein	--	221	
DSAG12_01227	hypothetical protein	--	185	
DSAG12_01228	hypothetical protein	--	193	
DSAG12_01229	hypothetical protein	--	57	
DSAG12_01230	protein phosphatase 1 regulatory subunit 7	K17550	219	
DSAG12_01231	translation initiation factor 1A	K03236	212	
DSAG12_01232	hypothetical protein	--	197	
DSAG12_01233	hypothetical protein	--	171	
DSAG12_01234	triphosphoribosyl-dephospho-CoA synthase	K05966	330	
DSAG12_01235	hypothetical protein	--	127	
DSAG12_01236	ribulose-bisphosphate carboxylase large chain	K01601	305	
DSAG12_01237	ribose 1,5-bisphosphate isomerase	K18237	61	
DSAG12_01238	5-(carboxyamino)imidazole ribonucleotide mutase	K01588	150	
DSAG12_01239	hypothetical protein	--	195	

DSAG12_01240	adenylyltransferase and sulfurtransferase	K11996	311
DSAG12_01241	hypothetical protein	--	215
DSAG12_01242	hypothetical protein	--	141
DSAG12_01243	beta-glucuronidase	K01195	258
DSAG12_01244	hypothetical protein	--	237
DSAG12_01245	hypothetical protein	--	185
DSAG12_01246	hypothetical protein	--	187
DSAG12_01247	hypothetical protein	--	104
DSAG12_01248	3-dehydroquinate dehydratase I	K03785	174
DSAG12_01249	shikimate dehydrogenase	K00014	57
			putative homolog of eukaryotic ribosomal protein L22e
DSAG12_01250		K07041	258
DSAG12_01251	ferredoxin-type protein NapH	K02574	241
DSAG12_01252	hypothetical protein	--	179
DSAG12_01253	hypothetical protein	--	210
DSAG12_01254	hypothetical protein	K09121	210
DSAG12_01255	hypothetical protein	--	356
DSAG12_01256	ribosomal RNA methyltransferase Nop2	K14835	84
DSAG12_01257	60S ribosome subunit biogenesis protein NIP7	K07565	151
DSAG12_01258	hypothetical protein	--	220
DSAG12_01259	hypothetical protein	--	235
DSAG12_01260	ABC-2 type transport system permease protein	K01992	195
DSAG12_01261	ABC-2 type transport system ATP-binding protein	K01990	177
DSAG12_01262	hypothetical protein	--	172
DSAG12_01263	tRNA-Gln		186
DSAG12_01264	adenylate cyclase, class 2	K05873	272
DSAG12_01265	uncharacterized protein	K06950	208
DSAG12_01266		K00680	203
DSAG12_01267	hypothetical protein	--	165
DSAG12_01268	hypothetical protein	--	175
DSAG12_01269	hypothetical protein	--	99
DSAG12_01270	hypothetical protein	--	202
DSAG12_01271	hypothetical protein	--	188
DSAG12_01272	hypothetical protein	--	114
DSAG12_01273	FKBP-type peptidyl-prolyl cis-trans isomerase SlyD	K03775	184
DSAG12_01274		K07024	175
DSAG12_01275	hypothetical protein	--	200
DSAG12_01276	tRNA wybutosine-synthesizing protein 2	K07055	198
DSAG12_01277	hypothetical protein	--	0
DSAG12_01278	hypothetical protein	--	140
DSAG12_01279	L-aspartate oxidase	K00278	183
DSAG12_01280	hypothetical protein	--	225
DSAG12_01281	3-hydroxypropionyl-coenzyme A dehydratase	K15019	177
DSAG12_01282	butyryl-CoA dehydrogenase	K00248	188
DSAG12_01283	glycoside/pentoside/hexuronide:cation symporter, GPH family	K03292	195
DSAG12_01284	hypothetical protein	--	103
DSAG12_01285	protein transport protein SEC24	K14007	227
DSAG12_01286	thioredoxin reductase (NADPH)	K00384	134
DSAG12_01287	23S rRNA (adenine2503-C2)-methyltransferase	K06941	235
DSAG12_01288	long-chain acyl-CoA synthetase	K01897	143
DSAG12_01289	serine protease AprX	K17734	196
DSAG12_01290	hypothetical protein	--	184
DSAG12_01291	NADH-quinone oxidoreductase subunit C/D	K13378	96
DSAG12_01292	hypothetical protein	--	207
DSAG12_01293	hypothetical protein	--	243
DSAG12_01294	dUTP pyrophosphatase	K01520	155
DSAG12_01295	hypothetical protein	--	245
DSAG12_01296	cysteine desulfurase	K04487	212
DSAG12_01297	arginyl-tRNA synthetase	K01887	231
DSAG12_01298	ribose 5-phosphate isomerase A	K01807	159
DSAG12_01299	hypothetical protein	--	190
DSAG12_01300	hypothetical protein	--	159
DSAG12_01301	prolyl-tRNA synthetase	K01881	174
DSAG12_01302	hypothetical protein	--	250
DSAG12_01303	hypothetical protein	--	174
DSAG12_01304	mycothiol synthase	K15520	125
DSAG12_01305	hypothetical protein	--	149
DSAG12_01306	adenosylhomocysteinase	K01251	175
DSAG12_01307	hypothetical protein	--	204
DSAG12_01308	hypothetical protein	--	168
DSAG12_01309		K00257	110
DSAG12_01310	hypothetical protein	--	0
DSAG12_01311	hypothetical protein	--	224
DSAG12_01312	hypothetical protein	--	160
DSAG12_01313	proteasome beta subunit	K03433	233
DSAG12_01314	hypothetical protein	K09730	54
DSAG12_01315	hypothetical protein	--	164
DSAG12_01316	hypothetical protein	--	232

DSAG12_01317	endonuclease III	K10773	262
DSAG12_01318	two-component system, NtrC family, response regulator AtoC	K07714	170
DSAG12_01319	two-component system, NtrC family, sensor kinase	K02482	227
DSAG12_01320	protein-tyrosine phosphatase	K01104	187
DSAG12_01321	histidinol-phosphatase (PHP family)	K04486	262
DSAG12_01322	hypothetical protein	--	164
DSAG12_01323	hydroxyacylglutathione hydrolase	K01069	201
DSAG12_01324	hypothetical protein	--	257
DSAG12_01325	hypothetical protein	--	273
DSAG12_01326		K06944	155
DSAG12_01327	hypothetical protein	--	150
DSAG12_01328	drug/metabolite transporter, DME family	K03298	222
DSAG12_01329	hypothetical protein	--	102
DSAG12_01330		K00540	126
DSAG12_01331	GTP-binding protein	K03979	201
DSAG12_01332	glycoside/pentoside/hexuronide:cation symporter, GPH family	K03292	180
DSAG12_01333	hypothetical protein	--	138
DSAG12_01334	hypothetical protein	--	154
DSAG12_01335	glycoside/pentoside/hexuronide:cation symporter, GPH family	K03292	146
DSAG12_01336	hypothetical protein	--	159
DSAG12_01337	hypothetical protein	--	140
DSAG12_01338	NitT/TauT family transport system ATP-binding protein	K02049	163
DSAG12_01339	NitT/TauT family transport system permease protein	K02050	139
DSAG12_01340	hypothetical protein	--	159
DSAG12_01341	NitT/TauT family transport system substrate-binding protein	K02051	78
DSAG12_01342	hypothetical protein	--	254
DSAG12_01343	hypothetical protein	--	150
DSAG12_01344	hypothetical protein	--	187
DSAG12_01345	tRNA-Thr	Intron(1449E)	166
DSAG12_01346	hypothetical protein	--	243
DSAG12_01347	hypothetical protein	--	55
DSAG12_01348	hypothetical protein	--	68
DSAG12_01349	hypothetical protein	--	0
DSAG12_01350	protein-S-isoprenylcysteine O-methyltransferase	K00587	270
DSAG12_01351	hypothetical protein	--	176
DSAG12_01352	endoglucanase	K01179	36
DSAG12_01353	tRNA-Met	Intron(1456E)	162
DSAG12_01354	hypothetical protein	--	210
DSAG12_01355	hypothetical protein	--	154
DSAG12_01356	hypothetical protein	--	229
DSAG12_01357	hypothetical protein	--	190
DSAG12_01358	hypothetical protein	--	211
DSAG12_01359	hypothetical protein	--	198
DSAG12_01360	hypothetical protein	--	111
DSAG12_01361	MFS transporter, DHA3 family, macrolide efflux protein	K08217	260
DSAG12_01362	hypothetical protein	--	170
DSAG12_01363		K00540	199
DSAG12_01364	D-alanine-D-alanine ligase	K01921	163
DSAG12_01365	Ras-related protein Rab-4B	K07880	622
DSAG12_01366	hypothetical protein	--	283
DSAG12_01367	methylthioribose-1-phosphate isomerase	K08963	131
DSAG12_01368	translation initiation factor IF-2	K02519	75
DSAG12_01369		K07005	189
DSAG12_01370	hypothetical protein	--	344
DSAG12_01371	7, 8-dihydropterin-6-yl-methyl-4-(beta-D- ribofuranosyl)aminobenzene 5'-phosphate synthase	K06897	393
DSAG12_01372	hypothetical protein	--	198
DSAG12_01373	hypothetical protein	--	125
DSAG12_01374	hypothetical protein	K09133	243
DSAG12_01375	hypothetical protein	--	107
DSAG12_01376	hypothetical protein	--	187
DSAG12_01377	trans-2,3-dihydro-3-hydroxyanthranilate isomerase	K06998	167
DSAG12_01378	hypothetical protein	--	353
DSAG12_01379	hypothetical protein	--	198
DSAG12_01380	hypothetical protein	--	242
DSAG12_01381	putative acetyltransferase	K03826	255
DSAG12_01382	hypothetical protein	--	158
DSAG12_01383	hypothetical protein	--	202
DSAG12_01384	hypothetical protein	--	182
DSAG12_01385	hypothetical protein	--	188
DSAG12_01386	hypothetical protein	--	172
DSAG12_01387	hypothetical protein	--	208
DSAG12_01388	hypothetical protein	--	195
DSAG12_01389	tRNA-Asp	Intron(14894)	188
DSAG12_01390	phosphoglycolate phosphatase	K01091	137
DSAG12_01391	hypothetical protein	--	186
DSAG12_01392	hypothetical protein	--	118
DSAG12_01393	hypothetical protein	--	169
DSAG12_01394	hypothetical protein	--	186

DSAG12_01395	hypothetical protein	--	197
DSAG12_01396	aminotransferase	K10907	196
DSAG12_01397	hypothetical protein	--	161
DSAG12_01398	homoserine dehydrogenase	K00003	78
DSAG12_01399	transposase	K07486	233
DSAG12_01400	hypothetical protein	--	0
DSAG12_01401	exodeoxyribonuclease III	K01142	142
DSAG12_01402	aldehyde:ferredoxin oxidoreductase	K03738	153
DSAG12_01403	two-component system, cell cycle sensor histidine kinase and response regulator CckA	K13587	188
DSAG12_01404	hypothetical protein	--	130
DSAG12_01405	retinol dehydrogenase 13	K11161	198
DSAG12_01406	hypothetical protein	--	191
DSAG12_01407	hypothetical protein	--	256
DSAG12_01408	hydroxyacylglutathione hydrolase	K01069	135
DSAG12_01409	Ras-related protein Rab-11A	K07904	266
DSAG12_01410	hypothetical protein	--	192
DSAG12_01411	hypothetical protein	--	171
DSAG12_01412	inorganic pyrophosphatase	K01507	175
DSAG12_01413	hypothetical protein	--	277
DSAG12_01414	cystathione beta-lyase	K14155	193
DSAG12_01415	hypothetical protein	--	251
DSAG12_01416	hypothetical protein	--	191
DSAG12_01417	hypothetical protein	--	0
DSAG12_01418		K00540	239
DSAG12_01419	geranylgeranyl diphosphate synthase, type I	K13787	560
DSAG12_01420	hypothetical protein	--	215
DSAG12_01421	hypothetical protein	--	162 small GTP-binding domain protein
DSAG12_01422	selenide, water dikinase	K01008	191
DSAG12_01423	hypothetical protein	--	169
DSAG12_01424	translation initiation factor 2 subunit 3	K03242	187
DSAG12_01425	acetylornithine aminotransferase	K00818	99
DSAG12_01426	hypothetical protein	--	216
DSAG12_01427		K00680	176
DSAG12_01428	arsenate reductase	K03741	133
DSAG12_01429	hypothetical protein	--	154
DSAG12_01430	hypothetical protein	--	163
DSAG12_01431	TatD DNase family protein	K03424	188
DSAG12_01432	hypothetical protein	--	130
DSAG12_01433	hypothetical protein	--	150
DSAG12_01434	hypothetical protein	--	261
DSAG12_01435	hypothetical protein	--	165
DSAG12_01436	hypothetical protein	--	220
DSAG12_01437	hypothetical protein	--	226
DSAG12_01438	hypothetical protein	--	216
DSAG12_01439	hypothetical protein	--	155
DSAG12_01440	hypothetical protein	--	182
DSAG12_01441	hypothetical protein	--	102
DSAG12_01442	hypothetical protein	--	152
DSAG12_01443	hypothetical protein	--	212
DSAG12_01444	hypothetical protein	--	7
DSAG12_01445	integrase/recombinase XerD	K04763	1
DSAG12_01446	hypothetical protein	--	5
DSAG12_01447	hypothetical protein	--	0
DSAG12_01448	lysophospholipase	K01048	0
DSAG12_01449	hypothetical protein	--	1
DSAG12_01450	hypothetical protein	--	0
DSAG12_01451	hypothetical protein	--	4
DSAG12_01452	GMP synthase (glutamine-hydrolysing)	K01951	6
DSAG12_01453		K00680	1
DSAG12_01454	hypothetical protein	--	7
DSAG12_01455	hypothetical protein	--	6
DSAG12_01456	hypothetical protein	--	1
DSAG12_01457	tRNA-Val		6
DSAG12_01458	DNA-directed RNA polymerase subunit K	K03055	7
DSAG12_01459	hypothetical protein	--	147
DSAG12_01460	hypothetical protein	--	159
DSAG12_01461	fanconi anemia group M protein	K10896	225
DSAG12_01462	histidinol-phosphatase (PHP family)	K04486	146
DSAG12_01463	hypothetical protein	--	168
DSAG12_01464	actin beta/gamma 1	K05692	253
DSAG12_01465	hypothetical protein	--	257
DSAG12_01466	hypothetical protein	--	0
DSAG12_01467	hypothetical protein	--	148
DSAG12_01468	hypothetical protein	--	163
DSAG12_01469	4-aminobutyrate aminotransferase	K00823	138
DSAG12_01470	hypothetical protein	--	149
DSAG12_01471	hypothetical protein	--	0
DSAG12_01472	alanyl-tRNA synthetase	K01872	131

DSAG12_01473	hypothetical protein	--	82
DSAG12_01474	hypothetical protein	--	107
DSAG12_01475	hypothetical protein	--	208
DSAG12_01476	hypothetical protein	--	139
DSAG12_01477	hypothetical protein	--	136
DSAG12_01478	hypothetical protein	--	155
DSAG12_01479	ATP-binding cassette, subfamily B, bacterial	K06147	159
DSAG12_01480	hypothetical protein	--	169
DSAG12_01481	hypothetical protein	--	221
DSAG12_01482	Lrp/AsnC family transcriptional regulator, regulator for asnA, asnC and gidA	K03718	45
DSAG12_01483	Lrp/AsnC family transcriptional regulator, regulator for asnA, asnC and gidA	K03718	244
DSAG12_01484	hypothetical protein	--	241
DSAG12_01485	hypothetical protein	--	189
DSAG12_01486	hypothetical protein	--	257
DSAG12_01487	glycogen(starch) synthase	K16150	123
DSAG12_01488	mannose-1-phosphate guanylyltransferase / phosphomannomutase	K16881	163
DSAG12_01489	mannose-1-phosphate guanylyltransferase	K00966	219
DSAG12_01490	Ras-related protein Rab-21	K07890	178
DSAG12_01491	hypothetical protein	--	200
DSAG12_01492	hypothetical protein	--	222
DSAG12_01493	large subunit ribosomal protein L38e	K02923	0
DSAG12_01494	peptidyl-tRNA hydrolase, PTH2 family	K04794	228
DSAG12_01495	CopG family transcriptional regulator, nickel-responsive regulator	K07722	219
DSAG12_01496	nicotinate-nucleotide pyrophosphorylase (carboxylating)	K00767	183
DSAG12_01497		K03423	38
DSAG12_01498	hypothetical protein	K09141	34
DSAG12_01499	dihydroorotase	K01465	317
DSAG12_01500	signal recognition particle subunit SRP54	K03106	64
DSAG12_01501	hypothetical protein	--	127
DSAG12_01502	hypothetical protein	--	292
DSAG12_01503	putative transposase	K07491	199
DSAG12_01504	putative transposase	K07491	218
DSAG12_01505	beta-phosphoglucomutase	K01838	205 small GTP-binding domain protein
DSAG12_01506	hypothetical protein	--	115
DSAG12_01507	translation initiation factor 5A	K03263	285
DSAG12_01508	NAD+ kinase	K00858	50
DSAG12_01509	UPF0271 protein	K07060	168
DSAG12_01510	flap endonuclease-1	K04799	157
DSAG12_01511	transitional endoplasmic reticulum ATPase	K13525	221
DSAG12_01512	hypothetical protein	--	222
DSAG12_01513		K06915	249
DSAG12_01514	hypothetical protein	--	199
DSAG12_01515	hypothetical protein	--	279
DSAG12_01516	hypothetical protein	--	191
DSAG12_01517	GMP synthase (glutamine-hydrolysing)	K01951	0
DSAG12_01518	hypothetical protein	--	113
DSAG12_01519	hypothetical protein	--	120
DSAG12_01520	hypothetical protein	--	91
DSAG12_01521	hypothetical protein	--	166
DSAG12_01522	hypothetical protein	--	220
DSAG12_01523	Ras-related protein Rab-3D	K07884	196
DSAG12_01524	hypothetical protein	--	216
DSAG12_01525		K07095	173
DSAG12_01526	hypothetical protein	--	224
DSAG12_01527	phosphoribosylformylglycinamide cyclo-ligase	K01933	306
DSAG12_01528	adenylosuccinate lyase	K01756	88
DSAG12_01529	hypothetical protein	--	195
DSAG12_01530	hypothetical protein	--	170
DSAG12_01531	TldD protein	K03568	189
DSAG12_01532	PmbA protein	K03592	186
DSAG12_01533	hypothetical protein	--	154
DSAG12_01534	hypothetical protein	--	267
DSAG12_01535	UDP-glucuronate decarboxylase	K08678	466
DSAG12_01536	hypothetical protein	--	194
DSAG12_01537	hypothetical protein	--	155
DSAG12_01538	hypothetical protein	--	148
DSAG12_01539	hypothetical protein	--	147
DSAG12_01540	hypothetical protein	--	147
DSAG12_01541	hypothetical protein	--	173
DSAG12_01542	hypothetical protein	--	151
DSAG12_01543	hypothetical protein	--	219
DSAG12_01544	hypothetical protein	--	244
DSAG12_01545	hypothetical protein	--	114
DSAG12_01546	ATP-binding cassette, subfamily B, bacterial	K06147	120
DSAG12_01547	ATP-binding cassette, subfamily B, bacterial	K06147	234
DSAG12_01548	hypothetical protein	--	182
DSAG12_01549	hypothetical protein	--	229
DSAG12_01550	replication factor C small subunit	K04801	143

DSAG12_01551	replication factor C small subunit	K04801	230
DSAG12_01552	replication factor C large subunit	K04800	110
DSAG12_01553	hypothetical protein	--	102
DSAG12_01554	putative adenine-specific DNA-methyltransferase	K07319	217
DSAG12_01555	putative adenine-specific DNA-methyltransferase	K07319	139
DSAG12_01556	MFS transporter, DHA1 family, multidrug resistance protein	K08161	202
DSAG12_01557	hypothetical protein	--	143
DSAG12_01558	hypothetical protein	--	170
DSAG12_01559	hypothetical protein	--	192
DSAG12_01560	transcription initiation factor TFIIIB	K03124	203
DSAG12_01561	hypothetical protein	--	191
DSAG12_01562	protein-tyrosine phosphatase	K01104	283
DSAG12_01563	Lrp/AsnC family transcriptional regulator, regulator for asnA, asnC and gidA	K03718	308
DSAG12_01564	hypothetical protein	--	113
DSAG12_01565	peptide/nickel transport system permease protein	K02033	115
DSAG12_01566	peptide/nickel transport system permease protein	K02034	178
DSAG12_01567	hypothetical protein	--	161
DSAG12_01568	ribosomal-protein-alanine N-acetyltransferase	K03790	201
DSAG12_01569	hypothetical protein	--	109
DSAG12_01570	glycine hydroxymethyltransferase	K00600	94
DSAG12_01571		K06889	157
DSAG12_01572	hypothetical protein	--	201
DSAG12_01573	hypothetical protein	--	109
DSAG12_01574	DNA-directed RNA polymerase subunit D	K03047	161
DSAG12_01575	hypothetical protein	--	180
DSAG12_01576	TetR/AcrR family transcriptional regulator, multidrug resistance operon repressor	K18136	0
DSAG12_01577	hypothetical protein	--	243
DSAG12_01578	small subunit ribosomal protein S9	K02996	49
DSAG12_01579	large subunit ribosomal protein L13	K02871	150
DSAG12_01580	large subunit ribosomal protein L18e	K02883	202
DSAG12_01581	hypothetical protein	--	230
DSAG12_01582	hypothetical protein	--	193
DSAG12_01583	hypothetical protein	--	223
DSAG12_01584	hypothetical protein	--	320
DSAG12_01585	hypothetical protein	--	178
DSAG12_01586	hypothetical protein	--	178
DSAG12_01587	3-phosphoshikimate 1-carboxyvinyltransferase	K00800	286
DSAG12_01588	hypothetical protein	--	278
DSAG12_01589	hypothetical protein	--	171
DSAG12_01590	hypothetical protein	--	199
DSAG12_01591	hypothetical protein	--	203
DSAG12_01592	hypothetical protein	--	209
DSAG12_01593	hypothetical protein	--	146
DSAG12_01594	hypothetical protein	--	191
DSAG12_01595	hypothetical protein	--	196
DSAG12_01596	Lrp/AsnC family transcriptional regulator, leucine-responsive regulatory protein	K03719	200
DSAG12_01597	hypothetical protein	--	158
DSAG12_01598	hypothetical protein	--	146
DSAG12_01599		K06997	158
DSAG12_01600	hypothetical protein	--	90
DSAG12_01601	phosphoenolpyruvate phosphomutase	K01841	291
DSAG12_01602	1,3-propanediol dehydrogenase	K00086	292
DSAG12_01603	phosphoenolpyruvate decarboxylase	K09459	485
DSAG12_01604	phosphoenolpyruvate phosphomutase	K01841	232
DSAG12_01605	serine racemase	K12235	185
DSAG12_01606	hypothetical protein	--	247
DSAG12_01607	hypothetical protein	--	122
DSAG12_01608	hypothetical protein	--	169
DSAG12_01609	hypothetical protein	--	72
DSAG12_01610		K07090	243
DSAG12_01611		K07050	41
DSAG12_01612	hypothetical protein	--	241
DSAG12_01613	hypothetical protein	--	97
DSAG12_01614	glycerol kinase	K00864	202
DSAG12_01615	hypothetical protein	--	138
DSAG12_01616	hypothetical protein	--	179
DSAG12_01617	hypothetical protein	--	175
DSAG12_01618	hypothetical protein	--	161
DSAG12_01619	hypothetical protein	--	206
DSAG12_01620	hypothetical protein	--	218
DSAG12_01621	hypothetical protein	--	217
DSAG12_01622	hypothetical protein	--	205
DSAG12_01623	DtxR family transcriptional regulator, Mn-dependent transcriptional regulator	K03709	200
DSAG12_01624	ferrous iron transport protein B	K04759	299
DSAG12_01625	hypothetical protein	--	24
DSAG12_01626	hypothetical protein	K09165	161
DSAG12_01627	carboxylesterase	K03928	202
DSAG12_01628	hypothetical protein	--	207



DSAG12_01629	beta-glucosidase	K05349	185	
DSAG12_01630	hypothetical protein	--	127	
DSAG12_01631	cobalt/nickel transport system ATP-binding protein / cobalt/nickel transport system permease protein	K02006 K02	255	
DSAG12_01632	cobalt/nickel transport system permease protein	K02008	178	
DSAG12_01633	hypothetical protein	--	105	
DSAG12_01634	cobalt/nickel transport system permease protein	K02007	130	
DSAG12_01635	hypothetical protein	--	170	
DSAG12_01636	hypothetical protein	--	131	
DSAG12_01637	hypothetical protein	--	153	
DSAG12_01638	hypothetical protein	--	133	
DSAG12_01639	molecular chaperone GrpE	K03687	199	
DSAG12_01640	hypothetical protein	--	114	
DSAG12_01641	phosphoenolpyruvate carboxykinase (GTP)	K01596	214	
DSAG12_01642	putative MFS transporter, AGZA family, xanthine/uracil permease	K06901	83	
DSAG12_01643	hypothetical protein	--	33	
DSAG12_01644	hypothetical protein	--	184	
DSAG12_01645	hypothetical protein	--	344	
DSAG12_01646	hypothetical protein	--	213	
DSAG12_01647	hypothetical protein	--	142	
DSAG12_01648	hypothetical protein	--	136	
DSAG12_01649	hypothetical protein	--	128	
DSAG12_01650	hypothetical protein	--	109	
DSAG12_01651	hypothetical protein	--	241	
DSAG12_01652	transcription initiation factor TFIIB	K03124	167	
DSAG12_01653	gelsolin	K05768	168	
DSAG12_01654	hypothetical protein	--	188	
DSAG12_01655	hypothetical protein	--	73	
DSAG12_01656	hypothetical protein	--	197	
DSAG12_01657	hypothetical protein	--	154	small GTP-binding domain protein
DSAG12_01658	hypothetical protein	--	0	
DSAG12_01659	transitional endoplasmic reticulum ATPase	K13525	252	
DSAG12_01660	HSP20 family protein	K13993	261	
DSAG12_01661	HSP20 family protein	K13993	267	
DSAG12_01662	MFS transporter, DHA3 family, macrolide efflux protein	K08217	192	
DSAG12_01663		K07052	376	
DSAG12_01664	hypothetical protein	--	245	
DSAG12_01665	fructokinase	K00847	211	
DSAG12_01666		K06990	256	
DSAG12_01667		K06948	178	
DSAG12_01668	hypothetical protein	--	180	
DSAG12_01669	hypothetical protein	--	223	
DSAG12_01670	hypothetical protein	--	257	
DSAG12_01671	carbon-nitrogen hydrolase family protein	K08590	340	hypothetical proteins with gelsolin-like domain
DSAG12_01672	tRNA-intron endonuclease, archaea type	K01170	250	
DSAG12_01673	hypothetical protein	--	27	
DSAG12_01674	V/A-type H <sup>+</sup> -transporting ATPase subunit I	K02123	173	
DSAG12_01675	V/A-type H <sup>+</sup> -transporting ATPase subunit D	K02120	106	
DSAG12_01676	V/A-type H <sup>+</sup> -transporting ATPase subunit B	K02118	262	
DSAG12_01677	V/A-type H <sup>+</sup> -transporting ATPase subunit A	K02117	419	
DSAG12_01678	hypothetical protein	--	399	
DSAG12_01679	V/A-type H <sup>+</sup> -transporting ATPase subunit F	K02122	194	
DSAG12_01680	hypothetical protein	--	237	
DSAG12_01681	V/A-type H <sup>+</sup> -transporting ATPase subunit C	K02119	251	
DSAG12_01682	V/A-type H <sup>+</sup> -transporting ATPase subunit K	K02124	171	
DSAG12_01683	hypothetical protein	K07220	191	
DSAG12_01684	hypothetical protein	--	183	
DSAG12_01685	hypothetical protein	--	210	
DSAG12_01686	UDPglucose 6-dehydrogenase	K00012	125	
DSAG12_01687	PUA domain protein	K07575	206	
DSAG12_01688	NADH dehydrogenase / NADH dehydrogenase	K00329 K0C	195	
DSAG12_01689	hypothetical protein	--	171	
DSAG12_01690	U6 snRNA-associated Sm-like protein LSm5	K12624	151	
DSAG12_01691	large subunit ribosomal protein L37e	K02922	127	
DSAG12_01692	hypothetical protein	--	183	
DSAG12_01693	hypothetical protein	--	138	
DSAG12_01694	glycoside/pentoside/hexuronide:cation symporter, GPH family	K03292	218	
DSAG12_01695	hypothetical protein	--	223	
DSAG12_01696		K07053	108	
DSAG12_01697	NAD-dependent deacetylase sirtuin 7	K11417	47	
DSAG12_01698	glycoside/pentoside/hexuronide:cation symporter, GPH family	K03292	128	
DSAG12_01699	hypothetical protein	--	148	
DSAG12_01700	hypothetical protein	--	253	
DSAG12_01701	dolichol-phosphate mannosyltransferase	K00721	308	
DSAG12_01702	hypothetical protein	--	226	
DSAG12_01703	hypothetical protein	--	145	
DSAG12_01704	hypothetical protein	--	223	

DSAG12_01705	all-trans-retinol 13,14-reductase	K09516	147
DSAG12_01706	glycoside/pentoside/hexuronide:cation symporter, GPH family	K03292	169
DSAG12_01707	all-trans-retinol 13,14-reductase	K09516	137
DSAG12_01708	hypothetical protein	--	80
DSAG12_01709	hypothetical protein	--	125
DSAG12_01710	putative ABC transport system permease protein	K02004	161
DSAG12_01711	hypothetical protein	--	202
DSAG12_01712	hypothetical protein	--	266
DSAG12_01713	putative ABC transport system permease protein	K02004	216
DSAG12_01714	putative ABC transport system ATP-binding protein	K02003	201
DSAG12_01715	hypothetical protein	--	165
DSAG12_01716	hypothetical protein	--	274
DSAG12_01717	malate dehydrogenase (oxaloacetate-decarboxylating)	K00027	205
DSAG12_01718	glycerol-3-phosphate dehydrogenase	K00111	162
DSAG12_01719	sarcosine oxidase, subunit alpha	K00302	191
DSAG12_01720	hypothetical protein	--	172
DSAG12_01721	amidohydrolase	K01436	203
DSAG12_01722	polar amino acid transport system substrate-binding protein	K02030	242
DSAG12_01723	hypothetical protein	--	241
DSAG12_01724	hypothetical protein	--	253
DSAG12_01725	hypothetical protein	--	236
DSAG12_01726	3-oxoacyl-[acyl-carrier protein] reductase	K00059	95
DSAG12_01727	glycerophosphoryl diester phosphodiesterase	K01126	145
DSAG12_01728	hypothetical protein	--	231
DSAG12_01729	transcription initiation factor TFIID TATA-box-binding protein	K03120	205
DSAG12_01730	hypothetical protein	--	170
DSAG12_01731	hypothetical protein	--	198
DSAG12_01732	hypothetical protein	--	231
DSAG12_01733	hypothetical protein	--	179
DSAG12_01734	transcription initiation factor TFIID TATA-box-binding protein	K03120	131
DSAG12_01735	Ras-related protein Rab-6A	K07893	249
DSAG12_01736	hypothetical protein	--	248
DSAG12_01737	acetyltransferase	K09181	238
DSAG12_01738	L-2-hydroxycarboxylate dehydrogenase (NAD+)	K05884	154
DSAG12_01739	hypothetical protein	--	205
DSAG12_01740	hypothetical protein	--	198
DSAG12_01741	hypothetical protein	--	129
DSAG12_01742	hypothetical protein	--	217
DSAG12_01743	beta-galactosidase	K01190	176
DSAG12_01744	ADP-dependent NAD(P)H-hydrate dehydratase / NAD(P)H-hydrate epimerase	K17758 K17	312
DSAG12_01745	hypothetical protein	--	202
DSAG12_01746	hypothetical protein	--	0
DSAG12_01747	hypothetical protein	--	84
DSAG12_01748	hypothetical protein	--	216
DSAG12_01749	hypothetical protein	--	165
DSAG12_01750	hypothetical protein	--	161
DSAG12_01751	hypothetical protein	--	125
DSAG12_01752	hypothetical protein	--	168
DSAG12_01753	hypothetical protein	--	134
DSAG12_01754	hypothetical protein	--	122
DSAG12_01755	hypothetical protein	--	176
DSAG12_01756	serpin B11/12	K13966	250
DSAG12_01757	serpin B11/12	K13966	270
DSAG12_01758	serpin B	K13963	182
DSAG12_01759	hypothetical protein	--	274
DSAG12_01760	methionyl aminopeptidase	K01265	211
DSAG12_01761	hypothetical protein	--	235
DSAG12_01762	hypothetical protein	--	231
DSAG12_01763	tRNA-Arg	--	232
DSAG12_01764	isopentenyl-diphosphate delta-isomerase	K01823	143
DSAG12_01765	hypothetical protein	--	288
DSAG12_01766	large subunit ribosomal protein L11	K02867	150
DSAG12_01767	large subunit ribosomal protein L1	K02863	105
DSAG12_01768	large subunit ribosomal protein L10	K02864	181
DSAG12_01769	large subunit ribosomal protein L12	K02869	237
DSAG12_01770	hypothetical protein	--	228
DSAG12_01771	hypothetical protein	--	157
DSAG12_01772	hypothetical protein	--	160
DSAG12_01773	hypothetical protein	K09717	168
DSAG12_01774	hypothetical protein	--	53
DSAG12_01775	hypothetical protein	--	164
DSAG12_01776	GTP cyclohydrolase I	K01495	190
DSAG12_01777	oleandomycin transport system permease protein	K18233	153
DSAG12_01778	ABC-2 type transport system ATP-binding protein	K01990	233
DSAG12_01779	hypothetical protein	--	149
DSAG12_01780	/ putative redox protein	K06889 K07	131
DSAG12_01781	hypothetical protein	--	0
DSAG12_01782	dihydrmethanopterin reductase (acceptor)	K18853	0

DSAG12_01783	hypothetical protein	--	195
DSAG12_01784	hypothetical protein	K09154	176
DSAG12_01785	hypothetical protein	K09739	213
DSAG12_01786	beta-ribofuranosylaminobenzene 5'-phosphate synthase	K06984	175
DSAG12_01787	hydrogenase expression/formation protein	K07388	253
DSAG12_01788	protein-tyrosine phosphatase	K01104	163
DSAG12_01789	small subunit ribosomal protein S2	K02967	213
DSAG12_01790	hypothetical protein	--	134
DSAG12_01791	hypothetical protein	K09955	37
DSAG12_01792	hypothetical protein	--	183
DSAG12_01793	small subunit ribosomal protein S8e	K02995	163
DSAG12_01794	hypothetical protein	--	58
DSAG12_01795	hypothetical protein	K09736	200
DSAG12_01796	ribose-phosphate pyrophosphokinase	K00948	188
DSAG12_01797	hypothetical protein	--	193
DSAG12_01798	Ca2+-transporting ATPase	K01537	0
DSAG12_01799	FAD synthetase	K14656	190
DSAG12_01800	CDP-paratose 2-epimerase	K12454	152
DSAG12_01801	translin	K07477	163
DSAG12_01802	ribulose-phosphate 3-epimerase	K01783	200
DSAG12_01803	Ras-related protein Rab-21	K07890	111
DSAG12_01804	hypothetical protein	--	126
DSAG12_01805	hypothetical protein	--	149
DSAG12_01806	hypothetical protein	--	206
DSAG12_01807	hypothetical protein	--	139
DSAG12_01808	hypothetical protein	--	284
DSAG12_01809	archaeitylinositol phosphate synthase	K17884	165
DSAG12_01810	hypothetical protein	--	186
DSAG12_01811	phosphomannomutase	K17497	90
DSAG12_01812	phosphatidylinositol alpha-mannosyltransferase	K08256	174
DSAG12_01813	mannose-1-phosphate guanylyltransferase	K00971	147
DSAG12_01814	dTDP-4-dehydrorhamnose reductase	K00067	122
DSAG12_01815	glucose-1-phosphate thymidyltransferase	K00973	222
DSAG12_01816	dTDP-4-dehydrorhamnose reductase	K00067	169
DSAG12_01817	dTDP-glucose 4,6-dehydratase	K01710	208
DSAG12_01818	GDPmannose 4,6-dehydratase	K01711	157
DSAG12_01819	hypothetical protein	--	171
DSAG12_01820	hypothetical protein	--	150
DSAG12_01821	hypothetical protein	--	188
DSAG12_01822	hypothetical protein	--	221 small GTP-binding domain protein
DSAG12_01823	hypothetical protein	K00680	89
DSAG12_01824	hypothetical protein	--	107
DSAG12_01825	hypothetical protein	--	172
DSAG12_01826	hypothetical protein	--	130
DSAG12_01827	hypothetical protein	K01043	42
DSAG12_01828	hypothetical protein	--	120
DSAG12_01829	dTDP-4-amino-4,6-dideoxygalactose transaminase	K02805	208
DSAG12_01830	GDP-L-fucose synthase	K02377	214
DSAG12_01831	hypothetical protein	--	210
DSAG12_01832	hypothetical protein	--	203
DSAG12_01833	CDP-6-deoxy-D-xylo-4-hexulose-3-dehydrase	K12452	187
DSAG12_01834	hypothetical protein	--	199
DSAG12_01835	hypothetical protein	K00680	203
DSAG12_01836	hypothetical protein	--	185
DSAG12_01837	pseudaminic acid synthase	K15898	179
DSAG12_01838	hypothetical protein	K00837	0
DSAG12_01839	hypothetical protein	K00837	4
DSAG12_01840	hypothetical protein	--	4
DSAG12_01841	ribosomal-protein-alanine N-acetyltransferase	K03790	8
DSAG12_01842	hypothetical protein	--	9
DSAG12_01843	UDP-N-acetylglucosamine 4,6-dehydratase	K15894	4
DSAG12_01844	hypothetical protein	--	2
DSAG12_01845	glycosyltransferase	K13002	9
DSAG12_01846	dolichol-phosphate mannosyltransferase	K00721	2
DSAG12_01847	hypothetical protein	--	8
DSAG12_01848	hypothetical protein	--	12
DSAG12_01849	hypothetical protein	--	5
DSAG12_01850	hypothetical protein	--	4
DSAG12_01851	hypothetical protein	--	8
DSAG12_01852	hypothetical protein	--	4
DSAG12_01853	UDP-N-acetylglucosamine 2-epimerase (non-hydrolysing)	K01791	1
DSAG12_01854	hypothetical protein	K01795	0
DSAG12_01855	dTDP-glucose 4,6-dehydratase	K01710	12
DSAG12_01856	hypothetical protein	--	9
DSAG12_01857	D-inositol-3-phosphate glycosyltransferase	K15521	6
DSAG12_01858	hypothetical protein	--	8
DSAG12_01859	hypothetical protein	--	2
DSAG12_01860	hypothetical protein	--	6

DSAG12_01861	UDP-N-acetylglucosamine 4-epimerase	K02473	11
DSAG12_01862	hypothetical protein	--	0
DSAG12_01863	putative acetyltransferase	K03828	4
DSAG12_01864	leucyl-tRNA synthetase	K01869	2
DSAG12_01865	UDP-N-acetyl-2-amino-2-deoxyglucuronate dehydrogenase	K13020	13
DSAG12_01866	hypothetical protein	--	4
DSAG12_01867	hypothetical protein	--	6
DSAG12_01868	hypothetical protein	--	8
DSAG12_01869	CDP-glycerol glycerophosphotransferase	K09809	7
DSAG12_01870	hypothetical protein	--	2
DSAG12_01871		K01726	7
DSAG12_01872	phosphoenolpyruvate phosphomutase	K01841	0
DSAG12_01873	MFS transporter, OPA family, glycerol-3-phosphate transporter	K02445	8
DSAG12_01874	ADP-ribose pyrophosphatase	K01515	10
DSAG12_01875	hypothetical protein	--	7
DSAG12_01876		K00754	5
DSAG12_01877	riboflavin kinase, archaea type	K07732	7
DSAG12_01878	hypothetical protein	--	7
DSAG12_01879	hypothetical protein	--	8
DSAG12_01880	hypothetical protein	--	5
DSAG12_01881	putative ABC transport system ATP-binding protein	K02003	0
DSAG12_01882	hypothetical protein	--	24
DSAG12_01883	hypothetical protein	--	17
DSAG12_01884	hypothetical protein	--	55
DSAG12_01885	slit 3	K06850	206
DSAG12_01886		K07047	226
DSAG12_01887	hypothetical protein	--	112
DSAG12_01888	hypothetical protein	--	6
DSAG12_01889	hypothetical protein	--	5
DSAG12_01890	3-hydroxybutyryl-CoA dehydratase	K17865	6
DSAG12_01891	hypothetical protein	--	12
DSAG12_01892	malonyl-CoA O-methyltransferase	K02169	7
DSAG12_01893	glyceraldehyde 3-phosphate dehydrogenase	K00134	0
DSAG12_01894	7, 8-dihydropterin-6-yl-methyl-4-(beta-D- ribofuranosyl)aminobenzene 5'-phosphate synthase	K06897	11
DSAG12_01895	hypothetical protein	--	12
DSAG12_01896	enoyl-CoA hydratase / 3-hydroxyacyl-CoA dehydrogenase	K15016	3
DSAG12_01897	hypothetical protein	--	100
DSAG12_01898	phosphoglycerate kinase	K00927	141
DSAG12_01899	uncharacterized protein	K06959	169
DSAG12_01900	hypothetical protein	--	246
DSAG12_01901	hypothetical protein	--	196
DSAG12_01902	hypothetical protein	--	116
DSAG12_01903	tRNA-Val		305
DSAG12_01904	hypothetical protein	--	170
DSAG12_01905	hypothetical protein	--	146
DSAG12_01906	zeta-carotene isomerase	K15744	132
DSAG12_01907	hypothetical protein	--	192
DSAG12_01908	hypothetical protein	--	229
DSAG12_01909	transposase	K07486	190
DSAG12_01910	hypothetical protein	--	209
DSAG12_01911		K06898	216
DSAG12_01912	site-specific DNA-methyltransferase (cytosine-N4-specific)	K00590	176
DSAG12_01913	putative adenine-specific DNA-methyltransferase	K07319	97
DSAG12_01914		K00936	130
DSAG12_01915	hypothetical protein	--	259
DSAG12_01916	DNA polymerase IV (archaeal DinB-like DNA polymerase)	K04479	188
DSAG12_01917	hypothetical protein	--	203
DSAG12_01918	hypothetical protein	--	187
DSAG12_01919	hypothetical protein	--	210
DSAG12_01920	hypothetical protein	--	251
DSAG12_01921	hypothetical protein	--	253
DSAG12_01922		K07062	65
DSAG12_01923	hypothetical protein	--	173
DSAG12_01924	hypothetical protein	--	186
DSAG12_01925	hypothetical protein	--	0
DSAG12_01926	hypothetical protein	--	54
DSAG12_01927	hypothetical protein	--	193
DSAG12_01928	phosphoglycolate phosphatase	K01091	109
DSAG12_01929	acetoin utilization protein AcuC	K04768	229
DSAG12_01930	hypothetical protein	--	171
DSAG12_01931	hypothetical protein	--	0
DSAG12_01932	hypothetical protein	--	127
DSAG12_01933	hypothetical protein	--	134
DSAG12_01934	hypothetical protein	--	214
DSAG12_01935	hypothetical protein	--	173
DSAG12_01936	Ras-related protein Rab-7A	K07897	199
DSAG12_01937	hypothetical protein	--	221
DSAG12_01938	hypothetical protein	--	0

DSAG12_01939	hypothetical protein	--	11
DSAG12_01940	hypothetical protein	--	176
DSAG12_01941	cell division protein FtsZ	K03531	204
DSAG12_01942	hypothetical protein	--	146
DSAG12_01943		K06995	10
DSAG12_01944	hypothetical protein	--	148
DSAG12_01945		K07065	161
DSAG12_01946	hypothetical protein	--	147
DSAG12_01947	hypothetical protein	--	97
DSAG12_01948	hypothetical protein	--	0
DSAG12_01949	NADPH2:quinone reductase	K00344	287
DSAG12_01950	hypothetical protein	--	305
DSAG12_01951	hypothetical protein	--	184
DSAG12_01952	hypothetical protein	--	131
DSAG12_01953	hypothetical protein	--	182
DSAG12_01954	helicase	K03726	271
DSAG12_01955	replicative DNA helicase Mcm	K10726	230
DSAG12_01956	hypothetical protein	--	155
DSAG12_01957	AAA family ATPase	K07392	152
DSAG12_01958	hypothetical protein	--	216
DSAG12_01959	hypothetical protein	--	190
DSAG12_01960	2-dehydropanoate 2-reductase	K00077	214
DSAG12_01961		K00936	312 small GTP-binding domain protein
DSAG12_01962	glycyl-tRNA synthetase	K01880	0
DSAG12_01963	hypothetical protein	--	6
DSAG12_01964	hypothetical protein	--	235
DSAG12_01965	hypothetical protein	--	241
DSAG12_01966	carboxypeptidase Taq	K01299	245
DSAG12_01967	glycoside/pentoside/hexuronide:cation symporter, GPH family	K03292	202
DSAG12_01968	hypothetical protein	--	97
DSAG12_01969	hypothetical protein	--	51
DSAG12_01970	hypothetical protein	--	89
DSAG12_01971	hypothetical protein	--	0
DSAG12_01972	hypothetical protein	--	195
DSAG12_01973	glutamate dehydrogenase (NAD(P)+)	K00261	0
DSAG12_01974	glutamate dehydrogenase (NADP+)	K00262	289
DSAG12_01975	hypothetical protein	--	257
DSAG12_01976	hypothetical protein	--	190
DSAG12_01977	hypothetical protein	--	7
DSAG12_01978	glutamate dehydrogenase (NADP+)	K00262	200
DSAG12_01979	hypothetical protein	--	234
DSAG12_01980	hypothetical protein	--	223
DSAG12_01981	hypothetical protein	--	238
DSAG12_01982	hypothetical protein	--	188
DSAG12_01983	Ras-related protein Rab-34	K07921	208
DSAG12_01984	hypothetical protein	--	58
DSAG12_01985	small subunit ribosomal protein S30e	K02983	76
DSAG12_01986	tRNA-Gln		185
DSAG12_01987	hypothetical protein	--	132
DSAG12_01988	hypothetical protein	--	251
DSAG12_01989	hypothetical protein	--	13
DSAG12_01990	acetolactate synthase I/II/III large subunit	K01652	144
DSAG12_01991	alkenylglycerophosphocholine/alkenylglycerophosphoethano lamine hydrolase	K18575	108
DSAG12_01992	dihydroxy-acid dehydratase	K01687	266
DSAG12_01993	hypothetical protein	--	230
DSAG12_01994	glycoside/pentoside/hexuronide:cation symporter, GPH family	K03292	99
DSAG12_01995	hypothetical protein	--	97
DSAG12_01996	flavin-binding kelch repeat F-box protein 1	K12116	154
DSAG12_01997	hypothetical protein	--	186
DSAG12_01998	hypothetical protein	--	241
DSAG12_01999	hypothetical protein	--	1313
DSAG12_02000	hypothetical protein	--	627
DSAG12_02001	beta-phosphoglucomutase	K01838	232
DSAG12_02002	hypothetical protein	--	129
DSAG12_02003	hypothetical protein	--	94
DSAG12_02004	serine/threonine-protein phosphatase PP1 catalytic subunit	K06269	295
DSAG12_02005	hypothetical protein	--	233
DSAG12_02006	hypothetical protein	--	213
DSAG12_02007	UDP-glucose 4-epimerase	K01784	233 putative membrane-bound protein with ubiquitin- like domain
DSAG12_02008	hypothetical protein	--	116
DSAG12_02009	methionyl aminopeptidase	K01265	202
DSAG12_02010		K07131	213
DSAG12_02011	dTMP kinase	K00943	73
DSAG12_02012	hypothetical protein	--	0
DSAG12_02013	hypothetical protein	--	130

DSAG12_02014	hypothetical protein	--	229	(dolichyl- diphosphooligosaccharide--protein glycosyltransferase subunit 1)
DSAG12_02015	hypothetical protein	--	58	
DSAG12_02016	MoxR-like ATPase	K03924	266	
DSAG12_02017	superkiller protein 3	K12600	119	
DSAG12_02018	two-component system, cell cycle sensor histidine kinase and response regulator CckA	K13587	250	
DSAG12_02019	hypothetical protein	--	233	
DSAG12_02020	hypothetical protein	--	205	
DSAG12_02021	hypothetical protein	K07502	162	
DSAG12_02022	hypothetical protein	K09122	237	
DSAG12_02023	hypothetical protein	--	198	
DSAG12_02024	hypothetical protein	--	180	
DSAG12_02025	formylmethanofuran dehydrogenase subunit E	K11261	192	
DSAG12_02026	MFS transporter, DHA1 family, multidrug resistance protein	K08153	98	
DSAG12_02027	long-chain acyl-CoA synthetase	K01897	139	
DSAG12_02028	long-chain acyl-CoA synthetase	K01897	6	
DSAG12_02029	cysteine synthase A	K01738	91	
DSAG12_02030	serine O-acetyltransferase	K00640	147	
DSAG12_02031	hypothetical protein	--	144	
DSAG12_02032	hypothetical protein	K09711	201	
DSAG12_02033	lipote-protein ligase A	K03800	237	
DSAG12_02034	biotin synthase	K01012	70	
DSAG12_02035	hypothetical protein	--	266	
DSAG12_02036	hypothetical protein	--	199	
DSAG12_02037	hypothetical protein	--	171	
DSAG12_02038	hypothetical protein	--	245	
DSAG12_02039	TldD protein	K03568	195	
DSAG12_02040	PmbA protein	K03592	156	
DSAG12_02041	Ras-related GTP-binding protein A/B	K16185	259	
DSAG12_02042	Ras-related GTP-binding protein A/B	K16185	299	
DSAG12_02043	hypothetical protein	--	216	
DSAG12_02044	thioredoxin 1	K03671	0	
DSAG12_02045	hypothetical protein	--	261	
DSAG12_02046	superkiller protein 3	K12600	270	
DSAG12_02047	hypothetical protein	--	171	
DSAG12_02048	hypothetical protein	--	152	
DSAG12_02049	triosephosphate isomerase (TIM)	K01803	171	
DSAG12_02050	hypothetical protein	--	182	
DSAG12_02051	hypothetical protein	--	160	
DSAG12_02052	energy-coupling factor transport system substrate-specific component	K16923	93	
DSAG12_02053	hypothetical protein	--	294	
DSAG12_02054	threonine synthase	K01733	251	
DSAG12_02055	drug/metabolite transporter, DME family	K03298	226	
DSAG12_02056	hypothetical protein	--	218	
DSAG12_02057	hypothetical protein	--	209	
DSAG12_02058	hypothetical protein	--	185	
DSAG12_02059	hypothetical protein	--	224	
DSAG12_02060	hypothetical protein	--	204	
DSAG12_02061	DNA excision repair protein ERCC-2	K10844	138	
DSAG12_02062	hemolysin III	K11068	289	
DSAG12_02063	starch synthase	K00703	205	
DSAG12_02064	uncharacterized protein	K06869	192	
DSAG12_02065	large subunit ribosomal protein L35Ae	K02917	186	
DSAG12_02066	hypothetical protein	--	178	
DSAG12_02067	hypothetical protein	--	189	
DSAG12_02068	hypothetical protein	K07062	218	
DSAG12_02069	hypothetical protein	--	130	
DSAG12_02070	hypothetical protein	--	300	
DSAG12_02071	hypothetical protein	--	0	
DSAG12_02072	hypothetical protein	--	186	
DSAG12_02073	hypothetical protein	--	176	
DSAG12_02074	charged multivesicular body protein 4	K12194	154	
DSAG12_02075	hypothetical protein	--	213	
DSAG12_02076	hypothetical protein	--	106	
DSAG12_02077	hypothetical protein	K07065	142	
DSAG12_02078	hypothetical protein	--	478	
DSAG12_02079	leucine-rich repeat-containing G protein-coupled receptor 6	K08399	146	
DSAG12_02080	pyruvate kinase	K00873	207	
DSAG12_02081	hypothetical protein	--	179	
DSAG12_02082	hypothetical protein	--	192	
DSAG12_02083	hypothetical protein	--	148	
DSAG12_02084	putative ABC transport system ATP-binding protein	K02021	189	
DSAG12_02085	ATP-binding cassette, subfamily B, bacterial	K06147	22	
DSAG12_02086	hypothetical protein	--	76	
DSAG12_02087	hypothetical protein	--	210	
DSAG12_02088	hypothetical protein	--	239	
DSAG12_02089	hypothetical protein	--	237	

DSAG12_02090	hypothetical protein	--	232
DSAG12_02091	hypothetical protein	--	134
DSAG12_02092	hypothetical protein	--	266
DSAG12_02093	transposase	K07486	256
DSAG12_02094	hypothetical protein	--	64
DSAG12_02095	hypothetical protein	--	64
DSAG12_02096	hypothetical protein	--	189
DSAG12_02097	Ras-related protein Rab-1A	K07874	0
DSAG12_02098	hypothetical protein	--	211
DSAG12_02099	hypothetical protein	--	133
DSAG12_02100	hypothetical protein	--	351 III)
DSAG12_02101	hypothetical protein	--	189
DSAG12_02102	hypothetical protein	--	166
DSAG12_02103	fanconi anemia group M protein	K10896	93
DSAG12_02104	hypothetical protein	--	69
DSAG12_02105	hypothetical protein	--	111
DSAG12_02106	nitrous oxidase accessory protein	K07218	232
DSAG12_02107	Ras-related protein Rab-11A	K07904	170
DSAG12_02108	hypothetical protein	--	198
DSAG12_02109	helicase	K03726	437
DSAG12_02110	hypothetical protein	--	216
DSAG12_02111	hypothetical protein	--	228
DSAG12_02112	hypothetical protein	--	203
DSAG12_02113	DNA repair protein RadA	K04483	186
DSAG12_02114	hypothetical protein	--	124
DSAG12_02115	hypothetical protein	--	225
DSAG12_02116	hypothetical protein	--	164
DSAG12_02117	hypothetical protein	--	58
DSAG12_02118	flap endonuclease-1	K04799	388
DSAG12_02119	hypothetical protein	--	164
DSAG12_02120	hypothetical protein	--	118
DSAG12_02121	hypothetical protein	--	168
DSAG12_02122	hypothetical protein	--	183 small GTP-binding domain protein
DSAG12_02123	hypothetical protein	--	254
DSAG12_02124		K06883	71
DSAG12_02125	hypothetical protein	--	252
DSAG12_02126	hypothetical protein	--	107
DSAG12_02127	hypothetical protein	--	173
DSAG12_02128	hypothetical protein	--	225
DSAG12_02129	hypothetical protein	--	172
DSAG12_02130	hypothetical protein	--	182
DSAG12_02131	hypothetical protein	--	211
DSAG12_02132	hypothetical protein	--	0
DSAG12_02133	fanconi anemia group M protein	K10896	129
DSAG12_02134	hypothetical protein	--	226
DSAG12_02135	hypothetical protein	--	261
DSAG12_02136	hypothetical protein	--	211
DSAG12_02137	hypothetical protein	--	220
DSAG12_02138	hypothetical protein	--	191
DSAG12_02139	hypothetical protein	--	256
DSAG12_02140	hypothetical protein	--	96
DSAG12_02141	hypothetical protein	--	0
DSAG12_02142	hypothetical protein	--	239
DSAG12_02143	hypothetical protein	--	224
DSAG12_02144	hypothetical protein	--	153
DSAG12_02145	fanconi anemia group M protein	K10896	267
DSAG12_02146	hypothetical protein	--	163
DSAG12_02147	hypothetical protein	--	97
DSAG12_02148	hypothetical protein	--	223
DSAG12_02149	hypothetical protein	--	162
DSAG12_02150	hypothetical protein	--	247
DSAG12_02151	hypothetical protein	--	212
DSAG12_02152	hypothetical protein	--	225
DSAG12_02153		K07131	235
DSAG12_02154	hypothetical protein	--	231
DSAG12_02155	aspartyl-tRNA synthetase	K01876	292
DSAG12_02156	tRNA pseudouridine13 synthase	K06176	106
DSAG12_02157	small subunit ribosomal protein S11	K02948	248
DSAG12_02158	small subunit ribosomal protein S4	K02986	155
DSAG12_02159	small subunit ribosomal protein S13	K02952	222
DSAG12_02160	4-hydroxybutyryl-CoA synthetase (ADP-forming)	K18593	101
DSAG12_02161	hypothetical protein	--	276
DSAG12_02162	NADPH2:quinone reductase	K00344	248
DSAG12_02163	hypothetical protein	--	165
DSAG12_02164	hypothetical protein	--	202
DSAG12_02165	hypothetical protein	--	117
DSAG12_02166	hypothetical protein	--	150
DSAG12_02167	hypothetical protein	--	223

DSAG12_02168	amidophosphoribosyltransferase	K00764	185
DSAG12_02169	phosphoribosylformylglycinamide synthase	K01952	240
DSAG12_02170	phosphoribosylformylglycinamide synthase	K01952	179
DSAG12_02171	hypothetical protein	--	276
DSAG12_02172	fusion protein PurCD	K13713	215
DSAG12_02173	dCTP diphosphatase	K16904	245
DSAG12_02174	3-oxoadipate enol-lactonase	K01055	246
DSAG12_02175		K07131	278
DSAG12_02176		K01932	220
DSAG12_02177	dihydropteroate synthase	K00796	268
DSAG12_02178	DNA gyrase subunit B	K02470	213
DSAG12_02179	DNA gyrase subunit A	K02469	246
DSAG12_02180	hypothetical protein	--	87
DSAG12_02181	hypothetical protein	--	222
DSAG12_02182	hypothetical protein	--	172
DSAG12_02183	hypothetical protein	--	274
DSAG12_02184	hypothetical protein	--	188
DSAG12_02185	hypothetical protein	--	213
DSAG12_02186	hypothetical protein	--	228
DSAG12_02187		K06883	159
DSAG12_02188	hypothetical protein	--	215
DSAG12_02189	hypothetical protein	--	144
DSAG12_02190	flotillin	K07192	157
DSAG12_02191	hypothetical protein	--	217
DSAG12_02192	hypothetical protein	--	111
DSAG12_02193	hypothetical protein	--	191
DSAG12_02194	hypothetical protein	--	230
DSAG12_02195	hypothetical protein	--	193
DSAG12_02196	hypothetical protein	--	221
DSAG12_02197	hypothetical protein	--	173
DSAG12_02198	3-deoxy-7-phosphoheptulonate synthase	K03856	195
DSAG12_02199	3-dehydroquininate synthase	K01735	100
DSAG12_02200	hypothetical protein	--	164
DSAG12_02201	asparaginyl-tRNA synthetase	K01893	172
DSAG12_02202	hypothetical protein	--	206
DSAG12_02203	hypothetical protein	K09989	200
DSAG12_02204	hypothetical protein	--	226
DSAG12_02205	hypothetical protein	--	237
DSAG12_02206	hypothetical protein	--	88
DSAG12_02207	hypothetical protein	--	186
DSAG12_02208	DNA ligase 1	K10747	207
DSAG12_02209	deoxyhypusine synthase	K00809	287
DSAG12_02210	arginine decarboxylase	K02626	38
DSAG12_02211	hypothetical protein	--	107
DSAG12_02212	hypothetical protein	--	177
DSAG12_02213	D-alanine-D-alanine ligase	K01921	234 small GTP-binding domain protein
DSAG12_02214	D-alanine-D-alanine ligase	K01921	102
DSAG12_02215	hypothetical protein	--	57
DSAG12_02216	AMP phosphorylase	K18931	308
DSAG12_02217	hypothetical protein	--	147
DSAG12_02218	hypothetical protein	--	235
DSAG12_02219	hypothetical protein	--	94
DSAG12_02220	hypothetical protein	--	176
DSAG12_02221	hypothetical protein	--	133
DSAG12_02222	hypothetical protein	--	148
DSAG12_02223	hypothetical protein	--	114
DSAG12_02224	hypothetical protein	--	214
DSAG12_02225	F420-non-reducing hydrogenase iron-sulfur subunit	K14127	201
DSAG12_02226	heterodisulfide reductase subunit A	K03388	137
DSAG12_02227	heterodisulfide reductase subunit A	K03388	225
DSAG12_02228	heterodisulfide reductase subunit A	K03388	194
DSAG12_02229	hypothetical protein	--	184
DSAG12_02230	hypothetical protein	--	185
DSAG12_02231	hypothetical protein	--	90
DSAG12_02232	phosphonate transport system ATP-binding protein	K02041	146
DSAG12_02233	hemin transport system ATP-binding protein	K09814	237
DSAG12_02234	hypothetical protein	--	197
DSAG12_02235	hypothetical protein	--	184
DSAG12_02236	hypothetical protein	--	151
DSAG12_02237	hypothetical protein	--	181
DSAG12_02238	hypothetical protein	--	57
DSAG12_02239	hypothetical protein	--	226
DSAG12_02240	hypothetical protein	--	177
DSAG12_02241	hypothetical protein	--	50
DSAG12_02242	hypothetical protein	--	0
DSAG12_02243	hypothetical protein	--	231
DSAG12_02244	hypothetical protein	--	192
DSAG12_02245	hypothetical protein	--	218



DSAG12_02246	hypothetical protein	--	76
DSAG12_02247	hypothetical protein	--	137
DSAG12_02248	hypothetical protein	--	247
DSAG12_02249	ribokinase	K00852	39
DSAG12_02250	hypothetical protein	--	89
DSAG12_02251	glycoside/pentoside/hexuronide:cation symporter, GPH family	K03292	115
DSAG12_02252	glucosamine--fructose-6-phosphate aminotransferase (isomerizing)	K00820	349
DSAG12_02253	hypothetical protein	--	183
DSAG12_02254	hypothetical protein	--	5
DSAG12_02255	hypothetical protein	--	215
DSAG12_02256	hypothetical protein	--	100
DSAG12_02257	isoleucyl-tRNA synthetase	K01870	102
DSAG12_02258	hypothetical protein	--	87
DSAG12_02259	hypothetical protein	--	105
DSAG12_02260	hypothetical protein	--	134
DSAG12_02261	hypothetical protein	--	80
DSAG12_02262	hypothetical protein	--	101
DSAG12_02263	hypothetical protein	--	162
DSAG12_02264	hypothetical protein	--	120
DSAG12_02265	phosphoribosylamine--glycine ligase	K01945	125
DSAG12_02266	N-glycosylase/DNA lyase	K03660	94
DSAG12_02267	hypothetical protein	--	125
DSAG12_02268	hypothetical protein	--	121
DSAG12_02269	hypothetical protein	--	0
DSAG12_02270	hypothetical protein	--	139
DSAG12_02271	phosphomannomutase / phosphoglucomutase	K15778	176
DSAG12_02272	nitric oxide dioxygenase	K05916	146
DSAG12_02273	hypothetical protein	--	150
DSAG12_02274		K06940	0
DSAG12_02275	alkylated DNA repair protein alkB homolog 8	K10770	8
DSAG12_02276	hypothetical protein	--	184
DSAG12_02277	hypothetical protein	--	203
DSAG12_02278	hypothetical protein	--	224
DSAG12_02279	hypothetical protein	--	274
DSAG12_02280	hypothetical protein	--	174
DSAG12_02281	hypothetical protein	--	110
DSAG12_02282	hypothetical protein	--	88
DSAG12_02283	hypothetical protein	--	185
DSAG12_02284	hypothetical protein	--	215
DSAG12_02285	hypothetical protein	--	245
DSAG12_02286	hypothetical protein	--	244
DSAG12_02287	glycerophosphoryl diester phosphodiesterase	K01126	130
DSAG12_02288		K06966	181
DSAG12_02289		K07123	152
DSAG12_02290	hypothetical protein	--	118
DSAG12_02291	hypothetical protein	--	187
DSAG12_02292	hypothetical protein	--	165
DSAG12_02293	hypothetical protein	--	221
DSAG12_02294	endoglucanase	K01179	138
DSAG12_02295	hypothetical protein	--	166
DSAG12_02296	menaquinone-dependent protoporphyrinogen oxidase	K00230	192
DSAG12_02297	ornithine--oxo-acid transaminase	K00819	90
DSAG12_02298	carbamate kinase	K00926	102
DSAG12_02299	ornithine carbamoyltransferase	K00611	245
DSAG12_02300	hypothetical protein	--	245
DSAG12_02301	16S rRNA (cytosine967-C5)-methyltransferase	K03500	105
DSAG12_02302	hypothetical protein	--	185
DSAG12_02303		K01463	172
DSAG12_02304	hypothetical protein	--	154
DSAG12_02305	hypothetical protein	--	126
DSAG12_02306	hypothetical protein	--	143
DSAG12_02307	hypothetical protein	--	195
DSAG12_02308	acetyl-CoA C-acetyltransferase	K00626	157
DSAG12_02309	hypothetical protein	--	138
DSAG12_02310	hypothetical protein	--	307
DSAG12_02311	hypothetical protein	--	486
DSAG12_02312	2,4-dienoyl-CoA reductase (NADPH2)	K00219	249
DSAG12_02313	hypothetical protein	--	194
DSAG12_02314	hypothetical protein	--	156
DSAG12_02315	hypothetical protein	--	173
DSAG12_02316	hypothetical protein	--	215
DSAG12_02317	hypothetical protein	--	175
DSAG12_02318	beta-glucuronidase	K01195	184 small GTP-binding domain protein
DSAG12_02319	hypothetical protein	--	249
DSAG12_02320	hypothetical protein	--	159
DSAG12_02321	HSP20 family protein	K13993	162
DSAG12_02322	hypothetical protein	--	248
DSAG12_02323	hypothetical protein	--	90

DSAG12_02324		K07062	169
DSAG12_02325	aldehyde:ferredoxin oxidoreductase	K03738	347
DSAG12_02326	hypothetical protein	--	285
DSAG12_02327	hypothetical protein	--	286
DSAG12_02328	hypothetical protein	--	479
DSAG12_02329	orotate phosphoribosyltransferase	K00762	164
DSAG12_02330	signal peptidase, endoplasmic reticulum-type	K13280	152
DSAG12_02331	signal peptidase, endoplasmic reticulum-type	K13280	213
DSAG12_02332	carboxylesterase	K03928	194
DSAG12_02333	modification methylase	K13581	255
DSAG12_02334	hypothetical protein	--	110
DSAG12_02335	NAD-dependent deacetylase	K12410	123
DSAG12_02336	hypothetical protein	--	329
DSAG12_02337	diaminopropionate ammonia-lyase	K01751	187
DSAG12_02338	indolepyruvate ferredoxin oxidoreductase, beta subunit	K00180	208
DSAG12_02339	indolepyruvate ferredoxin oxidoreductase, alpha subunit	K00179	147
DSAG12_02340	putative membrane protein	K00389	215
DSAG12_02341	D-glycerate 3-kinase	K15918	185
DSAG12_02342	hypothetical protein	--	146
DSAG12_02343	hypothetical protein	--	114
DSAG12_02344	hypothetical protein	--	147
DSAG12_02345	hypothetical protein	--	193 small GTP-binding domain protein
DSAG12_02346	hypothetical protein	--	164
DSAG12_02347	hypothetical protein	--	235
DSAG12_02348	hypothetical protein	--	132
DSAG12_02349	internalin A	K13730	188
DSAG12_02350	hypothetical protein	--	154
DSAG12_02351	hypothetical protein	--	29
DSAG12_02352	16S rRNA (cytosine967-C5)-methyltransferase	K03500	118
DSAG12_02353	hypothetical protein	--	224
DSAG12_02354	hypothetical protein	--	176
DSAG12_02355	inorganic phosphate transporter, PiT family	K03306	255
DSAG12_02356	hypothetical protein	--	222
DSAG12_02357	CBS domain-containing membrane protein	K07168	157
DSAG12_02358		K00540	218
DSAG12_02359	hypothetical protein	--	188
DSAG12_02360	fanconi anemia group M protein	K10896	181
DSAG12_02361	hypothetical protein	--	186
DSAG12_02362	hypothetical protein	--	170
DSAG12_02363	hypothetical protein	--	192
DSAG12_02364	NAD+ diphosphatase	K03426	163
DSAG12_02365	hypothetical protein	--	203
DSAG12_02366	hypothetical protein	--	141
DSAG12_02367	sarcosine oxidase, subunit beta	K00303	202
DSAG12_02368	hypothetical protein	--	121
DSAG12_02369	hypothetical protein	--	162
DSAG12_02370	hypothetical protein	--	148
DSAG12_02371	formylmethanofuran--tetrahydromethanopterin N-formyltransferase	K00672	89
DSAG12_02372	hypothetical protein	--	0
DSAG12_02373	hypothetical protein	--	207
DSAG12_02374	archaeetidylinositol phosphate synthase	K17884	81
DSAG12_02375	hypothetical protein	--	176
DSAG12_02376	hypothetical protein	--	232
DSAG12_02377	Ras-related protein Rab-30	K07917	203
DSAG12_02378	hypothetical protein	--	205
DSAG12_02379	hypothetical protein	--	303
DSAG12_02380	hypothetical protein	--	248 small GTP-binding domain protein
DSAG12_02381	hypothetical protein	--	237
DSAG12_02382	glycolate oxidase	K00104	268
DSAG12_02383	heterodisulfide reductase subunit D	K08264	56
DSAG12_02384	NAD-dependent deacetylase	K12410	247
DSAG12_02385		K06911	180
DSAG12_02386	hypothetical protein	--	131
DSAG12_02387	hypothetical protein	--	230
DSAG12_02388	hypothetical protein	--	160
DSAG12_02389	hypothetical protein	--	202
DSAG12_02390	hypothetical protein	--	117
DSAG12_02391	hypothetical protein	--	86
DSAG12_02392	hypothetical protein	--	187
DSAG12_02393	hypothetical protein	--	199
DSAG12_02394	laminin, alpha 3/5	K06240	83
DSAG12_02395	hypothetical protein	--	237
DSAG12_02396	hypothetical protein	--	236
DSAG12_02397	hypothetical protein	--	279
DSAG12_02398	hypothetical protein	--	97
DSAG12_02399	hypothetical protein	--	133
DSAG12_02400	glyoxylate reductase	K00015	156
DSAG12_02401	hypothetical protein	--	73

DSAG12_02402	2'-5' RNA ligase	K01975	126
DSAG12_02403	Ras-related GTP-binding protein C/D	K16186	162
DSAG12_02404	orotidine-5'-phosphate decarboxylase	K01591	150
DSAG12_02405		K07024	115
DSAG12_02406	hypothetical protein	--	172 small GTP-binding domain protein
DSAG12_02407	ADP-ribosylation factor-like protein 8	K07955	89
DSAG12_02408	hypothetical protein	--	148
DSAG12_02409	hypothetical protein	--	154
DSAG12_02410	hypothetical protein	--	155
DSAG12_02411	elongation factor 2	K03234	318
DSAG12_02412		K00936	326
DSAG12_02413	two-component system, cell cycle response regulator DivK	K11443	201
DSAG12_02414	two-component system, cell cycle response regulator DivK	K11443	245
DSAG12_02415	hypothetical protein	--	224
DSAG12_02416		K06944	213
DSAG12_02417	two-component system, cell cycle response regulator DivK	K11443	187
DSAG12_02418	hypothetical protein	--	203
DSAG12_02419	hypothetical protein	--	208
DSAG12_02420	hypothetical protein	--	140
DSAG12_02421	hypothetical protein	--	131
DSAG12_02422	two-component system, cell cycle response regulator DivK	K11443	67
DSAG12_02423	hypothetical protein	--	0
DSAG12_02424	hypothetical protein	--	258
DSAG12_02425	Ca-activated chloride channel homolog	K07114	217
DSAG12_02426	hypothetical protein	--	218
DSAG12_02427	energy-coupling factor transport system permease protein / energy-coupling factor transport system ATP-binding protein / energy-coupling factor transport system ATP-binding protein	K16785 K16	187
DSAG12_02428	energy-coupling factor transport system substrate-specific component	K16925	37
DSAG12_02429	hypothetical protein	--	73
DSAG12_02430	hypothetical protein	--	195
DSAG12_02431	hypothetical protein	--	144
DSAG12_02432	hypothetical protein	--	132
DSAG12_02433	isocitrate dehydrogenase	K00031	209
DSAG12_02434	ATP-citrate lyase alpha-subunit	K15230	204
DSAG12_02435	ATP-citrate lyase beta-subunit	K15231	176
DSAG12_02436	aconitate hydratase	K01681	169
DSAG12_02437	hypothetical protein	--	265 small GTP-binding domain protein
DSAG12_02438	sulfur carrier protein	K03154	206
DSAG12_02439	peptidyl-prolyl isomerase F (cyclophilin D)	K09565	183
DSAG12_02440	hypothetical protein	--	152
DSAG12_02441	acetylmithine deacetylase	K01438	234
DSAG12_02442	hypothetical protein	--	166
DSAG12_02443	hypothetical protein	--	66
DSAG12_02444	aldehyde:ferredoxin oxidoreductase	K03738	61
DSAG12_02445	CopG family transcriptional regulator, nickel-responsive regulator	K07722	125
DSAG12_02446	hypothetical protein	--	197
DSAG12_02447	acetyl-CoA synthetase (ADP-forming)	K01905	143
DSAG12_02448	hypothetical protein	--	168
DSAG12_02449	hypothetical protein	--	143
DSAG12_02450	large subunit ribosomal protein L10e	K02866	185
DSAG12_02451	hypothetical protein	--	109
DSAG12_02452	DtxR family transcriptional regulator, Mn-dependent transcriptional regulator	K03709	0
DSAG12_02453	hypothetical protein	--	84
DSAG12_02454	hypothetical protein	--	175
DSAG12_02455	hypothetical protein	--	127
DSAG12_02456	hypothetical protein	--	237
DSAG12_02457	DNA topoisomerase I	K03168	150
DSAG12_02458	DNA replication ATP-dependent helicase Dna2	K10742	157
DSAG12_02459	hypothetical protein	--	136
DSAG12_02460	hypothetical protein	--	172
DSAG12_02461	dynein light chain roadblock-type	K10419	205
DSAG12_02462	hypothetical protein	--	461
DSAG12_02463	hypothetical protein	--	159
DSAG12_02464	bacterial/archaeal transporter family protein	K08978	309
DSAG12_02465	UDP-N-acetylglucosamine 3-dehydrogenase	K18855	315
DSAG12_02466	3-amino-5-hydroxybenzoate synthase	K16016	242
DSAG12_02467	hypothetical protein	--	283
DSAG12_02468	aldehyde:ferredoxin oxidoreductase	K03738	157
DSAG12_02469	hypothetical protein	--	18
DSAG12_02470	LAO/AO transport system kinase	K07588	177
DSAG12_02471	methylmalonyl-CoA mutase, C-terminal domain	K01849	138
DSAG12_02472	methylmalonyl-CoA mutase, N-terminal domain	K01848	236
DSAG12_02473	cob(I)alamin adenosyltransferase	K00798	177
DSAG12_02474	hypothetical protein	--	219
DSAG12_02475	digeranylgeranylglycerophospholipid reductase	K17830	283
DSAG12_02476	hypothetical protein	--	151
DSAG12_02477	hypothetical protein	--	179
DSAG12_02478		K07124	197

DSAG12_02479	MFS transporter, DHA1 family, multidrug resistance protein	K08153	224	
DSAG12_02480	Ras-related protein Rab-9A	K07899	277	
DSAG12_02481	Ras-related protein Rab-27A	K07885	0	
DSAG12_02482	thioredoxin 1	K03671	373	
DSAG12_02483		K07013	206	
DSAG12_02484	2-isopropylmalate synthase	K01649	151	
DSAG12_02485	hypothetical protein	--	165	
DSAG12_02486	putative endonuclease	K07461	157	
DSAG12_02487	O-phosphoserine-tRNA(Sec) kinase	K10837	179	
DSAG12_02488	transitional endoplasmic reticulum ATPase	K13525	142	
DSAG12_02489	NAD+ kinase	K00858	217	
DSAG12_02490	hypothetical protein	--	191	
DSAG12_02491	tyrosine phenol-lyase	K01668	224	
DSAG12_02492	indolepyruvate ferredoxin oxidoreductase, beta subunit	K00180	146	
DSAG12_02493	indolepyruvate ferredoxin oxidoreductase, alpha subunit	K00179	139	
DSAG12_02494	penicillin amidase	K01434	153	
DSAG12_02495	hypothetical protein	--	132	
DSAG12_02496	hypothetical protein	--	111	
DSAG12_02497	acetyl-CoA synthetase (ADP-forming)	K01905	206	
DSAG12_02498	hypothetical protein	--	208	
DSAG12_02499	hypothetical protein	--	191	
DSAG12_02500	hypothetical protein	--	238	
DSAG12_02501	methionyl-tRNA synthetase	K01874	130	
DSAG12_02502	hypothetical protein	--	219	
DSAG12_02503	hypothetical protein	K09721	194	
DSAG12_02504	beta-galactosidase	K01190	255	
DSAG12_02505	hypothetical protein	--	158	
DSAG12_02506	alpha-mannosidase	K01191	175	
DSAG12_02507	hypothetical protein	--	193	
DSAG12_02508	hypothetical protein	--	163	
DSAG12_02509	hypothetical protein	--	36	
DSAG12_02510	hypothetical protein	--	147	
DSAG12_02511	hypothetical protein	--	156	
DSAG12_02512	hypothetical protein	--	175	small GTP-binding domain protein
DSAG12_02513	peroxiredoxin Q/BCP	K03564	195	
DSAG12_02514	hypothetical protein	--	107	
DSAG12_02515	hypothetical protein	--	178	
DSAG12_02516	hypothetical protein	--	21	
DSAG12_02517	hypothetical protein	--	167	
DSAG12_02518	hypothetical protein	--	119	
DSAG12_02519		K07052	139	
DSAG12_02520	hypothetical protein	--	260	
DSAG12_02521	hypothetical protein	--	206	
DSAG12_02522	hypothetical protein	--	193	hypothetical proteins with gelsolin-like domain
DSAG12_02523	hypothetical protein	--	279	
DSAG12_02524	putative hydrolase of the HAD superfamily	K07025	203	
DSAG12_02525	hypothetical protein	--	261	
DSAG12_02526	hypothetical protein	--	238	
DSAG12_02527	hypothetical protein	--	149	
DSAG12_02528	hypothetical protein	--	252	
DSAG12_02529	hypothetical protein	--	226	
DSAG12_02530	hypothetical protein	--	54	
DSAG12_02531	hypothetical protein	--	145	
DSAG12_02532	hypothetical protein	--	223	
DSAG12_02533	hypothetical protein	--	195	
DSAG12_02534	two-component system, OmpR family, sensor kinase	K02484	213	
DSAG12_02535	hypothetical protein	--	116	
DSAG12_02536	hypothetical protein	--	205	
DSAG12_02537	arylformamidase	K07130	128	
DSAG12_02538	protein phosphatase	K01090	177	
DSAG12_02539	hypothetical protein	--	175	
DSAG12_02540	hypothetical protein	--	78	
DSAG12_02541	O-acetylserine/cysteine efflux transporter	K15268	158	
DSAG12_02542	hypothetical protein	--	159	
DSAG12_02543	menaquinone-dependent protoporphyrinogen oxidase	K00230	0	
DSAG12_02544	hypothetical protein	--	166	
DSAG12_02545	alpha-mannosidase	K01191	307	
DSAG12_02546	hypothetical protein	--	0	
DSAG12_02547	hypothetical protein	--	102	
DSAG12_02548	hypothetical protein	--	250	
DSAG12_02549	hypothetical protein	--	306	
DSAG12_02550	two-component system, cell cycle sensor histidine kinase and response regulator CckA	K13587	233	
DSAG12_02551	hypothetical protein	--	125	
DSAG12_02552	hypothetical protein	--	125	
DSAG12_02553	hypothetical protein	--	188	
DSAG12_02554	hypothetical protein	--	96	
DSAG12_02555	DNA excision repair protein ERCC-2	K10844	49	

DSAG12_02556	putative acetyltransferase	K03828	42
DSAG12_02557	L-serine dehydratase	K01752	157
DSAG12_02558	putative ABC transport system ATP-binding protein	K02003	166
DSAG12_02559	hypothetical protein	--	146
DSAG12_02560	putative ABC transport system ATP-binding protein	K02003	203
DSAG12_02561	hypothetical protein	--	164
DSAG12_02562	hypothetical protein	--	195
DSAG12_02563	hypothetical protein	--	61
DSAG12_02564	hypothetical protein	--	128
DSAG12_02565	protease I	K05520	231
DSAG12_02566	hypothetical protein	--	0
DSAG12_02567	hypothetical protein	--	48
DSAG12_02568	hypothetical protein	--	183
DSAG12_02569	hypothetical protein	--	139
DSAG12_02570	hypothetical protein	--	148
DSAG12_02571	hypothetical protein	--	198
DSAG12_02572		K06883	115
DSAG12_02573	hypothetical protein	--	188
DSAG12_02574	hypothetical protein	--	116
DSAG12_02575	hypothetical protein	--	206
DSAG12_02576	hypothetical protein	--	123
DSAG12_02577	xylulokinase	K00854	188
DSAG12_02578	glycerol kinase	K00864	194
DSAG12_02579	hypothetical protein	--	117
DSAG12_02580	hypothetical protein	--	188
DSAG12_02581	hypothetical protein	--	136
DSAG12_02582	hypothetical protein	--	158
DSAG12_02583	hypothetical protein	--	68
DSAG12_02584	hypothetical protein	--	188
DSAG12_02585	hypothetical protein	--	184
DSAG12_02586	hypothetical protein	--	139
DSAG12_02587	hypothetical protein	--	182
DSAG12_02588	hypothetical protein	--	158
DSAG12_02589	hypothetical protein	--	172
DSAG12_02590	hypothetical protein	--	186
DSAG12_02591	hypothetical protein	--	118
DSAG12_02592	hypothetical protein	--	220
DSAG12_02593	hypothetical protein	--	236
DSAG12_02594	hypothetical protein	--	265
DSAG12_02595	hypothetical protein	--	243
DSAG12_02596	ATP-dependent helicase IRC3	K17677	137
DSAG12_02597	hypothetical protein	--	127
DSAG12_02598	hypothetical protein	--	306
DSAG12_02599	ribonuclease III	K03685	179
DSAG12_02600	hypothetical protein	--	135
DSAG12_02601	hypothetical protein	--	159
DSAG12_02602	hypothetical protein	--	241
DSAG12_02603	hypothetical protein	--	151
DSAG12_02604	RelE protein	K06218	203
DSAG12_02605	hypothetical protein	--	163
DSAG12_02606	hypothetical protein	--	96
DSAG12_02607	hypothetical protein	--	171
DSAG12_02608	hypothetical protein	--	134
DSAG12_02609	hypothetical protein	--	292
DSAG12_02610	hypothetical protein	--	217
DSAG12_02611	hypothetical protein	--	214
DSAG12_02612	hypothetical protein	--	274
DSAG12_02613	protein scribble	K16175	0
DSAG12_02614	hypothetical protein	--	55
DSAG12_02615	hypothetical protein	--	134
DSAG12_02616	hypothetical protein	--	88
DSAG12_02617	hypothetical protein	--	152
DSAG12_02618	hypothetical protein	--	0
DSAG12_02619	hypothetical protein	--	0
DSAG12_02620	hypothetical protein	--	100
DSAG12_02621	hypothetical protein	--	201
DSAG12_02622	hypothetical protein	--	108
DSAG12_02623	hypothetical protein	--	203
DSAG12_02624	hypothetical protein	--	130
DSAG12_02625	hypothetical protein	--	138
DSAG12_02626	hypothetical protein	--	135
DSAG12_02627	acetyl-CoA synthetase	K01895	125
DSAG12_02628	hypothetical protein	--	200
DSAG12_02629	hypothetical protein	--	139
DSAG12_02630	putative RecB family exonuclease	K07464	113
DSAG12_02631	hypothetical protein	--	226
DSAG12_02632	hypothetical protein	--	243
DSAG12_02633	hypothetical protein	--	184

DSAG12_02634	hypothetical protein	--	31
DSAG12_02635	hypothetical protein	--	143
DSAG12_02636	hypothetical protein	--	165
DSAG12_02637		K07052	168
DSAG12_02638	hypothetical protein	--	82
DSAG12_02639	hypothetical protein	--	0
DSAG12_02640	transposase	K07486	180
DSAG12_02641	acetyl-CoA synthetase	K01895	0
DSAG12_02642	hypothetical protein	--	88
DSAG12_02643	hypothetical protein	--	93
DSAG12_02644	hypothetical protein	--	107
DSAG12_02645	hypothetical protein	--	126
DSAG12_02646	hypothetical protein	--	65
DSAG12_02647	hypothetical protein	--	172
DSAG12_02648	hypothetical protein	--	0
DSAG12_02649	hypothetical protein	--	98
DSAG12_02650	hypothetical protein	--	107
DSAG12_02651	hypothetical protein	--	126
DSAG12_02652	hypothetical protein	--	103
DSAG12_02653	hypothetical protein	--	33
DSAG12_02654	hypothetical protein	--	227
DSAG12_02655	hypothetical protein	--	132
DSAG12_02656	hypothetical protein	--	124
DSAG12_02657	hypothetical protein	--	114
DSAG12_02658	hypothetical protein	--	184
DSAG12_02659	inner membrane protein	K07038	32
DSAG12_02660	hypothetical protein	--	148
DSAG12_02661	hypothetical protein	--	78
DSAG12_02662	hypothetical protein	--	170
DSAG12_02663	pyruvate formate lyase activating enzyme	K04069	165
DSAG12_02664	hypothetical protein	--	72
DSAG12_02665	hypothetical protein	--	170
DSAG12_02666	hypothetical protein	--	0
DSAG12_02667	hypothetical protein	--	84
DSAG12_02668	archaea-specific RecJ-like exonuclease	K07463	65
DSAG12_02669	hypothetical protein	--	189
DSAG12_02670	kynureninase	K01556	164
DSAG12_02671	hypothetical protein	--	212
DSAG12_02672	hypothetical protein	--	138
DSAG12_02673	putative protease	K08303	83
DSAG12_02674	ATP-dependent RNA helicase DeaD	K05592	92
DSAG12_02675	hypothetical protein	--	108
DSAG12_02676	hypothetical protein	--	202
DSAG12_02677	hypothetical protein	--	265
DSAG12_02678	hypothetical protein	--	155
DSAG12_02679	bifunctional UDP-N-acetylglucosamine pyrophosphorylase / Glucosamine-1-phosphate N-acetyltransferase	K04042	27
DSAG12_02680		K00100	391
DSAG12_02681	small subunit ribosomal protein S3Ae	K02984	142
DSAG12_02682	small subunit ribosomal protein S15	K02956	139
DSAG12_02683	hypothetical protein	--	150
DSAG12_02684	hypothetical protein	--	149
DSAG12_02685	hypothetical protein	--	145
DSAG12_02686	acetaminophen N-glucosyltransferase / 2-methoxy-0-polyphenyl-1,4-benzoquinone methide	K03183	181
DSAG12_02687	XTP/dITP diphosphohydrolase	K02428	143
DSAG12_02688	hypothetical protein	--	217
DSAG12_02689	hypothetical protein	--	45
DSAG12_02690	Xaa-Pro dipeptidase	K01271	123
DSAG12_02691	hypothetical protein	--	74
DSAG12_02692	hypothetical protein	--	134
DSAG12_02693	hypothetical protein	--	147
DSAG12_02694	guanidinopropionase	K18459	335
DSAG12_02695	deoxyhypusine synthase	K00809	41
DSAG12_02696		K07079	118
DSAG12_02697	hypothetical protein	--	120
DSAG12_02698	hypothetical protein	--	187
DSAG12_02699	hypothetical protein	--	144
DSAG12_02700	acetaminophen N-glucosyltransferase / 2-methoxy-0-polyphenyl-1,4-benzoquinone methide	K03183	185
DSAG12_02701	hypothetical protein	--	193
DSAG12_02702		K07052	189
DSAG12_02703	MFS transporter, DHA1 family, multidrug resistance protein	K08153	229
DSAG12_02704	hypothetical protein	--	116
DSAG12_02705	hypothetical protein	--	252
DSAG12_02706	acyl-CoA synthetase	K00142	35
DSAG12_02707	hypothetical protein	--	231
DSAG12_02708	hypothetical protein	--	122
DSAG12_02709	small subunit ribosomal protein S10	K02946	198
DSAG12_02710	hypothetical protein	--	79

DSAG12_02711	hypothetical protein	--	167
DSAG12_02712	hypothetical protein	--	217
DSAG12_02713		K07057	194
DSAG12_02714	hypothetical protein	--	161
DSAG12_02715	hypothetical protein	--	187
DSAG12_02716	tRNA-Ser		134
DSAG12_02717	inorganic phosphate transporter, PIT family	K03306	169
DSAG12_02718	hypothetical protein	--	180
DSAG12_02719	hypothetical protein	--	239
DSAG12_02720	hypothetical protein	--	205
DSAG12_02721	ribosomal-protein-alanine N-acetyltransferase	K03790	228
DSAG12_02722	hypothetical protein	--	58
DSAG12_02723	hypothetical protein	--	0
DSAG12_02724	glycine C-acetyltransferase	K00639	214
DSAG12_02725	UDP-glucose 4-epimerase	K01784	190
DSAG12_02726	hypothetical protein	--	166
DSAG12_02727	hypothetical protein	--	125
DSAG12_02728		K07018	65
DSAG12_02729	hypothetical protein	--	142
DSAG12_02730	hypothetical protein	--	212
DSAG12_02731	Xaa-Pro aminopeptidase	K01262	138
DSAG12_02732	hypothetical protein	--	170
DSAG12_02733	hypothetical protein	--	170
DSAG12_02734	hypothetical protein	--	191
DSAG12_02735	hypothetical protein	--	187
DSAG12_02736	COMPASS component SWD3	K14963	201
DSAG12_02737	spermidine synthase	K00797	217
DSAG12_02738	hypothetical protein	--	128
DSAG12_02739	hypothetical protein	--	5
DSAG12_02740	tRNA 2-thiouridine synthesizing protein A	K04085	95
DSAG12_02741	adenylylsulfate reductase, subunit B	K00395	148
DSAG12_02742	hypothetical protein	--	172
DSAG12_02743	formate dehydrogenase, beta subunit	K00125	146
DSAG12_02744	hypothetical protein	--	202
DSAG12_02745	hypothetical protein	--	170
DSAG12_02746	hypothetical protein	--	274
DSAG12_02747	hypothetical protein	--	299
DSAG12_02748	hypothetical protein	--	30
DSAG12_02749	hypothetical protein	--	128
DSAG12_02750	hypothetical protein	--	156
DSAG12_02751	hypothetical protein	--	174
DSAG12_02752	hypothetical protein	--	87
DSAG12_02753	hypothetical protein	--	147
DSAG12_02754	hypothetical protein	--	142
DSAG12_02755	hypothetical protein	--	161
DSAG12_02756	hypothetical protein	--	0
DSAG12_02757	hypothetical protein	--	241
DSAG12_02758	hypothetical protein	--	202
DSAG12_02759	hypothetical protein	--	118
DSAG12_02760	phenylglyoxylate dehydrogenase beta subunit	K18356	164
DSAG12_02761	aldehyde:ferredoxin oxidoreductase	K03738	100
DSAG12_02762	hypothetical protein	--	155
DSAG12_02763	F420-non-reducing hydrogenase iron-sulfur subunit	K14127	230
DSAG12_02764	heterodisulfide reductase subunit A	K03388	254
DSAG12_02765	heterodisulfide reductase subunit C	K03390	221
DSAG12_02766	hypothetical protein	--	129
DSAG12_02767	4Fe-4S ferredoxin	K00205	112
DSAG12_02768	hypothetical protein	--	164
DSAG12_02769	hypothetical protein	--	196
DSAG12_02770		K07052	195
DSAG12_02771	hypothetical protein	--	233
DSAG12_02772	antitoxin MazE	K07172	135
DSAG12_02773	mRNA interferase MazF	K07171	120
DSAG12_02774	16S rRNA (cytosine967-C5)-methyltransferase	K03500	164
DSAG12_02775	hypothetical protein	--	211
DSAG12_02776	hypothetical protein	--	141
DSAG12_02777	hypothetical protein	--	130
DSAG12_02778	hypothetical protein	--	195
DSAG12_02779	cysteine synthase A	K01738	147
DSAG12_02780	hypothetical protein	--	243
DSAG12_02781	hypothetical protein	--	54
DSAG12_02782	AraC family transcriptional regulator, regulatory protein of adaptative response / methylated-DNA-[protein]-cysteine methyltransferase	K10778	136
DSAG12_02783	methylated-DNA-[protein]-cysteine S-methyltransferase	K00567	233
DSAG12_02784	hypothetical protein	--	123
DSAG12_02785	hypothetical protein	--	204
DSAG12_02786	small conductance mechanosensitive channel	K03442	109
DSAG12_02787	hypothetical protein	--	231

DSAG12_02788	3-hydroxyisobutyrate dehydrogenase	K00020	318
DSAG12_02789	hypothetical protein	--	26
DSAG12_02790	hypothetical protein	--	102
DSAG12_02791	NADH oxidase	K00359	125
DSAG12_02792	hypothetical protein	--	137
DSAG12_02793	integrase/recombinase XerC	K03733	31
DSAG12_02794	hypothetical protein	--	154
DSAG12_02795	hypothetical protein	--	171
DSAG12_02796	hypothetical protein	--	136
DSAG12_02797	hypothetical protein	--	124
DSAG12_02798	dGTPase	K01129	138
DSAG12_02799	hypothetical protein	--	148
DSAG12_02800	site-specific DNA-methyltransferase (cytosine-N4-specific)	K00590	190
DSAG12_02801	hypothetical protein	--	295
DSAG12_02802	hypothetical protein	--	171
DSAG12_02803	hypothetical protein	--	146
DSAG12_02804	hypothetical protein	--	257
DSAG12_02805	hypothetical protein	--	171
DSAG12_02806	ATP-binding cassette, subfamily B, bacterial MsbA	K11085	208
DSAG12_02807	ATP-binding cassette, subfamily B, bacterial	K06147	194
DSAG12_02808	hypothetical protein	--	0
DSAG12_02809	hypothetical protein	--	186
DSAG12_02810	hypothetical protein	--	163
DSAG12_02811	proline iminopeptidase	K01259	156
DSAG12_02812	hypothetical protein	--	0
DSAG12_02813	actin beta/gamma 1	K05692	64
DSAG12_02814	Ras-related protein Rab-14	K07881	107
DSAG12_02815	hypothetical protein	--	0
DSAG12_02816	hypothetical protein	--	181
DSAG12_02817	hypothetical protein	--	192
DSAG12_02818	hypothetical protein	--	124
DSAG12_02819	MFS transporter, OFA family, oxalate/formate antiporter	K08177	0
DSAG12_02820	hypothetical protein	--	233
DSAG12_02821	hypothetical protein	--	131
DSAG12_02822	hypothetical protein	--	258
DSAG12_02823	hypothetical protein	--	106
DSAG12_02824	hypothetical protein	--	173
DSAG12_02825	hypothetical protein	--	153
DSAG12_02826	hypothetical protein	--	171
DSAG12_02827	thioredoxin reductase (NADPH)	K00384	143
DSAG12_02828	thioredoxin 1	K03671	144
DSAG12_02829	hypothetical protein	--	157
DSAG12_02830	hypothetical protein	--	173
DSAG12_02831	hypothetical protein	--	203
DSAG12_02832	hypothetical protein	--	174
DSAG12_02833	putative transcriptional regulator	K07729	211
DSAG12_02834	hypothetical protein	--	238
DSAG12_02835	ABC-2 type transport system ATP-binding protein	K01990	135
DSAG12_02836	hypothetical protein	--	133
DSAG12_02837	hypothetical protein	--	82
DSAG12_02838	hypothetical protein	--	239
DSAG12_02839	hypothetical protein	--	61
DSAG12_02840	hypothetical protein	--	122
DSAG12_02841	hypothetical protein	--	197
DSAG12_02842	hypothetical protein	--	175
DSAG12_02843	thiosulfate/3-mercaptopyruvate sulfurtransferase	K01011	189
DSAG12_02844	2-oxoglutarate ferredoxin oxidoreductase subunit delta	K00176	193
DSAG12_02845	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	K00174	7
DSAG12_02846	2-oxoglutarate ferredoxin oxidoreductase subunit beta	K00175	6
DSAG12_02847	2-oxoglutarate ferredoxin oxidoreductase subunit gamma	K00177	253
DSAG12_02848	MFS transporter, DHA1 family, tetracycline resistance protein	K08151	157
DSAG12_02849	hypothetical protein	--	217
DSAG12_02850	Ras-related protein Rab-30	K07917	185
DSAG12_02851	hypothetical protein	--	140
DSAG12_02852	hypothetical protein	--	151
DSAG12_02853	hypothetical protein	--	0
DSAG12_02854	actin-related protein 6	K11662	104
DSAG12_02855	hypothetical protein	--	176
DSAG12_02856	hypothetical protein	--	47
DSAG12_02857	archaeal cell division control protein 6	K10725	212 related)
DSAG12_02858	serine/threonine protein kinase, bacterial	K08884	202 small GTP-binding domain protein
DSAG12_02859	hypothetical protein	--	244
DSAG12_02860		K00936	121
DSAG12_02861	NAD+ synthase	K01916	191
DSAG12_02862	aspartate aminotransferase	K00812	199
DSAG12_02863	hypothetical protein	--	11
DSAG12_02864	hypothetical protein	--	179
DSAG12_02865	hypothetical protein	--	71



DSAG12_02866	hypothetical protein	--	215
DSAG12_02867	acetyltransferase	K09181	205
DSAG12_02868	hypothetical protein	--	225
DSAG12_02869	hypothetical protein	--	206
DSAG12_02870	hypothetical protein	--	10
DSAG12_02871	hypothetical protein	--	283
DSAG12_02872	hypothetical protein	--	173
DSAG12_02873	adenylosuccinate synthase	K01939	223
DSAG12_02874	energy-coupling factor transport system substrate-specific component	K16927	157
DSAG12_02875	energy-coupling factor transport system ATP-binding protein / energy-coupling factor transport system ATP-binding protein	K16786 K16	133
DSAG12_02876	energy-coupling factor transport system permease protein	K16785	208
DSAG12_02877	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	K01834	21
DSAG12_02878	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	K01834	196
DSAG12_02879	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	K01834	186
DSAG12_02880	hypothetical protein	--	158
DSAG12_02881	hypothetical protein	--	93
DSAG12_02882	histidine triad (HIT) family protein	K02503	115
DSAG12_02883		K00680	164
DSAG12_02884	hypothetical protein	--	218
DSAG12_02885	hypothetical protein	--	141
DSAG12_02886		K06930	115
DSAG12_02887	hypothetical protein	--	174
DSAG12_02888	hypothetical protein	--	72
DSAG12_02889	hypothetical protein	--	255
DSAG12_02890	hypothetical protein	--	281
DSAG12_02891	hypothetical protein	--	164
DSAG12_02892	hypothetical protein	--	194
DSAG12_02893	MFS transporter, DHA1 family, tetracycline resistance protein	K08151	138
DSAG12_02894	hypothetical protein	--	231
DSAG12_02895	fructose-bisphosphate aldolase, class II	K01624	172
DSAG12_02896	arabinose-5-phosphate isomerase	K06041	138
DSAG12_02897	dipeptidase D	K01270	132
DSAG12_02898		K07059	145
DSAG12_02899	hypothetical protein	--	0
DSAG12_02900	2-hydroxy-3-keto-5-methylthiopentyl-1-phosphate phosphatase	K08966	195
DSAG12_02901	hypothetical protein	--	55
DSAG12_02902	hypothetical protein	--	219
DSAG12_02903	hypothetical protein	--	205
DSAG12_02904	hypothetical protein	--	184
DSAG12_02905	alkyldihydroxyacetonephosphate synthase	K00803	171
DSAG12_02906	heterodisulfide reductase subunit D	K08264	188
DSAG12_02907	glycerol kinase	K00864	228
DSAG12_02908	hypothetical protein	--	125
DSAG12_02909	hypothetical protein	--	226
DSAG12_02910	hypothetical protein	--	227
DSAG12_02911	tRNA-intron endonuclease, archaea type	K01170	181
DSAG12_02912	ATPase	K06865	178
DSAG12_02913	CDP-diacylglycerol--serine O-phosphatidyltransferase	K17103	180
DSAG12_02914	glycoside/pentoside/hexuronide:cation symporter, GPH family	K03292	130
DSAG12_02915	hypothetical protein	--	141
DSAG12_02916	hypothetical protein	--	275
DSAG12_02917	hypothetical protein	--	174
DSAG12_02918	protein scribble	K16175	219
DSAG12_02919	hypothetical protein	--	161
DSAG12_02920	hypothetical protein	--	168
DSAG12_02921		K06883	100
DSAG12_02922	hypothetical protein	--	217
DSAG12_02923	2,3-diketo-5-methylthiopentyl-1-phosphate enolase	K08965	193
DSAG12_02924	hypothetical protein	--	176
DSAG12_02925	xylulokinase	K00854	199
DSAG12_02926	hypothetical protein	--	171
DSAG12_02927	glutamate-1-semialdehyde 2,1-aminomutase	K01845	165
DSAG12_02928	hypothetical protein	--	224
DSAG12_02929	hypothetical protein	--	224
DSAG12_02930	hypothetical protein	--	161
DSAG12_02931	hypothetical protein	--	195
DSAG12_02932	hypothetical protein	--	262
DSAG12_02933		K06930	405
DSAG12_02934	hypothetical protein	--	93
DSAG12_02935	protoheme IX farnesyltransferase	K02301	300
DSAG12_02936	phytol kinase	K18678	571
DSAG12_02937	isopentenyl phosphate kinase	K06981	269
DSAG12_02938	hypothetical protein	--	208
DSAG12_02939	hypothetical protein	--	97
DSAG12_02940	hypothetical protein	--	0
DSAG12_02941	hypothetical protein	--	247
DSAG12_02942	hypothetical protein	--	194

DSAG12_02943	hypothetical protein	--	196
DSAG12_02944	hypothetical protein	--	146
DSAG12_02945	hypothetical protein	--	173
DSAG12_02946	hypothetical protein	--	155
DSAG12_02947	UDP-glucose 4-epimerase	K01784	97
DSAG12_02948	hypothetical protein	--	51
DSAG12_02949		K00936	150
DSAG12_02950	hypothetical protein	K07502	64
DSAG12_02951	hypothetical protein	--	247
DSAG12_02952	putative RecB family exonuclease	K07464	241
DSAG12_02953	hypothetical protein	--	205
DSAG12_02954	hypothetical protein	--	127
DSAG12_02955	hypothetical protein	--	81
DSAG12_02956		K07076	181
DSAG12_02957		K07076	170
DSAG12_02958	hypothetical protein	--	209
DSAG12_02959	hypothetical protein	--	170
DSAG12_02960	2-(1,2-epoxy-1,2-dihydrophenyl)acetyl-CoA isomerase	K15866	211
DSAG12_02961	hypothetical protein	--	117
DSAG12_02962	hypothetical protein	--	172
DSAG12_02963	hypothetical protein	--	153
DSAG12_02964	hypothetical protein	--	241
DSAG12_02965	DNA (cytosine-5)-methyltransferase 1	K00558	0
DSAG12_02966	A/G-specific adenine glycosylase	K03575	235
DSAG12_02967	hypothetical protein	--	181
DSAG12_02968		K06915	197
DSAG12_02969	exonuclease SbcC	K03546	65
DSAG12_02970	hypothetical protein	--	276
DSAG12_02971		K00936	64
DSAG12_02972	hypothetical protein	--	240
DSAG12_02973	hypothetical protein	--	183
DSAG12_02974	hypothetical protein	--	264
DSAG12_02975	hypothetical protein	--	175
DSAG12_02976	hypothetical protein	--	170
DSAG12_02977	hypothetical protein	--	178
DSAG12_02978	hypothetical protein	--	356
DSAG12_02979	COMPASS component SWD3	K14963	221
DSAG12_02980	E3 ubiquitin-protein ligase TRAF7	K10646	117
DSAG12_02981	hypothetical protein	--	209
DSAG12_02982	transcription initiation factor TRIID TATA-box-binding protein	K03120	153
DSAG12_02983	hypothetical protein	--	170
DSAG12_02984	hypothetical protein	--	201
DSAG12_02985		K07065	205
DSAG12_02986	hypothetical protein	--	172
DSAG12_02987	hypothetical protein	--	182
DSAG12_02988	hypothetical protein	--	200
DSAG12_02989	hypothetical protein	--	244
DSAG12_02990	hypothetical protein	--	132
DSAG12_02991	hypothetical protein	--	217
DSAG12_02992	hypothetical protein	--	178
DSAG12_02993	hypothetical protein	--	204
DSAG12_02994	tryptophan synthase beta chain	K01696	246
DSAG12_02995	hypothetical protein	--	16
DSAG12_02996	hypothetical protein	--	0
DSAG12_02997	hypothetical protein	--	0
DSAG12_02998	hypothetical protein	--	238
DSAG12_02999	A/G-specific adenine glycosylase	K03575	176
DSAG12_03000	hypothetical protein	--	188
DSAG12_03001	hypothetical protein	--	218
DSAG12_03002	ribosomal-protein-alanine N-acetyltransferase	K03790	59
DSAG12_03003	tripeptide aminopeptidase	K01258	164
DSAG12_03004	hypothetical protein	--	216
DSAG12_03005	hypothetical protein	--	209
DSAG12_03006	ABC-2 type transport system ATP-binding protein	K01990	131
DSAG12_03007	hypothetical protein	--	11
DSAG12_03008	hypothetical protein	--	15
DSAG12_03009	hypothetical protein	--	214
DSAG12_03010	hypothetical protein	--	8
DSAG12_03011	hypothetical protein	--	5
DSAG12_03012	MFS transporter, AAHS family, benzoate transport protein	K05548	9
DSAG12_03013	heterodisulfide reductase subunit D	K08264	6
DSAG12_03014	hypothetical protein	--	12
DSAG12_03015	hypothetical protein	--	4
DSAG12_03016	Ras-related protein Rab-7L1	K07916	7
DSAG12_03017	hypothetical protein	--	5
DSAG12_03018	hypothetical protein	--	0
DSAG12_03019	hypothetical protein	--	2

hypothetical proteins with gelsolin-like domain

DSAG12_03020	hypothetical protein	--	4
DSAG12_03021	hypothetical protein	--	8
DSAG12_03022	methylated-DNA-protein-cysteine methyltransferase related protein	K07443	7
DSAG12_03023	butyryl-CoA dehydrogenase	K00248	299
DSAG12_03024	tryptophanase	K01667	9
DSAG12_03025	hypothetical protein	--	68
DSAG12_03026	hypothetical protein	--	108
DSAG12_03027	myo-inositol-1-phosphate synthase	K01858	192
DSAG12_03028	hypothetical protein	--	262
DSAG12_03029	hypothetical protein	--	245
DSAG12_03030	hypothetical protein	--	205
DSAG12_03031	phosphomannomutase	K01840	160
DSAG12_03032	hypothetical protein	--	269
DSAG12_03033	hypothetical protein	--	52
DSAG12_03034	peptide/nickel transport system permease protein	K02034	83
DSAG12_03035	peptide/nickel transport system permease protein	K02033	119
DSAG12_03036	hypothetical protein	--	251
DSAG12_03037	oligopeptide transport system substrate-binding protein	K15580	197
DSAG12_03038	hypothetical protein	--	225
DSAG12_03039	hypothetical protein	--	209
DSAG12_03040	hypothetical protein	--	253
DSAG12_03041	hypothetical protein	--	81
DSAG12_03042	oligopeptide transport system ATP-binding protein	K15583	123
DSAG12_03043	peptide/nickel transport system ATP-binding protein / peptide/nickel transport system ATP-binding protein	K02031 K02	107
DSAG12_03044	hypothetical protein	--	0
DSAG12_03045	hypothetical protein	--	256
DSAG12_03046	quinolinate synthase	K03517	115
DSAG12_03047	thioredoxin reductase (NADPH)	K00384	65
DSAG12_03048	formate C-acetyltransferase	K00656	177
DSAG12_03049	pyruvate formate lyase activating enzyme	K04069	232
DSAG12_03050	hypothetical protein	--	193
DSAG12_03051	hypothetical protein	K01163	108
DSAG12_03052	hypothetical protein	--	155
DSAG12_03053	K(+)-stimulated pyrophosphate-energized sodium pump	K15987	184
DSAG12_03054	hypothetical protein	--	223
DSAG12_03055	hypothetical protein	--	73
DSAG12_03056	ABC-2 type transport system ATP-binding protein	K01990	160
DSAG12_03057	hypothetical protein	--	175
DSAG12_03058	hypothetical protein	--	209
DSAG12_03059	hypothetical protein	--	22
DSAG12_03060	hypothetical protein	--	118
DSAG12_03061	hypothetical protein	--	134
DSAG12_03062	8-amino-7-oxononanoate synthase	K00652	436
DSAG12_03063	hypothetical protein	--	231
DSAG12_03064	hypothetical protein	--	250
DSAG12_03065	hypothetical protein	--	203
DSAG12_03066		K06944	42
DSAG12_03067	hypothetical protein	--	117 small GTP-binding domain protein
DSAG12_03068	hypothetical protein	--	0
DSAG12_03069	hypothetical protein	--	0
DSAG12_03070	hypothetical protein	--	228
DSAG12_03071	hypothetical protein	--	177
DSAG12_03072	hypothetical protein	--	41
DSAG12_03073	hypothetical protein	--	66
DSAG12_03074	hypothetical protein	--	100
DSAG12_03075	hypothetical protein	--	275
DSAG12_03076	hypothetical protein	--	223
DSAG12_03077	probable phosphoglycerate mutase	K15634	178
DSAG12_03078	hypothetical protein	--	114
DSAG12_03079	tRNA-Ala		211
DSAG12_03080	NADPH2:quinone reductase	K00344	176
DSAG12_03081	hypothetical protein	--	132
DSAG12_03082	hypothetical protein	--	184 small GTP-binding domain protein
DSAG12_03083	hypothetical protein	--	198
DSAG12_03084	hypothetical protein	--	142
DSAG12_03085	hypothetical protein	--	4
DSAG12_03086	hypothetical protein	--	319
DSAG12_03087	hypothetical protein	--	266
DSAG12_03088	tRNA-dihydrouridine synthase B	K05540	148
DSAG12_03089	hypothetical protein	--	4647
DSAG12_03090	hypothetical protein	--	160
DSAG12_03091	hypothetical protein	--	270
DSAG12_03092	hypothetical protein	--	135
DSAG12_03093	hypothetical protein	--	215
DSAG12_03094	hypothetical protein	--	252
DSAG12_03095	hypothetical protein	--	362
DSAG12_03096	putative adenine-specific DNA-methyltransferase	K07319	120

DSAG12_03097	hypothetical protein	--	205
DSAG12_03098	putative adenine-specific DNA-methyltransferase	K07319	0
DSAG12_03099	hypothetical protein	--	224
DSAG12_03100	1-acyl-sn-glycerol-3-phosphate acyltransferase	K00655	224
DSAG12_03101	hypothetical protein	--	228
DSAG12_03102	hypothetical protein	--	158
DSAG12_03103		K07052	1002
DSAG12_03104	hypothetical protein	--	224
DSAG12_03105	hypothetical protein	--	0
DSAG12_03106	actin-related protein 2	K17260	195
DSAG12_03107	hypothetical protein	--	408
DSAG12_03108	hypothetical protein	--	143
DSAG12_03109	hypothetical protein	--	138
DSAG12_03110	hypothetical protein	--	197
DSAG12_03111	hypothetical protein	--	165
DSAG12_03112	hypothetical protein	--	121
DSAG12_03113	hypothetical protein	--	109
DSAG12_03114	diacylglycerol kinase (ATP)	K07029	167
DSAG12_03115	hypothetical protein	--	206
DSAG12_03116	hypothetical protein	--	265
DSAG12_03117	hypothetical protein	--	176
DSAG12_03118	DNA-3-methyladenine glycosylase I	K01246	193
DSAG12_03119	undecaprenyl-diphosphatase	K06153	197
DSAG12_03120	alcohol dehydrogenase, propanol-preferring	K13953	0
DSAG12_03121	hypothetical protein	--	203
DSAG12_03122	cold shock protein (beta-ribbon, CspA family)	K03704	160
DSAG12_03123	hypothetical protein	--	170
DSAG12_03124	hypothetical protein	--	0
DSAG12_03125	hypothetical protein	--	202
DSAG12_03126	hypothetical protein	--	188
DSAG12_03127	peroxiredoxin Q/BCP	K03564	191
DSAG12_03128	transcription initiation factor TFIIB	K03124	284
DSAG12_03129	hypothetical protein	--	163
DSAG12_03130	hypothetical protein	--	183
DSAG12_03131	hypothetical protein	--	217
DSAG12_03132	hypothetical protein	--	149
DSAG12_03133	exonuclease SbcC	K03546	197
DSAG12_03134	hypothetical protein	--	0
DSAG12_03135	hypothetical protein	--	180
DSAG12_03136	hypothetical protein	--	120
DSAG12_03137	hypothetical protein	--	0
DSAG12_03138	hypothetical protein	--	209
DSAG12_03139	hypothetical protein	--	139
DSAG12_03140	hypothetical protein	--	229
DSAG12_03141	hypothetical protein	--	135
DSAG12_03142	hypothetical protein	--	184
DSAG12_03143	ribonuclease P protein subunit RPR2	K03540	209
DSAG12_03144	rRNA small subunit pseudouridine methyltransferase Nep1	K14568	188
DSAG12_03145	hypothetical protein	--	156
DSAG12_03146	hypothetical protein	--	197
DSAG12_03147	hypothetical protein	--	209
DSAG12_03148	hypothetical protein	--	238
DSAG12_03149	hypothetical protein	--	186
DSAG12_03150	nitric oxide reductase NorQ protein	K04748	225
DSAG12_03151	ABC-2 type transport system ATP-binding protein	K01990	194
DSAG12_03152	ABC-2 type transport system permease protein	K01992	54
DSAG12_03153	hypothetical protein	--	9
DSAG12_03154	hypothetical protein	--	0
DSAG12_03155	hypothetical protein	--	182
DSAG12_03156	hypothetical protein	--	159
DSAG12_03157	hypothetical protein	--	257
DSAG12_03158	tRNA-Gly		0
DSAG12_03159	glycoside/pentose/hexuronide:cation symporter, GPH family	K03292	297
DSAG12_03160	hypothetical protein	--	40
DSAG12_03161	heterodisulfide reductase subunit C	K03390	52
DSAG12_03162		K05912	171
DSAG12_03163	heterodisulfide reductase subunit A	K03388	201
DSAG12_03164	anaerobic sulfite reductase subunit A	K16950	162
DSAG12_03165	sulfhydrogenase subunit gamma (sulfur reductase)	K17995	119
DSAG12_03166	hypothetical protein	--	186
DSAG12_03167	hypothetical protein	--	190
DSAG12_03168	hypothetical protein	--	124
DSAG12_03169	hypothetical protein	--	182
DSAG12_03170	hypothetical protein	--	225
DSAG12_03171	tRNA-Phe		169
DSAG12_03172	isovaleryl-CoA dehydrogenase	K00253	205
DSAG12_03173	hypothetical protein	--	227
DSAG12_03174	hypothetical protein	--	101

DSAG12_03175	MFS transporter, DHA3 family, macrolide efflux protein	K08217	213
DSAG12_03176	hypothetical protein	--	151
DSAG12_03177	hypothetical protein	--	157
DSAG12_03178	bifunctional enzyme Fae/Hps	K13812	214
DSAG12_03179	hypothetical protein	--	195
DSAG12_03180	hypothetical protein	--	62
DSAG12_03181	fanconi anemia group M protein	K10896	171
DSAG12_03182	fanconi anemia group M protein	K10896	265
DSAG12_03183	8-oxo-dGTP diphosphatase	K03574	1044
DSAG12_03184	hypothetical protein	--	180
DSAG12_03185	hypothetical protein	--	150
DSAG12_03186	5'-nucleotidase	K01081	186
DSAG12_03187	5'-nucleotidase	K01081	197
DSAG12_03188	methylenetetrahydrofolate dehydrogenase (NADPH) / methylenetetrahydrofolate oxidase	K01491	178
DSAG12_03189	amidophosphoribosyltransferase	K00764	191
DSAG12_03190	hypothetical protein	K09126	157
DSAG12_03191	chloride channel protein, ClC family	K03281	137
DSAG12_03192	hypothetical protein	--	109
DSAG12_03193	hypothetical protein	--	187
DSAG12_03194	hypothetical protein	--	151
DSAG12_03195	hypothetical protein	--	148
DSAG12_03196	butyryl-CoA dehydrogenase	K00248	229
DSAG12_03197	glycolate oxidase	K00104	206
DSAG12_03198	hypothetical protein	--	189
DSAG12_03199	excinuclease ABC subunit B	K03702	133
DSAG12_03200	excinuclease ABC subunit A	K03701	149
DSAG12_03201	hypothetical protein	--	147
DSAG12_03202	hypothetical protein	--	141
DSAG12_03203	3'-5' exonuclease	K03698	271
DSAG12_03204	hypothetical protein	--	188
DSAG12_03205	hypothetical protein	--	5
DSAG12_03206	hypothetical protein	--	9
DSAG12_03207	3-oxo-5-alpha-steroid 4-dehydrogenase 1	K12343	5
DSAG12_03208	hypothetical protein	--	222
DSAG12_03209	long-chain acyl-CoA synthetase	K01897	196
DSAG12_03210	hypothetical protein	--	172
DSAG12_03211	hypothetical protein	K01362	92
DSAG12_03212	hypothetical protein	--	198
DSAG12_03213	hypothetical protein	--	171
DSAG12_03214	hypothetical protein	K06940	0
DSAG12_03215	cysteinyl-tRNA synthetase	K01883	219
DSAG12_03216	hypothetical protein	--	233
DSAG12_03217	tRNA nucleotidyltransferase (CCA-adding enzyme)	K07558	227
DSAG12_03218	hypothetical protein	--	214
DSAG12_03219	elongation factor 2	K03234	273
DSAG12_03220	hypothetical protein	--	174
DSAG12_03221	hypothetical protein	--	228
DSAG12_03222	hypothetical protein	K06936	213
DSAG12_03223	archaeosine synthase	K07557	334
DSAG12_03224	hypothetical protein	--	230
DSAG12_03225	arsenite-transporting ATPase	K01551	181
DSAG12_03226	ATP-dependent Clp protease ATP-binding subunit ClpB	K03695	195
DSAG12_03227	hypothetical protein	--	0
DSAG12_03228	putative copper resistance protein D	K07245	0
DSAG12_03229	DNA primase	K02316	277
DSAG12_03230	hypothetical protein	--	0
DSAG12_03231	fused signal recognition particle receptor	K03110	290
DSAG12_03232	prefoldin alpha subunit	K04797	196
DSAG12_03233	large subunit ribosomal protein LX	K02944	213
DSAG12_03234	translation initiation factor 6	K03264	150
DSAG12_03235	hypothetical protein	--	434
DSAG12_03236	programmed cell death protein 5	K06875	536
DSAG12_03237	small subunit ribosomal protein S19e	K02966	193
DSAG12_03238	methionyl-tRNA synthetase	K01874	130
DSAG12_03239	diacylglycerol kinase (ATP)	K07029	0
DSAG12_03240	hypothetical protein	--	194
DSAG12_03241	hypothetical protein	--	141
DSAG12_03242	hypothetical protein	--	124
DSAG12_03243	macrolide transport system ATP-binding/permease protein	K05685	201
DSAG12_03244	hypothetical protein	--	300
DSAG12_03245	archaea-specific helicase	K03725	179
DSAG12_03246	glycoside/pentoside/hexuronide:cation symporter, GPH family	K03292	116
DSAG12_03247	hypothetical protein	--	165
DSAG12_03248	hypothetical protein	--	212
DSAG12_03249	hypothetical protein	--	159
DSAG12_03250	hypothetical protein	--	220
DSAG12_03251	hypothetical protein	--	194
DSAG12_03252	hypothetical protein	--	157

DSAG12_03253	MarR family transcriptional regulator, transcriptional regulator for hemolysin	K06075	147
DSAG12_03254	MFS transporter, DHA3 family, macrolide efflux protein	K08217	225
DSAG12_03255		K00358	355
DSAG12_03256	dihydrolypoamide dehydrogenase	K00382	191
DSAG12_03257	hypothetical protein	--	104
DSAG12_03258	maltose/moltooligosaccharide transporter	K16211	244
DSAG12_03259	hypothetical protein	--	238
DSAG12_03260	hypothetical protein	--	24
DSAG12_03261	3-oxoacyl-[acyl-carrier protein] reductase	K00059	242
DSAG12_03262	hypothetical protein	--	201
DSAG12_03263	hypothetical protein	--	159
DSAG12_03264	hypothetical protein	--	210
DSAG12_03265	2-dehydro-3-deoxyphosphogluconate aldolase / (4S)-4-hydroxy-2-oxoglutarate aldolase	K01625	183
DSAG12_03266	2-dehydro-3-deoxygluconokinase	K00874	218
DSAG12_03267	hypothetical protein	--	186
DSAG12_03268	hypothetical protein	--	232
DSAG12_03269	hypothetical protein	--	192
DSAG12_03270	NADH-quinone oxidoreductase subunit E	K00334	180
DSAG12_03271	NADH-quinone oxidoreductase subunit F	K00335	171
DSAG12_03272	formate dehydrogenase major subunit	K00123	277
DSAG12_03273	hypothetical protein	--	120
DSAG12_03274	energy-coupling factor transport system ATP-binding protein	K16786	256
DSAG12_03275	energy-coupling factor transport system permease protein	K16785	166
DSAG12_03276	hypothetical protein	--	179
DSAG12_03277	hypothetical protein	--	226
DSAG12_03278	ribonuclease Z	K00784	268
DSAG12_03279	hypothetical protein	--	203
DSAG12_03280	hypothetical protein	--	165
DSAG12_03281	serine/threonine-protein phosphatase 5	K04460	232
DSAG12_03282		K07022	232
DSAG12_03283	hypothetical protein	--	85
DSAG12_03284	zinc transporter, ZIP family	K07238	200
DSAG12_03285	alpha-mannosidase	K01191	389
DSAG12_03286	hypothetical protein	--	144
DSAG12_03287	hypothetical protein	--	134
DSAG12_03288	serine/threonine-protein phosphatase 5	K04460	251
DSAG12_03289	indolepyruvate ferredoxin oxidoreductase, beta subunit	K00180	75
DSAG12_03290	indolepyruvate ferredoxin oxidoreductase, alpha subunit	K00179	178
DSAG12_03291	cytochrome c-type biogenesis protein	K06196	142
DSAG12_03292	hypothetical protein	--	66
DSAG12_03293	hypothetical protein	--	220
DSAG12_03294	hypothetical protein	--	158
DSAG12_03295	pimeloyl-[acyl-carrier protein] methyl ester esterase	K02170	159
DSAG12_03296	hypothetical protein	--	86
DSAG12_03297	hypothetical protein	--	128
DSAG12_03298	pimeloyl-[acyl-carrier protein] methyl ester esterase	K02170	0
DSAG12_03299	alpha-N-acetylglucosaminidase	K01205	240
DSAG12_03300	molybdopterin synthase sulfur carrier subunit	K03636	259
DSAG12_03301	hypothetical protein	--	21
DSAG12_03302	all-trans-retinol 13,14-reductase	K09516	87
DSAG12_03303	hypothetical protein	--	215
DSAG12_03304	hypothetical protein	--	215
DSAG12_03305	hypothetical protein	--	192
DSAG12_03306	hypothetical protein	--	185
DSAG12_03307	hypothetical protein	--	168
DSAG12_03308	hypothetical protein	--	122
DSAG12_03309	hypothetical protein	--	0
DSAG12_03310	hypothetical protein	--	111
DSAG12_03311	hypothetical protein	--	116
DSAG12_03312	hypothetical protein	--	193
DSAG12_03313	tRNA-Arg	Intron(37429	158
DSAG12_03314	acetaminophen:quinone methyltransferase / 2-methoxy-6-polypropenyl-1,4-benzoquinol	K03183	151
DSAG12_03315	hypothetical protein	--	248
DSAG12_03316	hypothetical protein	--	145
DSAG12_03317	translation initiation factor 5B	K03243	244
DSAG12_03318	hypothetical protein	--	153
DSAG12_03319	hypothetical protein	--	216
DSAG12_03320	small subunit ribosomal protein S6e	K02991	235
DSAG12_03321	hypothetical protein	--	209
DSAG12_03322	hypothetical protein	--	174
DSAG12_03323	hypothetical protein	--	198
DSAG12_03324	small subunit ribosomal protein S28e	K02979	144
DSAG12_03325	large subunit ribosomal protein L7Ae	K02936	231
DSAG12_03326	hypothetical protein	--	197
DSAG12_03327	hypothetical protein	--	215
DSAG12_03328	tRNA-His	Intron(3759C	266
DSAG12_03329	hypothetical protein	--	209
DSAG12_03330	hypothetical protein	--	109

DSAG12_03331	hypothetical protein	--	166
DSAG12_03332	hypothetical protein	--	231
DSAG12_03333	hypothetical protein	--	212
DSAG12_03334	histidyl-tRNA synthetase	K01892	175
DSAG12_03335	hypothetical protein	--	176
DSAG12_03336	hypothetical protein	--	149
DSAG12_03337	cold shock protein (beta-ribbon, CspA family)	K03704	146
DSAG12_03338		K01112	54
DSAG12_03339	bilin biosynthesis protein	K05384	230
DSAG12_03340	bifunctional tRNA threonylcarbamoyladenosine biosynthesis protein	K15904	53
DSAG12_03341	small subunit ribosomal protein S27Ae	K02977	207
DSAG12_03342	small subunit ribosomal protein S24e	K02974	156
DSAG12_03343	hypothetical protein	K09735	187
DSAG12_03344	hypothetical protein	--	185
DSAG12_03345	hypothetical protein	--	201
DSAG12_03346	hypothetical protein	--	225
DSAG12_03347	hypothetical protein	--	172
DSAG12_03348	enterochelin esterase and related enzymes	K07214	50
DSAG12_03349	DNA-directed RNA polymerase subunit E'	K03049	203
DSAG12_03350	hypothetical protein	--	213
DSAG12_03351	medium-chain acyl-[acyl-carrier-protein] hydrolase	K01071	245
DSAG12_03352	hypothetical protein	--	178
DSAG12_03353	hypothetical protein	--	221
DSAG12_03354	hypothetical protein	--	102
DSAG12_03355	hypothetical protein	--	204
DSAG12_03356	hypothetical protein	--	160
DSAG12_03357	hypothetical protein	--	36
DSAG12_03358	3-oxoacyl-[acyl-carrier protein] reductase	K00059	182
DSAG12_03359	3-oxoacyl-[acyl-carrier protein] reductase	K00059	188
DSAG12_03360	hypothetical protein	--	55
DSAG12_03361	glycerophosphoinositol inositolphosphodiesterase	K01124	246
DSAG12_03362	3-oxoacyl-[acyl-carrier protein] reductase	K00059	195
DSAG12_03363	3-oxoacyl-[acyl-carrier protein] reductase	K00059	139
DSAG12_03364	hypothetical protein	--	168
DSAG12_03365		K00540	47
DSAG12_03366		K07095	173
DSAG12_03367	hypothetical protein	--	178
DSAG12_03368	hypothetical protein	--	122
DSAG12_03369	hypothetical protein	--	161
DSAG12_03370	LL-diaminopimelate aminotransferase	K10206	151
DSAG12_03371	electron transfer flavoprotein alpha subunit	K03522	140
DSAG12_03372	electron transfer flavoprotein beta subunit	K03521	182
DSAG12_03373	hypothetical protein	--	159
DSAG12_03374	acyl-CoA dehydrogenase	K00249	192
DSAG12_03375	ATP-binding protein involved in chromosome partitioning	K03593	261
DSAG12_03376		K01529	239
DSAG12_03377		K07076	144
DSAG12_03378	hypothetical protein	--	86
DSAG12_03379	indolepyruvate ferredoxin oxidoreductase, alpha subunit	K00179	233
DSAG12_03380	indolepyruvate ferredoxin oxidoreductase, beta subunit	K00180	0
DSAG12_03381	Lrp/AsnC family transcriptional regulator, regulator for asnA, asnC and gidA	K03718	192
DSAG12_03382		K07076	125
DSAG12_03383	hypothetical protein	--	227
DSAG12_03384	hypothetical protein	--	107
DSAG12_03385	hypothetical protein	--	184
DSAG12_03386	hypothetical protein	--	165
DSAG12_03387	anaerobic nitric oxide reductase flavorubredoxin	K12264	187
DSAG12_03388	phosphoglycolate phosphatase	K01091	107
DSAG12_03389	hypothetical protein	--	151
DSAG12_03390	heterodisulfide reductase subunit D	K08264	186
DSAG12_03391	hypothetical protein	--	160
DSAG12_03392	hypothetical protein	--	205
DSAG12_03393	phosphoglycolate phosphatase	K01091	231
DSAG12_03394	hypothetical protein	--	181
DSAG12_03395	hypothetical protein	--	182
DSAG12_03396	hypothetical protein	--	103
DSAG12_03397	adenine-specific DNA-methyltransferase	K07317	211
DSAG12_03398	hypothetical protein	--	251
DSAG12_03399	hypothetical protein	--	221
DSAG12_03400	hypothetical protein	--	164
DSAG12_03401	digeranylgeranyl glycerophospholipid reductase	K17830	169
DSAG12_03402	hypothetical protein	--	181
DSAG12_03403	superkiller protein 3	K12600	88
DSAG12_03404	hypothetical protein	--	257
DSAG12_03405	thioredoxin 1	K03671	151
DSAG12_03406	oligopeptide transport system ATP-binding protein	K10823	189
DSAG12_03407	peptide/nickel transport system ATP-binding protein	K02031	181
DSAG12_03408	oligopeptide transport system permease protein	K15582	194

DSAG12_03409	peptide/nickel transport system permease protein	K02033	0
DSAG12_03410	hypothetical protein	--	143
DSAG12_03411	peptide/nickel transport system substrate-binding protein	K02035	106
DSAG12_03412	hypothetical protein	--	249
DSAG12_03413	hypothetical protein	--	208
DSAG12_03414	hypothetical protein	--	0
DSAG12_03415	26S proteasome regulatory subunit N11	K03030	113
DSAG12_03416	hypothetical protein	--	323
DSAG12_03417	transcription initiation factor TFIIB	K03124	216
DSAG12_03418	hypothetical protein	--	214
DSAG12_03419	hypothetical protein	--	243
DSAG12_03420	internalin A	K13730	437
DSAG12_03421		K07131	178
DSAG12_03422	hypothetical protein	--	201
DSAG12_03423	hypothetical protein	--	283
DSAG12_03424	lysophospholipase	K01048	572
DSAG12_03425	hypothetical protein	--	2408
DSAG12_03426	ribonuclease Z	K00784	218
DSAG12_03427	hypothetical protein	--	165
DSAG12_03428	hypothetical protein	--	179
DSAG12_03429	hypothetical protein	--	183
DSAG12_03430	ribosomal-protein-alanine N-acetyltransferase	K03790	145
DSAG12_03431	hypothetical protein	--	209
DSAG12_03432	glutamine synthetase	K01915	292
DSAG12_03433	hypothetical protein	--	226
DSAG12_03434	CTP synthase	K01937	172
DSAG12_03435	magnesium chelatase subunit D	K03404	366
DSAG12_03436	hypothetical protein	--	98
DSAG12_03437	hypothetical protein	--	209
DSAG12_03438	hypothetical protein	--	150
DSAG12_03439	hypothetical protein	--	131
DSAG12_03440	L-ribulose-5-phosphate 4-epimerase	K01786	258
DSAG12_03441	segregation and condensation protein B	K06024	200
DSAG12_03442	acylglycerol lipase	K01054	156
DSAG12_03443		K01453	81
DSAG12_03444	hypothetical protein	--	11
DSAG12_03445	chromosome segregation protein	K03529	188
DSAG12_03446	hypothetical protein	--	126
DSAG12_03447		K07024	0
DSAG12_03448	Trp repressor binding protein	K03809	313
DSAG12_03449	chorismate synthase	K01736	215
DSAG12_03450	ribose 1,5-bisphosphokinase	K05774	159
DSAG12_03451	hypothetical protein	--	218
DSAG12_03452	hypothetical protein	--	207
DSAG12_03453	hypothetical protein	--	119
DSAG12_03454	hypothetical protein	--	134
DSAG12_03455	hypothetical protein	--	180
DSAG12_03456	peptide/nickel transport system substrate-binding protein	K02035	55
DSAG12_03457	molecular chaperone DnaK	K04043	159
DSAG12_03458	molecular chaperone DnaJ	K03686	139
DSAG12_03459	hypothetical protein	--	163
DSAG12_03460	hypothetical protein	--	236
DSAG12_03461	tRNA-Gly		220
DSAG12_03462	glycerophosphoryl diester phosphodiesterase	K01126	180
DSAG12_03463	uncharacterized protein	K06950	232
DSAG12_03464	hypothetical protein	--	185
DSAG12_03465	Rab family, other	K07976	164
DSAG12_03466	ribonuclease J	K12574	175
DSAG12_03467	transcription initiation factor TFIID TATA-box-binding protein	K03120	127
DSAG12_03468	hypothetical protein	--	214
DSAG12_03469	ribosomal-protein-alanine N-acetyltransferase	K03790	190
DSAG12_03470	phosphatidylserine decarboxylase	K01613	226
DSAG12_03471	hypothetical protein	--	210
DSAG12_03472	hypothetical protein	--	104
DSAG12_03473	hypothetical protein	--	570
DSAG12_03474	hypothetical protein	--	133
DSAG12_03475	hypothetical protein	--	90
DSAG12_03476	hydrogenase expression/formation protein HypE	K04655	248
DSAG12_03477	esterase / lipase	K01066	213
DSAG12_03478	fumarate hydratase, class I	K01676	199
DSAG12_03479	fumarate hydratase subunit alpha	K01677	183
DSAG12_03480	hypothetical protein	--	231
DSAG12_03481	molybdopterin-guanine dinucleotide biosynthesis protein B	K03753	25
DSAG12_03482	hypothetical protein	--	157
DSAG12_03483	hypothetical protein	--	167
DSAG12_03484	hypothetical protein	--	49
DSAG12_03485	hypothetical protein	--	161
DSAG12_03486	hypothetical protein	--	178



DSAG12_03487	hypothetical protein	--	171
DSAG12_03488	putative transposase	K07491	173
DSAG12_03489	hypothetical protein	--	16
DSAG12_03490	hypothetical protein	--	177
DSAG12_03491	hypothetical protein	--	121
DSAG12_03492	hypothetical protein	--	157
DSAG12_03493	hypothetical protein	--	191
DSAG12_03494	hypothetical protein	--	205
DSAG12_03495	hypothetical protein	--	173
DSAG12_03496	hypothetical protein	--	217
DSAG12_03497		K07102	232
DSAG12_03498	hypothetical protein	--	189
DSAG12_03499	hypothetical protein	--	150
DSAG12_03500	hypothetical protein	--	218
DSAG12_03501	fanconi anemia group M protein	K10896	198
DSAG12_03502	hypothetical protein	--	187
DSAG12_03503	hypothetical protein	--	156
DSAG12_03504	hypothetical protein	--	148
DSAG12_03505	hypothetical protein	--	218
DSAG12_03506	hypothetical protein	--	179
DSAG12_03507	fanconi anemia group M protein	K10896	213
DSAG12_03508	hypothetical protein	--	184
DSAG12_03509	hypothetical protein	--	178
DSAG12_03510	hypothetical protein	--	135
DSAG12_03511	hypothetical protein	--	214
DSAG12_03512	hypothetical protein	--	180
DSAG12_03513	hypothetical protein	--	180
DSAG12_03514	hypothetical protein	--	183
DSAG12_03515	hypothetical protein	--	75
DSAG12_03516		K06883	146
DSAG12_03517	hypothetical protein	--	169
DSAG12_03518	hypothetical protein	--	244
DSAG12_03519	hypothetical protein	--	641
DSAG12_03520	hypothetical protein	--	341
DSAG12_03521	hypothetical protein	--	111
DSAG12_03522	hypothetical protein	--	196
DSAG12_03523	hypothetical protein	--	0
DSAG12_03524	hypothetical protein	--	183
DSAG12_03525	leucine-rich repeat kinase 2	K08844	204
DSAG12_03526	flap endonuclease-1	K04799	212
DSAG12_03527	hypothetical protein	--	162
DSAG12_03528	hypothetical protein	--	203
DSAG12_03529	hypothetical protein	--	275
DSAG12_03530	DNA repair protein RadA	K04483	159
DSAG12_03531	hypothetical protein	--	150
DSAG12_03532	hypothetical protein	--	207
DSAG12_03533	hypothetical protein	--	166
DSAG12_03534	hypothetical protein	--	131
DSAG12_03535	hypothetical protein	--	148
DSAG12_03536	hypothetical protein	--	213
DSAG12_03537	hypothetical protein	--	196
DSAG12_03538	helicase	K03726	193
DSAG12_03539	hypothetical protein	--	203
DSAG12_03540	hypothetical protein	--	210
DSAG12_03541	hypothetical protein	--	217
DSAG12_03542	hypothetical protein	--	148
DSAG12_03543	helicase	K03726	117
DSAG12_03544	hypothetical protein	--	213
DSAG12_03545	hypothetical protein	--	0
DSAG12_03546	fanconi anemia group M protein	K10896	0
DSAG12_03547	hypothetical protein	--	0
DSAG12_03548	hypothetical protein	--	0
DSAG12_03549	hypothetical protein	--	0
DSAG12_03550	mTERF domain-containing protein, mitochondrial	K15032	0
DSAG12_03551	hypothetical protein	--	0
DSAG12_03552	hypothetical protein	--	0
DSAG12_03553	hypothetical protein	--	0
DSAG12_03554	hypothetical protein	--	0
DSAG12_03555	hypothetical protein	--	0
DSAG12_03556	hypothetical protein	--	0
DSAG12_03557	hypothetical protein	--	0
DSAG12_03558	hypothetical protein	--	0
DSAG12_03559	hypothetical protein	--	0
DSAG12_03560	small subunit ribosomal protein S26e	K02976	0
DSAG12_03561	archaeitylinositol phosphate synthase	K17884	0
DSAG12_03562	hypothetical protein	--	0
DSAG12_03563	hypothetical protein	--	0
DSAG12_03564	hypothetical protein	--	0

DSAG12_03565	hypothetical protein	--	0
DSAG12_03566	hypothetical protein	--	0
DSAG12_03567	transcription initiation factor TFIIB	K03124	0
DSAG12_03568	RNA-binding protein	K07569	0
DSAG12_03569	GTP-binding protein	K03978	0
DSAG12_03570	hypothetical protein	--	0
DSAG12_03571	phosphoglycolate phosphatase	K01091	0
DSAG12_03572	threonyl-tRNA synthetase	K01868	0
DSAG12_03573	tRNA wybutosine-synthesizing protein 1	K15449	0
DSAG12_03574	hypothetical protein	--	0
DSAG12_03575	hypothetical protein	--	0
DSAG12_03576	hypothetical protein	--	0
DSAG12_03577	hypothetical protein	--	6
DSAG12_03578	hypothetical protein	--	0
DSAG12_03579	hypothetical protein	--	0
DSAG12_03580	hypothetical protein	--	0
DSAG12_03581	hypothetical protein	--	0
DSAG12_03582	putative ABC transport system ATP-binding protein	K02003	0
DSAG12_03583	hypothetical protein	--	0
DSAG12_03584	hypothetical protein	--	0
DSAG12_03585	hypothetical protein	--	0
DSAG12_03586	hypothetical protein	--	0
DSAG12_03587	putative ABC transport system ATP-binding protein	K02003	0
DSAG12_03588	deoxyribonuclease IV	K01151	0
DSAG12_03589	hypothetical protein	--	0
DSAG12_03590	hypothetical protein	--	0
DSAG12_03591	5-formyltetrahydrofolate cyclo-ligase	K01934	0
DSAG12_03592	phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP cyclohydrolase	K00602	0
DSAG12_03593	hypothetical protein	--	0
DSAG12_03594	IMP dehydrogenase	K00088	0
DSAG12_03595	Ras-related protein Rab-1A	K07874	0
DSAG12_03596	uncharacterized protein	K06950	0
DSAG12_03597	hypothetical protein	--	0
DSAG12_03598	adenylyltransferase and sulfurtransferase	K11996	0
DSAG12_03599	sulfite reductase (ferredoxin)	K00392	0
DSAG12_03600	methanogen homoacoinitase small subunit	K16793	0
DSAG12_03601	methanogen homoacoinitase large subunit	K16792	0
DSAG12_03602	adenylate kinase	K00939	0
DSAG12_03603	hypothetical protein	--	0
DSAG12_03604	branched-chain amino acid aminotransferase	K00826	0
DSAG12_03605	branched-chain amino acid aminotransferase	K00826	0
DSAG12_03606	transposase	K07486	0
DSAG12_03607	hypothetical protein	--	0
DSAG12_03608	hypothetical protein	--	0
DSAG12_03609		K00936	0
DSAG12_03610	hypothetical protein	--	0
DSAG12_03611	hypothetical protein	--	0
DSAG12_03612	hypothetical protein	--	0
DSAG12_03613	acylphosphatase	K01512	0
DSAG12_03614	hypothetical protein	--	0
DSAG12_03615	pantetheine-phosphate adenylyltransferase	K02201	0
DSAG12_03616	phenylalanyl-tRNA synthetase alpha chain	K01889	0
DSAG12_03617	phenylalanyl-tRNA synthetase beta chain	K01890	0
DSAG12_03618	hypothetical protein	--	0
DSAG12_03619	ribonuclease PH	K00989	0
DSAG12_03620	chorismate mutase / prephenate dehydratase	K14170	0
DSAG12_03621	hypothetical protein	--	0
DSAG12_03622	Ca <sup>2+</sup> -transporting ATPase	K01537	0
DSAG12_03623	hypothetical protein	--	0
DSAG12_03624	hypothetical protein	--	0
DSAG12_03625	ribonuclease III	K03685	0
DSAG12_03626	acetate acetyltransferase / 2-methoxy- $\alpha$ -polypropenyl-1,4-benzoquinol methide	K03183	125
DSAG12_03627	hypothetical protein	--	209
DSAG12_03628	aminoglycoside 2"-phosphotransferase	K17910	188
DSAG12_03629	ESCRT-II complex subunit VPS22	K12188	151
DSAG12_03630	ESCRT-II complex subunit VPS25	K12189	82
DSAG12_03631	vacuolar protein-sorting-associated protein 4	K12196	150
DSAG12_03632	hypothetical protein	--	127
DSAG12_03633	hypothetical protein	--	226
DSAG12_03634	hypothetical protein	--	150
DSAG12_03635	hypothetical protein	--	142 small GTP-binding domain protein
DSAG12_03636	hypothetical protein	--	191
DSAG12_03637	hypothetical protein	--	216
DSAG12_03638	hypothetical protein	--	249
DSAG12_03639	hypothetical protein	--	174
DSAG12_03640	3-dehydrosphinganine reductase	K04708	72
DSAG12_03641	hypothetical protein	--	159
DSAG12_03642	charged multivesicular body protein 1	K12197	188

DSAG12_03643	oligoendopeptidase F	K08602	231
DSAG12_03644	charged multivesicular body protein 1	K12197	251
DSAG12_03645	two-component system, NtrC family, sensor kinase	K02482	181
DSAG12_03646	hypothetical protein	--	111
DSAG12_03647	hypothetical protein	--	223
DSAG12_03648	hypothetical protein	--	257
DSAG12_03649	hypothetical protein	--	232
DSAG12_03650	hypothetical protein	--	221
DSAG12_03651	F420-non-reducing hydrogenase iron-sulfur subunit	K14127	133
DSAG12_03652	heterodisulfide reductase subunit A	K03388	159
DSAG12_03653	hypothetical protein	--	179
DSAG12_03654	heterodisulfide reductase subunit A	K03388	237
DSAG12_03655	heterodisulfide reductase subunit A	K03388	135
DSAG12_03656	heterodisulfide reductase subunit B	K03389	119
DSAG12_03657	heterodisulfide reductase subunit C	K03390	106
DSAG12_03658	2-iminobutanoate/2-iminopropanoate deaminase	K09022	200
DSAG12_03659	hypothetical protein	--	96
DSAG12_03660	thiamine biosynthesis protein ThiI	K03151	243
DSAG12_03661	ribokinase	K00852	197
DSAG12_03662	hypothetical protein	--	178
DSAG12_03663	ATP-binding cassette, sub-family E, member 1	K06174	129
DSAG12_03664	hypothetical protein	--	191
DSAG12_03665	hypothetical protein	--	33
DSAG12_03666	hypothetical protein	--	152
DSAG12_03667	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	K01834	241
DSAG12_03668	hypothetical protein	K06900	175
DSAG12_03669	hypothetical protein	--	86
DSAG12_03670	hypothetical protein	--	243
DSAG12_03671	glutamine synthetase	K01915	232
DSAG12_03672	glucosamine--fructose-6-phosphate aminotransferase (isomerizing)	K00820	9
DSAG12_03673	hypothetical protein	--	501
DSAG12_03674	COP9 signalosome complex subunit 5	K09613	52
DSAG12_03675	tRNA-dihydrouridine synthase B	K05540	95
DSAG12_03676	starch phosphorylase	K00688	161
DSAG12_03677	hypothetical protein	--	216
DSAG12_03678	DNA repair protein RadA	K04483	136
DSAG12_03679	hypothetical protein	K00540	65
DSAG12_03680	dimethylargininase	K01482	241
DSAG12_03681	hypothetical protein	--	116
DSAG12_03682	hypothetical protein	--	196
DSAG12_03683	hypothetical protein	K07131	204
DSAG12_03684	glucose-6-phosphate isomerase	K01810	0
DSAG12_03685	hypothetical protein	--	187
DSAG12_03686	acetyltransferase	K09181	0
DSAG12_03687	hypothetical protein	K06889	122
DSAG12_03688	hypothetical protein	--	239
DSAG12_03689	hypothetical protein	--	139
DSAG12_03690	lipid A 4'-phosphatase	K12978	153
DSAG12_03691	hypothetical protein	--	155
DSAG12_03692	hypothetical protein	--	0
DSAG12_03693	putative hydrolase of the HAD superfamily	K07025	168
DSAG12_03694	hypothetical protein	--	181
DSAG12_03695	hypothetical protein	--	136
DSAG12_03696	hypothetical protein	--	197
DSAG12_03697	hypothetical protein	--	185
DSAG12_03698	hypothetical protein	--	256
DSAG12_03699	hypothetical protein	--	182
DSAG12_03700	hypothetical protein	--	113
DSAG12_03701	hypothetical protein	--	141
DSAG12_03702	NTE family protein	K07001	93
DSAG12_03703	hypothetical protein	--	178
DSAG12_03704	hypothetical protein	--	45
DSAG12_03705	hypothetical protein	--	174
DSAG12_03706	hypothetical protein	--	0
DSAG12_03707	hypothetical protein	--	157
DSAG12_03708	hypothetical protein	--	202
DSAG12_03709	hypothetical protein	--	173
DSAG12_03710	hypothetical protein	--	235
DSAG12_03711	hypothetical protein	--	232
DSAG12_03712	hypothetical protein	--	244
DSAG12_03713	hypothetical protein	--	191
DSAG12_03714	translation initiation factor 4G	K03260	549
DSAG12_03715	hypothetical protein	--	229
DSAG12_03716	hypothetical protein	--	213
DSAG12_03717	hypothetical protein	--	215
DSAG12_03718	hypothetical protein	--	193
DSAG12_03719	hypothetical protein	--	223
DSAG12_03696	hypothetical protein	--	197
DSAG12_03697	hypothetical protein	--	185
DSAG12_03698	hypothetical protein	--	256
DSAG12_03699	hypothetical protein	--	182
DSAG12_03700	hypothetical protein	--	113
DSAG12_03701	hypothetical protein	--	141
DSAG12_03702	NTE family protein	K07001	93
DSAG12_03703	hypothetical protein	--	178
DSAG12_03704	hypothetical protein	--	45
DSAG12_03705	hypothetical protein	--	174
DSAG12_03706	hypothetical protein	--	0
DSAG12_03707	hypothetical protein	--	157
DSAG12_03708	hypothetical protein	--	202
DSAG12_03709	hypothetical protein	--	173
DSAG12_03710	hypothetical protein	--	235
DSAG12_03711	hypothetical protein	--	232
DSAG12_03712	hypothetical protein	--	244
DSAG12_03713	hypothetical protein	--	191
DSAG12_03714	translation initiation factor 4G	K03260	549
DSAG12_03715	hypothetical protein	--	229
DSAG12_03716	hypothetical protein	--	213
DSAG12_03717	hypothetical protein	--	215
DSAG12_03718	hypothetical protein	--	193
DSAG12_03719	hypothetical protein	--	223

DSAG12_03720	hypothetical protein	--	277
DSAG12_03721	hypothetical protein	--	198
DSAG12_03722	hypothetical protein	--	231
DSAG12_03723	hypothetical protein	--	244
DSAG12_03724	alpha-ribazole phosphatase	K02226	210
DSAG12_03725	hypothetical protein	--	205
DSAG12_03726	hypothetical protein	--	151
DSAG12_03727	hypothetical protein	--	77
DSAG12_03728	hypothetical protein	--	179
DSAG12_03729	hypothetical protein	--	228
DSAG12_03730	tyrosyl-tRNA synthetase	K01866	160
DSAG12_03731	hypothetical protein	--	214
DSAG12_03732	ABC-2 type transport system ATP-binding protein	K01990	208
DSAG12_03733	pyruvate, orthophosphate dikinase	K01006	205
DSAG12_03734	Ras-related protein Rab-11A	K07904	284
DSAG12_03735	hypothetical protein	--	175
DSAG12_03736	ribonucleoside-triphosphate reductase	K00527	227
DSAG12_03737	aspartate carbamoyltransferase catalytic subunit	K00609	146
DSAG12_03738	hypothetical protein	--	128
DSAG12_03739	large subunit ribosomal protein L44e	K02929	239
DSAG12_03740	small subunit ribosomal protein S27e	K02978	191
DSAG12_03741	transcription elongation factor	K03057	164
DSAG12_03742	hypothetical protein	--	172
DSAG12_03743	proliferating cell nuclear antigen	K04802	206
DSAG12_03744	pyruvate, water dikinase	K01007	304
DSAG12_03745	hypothetical protein	--	208
DSAG12_03746	high-affinity iron transporter	K07243	290
DSAG12_03747	hypothetical protein	--	192
DSAG12_03748	hypothetical protein	--	196
DSAG12_03749	hypothetical protein	--	195
DSAG12_03750	DNA primase large subunit	K18882	160
DSAG12_03751	DNA primase small subunit	K02683	460
DSAG12_03752	hypothetical protein	--	231
DSAG12_03753	H/ACA ribonucleoprotein complex subunit 3	K11130	168
DSAG12_03754	translation initiation factor 2 subunit 1	K03237	195
DSAG12_03755	hypothetical protein	--	201
DSAG12_03756	hypothetical protein	--	244
DSAG12_03757	hypothetical protein	--	213
DSAG12_03758	Lrp/AsnC family transcriptional regulator, regulator for asnA, asnC and gidA	K03718	187
DSAG12_03759	cation:H <sup>+</sup> antiporter	K07301	182
DSAG12_03760	hypothetical protein	--	234
DSAG12_03761	adenylsulfate reductase, subunit B	K00395	154
DSAG12_03762	hypothetical protein	--	155
DSAG12_03763	arsenite transporter, ACR3 family	K03325	152
DSAG12_03764	hypothetical protein	--	209
DSAG12_03765	protein-S-isoprenylcysteine O-methyltransferase	K00587	171
DSAG12_03766	putative protease	K08303	141
DSAG12_03767	hypothetical protein	--	195
DSAG12_03768	phosphoglycolate phosphatase	K01091	253
DSAG12_03769	MFS transporter, DHA3 family, tetracycline resistance protein	K18214	193
DSAG12_03770	hypothetical protein	--	208
DSAG12_03771	hypothetical protein	--	138
DSAG12_03772	hypothetical protein	--	258
DSAG12_03773	hypothetical protein	--	212
DSAG12_03774	HSP20 family protein	K13993	173
DSAG12_03775	hypothetical protein	--	186
DSAG12_03776	hypothetical protein	--	211
DSAG12_03777	hypothetical protein	--	232
DSAG12_03778	hypothetical protein	--	149
DSAG12_03779	hypothetical protein	--	163
DSAG12_03780	hypothetical protein	--	142
DSAG12_03781	hypothetical protein	--	229
DSAG12_03782	Arf/Sar family, other	K07977	222
DSAG12_03783	hypothetical protein	--	102
DSAG12_03784	ADP-ribose pyrophosphatase	K01515	125
DSAG12_03785		K07076	212
DSAG12_03786		K07076	188
DSAG12_03787	hypothetical protein	--	194
DSAG12_03788	glycerol-3-phosphate dehydrogenase subunit B	K00112	180
DSAG12_03789	glycerol-3-phosphate dehydrogenase	K00111	236
DSAG12_03790	hypothetical protein	--	102
DSAG12_03791	sulfoxyruvate decarboxylase subunit beta	K13039	176
DSAG12_03792	phosphonopyruvate decarboxylase	K09459	146
DSAG12_03793	phosphinothricin acetyltransferase	K03823	216
DSAG12_03794	hypothetical protein	--	218
DSAG12_03795	carboxy-terminal domain RNA polymerase II polypeptide A small phosphatase	K15731	233
DSAG12_03796	hypothetical protein	--	204
DSAG12_03797	hypothetical protein	--	143

DSAG12_03798	MFS transporter, DHA1 family, multidrug resistance protein	K08153	226
DSAG12_03799	thiamine pyrophosphokinase	K00949	169
DSAG12_03800	hypothetical protein	--	210
DSAG12_03801	thiamine transport system substrate-binding protein	K02064	285
DSAG12_03802	thiamine transport system permease protein	K02063	170
DSAG12_03803	iron(III) transport system ATP-binding protein	K02010	122
DSAG12_03804	hypothetical protein	--	145
DSAG12_03805	tRNA-Arg	Intron(43144)	246
DSAG12_03806	hypothetical protein	--	199
DSAG12_03807	hypothetical protein	--	73
DSAG12_03808	small subunit ribosomal protein S7	K02992	69
DSAG12_03809	small subunit ribosomal protein S12	K02950	179
DSAG12_03810	large subunit ribosomal protein L30e	K02908	115
DSAG12_03811	hypothetical protein	--	183
DSAG12_03812	hypothetical protein	--	224
DSAG12_03813	hypothetical protein	--	129
DSAG12_03814	hypothetical protein	--	229
DSAG12_03815	hypothetical protein	--	154
DSAG12_03816	tryptophanyl-tRNA synthetase	K01867	157
DSAG12_03817	hypothetical protein	--	194
DSAG12_03818	hypothetical protein	--	180
DSAG12_03819	DNA-directed RNA polymerase subunit A"	K03042	207
DSAG12_03820	DNA-directed RNA polymerase subunit A'	K03041	113
DSAG12_03821	hypothetical protein	--	32
DSAG12_03822	hypothetical protein	--	242
DSAG12_03823	D-3-phosphoglycerate dehydrogenase	K00058	13
DSAG12_03824	hypothetical protein	--	3
DSAG12_03825	hypothetical protein	--	3
DSAG12_03826	acetyl-CoA synthetase (ADP-forming)	K01905	111
DSAG12_03827	hypothetical protein	--	154
DSAG12_03828	Ca <sup>2+</sup> -transporting ATPase	K01537	148
DSAG12_03829	nicotinamide-nucleotide amidase	K03742	108
DSAG12_03830	hypothetical protein	--	173
DSAG12_03831	hypothetical protein	--	203
DSAG12_03832	two-component system, NtrC family, C4-dicarboxylate transport sensor histidine kinase DctB	K10125	105
DSAG12_03833	acetyl-CoA C-acetyltransferase	K00626	91
DSAG12_03834	DNA polymerase I	K02319	221
DSAG12_03835	hypothetical protein	--	240
DSAG12_03836	tRNA-Thr	Intron(43643)	177
DSAG12_03837	hypothetical protein	--	203
DSAG12_03838	hypothetical protein	--	203
DSAG12_03839	hypothetical protein	--	243
DSAG12_03840	hypothetical protein	--	0
DSAG12_03841	ABC-2 type transport system permease protein	K01992	151
DSAG12_03842	ABC-2 type transport system ATP-binding protein	K01990	56
DSAG12_03843	hypothetical protein	--	268
DSAG12_03844	hypothetical protein	--	277
DSAG12_03845	hypothetical protein	--	450
DSAG12_03846	hypothetical protein	--	297
DSAG12_03847	hypothetical protein	--	0
DSAG12_03848	glucans biosynthesis protein C	K11941	245
DSAG12_03849	phenylacetate-CoA ligase	K01912	157
DSAG12_03850	hypothetical protein	--	258
DSAG12_03851	ribosomal-protein-alanine N-acetyltransferase	K03790	0
DSAG12_03852	hypothetical protein	--	165
DSAG12_03853	hypothetical protein	--	0
DSAG12_03854	hypothetical protein	--	186
DSAG12_03855	hypothetical protein	--	838
DSAG12_03856	hypothetical protein	--	165
DSAG12_03857	MFS transporter, DHA3 family, macrolide efflux protein	K08217	116
DSAG12_03858	aminopeptidase	K01269	121
DSAG12_03859	Fur family transcriptional regulator, peroxide stress response regulator	K09825	105
DSAG12_03860	catalase-peroxidase	K03782	221
DSAG12_03861	hypothetical protein	--	258
DSAG12_03862	hypothetical protein	--	0
DSAG12_03863	hypothetical protein	--	99
DSAG12_03864	hypothetical protein	--	164
DSAG12_03865	hypothetical protein	--	178
DSAG12_03866	hydrogenase expression/formation protein HypD	K04654	165
DSAG12_03867	hydrogenase 3 maturation protease	K08315	172
DSAG12_03868	hydrogenase expression/formation protein HypE	K04655	0
DSAG12_03869	hydrogenase maturation protein HypF	K04656	133
DSAG12_03870	lysophospholipase	K01048	157
DSAG12_03871	putative hydrolase of the HAD superfamily	K07025	187
DSAG12_03872	hypothetical protein	--	196
DSAG12_03873	hydrogenase expression/formation protein HypC	K04653	195
DSAG12_03874	ArsR family transcriptional regulator	K03892	94
DSAG12_03875	Cd <sup>2+</sup> /Zn <sup>2+</sup> -exporting ATPase	K01534	212

DSAG12_03876	hypothetical protein	--	224
DSAG12_03877	F420-non-reducing hydrogenase large subunit	K14126	187
DSAG12_03878	heterodisulfide reductase subunit B	K03389	163
DSAG12_03879	heterodisulfide reductase subunit C	K03390	286
DSAG12_03880	F420-non-reducing hydrogenase small subunit	K14128	229
DSAG12_03881	hypothetical protein	--	230
DSAG12_03882	tRNA 2-thiouridine synthesizing protein C	K07236	190
DSAG12_03883	tRNA 2-thiouridine synthesizing protein D	K07235	181
DSAG12_03884		K07112	5
DSAG12_03885	tRNA 2-thiouridine synthesizing protein A	K04085	8
DSAG12_03886	hypothetical protein	--	6
DSAG12_03887	mono-ADP-ribosyltransferase sirtuin 6	K11416	8
DSAG12_03888	hypothetical protein	--	4
DSAG12_03889	anaerobic magnesium-protoporphyrin IX monomethyl ester cyclase	K04034	244
DSAG12_03890	hypothetical protein	--	301
DSAG12_03891	UDP-glucose 4-epimerase	K01784	138
DSAG12_03892	aminoglycoside N3'-acetyltransferase	K00662	232
DSAG12_03893	hypothetical protein	--	269
DSAG12_03894	hypothetical protein	--	0
DSAG12_03895	hypothetical protein	--	178
DSAG12_03896	hypothetical protein	--	144
DSAG12_03897	hypothetical protein	--	179
DSAG12_03898	titin	K12567	113
DSAG12_03899			166
DSAG12_03900			197
DSAG12_03901			217
DSAG12_03902			268
DSAG12_03903			163
DSAG12_03904			216
DSAG12_03905			104
DSAG12_03906			156
DSAG12_03907			340
DSAG12_03908			187
DSAG12_03909			233
DSAG12_03910			83
DSAG12_03911			117
DSAG12_03912			226
DSAG12_03913			205
DSAG12_03914			177
DSAG12_03915			171
DSAG12_03916			114
DSAG12_03917			137
DSAG12_03918			175
DSAG12_03919			218
DSAG12_03920			163
DSAG12_03921			178
DSAG12_03922			253
DSAG12_03923			200
DSAG12_03924			173
DSAG12_03925			79
DSAG12_03926			210
DSAG12_03927			225
DSAG12_03928			217
DSAG12_03929			200
DSAG12_03930			204
DSAG12_03931			232
DSAG12_03932			126
DSAG12_03933			323
DSAG12_03934			180
DSAG12_03935			133
DSAG12_03936			178
DSAG12_03937			221
DSAG12_03938			160
DSAG12_03939			243
DSAG12_03940			172
DSAG12_03941			233
DSAG12_03942			248
DSAG12_03943			229
DSAG12_03944			171
DSAG12_03945			158
DSAG12_03946			64
DSAG12_03947			96
DSAG12_03948			224
DSAG12_03949			290
DSAG12_03950			285
DSAG12_03951			248
DSAG12_03952			273
DSAG12_03953			266
DSAG12_03954			63
DSAG12_03955			155

DSAG12_03956	129
DSAG12_03957	217
DSAG12_03958	57
DSAG12_03959	174
DSAG12_03960	73
DSAG12_03961	60
DSAG12_03962	327
DSAG12_03963	179
DSAG12_03964	157
DSAG12_03965	250
DSAG12_03966	175
DSAG12_03967	159
DSAG12_03968	203
DSAG12_03969	335
DSAG12_03970	126
DSAG12_03971	224

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