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1 **Effect of oxygen on the anaerobic methanotroph ‘*Candidatus Methylomirabilis***  
2 **oxyfera’’: kinetic and transcriptional analysis**

3  
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23 Keywords: anaerobic methane oxidation, denitrification, '*Candidatus* Methyloirabilis oxyfera',  
24 oxidative stress, transcriptome.

25  
26 Abbreviations: AMO, ammonium monooxygenase; AOX, cyanide-insensitive alternative  
27 oxidase; CcO, cytochrome *c* oxidase; DTT, dithiothreitol; MOPS, 3-(N-morpholino)  
28 propanesulfonic acid; pMMO, particulate methane monooxygenase; PMSF,  
29 phenylmethanesulfonyl fluoride; ROS, reactive oxygen species; SHAM, salicylhydroxamic acid;  
30 TMPD, N,N,N',N'-tetramethyl-p-phenyldiamine; TOR, terminal oxygen reductase; UbqO,  
31 ubiquinol.

### 33 **SUMMARY**

34 '*Candidatus* Methyloirabilis oxyfera' is a denitrifying methanotroph that performs nitrite-  
35 dependent anaerobic methane oxidation through a newly discovered intra-aerobic pathway. In  
36 this study, we investigated the response of a *M. oxyfera* enrichment culture to oxygen. Addition  
37 of either 2 or 8% oxygen resulted in an instant decrease of methane and nitrite conversion rates.  
38 Oxygen exposure also led to a deviation in the nitrite to methane oxidation stoichiometry.  
39 Oxygen-uptake and inhibition studies with cell-free extracts displayed a change from cytochrome  
40 *c* to quinol as electron donor after exposure to oxygen. The change in global gene expression was  
41 monitored by deep sequencing of cDNA using Illumina technology. After 24 h of oxygen  
42 exposure, transcription levels of 1109 (out of 2303) genes changed significantly when compared  
43 to the anoxic period. Most of the genes encoding enzymes of the methane oxidation pathway  
44 were constitutively expressed. Genes from the denitrification pathway, with exception of one of  
45 the putative nitric oxide reductases, *norZ2*, were severely down-regulated. The majority of known  
46 genes involved in the vital cellular functions, such as nucleic acid and protein biosynthesis and

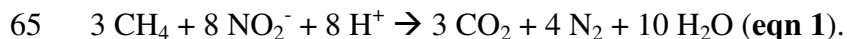
47 cell division processes, were down-regulated. The alkyl hydroperoxide reductase, *alpC*, and  
48 genes involved in the synthesis/repair of the iron-sulfur clusters were among the few up-regulated  
49 genes. Further, transcription of the *pmoCAB* genes of aerobic methanotrophs present in the non-  
50 *M. oxyfera* community were triggered by the presence of oxygen. Our results show that oxygen-  
51 exposed cells of *M. oxyfera* were under oxidative stress and that in spite of its oxygenic capacity,  
52 exposure to microaerophilic conditions has an overall detrimental effect.

53

## 54 INTRODUCTION

55 Methane munching microbes play an important role in the global carbon cycle and mitigate the  
56 greenhouse effect by oxidizing methane before it reaches the atmosphere (Hanson and Hanson,  
57 1996). This process can be performed either aerobically by methanotrophic bacteria  
58 (methanotrophs), members of the phyla *Proteobacteria* and *Verrucomicrobia*, or anaerobically by  
59 sulfate-dependent methanotrophic archaea (Knittel and Boetius, 2009; Op den Camp et al., 2009).  
60 Recently, a new group of bacterial methanotrophs affiliated to the 'NC10' phylum was  
61 discovered (Raghoebarsing et al., 2006). The representative bacterium, tentatively named  
62 '*Candidatus Methyloirabilis oxyfera*', performs nitrite-dependent anaerobic methane oxidation,  
63 with the following stoichiometry (Raghoebarsing et al., 2006; Ettwig et al., 2010):

64



66

67 Interestingly, this process is performed via a classical aerobic methane oxidation pathway in the  
68 total absence of externally supplied O<sub>2</sub> (Ettwig et al., 2010). This apparent paradox is explained  
69 by the unique ability of *M. oxyfera* to produce intracellular O<sub>2</sub> through an alternative  
70 denitrification pathway that does not involve nitrous oxide (N<sub>2</sub>O) as an intermediate. In this

71 pathway, the nitric oxide (NO) generated from the reduction of nitrite (NO<sub>2</sub><sup>-</sup>) is suggested to be  
72 disproportionated into dinitrogen gas (N<sub>2</sub>) and O<sub>2</sub> (Fig. 1) (Ettwig et al., 2010; Wu et al., 2011a).  
73 The majority of the generated O<sub>2</sub> is used for activation and oxidation of methane in the strictly  
74 O<sub>2</sub>-dependent reaction catalyzed by particulate methane monooxygenase (pMMO). It has been  
75 proposed that the remainder of the O<sub>2</sub> is used by other processes, like ‘normal’ respiration by  
76 terminal O<sub>2</sub> reductases (TOR). The presence of four sets genes encoding TORs in the genome of  
77 *M. oxyfera* and the previously reported functional production of a *bo*-type ubiquinol (UbqO)  
78 TOR suggests that this organism is capable of nitrite and O<sub>2</sub> co-respiration (Wu et al., 2011b).

79 Thus far, *M. oxyfera* and *M. oxyfera*-like bacteria have been found in various freshwater  
80 habitats, in close proximity to the oxic/anoxic interface (Raghoebarsing et al., 2006; Ettwig et al.,  
81 2008; Hu et al., 2011; Luesken et al., 2011b; Luesken et al., 2011a). Such habitats are subjected  
82 to fluctuations in O<sub>2</sub> concentrations and in transient exposure to O<sub>2</sub>. Thus, being able to profit or  
83 simply tolerate external O<sub>2</sub> might be essential for the survival and competitive fitness of *M.*  
84 *oxyfera* cells in natural O<sub>2</sub> limited ecological habitats.

85 The effects of O<sub>2</sub> exposure on organisms can be manifold. In *M. oxyfera* it could enhance  
86 the rates of O<sub>2</sub>-dependent reactions, such as the ones catalyzed by pMMO and TORs. During  
87 electron transport, more energy is conserved by O<sub>2</sub> respiration due to the involvement of TORs,  
88 when compared to denitrification; hence, an O<sub>2</sub> surplus could be beneficial to *M. oxyfera*. On the  
89 other hand, the denitrification pathway itself, which is often O<sub>2</sub>-sensitive, can be inhibited.  
90 Studies have shown that O<sub>2</sub> can suppress the synthesis of denitrifying enzymes and reversibly  
91 inhibit their activity. The extent of this effect is species dependent and the O<sub>2</sub>-tolerance varies  
92 greatly among microbes. *Thiomicrospira denitrificans* requires absolute anoxia for  
93 denitrification, while *Paracoccus pantothropus* can still denitrify at 90 % air saturation (Hoor,  
94 1975; Robertson and Kuenen, 1984; Zumft, 1997). This variation seems mainly caused by

95 differences in sensitivity of enzymes and regulators involved in the reactions of the denitrification  
96 pathway. In some denitrifiers, higher growth rates were observed when O<sub>2</sub> and nitrate were  
97 simultaneously used as electron acceptors (Robertson and Kuenen, 1984; Bonin and Gilewicz,  
98 1991). Interestingly, the strict aerobe *Methylothermobacter mobilis* denitrifies when grown in methanol,  
99 but only to N<sub>2</sub>O as end product (Kalyuzhnaya et al., 2009).

100 In addition to the possible effects on the central energy metabolism, a direct consequence  
101 of increased O<sub>2</sub> utilization as terminal electron acceptor is the concomitant increase in the  
102 formation of highly reactive O<sub>2</sub> species (ROS) which are derived from the partial reduction of O<sub>2</sub>.  
103 The increased intracellular ROS can damage essential cellular components when not scavenged  
104 (Fridovich, 1978; Imlay et al., 1988). To counteract this effect, many organisms have developed  
105 O<sub>2</sub>-detoxification systems: superoxide anions (O<sub>2</sub><sup>-</sup>) are converted to hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>) by  
106 superoxide dismutase (SOD), and H<sub>2</sub>O<sub>2</sub> is eliminated by the action of catalases and peroxidases  
107 (Farr and Kogoma, 1991).

108 The response of *M. oxyfera* to O<sub>2</sub> has not been investigated so far. Here, cells from a *M.*  
109 *oxyfera* enrichment culture were exposed to two different O<sub>2</sub> concentrations (2 and 8 %). Kinetics  
110 of substrate utilization under anoxic conditions and upon O<sub>2</sub> exposure was measured. For the  
111 cells treated with 8 % O<sub>2</sub>, the differential O<sub>2</sub> reduction potential by the cell-free extracts was  
112 measured and the total mRNA profiles were examined to evaluate the changes in global gene  
113 expression.

114

## 115 **RESULTS**

### 116 **Effects of O<sub>2</sub> on nitrite-dependent anaerobic methane oxidation rates**

117 Biomass from a *M. oxyfera* enrichment culture was exposed to O<sub>2</sub> in two different experiments (2  
118 and 8 % O<sub>2</sub>). In the anoxic period of both experiments, as well as in the control experiment, the

119 methane and nitrite conversion rates occurred close to the expected 3 CH<sub>4</sub>: 8 NO<sub>2</sub><sup>-</sup> (see eqn 1)  
120 stoichiometry (Raghoebarsing et al., 2006) (Fig. 2 and Table 1). After addition of O<sub>2</sub>, the  
121 methane and nitrite conversions decreased instantaneously and the stoichiometry deviated  
122 substantially (1 CH<sub>4</sub>: 2 NO<sub>2</sub><sup>-</sup>) from the theoretical values (Fig. 2 and Table 1).

123 In the second experiment (8 % O<sub>2</sub>), the produced dinitrogen gas was analyzed for the  
124 masses <sup>15-15</sup>N<sub>2</sub>, <sup>15-14</sup>N<sub>2</sub> and <sup>14-14</sup>N<sub>2</sub> because unlabeled residual nitrite was present in the *M. oxyfera*  
125 biomass before labeled nitrite was added. The production rate of <sup>15-15</sup>N<sub>2</sub> was 1.3 nmol min<sup>-1</sup> mg  
126 protein<sup>-1</sup> and in total 1.8 nmol N<sub>2</sub> min<sup>-1</sup> mg protein<sup>-1</sup> was formed. The initial concentration of O<sub>2</sub>  
127 (8 %) was depleted within 42 h. In the following anoxic period (69.5 to 77.5 h), the anaerobic  
128 methane oxidation coupled to denitrification did not fully recover. The measured anoxic  
129 conversion of methane during this period was 0.7 nmol min<sup>-1</sup> mg protein<sup>-1</sup>, which was lower than  
130 the initial methane oxidation rate measured. In the anoxic control (0.14 g protein), kept in parallel  
131 for 79 h, the methane and nitrite conversions were close to the rates in the anoxic period from the  
132 second experiment (8 % O<sub>2</sub>).

133

#### 134 **Effects in the O<sub>2</sub>-uptake by cell-free extracts**

135 O<sub>2</sub> consumption by cell-extracts of *M. oxyfera* culture under anoxic (t = 0) and after 24 h of  
136 exposure to 8 % of O<sub>2</sub> was assessed using specific reductants: TMPD/cyt *c* or UbqO (Table 2).  
137 CN<sup>-</sup> and SHAM were used as specific inhibitors for heme-copper TORs (Garcia-Horsman et al.,  
138 1994) and diiron alternative O<sub>2</sub> reductase (AOX) (Schonbaum et al., 1971), respectively. The  
139 total O<sub>2</sub>-uptake capacity by *M. oxyfera* cell-free extracts was not significantly affected by O<sub>2</sub>  
140 exposure. Under anoxic conditions, a higher activity for TMPD/cyt *c*-dependent O<sub>2</sub>-uptake was  
141 observed. UbqO-dependent O<sub>2</sub>-uptake only accounted for about 20 % of the total reduced O<sub>2</sub>.  
142 When assayed with inhibitors, the UbqO-dependent O<sub>2</sub>-uptake was insensitive to both CN<sup>-</sup> and

143 SHAM. In contrast, the TMPD/cyt *c*-dependent respiration was inhibited up to 50 % by CN<sup>-</sup>.  
144 Thus, under anoxic conditions, 50 % of the total consumed O<sub>2</sub> can be assigned to the activity of  
145 TOR(s). After exposure to O<sub>2</sub>, a shift to UbqO-dependent O<sub>2</sub>-uptake was observed. The  
146 TMPD/cyt *c* O<sub>2</sub>-uptake was 2-fold lower in comparison to the samples from the anoxic condition  
147 and the UbqO-dependent O<sub>2</sub>-uptake increased up to 3-fold. Now, the TMPD/cyt *c* O<sub>2</sub>-uptake was  
148 not significantly affected by CN<sup>-</sup>, whereas the UbqO-dependent O<sub>2</sub>-uptake inhibited by CN<sup>-</sup> and  
149 SHAM, respectively. This results show that exposure to O<sub>2</sub> stimulated the UbqO-dependent O<sub>2</sub>-  
150 uptake. Still, only 33 % of the total O<sub>2</sub> consumption can be assigned to TOR enzymes.

151

### 152 **Changes in transcript levels upon O<sub>2</sub> exposure**

153 We monitored the change in the gene expression of *M. oxyfera* by comparing the transcript  
154 profiles of cells under anoxic conditions (t = 0) and after 24 h of exposure to 8 % of O<sub>2</sub> (Tables 3-  
155 5 and Supplementary Table 1). From 2303 transcripts, 148 were up-regulated, 961 down-  
156 regulated, and 856 transcripts did not change significantly. Some transcripts were only detected  
157 under anoxic (296) or O<sub>2</sub> exposed conditions (42).

158 The analysis of the cellular functions of proteins encoded by genes showing differential  
159 transcription can elucidate the mechanisms by which O<sub>2</sub> exposure affects *M. oxyfera*. From this  
160 point of view, three major groups could be distinguished, which include genes encoding enzymes  
161 involved in the (i) central energy metabolism; (ii) direct response to the presence of O<sub>2</sub>, such as  
162 TORs and ROS defense; (iii) protein and nucleic acid synthesis process, and cell division  
163 processes.

164

### 165 ***Genes involved in the central energy metabolism***



166 The transcription profile of genes encoding enzymes involved in methane oxidation were not  
167 significantly affected by exposure to O<sub>2</sub> (Table 3). Out of 18 transcripts, including a variety of  
168 enzymes that catalyze the oxidation of methane to carbon dioxide, only 5 were down-regulated.  
169 These comprised genes encoding enzymes that catalyze partial reactions succeeding the  
170 formation of formaldehyde, such as formaldehyde activating enzyme (*fae*) and formate  
171 dehydrogenase (*fdh*).

172 The denitrification pathway, on the other hand, was more significantly affected by the  
173 presence of O<sub>2</sub>. From the 13 genes, 9 were down-regulated (Table 4). The expression of gene  
174 clusters encoding for nitrate reductase (NAR) and nitrite reductase (NIR) were notably  
175 suppressed, with several genes showing a 10-fold lower expression. Interestingly, two gene  
176 transcripts that were not suppressed by O<sub>2</sub> were the ones that encode for the putative nitric oxide  
177 reductase (NOR) enzyme: *norZ3* was transcribed at the same level and *norZ2* was up-regulated  
178 up to 7.5-fold.

179

### 180 ***Genes involved in direct response to the presence of O<sub>2</sub>: ROS defense system and TORs***

181 A direct effect of the presence of O<sub>2</sub> is the production of ROS, which can cause damage at  
182 various cellular levels if it exceeds the capacity of the cell defense system. Analysis of the  
183 genome of *M. oxyfera* showed that it contained a repertoire of genes potentially encoding  
184 enzymes that are implicated in the defense against ROS: (i) a Fe-SOD (*sodB*), (ii) three *haem* iron  
185 peroxidases (2 *ccp*; 1 *dyp*) (iii) a non-*haem* iron rubrerythrins (*rbr*) and an alkyl  
186 hydroxyperoxidase reductase (*ahpC*). A catalase-encoding gene was not present in the genome.  
187 Differential expressions of these genes are shown in Table 5. The *sodB* gene encoding SOD,  
188 which catalyzes dismutation of O<sub>2</sub><sup>-</sup> to hydrogen peroxide, was constitutively expressed.  
189 Interestingly, two of the peroxidases and *rbr* were down-regulated. *AhpC*, a hydrogen peroxide

190 scavenger and member of the thioredoxin fold superfamily (Schröder and Ponting, 1998), was the  
191 only gene of O<sub>2</sub> defense that was up-regulated (4-fold) upon O<sub>2</sub> exposure.

192 The genome of *M. oxyfera* contains four gene clusters encodings TORs; these include two  
193 heme-copper cytochrome *c*-dependent TORs, one heme-copper UbqO-dependent TOR and a  
194 diiron cyanide insensitive AOX (Wu et al., 2011b). It was expected that an O<sub>2</sub> surplus would  
195 induce the expression of TORs as more substrate was available. However, the expressions of  
196 these genes did not change significantly (Table 5).

197

### 198 ***Genes involved in the protein synthesis, nucleic acids synthesis, and cell division***

199 Differential analysis of the genes involved in the protein synthesis and repair suggests that *M.*  
200 *oxyfera* was under oxidative stress after O<sub>2</sub> exposure (Supplementary Table 1). Overall, genes  
201 involved in cell division were repressed in the presence of external O<sub>2</sub>; these include for instance  
202 genes belonging to the *fts* operon and the rod-shape maintaining bacterial actin homologue *mreB*  
203 (Cabeen and Jacobs-Wagner, 2005). The majority of the genes involved in DNA replication were  
204 either constitutively expressed or down-regulated. Exceptionally, *dnaK*, which is also implicated  
205 in the hyperosmotic shock (Bianchi and Baneyx, 1999), was up-regulated.

206 Proteins containing iron-sulfur (Fe/S) clusters are very prone to O<sub>2</sub><sup>-</sup> attack. Exposure of *M.*  
207 *oxyfera* to O<sub>2</sub> resulted in an increased expression of *nifU/nifS* and SUF operon (*sufABCDSE*)  
208 genes which encode for proteins involved in Fe/S biosynthesis and/or repair (Ayala-Castro et al.,  
209 2008). It is noteworthy that the gene encoding for the flavin-containing glycolate oxidase and  
210 chaperone-like peptidyl-prolyl cis-trans isomerase (PPIase) were repressed after O<sub>2</sub> exposure.

211

### 212 **Analysis of non-*M. oxyfera* community**

213 Due to the complexity of the enrichment culture used, O<sub>2</sub> can affect not only *M. oxyfera* but also  
214 the non-*M. oxyfera* community. Thus, the community composition of the culture was monitored  
215 using FISH and complemented by the analysis of the total *pmo* gene transcripts under anoxic and  
216 O<sub>2</sub> exposed conditions. When monitored by FISH, no significant differences were observed  
217 between the anoxic and oxic periods, using general probes targeting organisms like  $\alpha$ -,  $\beta$ - and  $\gamma$ -  
218 *Proteobacteria*, and specific probes targeting *M. oxyfera* (Supplementary Figure 1). This was  
219 corroborated by 70 % percentage of Illumina reads that matched to *M. oxyfera* in both periods.  
220 Examination of the total *pmo* gene transcripts showed that O<sub>2</sub> triggered the onset of transcription  
221 of *pmo* genes from various aerobic methanotrophs and *amo* genes from *Nitrosomonas* (Table 6).  
222 However, the majority of *pmo* transcripts matched to *M. oxyfera* in both periods.

223

## 224 **DISCUSSION**

225 Three properties of *M. oxyfera* make it a very interesting system to study the effects of O<sub>2</sub>: (i) the  
226 ability to perform anaerobic methane oxidation coupled to denitrification, (ii) the ability to  
227 produce O<sub>2</sub> intra-aerobically, and (iii) the possession of an apparently suitable ROS defense  
228 system. In this study, the effects of aerobic conditions (2 and 8 %) on anoxic incubations of *M.*  
229 *oxyfera* were investigated using a complementary array of methods.

230 The anoxic *M. oxyfera* incubations showed methane oxidation coupled to nitrite reduction  
231 close to the expected 3:8 stoichiometry as reported previously (Raghoebarsing et al., 2006)  
232 (Table 1). Addition of either 2 or 8 % O<sub>2</sub> resulted in an instant decrease in the nitrite conversion  
233 rates leaving only 43 and 19 % of the original nitrite converting activity, respectively (Fig. 2 and  
234 Table 1). This decrease is strongly corroborated by the decrease in expression levels of nitrate  
235 and nitrite reductase genes. Substrate limitation can be ruled out since both methane and nitrite

236 were present in sufficient amounts throughout the experiment. Therefore, the observed decrease  
237 in activity is most likely a direct effect of the O<sub>2</sub> added to the incubations. Upon O<sub>2</sub> depletion, it  
238 appeared that *M. oxyfera* does not resume activity to its original capacity. The above mentioned  
239 findings are highly interesting, taken into account that *M. oxyfera* is an oxygenic bacterium. One  
240 possible explanation is that being a slow-growing and slow-metabolizing organism, both the ROS  
241 defense system and the electron transport chain in *M. oxyfera* have a low capacity, and thus, a  
242 surplus of O<sub>2</sub> does not result in a complete transfer of electrons to O<sub>2</sub> and efficient elimination of  
243 ROS.

244           After O<sub>2</sub> addition, both the methane and nitrite conversion rates decreased but also the  
245 stoichiometry shifted towards methane oxidation independent of denitrification. This effect could  
246 be due to an increased susceptibility of the denitrification enzymes to oxidative conditions, a  
247 preference for O<sub>2</sub> as electron acceptor, or a combination of these effects. In line with the observed  
248 shift in the stoichiometry and the susceptibility of enzymes involved in denitrification, the  
249 majority of genes involved in the denitrification pathway were down-regulated upon exposure to  
250 8 % O<sub>2</sub> (Table 4). Interestingly, the transcription of the *norZ2* gene encoding for the nitric oxide  
251 reductase (NOR) was highly induced by O<sub>2</sub>. The *norZ2* gene is one of the candidate enzymes for  
252 NO disproportionation, the reaction responsible for the oxygenic capacity of *M. oxyfera* (Ettwig  
253 et al., 2010). NOR enzymes can have O<sub>2</sub> reductase activity. For instance, the *cb*-type NOR from  
254 *P. denitrificans*, reduces O<sub>2</sub> to water as a side reaction (Fujiwara and Fukumori, 1996). Thus, it is  
255 conceivable that under oxidative conditions, the up-regulation of *norZ2* serves for O<sub>2</sub> respiration  
256 or detoxification. Nevertheless, further investigation is necessary to test these hypotheses. Due to  
257 the community complexity of the enrichment culture, it is also possible that the surplus of  
258 methane, uncoupled to nitrite reduction, was consumed by other members of the community,  
259 such as aerobic methanotrophs. Although no significant variation in the non-*M. oxyfera*

260 community was observed using FISH, a more sensitive analysis of *pmo* gene transcripts showed  
261 that O<sub>2</sub> triggered the onset of *pmo* transcription of a variety of aerobic methanotrophs (Table 6).  
262 Thus, it is likely that a small part of the methane oxidation observed in the oxic period is due to  
263 the activity of aerobic methanotrophs. In addition, at both O<sub>2</sub> concentrations tested, O<sub>2</sub> reduction  
264 occurred at rates higher than could be assigned to methane oxidation alone. The source of the  
265 excess of O<sub>2</sub> consumed might be heterotrophic, given that internal substrates can be generated by  
266 decaying biomass or by using reserve material.

267 O<sub>2</sub>-uptake and inhibition studies using specific inhibitors showed that the TOR-dependent  
268 activity decreased from 50 % in the anoxic period to 33 % when exposed to 8 % O<sub>2</sub> (Table 2). O<sub>2</sub>  
269 exposure also resulted in a shift in the electron donor specificity: under anoxic conditions, the  
270 major part of O<sub>2</sub> consumption can be assigned to a cytochrome *c*-dependent TORs, whereas after  
271 O<sub>2</sub> exposure the UbqO TOR activity was dominant. Despite of this variation, no significant  
272 variation in the level of transcripts was found for the four TORs. This shift could be due to (i)  
273 regulation of these enzymes at the translation level; (ii) O<sub>2</sub>-consumption by aerobic  
274 methanotrophs; and alternatively, (iii) it is possible that at least part of the increased UbqO-  
275 respiration derives from NOR activity, which would be consistent with the marked up-regulation  
276 of *norZ2*.

277 Genome analysis suggests that *M. oxyfera* is suitably equipped with a ROS defense  
278 system. Among genes implicated in the ROS systems, only *alpC* was induced in O<sub>2</sub> treated cells.  
279 Two of the *haem* iron peroxidases and *rbr* were down-regulated. The exact physiological role of  
280 rubrerythrins in defense against oxidative stress has not been entirely elucidated. However, a  
281 peroxidase activity has been suggested (Sztukowska et al., 2002). The constitutive expression of  
282 the other *ccp* (DAMO\_1666) and *sodB* may serve to provide *M. oxyfera* with a standby defense  
283 against the internally produced O<sub>2</sub>, whereas *alpC* functions as a major peroxide scavenger under

284 oxidative conditions. In the strict anaerobe *Clostridium perfringens*, transcription of both *sodB*  
285 and *rbr* did not change in O<sub>2</sub> treated cells (Geissmann et al., 1999). On the other hand, increased  
286 levels of SOD have been reported for anaerobically grown cultures of *Streptococcus faecalis* and  
287 *Escherichia coli* B exposed to O<sub>2</sub> (Gregory and Fridovich, 1973). These observations suggest the  
288 response to O<sub>2</sub> among microorganism in not uniformly similar.

289 Two additional observations support the notion that *M. oxyfera* was under oxidative stress  
290 upon O<sub>2</sub> exposure. First, the majority of the differentially expressed genes were down-regulated  
291 (961 down, 148 up). Secondly, most of the genes involved in various vital cellular functions were  
292 among the down-regulated ones. For example, genes involved in DNA replication, protein  
293 folding and stabilization, and cell division, including *mreB* and the one from *fts* operon, were  
294 down-regulated. The lower amounts of the chaperone-like PPIase transcripts is a factor that could  
295 prevent the folding/stabilization of *de novo* synthesized proteins (Ideno et al., 2001) as previously  
296 reported for O<sub>2</sub>-treated cells of the strict anaerobe *Desulfovibrio vulgaris* (Fournier et al., 2006).  
297 Flavin-containing proteins, such as glycolate oxidase, may generate hydrogen peroxide in  
298 response to O<sub>2</sub>. Lower expression of glycolate oxidase by *M. oxyfera* might serve the means of  
299 preventing excessive hydrogen peroxide formation. In *Desulfovibrio vulgaris* lower levels of  
300 glycolate oxidase were detected in the O<sub>2</sub> treated cells (Fournier et al., 2006). The genes encoded  
301 by the *nifU/nifS* and *SUF* operon have a role of synthesis and repair of Fe/S clusters (Dos Santos  
302 et al., 2004); induction of these genes point to Fe/S clusters damage in the O<sub>2</sub> treated *M. oxyfera*  
303 cells.

304 Despite the long duration of our experiment, the question remains whether in a continuous  
305 culture with alternating oxic/anoxic conditions as described by (Strous et al., 1997) *M. oxyfera*  
306 would adapt to or even benefit from microaerophilic conditions. In conclusion, the applied O<sub>2</sub>  
307 conditions in this study have an overall damaging effect in *M. oxyfera*. The inhibition of the

308 central energy metabolism and the deviation in the stoichiometry when cells are exposed to O<sub>2</sub>  
309 suggests that O<sub>2</sub> production and consumption by *M. oxyfera* is a tightly controlled process.

310

## 311 **EXPERIMENTAL PROCEDURES**

### 312 ***M. oxyfera* enrichment culture**

313 *M. oxyfera* was enriched in an anoxic sequencing batch reactor (15 L) at 30 °C as described  
314 before (Ettwig et al., 2009). During prolonged enrichment (> 6 months), O<sub>2</sub> levels were always  
315 below the detection level as monitored by a Clark-type O<sub>2</sub> electrode. *M. oxyfera* made up about  
316 70-80 % of the total bacterial population, as shown by FISH and metagenome analysis.

317

### 318 **Experimental set-up**

319 As the O<sub>2</sub> tolerance of *M. oxyfera* was unknown, two experiments with different O<sub>2</sub>  
320 concentrations were performed, one with initially 2 % pure O<sub>2</sub> in the headspace and one with  
321 initially 8 % pure O<sub>2</sub>. Experiments were carried out at 30°C in bottles with a total volume of 2.3  
322 L or 1.1 L. Biomass from the *M. oxyfera* enrichment was used to inoculate the bottles, which  
323 were equipped with a gas and liquid sampling ports. To buffer the liquid 3-(N-morpholino)  
324 propanesulfonic acid (MOPS) was added to a final concentration of 30 mM resulting in a pH of  
325 7.2. The headspace of the bottles including MOPS, were flushed with helium for 30 min prior to  
326 the experiment. In both experiments biomass from the *M. oxyfera* enrichment culture containing  
327 0-10 mg L<sup>-1</sup> nitrite was pumped directly into the anoxic bottles using Masterflex easy-load II  
328 pumps with 16 mm Norprene tubing (Cole Parmer, USA), to prevent exposure to air.  
329 Overpressure was obtained by adding either 150 or 100 mL of helium to the first and second  
330 experiments, respectively. There was an incubation period of approximately 12 h to reach

331 equilibrium for the added gasses, before the measurements started. Bottles were stirred at 150  
332 rpm during the course of the experiment.

333 In the first experiment, a 2.3 L bottle was inoculated with 1 L biomass. Labeled nitrite  
334 (stock solution: 1 M  $^{15}\text{NO}_2^-$ ) was directly added to the bottle, with a final concentration of 3 mM.  
335 Subsequently labeled methane (50 mL  $^{13}\text{CH}_4$ ) was added to the headspace of the bottle. At  $t = 27$   
336 h, 20 mL of pure  $\text{O}_2$  was supplied to the headspace and at  $t = 49$  h another 10 mL of  $\text{O}_2$  was  
337 added to the bottle.

338 In the second experiment, a 1.1 L bottle was inoculated with 700 mL bottle. At the  
339 start of the experiment, before addition of  $^{15}\text{NO}_2^-$ , the residual nitrite concentration was 0.2 mM.  
340 The stock solution of labeled nitrite (1 M  $^{15}\text{NO}_2^-$ ) was first diluted in medium [according to  
341 (Ettwig et al., 2009) without  $\text{NO}_2^-$ ] to 60 mM and subsequently added to the bottle with a final  
342 concentration of 2.5 mM nitrite. The total volume of the sample was 750 mL. Labeled methane  
343 (40 mL  $^{13}\text{CH}_4$ ) was injected in the headspace, followed by argon (0.3 %), which was used as  
344 internal control for leakage and remained constant throughout the experiment. After an anoxic  
345 period of 27.5 h, 30 mL of pure  $\text{O}_2$  was added to the culture, resulting in a headspace  
346 concentration of 8 %. This experiment was prolonged until the initial  $\text{O}_2$  concentration (8%) was  
347 depleted. Subsequently, methane was measured in this second anoxic period from  $t = 69.5$  to 77.5  
348 h.

349 A control experiment was run in parallel, where 30 mL of helium instead of pure  $\text{O}_2$  was  
350 added. Samples (70 mL) for the  $\text{O}_2$ -uptake assays were taken after 24 h of  $\text{O}_2$  exposure and RNA  
351 was extracted for deep sequencing of cDNA using Illumina technology (see below).

352 Gas samples were taken for  $\text{CH}_4$  analysis using gas chromatography (100  $\mu\text{l}$  per  
353 injection);  $\text{N}_2$  and  $\text{O}_2$  were analyzed using a gas chromatograph coupled to a mass spectrometer  
354 (30  $\mu\text{l}$  per injection) as described below.



355

## 356 **Transcriptomics**

357 Total RNA was extracted from samples (6 mL) from the anoxic bottle culture and after 24 h  
358 exposure to 8 % O<sub>2</sub> using the RiboPure™ – Bacteria kit (Ambion, AM1925, The Netherlands),  
359 according to the manufacturer's instructions. After isolation, an additional DNase treatment was  
360 performed. Quality was assessed by 1.2 % agarose gel electrophoresis and concentrations were  
361 measured with NanoDrop ND-1000 spectrophotometer (Isogen Life science). First-strand cDNA  
362 was synthesized with random primers using the RevertAid™ H Minus First Strand cDNA  
363 Synthesis Kit, and the second strand was synthesized using DNA polymerase (Fermentas Life  
364 Sciences) according to the manufacturer's instructions. Purification of dsDNA was performed  
365 using the phenol chloroform method. Single-end Illumina sequencing was performed as  
366 described previously (Ettwig et al., 2010). The obtained Illumina reads (read length: 75 nt;  
367 27,890,382 for oxic conditions and 30,582,570 reads under anoxic conditions; Supplementary  
368 Table 1) were mapped with CLC bio genomics software to the genome assembly of *M. oxyfera*  
369 (NCBI accession number GSE18535) excluding the rRNA genes. Reads were counted if they had  
370 a minimum identity of 90% and minimum length coverage of 90% to the *M. oxyfera* genes.  
371 Excluding the rRNA genes, 158,159 reads were mapped to *M. oxyfera* genes for the oxic period  
372 and 250,081 for the anoxic period. This resulted in a average coverage, defined as  $N \times L/G$ , were  
373  $N$  is the number of reads,  $L$  the average read length and  $G$  length of the genome, of 4.5 and 7.2-  
374 fold for the anoxic and oxic conditions, respectively. The percentages of total reads mapped to *M.*  
375 *oxyfera* including ribosomal RNA in anoxic and oxic conditions were 73.8 % and 69.3 %,   
376 respectively. The relative expression of the *M. oxyfera* genes was calculated as described  
377 previously (Ettwig et al., 2010). Only differential expressions with a 2-fold lower or higher than  
378 average coverage were considered significant. In order to analyze reads that had a match with

379 methane monooxygenase genes, 7076 pmo genes were downloaded from NCBI (14 June 2011).  
380 Illumina reads were mapped with a minimum DNA identity of 66% and minimum length  
381 coverage of 80%. In this way, 2282 and 2110 reads were obtained for the anoxic and oxic period,  
382 respectively. To assess the diversity in those reads, a Blastx (and Blastn) analysis versus the non  
383 redundant NCBI data base was performed using an E value of 0.0001.

384

### 385 **Preparation of cell-free extracts**

386 Approximately 1.6 g of biomass (wet weight) from the anoxic period and biomass exposed to 24  
387 h of 8 % O<sub>2</sub> was collected and washed three times in 20 mM Tris-HCl, pH 8.0. Cells were  
388 resuspended in 10 ml buffer, containing 20 mM Tris-HCl, pH 8.0, 50 mM sodium  
389 pyrophosphate, 0.5 mM phenylmethanesulfonyl fluoride (PMSF), and a few grains of solid  
390 DNase. Cells were broken by sonication, cell debris was removed by centrifugation (6000 x g,  
391 15 min, 4 °C) and the supernatant was collected as cell-free extract.

392

### 393 **O<sub>2</sub> reduction measurements**

394 O<sub>2</sub> consumption by the *M. oxyfera* cell-free extracts was measured polarographically at 30 °C  
395 using a microsensor Clarke-type electrode (Unisense, Denmark). Anoxic stock solutions of the  
396 substrates and inhibitors were prepared in 100% helium gas prior to injection to the reaction  
397 mixtures. Bovine heart cytochrome *c* (10 μM) and N,N,N',N'-tetramethyl-p-phenyldiamine  
398 (TMPD; 2 mM) O<sub>2</sub> reductase activities were assayed in the presence of 2 mM sodium ascorbate.  
399 Ubiquinone-1 (Q<sub>1</sub>; 60 μM) reduced with 10 mM DTT was used to assay UbqO O<sub>2</sub> reductase  
400 activity. In the inhibitions assay, the samples were pre-incubated with cyanide (CN<sup>-</sup>; 5 mM) or  
401 salicylhydroxamic acid (SHAM; 5 mM) for 1 h. The donor-specific O<sub>2</sub> consumption rates were

402 corrected for the auto-oxidation and endogenous respiration rates as described by (Wu et al.,  
403 2011b).

404

#### 405 **Fluorescence *in situ* Hybridization (FISH)**

406 Biomass samples (2 mL) from the anoxic and oxic period were fixed and hybridized according to  
407 (Luesken et al., 2011b) using 20-50 % formamide, depending on the specificity of the  
408 oligonucleotide probes. The following probes were used: S-\*-DBACT-0193-a-A-18  
409 (DBACT193) and S-\*-DBACT-1027-a-A-18 (DBACT1027), specific for dominant bacteria  
410 affiliated with the 'NC10' phylum (Raghoebarsing et al., 2006); S-D-Bact-0338-a-A-18  
411 (EUB338), specific for most *Bacteria* (Amann et al., 1990); L-C-gProt-1027-a-A-17 (GAM42a),  
412 specific for  $\gamma$ -*Proteobacteria* (Manz et al., 1992); L-C-bProt-1027-a-A-17 (BET42a), specific for  
413  $\beta$ -*Proteobacteria* (Manz et al., 1992), S-Sc-aProt-0968-a-A-18 (ALF 968), specific for  $\alpha$ -  
414 *Proteobacteria*, except *Rickettsiales* (Neef, 1997) and S-P-Planc-0046-a-A-18 (PLA 46), specific  
415 for *Planctomycetes* (Neef et al., 1998). The slides were examined using a Zeiss Axioplan II  
416 epifluorescence microscope with digital video camera and image analysis software (Axiovision,  
417 Zeiss, Germany).

418

#### 419 **Analytical methods**

420 For routine nitrite analysis, Merckoquant test strips (0 to 80 mg L<sup>-1</sup> nitrite; Merck, Germany)  
421 were used. Nitrite and nitrate samples (1 mL) from the batch experiments were measured  
422 colorimetrically (Kartal et al., 2006). Methane concentrations were determined by gas  
423 chromatography (Ettwig et al., 2008). To analyze N<sub>2</sub> (labeled and non-labeled) and O<sub>2</sub>, gas  
424 chromatography was used (6890 series; Agilent, USA) with a Porapak Q column at 80 °C (4 min)

425 using helium as carrier gas (flow rate, 24 mL min<sup>-1</sup>). The gas chromatograph was coupled to a  
426 mass spectrometer (Agilent 5975C inert MSD; Agilent, USA). Molecular masses of 32 Da (O<sub>2</sub>)  
427 and 28 to 30 Da (N<sub>2</sub>) were quantified and analyzed using Enhanced MSD Chem Station software  
428 (version E.02.00.493; Agilent). The total protein content in the incubations was determined by  
429 the bicinchoninic acid assay (BCA, Pierce, USA) according to manufacturer's protocol. Bovine  
430 serum albumin (BSA; Thermo Scientific, USA) was used as a standard. The protein content of  
431 the cell-free extracts was determined as described previously (Bradford, 1976) using a Bio-Rad  
432 protein assay kit (Bio-Rad, Veenendaal) with BSA as standard.

433

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438 and MS by ERC (242635).

439

#### 440 **SUPPLEMENTARY DATA**

441 -Supplementary Figure 1: Example of the community composition and its abundant members  
442 visualized using Fluorescent *in situ* Hybridization (FISH) in the anoxic and oxic period.  
443 The general bacterial probe EUB338 (Cy5, dark blue) was combined with specific probe  
444 DBACT1027 for 'NC10' affiliated bacteria (Cy3, red).. (A) In the anoxic period *M.*  
445 *oxyfera* dominates the population with 70-80 %. (B) On t = 31.5 h (5 h after addition of 8  
446 % O<sub>2</sub>) no differences could be observed compared to the anoxic period. (C) After 99 h (72

447 h after the addition of O<sub>2</sub>) the population was still dominated by *M. oxyfera*. Scale bars =  
448 20 μm.

449 -Supplementary Table 1 (XLS file): Illumina reads (75 nt) of *M. oxyfera* incubations under  
450 anoxic and oxic conditions mapped on the *M. oxyfera* genome (NCBI accession number  
451 GSE18535) using CLC bio genomics software.

452

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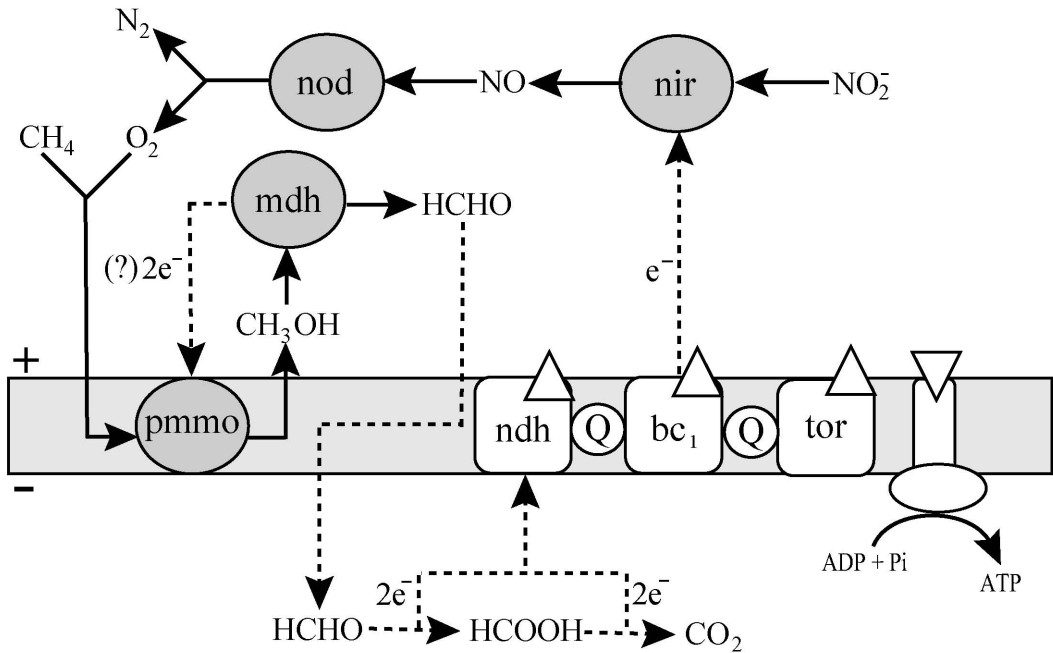
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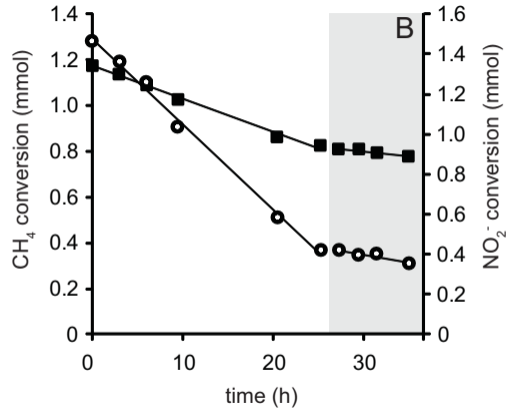
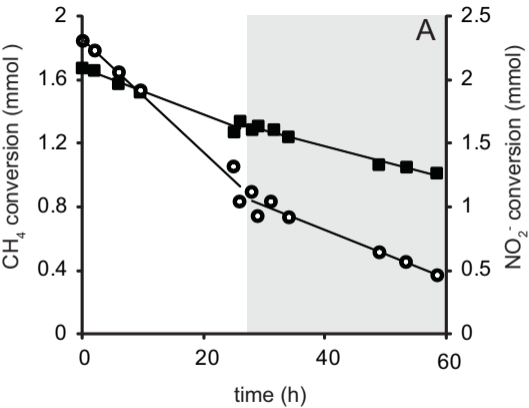
558 **Figure captions**

559  
560 **Figure 1.** Postulated model for central catabolism and energy conservation in *M. oxyfera*. Open  
561 triangles, direction of proton flow. Abbreviations; *bc<sub>1</sub>*, cytochrome *bc<sub>1</sub>* complex; mdh, methanol  
562 dehydrogenase; ndh, NAD(P)H dehydrogenase complex; nir, nitrate reductase; nod, nitric oxide  
563 dismutase; pmmo, particulate methane monooxygenase; Q, co-enzyme Q. Adapted from (Wu et  
564 al., 2011a).

565  
566 **Figure 2.** Methane (closed squares) and nitrite (open circles) consumption by the whole  
567 enrichment culture performing nitrite-dependent anaerobic methane oxidation. (A) In the anoxic  
568 period (white background) methane and nitrite were converted according to stoichiometry  
569 (eqn.1). After addition of O<sub>2</sub> (gray background) the conversions rates of methane and nitrite  
570 decreased by 25 and 57 %, respectively.(B) In the second activity experiment conversions of  
571 methane and nitrite in the oxic period (gray background) compared to the anoxic period (white  
572 background) decreased by 72 and 81 %, respectively.

573





**Table 1.** Methane, nitrite and O<sub>2</sub> conversion rates under anoxic conditions and after exposure to either 2 or 8 % of pure O<sub>2</sub>. The control experiment received 30 mL of helium after 28.5 h, thus remained anoxic with stable conversion rates (the control was measured until t = 79 h).

| Experiment | Anoxic  |                              | Oxic  |                              |                |
|------------|---|------------------------------|---|------------------------------|----------------|
|            | nmol min <sup>-1</sup> mg protein <sup>-1</sup> |                              | nmol min <sup>-1</sup> mg protein <sup>-1</sup> |                              |                |
|            | CH <sub>4</sub>                                 | NO <sub>2</sub> <sup>-</sup> | CH <sub>4</sub>                                 | NO <sub>2</sub> <sup>-</sup> | O <sub>2</sub> |
| 2%         | 0.7   | 2.3                          | 0.5   | 1.0                          | 0.9            |
| 8%         | 1.8   | 5.3                          | 0.5   | 1.0                          | 4.0            |
| Control    | 2.1   | 5.6                          | —   | —                            | —              |

**Table 2.** O<sub>2</sub> reduction activity and inhibition of *M. oxyfera* cell-free extracts from the anoxic condition and after 24 h exposure to 8 % O<sub>2</sub>.

| Substrate                     | O <sub>2</sub> consumption activity <sup>#</sup><br>(nmol min <sup>-1</sup> mg of protein <sup>-1</sup> ) |          |
|-------------------------------|---|----------|
|                               | Anoxic  | Oxic     |
| TMPD + cyt <i>c</i>           | 341 ± 22  | 148 ± 9  |
| +5 mM CN <sup>-</sup>         | 170 ± 19  | 125 ± 2  |
| Q <sub>1</sub> H <sub>2</sub> | 66 ± 9  | 169 ± 14 |
| +5 mM CN <sup>-</sup>         | 86 ± 6  | 109 ± 7  |
| +5 mM SHAM                    | 67 ± 4  | 125 ± 2  |

<sup>#</sup>Results are the means with standard deviations from at least three independent assays. Cell-free extract protein concentrations in the (0.5 mL) polarographic chamber during the assay ranged between 0.8 and 2.7 mg mL<sup>-1</sup>.

**Table 3.** Transcriptome analysis of genes encoding enzymes involved in the methane oxidation pathway of *M. oxyfera* under anoxic conditions and after 24 h exposure to 8 % O<sub>2</sub>. Grey = down-regulated genes; white = constitutively expressed.

| Enzyme  | Gene           | ORF identifier | Anoxic                  |                  | Oxic                    |                  | Ratio (oxic vs. anoxic) |
|---|----------------|----------------|-------------------------|------------------|-------------------------|------------------|-------------------------|
|   |                |                | # unique reads detected | average coverage | # unique reads detected | average coverage |                         |
| Methane monooxygenase   | <i>pmoA1</i>   | DAMO_2450      | 995                     | 13.6             | 700                     | 15.2             | 1.1                     |
|   | <i>pmoB1</i>   | DAMO_2448      | 1066                    | 8.4              | 412                     | 5.2              | 0.6                     |
| Methanol dehydrogenase  | <i>mxnF3</i>   | DAMO_0134      | 435                     | 2.4              | 148                     | 1.3              | 0.5                     |
|   | <i>mxnJ3</i>   | DAMO_0136      | 113                     | 1.3              | 65                      | 1.2              | 0.9                     |
|   | <i>mxnG3</i>   | DAMO_0138      | 46                      | 0.9              | 18                      | 0.6              | 0.6                     |
| Formaldehyde activating enzyme  | <i>fae</i>     | DAMO_0454      | 4573                    | 91.6             | 764                     | 24.2             | 0.3                     |
| Methylene H <sub>4</sub> MTP dehydrogenase  | <i>mdB</i>     | DAMO_0455      | 395                     | 4.5              | 190                     | 3.4              | 0.8                     |
| Methenyl H <sub>4</sub> MPT cyclohydrogenase                                      | <i>mch</i>     | DAMO_0461      | 38                      | 0.4              | 7                       | 0.1              | 0.3                     |
| Formyltransferase/hydrolase complex   | <i>fdhA</i>    | DAMO_0458      | 523                     | 3.2              | 311                     | 3                | 0.9                     |
|   | <i>fhcA</i>    | DAMO_0457      | 392                     | 2.5              | 195                     | 2.3              | 0.9                     |
|   | <i>fhcB1</i>   | DAMO_1135      | 14                      | 0.4              | 9                       | 0.4              | 1                       |
|   | <i>fhcB2</i>   | DAMO_1136      | 58                      | 0.6              | 6                       | 0.1              | 0.2                     |
|   | <i>fhcC</i>    | DAMO_0460      | 405                     | 5                | 131                     | 2.6              | 0.5                     |
|   | <i>fhcD</i>    | DAMO_0459      | 272                     | 3                | 117                     | 2                | 0.7                     |
| Methylene H <sub>4</sub> F dehydrogenase/Methenyl H <sub>4</sub> F cyclohydrolase | <i>folD</i>    | DAMO_1852      | 89                      | 1                | 38                      | 0.7              | 0.7                     |
| Formyl H <sub>4</sub> F deformylase   | <i>purU</i>    | DAMO_2586      | 82                      | 1                | 28                      | 0.5              | 0.5                     |
| Formate dehydrogenase   | <i>fdhA2</i>   | DAMO_0853      | 145                     | 0.5              | 17                      | 0.1              | 0.2                     |
|   | <i>fdhB/C2</i> | DAMO_0854      | 145                     | 0.7              | 31                      | 0.2              | 0.3                     |

**Table 4.** Transcriptome analysis of genes encoding enzymes involved in the denitrification pathway in *M. oxyfe* under anoxic conditions and after 24 h exposure to 8 % O<sub>2</sub>. Light grey = down-regulated genes; dark grey = up-regulated genes; white = constitutively expressed.

| Enzyme                        | Gene                       | ORF identifier | Anoxic                  |                  | Oxic                    |                  | Ratio (oxic vs. anoxic) |
|-------------------------------|----------------------------|----------------|-------------------------|------------------|-------------------------|------------------|-------------------------|
|                               |                            |                | # unique reads detected | average coverage | # unique reads detected | average coverage |                         |
| Nitrate reductase             | <i>narG</i>                | DAMO_0778      | 1452                    | 4                | 190                     | 0.8              | 0.2                     |
|                               | <i>narH</i>                | DAMO_0776      | 2732                    | 17.9             | 193                     | 2                | 0.1                     |
|                               | <i>narL</i>                | DAMO_0774      | 259                     | 3.8              | 27                      | 0.6              | 0.2                     |
|                               | <i>narJ</i>                | DAMO_0775      | 353                     | 3.9              | 30                      | 0.5              | 0.1                     |
| Periplasmic nitrate reductase | <i>napA</i>                | DAMO_2411      | 250                     | 1.1              | 72                      | 0.5              | 0.5                     |
|                               | <i>napB</i>                | DAMO_2410      | 8                       | 0.2              | 2                       | 0.1              | 0.4                     |
| Nitrite reductase             | <i>nirS</i>                | DAMO_2415      | 2134                    | 13               | 113                     | 1.1              | 0.1                     |
|                               | <i>nirJ</i>                | DAMO_2413      | 116                     | 1                | 48                      | 0.6              | 0.7                     |
|                               | <i>nirF</i>                | DAMO_2412      | 88                      | 0.7              | 35                      | 0.5              | 0.6                     |
|                               | <i>nirD/nirG/nirH/nirL</i> | DAMO_2409      | 48                      | 0.4              | 10                      | 0.1              | 0.3                     |
| Nitric oxide reductase        | <i>norZ1</i>               | DAMO_1889      | 201                     | 0.9              | 38                      | 0.3              | 0.3                     |
|                               | <i>norZ2</i>               | DAMO_2434      | 2229                    | 9.2              | 10609                   | 69.4             | 7.5                     |
|                               | <i>norZ3</i>               | DAMO_2437      | 9380                    | 38.7             | 7715                    | 50.3             | 1.3                     |

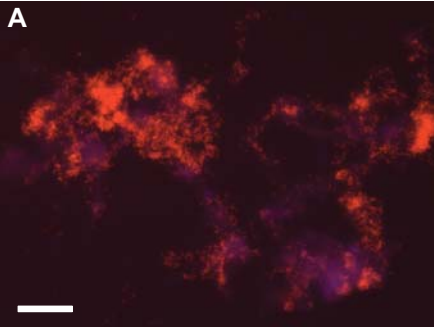
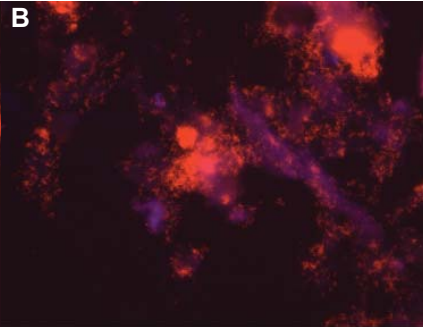
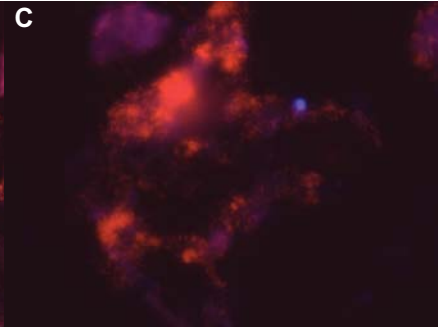


**Table 5.** Transcriptome analysis of genes encoding enzymes involved in the response to oxidative stress and TORs in *M. oxyfera* under anoxic conditions and after 24 h exposure to 8 % O<sub>2</sub>. Light grey = down-regulated genes; dark grey = up-regulated genes; white = constitutively expressed.

| Enzyme                                 | Gene        | ORF identifier | Anoxic                  |                  | Oxic                    |                  | Ratio (oxic vs. anoxic) |
|--|-------------|----------------|-------------------------|------------------|-------------------------|------------------|-------------------------|
|  |             |                | # unique reads detected | average coverage | # unique reads detected | average coverage |                         |
| Cyt <i>c</i> -dependent TOR            | <i>cox1</i> | DAMO_1165      | 103                     | 0.6              | 31                      | 0.3              | 0.5                     |
|  | <i>cox2</i> | DAMO_1166      | 93                      | 1.3              | 41                      | 0.9              | 0.7                     |
|  | <i>cox3</i> | DAMO_1164      | 43                      | 0.8              | 5                       | 0.1              | 0.2                     |
|  | <i>cox4</i> | DAMO_1162      | 13                      | 0.5              | 4                       | 0.2              | 0.5                     |
| Cyt <i>c</i> -dependent TOR            | <i>cbaA</i> | DAMO_0801      | 267                     | 1.9              | 138                     | 1.6              | 0.8                     |
|  | <i>cbaB</i> | DAMO_0802      | 166                     | 3                | 164                     | 4.7              | 1.6                     |
| UbqO-dependent TOR                     | <i>cyoB</i> | DAMO_1118      | 73                      | 0.5              | 16                      | 0.2              | 0.3                     |
|  | <i>cyoA</i> | DAMO_1119      | 19                      | 0.3              | 5                       | 0.1              | 0.4                     |
| Diiron cyanide-insensitive AOX         | <i>aox</i>  | DAMO_2910      | 41                      | 0.6              | 39                      | 0.9              | 1.5                     |
| Dyp-type peroxidase                    | <i>dyp</i>  | DAMO_0362      | 35                      | 0.4              | 3                       | 0.1              | 0.1                     |
| Di-haem cytochrome <i>c</i> peroxidase | <i>ccp</i>  | DAMO_1661      | 41                      | 0.6              | 5                       | 0.1              | 0.1                     |
|  | <i>ccp</i>  | DAMO_1666      | 93                      | 0.6              | 41                      | 0.4              | 0.6                     |
| Alkyl hydroperoxidase                  | <i>ahpC</i> | DAMO_1985      | 97                      | 1.6              | 253                     | 6.6              | 4.1                     |
| Superoxide dismutase                   | <i>sodB</i> | DAMO_0395      | 215                     | 3.6              | 80                      | 2.1              | 0.6                     |
| Rubrerythrin                           | <i>rbr</i>  | DAMO_1284      | 129                     | 2.6              | 31                      | 1                | 0.4                     |

**Table 6.** Analysis of *M. oxyfera* and non-*M. oxyfera pmo* and *amo* gene cluster transcripts under anoxic conditions (2282 reads) and after 24 h exposure to 8 % O<sub>2</sub> (2110 reads).

| Organism                | Anoxic  |      | Oxic    |      |
|-------------------------|---------|------|---------|------|
|                         | # reads | %    | # reads | %    |
| <i>M. oxyfera</i>       | 2275    | 99.7 | 1911    | 90.6 |
| <i>Methylobacter</i>    | 0       | 0    | 4       | 0.2  |
| <i>Methylovulum</i>     | 0       | 0    | 11      | 0.5  |
| <i>Methylomicrobium</i> | 0       | 0    | 9       | 0.4  |
| <i>Methylomonas</i>     | 4       | 0.2  | 108     | 5.1  |
| <i>Methyococcus</i>     | 1       | 0    | 24      | 1.1  |
| <i>Methylosinus</i>     | 0       | 0    | 15      | 0.7  |
| <i>Methylocystis</i>    | 2       | 0.1  | 28      | 1.3  |
| <i>Nitrosomonas</i>     | 0       | 0    | 2       | 0.1  |

**A****B****C**

**Supplementary Table 1.** Transcriptome analysis of *M. oxyfera* genes under anoxic conditions and after 24 h exposure to 8 % O<sub>2</sub>.

From the 2303 transcripts detected, 148 were up-regulated, 961 down-regulated, 856 transcripts did not change significantly, 296 were only detected under anoxic and 42 only upon O<sub>2</sub> exposure.

| ORF identifier | Description  | Gene length | Anoxic                  |          | Oxic             |                         |          | Ratio (oxic vs. anoxic) |                  |
|----------------|--|-------------|-------------------------|----------|------------------|-------------------------|----------|-------------------------|------------------|
|                |  |             | # unique reads detected | coverage | average coverage | # unique reads detected | coverage |                         | average coverage |
| DAMO_0001      | Chromosomal replication initiator protein dnaA   | 1359        | 104                     | 5.5      | 0.8              | 4                       | 0.2      | 0.0                     | 0.1              |
| DAMO_0002      | putative dihydroflavonol-4-reductase (DFR)   | 993         | 30                      | 2.2      | 0.3              | 4                       | 0.3      | 0.1                     | 0.2              |
| DAMO_0003      | Cytochrome c biogenesis protein CcdA   | 750         | 149                     | 14.3     | 2.0              | 29                      | 2.8      | 0.6                     | 0.3              |
| DAMO_0004      | putative Peptidase M16 domain protein, involved in ppq synthesis (ppqG)                                    | 1347        | 39                      | 2.1      | 0.3              | 13                      | 0.7      | 0.2                     | 0.5              |
| DAMO_0005      | putative Zn-dependent protease, involved in ppq synthesis (ppqF)   | 1284        | 41                      | 2.3      | 0.3              | 12                      | 0.7      | 0.1                     | 0.5              |
| DAMO_0006      | exported protein of unknown function   | 471         | 1                       | 0.2      | 0.0              | 5                       | 0.8      | 0.2                     | 7.9              |
| DAMO_0007      | Peptidase S1 and S6, chymotrypsin/Hap  | 1119        | 214                     | 13.8     | 1.9              | 51                      | 3.3      | 0.7                     | 0.4              |
| DAMO_0008      | protein of unknown function  | 162         | 4                       | 1.8      | 0.2              | 3                       | 1.3      | 0.3                     | 1.2              |
| DAMO_0009      | Lipase (Class 3)   | 1089        | 4                       | 0.3      | 0.0              | 0                       | 0.0      | 0.0                     | 0.0              |
| DAMO_0010      | Inositol-1-monophosphatase (IMPase) (Inositol-1- phosphatase) (I-1-Pase)                                   | 783         | 59                      | 5.4      | 0.8              | 35                      | 3.2      | 0.7                     | 0.9              |
| DAMO_0011      | protein of unknown function  | 180         | 26                      | 10.4     | 1.4              | 5                       | 2.0      | 0.4                     | 0.3              |
| DAMO_0012      | Carbon starvation protein A  | 1695        | 31                      | 1.3      | 0.2              | 11                      | 0.5      | 0.1                     | 0.6              |
| DAMO_0013      | Uncharacterized 28.2 kDa protein in hemB 3'region  | 783         | 36                      | 3.3      | 0.5              | 19                      | 1.7      | 0.4                     | 0.8              |
| DAMO_0014      | conserved protein of unknown function  | 321         | 184                     | 41.3     | 5.8              | 388                     | 87.0     | 19.2                    | 3.3              |
| DAMO_0015      | protein of unknown function  | 390         | 14                      | 2.6      | 0.4              | 1                       | 0.2      | 0.0                     | 0.1              |
| DAMO_0016      | protein of unknown function  | 195         | 22                      | 8.1      | 1.1              | 5                       | 1.8      | 0.4                     | 0.4              |
| DAMO_0017      | protein of unknown function  | 201         | 4                       | 1.4      | 0.2              | 8                       | 2.9      | 0.6                     | 3.2              |
| DAMO_0018      | Universal stress protein-like (fragment)   | 471         | 35                      | 5.4      | 0.7              | 78                      | 11.9     | 2.6                     | 3.5              |
| DAMO_0019      | protein of unknown function  | 150         | 0                       | 0.0      | 0.0              | 0                       | 0.0      | 0.0                     | —                |
| DAMO_0021      | Kelch repeat-containing protein precursor  | 942         | 0                       | 0.0      | 0.0              | 0                       | 0.0      | 0.0                     | —                |
| DAMO_0022      | conserved protein of unknown function  | 174         | 0                       | 0.0      | 0.0              | 0                       | 0.0      | 0.0                     | —                |
| DAMO_0023      | protein of unknown function  | 414         | 0                       | 0.0      | 0.0              | 0                       | 0.0      | 0.0                     | —                |
| DAMO_0025      | protein of unknown function  | 243         | 0                       | 0.0      | 0.0              | 0                       | 0.0      | 0.0                     | —                |
| DAMO_0026      | Maturase; integron/retron-type RNA-directed DNA polymerase (Reverse transcriptase); part of type II intron | 1338        | 0                       | 0.0      | 0.0              | 0                       | 0.0      | 0.0                     | —                |
| DAMO_0027      | protein of unknown function  | 108         | 0                       | 0.0      | 0.0              | 0                       | 0.0      | 0.0                     | —                |
| DAMO_0028      | protein of unknown function  | 624         | 0                       | 0.0      | 0.0              | 0                       | 0.0      | 0.0                     | —                |
| DAMO_0029      | transposase  | 1359        | 1                       | 0.1      | 0.0              | 0                       | 0.0      | 0.0                     | 0.0              |
| DAMO_0031      | putative insertion sequence IS21 ATP-binding protein   | 771         | 157                     | 14.7     | 2.0              | 18                      | 1.7      | 0.4                     | 0.2              |
| DAMO_0032      | transposase  | 1530        | 171                     | 8.0      | 1.1              | 20                      | 0.9      | 0.2                     | 0.2              |
| DAMO_0034      | conserved hypothetical protein   | 279         | 37                      | 9.5      | 1.3              | 21                      | 5.4      | 1.2                     | 0.9              |
| DAMO_0035      | putative Dehydrogenases  | 1194        | 22                      | 1.3      | 0.2              | 6                       | 0.4      | 0.1                     | 0.4              |
| DAMO_0036      | copper-transporting P-type ATPase  | 2649        | 77                      | 2.1      | 0.3              | 51                      | 1.4      | 0.3                     | 1.0              |
| DAMO_0038      | conserved protein of unknown function  | 99          | 19                      | 13.8     | 1.9              | 4                       | 2.9      | 0.6                     | 0.3              |
| DAMO_0039      | YHS domain protein   | 147         | 0                       | 0.0      | 0.0              | 0                       | 0.0      | 0.0                     | —                |
| DAMO_0040      | conserved membrane protein of unknown function   | 1167        | 24                      | 1.5      | 0.2              | 8                       | 0.5      | 0.1                     | 0.5              |
| DAMO_0041      | ABC-type transporter, permease component   | 1158        | 31                      | 1.9      | 0.3              | 5                       | 0.3      | 0.1                     | 0.3              |
| DAMO_0042      | putative ABC transporter, ATP-binding protein  | 723         | 17                      | 1.7      | 0.2              | 2                       | 0.2      | 0.0                     | 0.2              |
| DAMO_0043      | Secretion protein HlyD   | 1212        | 25                      | 1.5      | 0.2              | 3                       | 0.2      | 0.0                     | 0.2              |
| DAMO_0044      | putative nucleoside phosphorylase (modular protein)  | 816         | 14                      | 1.2      | 0.2              | 6                       | 0.5      | 0.1                     | 0.7              |
| DAMO_0045      | Squalene--hopene cyclase   | 1965        | 185                     | 6.8      | 0.9              | 29                      | 1.1      | 0.2                     | 0.2              |
| DAMO_0046      | Radical SAM (fragment)   | 474         | 63                      | 9.6      | 1.3              | 19                      | 2.9      | 0.6                     | 0.5              |
| DAMO_0047      | Radical SAM domain protein (fragment)  | 699         | 88                      | 9.1      | 1.3              | 39                      | 4.0      | 0.9                     | 0.7              |
| DAMO_0048      | exported protein of unknown function   | 207         | 3                       | 1.0      | 0.1              | 0                       | 0.0      | 0.0                     | 0.0              |
| DAMO_0051      | putative DegT/DnrJ/EryC1/StrS aminotransferase protein family  | 1119        | 39                      | 2.5      | 0.3              | 29                      | 1.9      | 0.4                     | 1.2              |
| DAMO_0052      | S-adenosylmethionine decarboxylase   | 435         | 532                     | 88.1     | 12.3             | 312                     | 51.6     | 11.4                    | 0.9              |

|           |   |      |     |      |     |     |      |     |     |
|-----------|---|------|-----|------|-----|-----|------|-----|-----|
| DAMO_0053 | Spermidine synthase (Putrescine aminopropyltransferase) (PAPT) (SPDSY)                            | 918  | 134 | 10.5 | 1.5 | 25  | 2.0  | 0.4 | 0.3 |
| DAMO_0054 | Arginine decarboxylase  | 1464 | 128 | 6.3  | 0.9 | 36  | 1.8  | 0.4 | 0.4 |
| DAMO_0055 | Protein-export membrane protein secD  | 1548 | 47  | 2.2  | 0.3 | 7   | 0.3  | 0.1 | 0.2 |
| DAMO_0056 | Protein-export membrane protein secF  | 939  | 51  | 3.9  | 0.5 | 7   | 0.5  | 0.1 | 0.2 |
| DAMO_0057 | Phosphoheptose isomerase (Sedoheptulose 7-phosphate isomerase)                                    | 678  | 54  | 5.7  | 0.8 | 12  | 1.3  | 0.3 | 0.4 |
| DAMO_0058 | putative Serine-type D-Ala-D-Ala carboxypeptidase   | 1068 | 148 | 10.0 | 1.4 | 20  | 1.3  | 0.3 | 0.2 |
| DAMO_0059 | DNA processing chain A (DprA/Smf)   | 1140 | 31  | 2.0  | 0.3 | 7   | 0.4  | 0.1 | 0.4 |
| DAMO_0060 | DNA topoisomerase I   | 2478 | 148 | 4.3  | 0.6 | 16  | 0.5  | 0.1 | 0.2 |
| DAMO_0061 | conserved hypothetical protein; putative glucose-inhibited division protein (gid)                 | 1332 | 82  | 4.4  | 0.6 | 13  | 0.7  | 0.2 | 0.3 |
| DAMO_0062 | conserved protein of unknown function   | 417  | 1   | 0.2  | 0.0 | 0   | 0.0  | 0.0 | 0.0 |
| DAMO_0063 | putative Transcription regulator, SpoVT/AbrB family   | 276  | 6   | 1.6  | 0.2 | 7   | 1.8  | 0.4 | 1.8 |
| DAMO_0064 | transposase (fragment)  | 201  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0066 | membrane protein of unknown function  | 639  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0068 | protein of unknown function   | 378  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0069 | conserved protein of unknown function   | 1158 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0070 | Tyrosine recombinase xerC   | 1050 | 74  | 5.1  | 0.7 | 20  | 1.4  | 0.3 | 0.4 |
| DAMO_0071 | ATP-dependent protease hslV (protease subunit of a proteasome-like degradation complex)           | 480  | 44  | 6.6  | 0.9 | 6   | 0.9  | 0.2 | 0.2 |
| DAMO_0072 | ATPase component of the HslUV protease, also functions as molecular chaperone; heat shock protein | 1356 | 51  | 2.7  | 0.4 | 10  | 0.5  | 0.1 | 0.3 |
| DAMO_0073 | acetylglutamate kinase (NAG kinase) (AGK)   | 912  | 65  | 5.1  | 0.7 | 4   | 0.3  | 0.1 | 0.1 |
| DAMO_0074 | acetylornithine transaminase (NAcOATase and DapATase), PLP-dependent                              | 1200 | 46  | 2.8  | 0.4 | 4   | 0.2  | 0.1 | 0.1 |
| DAMO_0075 | ornithine carbamoyltransferase (OTCase)   | 936  | 87  | 6.7  | 0.9 | 12  | 0.9  | 0.2 | 0.2 |
| DAMO_0076 | conserved protein of unknown function   | 249  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0078 | protein of unknown function   | 375  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0079 | conserved protein of unknown function   | 1119 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0080 | protein of unknown function   | 285  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0081 | protein of unknown function   | 195  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0082 | conserved protein of unknown function   | 1263 | 5   | 0.3  | 0.0 | 0   | 0.0  | 0.0 | 0.0 |
| DAMO_0083 | DNA repair protein radC homolog   | 711  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0084 | protein of unknown function   | 447  | 1   | 0.2  | 0.0 | 3   | 0.5  | 0.1 | 4.7 |
| DAMO_0085 | Argininosuccinate synthase (Citrulline--aspartate ligase)   | 1233 | 152 | 8.9  | 1.2 | 21  | 1.2  | 0.3 | 0.2 |
| DAMO_0086 | argininosuccinate lyase   | 1398 | 151 | 7.8  | 1.1 | 13  | 0.7  | 0.1 | 0.1 |
| DAMO_0087 | putative Fibronectin, type III precursor  | 1047 | 17  | 1.2  | 0.2 | 1   | 0.1  | 0.0 | 0.1 |
| DAMO_0088 | Selenocysteine-specific elongation factor (SelB translation factor)                               | 1950 | 473 | 17.5 | 2.4 | 820 | 30.3 | 6.7 | 2.7 |
| DAMO_0089 | Sec-independent protein translocase protein tatA/E homolog  | 207  | 67  | 23.3 | 3.2 | 47  | 16.3 | 3.6 | 1.1 |
| DAMO_0090 | UDP-glucose 6-dehydrogenase (UDP-Glc dehydrogenase) (UDP-GlcDH) (UDPGDH)                          | 1323 | 13  | 0.7  | 0.1 | 4   | 0.2  | 0.0 | 0.5 |
| DAMO_0091 | protein of unknown function   | 186  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0092 | protein of unknown function   | 123  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0093 | nicotinamide nucleotide transhydrogenase, subunit alpha1  | 1155 | 373 | 23.3 | 3.2 | 56  | 3.5  | 0.8 | 0.2 |
| DAMO_0094 | nicotinamide nucleotide transhydrogenase, subunit alpha2  | 297  | 9   | 2.2  | 0.3 | 0   | 0.0  | 0.0 | 0.0 |
| DAMO_0095 | pyridine nucleotide transhydrogenase (proton pump), beta subunit                                  | 1380 | 26  | 1.4  | 0.2 | 7   | 0.4  | 0.1 | 0.4 |
| DAMO_0096 | conserved protein of unknown function   | 1155 | 22  | 1.4  | 0.2 | 2   | 0.1  | 0.0 | 0.1 |
| DAMO_0097 | putative Diaminopimelate decarboxylase  | 1308 | 55  | 3.0  | 0.4 | 9   | 0.5  | 0.1 | 0.3 |
| DAMO_0098 | putative TonB-dependent receptor  | 2178 | 145 | 4.8  | 0.7 | 15  | 0.5  | 0.1 | 0.2 |
| DAMO_0099 | putative Sensor protein   | 1479 | 100 | 4.9  | 0.7 | 29  | 1.4  | 0.3 | 0.5 |
| DAMO_0100 | Two component, sigma54 specific, transcriptional regulator, Fis family                            | 1419 | 202 | 10.2 | 1.4 | 41  | 2.1  | 0.5 | 0.3 |
| DAMO_0102 | putative TonB-dependent siderophore receptor  | 2238 | 4   | 0.1  | 0.0 | 1   | 0.0  | 0.0 | 0.4 |
| DAMO_0103 | protein of unknown function   | 243  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0104 | putative Histidine kinase   | 1470 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0105 | Two component, sigma54 specific, transcriptional regulator, Fis family                            | 1377 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0106 | protein of unknown function   | 273  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0107 | PilT protein-like (fragment)  | 405  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0108 | protein of unknown function   | 204  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0109 | protein of unknown function   | 351  | 1   | 0.2  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0111 | protein of unknown function   | 252  | 1   | 0.3  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0112 | Methanol dehydrogenase large subunit (mxAF1)  | 1806 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0113 | Conserved hypothetical protein; putative mxa  | 897  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |

|           |   |      |      |       |      |     |       |      |     |
|-----------|---|------|------|-------|------|-----|-------|------|-----|
| DAMO_0114 | mxgG (Cytochrome c1 precursor) involved in Methanol dehydrogenase (mxgG1)                                 | 504  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0115 | Methanol dehydrogenase, small subunit (mxgA)  | 285  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0116 | Conserved hypothetical protein; putative mxgR, involved in methanol dehydrogenase                         | 1020 | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0117 | Conserved hypothetical protein; putative mxgS, involved in methanol dehydrogenase                         | 888  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0118 | Putative mxgA protein, involved in Ca <sup>2+</sup> insertion in methanol dehydrogenase                   | 954  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0119 | Putative mxgC protein, involved in Ca <sup>2+</sup> insertion in methanol dehydrogenase                   | 987  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0120 | Putative mxgK protein, involved in Ca <sup>2+</sup> insertion into methanol dehydrogenase                 | 567  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0121 | Putative fused mxgL and mxgD proteins, involved in Ca <sup>2+</sup> insertion into methanol dehydrogenase | 1620 | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0122 | conserved hypothetical protein; putative mxgE, involved in methanol dehydrogenase (mxgE1)                 | 1002 | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0124 | Methanol dehydrogenase large subunit homolog  | 1905 | 1    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0125 | Conserved hypothetical protein; putative mxg  | 1719 | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0127 | mxgG (Cytochrome c1 precursor) involved in Methanol dehydrogenase (mxgG2)                                 | 600  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0128 | conserved hypothetical protein; putative mxgE, involved in methanol dehydrogenase (mxgE2)                 | 969  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0129 | putative TonB-dependent receptor  | 2346 | 30   | 0.9   | 0.1  | 2   | 0.1   | 0.0  | 0.1 |
| DAMO_0130 | protein of unknown function   | 186  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0131 | putative TonB-like protein  | 978  | 88   | 6.5   | 0.9  | 23  | 1.7   | 0.4  | 0.4 |
| DAMO_0132 | exported protein of unknown function  | 1236 | 444  | 25.9  | 3.6  | 184 | 10.7  | 2.4  | 0.7 |
| DAMO_0133 | exported protein of unknown function  | 2058 | 127  | 4.4   | 0.6  | 15  | 0.5   | 0.1  | 0.2 |
| DAMO_0134 | Methanol dehydrogenase large subunit homolog  | 1842 | 435  | 17.0  | 2.4  | 148 | 5.8   | 1.3  | 0.5 |
| DAMO_0136 | Conserved hypothetical protein; putative mxg  | 891  | 113  | 9.1   | 1.3  | 65  | 5.3   | 1.2  | 0.9 |
| DAMO_0138 | mxgG (cytochrome c1 precursor) involved in methanol dehydrogenase (mxgG3)                                 | 495  | 46   | 6.7   | 0.9  | 18  | 2.6   | 0.6  | 0.6 |
| DAMO_0139 | exported protein of unknown function  | 429  | 32   | 5.4   | 0.7  | 147 | 24.7  | 5.4  | 7.3 |
| DAMO_0140 | Cold shock protein, DNA binding   | 207  | 1430 | 497.4 | 69.3 | 353 | 122.8 | 27.1 | 0.4 |
| DAMO_0141 | membrane protein of unknown function  | 531  | 7    | 0.9   | 0.1  | 1   | 0.1   | 0.0  | 0.2 |
| DAMO_0142 | conserved protein of unknown function   | 483  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0143 | conserved exported protein of unknown function  | 534  | 32   | 4.3   | 0.6  | 22  | 3.0   | 0.7  | 1.1 |
| DAMO_0145 | putative dioxygenase VC_1345  | 1242 | 88   | 5.1   | 0.7  | 82  | 4.8   | 1.0  | 1.5 |
| DAMO_0146 | protein of unknown function   | 684  | 114  | 12.0  | 1.7  | 81  | 8.5   | 1.9  | 1.1 |
| DAMO_0147 | protein of unknown function   | 762  | 87   | 8.2   | 1.1  | 88  | 8.3   | 1.8  | 1.6 |
| DAMO_0148 | protein of unknown function   | 690  | 118  | 12.3  | 1.7  | 68  | 7.1   | 1.6  | 0.9 |
| DAMO_0149 | conserved protein of unknown function   | 810  | 188  | 16.7  | 2.3  | 218 | 19.4  | 4.3  | 1.8 |
| DAMO_0150 | conserved protein of unknown function   | 234  | 0    | 0.0   | 0.0  | 4   | 1.2   | 0.3  | —   |
| DAMO_0151 | conserved protein of unknown function   | 303  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0152 | putative aldehyde dehydrogenase ycbD  | 1491 | 396  | 19.1  | 2.7  | 402 | 19.4  | 4.3  | 1.6 |
| DAMO_0153 | Amidino transferase family protein  | 807  | 113  | 10.1  | 1.4  | 191 | 17.0  | 3.8  | 2.7 |
| DAMO_0154 | succinylornithine transaminase, also has acetylornithine transaminase activity, PLP-dependent             | 1188 | 190  | 11.5  | 1.6  | 219 | 13.3  | 2.9  | 1.8 |
| DAMO_0155 | protein of unknown function   | 168  | 54   | 23.1  | 3.2  | 16  | 6.9   | 1.5  | 0.5 |
| DAMO_0156 | Putative acetolactate synthase large subunit  | 1626 | 245  | 10.8  | 1.5  | 222 | 9.8   | 2.2  | 1.4 |
| DAMO_0158 | Putative outer membrane protein (modular protein)   | 1500 | 4    | 0.2   | 0.0  | 0   | 0.0   | 0.0  | 0.0 |
| DAMO_0159 | Orotate phosphoribosyltransferase (modular protein)   | 513  | 436  | 61.2  | 8.5  | 144 | 20.2  | 4.5  | 0.5 |
| DAMO_0160 | conserved protein of unknown function   | 1878 | 96   | 3.7   | 0.5  | 23  | 0.9   | 0.2  | 0.4 |
| DAMO_0161 | conserved protein of unknown function   | 645  | 84   | 9.4   | 1.3  | 31  | 3.5   | 0.8  | 0.6 |
| DAMO_0162 | membrane protein of unknown function  | 1797 | 94   | 3.8   | 0.5  | 102 | 4.1   | 0.9  | 1.7 |
| DAMO_0163 | exported protein of unknown function  | 465  | 1    | 0.2   | 0.0  | 0   | 0.0   | 0.0  | 0.0 |
| DAMO_0164 | membrane protein of unknown function  | 1461 | 14   | 0.7   | 0.1  | 5   | 0.2   | 0.1  | 0.6 |
| DAMO_0165 | putative peroxiredoxin (Thioredoxin reductase) (26 kDa antigen)   | 600  | 66   | 7.9   | 1.1  | 14  | 1.7   | 0.4  | 0.3 |
| DAMO_0166 | conserved exported protein of unknown function  | 321  | 24   | 5.4   | 0.8  | 0   | 0.0   | 0.0  | 0.0 |
| DAMO_0167 | conserved exported protein of unknown function  | 810  | 186  | 16.5  | 2.3  | 14  | 1.2   | 0.3  | 0.1 |
| DAMO_0170 | conserved hypothetical protein; putative quinoprotein amine dehydrogenase, beta chain-like                | 978  | 44   | 3.2   | 0.5  | 12  | 0.9   | 0.2  | 0.4 |
| DAMO_0171 | conserved protein of unknown function   | 276  | 37   | 9.7   | 1.3  | 20  | 5.2   | 1.1  | 0.9 |
| DAMO_0172 | protein of unknown function   | 543  | 54   | 7.2   | 1.0  | 19  | 2.5   | 0.6  | 0.6 |
| DAMO_0173 | conserved protein of unknown function   | 222  | 8    | 2.6   | 0.4  | 2   | 0.6   | 0.1  | 0.4 |
| DAMO_0174 | fructose 1,6-bisphosphatase II  | 1014 | 63   | 4.5   | 0.6  | 0   | 0.0   | 0.0  | 0.0 |
| DAMO_0175 | Fructose-bisphosphate aldolase  | 1065 | 300  | 20.3  | 2.8  | 50  | 3.4   | 0.7  | 0.3 |
| DAMO_0176 | Ribulose-phosphate 3-epimerase  | 666  | 82   | 8.9   | 1.2  | 8   | 0.9   | 0.2  | 0.2 |
| DAMO_0177 | Peptidase M48, Ste24p precursor   | 801  | 108  | 9.7   | 1.4  | 10  | 0.9   | 0.2  | 0.1 |

|           |  |      |     |       |      |     |       |      |      |
|-----------|--|------|-----|-------|------|-----|-------|------|------|
| DAMO_0178 | Cellulase precursor                                  | 1176 | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0179 | exported protein of unknown function                 | 1521 | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0180 | exported protein of unknown function                 | 492  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0181 | protein of unknown function                          | 426  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0182 | putative Cellulose synthase (UDP-forming)            | 2145 | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0183 | exported protein of unknown function                 | 156  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0185 | Acetyl-coenzyme A synthetase (Acetate--CoA ligase)   | 1950 | 109 | 4.0   | 0.6  | 13  | 0.5   | 0.1  | 0.2  |
| DAMO_0186 | putative Lipoprotein                                 | 675  | 75  | 8.0   | 1.1  | 12  | 1.3   | 0.3  | 0.3  |
| DAMO_0188 | exported protein of unknown function                 | 3021 | 20  | 0.5   | 0.1  | 3   | 0.1   | 0.0  | 0.2  |
| DAMO_0189 | Two component transcriptional regulator, LuxR family | 651  | 2   | 0.2   | 0.0  | 24  | 2.7   | 0.6  | 19.0 |
| DAMO_0190 | protein of unknown function                          | 201  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0191 | protein of unknown function                          | 489  | 4   | 0.6   | 0.1  | 19  | 2.8   | 0.6  | 7.5  |
| DAMO_0192 | exported protein of unknown function                 | 1317 | 2   | 0.1   | 0.0  | 14  | 0.8   | 0.2  | 11.1 |
| DAMO_0193 | putative Polysaccharide export protein               | 1089 | 3   | 0.2   | 0.0  | 11  | 0.7   | 0.2  | 5.8  |
| DAMO_0194 | putative Protein-tyrosine kinase                     | 2310 | 17  | 0.5   | 0.1  | 94  | 2.9   | 0.6  | 8.7  |
| DAMO_0196 | exported protein of unknown function                 | 1281 | 1   | 0.1   | 0.0  | 16  | 0.9   | 0.2  | 25.3 |
| DAMO_0197 | putative Similar to glycosyl transferase             | 1446 | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0199 | membrane protein of unknown function                 | 1404 | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0200 | membrane protein of unknown function                 | 1590 | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0201 | protein of unknown function                          | 816  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0202 | protein of unknown function                          | 312  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0203 | putative Glycosyl transferase group 1                | 1170 | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0204 | putative Glycosyltransferase, group 1 family protein | 1140 | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0205 | putative Glycosyl transferase, group 1               | 1230 | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0206 | exported protein of unknown function                 | 1944 | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0207 | conserved protein of unknown function                | 993  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0208 | conserved protein of unknown function                | 882  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0210 | putative Glycosyl transferase, group 1               | 1194 | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0211 | protein of unknown function                          | 819  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0212 | protein of unknown function                          | 1011 | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0214 | conserved exported protein of unknown function       | 2031 | 14  | 0.5   | 0.1  | 0   | 0.0   | 0.0  | —    |
| DAMO_0215 | conserved protein of unknown function                | 399  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0216 | protein of unknown function                          | 246  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0217 | ATPase (AAA+ superfamily)-like protein               | 1194 | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0218 | UDP-glucose/GDP-mannose dehydrogenase                | 1323 | 9   | 0.5   | 0.1  | 0   | 0.0   | 0.0  | —    |
| DAMO_0219 | exported protein of unknown function                 | 561  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0220 | protein of unknown function                          | 930  | 12  | 0.9   | 0.1  | 1   | 0.1   | 0.0  | 0.1  |
| DAMO_0221 | exported protein of unknown function                 | 1782 | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0223 | exported protein of unknown function                 | 1524 | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0224 | membrane protein of unknown function                 | 756  | 1   | 0.1   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0225 | membrane protein of unknown function                 | 1131 | 1   | 0.1   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0226 | Undecaprenol glycosyltransferase (fragment)          | 942  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0227 | putative restriction endonuclease-like               | 351  | 342 | 70.2  | 9.8  | 66  | 13.5  | 3.0  | 0.3  |
| DAMO_0229 | exported protein of unknown function                 | 648  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0230 | membrane protein of unknown function                 | 519  | 0   | 0.0   | 0.0  | 2   | 0.3   | 0.1  | —    |
| DAMO_0231 | membrane protein of unknown function                 | 171  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0232 | protein of unknown function                          | 1170 | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0233 | exported protein of unknown function                 | 573  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0235 | exported protein of unknown function                 | 1383 | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0236 | protein of unknown function                          | 174  | 801 | 331.4 | 46.2 | 328 | 135.7 | 29.9 | 0.6  |
| DAMO_0237 | exported protein of unknown function                 | 216  | 47  | 15.7  | 2.2  | 12  | 4.0   | 0.9  | 0.4  |
| DAMO_0238 | conserved protein of unknown function                | 381  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0239 | putative DNA polymerase, beta-like region            | 327  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0240 | protein of unknown function                          | 231  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0241 | protein of unknown function                          | 198  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |
| DAMO_0242 | exported protein of unknown function                 | 600  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —    |

|           |  |      |     |      |     |     |      |     |     |
|-----------|--|------|-----|------|-----|-----|------|-----|-----|
| DAMO_0244 | protein of unknown function  | 105  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0245 | protein of unknown function  | 699  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0246 | exported protein of unknown function   | 921  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0247 | protein of unknown function  | 1164 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0248 | protein of unknown function  | 222  | 1   | 0.3  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0249 | putative Glycosyl transferase family 2                                       | 1152 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0250 | membrane protein of unknown function   | 1632 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0251 | ABC transporter permease protein   | 792  | 0   | 0.0  | 0.0 | 1   | 0.1  | 0.0 | —   |
| DAMO_0252 | Wzt  | 1269 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0253 | conserved protein of unknown function  | 1014 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0254 | protein of unknown function  | 663  | 2   | 0.2  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0255 | protein of unknown function  | 4383 | 28  | 0.5  | 0.1 | 13  | 0.2  | 0.0 | 0.7 |
| DAMO_0256 | protein of unknown function  | 1311 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0257 | Glycosyl transferase family 2 (fragment)                                     | 906  | 3   | 0.2  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0258 | protein of unknown function  | 1995 | 1   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0259 | Spore coat polysaccharide biosynthesis protein spsK                          | 867  | 16  | 1.3  | 0.2 | 1   | 0.1  | 0.0 | 0.1 |
| DAMO_0260 | putative transcriptional regulator, CopG family                              | 249  | 5   | 1.4  | 0.2 | 0   | 0.0  | 0.0 | —   |
| DAMO_0261 | conserved protein of unknown function  | 411  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0262 | putative Glycosyl transferase, family 2                                      | 993  | 74  | 5.4  | 0.7 | 26  | 1.9  | 0.4 | 0.6 |
| DAMO_0263 | Glycosyltransferase  | 1230 | 68  | 4.0  | 0.6 | 14  | 0.8  | 0.2 | 0.3 |
| DAMO_0264 | Similar to capsular polysaccharide synthesis protein                         | 1404 | 77  | 3.9  | 0.6 | 26  | 1.3  | 0.3 | 0.5 |
| DAMO_0266 | UDP-glucose 4-epimerase (EC 5.1.3.2  | 921  | 20  | 1.6  | 0.2 | 5   | 0.4  | 0.1 | 0.4 |
| DAMO_0267 | PfkB domain protein  | 960  | 64  | 4.8  | 0.7 | 19  | 1.4  | 0.3 | 0.5 |
| DAMO_0268 | CTP synthase (UTP--ammonia ligase) (CTP synthetase)                          | 1608 | 299 | 13.4 | 1.9 | 140 | 6.3  | 1.4 | 0.7 |
| DAMO_0269 | 2-dehydro-3-deoxyphosphooctonate aldolase KDO-8-phosphate synthetase, KDOPS) | 840  | 90  | 7.7  | 1.1 | 60  | 5.1  | 1.1 | 1.1 |
| DAMO_0270 | Putative ABC transporter (permease and ATP-binding protein)                  | 1827 | 22  | 0.9  | 0.1 | 3   | 0.1  | 0.0 | 0.2 |
| DAMO_0271 | Similar to glucosyl-transferase (modular protein)                            | 1080 | 11  | 0.7  | 0.1 | 2   | 0.1  | 0.0 | 0.3 |
| DAMO_0272 | membrane protein of unknown function   | 2325 | 38  | 1.2  | 0.2 | 12  | 0.4  | 0.1 | 0.5 |
| DAMO_0273 | Arabinose 5-phosphate isomerase  | 960  | 26  | 2.0  | 0.3 | 7   | 0.5  | 0.1 | 0.4 |
| DAMO_0274 | membrane protein of unknown function   | 1611 | 44  | 2.0  | 0.3 | 17  | 0.8  | 0.2 | 0.6 |
| DAMO_0275 | 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase                         | 597  | 8   | 1.0  | 0.1 | 4   | 0.5  | 0.1 | 0.8 |
| DAMO_0276 | methionine adenosyltransferase 1 (AdoMet synthetase)                         | 1158 | 159 | 9.9  | 1.4 | 32  | 2.0  | 0.4 | 0.3 |
| DAMO_0277 | Peptidylprolyl isomerase (modular protein)                                   | 672  | 446 | 47.8 | 6.7 | 54  | 5.8  | 1.3 | 0.2 |
| DAMO_0278 | protein of unknown function  | 189  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0279 | protein of unknown function  | 330  | 205 | 44.7 | 6.2 | 111 | 24.2 | 5.3 | 0.9 |
| DAMO_0280 | protein of unknown function  | 411  | 54  | 9.5  | 1.3 | 12  | 2.1  | 0.5 | 0.4 |
| DAMO_0282 | protein of unknown function  | 315  | 56  | 12.8 | 1.8 | 28  | 6.4  | 1.4 | 0.8 |
| DAMO_0284 | conserved protein of unknown function  | 363  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0285 | Putative transcriptional regulator (fragment)                                | 282  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0286 | protein of unknown function  | 156  | 9   | 4.2  | 0.6 | 2   | 0.9  | 0.2 | 0.4 |
| DAMO_0287 | Adenosylhomocysteinase (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase)     | 1443 | 314 | 15.7 | 2.2 | 62  | 3.1  | 0.7 | 0.3 |
| DAMO_0290 | protein of unknown function  | 183  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0292 | protein of unknown function  | 1848 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0293 | putative Glycosyl transferase  | 1581 | 1   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | 0.0 |
| DAMO_0294 | protein of unknown function  | 2001 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0295 | putative Glycosyl transferase family 2 precursor                             | 1464 | 1   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | 0.0 |
| DAMO_0296 | exported protein of unknown function   | 900  | 31  | 2.5  | 0.3 | 0   | 0.0  | 0.0 | 0.0 |
| DAMO_0297 | membrane protein of unknown function   | 2133 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0298 | protein of unknown function  | 342  | 6   | 1.3  | 0.2 | 4   | 0.8  | 0.2 | 1.1 |
| DAMO_0299 | putative cell wall or antigenic protei                                       | 1038 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0300 | putative Collagen triple helix repeat  | 1035 | 1   | 0.1  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0301 | conserved membrane protein of unknown function                               | 1923 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0302 | protein of unknown function  | 756  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0303 | Glycosyltransferase involved in cell wall biogenesis                         | 969  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0304 | conserved membrane protein of unknown function                               | 2100 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0306 | RRM domain (fragment)  | 186  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |



|           |  |      |     |      |      |     |      |     |     |
|-----------|--|------|-----|------|------|-----|------|-----|-----|
| DAMO_0307 | protein of unknown function  | 147  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_0308 | exported protein of unknown function   | 951  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_0309 | membrane protein of unknown function   | 975  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_0310 | Radical SAM domain protein precursor   | 1362 | 110 | 5.8  | 0.8  | 17  | 0.9  | 0.2 | 0.2 |
| DAMO_0311 | Glycosyl transferase, family 2   | 753  | 45  | 4.3  | 0.6  | 1   | 0.1  | 0.0 | —   |
| DAMO_0312 | exported protein of unknown function   | 921  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_0313 | Glycosyl transferase, family 2   | 735  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_0314 | putative Permease YjgP/YjgQ  | 1089 | 24  | 1.6  | 0.2  | 19  | 1.3  | 0.3 | 1.3 |
| DAMO_0315 | putative Permease YjgP/YjgQ family protein   | 1281 | 51  | 2.9  | 0.4  | 19  | 1.1  | 0.2 | 0.6 |
| DAMO_0316 | membrane protein of unknown function   | 966  | 17  | 1.3  | 0.2  | 9   | 0.7  | 0.1 | 0.8 |
| DAMO_0317 | exported protein of unknown function   | 1686 | 72  | 3.1  | 0.4  | 26  | 1.1  | 0.2 | 0.6 |
| DAMO_0318 | protein of unknown function  | 441  | 79  | 12.9 | 1.8  | 20  | 3.3  | 0.7 | 0.4 |
| DAMO_0319 | putative Metallo-beta-lactamase superfamily  | 2505 | 40  | 1.1  | 0.2  | 14  | 0.4  | 0.1 | 0.6 |
| DAMO_0320 | protein of unknown function  | 138  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_0321 | Exodeoxyribonuclease 7 large subunit large subunit   | 1242 | 204 | 11.8 | 1.6  | 47  | 2.7  | 0.6 | 0.4 |
| DAMO_0322 | exodeoxyribonuclease small subunit (modular protein)   | 264  | 1   | 0.3  | 0.0  | 0   | 0.0  | 0.0 | 0.0 |
| DAMO_0323 | Putative Geranyltranstransferas  | 939  | 209 | 16.0 | 2.2  | 30  | 2.3  | 0.5 | 0.2 |
| DAMO_0324 | putative rRNA methylase  | 885  | 111 | 9.0  | 1.3  | 14  | 1.1  | 0.3 | 0.2 |
| DAMO_0325 | putative inorganic polyphosphate/ATP-NAD kinas   | 855  | 78  | 6.6  | 0.9  | 8   | 0.7  | 0.1 | 0.2 |
| DAMO_0326 | DNA repair protein recN (Recombination protein N)  | 1716 | 150 | 6.3  | 0.9  | 19  | 0.8  | 0.2 | 0.2 |
| DAMO_0327 | 50S ribosomal protein L21  | 312  | 35  | 8.1  | 1.1  | 15  | 3.5  | 0.8 | 0.7 |
| DAMO_0328 | 50S ribosomal subunit protein L27  | 255  | 259 | 73.1 | 10.2 | 77  | 21.7 | 4.8 | 0.5 |
| DAMO_0330 | GTP-binding protein with nucleoside triP hydrolase domain; DNA-binding GTPase involved in cell partitioning; multic    | 1062 | 46  | 3.1  | 0.4  | 9   | 0.6  | 0.1 | 0.3 |
| DAMO_0331 | gamma-glutamate kinase   | 1152 | 73  | 4.6  | 0.6  | 12  | 0.8  | 0.2 | 0.3 |
| DAMO_0332 | gamma-glutamylphosphate reductase  | 1263 | 105 | 6.0  | 0.8  | 19  | 1.1  | 0.2 | 0.3 |
| DAMO_0333 | putative nicotinate-nucleotide adenylyltransferase diphosphorylase) (Nicotinate mononucleotide adenylyltransferase) (I | 693  | 61  | 6.3  | 0.9  | 18  | 1.9  | 0.4 | 0.5 |
| DAMO_0334 | conserved protein of unknown function  | 435  | 19  | 3.1  | 0.4  | 2   | 0.3  | 0.1 | 0.2 |
| DAMO_0335 | Transcriptional regulators, TraR/DksA family   | 354  | 458 | 93.2 | 13.0 | 113 | 23.0 | 5.1 | 0.4 |
| DAMO_0337 | protein of unknown function  | 498  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_0336 | putative competence protein F (COMF) (fragment)  | 519  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_0338 | protein of unknown function  | 381  | 2   | 0.4  | 0.1  | 0   | 0.0  | 0.0 | —   |
| DAMO_0339 | Glyceraldehyde-3-phosphate dehydrogenas  | 1002 | 182 | 13.1 | 1.8  | 25  | 1.8  | 0.4 | 0.2 |
| DAMO_0340 | Phosphoglycerate kinase, partial 5' end  | 384  | 40  | 7.5  | 1.0  | 2   | 0.4  | 0.1 | 0.1 |
| DAMO_0341 | Phosphoglycerate kinase, partial 3' end  | 849  | 65  | 5.5  | 0.8  | 15  | 1.3  | 0.3 | 0.4 |
| DAMO_0342 | Triosephosphate isomerase (TIM) (Triose-phosphate isomerase)   | 759  | 75  | 7.1  | 1.0  | 14  | 1.3  | 0.3 | 0.3 |
| DAMO_0343 | putative Protein-export membrane protein, secG-like  | 372  | 44  | 8.5  | 1.2  | 0   | 0.0  | 0.0 | 0.0 |
| DAMO_0345 | protein of unknown function  | 333  | 5   | 1.1  | 0.2  | 0   | 0.0  | 0.0 | 0.0 |
| DAMO_0346 | conserved protein of unknown function  | 1794 | 109 | 4.4  | 0.6  | 15  | 0.6  | 0.1 | 0.2 |
| DAMO_0347 | conserved protein of unknown function  | 1140 | 18  | 1.1  | 0.2  | 5   | 0.3  | 0.1 | 0.4 |
| DAMO_0348 | conserved membrane protein of unknown function   | 1317 | 36  | 2.0  | 0.3  | 6   | 0.3  | 0.1 | 0.3 |
| DAMO_0349 | conserved membrane protein of unknown function   | 639  | 72  | 8.1  | 1.1  | 15  | 1.7  | 0.4 | 0.3 |
| DAMO_0350 | conserved protein of unknown function  | 882  | 38  | 3.1  | 0.4  | 4   | 0.3  | 0.1 | 0.2 |
| DAMO_0351 | conserved membrane protein of unknown function   | 768  | 32  | 3.0  | 0.4  | 76  | 7.1  | 1.6 | 3.8 |
| DAMO_0353 | conserved protein of unknown function  | 117  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_0354 | conserved protein of unknown function  | 222  | 3   | 1.0  | 0.1  | 0   | 0.0  | 0.0 | 0.0 |
| DAMO_0355 | protein of unknown function  | 240  | 2   | 0.6  | 0.1  | 1   | 0.3  | 0.1 | 0.8 |
| DAMO_0356 | Type I restriction-modification system specificity determinant (fragment)  | 141  | 8   | 4.1  | 0.6  | 0   | 0.0  | 0.0 | 0.0 |
| DAMO_0357 | protein of unknown function  | 1302 | 345 | 19.1 | 2.7  | 104 | 5.8  | 1.3 | 0.5 |
| DAMO_0358 | protein of unknown function  | 204  | 60  | 21.2 | 3.0  | 14  | 4.9  | 1.1 | 0.4 |
| DAMO_0359 | protein of unknown function  | 174  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_0360 | ATPase, AAA+ superfamily   | 1248 | 1   | 0.1  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_0361 | OsmC family protein  | 453  | 6   | 1.0  | 0.1  | 1   | 0.2  | 0.0 | 0.3 |
| DAMO_0362 | Dyp-type peroxidase  | 882  | 35  | 2.9  | 0.4  | 3   | 0.2  | 0.1 | 0.1 |
| DAMO_0363 | Prevent-host-death family protein  | 243  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_0364 | Addiction module toxin, Txe/YoeB family  | 267  | 18  | 4.9  | 0.7  | 4   | 1.1  | 0.2 | 0.4 |
| DAMO_0367 | protein of unknown function  | 219  | 2   | 0.7  | 0.1  | 0   | 0.0  | 0.0 | —   |

|           |  |      |     |      |     |     |      |     |     |
|-----------|--|------|-----|------|-----|-----|------|-----|-----|
| DAMO_0369 | exported protein of unknown function   | 984  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0371 | putative 3-hydroxydecanoyl-ACP dehydratase   | 582  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0372 | protein of unknown function  | 306  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0373 | protein of unknown function  | 321  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0374 | transposase  | 852  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0375 | protein of unknown function  | 105  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0376 | protein of unknown function  | 240  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0377 | exported protein of unknown function   | 570  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0378 | protein of unknown function  | 267  | 4   | 1.1  | 0.2 | 0   | 0.0  | 0.0 | —   |
| DAMO_0379 | conserved protein of unknown function  | 285  | 26  | 6.6  | 0.9 | 47  | 11.9 | 2.6 | 2.9 |
| DAMO_0380 | conserved protein of unknown function  | 261  | 6   | 1.7  | 0.2 | 0   | 0.0  | 0.0 | 0.0 |
| DAMO_0381 | Transcriptional regulator, XRE family protein  | 288  | 28  | 7.0  | 1.0 | 3   | 0.8  | 0.2 | 0.2 |
| DAMO_0382 | Plasmid maintenance system killer  | 282  | 29  | 7.4  | 1.0 | 10  | 2.6  | 0.6 | 0.5 |
| DAMO_0383 | conserved protein of unknown function  | 990  | 44  | 3.2  | 0.4 | 9   | 0.7  | 0.1 | 0.3 |
| DAMO_0384 | protein of unknown function  | 318  | 7   | 1.6  | 0.2 | 3   | 0.7  | 0.1 | 0.7 |
| DAMO_0385 | protein of unknown function  | 90   | 1   | 0.8  | 0.1 | 3   | 2.4  | 0.5 | 4.7 |
| DAMO_0386 | Aconitate hydratase  | 1929 | 709 | 26.5 | 3.7 | 824 | 30.8 | 6.8 | 1.8 |
| DAMO_0387 | protein of unknown function  | 72   | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0388 | conserved exported protein of unknown function   | 345  | 27  | 5.6  | 0.8 | 1   | 0.2  | 0.0 | 0.1 |
| DAMO_0389 | Putative integron gene cassette protein (modular protein)  | 363  | 1   | 0.2  | 0.0 | 0   | 0.0  | 0.0 | 0.0 |
| DAMO_0390 | DNA polymerase IV, devoid of proofreading, damage-inducible protein P  | 1212 | 78  | 4.6  | 0.6 | 16  | 1.0  | 0.2 | 0.3 |
| DAMO_0391 | protein of unknown function  | 525  | 49  | 6.7  | 0.9 | 8   | 1.1  | 0.2 | 0.3 |
| DAMO_0392 | putative DNA-binding protein   | 381  | 105 | 19.8 | 2.8 | 33  | 6.2  | 1.4 | 0.5 |
| DAMO_0393 | Helicase, RecD/TraA family   | 2256 | 484 | 15.4 | 2.2 | 176 | 5.6  | 1.2 | 0.6 |
| DAMO_0394 | conserved protein of unknown function  | 204  | 39  | 13.8 | 1.9 | 28  | 9.9  | 2.2 | 1.1 |
| DAMO_0395 | Superoxide dismutase   | 603  | 215 | 25.7 | 3.6 | 80  | 9.6  | 2.1 | 0.6 |
| DAMO_0396 | ATP-dependent DNA helicase RecQ  | 1869 | 170 | 6.5  | 0.9 | 19  | 0.7  | 0.2 | 0.2 |
| DAMO_0397 | protein of unknown function  | 198  | 1   | 0.4  | 0.1 | 0   | 0.0  | 0.0 | 0.0 |
| DAMO_0398 | conserved protein of unknown function  | 594  | 76  | 9.2  | 1.3 | 132 | 16.0 | 3.5 | 2.7 |
| DAMO_0399 | conserved protein of unknown function  | 321  | 25  | 5.6  | 0.8 | 14  | 3.1  | 0.7 | 0.9 |
| DAMO_0400 | conserved protein of unknown function  | 504  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0401 | Integrase, catalytic region  | 1005 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0402 | protein of unknown function  | 270  | 65  | 17.3 | 2.4 | 23  | 6.1  | 1.4 | 0.6 |
| DAMO_0403 | protein of unknown function  | 912  | 59  | 4.7  | 0.6 | 17  | 1.3  | 0.3 | 0.5 |
| DAMO_0405 | putative Selenium-binding protein, precursor   | 1251 | 105 | 6.0  | 0.8 | 107 | 6.2  | 1.4 | 1.6 |
| DAMO_0407 | Amino acid permease-associated region  | 1941 | 76  | 2.8  | 0.4 | 19  | 0.7  | 0.2 | 0.4 |
| DAMO_0408 | protein of unknown function  | 84   | 1   | 0.9  | 0.1 | 0   | 0.0  | 0.0 | 0.0 |
| DAMO_0409 | conserved hypothetical protein; putative potassium-transporting ATPase, KdpF subunit                             | 93   | 2   | 1.5  | 0.2 | 0   | 0.0  | 0.0 | 0.0 |
| DAMO_0410 | high-affinity potassium transport system P-type ATPase, A chain  | 1806 | 95  | 3.8  | 0.5 | 34  | 1.4  | 0.3 | 0.6 |
| DAMO_0411 | fragment of P-type ATPase, high-affinity potassium transport system, B chain, a phosphatase-like domain (part 1) | 1503 | 68  | 3.3  | 0.5 | 12  | 0.6  | 0.1 | 0.3 |
| DAMO_0412 | fragment of P-type ATPase, high-affinity potassium transport system, B chain, a phosphatase-like domain (part 2) | 585  | 39  | 4.8  | 0.7 | 5   | 0.6  | 0.1 | 0.2 |
| DAMO_0413 | P-type ATPase, high-affinity potassium transport system, C chain   | 573  | 19  | 2.4  | 0.3 | 5   | 0.6  | 0.1 | 0.4 |
| DAMO_0414 | sensory histidine kinase in two-component regulatory system with KdpE, regulation of potassium translocation     | 2703 | 226 | 6.0  | 0.8 | 182 | 4.8  | 1.1 | 1.3 |
| DAMO_0415 | response regulator in two-component regulatory system with KdpD, regulation of potassium translocation           | 762  | 64  | 6.0  | 0.8 | 27  | 2.6  | 0.6 | 0.7 |
| DAMO_0416 | putative Histidine kinase  | 2829 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0417 | protein of unknown function  | 252  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0418 | protein of unknown function  | 222  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0419 | Predicted aminopeptidase   | 933  | 46  | 3.5  | 0.5 | 43  | 3.3  | 0.7 | 1.5 |
| DAMO_0420 | exported protein of unknown function   | 336  | 51  | 10.9 | 1.5 | 54  | 11.6 | 2.5 | 1.7 |
| DAMO_0421 | Putative ATP-dependent RNA helicase with P-loop hydrolase domain (rhIE gene)                                     | 1440 | 269 | 13.5 | 1.9 | 79  | 4.0  | 0.9 | 0.5 |
| DAMO_0422 | protein of unknown function  | 186  | 1   | 0.4  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_0423 | protein of unknown function  | 168  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0425 | conserved protein of unknown function  | 618  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0428 | protein of unknown function  | 333  | 1   | 0.2  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0429 | protein of unknown function  | 192  | 8   | 3.0  | 0.4 | 1   | 0.4  | 0.1 | 0.2 |
| DAMO_0430 | conserved protein of unknown function  | 198  | 1   | 0.4  | 0.1 | 0   | 0.0  | 0.0 | —   |

|           |  |      |      |       |      |     |       |      |     |
|-----------|--|------|------|-------|------|-----|-------|------|-----|
| DAMO_0431 | protein of unknown function  | 654  | 6    | 0.7   | 0.1  | 11  | 1.2   | 0.3  | 2.9 |
| DAMO_0432 | membrane protein of unknown function   | 552  | 10   | 1.3   | 0.2  | 7   | 0.9   | 0.2  | 1.1 |
| DAMO_0433 | DNA-methyltransferase  | 831  | 17   | 1.5   | 0.2  | 19  | 1.6   | 0.4  | 1.8 |
| DAMO_0434 | conserved protein of unknown function  | 2646 | 26   | 0.7   | 0.1  | 10  | 0.3   | 0.1  | 0.6 |
| DAMO_0435 | conserved protein of unknown function  | 177  | 3    | 1.2   | 0.2  | 0   | 0.0   | 0.0  | —   |
| DAMO_0437 | protein of unknown function  | 525  | 27   | 3.7   | 0.5  | 5   | 0.7   | 0.2  | 0.3 |
| DAMO_0438 | membrane protein of unknown function   | 309  | 24   | 5.6   | 0.8  | 1   | 0.2   | 0.1  | 0.1 |
| DAMO_0439 | conserved protein of unknown function  | 333  | 2    | 0.4   | 0.1  | 0   | 0.0   | 0.0  | —   |
| DAMO_0440 | conserved protein of unknown function  | 312  | 14   | 3.2   | 0.5  | 5   | 1.2   | 0.3  | 0.6 |
| DAMO_0441 | Lipoprotein ylpA precursor   | 741  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0442 | Orotate phosphoribosyltransferase (OPRT)   | 627  | 138  | 15.8  | 2.2  | 17  | 2.0   | 0.4  | 0.2 |
| DAMO_0443 | Peptide methionine sulfoxide reductase msr   | 441  | 51   | 8.3   | 1.2  | 53  | 8.7   | 1.9  | 1.6 |
| DAMO_0444 | conserved exported protein of unknown function   | 816  | 143  | 12.6  | 1.8  | 391 | 34.5  | 7.6  | 4.3 |
| DAMO_0445 | Membrane protein, putative (fragment)  | 675  | 50   | 5.3   | 0.7  | 87  | 9.3   | 2.0  | 2.8 |
| DAMO_0446 | conserved exported protein of unknown function   | 693  | 61   | 6.3   | 0.9  | 71  | 7.4   | 1.6  | 1.8 |
| DAMO_0447 | Protein mazG   | 801  | 98   | 8.8   | 1.2  | 192 | 17.3  | 3.8  | 3.1 |
| DAMO_0448 | Zinc/iron transporter  | 738  | 42   | 4.1   | 0.6  | 2   | 0.2   | 0.0  | 0.1 |
| DAMO_0449 | conserved exported protein of unknown function   | 1941 | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0450 | Lytic transglycosylase, catalytic precursor  | 720  | 31   | 3.1   | 0.4  | 5   | 0.5   | 0.1  | 0.3 |
| DAMO_0451 | conserved protein of unknown function  | 258  | 9    | 2.5   | 0.3  | 3   | 0.8   | 0.2  | 0.5 |
| DAMO_0452 | protein of unknown function  | 213  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0454 | Formaldehyde activating enzyme (Fae)   | 501  | 4573 | 657.2 | 91.6 | 764 | 109.8 | 24.2 | 0.3 |
| DAMO_0455 | putative methylene tetrahydromethanopterin dehydrogenase (mtdB)  | 885  | 395  | 32.1  | 4.5  | 190 | 15.5  | 3.4  | 0.8 |
| DAMO_0456 | Putative formylmethanofuran dehydrogenase, subunit D (FwdD)  | 339  | 112  | 23.8  | 3.3  | 18  | 3.8   | 0.8  | 0.3 |
| DAMO_0457 | Formyltransferase/hydrolase complex subunit bet  | 1356 | 342  | 18.2  | 2.5  | 195 | 10.4  | 2.3  | 0.9 |
| DAMO_0458 | Formyltransferase/hydrolase complex subunit alph   | 1647 | 523  | 22.9  | 3.2  | 311 | 13.6  | 3.0  | 0.9 |
| DAMO_0459 | Formyltransferase/hydrolase complex subunit epsilon (fhcD)   | 915  | 272  | 21.4  | 3.0  | 117 | 9.2   | 2.0  | 0.7 |
| DAMO_0460 | Formyltransferase/hydrolase complex subunit gamm   | 810  | 405  | 36.0  | 5.0  | 131 | 11.6  | 2.6  | 0.5 |
| DAMO_0461 | Methenyltetrahydromethanopterin cyclohydrolas  | 939  | 38   | 2.9   | 0.4  | 7   | 0.5   | 0.1  | 0.3 |
| DAMO_0462 | conserved hypothetical protein; putative Glutathione synthase, possibly involved in H4MPT biosynthesis (homologous   | 876  | 101  | 8.3   | 1.2  | 36  | 3.0   | 0.7  | 0.6 |
| DAMO_0463 | conserved hypothetical protein; putative protein involved in H4MPT cofactor biosynthesis (homologous to orf7 of M. c | 858  | 16   | 1.3   | 0.2  | 1   | 0.1   | 0.0  | 0.1 |
| DAMO_0464 | Acetyl-CoA synthetase / acetyltransferase (GNAT) family protein  | 2667 | 14   | 0.4   | 0.1  | 0   | 0.0   | 0.0  | —   |
| DAMO_0465 | putative Alpha/beta hydrolase fold   | 951  | 5    | 0.4   | 0.1  | 0   | 0.0   | 0.0  | —   |
| DAMO_0466 | Aminotransferase class-III   | 1395 | 3    | 0.2   | 0.0  | 1   | 0.1   | 0.0  | 0.5 |
| DAMO_0467 | putative 2,3-diketo-5-methylthio-1-phosphopentane phosphatase (phosphoserine phosphatase) (serB)                     | 744  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0469 | exported protein of unknown function   | 387  | 5    | 0.9   | 0.1  | 1   | 0.2   | 0.0  | 0.3 |
| DAMO_0470 | Putative beta-ribofuranosylaminobenzene 5'-phosphate synthase. Involved in methanopterin biosynthesis (orf4)         | 960  | 145  | 10.9  | 1.5  | 24  | 1.8   | 0.4  | 0.3 |
| DAMO_0471 | conserved protein of unknown function  | 570  | 17   | 2.1   | 0.3  | 7   | 0.9   | 0.2  | 0.7 |
| DAMO_0472 | conserved protein of unknown function  | 1356 | 142  | 7.5   | 1.1  | 33  | 1.8   | 0.4  | 0.4 |
| DAMO_0473 | 3-oxoacyl-(Acyl-carrier protein) reductase   | 750  | 56   | 5.4   | 0.7  | 14  | 1.3   | 0.3  | 0.4 |
| DAMO_0474 | Biotin synthetase (Fragment)   | 1071 | 95   | 6.4   | 0.9  | 6   | 0.4   | 0.1  | 0.1 |
| DAMO_0475 | Adenosylmethionine-8-amino-7-oxononanoate aminotransferase (7,8-diamino-pelargonic acid aminotransferase) (DAF       | 1344 | 109  | 5.8   | 0.8  | 12  | 0.6   | 0.1  | 0.2 |
| DAMO_0476 | Dethiobiotin synthetase (Dethiobiotin synthase   | 738  | 3    | 0.3   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0477 | RlpA-like lipoprotein precursor (fragment)   | 660  | 7    | 0.8   | 0.1  | 2   | 0.2   | 0.0  | 0.5 |
| DAMO_0478 | putative Histidine kinase  | 2946 | 4    | 0.1   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0479 | Two-component response regulator (fragment)  | 990  | 9    | 0.7   | 0.1  | 0   | 0.0   | 0.0  | —   |
| DAMO_0480 | putative Histidine kinase  | 2094 | 32   | 1.1   | 0.2  | 8   | 0.3   | 0.1  | 0.4 |
| DAMO_0481 | protein of unknown function  | 705  | 2    | 0.2   | 0.0  | 1   | 0.1   | 0.0  | 0.8 |
| DAMO_0482 | putative Haloacid dehalogenase-like hydrolase domain-containing protein 3  | 696  | 49   | 5.1   | 0.7  | 10  | 1.0   | 0.2  | 0.3 |
| DAMO_0483 | conserved protein of unknown function  | 675  | 19   | 2.0   | 0.3  | 6   | 0.6   | 0.1  | 0.5 |
| DAMO_0484 | Glucokinase (Glucose kinase)   | 1023 | 61   | 4.3   | 0.6  | 11  | 0.8   | 0.2  | 0.3 |
| DAMO_0485 | 6-phosphogluconolactonase (6PGL)   | 768  | 44   | 4.1   | 0.6  | 0   | 0.0   | 0.0  | —   |
| DAMO_0486 | glucose-6-phosphate 1-dehydrogenase  | 1596 | 288  | 13.0  | 1.8  | 57  | 2.6   | 0.6  | 0.3 |
| DAMO_0487 | putative 6-phosphogluconate dehydrogenas   | 984  | 38   | 2.8   | 0.4  | 3   | 0.2   | 0.0  | 0.1 |
| DAMO_0488 | putative bifunctional: transaldolas  | 1743 | 125  | 5.2   | 0.7  | 26  | 1.1   | 0.2  | 0.3 |
| DAMO_0489 | protein of unknown function  | 459  | 4    | 0.6   | 0.1  | 0   | 0.0   | 0.0  | —   |

|           |  |      |      |      |     |     |      |     |     |
|-----------|--|------|------|------|-----|-----|------|-----|-----|
| DAMO_0490 | protein of unknown function  | 570  | 13   | 1.6  | 0.2 | 18  | 2.3  | 0.5 | 2.2 |
| DAMO_0491 | protein of unknown function  | 387  | 0    | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0492 | protein of unknown function  | 189  | 0    | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0493 | conserved exported protein of unknown function   | 336  | 73   | 15.6 | 2.2 | 21  | 4.5  | 1.0 | 0.5 |
| DAMO_0494 | TolQ protein   | 720  | 227  | 22.7 | 3.2 | 82  | 8.2  | 1.8 | 0.6 |
| DAMO_0495 | Biopolymer transport protein exbD  | 438  | 83   | 13.6 | 1.9 | 48  | 7.9  | 1.7 | 0.9 |
| DAMO_0496 | protein of unknown function  | 837  | 8    | 0.7  | 0.1 | 2   | 0.2  | 0.0 | 0.4 |
| DAMO_0497 | Protein tolB precursor   | 1353 | 96   | 5.1  | 0.7 | 33  | 1.8  | 0.4 | 0.5 |
| DAMO_0498 | OmpA/MotB domain protein precursor   | 645  | 45   | 5.0  | 0.7 | 5   | 0.6  | 0.1 | 0.2 |
| DAMO_0499 | exported protein of unknown function   | 1260 | 81   | 4.6  | 0.6 | 25  | 1.4  | 0.3 | 0.5 |
| DAMO_0500 | membrane protein of unknown function   | 492  | 24   | 3.5  | 0.5 | 6   | 0.9  | 0.2 | 0.4 |
| DAMO_0501 | 3-isopropylmalate dehydrogenase (Beta-IPM dehydrogenase) (IMDH) (3-IPM-DH)   | 1080 | 31   | 2.1  | 0.3 | 5   | 0.3  | 0.1 | 0.3 |
| DAMO_0502 | putative GTP-binding protein engB  | 693  | 21   | 2.2  | 0.3 | 9   | 0.9  | 0.2 | 0.7 |
| DAMO_0503 | putative TPR domain protein  | 1758 | 211  | 8.6  | 1.2 | 423 | 17.3 | 3.8 | 3.2 |
| DAMO_0504 | protein of unknown function  | 822  | 79   | 6.9  | 1.0 | 57  | 5.0  | 1.1 | 1.1 |
| DAMO_0505 | protein of unknown function  | 603  | 19   | 2.3  | 0.3 | 13  | 1.6  | 0.3 | 1.1 |
| DAMO_0506 | protein of unknown function  | 273  | 79   | 20.8 | 2.9 | 37  | 9.8  | 2.2 | 0.7 |
| DAMO_0507 | Ribose-phosphate pyrophosphokinase (RPPK) synthetase) (PRPP synthetase)  | 939  | 110  | 8.4  | 1.2 | 44  | 3.4  | 0.7 | 0.6 |
| DAMO_0508 | 50S ribosomal protein L25 (General stress protein CTC)   | 663  | 70   | 7.6  | 1.1 | 27  | 2.9  | 0.6 | 0.6 |
| DAMO_0509 | peptidyl-tRNA hydrolase  | 576  | 18   | 2.3  | 0.3 | 2   | 0.3  | 0.1 | 0.2 |
| DAMO_0510 | 30S ribosomal protein S6 (modular protein)   | 381  | 189  | 35.7 | 5.0 | 61  | 11.5 | 2.5 | 0.5 |
| DAMO_0511 | Single-stranded DNA-binding protein 2 (SSB 2   | 384  | 20   | 3.8  | 0.5 | 4   | 0.8  | 0.2 | 0.3 |
| DAMO_0512 | 30S ribosomal subunit protein S18  | 237  | 28   | 8.5  | 1.2 | 9   | 2.7  | 0.6 | 0.5 |
| DAMO_0513 | conserved membrane protein of unknown function   | 951  | 114  | 8.6  | 1.2 | 19  | 1.4  | 0.3 | 0.3 |
| DAMO_0514 | 50S ribosomal protein L9   | 450  | 46   | 7.4  | 1.0 | 5   | 0.8  | 0.2 | 0.2 |
| DAMO_0515 | putative replicative DNA helicase, dnaB  | 1395 | 144  | 7.4  | 1.0 | 30  | 1.5  | 0.3 | 0.3 |
| DAMO_0516 | DNA repair protein (DNA repair protein)  | 1380 | 240  | 12.5 | 1.7 | 92  | 4.8  | 1.1 | 0.6 |
| DAMO_0517 | protein of unknown function  | 72   | 0    | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0518 | CarD-like transcriptional regulator  | 489  | 96   | 14.1 | 2.0 | 99  | 14.6 | 3.2 | 1.6 |
| DAMO_0519 | conserved membrane protein of unknown function   | 1023 | 219  | 15.4 | 2.1 | 85  | 6.0  | 1.3 | 0.6 |
| DAMO_0520 | fragment of IspD/ispF bifunctional enzyme cytidylyltransferase (4-diphosphocytidyl-2C- methyl-D-erythritol synthase) | 621  | 44   | 5.1  | 0.7 | 6   | 0.7  | 0.2 | 0.2 |
| DAMO_0521 | fragment of IspD/ispF bifunctional enzyme cytidylyltransferase (4-diphosphocytidyl-2C- methyl-D-erythritol synthase) | 486  | 26   | 3.9  | 0.5 | 27  | 4.0  | 0.9 | 1.6 |
| DAMO_0522 | Cysteinylyl-tRNA synthetase (Cysteine--tRNA ligase   | 1593 | 79   | 3.6  | 0.5 | 32  | 1.4  | 0.3 | 0.6 |
| DAMO_0523 | putative enzyme  | 786  | 111  | 10.2 | 1.4 | 47  | 4.3  | 0.9 | 0.7 |
| DAMO_0524 | Elongation factor Tu (EF-Tu)   | 1203 | 0    | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0525 | protein of unknown function  | 312  | 208  | 48.0 | 6.7 | 40  | 9.2  | 2.0 | 0.3 |
| DAMO_0526 | Preprotein translocase subunit secE  | 195  | 141  | 52.1 | 7.3 | 12  | 4.4  | 1.0 | 0.1 |
| DAMO_0527 | component in transcription antitermination   | 531  | 124  | 16.8 | 2.3 | 84  | 11.4 | 2.5 | 1.1 |
| DAMO_0528 | 50S ribosomal subunit protein L11  | 423  | 107  | 18.2 | 2.5 | 31  | 5.3  | 1.2 | 0.5 |
| DAMO_0529 | 50S ribosomal subunit protein L1   | 708  | 220  | 22.4 | 3.1 | 85  | 8.6  | 1.9 | 0.6 |
| DAMO_0530 | 50S ribosomal subunit protein L10  | 516  | 29   | 4.0  | 0.6 | 3   | 0.4  | 0.1 | 0.2 |
| DAMO_0531 | 50S ribosomal subunit protein L7/L12   | 393  | 125  | 22.9 | 3.2 | 38  | 7.0  | 1.5 | 0.5 |
| DAMO_0532 | RNA polymerase, beta subunit   | 4017 | 1141 | 20.5 | 2.8 | 171 | 3.1  | 0.7 | 0.2 |
| DAMO_0533 | RNA polymerase, beta prime subunit   | 4098 | 1431 | 25.1 | 3.5 | 324 | 5.7  | 1.3 | 0.4 |
| DAMO_0534 | 30S ribosomal subunit protein S12  | 378  | 176  | 33.5 | 4.7 | 78  | 14.9 | 3.3 | 0.7 |
| DAMO_0535 | 30S ribosomal subunit protein S7   | 471  | 188  | 28.7 | 4.0 | 8   | 1.2  | 0.3 | 0.1 |
| DAMO_0536 | Elongation factor G (EF-G)   | 2094 | 428  | 14.7 | 2.1 | 83  | 2.9  | 0.6 | 0.3 |
| DAMO_0537 | Elongation factor Tu (EF-Tu)   | 1203 | 0    | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0538 | 30S ribosomal subunit protein S10  | 309  | 16   | 3.7  | 0.5 | 1   | 0.2  | 0.1 | 0.1 |
| DAMO_0539 | 50S ribosomal subunit protein L3   | 633  | 65   | 7.4  | 1.0 | 16  | 1.8  | 0.4 | 0.4 |
| DAMO_0540 | 50S ribosomal subunit protein L4   | 636  | 24   | 2.7  | 0.4 | 4   | 0.5  | 0.1 | 0.3 |
| DAMO_0541 | 50S ribosomal subunit protein L23  | 291  | 25   | 6.2  | 0.9 | 0   | 0.0  | 0.0 | 0.0 |
| DAMO_0542 | 50S ribosomal subunit protein L2   | 819  | 178  | 15.6 | 2.2 | 36  | 3.2  | 0.7 | 0.3 |
| DAMO_0543 | 30S ribosomal subunit protein S19  | 285  | 133  | 33.6 | 4.7 | 31  | 7.8  | 1.7 | 0.4 |
| DAMO_0544 | 50S ribosomal subunit protein L22  | 348  | 45   | 9.3  | 1.3 | 26  | 5.4  | 1.2 | 0.9 |
| DAMO_0545 | 30S ribosomal subunit protein S3   | 708  | 70   | 7.1  | 1.0 | 7   | 0.7  | 0.2 | 0.2 |

|           |  |      |     |      |      |     |      |     |     |
|-----------|--|------|-----|------|------|-----|------|-----|-----|
| DAMO_0546 | 50S ribosomal subunit protein L16  | 420  | 288 | 49.4 | 6.9  | 45  | 7.7  | 1.7 | 0.2 |
| DAMO_0547 | 50S ribosomal protein L29  | 222  | 12  | 3.9  | 0.5  | 4   | 1.3  | 0.3 | 0.5 |
| DAMO_0548 | 30S ribosomal subunit protein S17  | 270  | 140 | 37.3 | 5.2  | 16  | 4.3  | 0.9 | 0.2 |
| DAMO_0549 | 50S ribosomal subunit protein L14  | 348  | 179 | 37.0 | 5.2  | 41  | 8.5  | 1.9 | 0.4 |
| DAMO_0550 | 50S ribosomal subunit protein L24  | 333  | 66  | 14.3 | 2.0  | 14  | 3.0  | 0.7 | 0.3 |
| DAMO_0551 | 50S ribosomal subunit protein L5   | 618  | 21  | 2.4  | 0.3  | 12  | 1.4  | 0.3 | 0.9 |
| DAMO_0552 | 30S ribosomal protein S14 type Z   | 186  | 45  | 17.4 | 2.4  | 4   | 1.5  | 0.3 | 0.1 |
| DAMO_0553 | 30S ribosomal subunit protein S8, and regulator  | 396  | 39  | 7.1  | 1.0  | 6   | 1.1  | 0.2 | 0.2 |
| DAMO_0554 | 50S ribosomal subunit protein L6   | 537  | 51  | 6.8  | 1.0  | 11  | 1.5  | 0.3 | 0.3 |
| DAMO_0555 | 50S ribosomal subunit protein L18  | 369  | 21  | 4.1  | 0.6  | 5   | 1.0  | 0.2 | 0.4 |
| DAMO_0556 | 30S ribosomal subunit protein S5   | 510  | 99  | 14.0 | 1.9  | 24  | 3.4  | 0.7 | 0.4 |
| DAMO_0557 | 50S ribosomal subunit protein L30  | 201  | 15  | 5.4  | 0.7  | 1   | 0.4  | 0.1 | 0.1 |
| DAMO_0558 | 50S ribosomal subunit protein L15  | 447  | 173 | 27.9 | 3.9  | 25  | 4.0  | 0.9 | 0.2 |
| DAMO_0559 | Preprotein translocase secY subunit  | 1311 | 188 | 10.3 | 1.4  | 126 | 6.9  | 1.5 | 1.1 |
| DAMO_0560 | Adenylate kinase (ATP-AMP transphosphorylase)  | 648  | 61  | 6.8  | 0.9  | 7   | 0.8  | 0.2 | 0.2 |
| DAMO_0561 | methionine aminopeptidase  | 780  | 36  | 3.3  | 0.5  | 15  | 1.4  | 0.3 | 0.7 |
| DAMO_0562 | Translation initiation factor IF-1   | 219  | 20  | 6.6  | 0.9  | 15  | 4.9  | 1.1 | 1.2 |
| DAMO_0563 | protein of unknown function  | 540  | 547 | 72.9 | 10.2 | 244 | 32.5 | 7.2 | 0.7 |
| DAMO_0564 | 30S ribosomal subunit protein S11  | 411  | 108 | 18.9 | 2.6  | 51  | 8.9  | 2.0 | 0.7 |
| DAMO_0565 | 30S ribosomal subunit protein S4   | 579  | 256 | 31.8 | 4.4  | 104 | 12.9 | 2.8 | 0.6 |
| DAMO_0566 | DNA-directed RNA polymerase alpha chain  | 1029 | 298 | 20.9 | 2.9  | 174 | 12.2 | 2.7 | 0.9 |
| DAMO_0567 | 50S ribosomal protein L17  | 474  | 41  | 6.2  | 0.9  | 32  | 4.9  | 1.1 | 1.2 |
| DAMO_0568 | Elongation factor G (EF-G)   | 2085 | 52  | 1.8  | 0.3  | 15  | 0.5  | 0.1 | 0.5 |
| DAMO_0569 | conserved protein of unknown function  | 462  | 9   | 1.4  | 0.2  | 9   | 1.4  | 0.3 | 1.6 |
| DAMO_0570 | protein of unknown function  | 90   | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_0571 | Transcription elongation protein nusA (N utilization substance protein A) (L factor)                           | 1302 | 104 | 5.8  | 0.8  | 73  | 4.0  | 0.9 | 1.1 |
| DAMO_0572 | conserved protein of unknown function  | 636  | 33  | 3.7  | 0.5  | 10  | 1.1  | 0.2 | 0.5 |
| DAMO_0574 | translation initiation factor IF-2   | 2394 | 353 | 10.6 | 1.5  | 206 | 6.2  | 1.4 | 0.9 |
| DAMO_0575 | conserved protein of unknown function  | 288  | 47  | 11.8 | 1.6  | 33  | 8.3  | 1.8 | 1.1 |
| DAMO_0576 | Ribosome-binding factor A  | 360  | 20  | 4.0  | 0.6  | 11  | 2.2  | 0.5 | 0.9 |
| DAMO_0577 | PHP C-terminal domain protein  | 873  | 11  | 0.9  | 0.1  | 5   | 0.4  | 0.1 | 0.7 |
| DAMO_0578 | tRNA pseudouridine synthase B (tRNA pseudouridine 55 synthase) (Psi55 synthase) (tRNA-uridine isomerase) (tRNA | 942  | 87  | 6.6  | 0.9  | 27  | 2.1  | 0.5 | 0.5 |
| DAMO_0579 | Riboflavin biosynthesis protein RibF   | 1008 | 18  | 1.3  | 0.2  | 3   | 0.2  | 0.0 | 0.3 |
| DAMO_0580 | 30S ribosomal subunit protein S15  | 270  | 24  | 6.4  | 0.9  | 4   | 1.1  | 0.2 | 0.3 |
| DAMO_0581 | Polyribonucleotide nucleotidyltransferas   | 2088 | 468 | 16.1 | 2.2  | 283 | 9.8  | 2.2 | 1.0 |
| DAMO_0582 | putative enzyme  | 1254 | 242 | 13.9 | 1.9  | 124 | 7.1  | 1.6 | 0.8 |
| DAMO_0583 | Adenylosuccinate lyase (Adenylosuccinase) (ASL)  | 1266 | 120 | 6.8  | 1.0  | 31  | 1.8  | 0.4 | 0.4 |
| DAMO_0584 | Phosphoribosylformylglycinamide synthetase, PurS component   | 255  | 31  | 8.8  | 1.2  | 9   | 2.5  | 0.6 | 0.5 |
| DAMO_0585 | phosphoribosylformylglycinamide synthase I (FGAM synthase I)   | 723  | 64  | 6.4  | 0.9  | 23  | 2.3  | 0.5 | 0.6 |
| DAMO_0586 | Phosphoribosylformylglycinamide synthase I   | 2217 | 298 | 9.7  | 1.3  | 44  | 1.4  | 0.3 | 0.2 |
| DAMO_0587 | homoserine dehydrogenase (HDH)   | 1305 | 205 | 11.3 | 1.6  | 43  | 2.4  | 0.5 | 0.3 |
| DAMO_0588 | Threonine synthase   | 1065 | 113 | 7.6  | 1.1  | 16  | 1.1  | 0.2 | 0.2 |
| DAMO_0589 | conserved protein of unknown function  | 576  | 55  | 6.9  | 1.0  | 29  | 3.6  | 0.8 | 0.8 |
| DAMO_0590 | isovaleryl-CoA dehydrogenase   | 1152 | 66  | 4.1  | 0.6  | 19  | 1.2  | 0.3 | 0.5 |
| DAMO_0591 | conserved protein of unknown function  | 864  | 181 | 15.1 | 2.1  | 32  | 2.7  | 0.6 | 0.3 |
| DAMO_0592 | conserved protein of unknown function  | 147  | 35  | 17.1 | 2.4  | 10  | 4.9  | 1.1 | 0.5 |
| DAMO_0593 | conserved protein of unknown function  | 921  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_0594 | conserved protein of unknown function  | 243  | 69  | 20.4 | 2.8  | 44  | 13.0 | 2.9 | 1.0 |
| DAMO_0595 | conserved protein of unknown function  | 489  | 45  | 6.6  | 0.9  | 27  | 4.0  | 0.9 | 0.9 |
| DAMO_0596 | 3-oxoacid CoA-transferase, alpha subunit   | 972  | 71  | 5.3  | 0.7  | 10  | 0.7  | 0.2 | 0.2 |
| DAMO_0597 | Acyl CoA:acetate/3-ketoacid CoA transferase, beta subunit  | 795  | 38  | 3.4  | 0.5  | 5   | 0.5  | 0.1 | 0.2 |
| DAMO_0599 | protein of unknown function  | 603  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_0600 | protein of unknown function  | 312  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_0601 | protein of unknown function  | 378  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_0602 | protein of unknown function  | 201  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_0603 | conserved protein of unknown function  | 192  | 119 | 44.6 | 6.2  | 84  | 31.5 | 6.9 | 1.1 |

|           |   |      |     |      |     |     |      |     |     |
|-----------|---|------|-----|------|-----|-----|------|-----|-----|
| DAMO_0604 | protein of unknown function   | 258  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0605 | PilT protein-like protein   | 384  | 0   | 0.0  | 0.0 | 2   | 0.4  | 0.1 | —   |
| DAMO_0606 | Transcriptional regulator, AbrB family protein  | 276  | 2   | 0.5  | 0.1 | 1   | 0.3  | 0.1 | 0.8 |
| DAMO_0608 | heme-molybdoenzyme heme-containing subunit YedZ; cytochrome b subunit                 | 666  | 70  | 7.6  | 1.1 | 81  | 8.8  | 1.9 | 1.8 |
| DAMO_0609 | exported heme-molybdoenzyme molybdopterin-containing subunit YedY; TAT export         | 954  | 117 | 8.8  | 1.2 | 88  | 6.6  | 1.5 | 1.2 |
| DAMO_0610 | NUDIX hydrolase   | 561  | 46  | 5.9  | 0.8 | 29  | 3.7  | 0.8 | 1.0 |
| DAMO_0611 | conserved membrane protein of unknown function  | 1395 | 2   | 0.1  | 0.0 | 3   | 0.2  | 0.0 | 2.4 |
| DAMO_0612 | Radical SAM domain protein  | 1005 | 0   | 0.0  | 0.0 | 2   | 0.1  | 0.0 | —   |
| DAMO_0613 | Radical SAM domain protein  | 990  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0614 | Dolichol phosphate mannosyltransferase or dolichol phosphate beta glucosyltransferase | 675  | 1   | 0.1  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0615 | putative Methyltransferase type 11  | 810  | 1   | 0.1  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0616 | Predicted regulator of plasmid copy number  | 264  | 1   | 0.3  | 0.0 | 4   | 1.1  | 0.2 | 6.3 |
| DAMO_0617 | conserved protein of unknown function   | 279  | 2   | 0.5  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_0618 | protein of unknown function   | 243  | 0   | 0.0  | 0.0 | 1   | 0.3  | 0.1 | —   |
| DAMO_0619 | protein of unknown function   | 243  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0620 | conserved membrane protein of unknown function  | 537  | 4   | 0.5  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_0621 | conserved protein of unknown function   | 2637 | 162 | 4.4  | 0.6 | 156 | 4.3  | 0.9 | 1.5 |
| DAMO_0622 | peptide methionine sulfoxide reductase msrB   | 402  | 3   | 0.5  | 0.1 | 1   | 0.2  | 0.0 | 0.5 |
| DAMO_0623 | protein of unknown function   | 69   | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0624 | protein of unknown function   | 645  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0625 | protein of unknown function   | 264  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0626 | protein of unknown function   | 99   | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0627 | protein of unknown function   | 336  | 14  | 3.0  | 0.4 | 2   | 0.4  | 0.1 | 0.2 |
| DAMO_0628 | conserved protein of unknown function   | 168  | 17  | 7.3  | 1.0 | 3   | 1.3  | 0.3 | 0.3 |
| DAMO_0629 | conserved protein of unknown function   | 213  | 41  | 13.9 | 1.9 | 44  | 14.9 | 3.3 | 1.7 |
| DAMO_0630 | protein of unknown function   | 180  | 62  | 24.8 | 3.5 | 20  | 8.0  | 1.8 | 0.5 |
| DAMO_0631 | protein of unknown function   | 303  | 51  | 12.1 | 1.7 | 7   | 1.7  | 0.4 | 0.2 |
| DAMO_0632 | Uncharacterized HTH-type transcriptional regulator yddM                               | 294  | 125 | 30.6 | 4.3 | 40  | 9.8  | 2.2 | 0.5 |
| DAMO_0633 | protein of unknown function   | 231  | 62  | 19.3 | 2.7 | 16  | 5.0  | 1.1 | 0.4 |
| DAMO_0634 | conserved protein of unknown function   | 225  | 117 | 37.4 | 5.2 | 50  | 16.0 | 3.5 | 0.7 |
| DAMO_0635 | protein of unknown function   | 174  | 9   | 3.7  | 0.5 | 0   | 0.0  | 0.0 | 0.0 |
| DAMO_0636 | Helix-turn-helix motif  | 297  | 33  | 8.0  | 1.1 | 25  | 6.1  | 1.3 | 1.2 |
| DAMO_0637 | Plasmid maintenance system killer   | 285  | 17  | 4.3  | 0.6 | 19  | 4.8  | 1.1 | 1.8 |
| DAMO_0638 | Multimodular transpeptidase-transglycosylase  | 2049 | 31  | 1.1  | 0.2 | 25  | 0.9  | 0.2 | 1.3 |
| DAMO_0639 | conserved protein of unknown function   | 447  | 10  | 1.6  | 0.2 | 1   | 0.2  | 0.0 | 0.2 |
| DAMO_0640 | protein of unknown function   | 612  | 2   | 0.2  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0641 | protein of unknown function   | 177  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0642 | conserved protein of unknown function   | 303  | 0   | 0.0  | 0.0 | 1   | 0.2  | 0.1 | —   |
| DAMO_0643 | conserved protein of unknown function   | 297  | 0   | 0.0  | 0.0 | 4   | 1.0  | 0.2 | —   |
| DAMO_0644 | protein of unknown function   | 156  | 1   | 0.5  | 0.1 | 2   | 0.9  | 0.2 | 3.2 |
| DAMO_0645 | isovaleryl-CoA dehydrogenase  | 1140 | 119 | 7.5  | 1.0 | 43  | 2.7  | 0.6 | 0.6 |
| DAMO_0646 | protein fixA; electron transfer flavoprotein beta-subunit (Beta-ETF)                  | 801  | 62  | 5.6  | 0.8 | 16  | 1.4  | 0.3 | 0.4 |
| DAMO_0647 | protein FixB; electron transfer flavoprotein alpha chain                              | 990  | 121 | 8.8  | 1.2 | 33  | 2.4  | 0.5 | 0.4 |
| DAMO_0648 | protein of unknown function   | 351  | 29  | 5.9  | 0.8 | 5   | 1.0  | 0.2 | 0.3 |
| DAMO_0649 | putative iron-sulfur cluster-binding protein  | 1749 | 175 | 7.2  | 1.0 | 29  | 1.2  | 0.3 | 0.3 |
| DAMO_0650 | fragment of Methylmalonyl-CoA mutase large subunit                                    | 1695 | 313 | 13.3 | 1.9 | 136 | 5.8  | 1.3 | 0.7 |
| DAMO_0651 | fragment of Methylmalonyl-CoA mutase large subunit                                    | 414  | 30  | 5.2  | 0.7 | 31  | 5.4  | 1.2 | 1.6 |
| DAMO_0652 | Sterol carrier protein x/sterol carrier protein 2 related protein                     | 1311 | 147 | 8.1  | 1.1 | 49  | 2.7  | 0.6 | 0.5 |
| DAMO_0654 | protein of unknown function   | 567  | 158 | 20.1 | 2.8 | 167 | 21.2 | 4.7 | 1.7 |
| DAMO_0655 | conserved protein of unknown function   | 99   | 16  | 11.6 | 1.6 | 3   | 2.2  | 0.5 | 0.3 |
| DAMO_0656 | protein of unknown function   | 348  | 68  | 14.1 | 2.0 | 46  | 9.5  | 2.1 | 1.1 |
| DAMO_0657 | conserved protein of unknown function   | 174  | 26  | 10.8 | 1.5 | 13  | 5.4  | 1.2 | 0.8 |
| DAMO_0658 | General secretion pathway protein A   | 1725 | 549 | 22.9 | 3.2 | 216 | 9.0  | 2.0 | 0.6 |
| DAMO_0659 | protein of unknown function   | 813  | 400 | 35.4 | 4.9 | 36  | 3.2  | 0.7 | 0.1 |
| DAMO_0660 | protein of unknown function   | 432  | 230 | 38.3 | 5.3 | 45  | 7.5  | 1.7 | 0.3 |
| DAMO_0661 | protein of unknown function   | 198  | 3   | 1.1  | 0.2 | 0   | 0.0  | 0.0 | —   |

|           |  |      |     |      |     |     |      |     |     |
|-----------|--|------|-----|------|-----|-----|------|-----|-----|
| DAMO_0662 | Valyl-tRNA synthetase (Valine--tRNA ligase)  | 2817 | 601 | 15.4 | 2.1 | 159 | 4.1  | 0.9 | 0.4 |
| DAMO_0663 | BirA biofunctional protein, putative (fragment)  | 831  | 47  | 4.1  | 0.6 | 7   | 0.6  | 0.1 | 0.2 |
| DAMO_0664 | Type III pantothenate kinase (Pantothenic acid kinase) (PanK-III)  | 765  | 123 | 11.6 | 1.6 | 76  | 7.2  | 1.6 | 1.0 |
| DAMO_0665 | Sec-independent protein translocase protein tatA/E homolog (modular protein)   | 252  | 9   | 2.6  | 0.4 | 1   | 0.3  | 0.1 | 0.2 |
| DAMO_0666 | 50S ribosomal subunit protein L13  | 450  | 40  | 6.4  | 0.9 | 6   | 1.0  | 0.2 | 0.2 |
| DAMO_0667 | 30S ribosomal protein S9   | 396  | 57  | 10.4 | 1.4 | 8   | 1.5  | 0.3 | 0.2 |
| DAMO_0668 | N-acetyl-gamma-glutamyl-phosphate reductase (AGPR) dehydrogenase)  | 1071 | 51  | 3.4  | 0.5 | 3   | 0.2  | 0.0 | 0.1 |
| DAMO_0669 | arginine biosynthesis bifunctional protein   | 1218 | 103 | 6.1  | 0.8 | 24  | 1.4  | 0.3 | 0.4 |
| DAMO_0670 | protein of unknown function  | 159  | 6   | 2.7  | 0.4 | 1   | 0.5  | 0.1 | 0.3 |
| DAMO_0671 | 30S ribosomal protein S2   | 789  | 212 | 19.3 | 2.7 | 109 | 9.9  | 2.2 | 0.8 |
| DAMO_0672 | Elongation factor Ts (EF-Ts)   | 618  | 37  | 4.3  | 0.6 | 9   | 1.0  | 0.2 | 0.4 |
| DAMO_0673 | Uridylate kinase (UK) (Uridine monophosphate kinase) (UMP kinase)  | 729  | 116 | 11.5 | 1.6 | 51  | 5.0  | 1.1 | 0.7 |
| DAMO_0674 | Ribosome recycling factor (Ribosome-releasing factor) (RRF)  | 558  | 34  | 4.4  | 0.6 | 5   | 0.6  | 0.1 | 0.2 |
| DAMO_0675 | Phosphatidate cytidyltransferase (CDP- diacylglycerol synthase)  | 804  | 25  | 2.2  | 0.3 | 6   | 0.5  | 0.1 | 0.4 |
| DAMO_0676 | Apolipoprotein N-acyltransferase (ALP N-acyltransferase)   | 1581 | 19  | 0.9  | 0.1 | 2   | 0.1  | 0.0 | 0.2 |
| DAMO_0677 | Peptide chain release factor 2 (RF-2)  | 1005 | 28  | 2.0  | 0.3 | 13  | 0.9  | 0.2 | 0.7 |
| DAMO_0678 | conserved membrane protein of unknown function   | 348  | 4   | 0.8  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_0679 | conserved membrane protein of unknown function   | 342  | 1   | 0.2  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0680 | protein of unknown function  | 84   | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0681 | putative Peptidase, M23/M37 family   | 966  | 91  | 6.8  | 0.9 | 17  | 1.3  | 0.3 | 0.3 |
| DAMO_0682 | Preprotein translocase secA subunit  | 2826 | 438 | 11.2 | 1.6 | 163 | 4.2  | 0.9 | 0.6 |
| DAMO_0683 | conserved protein of unknown function  | 1149 | 210 | 13.2 | 1.8 | 40  | 2.5  | 0.6 | 0.3 |
| DAMO_0685 | protein of unknown function  | 324  | 6   | 1.3  | 0.2 | 0   | 0.0  | 0.0 | —   |
| DAMO_0686 | Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase   | 834  | 38  | 3.3  | 0.5 | 11  | 0.9  | 0.2 | 0.5 |
| DAMO_0687 | conserved protein of unknown function  | 1353 | 62  | 3.3  | 0.5 | 13  | 0.7  | 0.2 | 0.3 |
| DAMO_0689 | protein of unknown function  | 207  | 11  | 3.8  | 0.5 | 9   | 3.1  | 0.7 | 1.3 |
| DAMO_0690 | conserved protein of unknown function  | 198  | 122 | 44.4 | 6.2 | 53  | 19.3 | 4.2 | 0.7 |
| DAMO_0691 | conserved protein of unknown function  | 507  | 175 | 24.9 | 3.5 | 177 | 25.1 | 5.5 | 1.6 |
| DAMO_0692 | Molybdenum cofactor biosynthesis protein B   | 555  | 85  | 11.0 | 1.5 | 38  | 4.9  | 1.1 | 0.7 |
| DAMO_0693 | GTP cyclohydrolase I   | 249  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0694 | exported protein of unknown function   | 603  | 18  | 2.1  | 0.3 | 12  | 1.4  | 0.3 | 1.1 |
| DAMO_0695 | 6-phosphofructokinase  | 1251 | 60  | 3.5  | 0.5 | 19  | 1.1  | 0.2 | 0.5 |
| DAMO_0696 | putative Uncharacterized domain HDIG   | 1512 | 2   | 0.1  | 0.0 | 2   | 0.1  | 0.0 | 1.6 |
| DAMO_0697 | conserved protein of unknown function  | 207  | 33  | 11.5 | 1.6 | 71  | 24.7 | 5.4 | 3.4 |
| DAMO_0698 | serine acetyltransferase   | 705  | 37  | 3.8  | 0.5 | 27  | 2.8  | 0.6 | 1.2 |
| DAMO_0699 | glucose-1-phosphate adenylyltransferase  | 1254 | 87  | 5.0  | 0.7 | 35  | 2.0  | 0.4 | 0.6 |
| DAMO_0700 | putative Electron transfer oxidoreductase  | 1224 | 70  | 4.1  | 0.6 | 18  | 1.1  | 0.2 | 0.4 |
| DAMO_0701 | Methyltransferase type 11  | 723  | 142 | 14.1 | 2.0 | 146 | 14.5 | 3.2 | 1.6 |
| DAMO_0702 | putative Chalcone and stilbene synthase domain protein   | 1026 | 194 | 13.6 | 1.9 | 199 | 14.0 | 3.1 | 1.6 |
| DAMO_0703 | putative Sterol 24-C-methyltransferase   | 831  | 90  | 7.8  | 1.1 | 115 | 10.0 | 2.2 | 2.0 |
| DAMO_0704 | glycine cleavage system T-protei   | 1113 | 103 | 6.7  | 0.9 | 16  | 1.0  | 0.2 | 0.2 |
| DAMO_0705 | Glycine cleavage system H-protein  | 387  | 42  | 7.8  | 1.1 | 11  | 2.0  | 0.5 | 0.4 |
| DAMO_0706 | putative glycine dehydrogenase [decarboxylating] subunit 1 (Glycine decarboxylase subunit 1) (Glycine cleavage syste | 1350 | 127 | 6.8  | 0.9 | 16  | 0.9  | 0.2 | 0.2 |
| DAMO_0707 | putative glycine dehydrogenase [decarboxylating] subunit 2 (Glycine decarboxylase subunit 2) (Glycine cleavage syste | 1578 | 122 | 5.6  | 0.8 | 24  | 1.1  | 0.2 | 0.3 |
| DAMO_0708 | conserved protein of unknown function  | 507  | 41  | 5.8  | 0.8 | 10  | 1.4  | 0.3 | 0.4 |
| DAMO_0709 | conserved protein of unknown function  | 153  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0710 | conserved protein of unknown function  | 180  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0711 | conserved protein of unknown function  | 231  | 6   | 1.9  | 0.3 | 0   | 0.0  | 0.0 | —   |
| DAMO_0712 | toxin of the YafQ-DinJ toxin-antitoxin system  | 273  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0713 | antitoxin of YafQ-DinJ toxin-antitoxin system  | 261  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0714 | conserved protein of unknown function  | 354  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0715 | bifunctional: hydroxy-methylpyrimidine kinase (HMP kinase); hydroxy-phosphomethylpyrimidine kinase (HMP-P kin        | 795  | 89  | 8.1  | 1.1 | 5   | 0.5  | 0.1 | 0.1 |
| DAMO_0716 | Endonuclease V (Deoxyinosine 3'endonuclease  | 696  | 59  | 6.1  | 0.9 | 3   | 0.3  | 0.1 | 0.1 |
| DAMO_0717 | protein of unknown function  | 207  | 40  | 13.9 | 1.9 | 3   | 1.0  | 0.2 | 0.1 |
| DAMO_0718 | 3-oxoacyl-acyl carrier protein reductase   | 771  | 96  | 9.0  | 1.2 | 15  | 1.4  | 0.3 | 0.2 |
| DAMO_0720 | protein of unknown function  | 309  | 9   | 2.1  | 0.3 | 5   | 1.2  | 0.3 | 0.9 |

|           |   |      |      |       |      |      |      |      |     |
|-----------|---|------|------|-------|------|------|------|------|-----|
| DAMO_0721 | conserved protein of unknown function   | 504  | 0    | 0.0   | 0.0  | 0    | 0.0  | 0.0  | —   |
| DAMO_0722 | conserved protein of unknown function   | 1005 | 0    | 0.0   | 0.0  | 0    | 0.0  | 0.0  | —   |
| DAMO_0723 | Integrase, catalytic region   | 147  | 1    | 0.5   | 0.1  | 0    | 0.0  | 0.0  | —   |
| DAMO_0724 | conserved protein of unknown function   | 576  | 5    | 0.6   | 0.1  | 1    | 0.1  | 0.0  | 0.3 |
| DAMO_0725 | protein of unknown function   | 315  | 0    | 0.0   | 0.0  | 0    | 0.0  | 0.0  | —   |
| DAMO_0726 | 3-oxoacyl-[acyl-carrier-protein] reductas   | 762  | 0    | 0.0   | 0.0  | 0    | 0.0  | 0.0  | —   |
| DAMO_0727 | protein of unknown function   | 1827 | 0    | 0.0   | 0.0  | 0    | 0.0  | 0.0  | —   |
| DAMO_0728 | protein of unknown function   | 945  | 0    | 0.0   | 0.0  | 0    | 0.0  | 0.0  | —   |
| DAMO_0729 | conserved protein of unknown function   | 687  | 0    | 0.0   | 0.0  | 0    | 0.0  | 0.0  | —   |
| DAMO_0730 | membrane protein of unknown function  | 405  | 35   | 6.2   | 0.9  | 7    | 1.2  | 0.3  | 0.3 |
| DAMO_0731 | protein of unknown function   | 213  | 0    | 0.0   | 0.0  | 1    | 0.3  | 0.1  | —   |
| DAMO_0732 | conserved protein of unknown function   | 390  | 1    | 0.2   | 0.0  | 0    | 0.0  | 0.0  | —   |
| DAMO_0733 | protein of unknown function   | 222  | 0    | 0.0   | 0.0  | 0    | 0.0  | 0.0  | —   |
| DAMO_0734 | conserved hypothetical protein  | 549  | 1    | 0.1   | 0.0  | 0    | 0.0  | 0.0  | —   |
| DAMO_0735 | protein of unknown function   | 294  | 0    | 0.0   | 0.0  | 0    | 0.0  | 0.0  | —   |
| DAMO_0736 | protein of unknown function   | 228  | 3    | 0.9   | 0.1  | 0    | 0.0  | 0.0  | —   |
| DAMO_0737 | conserved protein of unknown function   | 285  | 7    | 1.8   | 0.2  | 10   | 2.5  | 0.6  | 2.3 |
| DAMO_0738 | Glycogen phosphorylase  | 2493 | 563  | 16.3  | 2.3  | 614  | 17.7 | 3.9  | 1.7 |
| DAMO_0739 | Histidine kinase  | 471  | 80   | 12.2  | 1.7  | 112  | 17.1 | 3.8  | 2.2 |
| DAMO_0741 | Anti-sigma B factor antagonist  | 348  | 60   | 12.4  | 1.7  | 82   | 17.0 | 3.7  | 2.2 |
| DAMO_0742 | conserved protein of unknown function   | 303  | 4    | 1.0   | 0.1  | 17   | 4.0  | 0.9  | 6.7 |
| DAMO_0743 | putative Sensor protein   | 3150 | 185  | 4.2   | 0.6  | 326  | 7.5  | 1.6  | 2.8 |
| DAMO_0744 | Response regulator receiver protein   | 1194 | 21   | 1.3   | 0.2  | 59   | 3.6  | 0.8  | 4.4 |
| DAMO_0746 | protein of unknown function   | 1212 | 59   | 3.5   | 0.5  | 0    | 0.0  | 0.0  | —   |
| DAMO_0747 | Similar to 2-oxoglutarate dehydrogenase complex E2 component  | 972  | 98   | 7.3   | 1.0  | 13   | 1.0  | 0.2  | 0.2 |
| DAMO_0748 | 2-oxoisovalerate dehydrogenase subunit beta beta chain) (BCKDH E1-beta)                               | 972  | 122  | 9.0   | 1.3  | 43   | 3.2  | 0.7  | 0.6 |
| DAMO_0749 | Similar to pyruvate dehydrogenase (Lipoamide) E1 component alpha chain                                | 1830 | 792  | 31.2  | 4.3  | 1121 | 44.1 | 9.7  | 2.2 |
| DAMO_0750 | conserved protein of unknown function   | 1485 | 220  | 10.7  | 1.5  | 306  | 14.8 | 3.3  | 2.2 |
| DAMO_0751 | putative proteasome component   | 852  | 262  | 22.1  | 3.1  | 175  | 14.8 | 3.3  | 1.1 |
| DAMO_0752 | putative proteasome A-type and B-type   | 696  | 70   | 7.2   | 1.0  | 72   | 7.4  | 1.6  | 1.6 |
| DAMO_0753 | putative proteasome A-type and B-type   | 1359 | 469  | 24.8  | 3.5  | 741  | 39.3 | 8.7  | 2.5 |
| DAMO_0754 | conserved protein of unknown function   | 1521 | 138  | 6.5   | 0.9  | 56   | 2.7  | 0.6  | 0.6 |
| DAMO_0755 | Putative cytosol aminopeptidase (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase) PepA           | 231  | 66   | 20.6  | 2.9  | 6    | 1.9  | 0.4  | 0.1 |
| DAMO_0756 | putative transport protein, belonging to the Major Facilitator Superfamily, of which narK is a member | 1224 | 15   | 0.9   | 0.1  | 8    | 0.5  | 0.1  | 0.8 |
| DAMO_0757 | Pfs, NACHT and Ankyrin domain protei  | 912  | 11   | 0.9   | 0.1  | 2    | 0.2  | 0.0  | 0.3 |
| DAMO_0758 | conserved protein of unknown function   | 714  | 168  | 16.9  | 2.4  | 179  | 18.1 | 4.0  | 1.7 |
| DAMO_0759 | conserved protein of unknown function   | 912  | 275  | 21.7  | 3.0  | 161  | 12.7 | 2.8  | 0.9 |
| DAMO_0761 | conserved protein of unknown function   | 912  | 169  | 13.3  | 1.9  | 241  | 19.0 | 4.2  | 2.3 |
| DAMO_0762 | protein of unknown function   | 93   | 2    | 1.5   | 0.2  | 0    | 0.0  | 0.0  | 0.0 |
| DAMO_0764 | conserved protein of unknown function   | 912  | 256  | 20.2  | 2.8  | 260  | 20.5 | 4.5  | 1.6 |
| DAMO_0765 | Pfs, NACHT and Ankyrin domain protei  | 819  | 330  | 29.0  | 4.0  | 336  | 29.5 | 6.5  | 1.6 |
| DAMO_0766 | FAD-dependent pyridine nucleotide-disulphide oxidoreductase precursor                                 | 1998 | 740  | 26.7  | 3.7  | 218  | 7.9  | 1.7  | 0.5 |
| DAMO_0767 | Rieske (2Fe-2S) domain protein precursor  | 519  | 95   | 13.2  | 1.8  | 94   | 13.0 | 2.9  | 1.6 |
| DAMO_0768 | Menaquinol-cytochrome c reductase cytochrome b subunit (modular protein)                              | 1482 | 399  | 19.4  | 2.7  | 485  | 23.6 | 5.2  | 1.9 |
| DAMO_0769 | hypothetical tetraheam c type cytochrome, part of bc1 complex, complex III                            | 792  | 744  | 67.6  | 9.4  | 312  | 28.4 | 6.3  | 0.7 |
| DAMO_0770 | protein of unknown function   | 237  | 83   | 25.2  | 3.5  | 33   | 10.0 | 2.2  | 0.6 |
| DAMO_0771 | conserved protein of unknown function   | 276  | 224  | 58.4  | 8.1  | 173  | 45.1 | 9.9  | 1.2 |
| DAMO_0772 | conserved protein of unknown function   | 279  | 151  | 39.0  | 5.4  | 247  | 63.7 | 14.0 | 2.6 |
| DAMO_0773 | putative C4-dicarboxylate transporter   | 1047 | 279  | 19.2  | 2.7  | 15   | 1.0  | 0.2  | 0.1 |
| DAMO_0774 | Nitrate reductase, gamma subunit  | 684  | 259  | 27.3  | 3.8  | 27   | 2.8  | 0.6  | 0.2 |
| DAMO_0775 | Protein necessary for nitrate reductase assembl   | 900  | 353  | 28.2  | 3.9  | 30   | 2.4  | 0.5  | 0.1 |
| DAMO_0776 | Nitrate reductase, beta subunit; may be more similar to nitrite oxidoreductase                        | 1530 | 2732 | 128.6 | 17.9 | 193  | 9.1  | 2.0  | 0.1 |
| DAMO_0777 | Protein of unknown function.  | 582  | 136  | 16.8  | 2.3  | 13   | 1.6  | 0.4  | 0.2 |
| DAMO_0778 | Nitrate reductase, alpha chain; may be more similar to a nitrite oxidoreductase                       | 3651 | 1452 | 28.6  | 4.0  | 190  | 3.7  | 0.8  | 0.2 |
| DAMO_0779 | conserved hypothetical protein; putative cytochrome c class I   | 1266 | 739  | 42.0  | 5.9  | 130  | 7.4  | 1.6  | 0.3 |
| DAMO_0780 | protein of unknown function   | 1263 | 25   | 1.4   | 0.2  | 16   | 0.9  | 0.2  | 1.0 |



|           |  |      |     |      |     |     |      |     |     |
|-----------|--|------|-----|------|-----|-----|------|-----|-----|
| DAMO_0781 | exported protein of unknown function   | 843  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0782 | protein of unknown function  | 246  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0783 | protein of unknown function  | 363  | 9   | 1.8  | 0.2 | 0   | 0.0  | 0.0 | —   |
| DAMO_0784 | protein of unknown function  | 459  | 2   | 0.3  | 0.0 | 1   | 0.2  | 0.0 | 0.8 |
| DAMO_0785 | conserved protein of unknown function  | 282  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0787 | protein of unknown function  | 123  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0788 | protein of unknown function  | 207  | 4   | 1.4  | 0.2 | 0   | 0.0  | 0.0 | —   |
| DAMO_0789 | PilT-like protein  | 387  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0790 | Prevent-host-death family protein  | 246  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0792 | protein of unknown function  | 213  | 14  | 4.7  | 0.7 | 1   | 0.3  | 0.1 | 0.1 |
| DAMO_0793 | protein of unknown function  | 192  | 9   | 3.4  | 0.5 | 3   | 1.1  | 0.2 | 0.5 |
| DAMO_0794 | ATPase (AAA+ superfamily)-like (fragment)  | 135  | 7   | 3.7  | 0.5 | 6   | 3.2  | 0.7 | 1.4 |
| DAMO_0795 | ATPase (AAA+ superfamily)-like (fragment)  | 750  | 195 | 18.7 | 2.6 | 42  | 4.0  | 0.9 | 0.3 |
| DAMO_0796 | protein of unknown function  | 294  | 24  | 5.9  | 0.8 | 11  | 2.7  | 0.6 | 0.7 |
| DAMO_0797 | protein of unknown function  | 876  | 140 | 11.5 | 1.6 | 138 | 11.3 | 2.5 | 1.6 |
| DAMO_0798 | exported protein of unknown function   | 210  | 63  | 21.6 | 3.0 | 53  | 18.2 | 4.0 | 1.3 |
| DAMO_0799 | protein of unknown function  | 636  | 148 | 16.8 | 2.3 | 48  | 5.4  | 1.2 | 0.5 |
| DAMO_0800 | protein of unknown function  | 66   | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0801 | Putative cytochrome c oxidase, subunit I   | 1404 | 267 | 13.7 | 1.9 | 138 | 7.1  | 1.6 | 0.8 |
| DAMO_0802 | Putative cytochrome c oxidase, subunit II  | 558  | 166 | 21.4 | 3.0 | 164 | 21.2 | 4.7 | 1.6 |
| DAMO_0803 | protein of unknown function  | 267  | 134 | 36.1 | 5.0 | 38  | 10.2 | 2.3 | 0.4 |
| DAMO_0804 | Transcriptional regulator, LysR family   | 915  | 48  | 3.8  | 0.5 | 16  | 1.3  | 0.3 | 0.5 |
| DAMO_0805 | putative Glycosyl transferase, group 1   | 1047 | 61  | 4.2  | 0.6 | 17  | 1.2  | 0.3 | 0.4 |
| DAMO_0806 | exported protein of unknown function   | 2010 | 424 | 15.2 | 2.1 | 88  | 3.2  | 0.7 | 0.3 |
| DAMO_0807 | Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (Asp/Glu-ADT subunit B)                       | 1494 | 401 | 19.3 | 2.7 | 115 | 5.5  | 1.2 | 0.5 |
| DAMO_0808 | conserved protein of unknown function  | 444  | 6   | 1.0  | 0.1 | 2   | 0.3  | 0.1 | 0.5 |
| DAMO_0809 | exported protein of unknown function   | 414  | 2   | 0.3  | 0.0 | 8   | 1.4  | 0.3 | 6.3 |
| DAMO_0810 | Glutamyl-tRNA(Gln) amidotransferase subunit  | 1461 | 147 | 7.2  | 1.0 | 55  | 2.7  | 0.6 | 0.6 |
| DAMO_0811 | Glutamyl-tRNA(Gln) amidotransferase subunit C  | 291  | 23  | 5.7  | 0.8 | 11  | 2.7  | 0.6 | 0.8 |
| DAMO_0812 | DNA helicase II  | 2190 | 238 | 7.8  | 1.1 | 82  | 2.7  | 0.6 | 0.5 |
| DAMO_0813 | conserved protein of unknown function  | 264  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0814 | PilT protein-like  | 402  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0815 | protein of unknown function  | 177  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0816 | exported protein of unknown function   | 639  | 7   | 0.8  | 0.1 | 1   | 0.1  | 0.0 | 0.2 |
| DAMO_0818 | putative deca-heme c-type cytochrome (fragment)  | 1002 | 112 | 8.0  | 1.1 | 12  | 0.9  | 0.2 | 0.2 |
| DAMO_0819 | exported protein of unknown function   | 2400 | 102 | 3.1  | 0.4 | 22  | 0.7  | 0.1 | 0.3 |
| DAMO_0820 | putative Plastoquinol--plastocyanin reductase  | 453  | 35  | 5.6  | 0.8 | 3   | 0.5  | 0.1 | 0.1 |
| DAMO_0821 | Cytochrome bc complex cytochrome b subunit   | 1089 | 63  | 4.2  | 0.6 | 15  | 1.0  | 0.2 | 0.4 |
| DAMO_0822 | exported protein of unknown function   | 1269 | 62  | 3.5  | 0.5 | 9   | 0.5  | 0.1 | 0.2 |
| DAMO_0824 | exported protein of unknown function   | 375  | 243 | 46.7 | 6.5 | 93  | 17.9 | 3.9 | 0.6 |
| DAMO_0825 | putative Cytochrome b subunit of formate dehydrogenase-like protein                                      | 2148 | 111 | 3.7  | 0.5 | 19  | 0.6  | 0.1 | 0.3 |
| DAMO_0826 | protein of unknown function  | 2199 | 152 | 5.0  | 0.7 | 67  | 2.2  | 0.5 | 0.7 |
| DAMO_0828 | protein of unknown function  | 546  | 51  | 6.7  | 0.9 | 34  | 4.5  | 1.0 | 1.1 |
| DAMO_0827 | exported protein of unknown function   | 222  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0829 | Ribonuclease T2 precursor  | 963  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0830 | Esterase/lipase/thioesterase family active site  | 747  | 1   | 0.1  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0831 | membrane protein of unknown function   | 534  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0832 | membrane protein of unknown function   | 1011 | 6   | 0.4  | 0.1 | 4   | 0.3  | 0.1 | 1.1 |
| DAMO_0833 | exported protein of unknown function   | 318  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_0834 | CDP-diacylglycerol-choline O-phosphatidyltransferase   | 732  | 53  | 5.2  | 0.7 | 6   | 0.6  | 0.1 | 0.2 |
| DAMO_0835 | exported protein of unknown function   | 951  | 40  | 3.0  | 0.4 | 0   | 0.0  | 0.0 | —   |
| DAMO_0836 | putative ABC-type uncharacterized transport system involved in gliding motility auxiliary component-like | 1614 | 143 | 6.4  | 0.9 | 117 | 5.2  | 1.2 | 1.3 |
| DAMO_0837 | ABC-type transport system involved in multi-copper enzyme maturation, permease component                 | 768  | 56  | 5.3  | 0.7 | 19  | 1.8  | 0.4 | 0.5 |
| DAMO_0838 | ABC transporter related  | 987  | 105 | 7.7  | 1.1 | 39  | 2.8  | 0.6 | 0.6 |
| DAMO_0839 | conserved protein of unknown function  | 891  | 12  | 1.0  | 0.1 | 2   | 0.2  | 0.0 | 0.3 |
| DAMO_0840 | conserved protein of unknown function  | 1059 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |

|           |  |      |      |       |      |     |       |      |     |
|-----------|--|------|------|-------|------|-----|-------|------|-----|
| DAMO_0841 | protein of unknown function  | 597  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0842 | conserved protein of unknown function  | 216  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0843 | Type-2 restriction enzyme MunI (R.MunI) (Type II restriction enzyme MunI) (Endonuclease MunI)                      | 600  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0844 | Modification methylase MunI (Adenine-specific methyltransferase MunI) (M.MunI)                                     | 744  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0845 | conserved exported protein of unknown function   | 249  | 1    | 0.3   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0846 | protein of unknown function  | 228  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0847 | conserved protein of unknown function  | 585  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0848 | protein of unknown function  | 267  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0849 | protein of unknown function  | 63   | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0850 | putative exoribonuclease II  | 1470 | 354  | 17.3  | 2.4  | 94  | 4.6   | 1.0  | 0.4 |
| DAMO_0851 | Conserved hypothetical protein   | 294  | 16   | 3.9   | 0.5  | 7   | 1.7   | 0.4  | 0.7 |
| DAMO_0852 | Conserved hypothetical protein   | 234  | 13   | 4.0   | 0.6  | 7   | 2.2   | 0.5  | 0.9 |
| DAMO_0853 | Formate dehydrogenase, alpha subunit (fdhA2)   | 2700 | 145  | 3.9   | 0.5  | 17  | 0.5   | 0.1  | 0.2 |
| DAMO_0854 | Putative dehydrogenase, similar to gamma (5') and beta (3') subunits of formate dehydrogenase and to nuoE and nuoF | 2133 | 145  | 4.9   | 0.7  | 31  | 1.0   | 0.2  | 0.3 |
| DAMO_0855 | protein of unknown function  | 264  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0856 | putative AsnC family transcriptional regulator   | 234  | 74   | 22.8  | 3.2  | 9   | 2.8   | 0.6  | 0.2 |
| DAMO_0857 | conserved hypothetical protein   | 216  | 325  | 108.3 | 15.1 | 127 | 42.3  | 9.3  | 0.6 |
| DAMO_0858 | hypothetical protein   | 306  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0859 | putative Nitrogen assimilation transcription regulation protein (ntrB) (synonyms:glnR, glnL)                       | 1218 | 77   | 4.6   | 0.6  | 24  | 1.4   | 0.3  | 0.5 |
| DAMO_0860 | putative Nitrogen assimilation transcription regulatory protein (ntrC)(synonyms:glnT, glnG)                        | 1464 | 101  | 5.0   | 0.7  | 15  | 0.7   | 0.2  | 0.2 |
| DAMO_0861 | putative transcriptional regulator, LysR family  | 939  | 112  | 8.6   | 1.2  | 10  | 0.8   | 0.2  | 0.1 |
| DAMO_0862 | putative phosphoribosylaminoimidazole-succinocarboxamide synthase (SAICAR synthetase) (ade1/pur7). Catalyses A'    | 936  | 50   | 3.8   | 0.5  | 11  | 0.8   | 0.2  | 0.3 |
| DAMO_0863 | hypothetical protein; putative membrane protein of unknown function  | 270  | 42   | 11.2  | 1.6  | 33  | 8.8   | 1.9  | 1.2 |
| DAMO_0864 | Putative nirD (nasD) assimilatory nitrite reductase, small subunit (Rieske (2Fe-2S) domain) protein                | 324  | 19   | 4.2   | 0.6  | 3   | 0.7   | 0.1  | 0.2 |
| DAMO_0865 | putative nirB (nasB) assimilatory nitrite reductase, large subunit [NAD(P)H]                                       | 2424 | 40   | 1.2   | 0.2  | 7   | 0.2   | 0.0  | 0.3 |
| DAMO_0866 | Glutamate synthase [NADPH] small chain   | 1446 | 108  | 5.4   | 0.7  | 30  | 1.5   | 0.3  | 0.4 |
| DAMO_0867 | Glutamate synthase [NADPH] large chain   | 4590 | 256  | 4.0   | 0.6  | 79  | 1.2   | 0.3  | 0.5 |
| DAMO_0868 | hypothetical protein   | 153  | 1    | 0.5   | 0.1  | 0   | 0.0   | 0.0  | —   |
| DAMO_0869 | putative Peptidoglycan glycosyltransferase   | 2439 | 3    | 0.1   | 0.0  | 10  | 0.3   | 0.1  | 5.3 |
| DAMO_0870 | exported protein of unknown function   | 1368 | 0    | 0.0   | 0.0  | 3   | 0.2   | 0.0  | —   |
| DAMO_0871 | protein of unknown function  | 288  | 177  | 44.3  | 6.2  | 102 | 25.5  | 5.6  | 0.9 |
| DAMO_0872 | Alpha/beta hydrolase fold  | 789  | 22   | 2.0   | 0.3  | 6   | 0.5   | 0.1  | 0.4 |
| DAMO_0873 | 3-isopropylmalate dehydratase small subunit  | 603  | 64   | 7.6   | 1.1  | 26  | 3.1   | 0.7  | 0.6 |
| DAMO_0874 | 3-isopropylmalate dehydratase large subunit 2 2)   | 1404 | 159  | 8.2   | 1.1  | 38  | 1.9   | 0.4  | 0.4 |
| DAMO_0875 | conserved exported protein of unknown function   | 372  | 98   | 19.0  | 2.6  | 46  | 8.9   | 2.0  | 0.7 |
| DAMO_0876 | protein of unknown function  | 63   | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0877 | protein of unknown function  | 219  | 1186 | 389.9 | 54.3 | 602 | 197.9 | 43.6 | 0.8 |
| DAMO_0878 | conserved protein of unknown function  | 291  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0879 | protein of unknown function  | 447  | 68   | 11.0  | 1.5  | 16  | 2.6   | 0.6  | 0.4 |
| DAMO_0880 | protein of unknown function  | 408  | 205  | 36.2  | 5.0  | 223 | 39.4  | 8.7  | 1.7 |
| DAMO_0881 | protein of unknown function  | 177  | 115  | 46.8  | 6.5  | 8   | 3.3   | 0.7  | 0.1 |
| DAMO_0882 | Short-chain dehydrogenase/reductase SDR  | 735  | 59   | 5.8   | 0.8  | 36  | 3.5   | 0.8  | 1.0 |
| DAMO_0883 | Beta-lactamase-like  | 678  | 23   | 2.4   | 0.3  | 11  | 1.2   | 0.3  | 0.8 |
| DAMO_0884 | protein of unknown function  | 1164 | 27   | 1.7   | 0.2  | 9   | 0.6   | 0.1  | 0.5 |
| DAMO_0885 | putative DNA-methyltransferase   | 531  | 2    | 0.3   | 0.0  | 1   | 0.1   | 0.0  | 0.8 |
| DAMO_0886 | protein of unknown function  | 267  | 1    | 0.3   | 0.0  | 1   | 0.3   | 0.1  | 1.6 |
| DAMO_0887 | Transcriptional regulatory protein zraR  | 1383 | 4    | 0.2   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0888 | protein of unknown function  | 69   | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0889 | exported protein of unknown function   | 798  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0890 | exported protein of unknown function   | 1083 | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0891 | conserved protein of unknown function  | 2166 | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0892 | Peptidase C1A, papain  | 915  | 33   | 2.6   | 0.4  | 14  | 1.1   | 0.2  | 0.7 |
| DAMO_0893 | protein of unknown function  | 174  | 1    | 0.4   | 0.1  | 0   | 0.0   | 0.0  | —   |
| DAMO_0894 | protein of unknown function  | 387  | 9    | 1.7   | 0.2  | 6   | 1.1   | 0.2  | 1.1 |
| DAMO_0895 | exported protein of unknown function   | 1056 | 65   | 4.4   | 0.6  | 62  | 4.2   | 0.9  | 1.5 |
| DAMO_0896 | protein of unknown function  | 273  | 9    | 2.4   | 0.3  | 0   | 0.0   | 0.0  | —   |

|           |  |      |      |       |      |       |        |       |      |
|-----------|--|------|------|-------|------|-------|--------|-------|------|
| DAMO_0897 | Ubiquinone/menaquinone biosynthesis methyltransferase ubiE   | 723  | 50   | 5.0   | 0.7  | 18    | 1.8    | 0.4   | 0.6  |
| DAMO_0898 | 4-hydroxybenzoate polyprenyltransferase-related protein  | 873  | 45   | 3.7   | 0.5  | 15    | 1.2    | 0.3   | 0.5  |
| DAMO_0899 | exported protein of unknown function   | 255  | 122  | 34.4  | 4.8  | 11    | 3.1    | 0.7   | 0.1  |
| DAMO_0900 | protein of unknown function  | 261  | 11   | 3.0   | 0.4  | 2     | 0.6    | 0.1   | 0.3  |
| DAMO_0901 | protein of unknown function  | 318  | 19   | 4.3   | 0.6  | 3     | 0.7    | 0.1   | 0.2  |
| DAMO_0902 | conserved protein of unknown function  | 513  | 2    | 0.3   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0903 | protein of unknown function  | 123  | 40   | 23.4  | 3.3  | 2     | 1.2    | 0.3   | 0.1  |
| DAMO_0904 | protein of unknown function  | 1011 | 20   | 1.4   | 0.2  | 4     | 0.3    | 0.1   | 0.3  |
| DAMO_0905 | Glycosyltransferase (fragment)   | 849  | 2    | 0.2   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0906 | putative O-antigen/LPS export system ATP-binding protein   | 795  | 2    | 0.2   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0907 | putative O-antigen export system permease protein rfbA   | 828  | 3    | 0.3   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0908 | GDP-mannose 4,6-dehydratase (GDP-D-mannose dehydratase)  | 987  | 1    | 0.1   | 0.0  | 1     | 0.1    | 0.0   | 1.6  |
| DAMO_0909 | dTDP-4-dehydrorhamnose 3,5-epimerase   | 525  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0910 | conserved protein of unknown function  | 846  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0911 | protein of unknown function  | 213  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0912 | bifunctional GDP-fucose synthetase: GDP-4-dehydro-6-deoxy-D-mannose epimerase; GDP-4-dehydro-6-L-deoxygalac          | 945  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0913 | DNA polymerase, beta domain protein region   | 423  | 3    | 0.5   | 0.1  | 0     | 0.0    | 0.0   | —    |
| DAMO_0914 | conserved protein of unknown function  | 273  | 18   | 4.7   | 0.7  | 2     | 0.5    | 0.1   | 0.2  |
| DAMO_0915 | putative HEPN domain protein   | 240  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0916 | conserved protein of unknown function  | 789  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0917 | putative Sulfotransferase domain superfamily   | 858  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0918 | protein of unknown function  | 1560 | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0919 | protein of unknown function  | 1242 | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0920 | protein of unknown function  | 1338 | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0921 | protein of unknown function  | 468  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0922 | protein of unknown function  | 240  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0923 | Genome sequencing data, contig C328  | 246  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0924 | conserved protein of unknown function  | 219  | 0    | 0.0   | 0.0  | 1     | 0.3    | 0.1   | —    |
| DAMO_0925 | protein of unknown function  | 165  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0926 | protein of unknown function  | 957  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0927 | putative CysN/CysC bifunctional enzyme: Sulfate adenylyltransferase (SAT) subunit 1 (N-terminal); Adenylyl-sulfate l | 573  | 0    | 0.0   | 0.0  | 1     | 0.1    | 0.0   | —    |
| DAMO_0928 | Glycosyl transferase, family 2 (modular protein)   | 1611 | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0929 | protein of unknown function  | 1260 | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0930 | protein of unknown function  | 864  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0931 | Methyltransferase 24   | 738  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0932 | Uncharacterized glycosyltransferase ykcC   | 942  | 2    | 0.2   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0933 | NAD-dependent epimerase/dehydratase  | 957  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0934 | Short-chain alcohol dehydrogenase  | 879  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0935 | Oxidoreductase domain protein  | 978  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0936 | protein of unknown function  | 435  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0937 | conserved protein of unknown function  | 201  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0938 | GHMP kinase  | 984  | 1    | 0.1   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0939 | Nucleotidyl transferase  | 717  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0940 | Sugar isomerase family protein   | 597  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0941 | putative phosphatase   | 564  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0942 | Transaldolase  | 717  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0943 | GDP-mannose 4,6-dehydratase (GDP-D-mannose dehydratase)  | 1041 | 65   | 4.5   | 0.6  | 18    | 1.2    | 0.3   | 0.4  |
| DAMO_0944 | conserved protein of unknown function  | 561  | 10   | 1.3   | 0.2  | 0     | 0.0    | 0.0   | —    |
| DAMO_0945 | protein of unknown function  | 183  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0946 | conserved protein of unknown function  | 324  | 2    | 0.4   | 0.1  | 1     | 0.2    | 0.0   | 0.8  |
| DAMO_0947 | protein of unknown function  | 324  | 0    | 0.0   | 0.0  | 0     | 0.0    | 0.0   | —    |
| DAMO_0948 | putative transporter, major facilitator family. narK is a member of this family                                      | 1179 | 206  | 12.6  | 1.8  | 25    | 1.5    | 0.3   | 0.2  |
| DAMO_0949 | putative 2-phosphosulfolactate phosphatase   | 726  | 21   | 2.1   | 0.3  | 13    | 1.3    | 0.3   | 1.0  |
| DAMO_0950 | protein of unknown function  | 153  | 12   | 5.6   | 0.8  | 1     | 0.5    | 0.1   | 0.1  |
| DAMO_0951 | conserved protein of unknown function  | 462  | 1090 | 169.9 | 23.7 | 10540 | 1642.6 | 362.0 | 15.3 |
| DAMO_0952 | protein of unknown function  | 201  | 22   | 7.9   | 1.1  | 4     | 1.4    | 0.3   | 0.3  |

|           |  |      |      |       |      |     |       |      |     |
|-----------|--|------|------|-------|------|-----|-------|------|-----|
| DAMO_0953 | protein of unknown function  | 618  | 32   | 3.7   | 0.5  | 35  | 4.1   | 0.9  | 1.7 |
| DAMO_0954 | conserved protein of unknown function                                    | 690  | 17   | 1.8   | 0.2  | 90  | 9.4   | 2.1  | 8.4 |
| DAMO_0955 | exported protein of unknown function                                     | 1044 | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0956 | protein of unknown function  | 192  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0957 | protein of unknown function  | 213  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0958 | protein of unknown function  | 165  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0959 | exported protein of unknown function                                     | 321  | 80   | 17.9  | 2.5  | 18  | 4.0   | 0.9  | 0.4 |
| DAMO_0960 | protein of unknown function  | 171  | 7    | 2.9   | 0.4  | 0   | 0.0   | 0.0  | —   |
| DAMO_0961 | Outer membrane efflux protein precursor                                  | 1281 | 174  | 9.8   | 1.4  | 24  | 1.3   | 0.3  | 0.2 |
| DAMO_0962 | Efflux transporter, RND family, MFP subuni                               | 1278 | 175  | 9.9   | 1.4  | 16  | 0.9   | 0.2  | 0.1 |
| DAMO_0963 | putative cation efflux system protein silA                               | 3153 | 299  | 6.8   | 1.0  | 45  | 1.0   | 0.2  | 0.2 |
| DAMO_0964 | putative Integral membrane protein, TerC famil                           | 114  | 12   | 7.6   | 1.1  | 0   | 0.0   | 0.0  | —   |
| DAMO_0965 | protein of unknown function  | 153  | 7    | 3.3   | 0.5  | 0   | 0.0   | 0.0  | —   |
| DAMO_0966 | Peptidase M50  | 1086 | 143  | 9.5   | 1.3  | 14  | 0.9   | 0.2  | 0.2 |
| DAMO_0967 | protein of unknown function  | 126  | 7    | 4.0   | 0.6  | 0   | 0.0   | 0.0  | —   |
| DAMO_0968 | protein of unknown function  | 210  | 1400 | 480.0 | 66.9 | 532 | 182.4 | 40.2 | 0.6 |
| DAMO_0969 | Similar to glycogen phosphorylase  | 1857 | 212  | 8.2   | 1.1  | 51  | 2.0   | 0.4  | 0.4 |
| DAMO_0970 | exported protein of unknown function                                     | 459  | 264  | 41.4  | 5.8  | 54  | 8.5   | 1.9  | 0.3 |
| DAMO_0971 | protein of unknown function  | 270  | 42   | 11.2  | 1.6  | 23  | 6.1   | 1.4  | 0.9 |
| DAMO_0972 | conserved protein of unknown function                                    | 288  | 4    | 1.0   | 0.1  | 0   | 0.0   | 0.0  | —   |
| DAMO_0973 | conserved protein of unknown function                                    | 243  | 5    | 1.5   | 0.2  | 0   | 0.0   | 0.0  | —   |
| DAMO_0974 | protein of unknown function  | 300  | 1    | 0.2   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0975 | Cell division protein ftsH homolog (ATP-dependent zinc-metallo protease) | 1851 | 312  | 12.1  | 1.7  | 78  | 3.0   | 0.7  | 0.4 |
| DAMO_0976 | protein of unknown function  | 87   | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0977 | protein of unknown function  | 447  | 10   | 1.6   | 0.2  | 29  | 4.7   | 1.0  | 4.6 |
| DAMO_0978 | conserved exported protein of unknown function                           | 1110 | 107  | 6.9   | 1.0  | 79  | 5.1   | 1.1  | 1.2 |
| DAMO_0979 | conserved protein of unknown function                                    | 417  | 3    | 0.5   | 0.1  | 1   | 0.2   | 0.0  | 0.5 |
| DAMO_0980 | Pyruvate flavodoxin/ferredoxin oxidoreductase domain protein             | 1977 | 359  | 13.1  | 1.8  | 221 | 8.0   | 1.8  | 1.0 |
| DAMO_0981 | Thiamine pyrophosphate enzyme domain protein TPP-binding                 | 1683 | 164  | 7.0   | 1.0  | 88  | 3.8   | 0.8  | 0.8 |
| DAMO_0982 | Putative pqq coenzyme synthesis protein (pqqE)                           | 1116 | 62   | 4.0   | 0.6  | 55  | 3.5   | 0.8  | 1.4 |
| DAMO_0983 | UspA   | 468  | 165  | 25.4  | 3.5  | 70  | 10.8  | 2.4  | 0.7 |
| DAMO_0984 | conserved protein of unknown function                                    | 1119 | 56   | 3.6   | 0.5  | 125 | 8.0   | 1.8  | 3.5 |
| DAMO_0985 | Adenylylsulfate kinase   | 600  | 67   | 8.0   | 1.1  | 33  | 4.0   | 0.9  | 0.8 |
| DAMO_0986 | protein of unknown function  | 273  | 4    | 1.1   | 0.1  | 3   | 0.8   | 0.2  | 1.2 |
| DAMO_0987 | putative HspC2 heat shock protein  | 444  | 199  | 32.3  | 4.5  | 714 | 115.8 | 25.5 | 5.7 |
| DAMO_0988 | conserved protein of unknown function                                    | 519  | 117  | 16.2  | 2.3  | 102 | 14.2  | 3.1  | 1.4 |
| DAMO_0989 | Methionine adenosyltransferase   | 1203 | 195  | 11.7  | 1.6  | 53  | 3.2   | 0.7  | 0.4 |
| DAMO_0990 | CBS domain containing membrane protein                                   | 645  | 100  | 11.2  | 1.6  | 117 | 13.1  | 2.9  | 1.9 |
| DAMO_0991 | protein of unknown function  | 813  | 118  | 10.5  | 1.5  | 50  | 4.4   | 1.0  | 0.7 |
| DAMO_0992 | Calcium-transporting ATPase  | 2754 | 202  | 5.3   | 0.7  | 113 | 3.0   | 0.7  | 0.9 |
| DAMO_0993 | protein of unknown function  | 327  | 2    | 0.4   | 0.1  | 3   | 0.7   | 0.1  | 2.4 |
| DAMO_0994 | putative GCN5-related N-acetyltransferase                                | 564  | 50   | 6.4   | 0.9  | 36  | 4.6   | 1.0  | 1.1 |
| DAMO_0995 | protein of unknown function  | 147  | 11   | 5.4   | 0.8  | 10  | 4.9   | 1.1  | 1.4 |
| DAMO_0996 | putative ATP-dependent protease  | 2472 | 266  | 7.7   | 1.1  | 137 | 4.0   | 0.9  | 0.8 |
| DAMO_0997 | protein of unknown function  | 63   | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_0998 | protein of unknown function  | 525  | 88   | 12.1  | 1.7  | 155 | 21.3  | 4.7  | 2.8 |
| DAMO_0999 | conserved protein of unknown function                                    | 486  | 114  | 16.9  | 2.4  | 224 | 33.2  | 7.3  | 3.1 |
| DAMO_1000 | conserved protein of unknown function                                    | 489  | 53   | 7.8   | 1.1  | 16  | 2.4   | 0.5  | 0.5 |
| DAMO_1001 | protein of unknown function  | 321  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1002 | transposase  | 852  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1003 | conserved protein of unknown function                                    | 480  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1004 | protein of unknown function  | 117  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1005 | putative Sel1 domain protein repeat-containing protein                   | 1113 | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1006 | conserved protein of unknown function                                    | 504  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1007 | Integrase, catalytic region  | 1005 | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1008 | protein of unknown function  | 240  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |

|           |   |      |     |      |     |     |      |      |     |
|-----------|---|------|-----|------|-----|-----|------|------|-----|
| DAMO_1009 | conserved protein of unknown function   | 267  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_1010 | protein of unknown function   | 168  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_1011 | putative Vesicle-fusing ATPase  | 2283 | 494 | 15.6 | 2.2 | 62  | 2.0  | 0.4  | 0.2 |
| DAMO_1012 | protein of unknown function   | 201  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_1013 | protein of unknown function   | 192  | 3   | 1.1  | 0.2 | 0   | 0.0  | 0.0  | —   |
| DAMO_1014 | protein of unknown function   | 474  | 7   | 1.1  | 0.1 | 0   | 0.0  | 0.0  | —   |
| DAMO_1015 | protein of unknown function   | 240  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_1016 | Rhodanese-related sulfurtransferase-like protein precursor  | 888  | 31  | 2.5  | 0.4 | 6   | 0.5  | 0.1  | 0.3 |
| DAMO_1017 | Galactose-1-phosphate uridylyltransferase   | 999  | 127 | 9.2  | 1.3 | 24  | 1.7  | 0.4  | 0.3 |
| DAMO_1018 | Pyrazinamidase/nicotinamidase (PZAase) (Nicotine deamidase) (NAMase)  | 606  | 10  | 1.2  | 0.2 | 2   | 0.2  | 0.1  | 0.3 |
| DAMO_1019 | Nicotinate phosphoribosyltransferase  | 1338 | 106 | 5.7  | 0.8 | 10  | 0.5  | 0.1  | 0.1 |
| DAMO_1020 | protein of unknown function   | 183  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_1021 | conserved protein of unknown function   | 576  | 150 | 18.8 | 2.6 | 69  | 8.6  | 1.9  | 0.7 |
| DAMO_1022 | Transcriptional regulator, BadM/Rrf2 family   | 411  | 11  | 1.9  | 0.3 | 2   | 0.4  | 0.1  | 0.3 |
| DAMO_1023 | pyridoxal-phosphate (PLP) dependent enzymes family; subunit of cysteine synthase A (O-acetylserine sulfhydrylase A) | 915  | 133 | 10.5 | 1.5 | 34  | 2.7  | 0.6  | 0.4 |
| DAMO_1024 | putative Molybdopterin biosynthesis protein moe   | 1149 | 100 | 6.3  | 0.9 | 77  | 4.8  | 1.1  | 1.2 |
| DAMO_1025 | putative permease   | 942  | 40  | 3.1  | 0.4 | 33  | 2.5  | 0.6  | 1.3 |
| DAMO_1026 | SirA family protein   | 243  | 25  | 7.4  | 1.0 | 23  | 6.8  | 1.5  | 1.5 |
| DAMO_1027 | conserved protein of unknown function   | 249  | 55  | 15.9 | 2.2 | 64  | 18.5 | 4.1  | 1.8 |
| DAMO_1028 | pyridoxal-phosphate (PLP) dependent enzymes family; subunit of cysteine synthase A (O-acetylserine sulfhydrylase A) | 936  | 265 | 20.4 | 2.8 | 799 | 61.5 | 13.5 | 4.8 |
| DAMO_1029 | putative Mov34/MPN/PAD-1 family protein   | 489  | 14  | 2.1  | 0.3 | 28  | 4.1  | 0.9  | 3.2 |
| DAMO_1030 | conserved membrane protein of unknown function  | 942  | 93  | 7.1  | 1.0 | 53  | 4.1  | 0.9  | 0.9 |
| DAMO_1031 | putative Sulfite/ferredoxin reductase (cysI)  | 1830 | 133 | 5.2  | 0.7 | 108 | 4.2  | 0.9  | 1.3 |
| DAMO_1032 | exported protein of unknown function  | 981  | 24  | 1.8  | 0.2 | 17  | 1.2  | 0.3  | 1.1 |
| DAMO_1033 | protein of unknown function   | 291  | 8   | 2.0  | 0.3 | 0   | 0.0  | 0.0  | —   |
| DAMO_1034 | phosphoadenosine phosphosulfate reductase(PAPS reductase, thioredoxin dependent) (PAdoPS reductase) (3'- phospho    | 786  | 98  | 9.0  | 1.3 | 99  | 9.1  | 2.0  | 1.6 |
| DAMO_1035 | Sulfate adenylyltransferase (Sulfate adenylyltransferase) (SAT) (ATP-sulfurylase)                                   | 1194 | 83  | 5.0  | 0.7 | 73  | 4.4  | 1.0  | 1.4 |
| DAMO_1036 | protein of unknown function   | 654  | 4   | 0.4  | 0.1 | 3   | 0.3  | 0.1  | 1.2 |
| DAMO_1037 | conserved protein of unknown function   | 240  | 49  | 14.7 | 2.0 | 13  | 3.9  | 0.9  | 0.4 |
| DAMO_1038 | conserved protein of unknown function   | 237  | 74  | 22.5 | 3.1 | 16  | 4.9  | 1.1  | 0.3 |
| DAMO_1039 | putative threonine synthase (TS)  | 1254 | 166 | 9.5  | 1.3 | 37  | 2.1  | 0.5  | 0.4 |
| DAMO_1040 | conserved protein of unknown function   | 279  | 82  | 21.2 | 2.9 | 28  | 7.2  | 1.6  | 0.5 |
| DAMO_1041 | exported protein of unknown function  | 549  | 6   | 0.8  | 0.1 | 0   | 0.0  | 0.0  | 0.0 |
| DAMO_1042 | exported protein of unknown function  | 417  | 5   | 0.9  | 0.1 | 1   | 0.2  | 0.0  | 0.3 |
| DAMO_1043 | exported protein of unknown function  | 123  | 1   | 0.6  | 0.1 | 0   | 0.0  | 0.0  | —   |
| DAMO_1044 | 4-hydroxy-3-methylbut-2-enyl diphosphate reductase 2  | 993  | 177 | 12.8 | 1.8 | 138 | 10.0 | 2.2  | 1.2 |
| DAMO_1045 | protein of unknown function   | 156  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_1046 | ACT domain-containing protein   | 414  | 111 | 19.3 | 2.7 | 68  | 11.8 | 2.6  | 1.0 |
| DAMO_1047 | putative lactam utilization protein   | 786  | 16  | 1.5  | 0.2 | 2   | 0.2  | 0.0  | 0.2 |
| DAMO_1048 | putative carboxylase  | 687  | 4   | 0.4  | 0.1 | 1   | 0.1  | 0.0  | 0.4 |
| DAMO_1049 | putative urea amidolyase-related protein  | 1089 | 14  | 0.9  | 0.1 | 2   | 0.1  | 0.0  | 0.2 |
| DAMO_1050 | protein of unknown function   | 543  | 1   | 0.1  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_1051 | protein of unknown function   | 408  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_1052 | putative galactose-1-phosphate uridyl transferas  | 999  | 136 | 9.8  | 1.4 | 32  | 2.3  | 0.5  | 0.4 |
| DAMO_1053 | Glutamine synthetase regulatory protein P-II  | 339  | 71  | 15.1 | 2.1 | 7   | 1.5  | 0.3  | 0.2 |
| DAMO_1054 | Glutamine synthetase, type I, C-termina   | 264  | 24  | 6.5  | 0.9 | 3   | 0.8  | 0.2  | 0.2 |
| DAMO_1055 | Glutamine synthetase, type I, N-termina   | 1140 | 305 | 19.3 | 2.7 | 33  | 2.1  | 0.5  | 0.2 |
| DAMO_1056 | conserved membrane protein of unknown function  | 426  | 81  | 13.7 | 1.9 | 19  | 3.2  | 0.7  | 0.4 |
| DAMO_1057 | putative Glutamate-ammonia-ligase adenylyltransferase ([Glutamate--ammonia-ligase] adenylyltransferase) (Glutamin   | 3147 | 87  | 2.0  | 0.3 | 28  | 0.6  | 0.1  | 0.5 |
| DAMO_1058 | protein of unknown function   | 411  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_1059 | conserved protein of unknown function   | 906  | 82  | 6.5  | 0.9 | 62  | 4.9  | 1.1  | 1.2 |
| DAMO_1060 | protein of unknown function   | 387  | 103 | 19.2 | 2.7 | 117 | 21.8 | 4.8  | 1.8 |
| DAMO_1062 | protein of unknown function   | 108  | 50  | 33.3 | 4.6 | 12  | 8.0  | 1.8  | 0.4 |
| DAMO_1063 | protein of unknown function   | 222  | 5   | 1.6  | 0.2 | 2   | 0.6  | 0.1  | 0.6 |
| DAMO_1064 | exported protein of unknown function  | 381  | 10  | 1.9  | 0.3 | 9   | 1.7  | 0.4  | 1.4 |
| DAMO_1065 | conserved membrane protein of unknown function  | 1791 | 45  | 1.8  | 0.3 | 2   | 0.1  | 0.0  | 0.1 |

|           |  |      |     |      |     |     |      |     |     |
|-----------|--|------|-----|------|-----|-----|------|-----|-----|
| DAMO_1066 | putative Long-chain-fatty-acid--CoA ligase   | 1092 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1067 | protein of unknown function  | 1104 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1068 | protein of unknown function  | 1302 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1069 | protein of unknown function  | 315  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1070 | protein of unknown function  | 447  | 0   | 0.0  | 0.0 | 2   | 0.3  | 0.1 | —   |
| DAMO_1071 | protein of unknown function  | 699  | 13  | 1.3  | 0.2 | 0   | 0.0  | 0.0 | —   |
| DAMO_1072 | protein of unknown function  | 462  | 7   | 1.1  | 0.2 | 4   | 0.6  | 0.1 | 0.9 |
| DAMO_1073 | Chaperone  | 2598 | 224 | 6.2  | 0.9 | 88  | 2.4  | 0.5 | 0.6 |
| DAMO_1074 | fragment of conserved hypothetical protein (part 1)  | 483  | 13  | 1.9  | 0.3 | 3   | 0.4  | 0.1 | 0.4 |
| DAMO_1075 | fragment of conserved hypothetical protein (part 2)  | 303  | 11  | 2.6  | 0.4 | 3   | 0.7  | 0.2 | 0.4 |
| DAMO_1076 | Peptidase M48, Ste24p precursor  | 759  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1077 | Serine hydroxymethyltransferase (glyA)   | 1269 | 312 | 17.7 | 2.5 | 151 | 8.6  | 1.9 | 0.8 |
| DAMO_1078 | conserved hypothetical protein with ATP cone domain  | 474  | 58  | 8.8  | 1.2 | 18  | 2.7  | 0.6 | 0.5 |
| DAMO_1079 | Glutamyl-tRNA reductase (GluTR)  | 1269 | 35  | 2.0  | 0.3 | 10  | 0.6  | 0.1 | 0.5 |
| DAMO_1080 | Porphobilinogen deaminase (PBG) synthase)  | 948  | 31  | 2.4  | 0.3 | 6   | 0.5  | 0.1 | 0.3 |
| DAMO_1081 | Uroporphyrinogen-III methylase and Uroporphyrinogen-III synthase                           | 1530 | 117 | 5.5  | 0.8 | 51  | 2.4  | 0.5 | 0.7 |
| DAMO_1082 | protein of unknown function  | 309  | 23  | 5.4  | 0.7 | 7   | 1.6  | 0.4 | 0.5 |
| DAMO_1083 | putative septum formation protein  | 591  | 44  | 5.4  | 0.7 | 5   | 0.6  | 0.1 | 0.2 |
| DAMO_1084 | protein of unknown function  | 162  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1085 | protein of unknown function  | 264  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1086 | protein of unknown function  | 186  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1087 | protein of unknown function  | 180  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1089 | protein of unknown function  | 237  | 2   | 0.6  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_1088 | conserved protein of unknown function  | 486  | 1   | 0.1  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1090 | protein of unknown function  | 93   | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1091 | putative aromatic acid decarboxylase   | 594  | 38  | 4.6  | 0.6 | 6   | 0.7  | 0.2 | 0.2 |
| DAMO_1092 | protein of unknown function  | 177  | 1   | 0.4  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_1093 | MotA/TolQ/ExbB proton channel precursor  | 678  | 23  | 2.4  | 0.3 | 4   | 0.4  | 0.1 | 0.3 |
| DAMO_1094 | TolR protein   | 381  | 50  | 9.4  | 1.3 | 17  | 3.2  | 0.7 | 0.5 |
| DAMO_1095 | conserved protein of unknown function  | 618  | 148 | 17.2 | 2.4 | 88  | 10.3 | 2.3 | 0.9 |
| DAMO_1096 | Apocytochrome f precursor (fragment)   | 120  | 10  | 6.0  | 0.8 | 1   | 0.6  | 0.1 | 0.2 |
| DAMO_1097 | Sec-independent protein translocase protein tatA/E homolog (modular protein)               | 288  | 16  | 4.0  | 0.6 | 3   | 0.8  | 0.2 | 0.3 |
| DAMO_1098 | putative Sec-independent protein translocase protein TatC                                  | 801  | 47  | 4.2  | 0.6 | 22  | 2.0  | 0.4 | 0.7 |
| DAMO_1099 | transcriptional repressor for high-affinity phosphate uptake (modular protein)             | 1356 | 474 | 25.2 | 3.5 | 319 | 16.9 | 3.7 | 1.1 |
| DAMO_1100 | high-affinity phosphate transport protein (ABC superfamily, atp_bind)                      | 747  | 135 | 13.0 | 1.8 | 111 | 10.7 | 2.4 | 1.3 |
| DAMO_1101 | conserved membrane protein of unknown function   | 1620 | 88  | 3.9  | 0.5 | 26  | 1.2  | 0.3 | 0.5 |
| DAMO_1102 | conserved membrane protein of unknown function   | 2271 | 132 | 4.2  | 0.6 | 38  | 1.2  | 0.3 | 0.5 |
| DAMO_1103 | Strongly similar to phosphate binding protein of ABC-type phosphate transport system       | 1011 | 106 | 7.5  | 1.1 | 78  | 5.6  | 1.2 | 1.2 |
| DAMO_1104 | putative Phosphate-selective porin O and P precursor                                       | 1398 | 66  | 3.4  | 0.5 | 22  | 1.1  | 0.2 | 0.5 |
| DAMO_1105 | protein of unknown function  | 360  | 1   | 0.2  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1106 | protein of unknown function  | 219  | 19  | 6.2  | 0.9 | 1   | 0.3  | 0.1 | 0.1 |
| DAMO_1107 | conserved protein of unknown function  | 372  | 21  | 4.1  | 0.6 | 3   | 0.6  | 0.1 | 0.2 |
| DAMO_1108 | S-adenosylmethionine synthetase (Methionine adenosyltransferase) (AdoMet synthetase) (MAT) | 1200 | 107 | 6.4  | 0.9 | 104 | 6.2  | 1.4 | 1.5 |
| DAMO_1109 | Cation-transporting ATPase   | 3117 | 5   | 0.1  | 0.0 | 1   | 0.0  | 0.0 | 0.3 |
| DAMO_1110 | conserved protein of unknown function  | 702  | 2   | 0.2  | 0.0 | 3   | 0.3  | 0.1 | 2.4 |
| DAMO_1111 | conserved protein of unknown function  | 507  | 0   | 0.0  | 0.0 | 3   | 0.4  | 0.1 | —   |
| DAMO_1112 | conserved exported protein of unknown function   | 291  | 5   | 1.2  | 0.2 | 2   | 0.5  | 0.1 | 0.6 |
| DAMO_1113 | CHU large protein; putative phytase (fragment)   | 1539 | 89  | 4.2  | 0.6 | 84  | 3.9  | 0.9 | 1.5 |
| DAMO_1114 | protein of unknown function  | 276  | 20  | 5.2  | 0.7 | 11  | 2.9  | 0.6 | 0.9 |
| DAMO_1115 | putative Histidine kinase  | 1833 | 63  | 2.5  | 0.3 | 9   | 0.4  | 0.1 | 0.2 |
| DAMO_1116 | putative Nucleotidyl transferase   | 957  | 87  | 6.5  | 0.9 | 7   | 0.5  | 0.1 | 0.1 |
| DAMO_1117 | protein of unknown function  | 198  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1118 | Putative cytochrome c oxidase, subunit I   | 1590 | 73  | 3.3  | 0.5 | 16  | 0.7  | 0.2 | 0.3 |
| DAMO_1119 | Putative cytochrome c oxidase, subunit II  | 558  | 19  | 2.5  | 0.3 | 5   | 0.6  | 0.1 | 0.4 |
| DAMO_1120 | DNA polymerase, beta domain protein regio  | 333  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1121 | HEPN domain protein  | 414  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |

|           |  |      |     |       |      |     |       |      |     |
|-----------|--|------|-----|-------|------|-----|-------|------|-----|
| DAMO_1122 | protein of unknown function  | 171  | 2   | 0.8   | 0.1  | 0   | 0.0   | 0.0  | —   |
| DAMO_1123 | Protein arsC (Arsenate reductase) (Arsenical pump modifier) (Low molecular weight protein-tyrosine-phosphatase)  | 486  | 23  | 3.4   | 0.5  | 5   | 0.7   | 0.2  | 0.3 |
| DAMO_1124 | conserved membrane protein of unknown function   | 1110 | 181 | 11.7  | 1.6  | 36  | 2.3   | 0.5  | 0.3 |
| DAMO_1125 | Arsenical resistance operon repressor  | 327  | 2   | 0.4   | 0.1  | 0   | 0.0   | 0.0  | —   |
| DAMO_1126 | Putative transcriptional accessory protein containing S1 RNA-binding domain                                      | 2325 | 248 | 7.7   | 1.1  | 59  | 1.8   | 0.4  | 0.4 |
| DAMO_1127 | conserved protein of unknown function  | 1089 | 103 | 6.8   | 0.9  | 26  | 1.7   | 0.4  | 0.4 |
| DAMO_1128 | putative Sensor protein yycG   | 1833 | 159 | 6.2   | 0.9  | 92  | 3.6   | 0.8  | 0.9 |
| DAMO_1129 | response regulator in two-component regulatory system with PhoR (or CreC), regulation of Pi uptake (OmpR family) | 684  | 61  | 6.4   | 0.9  | 47  | 4.9   | 1.1  | 1.2 |
| DAMO_1130 | putative transcriptional regulator, ModE family  | 339  | 86  | 18.3  | 2.5  | 39  | 8.3   | 1.8  | 0.7 |
| DAMO_1131 | Molybdenum-pterin binding protein (Mop); putative molybdenum transport component                                 | 207  | 59  | 20.5  | 2.9  | 70  | 24.3  | 5.4  | 1.9 |
| DAMO_1132 | ABC-type tungstate transport system permease component-like protein precursor                                    | 879  | 70  | 5.7   | 0.8  | 41  | 3.4   | 0.7  | 0.9 |
| DAMO_1133 | conserved exported protein of unknown function   | 1488 | 63  | 3.0   | 0.4  | 10  | 0.5   | 0.1  | 0.3 |
| DAMO_1134 | Putative formylmethanofuran dehydrogenase, subunit D (FwdD-2)  | 339  | 21  | 4.5   | 0.6  | 3   | 0.6   | 0.1  | 0.2 |
| DAMO_1135 | Formyltransferase/hydrolase complex, subunit B, 5' end   | 372  | 14  | 2.7   | 0.4  | 9   | 1.7   | 0.4  | 1.0 |
| DAMO_1136 | Formyltransferase/hydrolase complex, subunit B, 3' end   | 945  | 58  | 4.4   | 0.6  | 6   | 0.5   | 0.1  | 0.2 |
| DAMO_1137 | Putative NADH dehydrogenase; similar to formate dehydrogenase, beta subunit (fdhB1)                              | 1419 | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1138 | Formate dehydrogenase, alpha subunit (fdhA1)   | 2673 | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1139 | protein of unknown function  | 270  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1140 | SirA-like (fragment)   | 240  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1141 | Molybdenum ABC transporter, periplasmic molybdate-binding protein  | 867  | 70  | 5.8   | 0.8  | 39  | 3.2   | 0.7  | 0.9 |
| DAMO_1142 | Molybdenum ABC transporter (permease protein)  | 663  | 48  | 5.2   | 0.7  | 12  | 1.3   | 0.3  | 0.4 |
| DAMO_1143 | Molybdenum ABC transporter ATP-binding protein   | 1095 | 53  | 3.5   | 0.5  | 9   | 0.6   | 0.1  | 0.3 |
| DAMO_1144 | ABC-type tungstate transport permease protein  | 699  | 57  | 5.9   | 0.8  | 40  | 4.1   | 0.9  | 1.1 |
| DAMO_1145 | Tungsten transporter ATP binding protein   | 1092 | 20  | 1.3   | 0.2  | 10  | 0.7   | 0.1  | 0.8 |
| DAMO_1146 | conserved protein of unknown function  | 249  | 422 | 122.0 | 17.0 | 460 | 133.0 | 29.3 | 1.7 |
| DAMO_1147 | molybdenum cofactor biosynthesis protein C   | 498  | 165 | 23.9  | 3.3  | 54  | 7.8   | 1.7  | 0.5 |
| DAMO_1148 | Histone deacetylase/AcuC/AphA family protein   | 1140 | 16  | 1.0   | 0.1  | 5   | 0.3   | 0.1  | 0.5 |
| DAMO_1149 | conserved protein of unknown function  | 288  | 209 | 52.3  | 7.3  | 137 | 34.3  | 7.5  | 1.0 |
| DAMO_1150 | protein of unknown function  | 225  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1151 | response regulator PleD (with diguanylate cyclase and response regulator receiver domains) (fragment)            | 387  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1152 | protein of unknown function  | 321  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1153 | transposase  | 852  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1154 | Diguanylate cyclase (fragment)   | 318  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1155 | L-seryl-tRNA(Sec) selenium transferase   | 1431 | 48  | 2.4   | 0.3  | 23  | 1.2   | 0.3  | 0.8 |
| DAMO_1156 | thymidylate kinase   | 732  | 7   | 0.7   | 0.1  | 2   | 0.2   | 0.0  | 0.5 |
| DAMO_1157 | DNA polymerase III, delta prime subunit  | 1065 | 22  | 1.5   | 0.2  | 7   | 0.5   | 0.1  | 0.5 |
| DAMO_1158 | Stage 0 sporulation protein yaaT (modular protein)   | 900  | 15  | 1.2   | 0.2  | 9   | 0.7   | 0.2  | 0.9 |
| DAMO_1159 | Methionyl-tRNA synthetase (Methionine--tRNA ligase) (MetRS)  | 1941 | 133 | 4.9   | 0.7  | 40  | 1.5   | 0.3  | 0.5 |
| DAMO_1160 | Putative deoxyribonuclease (ycfH)  | 795  | 38  | 3.4   | 0.5  | 2   | 0.2   | 0.0  | 0.1 |
| DAMO_1161 | Glycine oxidase  | 1116 | 41  | 2.6   | 0.4  | 5   | 0.3   | 0.1  | 0.2 |
| DAMO_1162 | Conserved hypothetical protein   | 279  | 13  | 3.4   | 0.5  | 4   | 1.0   | 0.2  | 0.5 |
| DAMO_1163 | protein of unknown function  | 201  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1164 | Putative Cytochrome c oxidase, subunit III   | 567  | 43  | 5.5   | 0.8  | 5   | 0.6   | 0.1  | 0.2 |
| DAMO_1165 | Putative cytochrome c oxidase, subunit I   | 1725 | 103 | 4.3   | 0.6  | 31  | 1.3   | 0.3  | 0.5 |
| DAMO_1166 | Putative cytochrome c oxidase, subunit II  | 705  | 93  | 9.5   | 1.3  | 41  | 4.2   | 0.9  | 0.7 |
| DAMO_1167 | conserved exported protein of unknown function   | 3000 | 165 | 4.0   | 0.6  | 90  | 2.2   | 0.5  | 0.9 |
| DAMO_1168 | MscS Mechanosensitive ion channel  | 807  | 21  | 1.9   | 0.3  | 11  | 1.0   | 0.2  | 0.8 |
| DAMO_1169 | conserved exported protein of unknown function   | 771  | 33  | 3.1   | 0.4  | 8   | 0.7   | 0.2  | 0.4 |
| DAMO_1170 | mechanosensitive channel   | 435  | 270 | 44.7  | 6.2  | 58  | 9.6   | 2.1  | 0.3 |
| DAMO_1171 | protein of unknown function  | 669  | 2   | 0.2   | 0.0  | 5   | 0.5   | 0.1  | 4.0 |
| DAMO_1172 | exported protein of unknown function   | 501  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1173 | conserved protein of unknown function  | 168  | 12  | 5.1   | 0.7  | 4   | 1.7   | 0.4  | 0.5 |
| DAMO_1174 | protein of unknown function  | 1059 | 0   | 0.0   | 0.0  | 1   | 0.1   | 0.0  | —   |
| DAMO_1175 | protein of unknown function  | 234  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1176 | protein of unknown function  | 762  | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1177 | protein of unknown function  | 93   | 0   | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |

|           |   |      |      |       |      |     |      |      |     |
|-----------|---|------|------|-------|------|-----|------|------|-----|
| DAMO_1178 | transposase   | 936  | 0    | 0.0   | 0.0  | 0   | 0.0  | 0.0  | —   |
| DAMO_1179 | Ribonucleoside-diphosphate reductase  | 3591 | 423  | 8.5   | 1.2  | 56  | 1.1  | 0.2  | 0.2 |
| DAMO_1180 | Filamentation induced by cAMP protein Fic   | 1068 | 7    | 0.5   | 0.1  | 0   | 0.0  | 0.0  | —   |
| DAMO_1181 | exported protein of unknown function  | 165  | 0    | 0.0   | 0.0  | 0   | 0.0  | 0.0  | —   |
| DAMO_1182 | Deoxycytidine triphosphate deaminase (dCTP deaminase)   | 555  | 137  | 17.8  | 2.5  | 38  | 4.9  | 1.1  | 0.4 |
| DAMO_1183 | protein of unknown function   | 507  | 27   | 3.8   | 0.5  | 7   | 1.0  | 0.2  | 0.4 |
| DAMO_1184 | protein of unknown function   | 450  | 29   | 4.6   | 0.6  | 14  | 2.2  | 0.5  | 0.8 |
| DAMO_1185 | protein of unknown function   | 240  | 1417 | 425.1 | 59.2 | 249 | 74.7 | 16.5 | 0.3 |
| DAMO_1186 | protein of unknown function   | 183  | 0    | 0.0   | 0.0  | 0   | 0.0  | 0.0  | —   |
| DAMO_1187 | conserved exported protein of unknown function  | 618  | 10   | 1.2   | 0.2  | 9   | 1.0  | 0.2  | 1.4 |
| DAMO_1188 | putative OstA-like protein precursor  | 564  | 18   | 2.3   | 0.3  | 17  | 2.2  | 0.5  | 1.5 |
| DAMO_1189 | putative lipopolysaccharide transport protein B: ATP-binding component of ABC superfamily                         | 726  | 63   | 6.2   | 0.9  | 30  | 3.0  | 0.7  | 0.8 |
| DAMO_1190 | RNA polymerase sigma-54 factor  | 1425 | 200  | 10.1  | 1.4  | 109 | 5.5  | 1.2  | 0.9 |
| DAMO_1191 | Protein DR_1082   | 543  | 37   | 4.9   | 0.7  | 20  | 2.7  | 0.6  | 0.9 |
| DAMO_1192 | conserved protein of unknown function   | 867  | 118  | 9.8   | 1.4  | 31  | 2.6  | 0.6  | 0.4 |
| DAMO_1193 | conserved protein of unknown function   | 795  | 10   | 0.9   | 0.1  | 2   | 0.2  | 0.0  | 0.3 |
| DAMO_1194 | protein of unknown function   | 198  | 0    | 0.0   | 0.0  | 1   | 0.4  | 0.1  | —   |
| DAMO_1195 | CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (Phosphatidylglycerophosphate synthase) (PGP s | 588  | 47   | 5.8   | 0.8  | 8   | 1.0  | 0.2  | 0.3 |
| DAMO_1196 | conserved hypothetical protein; putative membrane protein   | 633  | 59   | 6.7   | 0.9  | 30  | 3.4  | 0.8  | 0.8 |
| DAMO_1197 | aspartokinase   | 1239 | 113  | 6.6   | 0.9  | 47  | 2.7  | 0.6  | 0.7 |
| DAMO_1198 | exported protein of unknown function  | 405  | 0    | 0.0   | 0.0  | 0   | 0.0  | 0.0  | —   |
| DAMO_1199 | Segregation and condensation protein A  | 738  | 30   | 2.9   | 0.4  | 3   | 0.3  | 0.1  | 0.2 |
| DAMO_1200 | Segregation and condensation protein B  | 639  | 20   | 2.3   | 0.3  | 4   | 0.5  | 0.1  | 0.3 |
| DAMO_1201 | Uncharacterized RNA pseudouridine synthase aq_146   | 849  | 11   | 0.9   | 0.1  | 4   | 0.3  | 0.1  | 0.6 |
| DAMO_1202 | P-protein [Includes: Chorismate mutase (CM); Prephenate dehydratase (PDT)]  | 1077 | 71   | 4.7   | 0.7  | 18  | 1.2  | 0.3  | 0.4 |
| DAMO_1203 | histidinol-phosphate aminotransferase   | 1137 | 57   | 3.6   | 0.5  | 14  | 0.9  | 0.2  | 0.4 |
| DAMO_1204 | Phospho-2-dehydro-3-deoxyheptonate aldolase synthetase) (3-deoxy-D-arabino- heptulosonate 7-phosphate synthase)   | 1014 | 94   | 6.7   | 0.9  | 11  | 0.8  | 0.2  | 0.2 |
| DAMO_1205 | Protein tyrC: Cyclohexadienyl dehydrogenas  | 948  | 35   | 2.7   | 0.4  | 3   | 0.2  | 0.1  | 0.1 |
| DAMO_1206 | putative GTPase   | 1170 | 50   | 3.1   | 0.4  | 9   | 0.6  | 0.1  | 0.3 |
| DAMO_1207 | CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase  | 633  | 5    | 0.6   | 0.1  | 8   | 0.9  | 0.2  | 2.5 |
| DAMO_1208 | Acetyl-coenzyme A synthetase (Acetate--CoA ligase   | 1953 | 0    | 0.0   | 0.0  | 0   | 0.0  | 0.0  | —   |
| DAMO_1209 | GTP-binding protein engA  | 1320 | 23   | 1.3   | 0.2  | 0   | 0.0  | 0.0  | —   |
| DAMO_1210 | GTP-binding protein YchF  | 1080 | 76   | 5.1   | 0.7  | 13  | 0.9  | 0.2  | 0.3 |
| DAMO_1211 | protein of unknown function   | 252  | 2    | 0.6   | 0.1  | 0   | 0.0  | 0.0  | 0.0 |
| DAMO_1212 | Exonuclease-like protein  | 489  | 75   | 11.0  | 1.5  | 18  | 2.7  | 0.6  | 0.4 |
| DAMO_1213 | tRNA 2-methylthioadenosine synthase-like protein  | 1344 | 28   | 1.5   | 0.2  | 5   | 0.3  | 0.1  | 0.3 |
| DAMO_1214 | 5'-methylthioadenosine phosphorylase  | 867  | 155  | 12.9  | 1.8  | 29  | 2.4  | 0.5  | 0.3 |
| DAMO_1215 | PfkB domain protein   | 909  | 41   | 3.2   | 0.5  | 3   | 0.2  | 0.1  | 0.1 |
| DAMO_1216 | putative propionyl-CoA carboxylase beta chain   | 1569 | 179  | 8.2   | 1.1  | 35  | 1.6  | 0.4  | 0.3 |
| DAMO_1217 | acetyl CoA carboxylase, biotin carboxylase subunit.   | 1503 | 19   | 0.9   | 0.1  | 4   | 0.2  | 0.0  | 0.3 |
| DAMO_1218 | Biotin/lipoic acid binding domain protein   | 507  | 8    | 1.1   | 0.2  | 1   | 0.1  | 0.0  | 0.2 |
| DAMO_1219 | Methylmalonyl-CoA mutase, N-terminal domain/subunit   | 1722 | 98   | 4.1   | 0.6  | 24  | 1.0  | 0.2  | 0.4 |
| DAMO_1220 | Methylmalonyl-CoA epimerase   | 411  | 0    | 0.0   | 0.0  | 0   | 0.0  | 0.0  | —   |
| DAMO_1221 | protein of unknown function   | 1830 | 29   | 1.1   | 0.2  | 3   | 0.1  | 0.0  | 0.2 |
| DAMO_1222 | Membrane protein involved in aromatic hydrocarbon degradation   | 1344 | 9    | 0.5   | 0.1  | 1   | 0.1  | 0.0  | 0.2 |
| DAMO_1223 | bacterioferritin (iron storage homoprotein)   | 468  | 28   | 4.3   | 0.6  | 10  | 1.5  | 0.3  | 0.6 |
| DAMO_1224 | protein of unknown function   | 1773 | 344  | 14.0  | 1.9  | 134 | 5.4  | 1.2  | 0.6 |
| DAMO_1225 | Molybdopterin converting factor, subunit 1  | 255  | 0    | 0.0   | 0.0  | 0   | 0.0  | 0.0  | —   |
| DAMO_1226 | Molybdopterin-converting factor subunit   | 423  | 60   | 10.2  | 1.4  | 45  | 7.7  | 1.7  | 1.2 |
| DAMO_1227 | Acyl-CoA dehydrogenase  | 1791 | 344  | 13.8  | 1.9  | 137 | 5.5  | 1.2  | 0.6 |
| DAMO_1228 | Acetyl-CoA acetyltransferase with thiolase domai  | 1191 | 43   | 2.6   | 0.4  | 19  | 1.1  | 0.3  | 0.7 |
| DAMO_1229 | 3-hydroxyacyl-CoA dehydrogenase/enoyl-CoA hydratase/isomerase family protein (fragment)                           | 216  | 7    | 2.3   | 0.3  | 1   | 0.3  | 0.1  | 0.2 |
| DAMO_1230 | 3-hydroxyacyl-CoA dehydrogenase NAD-binding precursor   | 2166 | 198  | 6.6   | 0.9  | 41  | 1.4  | 0.3  | 0.3 |
| DAMO_1231 | protein of unknown function   | 195  | 0    | 0.0   | 0.0  | 1   | 0.4  | 0.1  | —   |
| DAMO_1232 | protein of unknown function   | 519  | 0    | 0.0   | 0.0  | 0   | 0.0  | 0.0  | —   |
| DAMO_1233 | membrane protein of unknown function  | 468  | 0    | 0.0   | 0.0  | 0   | 0.0  | 0.0  | —   |



|           |  |      |     |      |     |     |      |      |      |
|-----------|--|------|-----|------|-----|-----|------|------|------|
| DAMO_1234 | PilT protein domain protein  | 411  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —    |
| DAMO_1235 | protein of unknown function  | 237  | 0   | 0.0  | 0.0 | 9   | 2.7  | 0.6  | —    |
| DAMO_1236 | exported protein of unknown function   | 1455 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —    |
| DAMO_1237 | protein of unknown function  | 249  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —    |
| DAMO_1238 | protein of unknown function  | 1068 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —    |
| DAMO_1239 | protein of unknown function  | 279  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —    |
| DAMO_1240 | protein of unknown function  | 333  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —    |
| DAMO_1241 | Putative mannan endo-1,4-beta-mannosidase 9 precursor (Beta-mannanase 9) (Endo-beta-1,4-mannanase 9) | 99   | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —    |
| DAMO_1242 | protein of unknown function  | 189  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —    |
| DAMO_1243 | conserved protein of unknown function  | 243  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —    |
| DAMO_1244 | conserved protein of unknown function  | 243  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —    |
| DAMO_1245 | protein of unknown function  | 531  | 1   | 0.1  | 0.0 | 0   | 0.0  | 0.0  | —    |
| DAMO_1246 | conserved protein of unknown function  | 117  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —    |
| DAMO_1247 | conserved protein of unknown function  | 225  | 77  | 24.6 | 3.4 | 10  | 3.2  | 0.7  | 0.2  |
| DAMO_1248 | conserved protein of unknown function  | 405  | 75  | 13.3 | 1.9 | 15  | 2.7  | 0.6  | 0.3  |
| DAMO_1249 | conserved membrane protein of unknown function   | 2718 | 659 | 17.5 | 2.4 | 137 | 3.6  | 0.8  | 0.3  |
| DAMO_1250 | 2-amino-3-ketobutyrate coenzyme A ligase (AKB ligase) (Glycine C-acetyltransferase)                  | 1233 | 79  | 4.6  | 0.6 | 13  | 0.8  | 0.2  | 0.3  |
| DAMO_1251 | protein of unknown function  | 276  | 2   | 0.5  | 0.1 | 0   | 0.0  | 0.0  | —    |
| DAMO_1252 | putative monovalent cation:proton antiporter (CPA2 family)   | 1704 | 2   | 0.1  | 0.0 | 1   | 0.0  | 0.0  | 0.8  |
| DAMO_1253 | protein of unknown function  | 261  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —    |
| DAMO_1254 | protein of unknown function  | 306  | 1   | 0.2  | 0.0 | 0   | 0.0  | 0.0  | —    |
| DAMO_1255 | protein of unknown function  | 357  | 34  | 6.9  | 1.0 | 5   | 1.0  | 0.2  | 0.2  |
| DAMO_1256 | Alpha-glucan phosphorylase   | 1704 | 207 | 8.7  | 1.2 | 52  | 2.2  | 0.5  | 0.4  |
| DAMO_1257 | protein of unknown function  | 183  | 17  | 6.7  | 0.9 | 1   | 0.4  | 0.1  | 0.1  |
| DAMO_1258 | protein of unknown function  | 498  | 77  | 11.1 | 1.6 | 645 | 93.3 | 20.5 | 13.2 |
| DAMO_1259 | Transcriptional regulator, TetR family   | 603  | 66  | 7.9  | 1.1 | 165 | 19.7 | 4.3  | 4.0  |
| DAMO_1260 | putative Macrolide-specific efflux protein macA precursor  | 1224 | 171 | 10.1 | 1.4 | 195 | 11.5 | 2.5  | 1.8  |
| DAMO_1261 | Acriflavin resistance protein (fragment)   | 3303 | 502 | 10.9 | 1.5 | 453 | 9.9  | 2.2  | 1.4  |
| DAMO_1262 | protein of unknown function  | 258  | 52  | 14.5 | 2.0 | 29  | 8.1  | 1.8  | 0.9  |
| DAMO_1263 | NADPH-dependent 7-cyano-7-deazaguanine reductas  | 366  | 29  | 5.7  | 0.8 | 7   | 1.4  | 0.3  | 0.4  |
| DAMO_1264 | TonB-dependent receptor, plug  | 2082 | 129 | 4.5  | 0.6 | 21  | 0.7  | 0.2  | 0.3  |
| DAMO_1265 | putative transmembrane protein   | 573  | 6   | 0.8  | 0.1 | 6   | 0.8  | 0.2  | 1.6  |
| DAMO_1266 | putative Histidine kinase  | 1587 | 13  | 0.6  | 0.1 | 2   | 0.1  | 0.0  | 0.2  |
| DAMO_1267 | Response regulator receiver protein  | 381  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —    |
| DAMO_1268 | Putative regulatory protein, FmdB famil  | 165  | 86  | 37.5 | 5.2 | 17  | 7.4  | 1.6  | 0.3  |
| DAMO_1269 | exported protein of unknown function   | 273  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —    |
| DAMO_1270 | protein of unknown function  | 264  | 1   | 0.3  | 0.0 | 0   | 0.0  | 0.0  | —    |
| DAMO_1271 | conserved protein of unknown function  | 1257 | 23  | 1.3  | 0.2 | 1   | 0.1  | 0.0  | 0.1  |
| DAMO_1272 | conserved protein of unknown function  | 1512 | 81  | 3.9  | 0.5 | 8   | 0.4  | 0.1  | 0.2  |
| DAMO_1273 | membrane protein of unknown function   | 1212 | 221 | 13.1 | 1.8 | 23  | 1.4  | 0.3  | 0.2  |
| DAMO_1274 | exported protein of unknown function   | 639  | 26  | 2.9  | 0.4 | 21  | 2.4  | 0.5  | 1.3  |
| DAMO_1275 | Anion transporter  | 1659 | 2   | 0.1  | 0.0 | 0   | 0.0  | 0.0  | —    |
| DAMO_1277 | protein of unknown function  | 66   | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —    |
| DAMO_1276 | protein of unknown function  | 108  | 3   | 2.0  | 0.3 | 0   | 0.0  | 0.0  | —    |
| DAMO_1278 | exported protein of unknown function   | 471  | 32  | 4.9  | 0.7 | 5   | 0.8  | 0.2  | 0.2  |
| DAMO_1279 | protein of unknown function  | 666  | 32  | 3.5  | 0.5 | 20  | 2.2  | 0.5  | 1.0  |
| DAMO_1280 | protein of unknown function  | 594  | 67  | 8.1  | 1.1 | 21  | 2.5  | 0.6  | 0.5  |
| DAMO_1281 | Integrase/recombinase (E2 protein) (fragment)  | 153  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —    |
| DAMO_1282 | Cellulase  | 2217 | 92  | 3.0  | 0.4 | 27  | 0.9  | 0.2  | 0.5  |
| DAMO_1283 | protein of unknown function  | 165  | 25  | 10.9 | 1.5 | 19  | 8.3  | 1.8  | 1.2  |
| DAMO_1284 | Rubryerythrin  | 504  | 129 | 18.4 | 2.6 | 31  | 4.4  | 1.0  | 0.4  |
| DAMO_1285 | protein of unknown function  | 276  | 52  | 13.6 | 1.9 | 29  | 7.6  | 1.7  | 0.9  |
| DAMO_1286 | conserved protein of unknown function  | 267  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —    |
| DAMO_1287 | transposase  | 1179 | 16  | 1.0  | 0.1 | 3   | 0.2  | 0.0  | 0.3  |
| DAMO_1288 | protein of unknown function  | 714  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —    |
| DAMO_1289 | protein of unknown function  | 198  | 2   | 0.7  | 0.1 | 0   | 0.0  | 0.0  | —    |

|           |   |      |     |      |     |     |      |     |     |
|-----------|---|------|-----|------|-----|-----|------|-----|-----|
| DAMO_1290 | protein of unknown function   | 156  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1291 | DNA replication and repair protein rec  | 150  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1292 | Error-prone DNA polymerase  | 3189 | 102 | 2.3  | 0.3 | 19  | 0.4  | 0.1 | 0.3 |
| DAMO_1293 | conserved protein of unknown function   | 1479 | 31  | 1.5  | 0.2 | 7   | 0.3  | 0.1 | 0.4 |
| DAMO_1294 | conserved protein of unknown function   | 645  | 7   | 0.8  | 0.1 | 3   | 0.3  | 0.1 | 0.7 |
| DAMO_1295 | conserved hypothetical protein; putative phage protein Gp37/Gp68  | 759  | 27  | 2.6  | 0.4 | 4   | 0.4  | 0.1 | 0.2 |
| DAMO_1296 | protein of unknown function   | 237  | 16  | 4.9  | 0.7 | 2   | 0.6  | 0.1 | 0.2 |
| DAMO_1297 | LexA repressor  | 594  | 25  | 3.0  | 0.4 | 11  | 1.3  | 0.3 | 0.7 |
| DAMO_1298 | putative response regulator in two-component regulatory system, sigma54 dependent transcriptional regulator.          | 1368 | 48  | 2.5  | 0.4 | 5   | 0.3  | 0.1 | 0.2 |
| DAMO_1299 | protein of unknown function   | 321  | 3   | 0.7  | 0.1 | 1   | 0.2  | 0.0 | 0.5 |
| DAMO_1300 | protein of unknown function   | 1659 | 7   | 0.3  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1301 | protein of unknown function   | 213  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1302 | protein of unknown function   | 1224 | 2   | 0.1  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1303 | protein of unknown function   | 228  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1304 | Patatin   | 1425 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1305 | protein of unknown function   | 222  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1306 | protein of unknown function   | 162  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1307 | protein of unknown function   | 243  | 3   | 0.9  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_1308 | Sensor protein (fragment)   | 951  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1309 | transposase   | 438  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1310 | protein of unknown function   | 300  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1311 | protein of unknown function   | 1173 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1312 | protein of unknown function   | 420  | 0   | 0.0  | 0.0 | 1   | 0.2  | 0.0 | —   |
| DAMO_1313 | conserved membrane protein of unknown function  | 1140 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1314 | protein of unknown function   | 180  | 23  | 9.2  | 1.3 | 22  | 8.8  | 1.9 | 1.5 |
| DAMO_1315 | protein of unknown function   | 171  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1316 | two component sigma-54-dependent hydrogenase transcriptional regulator, Fis family                                    | 1404 | 143 | 7.3  | 1.0 | 21  | 1.1  | 0.2 | 0.2 |
| DAMO_1317 | putative Histidine kinase   | 2064 | 98  | 3.4  | 0.5 | 14  | 0.5  | 0.1 | 0.2 |
| DAMO_1318 | protein of unknown function   | 327  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1319 | TPR repeat protein precursor  | 3663 | 63  | 1.2  | 0.2 | 6   | 0.1  | 0.0 | 0.2 |
| DAMO_1320 | protein of unknown function   | 270  | 3   | 0.8  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_1321 | protein of unknown function   | 354  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1322 | TonB-dependent receptor, plug (fragment)  | 528  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1323 | protein of unknown function   | 99   | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1324 | protein of unknown function   | 345  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1325 | protein of unknown function   | 1128 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1326 | Recombinase A (recA)  | 1056 | 464 | 31.6 | 4.4 | 82  | 5.6  | 1.2 | 0.3 |
| DAMO_1327 | Twitching mobility protein  | 1140 | 189 | 11.9 | 1.7 | 29  | 1.8  | 0.4 | 0.2 |
| DAMO_1328 | protein of unknown function   | 366  | 2   | 0.4  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_1329 | alanyl-tRNA synthetase  | 2661 | 185 | 5.0  | 0.7 | 31  | 0.8  | 0.2 | 0.3 |
| DAMO_1330 | conserved exported protein of unknown function  | 246  | 15  | 4.4  | 0.6 | 4   | 1.2  | 0.3 | 0.4 |
| DAMO_1331 | conserved protein of unknown function   | 645  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1332 | protein of unknown function   | 198  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1333 | Modification methylase BglI (M.BglI) (N(4)- cytosine- specific methyltransferase BglI) (BglI modification methyltran: | 1017 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1334 | protein of unknown function   | 174  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1335 | protein of unknown function   | 624  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1336 | protein of unknown function   | 204  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1337 | conserved protein of unknown function   | 1233 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1338 | conserved protein of unknown function   | 831  | 16  | 1.4  | 0.2 | 5   | 0.4  | 0.1 | 0.5 |
| DAMO_1339 | phosphatidylserine decarboxylase  | 627  | 6   | 0.7  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_1340 | CDP-diacylglycerol--serine O-phosphatidyltransferase  | 801  | 46  | 4.1  | 0.6 | 24  | 2.2  | 0.5 | 0.8 |
| DAMO_1341 | 2-isopropylmalate synthase (Alpha-isopropylmalate synthase) (Alpha-IPM synthetase)                                    | 1548 | 408 | 19.0 | 2.6 | 229 | 10.7 | 2.3 | 0.9 |
| DAMO_1342 | Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase) (ASADH)  | 1020 | 122 | 8.6  | 1.2 | 38  | 2.7  | 0.6 | 0.5 |
| DAMO_1343 | tRNA pseudouridine synthase A (tRNA-uridine isomerase I) (tRNA pseudouridylate synthase I)                            | 792  | 23  | 2.1  | 0.3 | 2   | 0.2  | 0.0 | 0.1 |
| DAMO_1344 | Multicopper oxidase family protein  | 1596 | 61  | 2.8  | 0.4 | 17  | 0.8  | 0.2 | 0.4 |
| DAMO_1345 | DSBA oxidoreductase precursor   | 1068 | 17  | 1.1  | 0.2 | 4   | 0.3  | 0.1 | 0.4 |

|           |  |      |     |      |     |     |      |      |     |
|-----------|--|------|-----|------|-----|-----|------|------|-----|
| DAMO_1346 | protein of unknown function  | 240  | 2   | 0.6  | 0.1 | 0   | 0.0  | 0.0  | —   |
| DAMO_1347 | putative cyclase   | 462  | 79  | 12.3 | 1.7 | 13  | 2.0  | 0.4  | 0.3 |
| DAMO_1348 | Type III restriction protein res subuni  | 1914 | 8   | 0.3  | 0.0 | 2   | 0.1  | 0.0  | 0.4 |
| DAMO_1349 | protein of unknown function  | 372  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_1350 | protein of unknown function  | 474  | 8   | 1.2  | 0.2 | 3   | 0.5  | 0.1  | 0.6 |
| DAMO_1351 | conserved protein of unknown function  | 324  | 30  | 6.7  | 0.9 | 21  | 4.7  | 1.0  | 1.1 |
| DAMO_1352 | protein of unknown function  | 132  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_1353 | protein of unknown function  | 204  | 23  | 8.1  | 1.1 | 10  | 3.5  | 0.8  | 0.7 |
| DAMO_1354 | protein of unknown function  | 471  | 5   | 0.8  | 0.1 | 4   | 0.6  | 0.1  | 1.3 |
| DAMO_1355 | leucine tRNA synthetase  | 2595 | 291 | 8.1  | 1.1 | 33  | 0.9  | 0.2  | 0.2 |
| DAMO_1356 | exported protein of unknown function   | 507  | 2   | 0.3  | 0.0 | 0   | 0.0  | 0.0  | 0.0 |
| DAMO_1357 | putative DNA polymerase III, delta subunit   | 1008 | 61  | 4.4  | 0.6 | 5   | 0.4  | 0.1  | 0.1 |
| DAMO_1358 | 30S ribosomal protein S20  | 273  | 200 | 52.7 | 7.4 | 16  | 4.2  | 0.9  | 0.1 |
| DAMO_1359 | putative Virulence factor MviN-like protei   | 252  | 2   | 0.6  | 0.1 | 0   | 0.0  | 0.0  | —   |
| DAMO_1360 | Virulence factor protein   | 1320 | 2   | 0.1  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_1361 | Acetolactate synthase large subunit (AHAS  | 1743 | 797 | 32.9 | 4.6 | 641 | 26.5 | 5.8  | 1.3 |
| DAMO_1362 | Acetolactate synthase small subuni   | 618  | 387 | 45.1 | 6.3 | 235 | 27.4 | 6.0  | 1.0 |
| DAMO_1363 | Ketol-acid reductoisomerase (Acetohydroxy-acid isomeroreductase) (Alpha-keto-beta-hydroxylacil reductoisomerase)       | 1005 | 384 | 27.5 | 3.8 | 793 | 56.8 | 12.5 | 3.3 |
| DAMO_1364 | 5,10-methylenetetrahydrofolate reductase   | 873  | 23  | 1.9  | 0.3 | 13  | 1.1  | 0.2  | 0.9 |
| DAMO_1365 | protein of unknown function  | 279  | 23  | 5.9  | 0.8 | 45  | 11.6 | 2.6  | 3.1 |
| DAMO_1366 | tRNA delta(2)-isopentenylpyrophosphate transferase isopentenyltransferase) (IPTase) (IPPT)                             | 945  | 103 | 7.8  | 1.1 | 114 | 8.7  | 1.9  | 1.8 |
| DAMO_1367 | 3-phosphoshikimate 1-carboxyvinyltransferase (5- enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase             | 1305 | 46  | 2.5  | 0.4 | 12  | 0.7  | 0.1  | 0.4 |
| DAMO_1368 | Cytidylate kinase (CK) (Cytidine monophosphate kinase) (CMP kinase)  | 702  | 20  | 2.1  | 0.3 | 15  | 1.5  | 0.3  | 1.2 |
| DAMO_1369 | 1-acyl-sn-glycerol-3-phosphate acyltransferases  | 717  | 8   | 0.8  | 0.1 | 0   | 0.0  | 0.0  | —   |
| DAMO_1370 | 30S ribosomal subunit protein S1   | 1734 | 201 | 8.3  | 1.2 | 94  | 3.9  | 0.9  | 0.7 |
| DAMO_1371 | Signal peptide peptidase SppA, 36K type precursor  | 873  | 47  | 3.9  | 0.5 | 5   | 0.4  | 0.1  | 0.2 |
| DAMO_1372 | protein of unknown function  | 390  | 1   | 0.2  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_1373 | Integration host factor beta-subunit (IHF-beta)  | 324  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_1374 | conserved protein of unknown function  | 459  | 9   | 1.4  | 0.2 | 7   | 1.1  | 0.2  | 1.2 |
| DAMO_1375 | conserved protein of unknown function  | 486  | 37  | 5.5  | 0.8 | 12  | 1.8  | 0.4  | 0.5 |
| DAMO_1376 | protein of unknown function  | 708  | 5   | 0.5  | 0.1 | 4   | 0.4  | 0.1  | 1.3 |
| DAMO_1377 | adenine phosphoribosyltransferase  | 522  | 17  | 2.3  | 0.3 | 7   | 1.0  | 0.2  | 0.7 |
| DAMO_1378 | protein of unknown function  | 216  | 5   | 1.7  | 0.2 | 0   | 0.0  | 0.0  | —   |
| DAMO_1379 | Protein-L-isoaspartate O-methyltransferase L-isoaspartyl methyltransferase) (L-isoaspartyl protein carboxyl methyltran | 642  | 91  | 10.2 | 1.4 | 9   | 1.0  | 0.2  | 0.2 |
| DAMO_1380 | 5'-nucleotidase surE (Nucleoside 5'-monophosphate phosphohydrolase)(survival protein, protein damage control)          | 789  | 41  | 3.7  | 0.5 | 7   | 0.6  | 0.1  | 0.3 |
| DAMO_1381 | Uncharacterized HTH-type transcriptional regulator in himA 3'region (Fragment) (modular protein)                       | 396  | 57  | 10.4 | 1.4 | 5   | 0.9  | 0.2  | 0.1 |
| DAMO_1382 | DNA-binding protein HU (DNA-binding protein II   | 282  | 239 | 61.0 | 8.5 | 241 | 61.5 | 13.6 | 1.6 |
| DAMO_1383 | membrane protein of unknown function   | 1425 | 28  | 1.4  | 0.2 | 18  | 0.9  | 0.2  | 1.0 |
| DAMO_1384 | conserved membrane protein of unknown function   | 1659 | 12  | 0.5  | 0.1 | 14  | 0.6  | 0.1  | 1.8 |
| DAMO_1385 | putative Fe-S oxidoreductase   | 792  | 22  | 2.0  | 0.3 | 10  | 0.9  | 0.2  | 0.7 |
| DAMO_1386 | Hypoxanthine-guanine phosphoribosyltransferas  | 567  | 16  | 2.0  | 0.3 | 8   | 1.0  | 0.2  | 0.8 |
| DAMO_1387 | conserved protein of unknown function  | 1317 | 235 | 12.8 | 1.8 | 190 | 10.4 | 2.3  | 1.3 |
| DAMO_1388 | aspartate aminotransferase A (AspAT)   | 1206 | 64  | 3.8  | 0.5 | 46  | 2.7  | 0.6  | 1.1 |
| DAMO_1389 | Phosphopantetheine adenylyltransferas  | 486  | 24  | 3.6  | 0.5 | 30  | 4.4  | 1.0  | 2.0 |
| DAMO_1390 | putative methyltransferase   | 558  | 13  | 1.7  | 0.2 | 4   | 0.5  | 0.1  | 0.5 |
| DAMO_1391 | protein of unknown function  | 90   | 10  | 8.0  | 1.1 | 6   | 4.8  | 1.1  | 0.9 |
| DAMO_1392 | GTP pyrophosphokinase (ATP:GTP 3'-pyrophosphotransferase) (ppGpp synthetase I) ((p)ppGpp synthetase)                   | 2139 | 313 | 10.5 | 1.5 | 339 | 11.4 | 2.5  | 1.7 |
| DAMO_1393 | conserved protein of unknown function  | 588  | 3   | 0.4  | 0.1 | 1   | 0.1  | 0.0  | 0.5 |
| DAMO_1394 | Extracellular ligand-binding receptor precursor  | 1197 | 1   | 0.1  | 0.0 | 1   | 0.1  | 0.0  | 1.6 |
| DAMO_1395 | high-affinity branched-chain amino acid ABC transporter (ATP-binding protein)  | 705  | 26  | 2.7  | 0.4 | 4   | 0.4  | 0.1  | 0.2 |
| DAMO_1396 | ABC transporter, permease protein (N-ter) and ATP-binding protein (C-ter); putative branched-chain amino acid transp   | 2091 | 25  | 0.9  | 0.1 | 3   | 0.1  | 0.0  | 0.2 |
| DAMO_1397 | high-affinity branched-chain amino acid ABC transporter (permease protein)   | 903  | 42  | 3.3  | 0.5 | 26  | 2.1  | 0.5  | 1.0 |
| DAMO_1398 | high-affinity branched-chain amino acid ABC transporter (substrate-binding protein)                                    | 1113 | 49  | 3.2  | 0.4 | 19  | 1.2  | 0.3  | 0.6 |
| DAMO_1399 | Thiamine-phosphate pyrophosphorylase (TMP pyrophosphorylase) (TMP-PPase) (Thiamine-phosphate synthase)                 | 645  | 111 | 12.4 | 1.7 | 8   | 0.9  | 0.2  | 0.1 |
| DAMO_1400 | Elongation factor P (EF-P)   | 561  | 121 | 15.5 | 2.2 | 39  | 5.0  | 1.1  | 0.5 |
| DAMO_1401 | 3-dehydroquinate dehydratase type 2  | 471  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |

|           |  |      |     |       |      |     |      |      |     |
|-----------|--|------|-----|-------|------|-----|------|------|-----|
| DAMO_1402 | fragment of bifunctional: shikimate kinase 2)  | 1095 | 16  | 1.1   | 0.1  | 1   | 0.1  | 0.0  | 0.1 |
| DAMO_1403 | fragment of bifunctional: shikimate kinase 1)  | 531  | 3   | 0.4   | 0.1  | 1   | 0.1  | 0.0  | 0.5 |
| DAMO_1404 | Chorismate synthas   | 1164 | 107 | 6.6   | 0.9  | 29  | 1.8  | 0.4  | 0.4 |
| DAMO_1405 | exported protein of unknown function   | 813  | 2   | 0.2   | 0.0  | 0   | 0.0  | 0.0  | —   |
| DAMO_1406 | protein of unknown function  | 186  | 0   | 0.0   | 0.0  | 0   | 0.0  | 0.0  | —   |
| DAMO_1407 | exported protein of unknown function   | 867  | 3   | 0.2   | 0.0  | 0   | 0.0  | 0.0  | —   |
| DAMO_1408 | protein of unknown function  | 2295 | 22  | 0.7   | 0.1  | 2   | 0.1  | 0.0  | 0.1 |
| DAMO_1409 | exported protein of unknown function   | 495  | 2   | 0.3   | 0.0  | 0   | 0.0  | 0.0  | —   |
| DAMO_1410 | protein of unknown function  | 621  | 5   | 0.6   | 0.1  | 2   | 0.2  | 0.1  | 0.6 |
| DAMO_1411 | putative Pili assembly protein   | 543  | 2   | 0.3   | 0.0  | 0   | 0.0  | 0.0  | —   |
| DAMO_1412 | Type IV pilus assembly protein PilM  | 1071 | 41  | 2.8   | 0.4  | 5   | 0.3  | 0.1  | 0.2 |
| DAMO_1413 | tryptophan synthase alpha chain  | 801  | 13  | 1.2   | 0.2  | 2   | 0.2  | 0.0  | 0.2 |
| DAMO_1414 | Tryptophan synthase beta chain   | 1236 | 55  | 3.2   | 0.4  | 8   | 0.5  | 0.1  | 0.2 |
| DAMO_1415 | N-(5'-phosphoribosyl)anthranilate isomeras   | 624  | 7   | 0.8   | 0.1  | 1   | 0.1  | 0.0  | 0.2 |
| DAMO_1416 | indole-3-glycerol-phosphate synthase (IGPS)  | 804  | 3   | 0.3   | 0.0  | 0   | 0.0  | 0.0  | —   |
| DAMO_1417 | anthranilate phosphoribosyltransferase   | 1098 | 92  | 6.0   | 0.8  | 5   | 0.3  | 0.1  | 0.1 |
| DAMO_1418 | fragment of Anthranilate synthase [Includes: Glutamine amidotransferase] (part 2)                                  | 567  | 89  | 11.3  | 1.6  | 26  | 3.3  | 0.7  | 0.5 |
| DAMO_1419 | fragment of Anthranilate synthase [Includes: Glutamine amidotransferase] (part 1)                                  | 1515 | 212 | 10.1  | 1.4  | 20  | 1.0  | 0.2  | 0.1 |
| DAMO_1420 | thioredoxin 1, redox factor  | 330  | 5   | 1.1   | 0.2  | 0   | 0.0  | 0.0  | —   |
| DAMO_1421 | protein of unknown function  | 1104 | 5   | 0.3   | 0.0  | 0   | 0.0  | 0.0  | —   |
| DAMO_1422 | Ribonuclease 3 (Ribonuclease III) (RNase III)  | 741  | 13  | 1.3   | 0.2  | 2   | 0.2  | 0.0  | 0.2 |
| DAMO_1423 | protein of unknown function  | 186  | 0   | 0.0   | 0.0  | 0   | 0.0  | 0.0  | —   |
| DAMO_1424 | putative Chromosome partition protein smc  | 3600 | 197 | 3.9   | 0.5  | 18  | 0.4  | 0.1  | 0.1 |
| DAMO_1425 | Cell division transporter substrate-binding protein FtsY (Signal recognition particle receptor)                    | 945  | 73  | 5.6   | 0.8  | 6   | 0.5  | 0.1  | 0.1 |
| DAMO_1426 | bifunctional: diaminohydroxyphosphoribosylaminopyrimidine deaminase reductase                                      | 1119 | 14  | 0.9   | 0.1  | 9   | 0.6  | 0.1  | 1.0 |
| DAMO_1427 | riboflavin synthase alpha chain  | 651  | 5   | 0.6   | 0.1  | 2   | 0.2  | 0.0  | 0.6 |
| DAMO_1428 | Riboflavin biosynthesis protein ribBA [Includes: 3,4-dihydroxy-2- butanone 4-phosphate synthase (DHBP synthase); C | 1215 | 129 | 7.6   | 1.1  | 24  | 1.4  | 0.3  | 0.3 |
| DAMO_1429 | riboflavin synthase, beta chain  | 465  | 53  | 8.2   | 1.1  | 39  | 6.0  | 1.3  | 1.2 |
| DAMO_1430 | N utilization substance protein B homolog (Protein nusB)   | 432  | 45  | 7.5   | 1.0  | 6   | 1.0  | 0.2  | 0.2 |
| DAMO_1431 | exported protein of unknown function   | 348  | 9   | 1.9   | 0.3  | 3   | 0.6  | 0.1  | 0.5 |
| DAMO_1432 | conserved protein of unknown function  | 552  | 7   | 0.9   | 0.1  | 1   | 0.1  | 0.0  | 0.2 |
| DAMO_1433 | 3-oxoacyl-[acyl-carrier-protein] synthase I  | 1221 | 239 | 14.1  | 2.0  | 31  | 1.8  | 0.4  | 0.2 |
| DAMO_1434 | Acyl carrier protein (ACP)   | 246  | 87  | 25.5  | 3.5  | 67  | 19.6 | 4.3  | 1.2 |
| DAMO_1435 | 3-oxoacyl-[acyl-carrier-protein] reductase   | 759  | 142 | 13.5  | 1.9  | 47  | 4.5  | 1.0  | 0.5 |
| DAMO_1436 | Malonyl CoA-acyl carrier protein transacylas   | 891  | 29  | 2.3   | 0.3  | 5   | 0.4  | 0.1  | 0.3 |
| DAMO_1437 | 3-oxoacyl-[acyl-carrier-protein] synthase II   | 984  | 174 | 12.7  | 1.8  | 82  | 6.0  | 1.3  | 0.7 |
| DAMO_1438 | fatty acid/phospholipid synthesis protein, methyltransferase domain  | 972  | 227 | 16.8  | 2.3  | 108 | 8.0  | 1.8  | 0.8 |
| DAMO_1439 | protein of unknown function  | 747  | 163 | 15.7  | 2.2  | 101 | 9.7  | 2.1  | 1.0 |
| DAMO_1440 | protein of unknown function  | 510  | 116 | 16.4  | 2.3  | 12  | 1.7  | 0.4  | 0.2 |
| DAMO_1441 | nucleoside diphosphate kinase (NDK) (NDP kinase  | 447  | 15  | 2.4   | 0.3  | 1   | 0.2  | 0.0  | 0.1 |
| DAMO_1442 | succinyl-CoA synthetase, alpha subunit, NAD(P)-binding   | 870  | 17  | 1.4   | 0.2  | 0   | 0.0  | 0.0  | —   |
| DAMO_1443 | succinyl-CoA synthetase, beta subunit  | 1179 | 17  | 1.0   | 0.1  | 2   | 0.1  | 0.0  | 0.2 |
| DAMO_1444 | protein of unknown function  | 303  | 3   | 0.7   | 0.1  | 0   | 0.0  | 0.0  | —   |
| DAMO_1445 | DEAD/DEAH box helicase domain protein  | 2943 | 61  | 1.5   | 0.2  | 9   | 0.2  | 0.0  | 0.2 |
| DAMO_1446 | Similar to phosphatidylethanolamine N-methyltransferase  | 624  | 217 | 25.0  | 3.5  | 50  | 5.8  | 1.3  | 0.4 |
| DAMO_1447 | conserved exported protein of unknown function   | 543  | 30  | 4.0   | 0.6  | 2   | 0.3  | 0.1  | 0.1 |
| DAMO_1448 | Peptidase M28  | 879  | 7   | 0.6   | 0.1  | 3   | 0.2  | 0.1  | 0.7 |
| DAMO_1449 | protein of unknown function  | 234  | 37  | 11.4  | 1.6  | 16  | 4.9  | 1.1  | 0.7 |
| DAMO_1450 | exported protein of unknown function   | 315  | 542 | 123.9 | 17.3 | 317 | 72.5 | 16.0 | 0.9 |
| DAMO_1451 | exported protein of unknown function   | 528  | 112 | 15.3  | 2.1  | 79  | 10.8 | 2.4  | 1.1 |
| DAMO_1452 | conserved exported protein of unknown function   | 618  | 45  | 5.2   | 0.7  | 20  | 2.3  | 0.5  | 0.7 |
| DAMO_1453 | exported protein of unknown function   | 369  | 0   | 0.0   | 0.0  | 0   | 0.0  | 0.0  | —   |
| DAMO_1454 | conserved exported protein of unknown function   | 522  | 17  | 2.3   | 0.3  | 9   | 1.2  | 0.3  | 0.8 |
| DAMO_1455 | putative 17 kDa surface antigen precursor  | 636  | 11  | 1.2   | 0.2  | 14  | 1.6  | 0.3  | 2.0 |
| DAMO_1456 | membrane protein of unknown function   | 1410 | 0   | 0.0   | 0.0  | 0   | 0.0  | 0.0  | —   |
| DAMO_1457 | protein of unknown function  | 219  | 0   | 0.0   | 0.0  | 0   | 0.0  | 0.0  | —   |

|           |  |      |     |      |     |     |     |     |      |
|-----------|--|------|-----|------|-----|-----|-----|-----|------|
| DAMO_1458 | Peptidase M20 domain-containing protein  | 1170 | 102 | 6.3  | 0.9 | 104 | 6.4 | 1.4 | 1.6  |
| DAMO_1459 | Glycosyl transferase family 2  | 690  | 0   | 0.0  | 0.0 | 0   | 0.0 | 0.0 | —    |
| DAMO_1460 | protein of unknown function  | 207  | 0   | 0.0  | 0.0 | 0   | 0.0 | 0.0 | —    |
| DAMO_1461 | anhydro-N-acetylmuramic acid kinase  | 1194 | 17  | 1.0  | 0.1 | 0   | 0.0 | 0.0 | —    |
| DAMO_1462 | conserved protein of unknown function  | 738  | 9   | 0.9  | 0.1 | 17  | 1.7 | 0.4 | 3.0  |
| DAMO_1463 | Silmilar to D-aminoacylase   | 1602 | 16  | 0.7  | 0.1 | 7   | 0.3 | 0.1 | 0.7  |
| DAMO_1464 | putative glutamine amidotransferase-like protein yvdE  | 720  | 57  | 5.7  | 0.8 | 3   | 0.3 | 0.1 | 0.1  |
| DAMO_1465 | exported protein of unknown function   | 645  | 2   | 0.2  | 0.0 | 2   | 0.2 | 0.0 | 1.6  |
| DAMO_1466 | Putative beta-N-acetylglucosaminidas   | 1065 | 9   | 0.6  | 0.1 | 1   | 0.1 | 0.0 | 0.2  |
| DAMO_1467 | exported protein of unknown function   | 735  | 27  | 2.6  | 0.4 | 5   | 0.5 | 0.1 | 0.3  |
| DAMO_1468 | putative SAM dependent methyltransferase   | 705  | 16  | 1.6  | 0.2 | 3   | 0.3 | 0.1 | 0.3  |
| DAMO_1469 | protein of unknown function  | 639  | 0   | 0.0  | 0.0 | 0   | 0.0 | 0.0 | —    |
| DAMO_1470 | exported protein of unknown function   | 630  | 0   | 0.0  | 0.0 | 2   | 0.2 | 0.1 | —    |
| DAMO_1471 | protein of unknown function  | 588  | 10  | 1.2  | 0.2 | 0   | 0.0 | 0.0 | —    |
| DAMO_1472 | DNA repair protein radC homolog  | 738  | 41  | 4.0  | 0.6 | 9   | 0.9 | 0.2 | 0.3  |
| DAMO_1473 | Natural resistance-associated macrophage protein precursor                                       | 1236 | 123 | 7.2  | 1.0 | 38  | 2.2 | 0.5 | 0.5  |
| DAMO_1474 | CBS:MgtE intracellular region  | 1230 | 182 | 10.7 | 1.5 | 19  | 1.1 | 0.2 | 0.2  |
| DAMO_1475 | protein of unknown function  | 624  | 2   | 0.2  | 0.0 | 0   | 0.0 | 0.0 | —    |
| DAMO_1476 | conserved protein of unknown function  | 291  | 15  | 3.7  | 0.5 | 0   | 0.0 | 0.0 | —    |
| DAMO_1477 | conserved protein of unknown function  | 204  | 1   | 0.4  | 0.0 | 0   | 0.0 | 0.0 | —    |
| DAMO_1478 | conserved protein of unknown function  | 240  | 1   | 0.3  | 0.0 | 1   | 0.3 | 0.1 | 1.6  |
| DAMO_1479 | protein of unknown function  | 243  | 0   | 0.0  | 0.0 | 0   | 0.0 | 0.0 | —    |
| DAMO_1480 | conserved protein of unknown function  | 258  | 3   | 0.8  | 0.1 | 5   | 1.4 | 0.3 | 2.6  |
| DAMO_1481 | conserved protein of unknown function  | 258  | 2   | 0.6  | 0.1 | 15  | 4.2 | 0.9 | 11.9 |
| DAMO_1482 | Integrase/recombinase (E2 protein) (fragment)  | 141  | 1   | 0.5  | 0.1 | 0   | 0.0 | 0.0 | —    |
| DAMO_1483 | protein of unknown function  | 90   | 0   | 0.0  | 0.0 | 0   | 0.0 | 0.0 | —    |
| DAMO_1484 | conserved protein of unknown function  | 306  | 0   | 0.0  | 0.0 | 0   | 0.0 | 0.0 | —    |
| DAMO_1485 | conserved protein of unknown function  | 270  | 0   | 0.0  | 0.0 | 0   | 0.0 | 0.0 | —    |
| DAMO_1486 | conserved protein of unknown function  | 114  | 0   | 0.0  | 0.0 | 0   | 0.0 | 0.0 | —    |
| DAMO_1487 | conserved protein of unknown function  | 144  | 0   | 0.0  | 0.0 | 0   | 0.0 | 0.0 | —    |
| DAMO_1488 | protein of unknown function  | 198  | 9   | 3.3  | 0.5 | 0   | 0.0 | 0.0 | —    |
| DAMO_1489 | conserved protein of unknown function  | 351  | 11  | 2.3  | 0.3 | 4   | 0.8 | 0.2 | 0.6  |
| DAMO_1490 | protein of unknown function  | 312  | 0   | 0.0  | 0.0 | 0   | 0.0 | 0.0 | —    |
| DAMO_1491 | membrane protein of unknown function   | 417  | 1   | 0.2  | 0.0 | 0   | 0.0 | 0.0 | —    |
| DAMO_1492 | conserved protein of unknown function  | 249  | 1   | 0.3  | 0.0 | 0   | 0.0 | 0.0 | —    |
| DAMO_1493 | conserved protein of unknown function  | 237  | 0   | 0.0  | 0.0 | 0   | 0.0 | 0.0 | —    |
| DAMO_1494 | protein of unknown function  | 957  | 0   | 0.0  | 0.0 | 0   | 0.0 | 0.0 | —    |
| DAMO_1495 | protein of unknown function  | 189  | 0   | 0.0  | 0.0 | 0   | 0.0 | 0.0 | —    |
| DAMO_1496 | protein of unknown function  | 618  | 0   | 0.0  | 0.0 | 0   | 0.0 | 0.0 | —    |
| DAMO_1497 | protein of unknown function  | 264  | 2   | 0.5  | 0.1 | 0   | 0.0 | 0.0 | —    |
| DAMO_1498 | protein of unknown function  | 171  | 37  | 15.6 | 2.2 | 7   | 2.9 | 0.6 | 0.3  |
| DAMO_1499 | Magnesium transporter  | 1386 | 113 | 5.9  | 0.8 | 10  | 0.5 | 0.1 | 0.1  |
| DAMO_1500 | H+ translocating pyrophosphate synthase pump)(Pyrophosphate-energized inorganic pyrophosphatase) | 2319 | 722 | 22.4 | 3.1 | 128 | 4.0 | 0.9 | 0.3  |
| DAMO_1501 | Amidophosphoribosyltransferase precurso  | 1419 | 172 | 8.7  | 1.2 | 100 | 5.1 | 1.1 | 0.9  |
| DAMO_1502 | Oligopeptidase A. Metallo peptidase. MEROPS family M03A (fragment)                               | 183  | 14  | 5.5  | 0.8 | 3   | 1.2 | 0.3 | 0.3  |
| DAMO_1503 | putative PLP-dependent aminotransferase, putative aspartate aminotransferase.                    | 1167 | 376 | 23.2 | 3.2 | 154 | 9.5 | 2.1 | 0.6  |
| DAMO_1504 | conserved protein of unknown function  | 552  | 76  | 9.9  | 1.4 | 24  | 3.1 | 0.7 | 0.5  |
| DAMO_1505 | protein of unknown function  | 261  | 0   | 0.0  | 0.0 | 0   | 0.0 | 0.0 | —    |
| DAMO_1506 | protein of unknown function  | 273  | 0   | 0.0  | 0.0 | 0   | 0.0 | 0.0 | —    |
| DAMO_1507 | Transcriptional regulator (fragment)   | 132  | 3   | 1.6  | 0.2 | 0   | 0.0 | 0.0 | —    |
| DAMO_1508 | arginyl-tRNA synthetase  | 1674 | 148 | 6.4  | 0.9 | 23  | 1.0 | 0.2 | 0.2  |
| DAMO_1509 | protein of unknown function  | 54   | 0   | 0.0  | 0.0 | 0   | 0.0 | 0.0 | —    |
| DAMO_1510 | Rhodanese-like   | 339  | 41  | 8.7  | 1.2 | 43  | 9.1 | 2.0 | 1.7  |
| DAMO_1511 | putative Alpha/beta hydrolase fold precursor   | 1071 | 55  | 3.7  | 0.5 | 4   | 0.3 | 0.1 | 0.1  |
| DAMO_1512 | Squalene/phytoene synthase   | 858  | 49  | 4.1  | 0.6 | 13  | 1.1 | 0.2 | 0.4  |
| DAMO_1513 | protein of unknown function  | 597  | 11  | 1.3  | 0.2 | 0   | 0.0 | 0.0 | 0.0  |

|           |   |      |     |      |     |     |      |     |     |
|-----------|---|------|-----|------|-----|-----|------|-----|-----|
| DAMO_1514 | putative phosphotransferase Gmet_3384   | 918  | 24  | 1.9  | 0.3 | 15  | 1.2  | 0.3 | 1.0 |
| DAMO_1515 | N-acetylglutamate synthase  | 471  | 1   | 0.2  | 0.0 | 1   | 0.2  | 0.0 | 1.6 |
| DAMO_1516 | putative RNA 3'-terminal phosphate cyclas   | 1116 | 20  | 1.3  | 0.2 | 6   | 0.4  | 0.1 | 0.5 |
| DAMO_1517 | protein of unknown function   | 207  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1518 | conserved protein of unknown function   | 435  | 19  | 3.1  | 0.4 | 8   | 1.3  | 0.3 | 0.7 |
| DAMO_1519 | Amino acid permease-associated region   | 1944 | 151 | 5.6  | 0.8 | 89  | 3.3  | 0.7 | 0.9 |
| DAMO_1520 | putative Trk system potassium uptake protein trk  | 660  | 44  | 4.8  | 0.7 | 20  | 2.2  | 0.5 | 0.7 |
| DAMO_1521 | TrkA-N domain protein   | 699  | 124 | 12.8 | 1.8 | 14  | 1.4  | 0.3 | 0.2 |
| DAMO_1522 | Alpha/beta hydrolase fold   | 777  | 4   | 0.4  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_1523 | glycerol-3-phosphate dehydrogenase (NAD+)   | 1041 | 131 | 9.1  | 1.3 | 27  | 1.9  | 0.4 | 0.3 |
| DAMO_1524 | Prolipoprotein diacylglyceryl transferase   | 789  | 95  | 8.7  | 1.2 | 63  | 5.7  | 1.3 | 1.0 |
| DAMO_1525 | O-antigen polymerase (fragment)   | 120  | 14  | 8.4  | 1.2 | 3   | 1.8  | 0.4 | 0.3 |
| DAMO_1526 | aldehyde dehydrogenase  | 1521 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1527 | K+-dependent Na+/Ca+ exchanger related-protein  | 930  | 51  | 3.9  | 0.6 | 34  | 2.6  | 0.6 | 1.1 |
| DAMO_1528 | Na(+)/H(+) antiporter nhaA (Sodium/proton antiporter nhaA)  | 1350 | 279 | 14.9 | 2.1 | 147 | 7.8  | 1.7 | 0.8 |
| DAMO_1529 | conserved exported protein of unknown function  | 423  | 80  | 13.6 | 1.9 | 77  | 13.1 | 2.9 | 1.5 |
| DAMO_1530 | conserved protein of unknown function   | 207  | 3   | 1.0  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_1531 | putative Trehalose-phosphatase (Trehalose 6-phosphate phosphatase) (TPP)  | 780  | 122 | 11.3 | 1.6 | 229 | 21.1 | 4.7 | 3.0 |
| DAMO_1532 | Two component transcriptional regulator, LuxR family  | 669  | 71  | 7.6  | 1.1 | 147 | 15.8 | 3.5 | 3.3 |
| DAMO_1533 | putative Multi-sensor signal transduction histidine kinase  | 1434 | 100 | 5.0  | 0.7 | 136 | 6.8  | 1.5 | 2.2 |
| DAMO_1534 | Putative sugar ABC transporter (ATP binding protein); putative glycerol 3-phosphate transport protein, ugpC-like prot | 1080 | 109 | 7.3  | 1.0 | 55  | 3.7  | 0.8 | 0.8 |
| DAMO_1535 | putative ABC transporter permease protein   | 837  | 242 | 20.8 | 2.9 | 164 | 14.1 | 3.1 | 1.1 |
| DAMO_1536 | Putative ABC transporter (permease protein)   | 876  | 132 | 10.8 | 1.5 | 104 | 8.5  | 1.9 | 1.2 |
| DAMO_1537 | putative sugar ABC transporter, periplasmic sugar-binding protein   | 1209 | 156 | 9.3  | 1.3 | 82  | 4.9  | 1.1 | 0.8 |
| DAMO_1538 | conserved membrane protein of unknown function  | 708  | 86  | 8.7  | 1.2 | 94  | 9.6  | 2.1 | 1.7 |
| DAMO_1539 | Glycosyl transferase, family 2  | 1254 | 134 | 7.7  | 1.1 | 58  | 3.3  | 0.7 | 0.7 |
| DAMO_1540 | Mannosyl-3-phosphoglycerate phosphatase   | 843  | 189 | 16.1 | 2.2 | 107 | 9.1  | 2.0 | 0.9 |
| DAMO_1541 | Conserved hypothetical protein; putative glycosyl transferase involved in cell wall biogenesis                        | 1209 | 234 | 13.9 | 1.9 | 249 | 14.8 | 3.3 | 1.7 |
| DAMO_1542 | Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains (fragment)                 | 396  | 196 | 35.6 | 5.0 | 216 | 39.3 | 8.7 | 1.7 |
| DAMO_1543 | Hydroxypyruvate reductase   | 1293 | 58  | 3.2  | 0.5 | 25  | 1.4  | 0.3 | 0.7 |
| DAMO_1544 | putative Sensor protein   | 1443 | 307 | 15.3 | 2.1 | 293 | 14.6 | 3.2 | 1.5 |
| DAMO_1545 | protein of unknown function   | 444  | 68  | 11.0 | 1.5 | 89  | 14.4 | 3.2 | 2.1 |
| DAMO_1546 | protein of unknown function   | 210  | 8   | 2.7  | 0.4 | 0   | 0.0  | 0.0 | —   |
| DAMO_1547 | putative Phosphomannomutase   | 2157 | 7   | 0.2  | 0.0 | 3   | 0.1  | 0.0 | 0.7 |
| DAMO_1548 | protein of unknown function   | 276  | 22  | 5.7  | 0.8 | 1   | 0.3  | 0.1 | 0.1 |
| DAMO_1549 | Transcription elongation factor greA (Transcript cleavage factor greA)  | 501  | 177 | 25.4 | 3.5 | 199 | 28.6 | 6.3 | 1.8 |
| DAMO_1550 | Glutamyl-tRNA synthetase (Glutamate--tRNA ligase)   | 1401 | 299 | 15.4 | 2.1 | 101 | 5.2  | 1.1 | 0.5 |
| DAMO_1551 | conserved protein of unknown function   | 180  | 27  | 10.8 | 1.5 | 0   | 0.0  | 0.0 | —   |
| DAMO_1552 | putative Ribosomal-protein-alanine acetyltransferase, RimI-like protein   | 480  | 34  | 5.1  | 0.7 | 7   | 1.1  | 0.2 | 0.3 |
| DAMO_1553 | Peptidase M22, glycoprotease  | 705  | 50  | 5.1  | 0.7 | 62  | 6.3  | 1.4 | 2.0 |
| DAMO_1554 | Major facilitator superfamily MFS_1   | 1260 | 101 | 5.8  | 0.8 | 35  | 2.0  | 0.4 | 0.5 |
| DAMO_1555 | conserved protein of unknown function   | 507  | 19  | 2.7  | 0.4 | 16  | 2.3  | 0.5 | 1.3 |
| DAMO_1556 | putative carbohydrate kinase  | 1596 | 119 | 5.4  | 0.7 | 37  | 1.7  | 0.4 | 0.5 |
| DAMO_1557 | acyl carrier protein synthase (ACP-CoA phosphopantetheinyltransferase)(Holo-ACP synthase)(holo-[acyl-carrier-prote    | 384  | 13  | 2.4  | 0.3 | 4   | 0.8  | 0.2 | 0.5 |
| DAMO_1558 | pyridoxal phosphate biosynthetic protein PdxJ (PNP synthase)  | 729  | 47  | 4.6  | 0.6 | 14  | 1.4  | 0.3 | 0.5 |
| DAMO_1559 | protein of unknown function   | 153  | 2   | 0.9  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_1560 | phosphoglucosamine mutase   | 1350 | 55  | 2.9  | 0.4 | 22  | 1.2  | 0.3 | 0.6 |
| DAMO_1561 | exported protein of unknown function  | 663  | 22  | 2.4  | 0.3 | 33  | 3.6  | 0.8 | 2.4 |
| DAMO_1562 | protein of unknown function   | 90   | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1563 | conserved membrane protein of unknown function  | 819  | 6   | 0.5  | 0.1 | 0   | 0.0  | 0.0 | 0.0 |
| DAMO_1564 | Dihydropteroate synthase (DHPS) (Dihydropteroate pyrophosphorylase)   | 852  | 13  | 1.1  | 0.2 | 5   | 0.4  | 0.1 | 0.6 |
| DAMO_1565 | Cell division protein FtsH; ATP-dependent zinc-metallo protease   | 1812 | 389 | 15.5 | 2.2 | 135 | 5.4  | 1.2 | 0.5 |
| DAMO_1566 | Putative ATPase; tRNA(Ile)-lysidine synthas   | 1407 | 89  | 4.6  | 0.6 | 12  | 0.6  | 0.1 | 0.2 |
| DAMO_1567 | protein of unknown function   | 177  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1568 | protein of unknown function   | 222  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1569 | exported protein of unknown function  | 771  | 2   | 0.2  | 0.0 | 2   | 0.2  | 0.0 | 1.6 |

|           |  |      |     |      |     |     |      |      |     |
|-----------|--|------|-----|------|-----|-----|------|------|-----|
| DAMO_1570 | Calcineurin-like phosphoesterase   | 681  | 28  | 3.0  | 0.4 | 7   | 0.7  | 0.2  | 0.4 |
| DAMO_1571 | protein of unknown function  | 246  | 198 | 58.0 | 8.1 | 168 | 49.2 | 10.8 | 1.3 |
| DAMO_1572 | membrane protein of unknown function   | 777  | 6   | 0.6  | 0.1 | 7   | 0.6  | 0.1  | 1.8 |
| DAMO_1573 | Xaa-Pro aminopeptidase   | 1152 | 34  | 2.1  | 0.3 | 7   | 0.4  | 0.1  | 0.3 |
| DAMO_1574 | membrane protein of unknown function   | 273  | 6   | 1.6  | 0.2 | 1   | 0.3  | 0.1  | 0.3 |
| DAMO_1575 | Thiamine biosynthesis protein thiC   | 1329 | 147 | 8.0  | 1.1 | 60  | 3.3  | 0.7  | 0.6 |
| DAMO_1576 | conserved exported protein of unknown function   | 1404 | 81  | 4.2  | 0.6 | 26  | 1.3  | 0.3  | 0.5 |
| DAMO_1577 | conserved protein of unknown function  | 1443 | 58  | 2.9  | 0.4 | 30  | 1.5  | 0.3  | 0.8 |
| DAMO_1578 | Thiamine biosynthesis enzyme ThiH and related uncharacterized enzymes  | 1074 | 69  | 4.6  | 0.6 | 39  | 2.6  | 0.6  | 0.9 |
| DAMO_1579 | conserved protein of unknown function  | 321  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_1580 | conserved protein of unknown function  | 228  | 1   | 0.3  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_1581 | protein of unknown function  | 360  | 8   | 1.6  | 0.2 | 6   | 1.2  | 0.3  | 1.2 |
| DAMO_1582 | Transcriptional regulator, XRE family protein  | 288  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_1583 | protein of unknown function  | 54   | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_1584 | Radical SAM domain protein   | 1137 | 423 | 26.8 | 3.7 | 193 | 12.2 | 2.7  | 0.7 |
| DAMO_1585 | exported protein of unknown function   | 330  | 13  | 2.8  | 0.4 | 3   | 0.7  | 0.1  | 0.4 |
| DAMO_1586 | Cytochrome c-type biogenesis protein cycL precursor  | 489  | 9   | 1.3  | 0.2 | 11  | 1.6  | 0.4  | 1.9 |
| DAMO_1587 | periplasmic thioredoxin (cytochrome c biogenesis)  | 519  | 44  | 6.1  | 0.9 | 21  | 2.9  | 0.6  | 0.8 |
| DAMO_1588 | Cytochrome c-type biogenesis protein cycK  | 2001 | 87  | 3.1  | 0.4 | 56  | 2.0  | 0.4  | 1.0 |
| DAMO_1589 | Cytochrome c-type biogenesis protein ccm   | 450  | 82  | 13.1 | 1.8 | 83  | 13.3 | 2.9  | 1.6 |
| DAMO_1590 | heme ABC transporter (heme exporter protein C), permease protein (cytochrome c biogenesis)                               | 699  | 58  | 6.0  | 0.8 | 67  | 6.9  | 1.5  | 1.8 |
| DAMO_1591 | Heme exporter, protein B   | 690  | 33  | 3.4  | 0.5 | 38  | 4.0  | 0.9  | 1.8 |
| DAMO_1592 | conserved protein of unknown function  | 756  | 99  | 9.4  | 1.3 | 125 | 11.9 | 2.6  | 2.0 |
| DAMO_1593 | Response regulator receiver modulated metal dependent phosphohydrolase (fragment)  | 1011 | 33  | 2.4  | 0.3 | 1   | 0.1  | 0.0  | —   |
| DAMO_1594 | lipoate biosynthesis protein B; Lipoate-protein ligase B   | 732  | 19  | 1.9  | 0.3 | 2   | 0.2  | 0.0  | 0.2 |
| DAMO_1595 | Dihydrolipoyl dehydrogenase (E3 component of pyruvate and 2-oxoglutarate dehydrogenases complexes)                       | 1407 | 108 | 5.5  | 0.8 | 12  | 0.6  | 0.1  | 0.2 |
| DAMO_1596 | Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (E2) dehydrogenase con         | 1248 | 131 | 7.6  | 1.1 | 27  | 1.6  | 0.3  | 0.3 |
| DAMO_1597 | Pyruvate dehydrogenase E1 component subunit beta   | 978  | 235 | 17.3 | 2.4 | 28  | 2.1  | 0.5  | 0.2 |
| DAMO_1598 | Pyruvate dehydrogenase E1 component, alpha subunit   | 972  | 211 | 15.6 | 2.2 | 32  | 2.4  | 0.5  | 0.2 |
| DAMO_1599 | Lipoyl synthase (Lipoic acid synthase) (Lipoate synthase) (Lipoyl-acyl-carrier protein synthase) (Sulfur insertion prote | 939  | 138 | 10.6 | 1.5 | 35  | 2.7  | 0.6  | 0.4 |
| DAMO_1600 | PHP-like   | 870  | 9   | 0.7  | 0.1 | 6   | 0.5  | 0.1  | 1.1 |
| DAMO_1601 | Putative formate dehydrogenase family accessory protein (FdhD)   | 810  | 131 | 11.6 | 1.6 | 145 | 12.9 | 2.8  | 1.8 |
| DAMO_1602 | conserved membrane protein of unknown function   | 750  | 31  | 3.0  | 0.4 | 8   | 0.8  | 0.2  | 0.4 |
| DAMO_1603 | conserved protein of unknown function  | 438  | 117 | 19.2 | 2.7 | 108 | 17.8 | 3.9  | 1.5 |
| DAMO_1604 | NADH-quinone oxidoreductase subunit I (NADH dehydrogenase I subunit I) (NDH-1 subunit I)                                 | 462  | 113 | 17.6 | 2.5 | 172 | 26.8 | 5.9  | 2.4 |
| DAMO_1605 | NADH-quinone oxidoreductase subunit 6 (NADH dehydrogenase I chain 6) (NDH-1 subunit 6)                                   | 546  | 138 | 18.2 | 2.5 | 129 | 17.0 | 3.7  | 1.5 |
| DAMO_1606 | Iron-binding protein IscA (iron-sulfur cluster assembly protein)   | 303  | 11  | 2.6  | 0.4 | 3   | 0.7  | 0.2  | 0.4 |
| DAMO_1607 | cysteine desulfurase (Nitrogenase metalloclusters biosynthesis protein nifS)   | 1227 | 173 | 10.2 | 1.4 | 259 | 15.2 | 3.3  | 2.4 |
| DAMO_1608 | conserved membrane protein of unknown function   | 1047 | 44  | 3.0  | 0.4 | 9   | 0.6  | 0.1  | 0.3 |
| DAMO_1609 | protein of unknown function  | 1203 | 113 | 6.8  | 0.9 | 39  | 2.3  | 0.5  | 0.5 |
| DAMO_1610 | putative 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (Phosphoglyceromutase                               | 1203 | 84  | 5.0  | 0.7 | 52  | 3.1  | 0.7  | 1.0 |
| DAMO_1611 | Molybdenum cofactor biosynthesis protein MoeA  | 1212 | 321 | 19.1 | 2.7 | 125 | 7.4  | 1.6  | 0.6 |
| DAMO_1612 | thioredoxin reductase, FAD/NAD(P)-binding  | 930  | 224 | 17.3 | 2.4 | 167 | 12.9 | 2.8  | 1.2 |
| DAMO_1613 | putative 4Fe-4S ferredoxin iron-sulfur binding domain protein precursor  | 531  | 372 | 50.4 | 7.0 | 385 | 52.2 | 11.5 | 1.6 |
| DAMO_1614 | NADH-ubiquinone oxidoreductase 20 kDa subuni   | 528  | 229 | 31.2 | 4.4 | 181 | 24.7 | 5.4  | 1.2 |
| DAMO_1615 | protein of unknown function  | 171  | 14  | 5.9  | 0.8 | 7   | 2.9  | 0.6  | 0.8 |
| DAMO_1616 | putative Molybdopterin oxidoreductase Fe4S4 region   | 1635 | 477 | 21.0 | 2.9 | 498 | 21.9 | 4.8  | 1.7 |
| DAMO_1617 | protein of unknown function  | 312  | 234 | 54.0 | 7.5 | 279 | 64.4 | 14.2 | 1.9 |
| DAMO_1618 | CBS domain containing protein (fragment)   | 231  | 82  | 25.6 | 3.6 | 55  | 17.1 | 3.8  | 1.1 |
| DAMO_1619 | 2-oxoglutarate ferredoxin oxidoreductase alpha subunit   | 1911 | 593 | 22.3 | 3.1 | 373 | 14.1 | 3.1  | 1.0 |
| DAMO_1620 | 2-oxoglutarate ferredoxin oxidoreductase subunit beta  | 1026 | 237 | 16.6 | 2.3 | 178 | 12.5 | 2.8  | 1.2 |
| DAMO_1621 | Thymidylate synthase complementing protein ThyX  | 783  | 74  | 6.8  | 0.9 | 32  | 2.9  | 0.6  | 0.7 |
| DAMO_1622 | protein of unknown function  | 429  | 10  | 1.7  | 0.2 | 3   | 0.5  | 0.1  | 0.5 |
| DAMO_1623 | protein of unknown function  | 120  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_1624 | protein of unknown function  | 513  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_1627 | protein of unknown function  | 1722 | 3   | 0.1  | 0.0 | 1   | 0.0  | 0.0  | 0.5 |

|           |  |      |      |      |     |     |      |     |     |
|-----------|--|------|------|------|-----|-----|------|-----|-----|
| DAMO_1628 | protein of unknown function  | 669  | 39   | 4.2  | 0.6 | 54  | 5.8  | 1.3 | 2.2 |
| DAMO_1629 | protein of unknown function  | 1605 | 26   | 1.2  | 0.2 | 21  | 0.9  | 0.2 | 1.3 |
| DAMO_1630 | phosphoribosylglycinamide formyltransferase (GART) transformylase)   | 1278 | 86   | 4.8  | 0.7 | 86  | 4.8  | 1.1 | 1.6 |
| DAMO_1631 | Bifunctional purine biosynthesis protein purH formyltransferase (AICAR transformylase); IMP cyclohydrolas        | 525  | 24   | 3.3  | 0.5 | 7   | 1.0  | 0.2 | 0.5 |
| DAMO_1632 | Phosphoribosylamine--glycine ligase (GARS  | 765  | 8    | 0.8  | 0.1 | 3   | 0.3  | 0.1 | 0.6 |
| DAMO_1633 | Phosphoribosylaminoimidazole carboxylase catalytic subunit (AIR carboxylase) (AIRC)                              | 756  | 23   | 2.2  | 0.3 | 8   | 0.8  | 0.2 | 0.6 |
| DAMO_1634 | conserved membrane protein of unknown function   | 1026 | 26   | 1.8  | 0.3 | 10  | 0.7  | 0.2 | 0.6 |
| DAMO_1635 | protein of unknown function  | 975  | 18   | 1.3  | 0.2 | 2   | 0.1  | 0.0 | 0.2 |
| DAMO_1636 | Glycosyl transferase, family 2   | 612  | 9    | 1.1  | 0.1 | 5   | 0.6  | 0.1 | 0.9 |
| DAMO_1637 | membrane protein of unknown function   | 924  | 20   | 1.6  | 0.2 | 7   | 0.5  | 0.1 | 0.6 |
| DAMO_1638 | putative Membrane-associated phospholipid phosphatase  | 675  | 157  | 16.7 | 2.3 | 32  | 3.4  | 0.8 | 0.3 |
| DAMO_1639 | Selenide, water dikinase (Selenophosphate synthetase) (Selenium donor protein)                                   | 804  | 7    | 0.6  | 0.1 | 1   | 0.1  | 0.0 | 0.2 |
| DAMO_1640 | protein of unknown function  | 1119 | 38   | 2.4  | 0.3 | 15  | 1.0  | 0.2 | 0.6 |
| DAMO_1641 | conserved protein of unknown function  | 1653 | 20   | 0.9  | 0.1 | 12  | 0.5  | 0.1 | 0.9 |
| DAMO_1642 | ADP-heptose:LPS heptosyl transferase I   | 966  | 40   | 3.0  | 0.4 | 15  | 1.1  | 0.2 | 0.6 |
| DAMO_1643 | ADP-heptose--LPS heptosyltransferase II (modular protein)  | 1125 | 10   | 0.6  | 0.1 | 2   | 0.1  | 0.0 | 0.3 |
| DAMO_1644 | Lipid A biosynthesis acyltransferase   | 1287 | 30   | 1.7  | 0.2 | 2   | 0.1  | 0.0 | 0.1 |
| DAMO_1645 | Tetraacyldisaccharide 4'-kinase (Lipid A 4'-kinase)  | 696  | 70   | 7.2  | 1.0 | 10  | 1.0  | 0.2 | 0.2 |
| DAMO_1646 | 3-deoxy-D-manno-octulosonic-acid transferase (KDO transferase)   | 1173 | 59   | 3.6  | 0.5 | 12  | 0.7  | 0.2 | 0.3 |
| DAMO_1647 | conserved protein of unknown function  | 948  | 44   | 3.3  | 0.5 | 4   | 0.3  | 0.1 | 0.1 |
| DAMO_1648 | Lipid-A-disaccharide synthase  | 801  | 55   | 4.9  | 0.7 | 10  | 0.9  | 0.2 | 0.3 |
| DAMO_1649 | Predicted dehydrogenase  | 777  | 27   | 2.5  | 0.3 | 9   | 0.8  | 0.2 | 0.5 |
| DAMO_1650 | conserved hypothetical protein   | 480  | 40   | 6.0  | 0.8 | 4   | 0.6  | 0.1 | 0.2 |
| DAMO_1651 | Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase (UDP-N-acetylglucosamine acyltransferase) | 1080 | 17   | 1.1  | 0.2 | 4   | 0.3  | 0.1 | 0.4 |
| DAMO_1652 | (3R)-hydroxymyristol acyl carrier protein dehydratase  | 549  | 93   | 12.2 | 1.7 | 24  | 3.1  | 0.7 | 0.4 |
| DAMO_1653 | UDP-3-O-(3-hydroxymyristoyl)-glucosamine N-acyltransferase   | 2304 | 112  | 3.5  | 0.5 | 15  | 0.5  | 0.1 | 0.2 |
| DAMO_1654 | putative Outer membrane chaperone Skp (OmpH) precursor   | 2433 | 1031 | 30.5 | 4.3 | 724 | 21.4 | 4.7 | 1.1 |
| DAMO_1655 | putative Surface antigen (D15) precursor   | 681  | 62   | 6.6  | 0.9 | 13  | 1.4  | 0.3 | 0.3 |
| DAMO_1656 | Chaperone  | 1251 | 148  | 8.5  | 1.2 | 31  | 1.8  | 0.4 | 0.3 |
| DAMO_1657 | lipoprotein-releasing system (ABC transporter), ATP-binding protein lolD   | 1503 | 268  | 12.8 | 1.8 | 91  | 4.4  | 1.0 | 0.5 |
| DAMO_1658 | Lipoprotein releasing system, transmembrane protein, LolC/E family   | 498  | 0    | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1659 | Lysyl-tRNA synthetase (Lysine--tRNA ligase   | 906  | 4    | 0.3  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1660 | protein of unknown function  | 978  | 29   | 2.1  | 0.3 | 5   | 0.4  | 0.1 | 0.3 |
| DAMO_1661 | Protoheme IX farnesyltransferase (Heme O synthase  | 1035 | 57   | 4.0  | 0.6 | 5   | 0.3  | 0.1 | 0.1 |
| DAMO_1662 | putative Cytochrome oxidase assembly precursor   | 726  | 30   | 3.0  | 0.4 | 4   | 0.4  | 0.1 | 0.2 |
| DAMO_1663 | Putative di-haem cytochrome c peroxidase   | 1173 | 219  | 13.4 | 1.9 | 31  | 1.9  | 0.4 | 0.2 |
| DAMO_1664 | putative lipoprotein   | 465  | 25   | 3.9  | 0.5 | 10  | 1.5  | 0.3 | 0.6 |
| DAMO_1665 | Metallophosphoesterase   | 876  | 16   | 1.3  | 0.2 | 7   | 0.6  | 0.1 | 0.7 |
| DAMO_1666 | conserved exported protein of unknown function   | 1026 | 58   | 4.1  | 0.6 | 23  | 1.6  | 0.4 | 0.6 |
| DAMO_1667 | conserved protein of unknown function  | 2658 | 164  | 4.4  | 0.6 | 60  | 1.6  | 0.4 | 0.6 |
| DAMO_1668 | Putative di-haem cytochrome c peroxidase   | 726  | 25   | 2.5  | 0.3 | 28  | 2.8  | 0.6 | 1.8 |
| DAMO_1669 | pyruvate phosphate dikinase  | 2571 | 207  | 5.8  | 0.8 | 72  | 2.0  | 0.4 | 0.6 |
| DAMO_1670 | conserved exported protein of unknown function   | 810  | 59   | 5.2  | 0.7 | 20  | 1.8  | 0.4 | 0.5 |
| DAMO_1671 | hypothetical octaheam cytochrome c   | 771  | 38   | 3.5  | 0.5 | 14  | 1.3  | 0.3 | 0.6 |
| DAMO_1672 | conserved membrane protein of unknown function   | 594  | 19   | 2.3  | 0.3 | 5   | 0.6  | 0.1 | 0.4 |
| DAMO_1673 | Strongly similar to cytochrome b6  | 168  | 3    | 1.3  | 0.2 | 0   | 0.0  | 0.0 | —   |
| DAMO_1674 | Similar to Rieske 2Fe-2S iron sulfur protei  | 852  | 0    | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1675 | protein of unknown function  | 321  | 0    | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1676 | transposase  | 270  | 9    | 2.4  | 0.3 | 2   | 0.5  | 0.1 | 0.4 |
| DAMO_1677 | protein of unknown function  | 174  | 11   | 4.6  | 0.6 | 0   | 0.0  | 0.0 | —   |
| DAMO_1678 | protein of unknown function  | 753  | 0    | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1679 | protein of unknown function  | 300  | 11   | 2.6  | 0.4 | 1   | 0.2  | 0.1 | 0.1 |
| DAMO_1680 | conserved protein of unknown function  | 285  | 0    | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1681 | Plasmid maintenance system antidote protein  | 204  | 0    | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1682 | Plasmid maintenance system killer  | 354  | 0    | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1683 | protein of unknown function  | 1377 | 30   | 1.6  | 0.2 | 1   | 0.1  | 0.0 | 0.1 |



|           |  |      |     |      |      |     |       |      |     |
|-----------|--|------|-----|------|------|-----|-------|------|-----|
| DAMO_1684 | protein of unknown function  | 507  | 626 | 88.9 | 12.4 | 946 | 134.3 | 29.6 | 2.4 |
| DAMO_1685 | ammonium transport protein (Amt family)                                  | 915  | 56  | 4.4  | 0.6  | 26  | 2.0   | 0.5  | 0.7 |
| DAMO_1686 | Universal stress protein family  | 1077 | 162 | 10.8 | 1.5  | 36  | 2.4   | 0.5  | 0.4 |
| DAMO_1687 | conserved protein of unknown function                                    | 342  | 43  | 9.1  | 1.3  | 9   | 1.9   | 0.4  | 0.3 |
| DAMO_1688 | putative ATPase of the MinD/MRP superfamil                               | 1329 | 133 | 7.2  | 1.0  | 24  | 1.3   | 0.3  | 0.3 |
| DAMO_1689 | conserved protein of unknown function                                    | 567  | 52  | 6.6  | 0.9  | 18  | 2.3   | 0.5  | 0.5 |
| DAMO_1690 | conserved membrane protein of unknown function                           | 666  | 109 | 11.8 | 1.6  | 27  | 2.9   | 0.6  | 0.4 |
| DAMO_1691 | protein of unknown function  | 231  | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1692 | putative Transcriptional regulator, Crp/Fnr family                       | 81   | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1693 | exported protein of unknown function                                     | 630  | 75  | 8.6  | 1.2  | 6   | 0.7   | 0.2  | 0.1 |
| DAMO_1694 | protein of unknown function  | 543  | 26  | 3.4  | 0.5  | 23  | 3.0   | 0.7  | 1.4 |
| DAMO_1695 | protein of unknown function  | 357  | 1   | 0.2  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1696 | Thiol-disulfide oxidoreductase resA                                      | 1377 | 35  | 1.8  | 0.3  | 5   | 0.3   | 0.1  | 0.2 |
| DAMO_1697 | protein of unknown function  | 1545 | 278 | 13.0 | 1.8  | 28  | 1.3   | 0.3  | 0.2 |
| DAMO_1698 | conserved exported protein of unknown function                           | 144  | 23  | 11.5 | 1.6  | 12  | 6.0   | 1.3  | 0.8 |
| DAMO_1699 | conserved membrane protein of unknown function                           | 588  | 108 | 13.2 | 1.8  | 2   | 0.2   | 0.1  | 0.0 |
| DAMO_1700 | protein of unknown function  | 462  | 27  | 4.2  | 0.6  | 2   | 0.3   | 0.1  | 0.1 |
| DAMO_1701 | Response regulator receiver  | 1329 | 129 | 7.0  | 1.0  | 8   | 0.4   | 0.1  | 0.1 |
| DAMO_1702 | membrane protein of unknown function                                     | 936  | 38  | 2.9  | 0.4  | 14  | 1.1   | 0.2  | 0.6 |
| DAMO_1703 | putative NADH dehydrogenase FAD-containing subunit transmembrane protein | 201  | 4   | 1.4  | 0.2  | 8   | 2.9   | 0.6  | 3.2 |
| DAMO_1704 | putative Micrococcal nuclease  | 399  | 0   | 0.0  | 0.0  | 9   | 1.6   | 0.4  | —   |
| DAMO_1705 | conserved protein of unknown function                                    | 336  | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1706 | PilT-like protein  | 426  | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1707 | DNA polymerase, beta-like region   | 624  | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1708 | HEPN domain protein  | 447  | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1709 | protein of unknown function  | 1017 | 161 | 11.4 | 1.6  | 33  | 2.3   | 0.5  | 0.3 |
| DAMO_1710 | conserved protein of unknown function                                    | 444  | 48  | 7.8  | 1.1  | 25  | 4.1   | 0.9  | 0.8 |
| DAMO_1711 | exported protein of unknown function                                     | 249  | 113 | 32.7 | 4.6  | 40  | 11.6  | 2.5  | 0.6 |
| DAMO_1712 | conserved protein of unknown function                                    | 387  | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1713 | protein of unknown function  | 717  | 29  | 2.9  | 0.4  | 3   | 0.3   | 0.1  | 0.2 |
| DAMO_1714 | protein of unknown function  | 1563 | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1715 | conserved exported protein of unknown function                           | 315  | 0   | 0.0  | 0.0  | 1   | 0.2   | 0.1  | —   |
| DAMO_1716 | protein of unknown function  | 714  | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1717 | Cytoplasmic domain of flagellar protein FhlB-like protein protein        | 1722 | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1718 | protein of unknown function  | 3027 | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1719 | Histidine kinase, HAMP region:chemotaxis sensory transducer              | 867  | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1720 | putative Histidine kinase  | 2913 | 4   | 0.1  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1721 | protein of unknown function  | 807  | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1722 | putative Histidine kinase  | 693  | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1723 | protein of unknown function  | 747  | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1724 | protein of unknown function  | 771  | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1725 | protein of unknown function  | 1707 | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1726 | protein of unknown function  | 2094 | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1727 | Histidine kinase, HAMP region:chemotaxis sensory transducer              | 345  | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1728 | Methyl-accepting chemotaxis sensory transducer precursor                 | 405  | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1729 | protein of unknown function  | 645  | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1730 | protein of unknown function  | 882  | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1731 | protein of unknown function  | 576  | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1732 | protein of unknown function  | 1380 | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1733 | protein of unknown function  | 861  | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1734 | RNA polymerase sigma factor whiG (modular protein)                       | 1167 | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1735 | Cobyrinic acid a,c-diamide synthase                                      | 2094 | 0   | 0.0  | 0.0  | 1   | 0.0   | 0.0  | —   |
| DAMO_1736 | putative Flagellar biosynthesis protein flh                              | 1080 | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1737 | Flagellar biosynthesis protein flhA                                      | 801  | 1   | 0.1  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1738 | Flagellar biosynthetic protein FlhB                                      | 270  | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_1739 | putative Flagellar biosynthetic protein fliR                             | 732  | 0   | 0.0  | 0.0  | 0   | 0.0   | 0.0  | —   |

|           |  |      |    |     |     |   |     |     |     |
|-----------|--|------|----|-----|-----|---|-----|-----|-----|
| DAMO_1740 | Flagellar biosynthetic protein fliQ  | 549  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1741 | Flagellar transport protein FliP   | 975  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1742 | protein of unknown function  | 1002 | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1743 | putative Flagellar motor switch phosphatase fliY fliY)   | 552  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1744 | putative Flagellar motor switch protein fliM   | 195  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1745 | putative Flagellar basal body-associated protein FliL  | 204  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1746 | Flagellar protein (fragment)   | 1158 | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1747 | protein of unknown function  | 1239 | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1748 | protein of unknown function  | 705  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1749 | putative Flagellar hook protein flgE   | 786  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1750 | putative basal-body rod modification protein flgD  | 2271 | 3  | 0.1 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1751 | protein of unknown function  | 765  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1752 | protein of unknown function  | 465  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1753 | exported protein of unknown function   | 1440 | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1754 | putative Flagellar biosynthesis chaperone  | 678  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1755 | flagellum-specific ATP synthase  | 1017 | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1756 | putative Flagellar assembly protein fliH   | 1620 | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1757 | Flagellar motor switch protein fliG  | 303  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1758 | Flagellar basal body M-ring protein  | 423  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1759 | conserved protein of unknown function  | 363  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1760 | flagellar basal-body rod protein Flg   | 1386 | 1  | 0.1 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1761 | putative Flagellar basal-body rod protein flgB   | 1338 | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1762 | putative response regulator in two-component regulatory system, sigma54 dependent transcriptional regulator. | 369  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1763 | putative Sensor protein  | 183  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1764 | putative response regulator receiver (CheY-like protein)   | 867  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1765 | protein of unknown function  | 927  | 1  | 0.1 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1766 | Chemotaxis protein   | 1464 | 3  | 0.1 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1767 | Outer membrane protein, OmpA/MotB family   | 1056 | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1768 | putative response regulator in two-component regulatory system, sigma54 dependent transcriptional regulator. | 192  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1769 | putative Histidine kinase  | 132  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1770 | protein of unknown function  | 1473 | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1771 | protein of unknown function  | 657  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1772 | putative Response regulator receiver modulated metal dependent phosphohydrolase                              | 348  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1773 | putative Response regulator receiver protein   | 336  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1774 | protein of unknown function  | 366  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1775 | protein of unknown function  | 1464 | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1776 | conserved protein of unknown function  | 408  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1777 | protein of unknown function  | 840  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1778 | conserved protein of unknown function  | 1869 | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1779 | putative flagellin   | 2346 | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1780 | protein of unknown function  | 2052 | 1  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1781 | putative Histidine kinase  | 879  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1782 | Sensor protein (fragment)  | 1692 | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1783 | putative HD domain protein   | 8883 | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1784 | protein of unknown function  | 1260 | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1785 | protein of unknown function  | 1059 | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1786 | putative Methyltransferase type 11   | 594  | 1  | 0.1 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1787 | NeuB family protein  | 1107 | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1788 | Formyl transferase domain protein  | 861  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1789 | GCN5-related N-acetyltransferase (fragment)  | 1155 | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1790 | putative NeuA  | 999  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1791 | putative polysaccharide biosynthesis protein   | 720  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1792 | conserved protein of unknown function  | 573  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1793 | exported protein of unknown function   | 180  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |
| DAMO_1794 | conserved protein of unknown function  | 231  | 12 | 3.7 | 0.5 | 3 | 0.9 | 0.2 | 0.4 |
| DAMO_1795 | protein of unknown function  | 177  | 0  | 0.0 | 0.0 | 0 | 0.0 | 0.0 | —   |

|           |   |      |     |      |     |     |      |     |     |
|-----------|---|------|-----|------|-----|-----|------|-----|-----|
| DAMO_1796 | conserved protein of unknown function   | 186  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1797 | conserved protein of unknown function   | 573  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1798 | protein of unknown function   | 564  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1799 | conserved protein of unknown function   | 489  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1800 | conserved protein of unknown function   | 252  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1801 | protein of unknown function   | 405  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1802 | Carbon storage regulator homolog (modular protein)  | 924  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1803 | putative Flagellar assembly factor fliW   | 402  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1804 | putative Flagellar hook-associated protein 3  | 1401 | 0   | 0.0  | 0.0 | 1   | 0.1  | 0.0 | —   |
| DAMO_1805 | Conserved hypothetical protein.   | 501  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1806 | putative Flagellar hook-associated protein  | 309  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1807 | protein of unknown function   | 351  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1808 | putative FlgM family protein  | 1119 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1809 | protein of unknown function   | 615  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1810 | Flagellar P-ring protein (basal body P-ring protein)  | 1056 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1811 | Flagellar L-ring protein (Basal body L-ring protein) (fragment)   | 789  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1812 | protein of unknown function   | 738  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1813 | Flagellar basal-body rod protein flgG (Distal rod protein)  | 1008 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1814 | Flagellar basal body and hook proteins  | 846  | 1   | 0.1  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1815 | Response regulator receiver modulated diguanylate cyclase (fragment)                                      | 327  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1816 | Metal-dependent phosphohydrolase, HD subdomain  | 699  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1817 | conserved protein of unknown function   | 555  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1818 | MotA/TolQ/ExbB proton channel precursor   | 759  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1819 | protein of unknown function   | 1215 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1820 | protein of unknown function   | 249  | 1   | 0.3  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1821 | Chemotaxis Response Regulator protein CheB-glutamate methylesterase                                       | 1062 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1822 | CheD, stimulates methylation of MCP proteins  | 561  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1823 | Chemotaxis protein methyltransferase  | 918  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1824 | Chemotaxis protein cheW   | 543  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1825 | putative Methyl-accepting chemotaxis I (Serine chemoreceptor protein) transmembrane protein               | 1875 | 0   | 0.0  | 0.0 | 1   | 0.0  | 0.0 | —   |
| DAMO_1826 | Chemotaxis protein cheA   | 1815 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1827 | Chemotaxis protein cheY   | 378  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1828 | protein of unknown function   | 93   | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1829 | protein of unknown function   | 771  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1830 | putative Histidine kinase   | 3087 | 0   | 0.0  | 0.0 | 15  | 0.3  | 0.1 | —   |
| DAMO_1831 | protein of unknown function   | 204  | 114 | 40.2 | 5.6 | 25  | 8.8  | 1.9 | 0.3 |
| DAMO_1833 | putative HAM1 protein   | 603  | 28  | 3.3  | 0.5 | 9   | 1.1  | 0.2 | 0.5 |
| DAMO_1834 | RNase PH  | 777  | 27  | 2.5  | 0.3 | 11  | 1.0  | 0.2 | 0.6 |
| DAMO_1835 | conserved protein of unknown function   | 552  | 4   | 0.5  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_1836 | putative N-acetylmuramoyl-L-alanine amidase   | 1368 | 11  | 0.6  | 0.1 | 2   | 0.1  | 0.0 | 0.3 |
| DAMO_1844 | Tyrosyl-tRNA synthetase (Tyrosine--tRNA ligase  | 1248 | 45  | 2.6  | 0.4 | 1   | 0.1  | 0.0 | —   |
| DAMO_1845 | protein of unknown function   | 294  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1846 | Penicillin-binding protein 1A (PBP-1a) (PBP1a   | 2220 | 64  | 2.1  | 0.3 | 19  | 0.6  | 0.1 | 0.5 |
| DAMO_1847 | protein of unknown function   | 621  | 37  | 4.3  | 0.6 | 7   | 0.8  | 0.2 | 0.3 |
| DAMO_1848 | conserved protein of unknown function   | 1128 | 31  | 2.0  | 0.3 | 20  | 1.3  | 0.3 | 1.0 |
| DAMO_1849 | putative alcohol dehydrogenase  | 1083 | 14  | 0.9  | 0.1 | 7   | 0.5  | 0.1 | 0.8 |
| DAMO_1850 | conserved protein of unknown function   | 363  | 19  | 3.8  | 0.5 | 11  | 2.2  | 0.5 | 0.9 |
| DAMO_1851 | protein of unknown function   | 306  | 2   | 0.5  | 0.1 | 3   | 0.7  | 0.2 | 2.4 |
| DAMO_1852 | bifunctional: 5,10-methylene-tetrahydrofolate dehydrogenase; 5,10-methenyl-tetrahydrofolate cyclohydrolas | 867  | 89  | 7.4  | 1.0 | 38  | 3.2  | 0.7 | 0.7 |
| DAMO_1853 | Metallo-phosphoesterase   | 777  | 57  | 5.3  | 0.7 | 12  | 1.1  | 0.2 | 0.3 |
| DAMO_1854 | conserved protein of unknown function   | 1566 | 109 | 5.0  | 0.7 | 38  | 1.7  | 0.4 | 0.6 |
| DAMO_1855 | protein of unknown function   | 336  | 35  | 7.5  | 1.0 | 26  | 5.6  | 1.2 | 1.2 |
| DAMO_1856 | protein of unknown function   | 318  | 205 | 46.4 | 6.5 | 120 | 27.2 | 6.0 | 0.9 |
| DAMO_1857 | Phenylalanyl-tRNA synthetase beta chai  | 2418 | 101 | 3.0  | 0.4 | 14  | 0.4  | 0.1 | 0.2 |
| DAMO_1858 | exported protein of unknown function  | 168  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1859 | conserved protein of unknown function   | 201  | 32  | 11.5 | 1.6 | 65  | 23.3 | 5.1 | 3.2 |

|           |  |      |     |       |      |     |      |     |     |
|-----------|--|------|-----|-------|------|-----|------|-----|-----|
| DAMO_1860 | PilT protein-like  | 357  | 85  | 17.1  | 2.4  | 94  | 19.0 | 4.2 | 1.7 |
| DAMO_1861 | Phenylalanyl-tRNA synthetase alpha chain   | 1053 | 105 | 7.2   | 1.0  | 23  | 1.6  | 0.3 | 0.3 |
| DAMO_1862 | 50S ribosomal subunit protein L20  | 360  | 179 | 35.8  | 5.0  | 51  | 10.2 | 2.2 | 0.5 |
| DAMO_1863 | 50S ribosomal protein L35  | 204  | 139 | 49.1  | 6.8  | 9   | 3.2  | 0.7 | 0.1 |
| DAMO_1864 | Translation initiation factor IF-3   | 492  | 953 | 139.5 | 19.4 | 222 | 32.5 | 7.2 | 0.4 |
| DAMO_1865 | Threonyl-tRNA synthetase (Threonine--tRNA ligase)  | 2043 | 443 | 15.6  | 2.2  | 70  | 2.5  | 0.5 | 0.2 |
| DAMO_1866 | putative response regulator in two-component regulatory system, sigma54 dependent transcriptional regulator. | 1383 | 65  | 3.4   | 0.5  | 14  | 0.7  | 0.2 | 0.3 |
| DAMO_1867 | putative Histidine kinase  | 1326 | 1   | 0.1   | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_1868 | GAF modulated sigma54 specific transcriptional regulator, Fis family (fragment)                              | 1737 | 2   | 0.1   | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_1869 | protein of unknown function  | 69   | 0   | 0.0   | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_1870 | exported protein of unknown function   | 900  | 50  | 4.0   | 0.6  | 35  | 2.8  | 0.6 | 1.1 |
| DAMO_1871 | protein of unknown function  | 204  | 0   | 0.0   | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_1872 | protein of unknown function  | 183  | 1   | 0.4   | 0.1  | 0   | 0.0  | 0.0 | —   |
| DAMO_1873 | conserved protein of unknown function  | 435  | 1   | 0.2   | 0.0  | 1   | 0.2  | 0.0 | 1.6 |
| DAMO_1874 | protein of unknown function  | 201  | 3   | 1.1   | 0.1  | 0   | 0.0  | 0.0 | 0.0 |
| DAMO_1875 | protein of unknown function  | 171  | 1   | 0.4   | 0.1  | 0   | 0.0  | 0.0 | 0.0 |
| DAMO_1876 | putative response regulator in two-component regulatory system, sigma 54-dependent.                          | 1383 | 15  | 0.8   | 0.1  | 21  | 1.1  | 0.2 | 2.2 |
| DAMO_1877 | putative Multi-sensor signal transduction histidine kinase precursor   | 1806 | 15  | 0.6   | 0.1  | 6   | 0.2  | 0.1 | 0.6 |
| DAMO_1878 | exported protein of unknown function   | 447  | 0   | 0.0   | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_1879 | protein of unknown function  | 441  | 25  | 4.1   | 0.6  | 3   | 0.5  | 0.1 | 0.2 |
| DAMO_1880 | conserved exported protein of unknown function   | 240  | 88  | 26.4  | 3.7  | 6   | 1.8  | 0.4 | 0.1 |
| DAMO_1881 | protein of unknown function  | 216  | 0   | 0.0   | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_1882 | ABC phosphonate-binding periplasmic protein precursor  | 876  | 44  | 3.6   | 0.5  | 33  | 2.7  | 0.6 | 1.2 |
| DAMO_1883 | Phosphonates import ATP-binding protein phnC (ABC superfamily, atp_bind)                                     | 819  | 7   | 0.6   | 0.1  | 1   | 0.1  | 0.0 | 0.2 |
| DAMO_1884 | putative phosphite transport system permease protein htxC  | 888  | 11  | 0.9   | 0.1  | 1   | 0.1  | 0.0 | 0.1 |
| DAMO_1885 | putative PhnE protein, phosphonate ABC transporter, putative membrane protein (modular protein)              | 1044 | 62  | 4.3   | 0.6  | 10  | 0.7  | 0.2 | 0.3 |
| DAMO_1886 | conserved protein of unknown function  | 567  | 4   | 0.5   | 0.1  | 0   | 0.0  | 0.0 | —   |
| DAMO_1887 | exported protein of unknown function   | 531  | 15  | 2.0   | 0.3  | 0   | 0.0  | 0.0 | —   |
| DAMO_1888 | protein of unknown function  | 261  | 0   | 0.0   | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_1889 | Nitric-oxide reductase, qNOR-like (norZ)   | 2193 | 201 | 6.6   | 0.9  | 38  | 1.2  | 0.3 | 0.3 |
| DAMO_1890 | conserved membrane protein of unknown function   | 1146 | 209 | 13.1  | 1.8  | 108 | 6.8  | 1.5 | 0.8 |
| DAMO_1891 | conserved protein of unknown function  | 444  | 0   | 0.0   | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_1892 | putative Ribbon-helix-helix protein  | 222  | 0   | 0.0   | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_1893 | protein of unknown function  | 483  | 0   | 0.0   | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_1894 | conserved protein of unknown function  | 1071 | 0   | 0.0   | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_1895 | N-6 DNA methylase (fragment)   | 150  | 0   | 0.0   | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_1896 | conserved protein of unknown function  | 492  | 47  | 6.9   | 1.0  | 6   | 0.9  | 0.2 | 0.2 |
| DAMO_1897 | Methionyl-tRNA formyltransferase   | 936  | 81  | 6.2   | 0.9  | 22  | 1.7  | 0.4 | 0.4 |
| DAMO_1898 | Sun protein  | 1404 | 71  | 3.6   | 0.5  | 32  | 1.6  | 0.4 | 0.7 |
| DAMO_1899 | exported protein of unknown function   | 585  | 4   | 0.5   | 0.1  | 1   | 0.1  | 0.0 | 0.4 |
| DAMO_1900 | protein of unknown function  | 255  | 147 | 41.5  | 5.8  | 49  | 13.8 | 3.0 | 0.5 |
| DAMO_1901 | protein of unknown function  | 228  | 205 | 64.7  | 9.0  | 29  | 9.2  | 2.0 | 0.2 |
| DAMO_1902 | protein of unknown function  | 1149 | 223 | 14.0  | 1.9  | 22  | 1.4  | 0.3 | 0.2 |
| DAMO_1903 | putative Heavy metal efflux pump, CzcB family  | 1263 | 133 | 7.6   | 1.1  | 17  | 1.0  | 0.2 | 0.2 |
| DAMO_1904 | putative cation efflux system protein  | 3084 | 344 | 8.0   | 1.1  | 40  | 0.9  | 0.2 | 0.2 |
| DAMO_1905 | exported protein of unknown function   | 336  | 326 | 69.9  | 9.7  | 207 | 44.4 | 9.8 | 1.0 |
| DAMO_1906 | conserved exported protein of unknown function   | 984  | 102 | 7.5   | 1.0  | 174 | 12.7 | 2.8 | 2.7 |
| DAMO_1907 | Copper resistance protein CopC precursor   | 372  | 4   | 0.8   | 0.1  | 9   | 1.7  | 0.4 | 3.6 |
| DAMO_1908 | membrane protein of unknown function   | 1197 | 7   | 0.4   | 0.1  | 1   | 0.1  | 0.0 | 0.2 |
| DAMO_1909 | exported protein of unknown function   | 294  | 5   | 1.2   | 0.2  | 6   | 1.5  | 0.3 | 1.9 |
| DAMO_1910 | conserved protein of unknown function  | 207  | 3   | 1.0   | 0.1  | 1   | 0.3  | 0.1 | 0.5 |
| DAMO_1911 | protein of unknown function  | 204  | 2   | 0.7   | 0.1  | 0   | 0.0  | 0.0 | —   |
| DAMO_1912 | protein of unknown function  | 201  | 0   | 0.0   | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_1913 | MotA/TolQ/ExbB proton channel  | 603  | 15  | 1.8   | 0.2  | 0   | 0.0  | 0.0 | —   |
| DAMO_1914 | Biopolymer transport protein ExbD/TolR   | 420  | 0   | 0.0   | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_1915 | putative Protein tonB2   | 873  | 0   | 0.0   | 0.0  | 0   | 0.0  | 0.0 | —   |

|           |   |      |      |       |      |      |       |      |     |
|-----------|---|------|------|-------|------|------|-------|------|-----|
| DAMO_1916 | TonB-dependent receptor   | 2343 | 1    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1917 | membrane protein of unknown function  | 1662 | 1    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1918 | exported protein of unknown function  | 744  | 220  | 21.3  | 3.0  | 185  | 17.9  | 3.9  | 1.3 |
| DAMO_1919 | protein of unknown function   | 282  | 17   | 4.3   | 0.6  | 4    | 1.0   | 0.2  | 0.4 |
| DAMO_1920 | Biotin/lipoyl attachment:Secretion protein HlyD precursor                     | 1176 | 22   | 1.3   | 0.2  | 5    | 0.3   | 0.1  | 0.4 |
| DAMO_1921 | conserved membrane protein of unknown function                                | 1203 | 11   | 0.7   | 0.1  | 4    | 0.2   | 0.1  | 0.6 |
| DAMO_1922 | putative ABC transporter, ATP-binding protein                                 | 687  | 9    | 0.9   | 0.1  | 1    | 0.1   | 0.0  | 0.2 |
| DAMO_1923 | putative RNA polymerase sigma factor  | 552  | 64   | 8.3   | 1.2  | 28   | 3.7   | 0.8  | 0.7 |
| DAMO_1924 | protein of unknown function   | 765  | 5    | 0.5   | 0.1  | 1    | 0.1   | 0.0  | 0.3 |
| DAMO_1925 | protein of unknown function   | 204  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1926 | protein of unknown function   | 198  | 1    | 0.4   | 0.1  | 3    | 1.1   | 0.2  | 4.7 |
| DAMO_1927 | protein of unknown function   | 243  | 2    | 0.6   | 0.1  | 0    | 0.0   | 0.0  | —   |
| DAMO_1928 | exported protein of unknown function  | 480  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1929 | protein of unknown function   | 288  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1930 | protein of unknown function   | 417  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1931 | putative Outer membrane efflux protein precursor                              | 1362 | 3    | 0.2   | 0.0  | 1    | 0.1   | 0.0  | 0.5 |
| DAMO_1932 | Secretion protein HlyD  | 1200 | 2    | 0.1   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1933 | putative cation/multidrug efflux pump of the AcrB/AcrD/AcrF family            | 3306 | 5    | 0.1   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1934 | protein of unknown function   | 450  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1935 | protein of unknown function   | 201  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1936 | protein of unknown function   | 105  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1937 | protein of unknown function   | 213  | 0    | 0.0   | 0.0  | 5    | 1.7   | 0.4  | —   |
| DAMO_1938 | Radical SAM domain protein  | 945  | 9    | 0.7   | 0.1  | 1    | 0.1   | 0.0  | 0.2 |
| DAMO_1939 | Zinc/iron permease  | 747  | 31   | 3.0   | 0.4  | 8    | 0.8   | 0.2  | 0.4 |
| DAMO_1940 | Methyltransferase type 11   | 699  | 33   | 3.4   | 0.5  | 12   | 1.2   | 0.3  | 0.6 |
| DAMO_1941 | conserved protein of unknown function   | 282  | 21   | 5.4   | 0.7  | 0    | 0.0   | 0.0  | —   |
| DAMO_1942 | protein of unknown function   | 174  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1943 | putative Zinc transporter zupT  | 756  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1944 | membrane protein of unknown function  | 1245 | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1945 | protein of unknown function   | 171  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1946 | conserved exported protein of unknown function                                | 2145 | 4    | 0.1   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1947 | protein of unknown function   | 75   | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1948 | exported protein of unknown function  | 306  | 567  | 133.4 | 18.6 | 197  | 46.4  | 10.2 | 0.5 |
| DAMO_1949 | protein of unknown function   | 117  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1950 | protein of unknown function   | 228  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1951 | protein of unknown function   | 522  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1952 | protein of unknown function   | 234  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1953 | exported protein of unknown function  | 480  | 41   | 6.2   | 0.9  | 85   | 12.8  | 2.8  | 3.3 |
| DAMO_1954 | exported protein of unknown function  | 729  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1955 | conserved protein of unknown function   | 261  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1956 | Conserved hypothetical protein  | 1245 | 5    | 0.3   | 0.0  | 2    | 0.1   | 0.0  | 0.6 |
| DAMO_1957 | Putative ABC transporter related precursor                                    | 681  | 10   | 1.1   | 0.1  | 1    | 0.1   | 0.0  | 0.2 |
| DAMO_1958 | conserved membrane protein of unknown function                                | 996  | 4    | 0.3   | 0.0  | 1    | 0.1   | 0.0  | 0.4 |
| DAMO_1959 | Putative nosL family protein  | 534  | 3    | 0.4   | 0.1  | 3    | 0.4   | 0.1  | 1.6 |
| DAMO_1960 | conserved exported protein of unknown function; contains a nosL family domain | 1377 | 128  | 6.7   | 0.9  | 94   | 4.9   | 1.1  | 1.2 |
| DAMO_1961 | exported protein of unknown function  | 369  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1962 | protein of unknown function   | 525  | 1    | 0.1   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1963 | TonB-dependent receptor protein   | 2319 | 44   | 1.4   | 0.2  | 14   | 0.4   | 0.1  | 0.5 |
| DAMO_1964 | conserved exported protein of unknown function                                | 867  | 8    | 0.7   | 0.1  | 2    | 0.2   | 0.0  | 0.4 |
| DAMO_1965 | conserved exported protein of unknown function                                | 339  | 1991 | 422.9 | 58.9 | 1549 | 329.0 | 72.5 | 1.2 |
| DAMO_1966 | B12-dependent homocysteine-N5-methyltetrahydrofolate transmethylase           | 3684 | 350  | 6.8   | 1.0  | 162  | 3.2   | 0.7  | 0.7 |
| DAMO_1967 | protein of unknown function   | 180  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1968 | exported protein of unknown function  | 1512 | 62   | 3.0   | 0.4  | 7    | 0.3   | 0.1  | 0.2 |
| DAMO_1969 | protein of unknown function   | 210  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1970 | protein of unknown function   | 132  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_1971 | DNA/RNA non-specific endonuclease (fragment)                                  | 1017 | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |

|           |   |      |     |      |     |     |      |     |     |
|-----------|---|------|-----|------|-----|-----|------|-----|-----|
| DAMO_1972 | exported protein of unknown function  | 1422 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1973 | Type I restriction enzyme EcoAI R protei  | 2370 | 4   | 0.1  | 0.0 | 1   | 0.0  | 0.0 | 0.4 |
| DAMO_1974 | conserved protein of unknown function   | 609  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1975 | conserved protein of unknown function   | 870  | 3   | 0.2  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1976 | Type I restriction enzyme EcoEI M protei  | 1512 | 40  | 1.9  | 0.3 | 1   | 0.0  | 0.0 | —   |
| DAMO_1977 | putative Restriction endonuclease S subunits  | 1173 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1978 | conserved protein of unknown function   | 240  | 1   | 0.3  | 0.0 | 1   | 0.3  | 0.1 | 1.6 |
| DAMO_1979 | protein of unknown function   | 327  | 15  | 3.3  | 0.5 | 0   | 0.0  | 0.0 | —   |
| DAMO_1980 | conserved exported protein of unknown function  | 1533 | 70  | 3.3  | 0.5 | 1   | 0.0  | 0.0 | —   |
| DAMO_1981 | Similar to periplasmic zinc binding protein   | 1062 | 26  | 1.8  | 0.2 | 0   | 0.0  | 0.0 | —   |
| DAMO_1982 | ABC transporter, ATPase subunit   | 771  | 33  | 3.1  | 0.4 | 20  | 1.9  | 0.4 | 1.0 |
| DAMO_1983 | membrane protein of unknown function  | 867  | 90  | 7.5  | 1.0 | 19  | 1.6  | 0.3 | 0.3 |
| DAMO_1984 | membrane protein of unknown function  | 645  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1985 | Thioredoxin peroxidase (AhpC, Alkyl hydroperoxide reductase)  | 609  | 97  | 11.5 | 1.6 | 253 | 29.9 | 6.6 | 4.1 |
| DAMO_1986 | protein of unknown function   | 261  | 2   | 0.6  | 0.1 | 3   | 0.8  | 0.2 | 2.4 |
| DAMO_1987 | conserved membrane protein of unknown function  | 483  | 50  | 7.5  | 1.0 | 41  | 6.1  | 1.3 | 1.3 |
| DAMO_1988 | Serine/threonine protein kinase (fragment)  | 774  | 3   | 0.3  | 0.0 | 2   | 0.2  | 0.0 | 1.1 |
| DAMO_1989 | bifunctional foylpolylglutamate synthase/dihydrofolate synthase protein (folC)  | 1359 | 43  | 2.3  | 0.3 | 24  | 1.3  | 0.3 | 0.9 |
| DAMO_1990 | bifunctional: N-acetyl glucosamine-1-phosphate uridyltransferase (N-terminal); glucosamine-1-phosphate acetyl transfi | 1389 | 147 | 7.6  | 1.1 | 72  | 3.7  | 0.8 | 0.8 |
| DAMO_1991 | L-glutamine:D-fructose-6-phosphate aminotransferase   | 1836 | 252 | 9.9  | 1.4 | 82  | 3.2  | 0.7 | 0.5 |
| DAMO_1992 | Succinate dehydrogenase subunit B   | 744  | 70  | 6.8  | 0.9 | 13  | 1.3  | 0.3 | 0.3 |
| DAMO_1993 | Succinate dehydrogenase flavoprotein subunit  | 1803 | 128 | 5.1  | 0.7 | 6   | 0.2  | 0.1 | 0.1 |
| DAMO_1994 | putative succinate dehydrogenase membrane anchor subunit (sdhD)   | 744  | 303 | 29.3 | 4.1 | 81  | 7.8  | 1.7 | 0.4 |
| DAMO_1995 | exported protein of unknown function  | 273  | 9   | 2.4  | 0.3 | 4   | 1.1  | 0.2 | 0.7 |
| DAMO_1996 | malate dehydrogenase  | 930  | 77  | 6.0  | 0.8 | 11  | 0.9  | 0.2 | 0.2 |
| DAMO_1997 | Isocitrate dehydrogenase [NADP] (IDH)   | 1419 | 255 | 12.9 | 1.8 | 59  | 3.0  | 0.7 | 0.4 |
| DAMO_1998 | protein of unknown function   | 2031 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_1999 | protein of unknown function   | 489  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2000 | conserved hypothetical protein; putative Appr-1-p processing enzyme family protein                                    | 513  | 96  | 13.5 | 1.9 | 25  | 3.5  | 0.8 | 0.4 |
| DAMO_2001 | putative glycine betaine/carnitine/choline ABC transporter (permease and substrate binding protein)                   | 1545 | 113 | 5.3  | 0.7 | 68  | 3.2  | 0.7 | 1.0 |
| DAMO_2002 | putative Glycine betaine/carnitine/choline ABC transporter (ATP-binding protein)                                      | 768  | 47  | 4.4  | 0.6 | 22  | 2.1  | 0.5 | 0.7 |
| DAMO_2003 | conserved hypothetical protein  | 972  | 33  | 2.4  | 0.3 | 9   | 0.7  | 0.1 | 0.4 |
| DAMO_2004 | protein of unknown function   | 54   | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2005 | protein of unknown function   | 270  | 33  | 8.8  | 1.2 | 22  | 5.9  | 1.3 | 1.1 |
| DAMO_2006 | protein of unknown function   | 198  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2007 | protein of unknown function   | 120  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2008 | protein of unknown function   | 768  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2009 | protein of unknown function   | 1848 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2010 | protein of unknown function   | 816  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2011 | protein of unknown function   | 483  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2012 | protein of unknown function   | 1455 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2013 | protein of unknown function   | 120  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2014 | protein of unknown function   | 291  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2015 | conserved protein of unknown function   | 252  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2016 | conserved protein of unknown function   | 363  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2017 | protein of unknown function   | 678  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2018 | protein of unknown function   | 150  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2019 | transposase   | 906  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2020 | Insertion element ISR1 uncharacterized 10 kDa protein A3  | 279  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2021 | protein of unknown function   | 183  | 5   | 2.0  | 0.3 | 1   | 0.4  | 0.1 | 0.3 |
| DAMO_2022 | protein of unknown function   | 165  | 5   | 2.2  | 0.3 | 0   | 0.0  | 0.0 | —   |
| DAMO_2023 | protein of unknown function   | 87   | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2024 | Helix-turn-helix protein, CopG  | 264  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2025 | protein of unknown function   | 459  | 1   | 0.2  | 0.0 | 1   | 0.2  | 0.0 | 1.6 |
| DAMO_2026 | conserved protein of unknown function   | 279  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2027 | protein of unknown function   | 198  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |

|           |  |      |     |      |     |     |      |     |     |
|-----------|--|------|-----|------|-----|-----|------|-----|-----|
| DAMO_2028 | protein of unknown function  | 801  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2029 | protein of unknown function  | 1011 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2030 | Transcriptional regulator, XRE family  | 345  | 9   | 1.9  | 0.3 | 2   | 0.4  | 0.1 | 0.4 |
| DAMO_2031 | AMP-dependent synthetase and ligase  | 1632 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2032 | putative Coproporphyrinogen dehydrogenase  | 1377 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2033 | membrane protein of unknown function   | 1083 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2034 | ABC transporter protein, membrane protei   | 141  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2035 | protein of unknown function  | 486  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2036 | protein of unknown function  | 774  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2037 | ComA operon protein 2  | 408  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2038 | membrane protein of unknown function   | 1194 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2039 | ABC transporter, permease protein  | 750  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2040 | conserved protein of unknown function  | 768  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2041 | putative ABC transporter, substrate binding protein  | 1074 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2042 | protein of unknown function  | 183  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2043 | protein of unknown function  | 15   | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2044 | conserved protein of unknown function  | 3810 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2045 | UvrD/REP helicase  | 2073 | 173 | 6.0  | 0.8 | 59  | 2.0  | 0.5 | 0.5 |
| DAMO_2046 | conserved protein of unknown function  | 3093 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2047 | putative DNA methylase   | 2823 | 188 | 4.8  | 0.7 | 25  | 0.6  | 0.1 | 0.2 |
| DAMO_2048 | protein of unknown function  | 414  | 8   | 1.4  | 0.2 | 3   | 0.5  | 0.1 | 0.6 |
| DAMO_2049 | Type III restriction enzyme, res subunit   | 3078 | 108 | 2.5  | 0.4 | 13  | 0.3  | 0.1 | 0.2 |
| DAMO_2050 | protein of unknown function  | 303  | 171 | 40.6 | 5.7 | 3   | 0.7  | 0.2 | —   |
| DAMO_2051 | protein of unknown function  | 189  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2052 | conserved protein of unknown function  | 885  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2053 | protein of unknown function  | 732  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2054 | protein of unknown function  | 756  | 30  | 2.9  | 0.4 | 3   | 0.3  | 0.1 | 0.2 |
| DAMO_2055 | protein of unknown function  | 396  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2056 | putative recombinase   | 1716 | 2   | 0.1  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2057 | putative pyruvate formate lyase activating enzyme 2 (yfgB)   | 1119 | 148 | 9.5  | 1.3 | 45  | 2.9  | 0.6 | 0.5 |
| DAMO_2058 | exported protein of unknown function   | 750  | 6   | 0.6  | 0.1 | 4   | 0.4  | 0.1 | 1.1 |
| DAMO_2059 | Aminodeoxychorismate lyase   | 1017 | 40  | 2.8  | 0.4 | 22  | 1.6  | 0.3 | 0.9 |
| DAMO_2060 | putative Holliday junction resolvase   | 435  | 10  | 1.7  | 0.2 | 15  | 2.5  | 0.5 | 2.4 |
| DAMO_2061 | conserved protein of unknown function  | 687  | 33  | 3.5  | 0.5 | 28  | 2.9  | 0.6 | 1.3 |
| DAMO_2062 | putative threonine synthase (TS) (modular protein)   | 1857 | 232 | 9.0  | 1.3 | 33  | 1.3  | 0.3 | 0.2 |
| DAMO_2063 | conserved protein of unknown function  | 414  | 8   | 1.4  | 0.2 | 6   | 1.0  | 0.2 | 1.2 |
| DAMO_2064 | putative peptidase, S54 (Rhomboid) family  | 696  | 20  | 2.1  | 0.3 | 7   | 0.7  | 0.2 | 0.6 |
| DAMO_2065 | Protein-L-isoaspartate O-methyltransferase L-isoaspartyl methyltransferase) (L-isoaspartyl protein carboxyl methyltran | 663  | 42  | 4.6  | 0.6 | 7   | 0.8  | 0.2 | 0.3 |
| DAMO_2066 | RNA polymerase sigma factor RpoS   | 861  | 152 | 12.7 | 1.8 | 370 | 30.9 | 6.8 | 3.8 |
| DAMO_2067 | conserved protein of unknown function  | 831  | 11  | 1.0  | 0.1 | 3   | 0.3  | 0.1 | 0.4 |
| DAMO_2068 | Thioesterase superfamily protein   | 402  | 17  | 3.0  | 0.4 | 7   | 1.3  | 0.3 | 0.7 |
| DAMO_2069 | protein of unknown function  | 222  | 71  | 23.0 | 3.2 | 8   | 2.6  | 0.6 | 0.2 |
| DAMO_2070 | protein of unknown function  | 240  | 0   | 0.0  | 0.0 | 2   | 0.6  | 0.1 | —   |
| DAMO_2071 | protein of unknown function  | 723  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2072 | protein of unknown function  | 4140 | 6   | 0.1  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2073 | putative Caspase-1, p20  | 843  | 1   | 0.1  | 0.0 | 2   | 0.2  | 0.0 | 3.2 |
| DAMO_2074 | Peptide methionine sulfoxide reductase msrB protein)   | 618  | 26  | 3.0  | 0.4 | 4   | 0.5  | 0.1 | 0.2 |
| DAMO_2075 | conserved exported protein of unknown function   | 396  | 23  | 4.2  | 0.6 | 12  | 2.2  | 0.5 | 0.8 |
| DAMO_2076 | exported protein of unknown function   | 339  | 64  | 13.6 | 1.9 | 41  | 8.7  | 1.9 | 1.0 |
| DAMO_2077 | Undecaprenyl pyrophosphate synthetase 2 (UPP synthetase 2) (Di-trans,poly-cis-decaprenylcistransferase 2               | 777  | 173 | 16.0 | 2.2 | 196 | 18.2 | 4.0 | 1.8 |
| DAMO_2078 | conserved membrane protein of unknown function   | 1089 | 93  | 6.1  | 0.9 | 81  | 5.4  | 1.2 | 1.4 |
| DAMO_2079 | protein of unknown function  | 939  | 74  | 5.7  | 0.8 | 4   | 0.3  | 0.1 | 0.1 |
| DAMO_2080 | iron-dicitrate transporter subunit ; ATP-binding component of ABC superfamily; KpLE2 phage-like element                | 834  | 14  | 1.2  | 0.2 | 1   | 0.1  | 0.0 | 0.1 |
| DAMO_2081 | iron-dicitrate transporter subunit ; membrane component of ABC superfamily; KpLE2 phage-like element                   | 1065 | 45  | 3.0  | 0.4 | 8   | 0.5  | 0.1 | 0.3 |
| DAMO_2082 | Periplasmic binding protein  | 897  | 12  | 1.0  | 0.1 | 6   | 0.5  | 0.1 | 0.8 |
| DAMO_2083 | putative TonB-dependent outer membrane receptor for cobalamin and Fe transport   | 2010 | 229 | 8.2  | 1.1 | 33  | 1.2  | 0.3 | 0.2 |

|           |   |      |      |       |      |      |       |      |     |
|-----------|---|------|------|-------|------|------|-------|------|-----|
| DAMO_2084 | protein of unknown function   | 204  | 39   | 13.8  | 1.9  | 9    | 3.2   | 0.7  | 0.4 |
| DAMO_2085 | protein of unknown function   | 249  | 99   | 28.6  | 4.0  | 4    | 1.2   | 0.3  | 0.1 |
| DAMO_2086 | Putative cobalamin synthase (CobS family)   | 822  | 4    | 0.4   | 0.0  | 2    | 0.2   | 0.0  | 0.8 |
| DAMO_2087 | Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase (anaerobic pathway of cobalamin biosynthes | 1059 | 34   | 2.3   | 0.3  | 3    | 0.2   | 0.0  | 0.1 |
| DAMO_2088 | adenosylcobinamide kinase/adenosylcobinamide-phosphate guanylyltransferase  | 564  | 14   | 1.8   | 0.2  | 2    | 0.3   | 0.1  | 0.2 |
| DAMO_2089 | putative Xylose isomerase domain protein TIM barrel   | 846  | 25   | 2.1   | 0.3  | 0    | 0.0   | 0.0  | —   |
| DAMO_2090 | Putative Cob(II)yrinic acid a,c-diamide reductase, bluB (modular protein)   | 768  | 8    | 0.8   | 0.1  | 1    | 0.1   | 0.0  | 0.2 |
| DAMO_2091 | protein of unknown function   | 87   | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2092 | protein of unknown function   | 243  | 88   | 26.1  | 3.6  | 18   | 5.3   | 1.2  | 0.3 |
| DAMO_2093 | putative histone H1 protein precursor   | 246  | 829  | 242.6 | 33.8 | 46   | 13.5  | 3.0  | 0.1 |
| DAMO_2094 | conserved exported protein of unknown function  | 237  | 1051 | 319.3 | 44.5 | 146  | 44.4  | 9.8  | 0.2 |
| DAMO_2095 | Multimodular transpeptidase-transglycosylase  | 2016 | 77   | 2.8   | 0.4  | 9    | 0.3   | 0.1  | 0.2 |
| DAMO_2096 | protein of unknown function   | 261  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2097 | putative lipoprotein  | 768  | 116  | 10.9  | 1.5  | 9    | 0.8   | 0.2  | 0.1 |
| DAMO_2098 | Quinone oxidoreductase (NADPH:quinone reductase)  | 969  | 47   | 3.5   | 0.5  | 8    | 0.6   | 0.1  | 0.3 |
| DAMO_2099 | protein of unknown function   | 354  | 20   | 4.1   | 0.6  | 5    | 1.0   | 0.2  | 0.4 |
| DAMO_2100 | protein of unknown function   | 240  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2101 | protein of unknown function   | 192  | 0    | 0.0   | 0.0  | 2    | 0.8   | 0.2  | —   |
| DAMO_2102 | protein of unknown function   | 696  | 79   | 8.2   | 1.1  | 24   | 2.5   | 0.5  | 0.5 |
| DAMO_2103 | Ribonuclease G (RNase G) (Cytoplasmic axial filament protein)   | 1533 | 417  | 19.6  | 2.7  | 345  | 16.2  | 3.6  | 1.3 |
| DAMO_2104 | Radical SAM domain protein  | 2604 | 182  | 5.0   | 0.7  | 64   | 1.8   | 0.4  | 0.6 |
| DAMO_2105 | protein of unknown function   | 714  | 9    | 0.9   | 0.1  | 52   | 5.2   | 1.2  | 9.1 |
| DAMO_2106 | protein of unknown function   | 120  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2107 | putative response regulator in two-component regulatory system (CheY-like protein)                                | 375  | 1    | 0.2   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2108 | putative Histidine kinase   | 2196 | 6    | 0.2   | 0.0  | 2    | 0.1   | 0.0  | 0.5 |
| DAMO_2109 | protein of unknown function   | 144  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2110 | protein of unknown function   | 483  | 1    | 0.1   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2111 | protein of unknown function   | 396  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2112 | protein of unknown function   | 252  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2113 | protein of unknown function   | 132  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2114 | Inorganic pyrophosphatase (Pyrophosphate phospho- hydrolase) (PPase)  | 507  | 2    | 0.3   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2115 | Major facilitator family transporter  | 1212 | 75   | 4.5   | 0.6  | 51   | 3.0   | 0.7  | 1.1 |
| DAMO_2116 | Phosphoribulokinase (Phosphopentokinase) (PRKase  | 918  | 4    | 0.3   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2117 | Cobyrinic acid a,c-diamide synthase (fragment)  | 141  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2118 | exported protein of unknown function  | 465  | 266  | 41.2  | 5.7  | 419  | 64.9  | 14.3 | 2.5 |
| DAMO_2119 | protein of unknown function   | 213  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2120 | putative Histidine kinase   | 2559 | 6    | 0.2   | 0.0  | 13   | 0.4   | 0.1  | 3.4 |
| DAMO_2121 | Putative Oxygen-independent coproporphyrinogen III oxidase (modular protein)                                      | 2454 | 20   | 0.6   | 0.1  | 1    | 0.0   | 0.0  | 0.1 |
| DAMO_2122 | conserved protein of unknown function   | 840  | 26   | 2.2   | 0.3  | 8    | 0.7   | 0.2  | 0.5 |
| DAMO_2123 | protein of unknown function   | 180  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2124 | 30S ribosomal protein S21   | 282  | 513  | 131.0 | 18.3 | 103  | 26.3  | 5.8  | 0.3 |
| DAMO_2125 | RNP-1 like RNA-binding protein (modular protein)  | 423  | 47   | 8.0   | 1.1  | 22   | 3.7   | 0.8  | 0.7 |
| DAMO_2126 | protein of unknown function   | 111  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2127 | conserved membrane protein of unknown function  | 1137 | 117  | 7.4   | 1.0  | 19   | 1.2   | 0.3  | 0.3 |
| DAMO_2128 | L-asparaginase (L-asparagine amidohydrolase   | 900  | 47   | 3.8   | 0.5  | 9    | 0.7   | 0.2  | 0.3 |
| DAMO_2129 | putative Uncharacterized metalloprotease yhf  | 1269 | 10   | 0.6   | 0.1  | 4    | 0.2   | 0.1  | 0.6 |
| DAMO_2130 | conserved protein of unknown function   | 486  | 0    | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2131 | putative ABC transporter (permease proteine)  | 1131 | 250  | 15.9  | 2.2  | 107  | 6.8   | 1.5  | 0.7 |
| DAMO_2132 | putative ABC transporter (ATP-binding protein)  | 993  | 62   | 4.5   | 0.6  | 27   | 2.0   | 0.4  | 0.7 |
| DAMO_2133 | Secretion protein HlyD precursor  | 1056 | 61   | 4.2   | 0.6  | 26   | 1.8   | 0.4  | 0.7 |
| DAMO_2134 | DNA ligase (Polydeoxyribonucleotide synthas   | 2055 | 515  | 18.0  | 2.5  | 1114 | 39.0  | 8.6  | 3.4 |
| DAMO_2135 | exported protein of unknown function  | 258  | 1179 | 329.0 | 45.8 | 1595 | 445.1 | 98.1 | 2.1 |
| DAMO_2136 | conserved protein of unknown function   | 282  | 6    | 1.5   | 0.2  | 1    | 0.3   | 0.1  | 0.3 |
| DAMO_2137 | Bifunctional protein pyrR [Includes: Pyrimidine operon regulatory protein; Uracil phosphoribosyltransferas        | 579  | 13   | 1.6   | 0.2  | 4    | 0.5   | 0.1  | 0.5 |
| DAMO_2138 | aspartate carbamoyltransferase (catalytic subunit)  | 930  | 14   | 1.1   | 0.2  | 2    | 0.2   | 0.0  | 0.2 |
| DAMO_2139 | dihydroorotase (DHOase)   | 1341 | 65   | 3.5   | 0.5  | 23   | 1.2   | 0.3  | 0.6 |



|           |  |      |     |      |     |     |      |     |     |
|-----------|--|------|-----|------|-----|-----|------|-----|-----|
| DAMO_2140 | carbamoyl phosphate synthetase, glutamine amidotransferase small subunit   | 1200 | 81  | 4.9  | 0.7 | 60  | 3.6  | 0.8 | 1.2 |
| DAMO_2141 | putative O-methyltransferase mdmC  | 660  | 35  | 3.8  | 0.5 | 18  | 2.0  | 0.4 | 0.8 |
| DAMO_2142 | carbamoyl phosphate synthase, large subunit  | 3300 | 246 | 5.4  | 0.7 | 49  | 1.1  | 0.2 | 0.3 |
| DAMO_2143 | putative Dihydroorotate dehydrogenase, electron transfer subunit   | 981  | 9   | 0.7  | 0.1 | 1   | 0.1  | 0.0 | 0.2 |
| DAMO_2144 | Aminodeoxychorismate synthase, subunit I   | 1467 | 102 | 5.0  | 0.7 | 25  | 1.2  | 0.3 | 0.4 |
| DAMO_2145 | Branched chain amino acid: 2-keto-4-methylthiobutyrate aminotransferase / branched chain amino acid aminotransfera | 897  | 46  | 3.7  | 0.5 | 13  | 1.0  | 0.2 | 0.4 |
| DAMO_2146 | Dihydroorotate dehydrogenase (Dihydroorotate oxidase) (DHOdehase) (DHODase) (DHOD)                                 | 948  | 43  | 3.3  | 0.5 | 6   | 0.5  | 0.1 | 0.2 |
| DAMO_2147 | Endonuclease III (DNA-(apurinic or apyrimidinic site) lyase)   | 675  | 69  | 7.4  | 1.0 | 17  | 1.8  | 0.4 | 0.4 |
| DAMO_2148 | protein of unknown function  | 522  | 75  | 10.3 | 1.4 | 17  | 2.3  | 0.5 | 0.4 |
| DAMO_2149 | protein of unknown function  | 327  | 14  | 3.1  | 0.4 | 0   | 0.0  | 0.0 | —   |
| DAMO_2150 | protein of unknown function  | 192  | 2   | 0.8  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_2151 | protein of unknown function  | 189  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2152 | putative Curli production assembly/transport component CsgG precursor  | 1038 | 72  | 5.0  | 0.7 | 8   | 0.6  | 0.1 | 0.2 |
| DAMO_2153 | protein of unknown function  | 621  | 29  | 3.4  | 0.5 | 19  | 2.2  | 0.5 | 1.0 |
| DAMO_2154 | exported protein of unknown function   | 348  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2155 | conserved exported protein of unknown function   | 930  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2156 | protein of unknown function  | 213  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2157 | transposase (fragment)   | 279  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2158 | protein of unknown function  | 270  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2159 | protein of unknown function  | 183  | 9   | 3.5  | 0.5 | 0   | 0.0  | 0.0 | —   |
| DAMO_2160 | conserved protein of unknown function  | 1284 | 159 | 8.9  | 1.2 | 83  | 4.7  | 1.0 | 0.8 |
| DAMO_2161 | protein of unknown function  | 291  | 1   | 0.2  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2162 | protein of unknown function  | 249  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2163 | D-fructose-1,6-bisphosphatase protein  | 1020 | 162 | 11.4 | 1.6 | 28  | 2.0  | 0.4 | 0.3 |
| DAMO_2164 | ribose 5-phosphate isomerase (Phosphoriboisomerase A) (PRI)  | 660  | 34  | 3.7  | 0.5 | 10  | 1.1  | 0.2 | 0.5 |
| DAMO_2165 | Ribulose bisphosphate carboxylase large chai   | 1464 | 285 | 14.0 | 2.0 | 112 | 5.5  | 1.2 | 0.6 |
| DAMO_2166 | Ribulose bisphosphate carboxylase small chai   | 423  | 139 | 23.7 | 3.3 | 100 | 17.0 | 3.8 | 1.1 |
| DAMO_2167 | putative CbbX-like protein, containing AAA-ATPase domain   | 963  | 286 | 21.4 | 3.0 | 60  | 4.5  | 1.0 | 0.3 |
| DAMO_2168 | Phosphoenolpyruvate carboxylase (PEPCase)  | 1497 | 270 | 13.0 | 1.8 | 70  | 3.4  | 0.7 | 0.4 |
| DAMO_2169 | exported protein of unknown function   | 240  | 16  | 4.8  | 0.7 | 5   | 1.5  | 0.3 | 0.5 |
| DAMO_2170 | Carbonic anhydrase   | 630  | 254 | 29.0 | 4.0 | 64  | 7.3  | 1.6 | 0.4 |
| DAMO_2171 | protein of unknown function  | 270  | 120 | 32.0 | 4.5 | 48  | 12.8 | 2.8 | 0.6 |
| DAMO_2172 | conserved protein of unknown function  | 342  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2173 | conserved protein of unknown function  | 258  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2174 | protein of unknown function  | 102  | 14  | 9.9  | 1.4 | 0   | 0.0  | 0.0 | —   |
| DAMO_2175 | protein of unknown function  | 375  | 2   | 0.4  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_2176 | protein of unknown function  | 192  | 6   | 2.3  | 0.3 | 0   | 0.0  | 0.0 | —   |
| DAMO_2177 | Alanine racemase   | 1179 | 200 | 12.2 | 1.7 | 86  | 5.3  | 1.2 | 0.7 |
| DAMO_2178 | putative Trigger factor (TF)   | 1296 | 104 | 5.8  | 0.8 | 39  | 2.2  | 0.5 | 0.6 |
| DAMO_2179 | ATP-dependent Clp protease proteolytic subuni  | 618  | 81  | 9.4  | 1.3 | 93  | 10.8 | 2.4 | 1.8 |
| DAMO_2180 | protein of unknown function  | 477  | 2   | 0.3  | 0.0 | 1   | 0.2  | 0.0 | 0.8 |
| DAMO_2181 | ATP-dependent Clp protease ATP-binding subunit clpX  | 1248 | 289 | 16.7 | 2.3 | 144 | 8.3  | 1.8 | 0.8 |
| DAMO_2182 | putative Tetratricopeptide TPR_2 precursor   | 915  | 34  | 2.7  | 0.4 | 13  | 1.0  | 0.2 | 0.6 |
| DAMO_2183 | Dimethyladenosine transferase dimethyltransferase) (16S rRNA dimethylase) (High level kasugamycin resistance prote | 939  | 35  | 2.7  | 0.4 | 5   | 0.4  | 0.1 | 0.2 |
| DAMO_2184 | Thiamine-monophosphate kinase  | 1038 | 38  | 2.6  | 0.4 | 2   | 0.1  | 0.0 | 0.1 |
| DAMO_2185 | protein of unknown function  | 444  | 49  | 7.9  | 1.1 | 1   | 0.2  | 0.0 | —   |
| DAMO_2186 | Enolase (2-phosphoglycerate dehydratase  | 1281 | 208 | 11.7 | 1.6 | 40  | 2.2  | 0.5 | 0.3 |
| DAMO_2187 | glutamate dehydrogenase (NAD(P)+) oxidoreductase protein   | 1266 | 110 | 6.3  | 0.9 | 34  | 1.9  | 0.4 | 0.5 |
| DAMO_2188 | conserved protein of unknown function  | 333  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2189 | protein of unknown function  | 366  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2190 | conserved protein of unknown function  | 300  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2191 | protein of unknown function  | 105  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2192 | protein of unknown function  | 324  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2193 | conserved protein of unknown function  | 294  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2194 | conserved protein of unknown function  | 306  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2195 | protein of unknown function  | 156  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |

|           |  |      |     |      |     |     |      |      |     |
|-----------|--|------|-----|------|-----|-----|------|------|-----|
| DAMO_2196 | conserved protein of unknown function  | 237  | 2   | 0.6  | 0.1 | 0   | 0.0  | 0.0  | —   |
| DAMO_2197 | conserved exported protein of unknown function   | 582  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2198 | Site-specific DNA-methyltransferas   | 294  | 1   | 0.2  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2199 | Type III restriction enzyme, res subuni  | 201  | 36  | 12.9 | 1.8 | 10  | 3.6  | 0.8  | 0.4 |
| DAMO_2200 | DNA polymerase, beta-like region   | 420  | 105 | 18.0 | 2.5 | 27  | 4.6  | 1.0  | 0.4 |
| DAMO_2201 | conserved protein of unknown function  | 417  | 24  | 4.1  | 0.6 | 7   | 1.2  | 0.3  | 0.5 |
| DAMO_2202 | conserved protein of unknown function  | 384  | 54  | 10.1 | 1.4 | 22  | 4.1  | 0.9  | 0.6 |
| DAMO_2203 | protein of unknown function  | 84   | 49  | 42.0 | 5.9 | 9   | 7.7  | 1.7  | 0.3 |
| DAMO_2204 | conserved protein of unknown function  | 429  | 174 | 29.2 | 4.1 | 45  | 7.6  | 1.7  | 0.4 |
| DAMO_2205 | putative oxidoreductase with FAD/NAD(P)-binding domain   | 1251 | 201 | 11.6 | 1.6 | 27  | 1.6  | 0.3  | 0.2 |
| DAMO_2206 | ABC transporter with duplicated ATPase domains   | 1908 | 180 | 6.8  | 0.9 | 37  | 1.4  | 0.3  | 0.3 |
| DAMO_2207 | putative transporter fused subunits of ABC superfamily: ATP-binding components                 | 1575 | 485 | 22.2 | 3.1 | 78  | 3.6  | 0.8  | 0.3 |
| DAMO_2208 | putative oxidoreductase  | 1005 | 137 | 9.8  | 1.4 | 27  | 1.9  | 0.4  | 0.3 |
| DAMO_2209 | protein of unknown function  | 996  | 120 | 8.7  | 1.2 | 15  | 1.1  | 0.2  | 0.2 |
| DAMO_2210 | protein of unknown function  | 168  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2211 | conserved exported protein of unknown function   | 417  | 218 | 37.6 | 5.2 | 174 | 30.0 | 6.6  | 1.3 |
| DAMO_2212 | protein of unknown function  | 309  | 62  | 14.4 | 2.0 | 18  | 4.2  | 0.9  | 0.5 |
| DAMO_2213 | conserved protein of unknown function  | 1521 | 129 | 6.1  | 0.9 | 52  | 2.5  | 0.5  | 0.6 |
| DAMO_2214 | putative helicase  | 2520 | 202 | 5.8  | 0.8 | 36  | 1.0  | 0.2  | 0.3 |
| DAMO_2215 | protein of unknown function  | 231  | 94  | 29.3 | 4.1 | 72  | 22.4 | 4.9  | 1.2 |
| DAMO_2216 | protein of unknown function  | 228  | 77  | 24.3 | 3.4 | 24  | 7.6  | 1.7  | 0.5 |
| DAMO_2217 | conserved exported protein of unknown function   | 666  | 113 | 12.2 | 1.7 | 16  | 1.7  | 0.4  | 0.2 |
| DAMO_2218 | putative Outer membrane efflux protein   | 1395 | 270 | 13.9 | 1.9 | 54  | 2.8  | 0.6  | 0.3 |
| DAMO_2219 | Mce-related protein  | 441  | 5   | 0.8  | 0.1 | 0   | 0.0  | 0.0  | —   |
| DAMO_2220 | Putative ABC transporter (ATP-binding protein)   | 747  | 164 | 15.8 | 2.2 | 41  | 4.0  | 0.9  | 0.4 |
| DAMO_2221 | toluene transporter subunit: membrane component of ABC superfamily                             | 771  | 67  | 6.3  | 0.9 | 12  | 1.1  | 0.2  | 0.3 |
| DAMO_2222 | protein of unknown function  | 225  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2223 | conserved protein of unknown function  | 663  | 124 | 13.5 | 1.9 | 47  | 5.1  | 1.1  | 0.6 |
| DAMO_2225 | conserved protein of unknown function  | 210  | 89  | 30.5 | 4.3 | 163 | 55.9 | 12.3 | 2.9 |
| DAMO_2224 | conserved protein of unknown function  | 177  | 33  | 13.4 | 1.9 | 42  | 17.1 | 3.8  | 2.0 |
| DAMO_2226 | conserved protein of unknown function  | 216  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2227 | conserved protein of unknown function  | 255  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2228 | exported protein of unknown function   | 411  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2229 | protein of unknown function  | 258  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2230 | Plasmid stabilization system   | 255  | 6   | 1.7  | 0.2 | 0   | 0.0  | 0.0  | —   |
| DAMO_2231 | protein of unknown function  | 279  | 34  | 8.8  | 1.2 | 10  | 2.6  | 0.6  | 0.5 |
| DAMO_2232 | protein of unknown function  | 141  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2233 | conserved protein of unknown function  | 366  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2234 | protein of unknown function  | 663  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2235 | protein of unknown function  | 456  | 78  | 12.3 | 1.7 | 22  | 3.5  | 0.8  | 0.4 |
| DAMO_2236 | Histidine biosynthesis bifunctional protein hisIE Phosphoribosyl-ATP pyrophosphatase (PRA-PH)] | 696  | 34  | 3.5  | 0.5 | 7   | 0.7  | 0.2  | 0.3 |
| DAMO_2237 | Imidazole glycerol phosphate synthase subunit hisF   | 840  | 80  | 6.9  | 1.0 | 31  | 2.7  | 0.6  | 0.6 |
| DAMO_2238 | N-(5'-phospho-L-ribosyl-formimino)-5-amino-1-(5  | 723  | 75  | 7.5  | 1.0 | 14  | 1.4  | 0.3  | 0.3 |
| DAMO_2239 | fragment of imidazole glycerol phosphate synthase subunit hisH (part 2)                        | 141  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2240 | protein of unknown function  | 186  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2241 | protein of unknown function  | 324  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2242 | fragment of imidazole glycerol phosphate synthase subunit hisH (part 1)                        | 633  | 55  | 6.3  | 0.9 | 26  | 3.0  | 0.7  | 0.7 |
| DAMO_2243 | imidazoleglycerol-phosphate dehydratase  | 588  | 74  | 9.1  | 1.3 | 43  | 5.3  | 1.2  | 0.9 |
| DAMO_2244 | Histidinol-phosphate aminotransferase 2 (Imidazole acetol-phosphate transaminase 2)            | 1080 | 64  | 4.3  | 0.6 | 51  | 3.4  | 0.7  | 1.3 |
| DAMO_2245 | histidinol dehydrogenase (HDH)   | 1290 | 110 | 6.1  | 0.9 | 46  | 2.6  | 0.6  | 0.7 |
| DAMO_2246 | ATP phosphoribosyltransferase (ATP-PRTase  | 684  | 56  | 5.9  | 0.8 | 26  | 2.7  | 0.6  | 0.7 |
| DAMO_2247 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase enolpyruvyl transferase 1) (EPT 1)           | 1281 | 129 | 7.3  | 1.0 | 53  | 3.0  | 0.7  | 0.6 |
| DAMO_2248 | Putative protein methyltransferase hemK modifies release factors RF-1 and RF-2                 | 894  | 48  | 3.9  | 0.5 | 19  | 1.5  | 0.3  | 0.6 |
| DAMO_2249 | peptide chain release factor 1   | 1077 | 161 | 10.8 | 1.5 | 108 | 7.2  | 1.6  | 1.1 |
| DAMO_2250 | putative 50S ribosomal protein L31 (modular protein)   | 279  | 48  | 12.4 | 1.7 | 64  | 16.5 | 3.6  | 2.1 |
| DAMO_2251 | Transcription termination factor Rho   | 1335 | 399 | 21.5 | 3.0 | 88  | 4.7  | 1.0  | 0.3 |

|           |   |      |     |      |     |     |      |     |     |
|-----------|---|------|-----|------|-----|-----|------|-----|-----|
| DAMO_2252 | Dephospho-CoA kinase  | 642  | 10  | 1.1  | 0.2 | 4   | 0.4  | 0.1 | 0.6 |
| DAMO_2253 | DNA polymerase I (POL I)  | 2622 | 112 | 3.1  | 0.4 | 53  | 1.5  | 0.3 | 0.7 |
| DAMO_2254 | Chaperone protein dnaJ, heat shock protei   | 1092 | 131 | 8.6  | 1.2 | 90  | 5.9  | 1.3 | 1.1 |
| DAMO_2255 | Protein grpE (HSP-70 cofactor)  | 645  | 54  | 6.0  | 0.8 | 52  | 5.8  | 1.3 | 1.5 |
| DAMO_2256 | Heat-inducible transcription repressor  | 1041 | 165 | 11.4 | 1.6 | 125 | 8.6  | 1.9 | 1.2 |
| DAMO_2257 | putative oxygen-independent coproporphyrinogen III oxidase (yggW)   | 1194 | 10  | 0.6  | 0.1 | 3   | 0.2  | 0.0 | 0.5 |
| DAMO_2258 | Peptidase S26A, signal peptidase I  | 639  | 22  | 2.5  | 0.3 | 16  | 1.8  | 0.4 | 1.2 |
| DAMO_2259 | GTP-binding elongation factor   | 1809 | 225 | 9.0  | 1.2 | 85  | 3.4  | 0.7 | 0.6 |
| DAMO_2260 | Polyprenyl synthetase   | 978  | 173 | 12.7 | 1.8 | 83  | 6.1  | 1.3 | 0.8 |
| DAMO_2261 | conserved membrane protein of unknown function  | 1701 | 95  | 4.0  | 0.6 | 22  | 0.9  | 0.2 | 0.4 |
| DAMO_2262 | putative Phosphoesterase, PA-phosphatase relate   | 663  | 123 | 13.4 | 1.9 | 34  | 3.7  | 0.8 | 0.4 |
| DAMO_2263 | Membrane protein-like precursor (fragment)  | 261  | 29  | 8.0  | 1.1 | 3   | 0.8  | 0.2 | 0.2 |
| DAMO_2264 | TrkA-N domain protein (fragment)  | 450  | 64  | 10.2 | 1.4 | 20  | 3.2  | 0.7 | 0.5 |
| DAMO_2265 | TrkA-N:TrkA-C precursor (fragment)  | 555  | 39  | 5.1  | 0.7 | 13  | 1.7  | 0.4 | 0.5 |
| DAMO_2266 | Intracellular protease, PfpI family   | 588  | 57  | 7.0  | 1.0 | 9   | 1.1  | 0.2 | 0.2 |
| DAMO_2267 | putative transcriptional regulator  | 315  | 3   | 0.7  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_2268 | conserved protein of unknown function   | 306  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2269 | conserved protein of unknown function   | 552  | 167 | 21.8 | 3.0 | 26  | 3.4  | 0.7 | 0.2 |
| DAMO_2270 | protein of unknown function   | 402  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2271 | exported protein of unknown function  | 540  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2272 | protein of unknown function   | 798  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2273 | protein of unknown function   | 399  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2274 | protein of unknown function   | 81   | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2275 | protein of unknown function   | 285  | 1   | 0.3  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2276 | protein of unknown function   | 81   | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2277 | Prevent-host-death family protein   | 219  | 46  | 15.1 | 2.1 | 7   | 2.3  | 0.5 | 0.2 |
| DAMO_2278 | PilT protein domain protein   | 399  | 85  | 15.3 | 2.1 | 11  | 2.0  | 0.4 | 0.2 |
| DAMO_2279 | protein of unknown function   | 174  | 87  | 36.0 | 5.0 | 51  | 21.1 | 4.7 | 0.9 |
| DAMO_2280 | protein of unknown function   | 399  | 98  | 17.7 | 2.5 | 5   | 0.9  | 0.2 | 0.1 |
| DAMO_2281 | exported protein of unknown function  | 567  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2282 | conserved protein of unknown function   | 387  | 3   | 0.6  | 0.1 | 1   | 0.2  | 0.0 | 0.5 |
| DAMO_2283 | Cation-transporting ATPase pacL   | 2706 | 88  | 2.3  | 0.3 | 23  | 0.6  | 0.1 | 0.4 |
| DAMO_2284 | putative formate transporter 1 (Formate channel 1)  | 822  | 66  | 5.8  | 0.8 | 76  | 6.7  | 1.5 | 1.8 |
| DAMO_2285 | Hydroxylamine oxidase precursor   | 1287 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2286 | MscS Mechanosensitive ion channel   | 813  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2287 | protein of unknown function   | 243  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2288 | Transcriptional regulator, IclR family  | 807  | 67  | 6.0  | 0.8 | 10  | 0.9  | 0.2 | 0.2 |
| DAMO_2289 | protein of unknown function   | 222  | 1   | 0.3  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2290 | putative enzyme   | 714  | 117 | 11.8 | 1.6 | 14  | 1.4  | 0.3 | 0.2 |
| DAMO_2291 | protein of unknown function   | 192  | 40  | 15.0 | 2.1 | 19  | 7.1  | 1.6 | 0.8 |
| DAMO_2292 | Cell division protein ftsZ  | 1179 | 278 | 17.0 | 2.4 | 126 | 7.7  | 1.7 | 0.7 |
| DAMO_2293 | cell division protein with ATPase domain, involved in recruitment of FtsK to Z ring                           | 1236 | 252 | 14.7 | 2.0 | 55  | 3.2  | 0.7 | 0.3 |
| DAMO_2294 | protein of unknown function   | 726  | 60  | 6.0  | 0.8 | 26  | 2.6  | 0.6 | 0.7 |
| DAMO_2295 | UDP-N-acetylenolpyruvoylglucosamine reductas  | 927  | 155 | 12.0 | 1.7 | 62  | 4.8  | 1.1 | 0.6 |
| DAMO_2296 | UDP-N-acetyl-muramate:alanine ligase, L-alanine adding enzyme   | 1428 | 202 | 10.2 | 1.4 | 52  | 2.6  | 0.6 | 0.4 |
| DAMO_2297 | UDP-N-acetylglucosamine:N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine trans  | 1164 | 250 | 15.5 | 2.2 | 99  | 6.1  | 1.3 | 0.6 |
| DAMO_2298 | essential cell division protein (stabilizes FtsZ ring)  | 1116 | 54  | 3.5  | 0.5 | 17  | 1.1  | 0.2 | 0.5 |
| DAMO_2299 | UDP-N-acetylmuramoylalanine-D-glutamate ligase  | 1383 | 50  | 2.6  | 0.4 | 21  | 1.1  | 0.2 | 0.7 |
| DAMO_2300 | phospho-N-acetylmuramoyl-pentapeptide transferase   | 1083 | 76  | 5.1  | 0.7 | 92  | 6.1  | 1.3 | 1.9 |
| DAMO_2301 | putative D-alanine--D-alanine ligase  | 1311 | 397 | 21.8 | 3.0 | 125 | 6.9  | 1.5 | 0.5 |
| DAMO_2302 | putative UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase   | 1707 | 303 | 12.8 | 1.8 | 78  | 3.3  | 0.7 | 0.4 |
| DAMO_2303 | Predicted hydrolases or acyltransferase   | 768  | 22  | 2.1  | 0.3 | 6   | 0.6  | 0.1 | 0.4 |
| DAMO_2304 | UDP-N-acetylmuramoylalanyl-D-glutamate 2,6-diaminopimelate ligase (UDP-N-acetylmuramyl-tripeptide synthetase) | 1515 | 457 | 21.7 | 3.0 | 60  | 2.9  | 0.6 | 0.2 |
| DAMO_2305 | division-specific transpeptidase, penicillin-binding protein  | 1794 | 163 | 6.5  | 0.9 | 43  | 1.7  | 0.4 | 0.4 |
| DAMO_2306 | protein of unknown function   | 405  | 3   | 0.5  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_2307 | S-adenosyl-dependent methyl transferase   | 906  | 37  | 2.9  | 0.4 | 4   | 0.3  | 0.1 | 0.2 |

|           |   |      |     |       |      |      |       |      |     |
|-----------|---|------|-----|-------|------|------|-------|------|-----|
| DAMO_2308 | Protein mraZ  | 450  | 649 | 103.8 | 14.5 | 71   | 11.4  | 2.5  | 0.2 |
| DAMO_2309 | pantothenate synthetase (Pantoate--beta-alanine ligase)   | 849  | 16  | 1.4   | 0.2  | 6    | 0.5   | 0.1  | 0.6 |
| DAMO_2310 | 3-methyl-2-oxobutanoate hydroxymethyltransferas   | 843  | 50  | 4.3   | 0.6  | 15   | 1.3   | 0.3  | 0.5 |
| DAMO_2311 | Deoxynucleoside kinase family protein   | 657  | 56  | 6.1   | 0.9  | 15   | 1.6   | 0.4  | 0.4 |
| DAMO_2312 | 7, 8-dihydro-6-hydroxymethylpterin-pyrophosphokinase (HPPK)                                     | 531  | 1   | 0.1   | 0.0  | 0    | 0.0   | 0.0  | 0.0 |
| DAMO_2313 | putative PLP-dependent aminotransferase, putative aspartate aminotransferase.                   | 1182 | 122 | 7.4   | 1.0  | 61   | 3.7   | 0.8  | 0.8 |
| DAMO_2314 | conserved protein of unknown function   | 762  | 89  | 8.4   | 1.2  | 51   | 4.8   | 1.1  | 0.9 |
| DAMO_2315 | Dihydrodipicolinate reductase (DHPR)  | 807  | 78  | 7.0   | 1.0  | 13   | 1.2   | 0.3  | 0.3 |
| DAMO_2316 | dihydrodipicolinate synthase  | 885  | 157 | 12.8  | 1.8  | 37   | 3.0   | 0.7  | 0.4 |
| DAMO_2317 | Diaminopimelate epimerase (DAP epimerase)   | 825  | 76  | 6.6   | 0.9  | 27   | 2.4   | 0.5  | 0.6 |
| DAMO_2318 | diaminopimelate decarboxylase   | 1257 | 393 | 22.5  | 3.1  | 199  | 11.4  | 2.5  | 0.8 |
| DAMO_2319 | protein of unknown function   | 303  | 0   | 0.0   | 0.0  | 1    | 0.2   | 0.1  | —   |
| DAMO_2320 | Type I site-specific deoxyribonuclease, HsdR family   | 2892 | 4   | 0.1   | 0.0  | 2    | 0.0   | 0.0  | 0.8 |
| DAMO_2321 | protein of unknown function   | 72   | 0   | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2322 | putative transcriptional regulator  | 1659 | 0   | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2323 | protein of unknown function   | 915  | 0   | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2324 | protein of unknown function   | 1353 | 0   | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2325 | putative Restriction modification system DNA specificity domain                                 | 1353 | 0   | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2326 | protein of unknown function   | 738  | 0   | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2329 | protein of unknown function   | 246  | 0   | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2330 | N-6 DNA methylase   | 1923 | 4   | 0.1   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2331 | protein of unknown function   | 165  | 0   | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2332 | Cold shock protein, DNA binding   | 204  | 241 | 85.1  | 11.9 | 26   | 9.2   | 2.0  | 0.2 |
| DAMO_2333 | UvrABC system protein B (Protein uvrB   | 2025 | 265 | 9.4   | 1.3  | 99   | 3.5   | 0.8  | 0.6 |
| DAMO_2334 | HNH endonuclease  | 597  | 461 | 55.6  | 7.7  | 34   | 4.1   | 0.9  | 0.1 |
| DAMO_2335 | putative Exopolyphosphatase   | 939  | 15  | 1.2   | 0.2  | 16   | 1.2   | 0.3  | 1.7 |
| DAMO_2336 | putative Fibronectin-binding protein / Fibrinogen-bindingprotein                                | 1863 | 70  | 2.7   | 0.4  | 26   | 1.0   | 0.2  | 0.6 |
| DAMO_2337 | Transcriptional regulator, MarR family  | 417  | 773 | 133.5 | 18.6 | 1486 | 256.6 | 56.5 | 3.0 |
| DAMO_2338 | protein of unknown function   | 129  | 55  | 30.7  | 4.3  | 73   | 40.7  | 9.0  | 2.1 |
| DAMO_2339 | Particulate methane monooxygenase, c-subunit  | 777  | 0   | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2340 | Conserved protein of unknown function; pmo  | 780  | 31  | 2.9   | 0.4  | 23   | 2.1   | 0.5  | 1.2 |
| DAMO_2341 | protein of unknown function   | 369  | 378 | 73.8  | 10.3 | 240  | 46.8  | 10.3 | 1.0 |
| DAMO_2342 | UvrABC system protein A (UvrA protein)(Excinuclease ABC subunit A)(Excinuclease ATPase subunit) | 2616 | 148 | 4.1   | 0.6  | 67   | 1.8   | 0.4  | 0.7 |
| DAMO_2343 | protein of unknown function   | 90   | 0   | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2344 | protein of unknown function   | 255  | 0   | 0.0   | 0.0  | 1    | 0.3   | 0.1  | —   |
| DAMO_2345 | conserved protein of unknown function   | 1029 | 242 | 16.9  | 2.4  | 46   | 3.2   | 0.7  | 0.3 |
| DAMO_2346 | membrane protein of unknown function  | 2256 | 1   | 0.0   | 0.0  | 3    | 0.1   | 0.0  | 4.7 |
| DAMO_2347 | protein of unknown function   | 207  | 0   | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2348 | protein of unknown function   | 201  | 0   | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2349 | protein of unknown function   | 705  | 0   | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |
| DAMO_2350 | protein of unknown function   | 204  | 3   | 1.1   | 0.1  | 0    | 0.0   | 0.0  | —   |
| DAMO_2351 | protein of unknown function   | 264  | 19  | 5.2   | 0.7  | 10   | 2.7   | 0.6  | 0.8 |
| DAMO_2352 | NAD-dependent epimerase/dehydratase   | 864  | 34  | 2.8   | 0.4  | 9    | 0.8   | 0.2  | 0.4 |
| DAMO_2353 | protein of unknown function   | 225  | 154 | 49.3  | 6.9  | 28   | 9.0   | 2.0  | 0.3 |
| DAMO_2354 | conserved exported protein of unknown function  | 909  | 116 | 9.2   | 1.3  | 27   | 2.1   | 0.5  | 0.4 |
| DAMO_2355 | conserved membrane protein of unknown function  | 609  | 2   | 0.2   | 0.0  | 0    | 0.0   | 0.0  | 0.0 |
| DAMO_2356 | protein of unknown function   | 2565 | 68  | 1.9   | 0.3  | 14   | 0.4   | 0.1  | 0.3 |
| DAMO_2357 | protein of unknown function   | 969  | 61  | 4.5   | 0.6  | 27   | 2.0   | 0.4  | 0.7 |
| DAMO_2358 | putative ABC transporter protein  | 960  | 35  | 2.6   | 0.4  | 6    | 0.5   | 0.1  | 0.3 |
| DAMO_2359 | protein of unknown function   | 996  | 44  | 3.2   | 0.4  | 13   | 0.9   | 0.2  | 0.5 |
| DAMO_2360 | protein of unknown function   | 957  | 66  | 5.0   | 0.7  | 11   | 0.8   | 0.2  | 0.3 |
| DAMO_2361 | protein of unknown function   | 921  | 14  | 1.1   | 0.2  | 10   | 0.8   | 0.2  | 1.1 |
| DAMO_2362 | protein of unknown function   | 327  | 85  | 18.7  | 2.6  | 20   | 4.4   | 1.0  | 0.4 |
| DAMO_2363 | Histidinol-phosphate aminotransferase (Imidazole acetol- phosphate transaminase)                | 1107 | 51  | 3.3   | 0.5  | 27   | 1.8   | 0.4  | 0.8 |
| DAMO_2364 | protein of unknown function   | 684  | 31  | 3.3   | 0.5  | 5    | 0.5   | 0.1  | 0.3 |
| DAMO_2365 | protein of unknown function   | 366  | 0   | 0.0   | 0.0  | 0    | 0.0   | 0.0  | —   |

|           |  |      |      |       |      |      |        |       |      |
|-----------|--|------|------|-------|------|------|--------|-------|------|
| DAMO_2366 | Transport-associated precursor   | 327  | 8    | 1.8   | 0.2  | 3    | 0.7    | 0.1   | 0.6  |
| DAMO_2367 | 4-hydroxythreonine-4-phosphate dehydrogenase (4  | 1041 | 457  | 31.6  | 4.4  | 250  | 17.3   | 3.8   | 0.9  |
| DAMO_2368 | exported protein of unknown function   | 585  | 258  | 31.8  | 4.4  | 105  | 12.9   | 2.8   | 0.6  |
| DAMO_2369 | conserved protein of unknown function  | 1014 | 29   | 2.1   | 0.3  | 4    | 0.3    | 0.1   | 0.2  |
| DAMO_2370 | putative Transcriptional regulator, AbrB family  | 219  | 8    | 2.6   | 0.4  | 4    | 1.3    | 0.3   | 0.8  |
| DAMO_2371 | Similar to tr  | 453  | 40   | 6.4   | 0.9  | 35   | 5.6    | 1.2   | 1.4  |
| DAMO_2372 | conserved protein of unknown function  | 1569 | 69   | 3.2   | 0.4  | 20   | 0.9    | 0.2   | 0.5  |
| DAMO_2373 | putative aldehyde-dehydrogenase-like protein y4uC  | 1419 | 182  | 9.2   | 1.3  | 90   | 4.6    | 1.0   | 0.8  |
| DAMO_2374 | protein of unknown function  | 84   | 12   | 10.3  | 1.4  | 4    | 3.4    | 0.8   | 0.5  |
| DAMO_2375 | Molybdenum cofactor biosynthesis protein A 1   | 936  | 57   | 4.4   | 0.6  | 37   | 2.8    | 0.6   | 1.0  |
| DAMO_2376 | protein of unknown function  | 144  | 5    | 2.5   | 0.3  | 0    | 0.0    | 0.0   | 0.0  |
| DAMO_2377 | 4Fe-4S ferredoxin iron-sulfur binding domain protein (modular protein)   | 342  | 530  | 111.6 | 15.5 | 4929 | 1037.7 | 228.7 | 14.7 |
| DAMO_2378 | conserved hypothetical protein (domain of unknown function DUF59)  | 312  | 94   | 21.7  | 3.0  | 582  | 134.3  | 29.6  | 9.8  |
| DAMO_2379 | NifU (FeS assembly protein). Function similar to nifS  | 477  | 28   | 4.2   | 0.6  | 55   | 8.3    | 1.8   | 3.1  |
| DAMO_2380 | Highly similar to cysteine desulfurase   | 1254 | 259  | 14.9  | 2.1  | 1059 | 60.8   | 13.4  | 6.5  |
| DAMO_2381 | sufD, needed for fhuF Fe-S center production/stability   | 1443 | 124  | 6.2   | 0.9  | 365  | 18.2   | 4.0   | 4.7  |
| DAMO_2382 | SufC, related to ABC transporter associated with Fe-S cluster assembly (ATP-binding protein)                           | 771  | 150  | 14.0  | 2.0  | 140  | 13.1   | 2.9   | 1.5  |
| DAMO_2383 | transport protein associated with Fe-S cluster assembly  | 1476 | 1252 | 61.1  | 8.5  | 3311 | 161.5  | 35.6  | 4.2  |
| DAMO_2384 | protein of unknown function  | 210  | 5    | 1.7   | 0.2  | 8    | 2.7    | 0.6   | 2.5  |
| DAMO_2385 | Protein mrp homolog  | 1083 | 532  | 35.4  | 4.9  | 659  | 43.8   | 9.7   | 2.0  |
| DAMO_2386 | protein of unknown function  | 336  | 87   | 18.6  | 2.6  | 75   | 16.1   | 3.5   | 1.4  |
| DAMO_2387 | protein of unknown function  | 396  | 88   | 16.0  | 2.2  | 149  | 27.1   | 6.0   | 2.7  |
| DAMO_2388 | protein of unknown function  | 186  | 0    | 0.0   | 0.0  | 0    | 0.0    | 0.0   | —    |
| DAMO_2389 | protein of unknown function  | 195  | 5    | 1.8   | 0.3  | 16   | 5.9    | 1.3   | 5.1  |
| DAMO_2390 | protein of unknown function  | 630  | 0    | 0.0   | 0.0  | 0    | 0.0    | 0.0   | —    |
| DAMO_2391 | protein of unknown function  | 171  | 0    | 0.0   | 0.0  | 0    | 0.0    | 0.0   | —    |
| DAMO_2392 | conserved protein of unknown function  | 336  | 0    | 0.0   | 0.0  | 0    | 0.0    | 0.0   | —    |
| DAMO_2393 | protein of unknown function  | 75   | 0    | 0.0   | 0.0  | 0    | 0.0    | 0.0   | —    |
| DAMO_2394 | conserved protein of unknown function  | 300  | 0    | 0.0   | 0.0  | 0    | 0.0    | 0.0   | —    |
| DAMO_2395 | protein of unknown function  | 237  | 0    | 0.0   | 0.0  | 0    | 0.0    | 0.0   | —    |
| DAMO_2396 | protein of unknown function  | 306  | 2    | 0.5   | 0.1  | 1    | 0.2    | 0.1   | 0.8  |
| DAMO_2397 | protein of unknown function  | 393  | 53   | 9.7   | 1.4  | 7    | 1.3    | 0.3   | 0.2  |
| DAMO_2398 | protein of unknown function  | 432  | 57   | 9.5   | 1.3  | 20   | 3.3    | 0.7   | 0.6  |
| DAMO_2399 | exported protein of unknown function   | 882  | 152  | 12.4  | 1.7  | 52   | 4.2    | 0.9   | 0.5  |
| DAMO_2400 | exported protein of unknown function   | 612  | 10   | 1.2   | 0.2  | 4    | 0.5    | 0.1   | 0.6  |
| DAMO_2401 | conserved hypothetical protein; YebC-like  | 750  | 224  | 21.5  | 3.0  | 108  | 10.4   | 2.3   | 0.8  |
| DAMO_2402 | Crossover junction endodeoxyribonuclease ruv   | 501  | 61   | 8.8   | 1.2  | 21   | 3.0    | 0.7   | 0.5  |
| DAMO_2403 | Holliday junction DNA helicase ruvA  | 627  | 18   | 2.1   | 0.3  | 5    | 0.6    | 0.1   | 0.4  |
| DAMO_2404 | Holliday junction DNA helicase ruvB  | 1056 | 216  | 14.7  | 2.1  | 87   | 5.9    | 1.3   | 0.6  |
| DAMO_2405 | conserved protein of unknown function  | 216  | 3    | 1.0   | 0.1  | 0    | 0.0    | 0.0   | 0.0  |
| DAMO_2406 | S-adenosylmethionine:tRNA ribosyltransferase-isomerase   | 1140 | 124  | 7.8   | 1.1  | 8    | 0.5    | 0.1   | 0.1  |
| DAMO_2407 | tRNA-guanine transglycosylase (queuine/archaeosine tRNA-ribosyltransferase)  | 1131 | 37   | 2.4   | 0.3  | 12   | 0.8    | 0.2   | 0.5  |
| DAMO_2408 | preprotein translocase (YajC)  | 342  | 5    | 1.1   | 0.1  | 3    | 0.6    | 0.1   | 0.9  |
| DAMO_2409 | Putative transcriptional regulator, AsnC family; likely to be a fused nirD/G and nirL/H, involved in heme D1 biosynthe | 1155 | 48   | 3.0   | 0.4  | 10   | 0.6    | 0.1   | 0.3  |
| DAMO_2410 | Putative periplasmic nitrate reductase, small subunit (napB); diheme cytochrome C                                      | 336  | 8    | 1.7   | 0.2  | 2    | 0.4    | 0.1   | 0.4  |
| DAMO_2411 | Periplasmic nitrate reductase, large subunit   | 2367 | 250  | 7.6   | 1.1  | 72   | 2.2    | 0.5   | 0.5  |
| DAMO_2412 | Putative heme D1 biosynthesis protein (nirF), involved in nitrite reductase biosynthesis                               | 1230 | 88   | 5.2   | 0.7  | 35   | 2.0    | 0.5   | 0.6  |
| DAMO_2413 | Putative heme D1 biosynthesis protein (nirJ) involved in nitrite reductase biosynthesis                                | 1221 | 116  | 6.8   | 1.0  | 48   | 2.8    | 0.6   | 0.7  |
| DAMO_2415 | protein of unknown function  | 1641 | 2134 | 93.6  | 13.0 | 113  | 5.0    | 1.1   | 0.1  |
| DAMO_2416 | Nitrate reductase, cytochrome cd1 type   | 1059 | 199  | 13.5  | 1.9  | 147  | 10.0   | 2.2   | 1.2  |
| DAMO_2417 | 5-methylthioribose-1-phosphate isomerase (MTNA)  | 2220 | 18   | 0.6   | 0.1  | 9    | 0.3    | 0.1   | 0.8  |
| DAMO_2418 | protein of unknown function  | 1206 | 8    | 0.5   | 0.1  | 11   | 0.7    | 0.1   | 2.2  |
| DAMO_2419 | Coenzyme A biosynthesis bifunctional protein coaBC Phosphopantothenoylecysteine decarboxylase (CoaC); Phosphop         | 735  | 26   | 2.5   | 0.4  | 16   | 1.6    | 0.3   | 1.0  |
| DAMO_2420 | protein of unknown function  | 330  | 3    | 0.7   | 0.1  | 8    | 1.7    | 0.4   | 4.2  |
| DAMO_2421 | exported protein of unknown function   | 975  | 7    | 0.5   | 0.1  | 5    | 0.4    | 0.1   | 1.1  |
| DAMO_2422 | exported protein of unknown function   | 696  | 116  | 12.0  | 1.7  | 63   | 6.5    | 1.4   | 0.9  |

|           |  |      |      |       |      |       |       |      |      |
|-----------|--|------|------|-------|------|-------|-------|------|------|
| DAMO_2423 | putative Primosomal protein N' (ATP-dependent helicase priA) (Replication factor Y)                            | 2601 | 61   | 1.7   | 0.2  | 18    | 0.5   | 0.1  | 0.5  |
| DAMO_2424 | SAM-dependent methyltransferase  | 801  | 42   | 3.8   | 0.5  | 9     | 0.8   | 0.2  | 0.3  |
| DAMO_2425 | Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase   | 858  | 49   | 4.1   | 0.6  | 10    | 0.8   | 0.2  | 0.3  |
| DAMO_2426 | NH(3)-dependent NAD(+) synthetase  | 822  | 49   | 4.3   | 0.6  | 43    | 3.8   | 0.8  | 1.4  |
| DAMO_2427 | membrane protein of unknown function   | 552  | 25   | 3.3   | 0.5  | 80    | 10.4  | 2.3  | 5.1  |
| DAMO_2428 | exported protein of unknown function   | 870  | 85   | 7.0   | 1.0  | 455   | 37.7  | 8.3  | 8.5  |
| DAMO_2429 | protein of unknown function  | 495  | 36   | 5.2   | 0.7  | 191   | 27.8  | 6.1  | 8.4  |
| DAMO_2430 | protein of unknown function  | 288  | 14   | 3.5   | 0.5  | 50    | 12.5  | 2.8  | 5.6  |
| DAMO_2431 | protein of unknown function  | 177  | 0    | 0.0   | 0.0  | 8     | 3.3   | 0.7  | —    |
| DAMO_2432 | exported protein of unknown function   | 381  | 0    | 0.0   | 0.0  | 1     | 0.2   | 0.0  | —    |
| DAMO_2433 | protein of unknown function  | 249  | 13   | 3.8   | 0.5  | 110   | 31.8  | 7.0  | 13.4 |
| DAMO_2434 | putative Cytochrome c oxidase subunit I precursor; nitric oxide-like (norZ)                                    | 2427 | 2229 | 66.1  | 9.2  | 10609 | 314.7 | 69.4 | 7.5  |
| DAMO_2435 | protein of unknown function  | 231  | 1    | 0.3   | 0.0  | 1     | 0.3   | 0.1  | 1.6  |
| DAMO_2436 | protein of unknown function  | 192  | 0    | 0.0   | 0.0  | 0     | 0.0   | 0.0  | —    |
| DAMO_2437 | putative Cytochrome c oxidase subunit I precursor; nitric oxide reductase-like (norZ)                          | 2433 | 9380 | 277.6 | 38.7 | 7715  | 228.3 | 50.3 | 1.3  |
| DAMO_2438 | protein of unknown function  | 174  | 0    | 0.0   | 0.0  | 0     | 0.0   | 0.0  | —    |
| DAMO_2439 | conserved protein of unknown function; putative transcriptional regulator                                      | 903  | 256  | 20.4  | 2.8  | 184   | 14.7  | 3.2  | 1.1  |
| DAMO_2440 | protein of unknown function  | 204  | 0    | 0.0   | 0.0  | 0     | 0.0   | 0.0  | —    |
| DAMO_2441 | protein of unknown function  | 345  | 25   | 5.2   | 0.7  | 0     | 0.0   | 0.0  | —    |
| DAMO_2442 | exported protein of unknown function   | 1524 | 221  | 10.4  | 1.5  | 25    | 1.2   | 0.3  | 0.2  |
| DAMO_2443 | protein of unknown function  | 252  | 0    | 0.0   | 0.0  | 2     | 0.6   | 0.1  | —    |
| DAMO_2444 | protein of unknown function  | 87   | 0    | 0.0   | 0.0  | 0     | 0.0   | 0.0  | —    |
| DAMO_2445 | Cell division protein FtsH; ATP-dependent zinc-metallo protease  | 1929 | 1005 | 37.5  | 5.2  | 2953  | 110.2 | 24.3 | 4.6  |
| DAMO_2446 | Conserved protein of unknown function; pmoD  | 765  | 10   | 0.9   | 0.1  | 10    | 0.9   | 0.2  | 1.6  |
| DAMO_2448 | protein of unknown function  | 1269 | 1066 | 60.5  | 8.4  | 412   | 23.4  | 5.2  | 0.6  |
| DAMO_2450 | Particulate methane monooxygenase, B-subuni  | 732  | 995  | 97.9  | 13.6 | 700   | 68.9  | 15.2 | 1.1  |
| DAMO_2451 | Hypothetical protein   | 777  | 0    | 0.0   | 0.0  | 0     | 0.0   | 0.0  | —    |
| DAMO_2452 | Particulate methane monooxygenase, A-subuni  | 168  | 10   | 4.3   | 0.6  | 3     | 1.3   | 0.3  | 0.5  |
| DAMO_2453 | Particulate methane monooxygenase, C-subuni  | 78   | 0    | 0.0   | 0.0  | 0     | 0.0   | 0.0  | —    |
| DAMO_2454 | protein of unknown function  | 1725 | 0    | 0.0   | 0.0  | 0     | 0.0   | 0.0  | —    |
| DAMO_2455 | protein of unknown function  | 1224 | 138  | 8.1   | 1.1  | 87    | 5.1   | 1.1  | 1.0  |
| DAMO_2456 | GAF modulated sigma54 specific transcriptional regulator, Fis family (fragment)                                | 438  | 125  | 20.5  | 2.9  | 53    | 8.7   | 1.9  | 0.7  |
| DAMO_2457 | ATP-dependent RNA helicase   | 1635 | 919  | 40.5  | 5.6  | 978   | 43.1  | 9.5  | 1.7  |
| DAMO_2458 | exported protein of unknown function   | 288  | 84   | 21.0  | 2.9  | 93    | 23.3  | 5.1  | 1.8  |
| DAMO_2459 | 60 kDa chaperonin (Protein Cpn60) (groEL protein)  | 561  | 75   | 9.6   | 1.3  | 12    | 1.5   | 0.3  | 0.3  |
| DAMO_2460 | chaperone Hsp10 (GroES), part of GroE chaperone system   | 2523 | 93   | 2.7   | 0.4  | 73    | 2.1   | 0.5  | 1.2  |
| DAMO_2461 | protein of unknown function  | 1425 | 60   | 3.0   | 0.4  | 13    | 0.7   | 0.1  | 0.3  |
| DAMO_2462 | Nucleotidyl transferase  | 372  | 6    | 1.2   | 0.2  | 6     | 1.2   | 0.3  | 1.6  |
| DAMO_2463 | Phosphoglucomutase/phosphomannomutase alpha/beta/alpha domain I  | 192  | 0    | 0.0   | 0.0  | 0     | 0.0   | 0.0  | —    |
| DAMO_2464 | putative Septum formation initiator (ftsB)   | 174  | 817  | 338.1 | 47.1 | 210   | 86.9  | 19.1 | 0.4  |
| DAMO_2465 | protein of unknown function  | 216  | 0    | 0.0   | 0.0  | 1     | 0.3   | 0.1  | —    |
| DAMO_2466 | 1-deoxy-D-xylulose 5-phosphate reductoisomerase reductoisomerase)  | 1155 | 227  | 14.2  | 2.0  | 260   | 16.2  | 3.6  | 1.8  |
| DAMO_2467 | putative Zinc metalloprotease  | 1131 | 85   | 5.4   | 0.8  | 63    | 4.0   | 0.9  | 1.2  |
| DAMO_2468 | 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase) | 1077 | 158  | 10.6  | 1.5  | 69    | 4.6   | 1.0  | 0.7  |
| DAMO_2469 | Prolyl-tRNA synthetase (Proline--tRNA ligase   | 1719 | 34   | 1.4   | 0.2  | 10    | 0.4   | 0.1  | 0.5  |
| DAMO_2470 | Conserved protein of unknown function; pmo   | 777  | 162  | 15.0  | 2.1  | 636   | 58.9  | 13.0 | 6.2  |
| DAMO_2471 | putative aspartate ammonia-lyase (L-aspartase)   | 1413 | 40   | 2.0   | 0.3  | 12    | 0.6   | 0.1  | 0.5  |
| DAMO_2472 | protein of unknown function  | 312  | 23   | 5.3   | 0.7  | 0     | 0.0   | 0.0  | —    |
| DAMO_2473 | Similar to hydroxylamine oxidoreductase hao  | 1389 | 398  | 20.6  | 2.9  | 55    | 2.9   | 0.6  | 0.2  |
| DAMO_2474 | conserved protein of unknown function  | 513  | 108  | 15.2  | 2.1  | 32    | 4.5   | 1.0  | 0.5  |
| DAMO_2475 | protein of unknown function  | 288  | 8    | 2.0   | 0.3  | 0     | 0.0   | 0.0  | —    |
| DAMO_2476 | protein of unknown function  | 708  | 83   | 8.4   | 1.2  | 17    | 1.7   | 0.4  | 0.3  |
| DAMO_2477 | putative GHMP kinase   | 1023 | 27   | 1.9   | 0.3  | 1     | 0.1   | 0.0  | 0.1  |
| DAMO_2478 | exported protein of unknown function   | 396  | 0    | 0.0   | 0.0  | 0     | 0.0   | 0.0  | —    |
| DAMO_2479 | exported protein of unknown function   | 2181 | 70   | 2.3   | 0.3  | 8     | 0.3   | 0.1  | 0.2  |
| DAMO_2480 | exported protein of unknown function   | 612  | 7    | 0.8   | 0.1  | 2     | 0.2   | 0.1  | 0.5  |

|           |  |      |     |      |     |     |      |      |     |
|-----------|--|------|-----|------|-----|-----|------|------|-----|
| DAMO_2481 | exported protein of unknown function   | 573  | 14  | 1.8  | 0.2 | 0   | 0.0  | 0.0  | —   |
| DAMO_2482 | protein of unknown function  | 1476 | 52  | 2.5  | 0.4 | 4   | 0.2  | 0.0  | 0.1 |
| DAMO_2483 | exported protein of unknown function   | 1071 | 25  | 1.7  | 0.2 | 2   | 0.1  | 0.0  | 0.1 |
| DAMO_2484 | protein of unknown function  | 816  | 21  | 1.9  | 0.3 | 3   | 0.3  | 0.1  | 0.2 |
| DAMO_2485 | putative General secretion pathway protein I, Gsp                                    | 531  | 21  | 2.8  | 0.4 | 1   | 0.1  | 0.0  | 0.1 |
| DAMO_2486 | exported protein of unknown function   | 585  | 48  | 5.9  | 0.8 | 12  | 1.5  | 0.3  | 0.4 |
| DAMO_2487 | pseudopilin, cryptic, general secretion pathway                                      | 507  | 5   | 0.7  | 0.1 | 0   | 0.0  | 0.0  | —   |
| DAMO_2488 | general secretory pathway component, cryptic   | 1227 | 542 | 31.8 | 4.4 | 123 | 7.2  | 1.6  | 0.4 |
| DAMO_2489 | putative General secretion pathway protein E (Type II traffic warden ATPase)         | 1722 | 332 | 13.9 | 1.9 | 223 | 9.3  | 2.1  | 1.1 |
| DAMO_2490 | protein of unknown function  | 195  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2491 | Short-chain dehydrogenase/reductase SDR precursor                                    | 870  | 286 | 23.7 | 3.3 | 126 | 10.4 | 2.3  | 0.7 |
| DAMO_2492 | putative cyclase   | 480  | 17  | 2.6  | 0.4 | 4   | 0.6  | 0.1  | 0.4 |
| DAMO_2493 | conserved protein of unknown function  | 309  | 2   | 0.5  | 0.1 | 0   | 0.0  | 0.0  | —   |
| DAMO_2494 | ABC-type multidrug/protein/lipid transport system, ATPase component                  | 1782 | 58  | 2.3  | 0.3 | 57  | 2.3  | 0.5  | 1.6 |
| DAMO_2495 | ABC transporter, ATPase subunit  | 1722 | 33  | 1.4  | 0.2 | 34  | 1.4  | 0.3  | 1.6 |
| DAMO_2496 | putative plasmid stabilization system protein  | 303  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2497 | Prevent-host-death family protein  | 276  | 27  | 7.0  | 1.0 | 19  | 5.0  | 1.1  | 1.1 |
| DAMO_2498 | Pyruvate formate-lyase activating enzyme   | 1056 | 52  | 3.5  | 0.5 | 60  | 4.1  | 0.9  | 1.8 |
| DAMO_2499 | Malate dehydrogenas  | 1770 | 472 | 19.2 | 2.7 | 154 | 6.3  | 1.4  | 0.5 |
| DAMO_2500 | protein of unknown function  | 486  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2501 | protein of unknown function  | 123  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2502 | conserved exported protein of unknown function                                       | 492  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2503 | protein of unknown function  | 246  | 56  | 16.4 | 2.3 | 14  | 4.1  | 0.9  | 0.4 |
| DAMO_2504 | conserved protein of unknown function  | 483  | 19  | 2.8  | 0.4 | 10  | 1.5  | 0.3  | 0.8 |
| DAMO_2505 | protein of unknown function  | 123  | 6   | 3.5  | 0.5 | 0   | 0.0  | 0.0  | —   |
| DAMO_2506 | Toxin higB-1   | 282  | 87  | 22.2 | 3.1 | 54  | 13.8 | 3.0  | 1.0 |
| DAMO_2507 | Antitoxin higA-1   | 315  | 73  | 16.7 | 2.3 | 37  | 8.5  | 1.9  | 0.8 |
| DAMO_2508 | putative enzyme  | 81   | 1   | 0.9  | 0.1 | 0   | 0.0  | 0.0  | —   |
| DAMO_2509 | conserved protein of unknown function  | 258  | 73  | 20.4 | 2.8 | 167 | 46.6 | 10.3 | 3.6 |
| DAMO_2510 | conserved protein of unknown function  | 321  | 119 | 26.7 | 3.7 | 36  | 8.1  | 1.8  | 0.5 |
| DAMO_2511 | conserved protein of unknown function  | 126  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2512 | conserved protein of unknown function  | 348  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2513 | protein of unknown function  | 189  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2514 | conserved protein of unknown function  | 447  | 6   | 1.0  | 0.1 | 0   | 0.0  | 0.0  | —   |
| DAMO_2515 | conserved protein of unknown function  | 267  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2516 | conserved protein of unknown function  | 411  | 24  | 4.2  | 0.6 | 5   | 0.9  | 0.2  | 0.3 |
| DAMO_2517 | conserved protein of unknown function  | 414  | 21  | 3.7  | 0.5 | 24  | 4.2  | 0.9  | 1.8 |
| DAMO_2518 | Indole-3-pyruvate decarboxylase (Indolepyruvate decarboxylase)                       | 1614 | 99  | 4.4  | 0.6 | 27  | 1.2  | 0.3  | 0.4 |
| DAMO_2519 | ATPase   | 1281 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2520 | conserved protein of unknown function  | 717  | 141 | 14.2 | 2.0 | 50  | 5.0  | 1.1  | 0.6 |
| DAMO_2521 | putative PilT protein-like   | 369  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2522 | protein of unknown function  | 261  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2523 | Ketohexokinase (Hepatic fructokinase)  | 906  | 10  | 0.8  | 0.1 | 3   | 0.2  | 0.1  | 0.5 |
| DAMO_2524 | conserved protein of unknown function  | 273  | 11  | 2.9  | 0.4 | 1   | 0.3  | 0.1  | 0.1 |
| DAMO_2525 | conserved protein of unknown function  | 240  | 34  | 10.2 | 1.4 | 117 | 35.1 | 7.7  | 5.4 |
| DAMO_2526 | putative endonuclease 4 (Endonuclease IV   | 891  | 22  | 1.8  | 0.2 | 3   | 0.2  | 0.1  | 0.2 |
| DAMO_2527 | Cell division ABC transpoter (ATP-binding protein)                                   | 663  | 215 | 23.3 | 3.3 | 84  | 9.1  | 2.0  | 0.6 |
| DAMO_2528 | putative Cell division protein FtsX  | 897  | 36  | 2.9  | 0.4 | 12  | 1.0  | 0.2  | 0.5 |
| DAMO_2529 | exported protein of unknown function   | 1236 | 43  | 2.5  | 0.3 | 9   | 0.5  | 0.1  | 0.3 |
| DAMO_2530 | Carboxy-terminal-processing protease precursor (C- terminal-processing protease)     | 1341 | 126 | 6.8  | 0.9 | 39  | 2.1  | 0.5  | 0.5 |
| DAMO_2531 | putative O-sialoglycoprotein endopeptidase, with actin-like ATPase domain (ygjD,gcp) | 1089 | 31  | 2.0  | 0.3 | 9   | 0.6  | 0.1  | 0.5 |
| DAMO_2532 | Peptide deformylase (PDF) (Polypeptide deformylase)                                  | 510  | 58  | 8.2  | 1.1 | 10  | 1.4  | 0.3  | 0.3 |
| DAMO_2533 | putative PpiC-type peptidyl-prolyl cis-trans isomerase                               | 1056 | 59  | 4.0  | 0.6 | 15  | 1.0  | 0.2  | 0.4 |
| DAMO_2534 | Transcription-repair-coupling factor (TRCF) (ATP- dependent helicase mfd)            | 3459 | 211 | 4.4  | 0.6 | 39  | 0.8  | 0.2  | 0.3 |
| DAMO_2535 | Cytidyltransferase-related domain  | 492  | 11  | 1.6  | 0.2 | 1   | 0.1  | 0.0  | 0.1 |
| DAMO_2536 | protein of unknown function  | 261  | 27  | 7.4  | 1.0 | 4   | 1.1  | 0.2  | 0.2 |

|           |   |      |      |       |       |      |        |       |     |
|-----------|---|------|------|-------|-------|------|--------|-------|-----|
| DAMO_2537 | exported protein of unknown function  | 675  | 32   | 3.4   | 0.5   | 8    | 0.9    | 0.2   | 0.4 |
| DAMO_2538 | protein of unknown function   | 357  | 3    | 0.6   | 0.1   | 3    | 0.6    | 0.1   | 1.6 |
| DAMO_2539 | membrane protein of unknown function  | 1437 | 33   | 1.7   | 0.2   | 15   | 0.8    | 0.2   | 0.7 |
| DAMO_2540 | Putative Multidrug efflux transporter, AcrB/AcrD/AcrF family protein  | 3114 | 444  | 10.3  | 1.4   | 648  | 15.0   | 3.3   | 2.3 |
| DAMO_2541 | protein of unknown function   | 1248 | 251  | 14.5  | 2.0   | 227  | 13.1   | 2.9   | 1.4 |
| DAMO_2542 | protein of unknown function   | 387  | 74   | 13.8  | 1.9   | 27   | 5.0    | 1.1   | 0.6 |
| DAMO_2543 | protein of unknown function   | 204  | 21   | 7.4   | 1.0   | 12   | 4.2    | 0.9   | 0.9 |
| DAMO_2544 | Phosphoribosylformylglycinamide cyclo-ligase synthase)  | 1110 | 142  | 9.2   | 1.3   | 19   | 1.2    | 0.3   | 0.2 |
| DAMO_2545 | exported protein of unknown function  | 1293 | 0    | 0.0   | 0.0   | 0    | 0.0    | 0.0   | —   |
| DAMO_2546 | Similarity  | 225  | 62   | 19.8  | 2.8   | 13   | 4.2    | 0.9   | 0.3 |
| DAMO_2547 | conserved protein of unknown function   | 240  | 13   | 3.9   | 0.5   | 1    | 0.3    | 0.1   | 0.1 |
| DAMO_2548 | protein of unknown function   | 225  | 1    | 0.3   | 0.0   | 1    | 0.3    | 0.1   | 1.6 |
| DAMO_2549 | PilT protein-like (fragment)  | 402  | 1    | 0.2   | 0.0   | 1    | 0.2    | 0.0   | 1.6 |
| DAMO_2550 | protein of unknown function   | 312  | 44   | 10.2  | 1.4   | 6    | 1.4    | 0.3   | 0.2 |
| DAMO_2551 | 3-hydroxybutyryl-CoA dehydrogenas   | 888  | 89   | 7.2   | 1.0   | 27   | 2.2    | 0.5   | 0.5 |
| DAMO_2552 | putative polynucleotide enzyme with nucleotide triphosphate hydrolase domain                                  | 1272 | 145  | 8.2   | 1.1   | 53   | 3.0    | 0.7   | 0.6 |
| DAMO_2553 | Orotidine 5'-phosphate decarboxylase (OMP decarboxylase) (OMPDCase) (OMPdecase)                               | 729  | 85   | 8.4   | 1.2   | 9    | 0.9    | 0.2   | 0.2 |
| DAMO_2554 | protein of unknown function   | 1260 | 104  | 5.9   | 0.8   | 42   | 2.4    | 0.5   | 0.6 |
| DAMO_2555 | exported protein of unknown function  | 396  | 11   | 2.0   | 0.3   | 0    | 0.0    | 0.0   | 0.0 |
| DAMO_2556 | protein of unknown function   | 201  | 9    | 3.2   | 0.4   | 3    | 1.1    | 0.2   | 0.5 |
| DAMO_2557 | protein of unknown function   | 231  | 0    | 0.0   | 0.0   | 0    | 0.0    | 0.0   | —   |
| DAMO_2558 | glycogen synthase   | 1467 | 69   | 3.4   | 0.5   | 9    | 0.4    | 0.1   | 0.2 |
| DAMO_2559 | protein of unknown function   | 186  | 170  | 65.8  | 9.2   | 10   | 3.9    | 0.9   | 0.1 |
| DAMO_2560 | protein of unknown function   | 207  | 2280 | 793.0 | 110.5 | 2966 | 1031.7 | 227.3 | 2.1 |
| DAMO_2561 | trans-translation protein, binds tmRNA and tRN  | 474  | 74   | 11.2  | 1.6   | 26   | 3.9    | 0.9   | 0.6 |
| DAMO_2562 | DNA-binding protein HU-beta (NS1) (HU-1)  | 273  | 1446 | 381.4 | 53.1  | 579  | 152.7  | 33.6  | 0.6 |
| DAMO_2563 | conserved protein of unknown function   | 528  | 10   | 1.4   | 0.2   | 4    | 0.5    | 0.1   | 0.6 |
| DAMO_2564 | Thiamine-phosphate pyrophosphorylase  | 570  | 15   | 1.9   | 0.3   | 8    | 1.0    | 0.2   | 0.8 |
| DAMO_2565 | thiamine biosynthesis protein ThiG  | 810  | 96   | 8.5   | 1.2   | 58   | 5.2    | 1.1   | 1.0 |
| DAMO_2566 | thiamine biosynthesis protein ThiS  | 207  | 0    | 0.0   | 0.0   | 2    | 0.7    | 0.2   | —   |
| DAMO_2567 | putative enoyl-CoA hydratase  | 804  | 33   | 3.0   | 0.4   | 11   | 1.0    | 0.2   | 0.5 |
| DAMO_2568 | conserved protein of unknown function   | 756  | 66   | 6.3   | 0.9   | 19   | 1.8    | 0.4   | 0.5 |
| DAMO_2569 | conserved membrane protein of unknown function  | 1206 | 123  | 7.3   | 1.0   | 11   | 0.7    | 0.1   | 0.1 |
| DAMO_2570 | conserved membrane protein of unknown function  | 882  | 68   | 5.6   | 0.8   | 12   | 1.0    | 0.2   | 0.3 |
| DAMO_2571 | Sodium channel protein type 11 subunit alpha neuron sodium channel 2) (NaN) (fragment)                        | 168  | 3    | 1.3   | 0.2   | 0    | 0.0    | 0.0   | —   |
| DAMO_2572 | Type I antifreeze protein   | 282  | 41   | 10.5  | 1.5   | 18   | 4.6    | 1.0   | 0.7 |
| DAMO_2573 | exported protein of unknown function  | 108  | 0    | 0.0   | 0.0   | 0    | 0.0    | 0.0   | —   |
| DAMO_2574 | conserved protein of unknown function   | 783  | 75   | 6.9   | 1.0   | 10   | 0.9    | 0.2   | 0.2 |
| DAMO_2575 | putative 5-methylthioadenosine/S-adenosylhomocysteine deaminase (MTA/SAH deaminase)                           | 1278 | 21   | 1.2   | 0.2   | 4    | 0.2    | 0.0   | 0.3 |
| DAMO_2576 | putative molybdopterin-guanine dinucleotide biosynthesis protein A  | 612  | 42   | 4.9   | 0.7   | 28   | 3.3    | 0.7   | 1.1 |
| DAMO_2577 | DNA-directed RNA polymerase subunit omega (RNAP omega subunit) (Transcriptase subunit omega) (RNA polymerase) | 447  | 45   | 7.2   | 1.0   | 28   | 4.5    | 1.0   | 1.0 |
| DAMO_2578 | Guanylate kinase (GMP kinase)   | 609  | 47   | 5.6   | 0.8   | 29   | 3.4    | 0.8   | 1.0 |
| DAMO_2579 | conserved protein of unknown function   | 285  | 100  | 25.3  | 3.5   | 53   | 13.4   | 3.0   | 0.8 |
| DAMO_2580 | conserved hypothetical protein  | 882  | 58   | 4.7   | 0.7   | 13   | 1.1    | 0.2   | 0.4 |
| DAMO_2581 | DNA mismatch repair protein MutS-like   | 1635 | 80   | 3.5   | 0.5   | 114  | 5.0    | 1.1   | 2.3 |
| DAMO_2582 | conserved protein of unknown function   | 288  | 0    | 0.0   | 0.0   | 0    | 0.0    | 0.0   | —   |
| DAMO_2583 | conserved protein of unknown function   | 270  | 0    | 0.0   | 0.0   | 0    | 0.0    | 0.0   | —   |
| DAMO_2584 | protein of unknown function   | 243  | 0    | 0.0   | 0.0   | 0    | 0.0    | 0.0   | —   |
| DAMO_2585 | conserved protein of unknown function   | 336  | 10   | 2.1   | 0.3   | 1    | 0.2    | 0.0   | 0.2 |
| DAMO_2586 | Putative formyltetrahydrofolate deformylas  | 861  | 82   | 6.9   | 1.0   | 28   | 2.3    | 0.5   | 0.5 |
| DAMO_2587 | Glutamate synthase (NADPH)  | 1503 | 1049 | 50.3  | 7.0   | 962  | 46.1   | 10.2  | 1.5 |
| DAMO_2588 | putative dihydroorotate dehydrogenase electron transfer subunit (modular protein)                             | 1647 | 863  | 37.7  | 5.3   | 714  | 31.2   | 6.9   | 1.3 |
| DAMO_2589 | Methyltransferase type 11   | 717  | 9    | 0.9   | 0.1   | 1    | 0.1    | 0.0   | 0.2 |
| DAMO_2590 | protein of unknown function   | 468  | 3    | 0.5   | 0.1   | 1    | 0.2    | 0.0   | 0.5 |
| DAMO_2591 | exported protein of unknown function  | 1272 | 40   | 2.3   | 0.3   | 5    | 0.3    | 0.1   | 0.2 |
| DAMO_2592 | conserved protein of unknown function   | 885  | 50   | 4.1   | 0.6   | 2    | 0.2    | 0.0   | 0.1 |



|           |  |      |     |      |     |     |      |      |     |
|-----------|--|------|-----|------|-----|-----|------|------|-----|
| DAMO_2593 | putative Histidine kinase  | 1716 | 26  | 1.1  | 0.2 | 3   | 0.1  | 0.0  | 0.2 |
| DAMO_2594 | putative response regulator in two-component regulatory system (CheY-like protein) | 372  | 3   | 0.6  | 0.1 | 3   | 0.6  | 0.1  | 1.6 |
| DAMO_2595 | putative DNA-binding response regulator in two-component system                    | 1386 | 42  | 2.2  | 0.3 | 13  | 0.7  | 0.1  | 0.5 |
| DAMO_2596 | protein of unknown function  | 192  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2597 | protein of unknown function  | 258  | 22  | 6.1  | 0.9 | 1   | 0.3  | 0.1  | 0.1 |
| DAMO_2598 | quinolinate synthetase A   | 963  | 580 | 43.4 | 6.0 | 85  | 6.4  | 1.4  | 0.2 |
| DAMO_2599 | quinolinate phosphoribosyltransferas   | 864  | 57  | 4.8  | 0.7 | 8   | 0.7  | 0.1  | 0.2 |
| DAMO_2600 | L-aspartate oxidase (Quinolinate synthetase B)                                     | 1554 | 187 | 8.7  | 1.2 | 25  | 1.2  | 0.3  | 0.2 |
| DAMO_2601 | Alcohol dehydrogenase, zinc-binding domain protein                                 | 1032 | 192 | 13.4 | 1.9 | 23  | 1.6  | 0.4  | 0.2 |
| DAMO_2602 | Glycerophosphodiester phosphodiesterase  | 768  | 30  | 2.8  | 0.4 | 8   | 0.8  | 0.2  | 0.4 |
| DAMO_2603 | protein of unknown function  | 315  | 1   | 0.2  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2604 | Long-chain-fatty-acid--CoA ligase (Long-chain acyl-CoA synthetase)                 | 1758 | 194 | 7.9  | 1.1 | 40  | 1.6  | 0.4  | 0.3 |
| DAMO_2605 | putative Protein export membrane protein, SecD/SecF family                         | 2907 | 300 | 7.4  | 1.0 | 103 | 2.6  | 0.6  | 0.5 |
| DAMO_2606 | conserved exported protein of unknown function                                     | 633  | 127 | 14.4 | 2.0 | 56  | 6.4  | 1.4  | 0.7 |
| DAMO_2607 | putative inositol-3-phosphate synthase   | 1374 | 118 | 6.2  | 0.9 | 52  | 2.7  | 0.6  | 0.7 |
| DAMO_2608 | membrane protein of unknown function   | 1200 | 16  | 1.0  | 0.1 | 4   | 0.2  | 0.1  | 0.4 |
| DAMO_2609 | putative Oxidoreductase domain protein   | 1083 | 5   | 0.3  | 0.0 | 0   | 0.0  | 0.0  | 0.0 |
| DAMO_2610 | Aminotransferase   | 1362 | 85  | 4.5  | 0.6 | 11  | 0.6  | 0.1  | 0.2 |
| DAMO_2611 | conserved protein of unknown function  | 873  | 14  | 1.2  | 0.2 | 4   | 0.3  | 0.1  | 0.5 |
| DAMO_2612 | putative Nucleotidyl transferase   | 639  | 48  | 5.4  | 0.8 | 7   | 0.8  | 0.2  | 0.2 |
| DAMO_2613 | putative HAD-superfamily hydrolase, subfamily IA, variant 3                        | 693  | 39  | 4.1  | 0.6 | 17  | 1.8  | 0.4  | 0.7 |
| DAMO_2614 | membrane protein of unknown function   | 1017 | 22  | 1.6  | 0.2 | 13  | 0.9  | 0.2  | 0.9 |
| DAMO_2615 | protein of unknown function  | 1554 | 234 | 10.8 | 1.5 | 50  | 2.3  | 0.5  | 0.3 |
| DAMO_2616 | protein of unknown function  | 1569 | 415 | 19.0 | 2.7 | 83  | 3.8  | 0.8  | 0.3 |
| DAMO_2617 | conserved protein of unknown function  | 594  | 78  | 9.5  | 1.3 | 4   | 0.5  | 0.1  | 0.1 |
| DAMO_2618 | putative competence-damage inducible protein                                       | 1341 | 141 | 7.6  | 1.1 | 29  | 1.6  | 0.3  | 0.3 |
| DAMO_2619 | putative Diguanylate kinase  | 1263 | 33  | 1.9  | 0.3 | 30  | 1.7  | 0.4  | 1.4 |
| DAMO_2620 | conserved protein of unknown function  | 492  | 26  | 3.8  | 0.5 | 12  | 1.8  | 0.4  | 0.7 |
| DAMO_2621 | putative Outer-membrane lipoprotein carrier protein precursor                      | 723  | 37  | 3.7  | 0.5 | 10  | 1.0  | 0.2  | 0.4 |
| DAMO_2622 | DNA translocase  | 2292 | 111 | 3.5  | 0.5 | 86  | 2.7  | 0.6  | 1.2 |
| DAMO_2623 | Ribonuclease J 1 (RNase J1)  | 1647 | 131 | 5.7  | 0.8 | 34  | 1.5  | 0.3  | 0.4 |
| DAMO_2624 | ATP-dependent protease La  | 2571 | 272 | 7.6  | 1.1 | 75  | 2.1  | 0.5  | 0.4 |
| DAMO_2625 | glucose-1-phosphate uridylyltransferase  | 906  | 138 | 11.0 | 1.5 | 62  | 4.9  | 1.1  | 0.7 |
| DAMO_2626 | OmpA/MotB precursor  | 750  | 288 | 27.6 | 3.9 | 60  | 5.8  | 1.3  | 0.3 |
| DAMO_2627 | protein of unknown function  | 303  | 1   | 0.2  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2628 | protein of unknown function  | 588  | 14  | 1.7  | 0.2 | 5   | 0.6  | 0.1  | 0.6 |
| DAMO_2629 | toluene transporter subunit: membrane component of ABC superfamily                 | 744  | 117 | 11.3 | 1.6 | 57  | 5.5  | 1.2  | 0.8 |
| DAMO_2630 | Putative ABC transporter (ATP-binding protein)                                     | 741  | 35  | 3.4  | 0.5 | 9   | 0.9  | 0.2  | 0.4 |
| DAMO_2631 | putative Mce family protein  | 960  | 46  | 3.5  | 0.5 | 15  | 1.1  | 0.2  | 0.5 |
| DAMO_2632 | Glycoside hydrolase, family 57   | 2484 | 88  | 2.6  | 0.4 | 33  | 1.0  | 0.2  | 0.6 |
| DAMO_2633 | CBS domain protein   | 1323 | 103 | 5.6  | 0.8 | 79  | 4.3  | 0.9  | 1.2 |
| DAMO_2634 | exported protein of unknown function   | 300  | 50  | 12.0 | 1.7 | 22  | 5.3  | 1.2  | 0.7 |
| DAMO_2635 | Conserved protein of unknown function; pmo   | 774  | 292 | 27.2 | 3.8 | 508 | 47.3 | 10.4 | 2.8 |
| DAMO_2636 | protein of unknown function  | 273  | 1   | 0.3  | 0.0 | 3   | 0.8  | 0.2  | 4.7 |
| DAMO_2637 | Guanine deaminase  | 1326 | 47  | 2.6  | 0.4 | 11  | 0.6  | 0.1  | 0.4 |
| DAMO_2638 | conserved protein of unknown function  | 1173 | 318 | 19.5 | 2.7 | 134 | 8.2  | 1.8  | 0.7 |
| DAMO_2639 | exported protein of unknown function   | 195  | 7   | 2.6  | 0.4 | 2   | 0.7  | 0.2  | 0.5 |
| DAMO_2640 | protein of unknown function  | 204  | 1   | 0.4  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2641 | HEAT domain protein repeat-containing protei                                       | 183  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2642 | conserved protein of unknown function  | 345  | 33  | 6.9  | 1.0 | 4   | 0.8  | 0.2  | 0.2 |
| DAMO_2643 | protein of unknown function  | 207  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2644 | glycine tRNA synthetase, alpha subunit   | 903  | 196 | 15.6 | 2.2 | 18  | 1.4  | 0.3  | 0.1 |
| DAMO_2645 | glycine tRNA synthetase, beta subunit  | 2070 | 310 | 10.8 | 1.5 | 43  | 1.5  | 0.3  | 0.2 |
| DAMO_2646 | putative Orotate phosphoribosyltransferase (OPRT                                   | 651  | 61  | 6.7  | 0.9 | 5   | 0.6  | 0.1  | 0.1 |
| DAMO_2647 | protein of unknown function  | 519  | 1   | 0.1  | 0.0 | 1   | 0.1  | 0.0  | 1.6 |
| DAMO_2648 | exported protein of unknown function   | 729  | 137 | 13.5 | 1.9 | 133 | 13.1 | 2.9  | 1.5 |

|           |  |      |     |      |     |     |      |      |     |
|-----------|--|------|-----|------|-----|-----|------|------|-----|
| DAMO_2649 | Transcriptional coactivator/pterin dehydratase   | 372  | 158 | 30.6 | 4.3 | 257 | 49.7 | 11.0 | 2.6 |
| DAMO_2650 | fructose 1,6-bisphosphatase II   | 1014 | 206 | 14.6 | 2.0 | 37  | 2.6  | 0.6  | 0.3 |
| DAMO_2651 | Transketolase (TK)   | 2010 | 134 | 4.8  | 0.7 | 39  | 1.4  | 0.3  | 0.5 |
| DAMO_2652 | Glyceraldehyde-3-phosphate dehydrogenas  | 1059 | 66  | 4.5  | 0.6 | 4   | 0.3  | 0.1  | 0.1 |
| DAMO_2653 | Putative Phosphoribulokinase/uridine kinase family   | 987  | 300 | 21.9 | 3.0 | 123 | 9.0  | 2.0  | 0.6 |
| DAMO_2654 | protein of unknown function  | 195  | 3   | 1.1  | 0.2 | 0   | 0.0  | 0.0  | 0.0 |
| DAMO_2655 | putative 6-pyruvoyl tetrahydropterin synthase  | 489  | 13  | 1.9  | 0.3 | 2   | 0.3  | 0.1  | 0.2 |
| DAMO_2656 | putative histidine biosynthesis protein  | 744  | 291 | 28.2 | 3.9 | 46  | 4.5  | 1.0  | 0.2 |
| DAMO_2657 | conserved protein of unknown function  | 1050 | 38  | 2.6  | 0.4 | 5   | 0.3  | 0.1  | 0.2 |
| DAMO_2658 | putative tetrahydromethanopterin biosynthesis protein  | 1035 | 66  | 4.6  | 0.6 | 14  | 1.0  | 0.2  | 0.3 |
| DAMO_2659 | putative conserved AdoMet-dependent methyltransferase with RNA interaction domain              | 2241 | 400 | 12.9 | 1.8 | 161 | 5.2  | 1.1  | 0.6 |
| DAMO_2660 | conserved protein of unknown function  | 963  | 22  | 1.6  | 0.2 | 3   | 0.2  | 0.0  | 0.2 |
| DAMO_2661 | transposase  | 204  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2662 | conserved protein of unknown function  | 1569 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2663 | protein of unknown function  | 309  | 3   | 0.7  | 0.1 | 0   | 0.0  | 0.0  | —   |
| DAMO_2664 | putative Yga2E   | 837  | 145 | 12.5 | 1.7 | 69  | 5.9  | 1.3  | 0.8 |
| DAMO_2665 | Transcriptional regulator, Cro/CI family   | 246  | 57  | 16.7 | 2.3 | 62  | 18.1 | 4.0  | 1.7 |
| DAMO_2666 | protein of unknown function  | 216  | 1   | 0.3  | 0.0 | 3   | 1.0  | 0.2  | 4.7 |
| DAMO_2668 | protein of unknown function  | 894  | 185 | 14.9 | 2.1 | 134 | 10.8 | 2.4  | 1.1 |
| DAMO_2667 | DNA adenine methylase Dam  | 255  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2669 | exported protein of unknown function   | 213  | 1   | 0.3  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2670 | TPR repeat (fragment)  | 732  | 16  | 1.6  | 0.2 | 5   | 0.5  | 0.1  | 0.5 |
| DAMO_2671 | TPR repeat (fragment)  | 1257 | 40  | 2.3  | 0.3 | 41  | 2.3  | 0.5  | 1.6 |
| DAMO_2672 | protein of unknown function  | 237  | 14  | 4.3  | 0.6 | 0   | 0.0  | 0.0  | 0.0 |
| DAMO_2673 | putative Delta 1-pyrroline-5-carboxylate synthetase  | 681  | 292 | 30.9 | 4.3 | 115 | 12.2 | 2.7  | 0.6 |
| DAMO_2674 | conserved protein of unknown function  | 711  | 209 | 21.2 | 2.9 | 26  | 2.6  | 0.6  | 0.2 |
| DAMO_2675 | conserved protein of unknown function  | 246  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2676 | conserved protein of unknown function  | 435  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2677 | protein of unknown function  | 309  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2679 | conserved protein of unknown function  | 264  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2678 | protein of unknown function  | 750  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2680 | protein of unknown function  | 336  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2681 | protein of unknown function  | 189  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2682 | conserved protein of unknown function  | 1446 | 193 | 9.6  | 1.3 | 40  | 2.0  | 0.4  | 0.3 |
| DAMO_2683 | exported protein of unknown function   | 183  | 5   | 2.0  | 0.3 | 0   | 0.0  | 0.0  | —   |
| DAMO_2684 | conserved protein of unknown function  | 252  | 12  | 3.4  | 0.5 | 2   | 0.6  | 0.1  | 0.3 |
| DAMO_2685 | exported protein of unknown function   | 390  | 46  | 8.5  | 1.2 | 5   | 0.9  | 0.2  | 0.2 |
| DAMO_2686 | protein of unknown function  | 315  | 4   | 0.9  | 0.1 | 0   | 0.0  | 0.0  | —   |
| DAMO_2687 | Prevent-host-death protein   | 279  | 1   | 0.3  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2688 | putative G-protein coupled receptor 124 precursor  | 210  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0  | —   |
| DAMO_2689 | Redox-sensing transcriptional repressor rex  | 651  | 45  | 5.0  | 0.7 | 4   | 0.4  | 0.1  | 0.1 |
| DAMO_2690 | NADH-quinone oxidoreductase chain N (NADH dehydrogenase I, chain N) (NDH-1, chain N)           | 1503 | 47  | 2.3  | 0.3 | 13  | 0.6  | 0.1  | 0.4 |
| DAMO_2691 | NADH-quinone oxidoreductase chain M (NADH dehydrogenase I, chain M) (NDH-1, chain M)           | 1620 | 59  | 2.6  | 0.4 | 15  | 0.7  | 0.1  | 0.4 |
| DAMO_2692 | NADH-quinone oxidoreductase chain L (NADH dehydrogenase I, chain L) (NDH-1, chain L)           | 1893 | 36  | 1.4  | 0.2 | 18  | 0.7  | 0.2  | 0.8 |
| DAMO_2693 | NADH-quinone oxidoreductase chain K (NADH dehydrogenase I, chain K) (NDH-1, chain K)           | 312  | 15  | 3.5  | 0.5 | 6   | 1.4  | 0.3  | 0.6 |
| DAMO_2694 | NADH-quinone oxidoreductase chain J (NADH dehydrogenase I, chain J) (NDH-1, chain J)           | 507  | 14  | 2.0  | 0.3 | 8   | 1.1  | 0.3  | 0.9 |
| DAMO_2695 | NADH-quinone oxidoreductase chain H (NADH dehydrogenase I, chain H) (NDH-1, chain H)           | 987  | 50  | 3.6  | 0.5 | 5   | 0.4  | 0.1  | 0.2 |
| DAMO_2696 | NADH-quinone oxidoreductase chain F (NADH dehydrogenase I, chain F) (NDH-1, chain F)           | 1284 | 52  | 2.9  | 0.4 | 6   | 0.3  | 0.1  | 0.2 |
| DAMO_2697 | NADH-quinone oxidoreductase subunit E 2 (NADH dehydrogenase I subunit E 2) (NDH-1 subunit E 2) | 516  | 10  | 1.4  | 0.2 | 0   | 0.0  | 0.0  | —   |
| DAMO_2698 | NADH-quinone oxidoreductase chain D (NADH dehydrogenase I, chain D) (NDH-1, chain D)           | 1173 | 85  | 5.2  | 0.7 | 28  | 1.7  | 0.4  | 0.5 |
| DAMO_2699 | NADH-quinone oxidoreductase  | 507  | 35  | 5.0  | 0.7 | 6   | 0.9  | 0.2  | 0.3 |
| DAMO_2700 | NADH-quinone oxidoreductase chain A (NADH dehydrogenase I, chain A) (NDH-1, chain A)           | 360  | 112 | 22.4 | 3.1 | 188 | 37.6 | 8.3  | 2.7 |
| DAMO_2701 | ATP synthase subunit C, membrane-bound, F0 sector; DCCD-binding (modular protein)              | 381  | 61  | 11.5 | 1.6 | 21  | 4.0  | 0.9  | 0.5 |
| DAMO_2702 | ATP synthase A chain   | 720  | 130 | 13.0 | 1.8 | 53  | 5.3  | 1.2  | 0.6 |
| DAMO_2703 | conserved exported protein of unknown function   | 216  | 28  | 9.3  | 1.3 | 44  | 14.7 | 3.2  | 2.5 |
| DAMO_2704 | NADH-quinone oxidoreductase chain N (NADH dehydrogenase I, chain N) (NDH-1, chain N)           | 1452 | 346 | 17.2 | 2.4 | 123 | 6.1  | 1.3  | 0.6 |

|           |   |      |      |       |      |     |       |      |     |
|-----------|---|------|------|-------|------|-----|-------|------|-----|
| DAMO_2705 | NADH-quinone oxidoreductase chain M (NADH dehydrogenase I, chain M) (NDH-1, chain M)                        | 1665 | 392  | 17.0  | 2.4  | 115 | 5.0   | 1.1  | 0.5 |
| DAMO_2706 | NADH-quinone oxidoreductase chain L (NADH dehydrogenase I, chain L) (NDH-1, chain L)                        | 2037 | 208  | 7.4   | 1.0  | 80  | 2.8   | 0.6  | 0.6 |
| DAMO_2707 | NADH-quinone oxidoreductase chain K (NADH dehydrogenase I, chain K) (NDH-1, chain K)                        | 309  | 37   | 8.6   | 1.2  | 12  | 2.8   | 0.6  | 0.5 |
| DAMO_2708 | NAD(P)H-quinone oxidoreductase chain 6 (NAD(P)H dehydrogenase I, chain 6) (NDH-1, chain 6)                  | 513  | 38   | 5.3   | 0.7  | 16  | 2.2   | 0.5  | 0.7 |
| DAMO_2709 | NADH-quinone oxidoreductase chain H (NADH dehydrogenase I, chain H) (NDH-1, chain H) (modular protein)      | 1176 | 94   | 5.8   | 0.8  | 22  | 1.3   | 0.3  | 0.4 |
| DAMO_2710 | NADH-quinone oxidoreductase chain D (NADH dehydrogenase I, chain D) (NDH-1, chain D)                        | 1134 | 138  | 8.8   | 1.2  | 48  | 3.0   | 0.7  | 0.6 |
| DAMO_2711 | NAD(P)H-quinone oxidoreductase subunit J (NAD(P)H dehydrogenase I, subunit J) (NDH-1, subunit J) (fragment) | 465  | 68   | 10.5  | 1.5  | 27  | 4.2   | 0.9  | 0.6 |
| DAMO_2712 | NADH-quinone oxidoreductase chain A (NADH dehydrogenase I, chain A) (NDH-1, chain A)                        | 360  | 47   | 9.4   | 1.3  | 9   | 1.8   | 0.4  | 0.3 |
| DAMO_2713 | protein of unknown function   | 225  | 65   | 20.8  | 2.9  | 12  | 3.8   | 0.8  | 0.3 |
| DAMO_2714 | putative Cytochrome c heme-binding site   | 354  | 26   | 5.3   | 0.7  | 14  | 2.8   | 0.6  | 0.9 |
| DAMO_2715 | Glutamate-1-semialdehyde 2,1-aminomutase (GSA   | 1320 | 139  | 7.6   | 1.1  | 126 | 6.9   | 1.5  | 1.4 |
| DAMO_2716 | Delta-aminolevulinic acid dehydratase   | 981  | 190  | 13.9  | 1.9  | 135 | 9.9   | 2.2  | 1.1 |
| DAMO_2717 | exported protein of unknown function  | 2298 | 37   | 1.2   | 0.2  | 1   | 0.0   | 0.0  | —   |
| DAMO_2718 | exported protein of unknown function  | 306  | 15   | 3.5   | 0.5  | 5   | 1.2   | 0.3  | 0.5 |
| DAMO_2719 | protein of unknown function   | 117  | 85   | 52.3  | 7.3  | 0   | 0.0   | 0.0  | —   |
| DAMO_2720 | conserved protein of unknown function   | 438  | 40   | 6.6   | 0.9  | 7   | 1.2   | 0.3  | 0.3 |
| DAMO_2721 | conserved protein of unknown function   | 288  | 83   | 20.8  | 2.9  | 113 | 28.3  | 6.2  | 2.2 |
| DAMO_2722 | Transcriptional regulator, AbrB famil   | 252  | 55   | 15.7  | 2.2  | 26  | 7.4   | 1.6  | 0.7 |
| DAMO_2723 | PilT protein-like   | 408  | 1    | 0.2   | 0.0  | 1   | 0.2   | 0.0  | 1.6 |
| DAMO_2724 | protein of unknown function   | 513  | 7    | 1.0   | 0.1  | 3   | 0.4   | 0.1  | 0.7 |
| DAMO_2725 | putative transcriptional regulator, AbrB family   | 228  | 62   | 19.6  | 2.7  | 34  | 10.7  | 2.4  | 0.9 |
| DAMO_2726 | Death-on-curing family protein  | 387  | 17   | 3.2   | 0.4  | 6   | 1.1   | 0.2  | 0.6 |
| DAMO_2728 | protein of unknown function   | 237  | 7    | 2.1   | 0.3  | 0   | 0.0   | 0.0  | —   |
| DAMO_2727 | protein of unknown function   | 249  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_2729 | protein of unknown function   | 207  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_2730 | protein of unknown function   | 357  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_2731 | protein of unknown function   | 159  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_2732 | protein of unknown function   | 189  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_2733 | protein of unknown function   | 360  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_2734 | CRISPR-associated protein Cas2  | 291  | 2    | 0.5   | 0.1  | 0   | 0.0   | 0.0  | —   |
| DAMO_2735 | CRISPR-associated protein Cas1/Cas4   | 1638 | 19   | 0.8   | 0.1  | 3   | 0.1   | 0.0  | 0.2 |
| DAMO_2736 | conserved protein of unknown function   | 1626 | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_2737 | conserved protein of unknown function   | 999  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_2738 | conserved protein of unknown function   | 2160 | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_2739 | conserved protein of unknown function   | 2580 | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_2740 | protein of unknown function   | 234  | 26   | 8.0   | 1.1  | 7   | 2.2   | 0.5  | 0.4 |
| DAMO_2741 | conserved protein of unknown function   | 228  | 2    | 0.6   | 0.1  | 0   | 0.0   | 0.0  | —   |
| DAMO_2743 | protein of unknown function   | 435  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_2742 | conserved protein of unknown function   | 687  | 1    | 0.1   | 0.0  | 1   | 0.1   | 0.0  | 1.6 |
| DAMO_2744 | protein of unknown function   | 615  | 4    | 0.5   | 0.1  | 3   | 0.4   | 0.1  | 1.2 |
| DAMO_2745 | protein of unknown function   | 162  | 67   | 29.8  | 4.1  | 44  | 19.6  | 4.3  | 1.0 |
| DAMO_2746 | Conserved membrane protein  | 435  | 247  | 40.9  | 5.7  | 152 | 25.2  | 5.5  | 1.0 |
| DAMO_2747 | putative Helix-turn-helix, type 11 domain protein   | 990  | 24   | 1.7   | 0.2  | 2   | 0.1   | 0.0  | 0.1 |
| DAMO_2748 | conserved protein of unknown function   | 405  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_2749 | conserved protein of unknown function   | 207  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_2750 | PHP C-terminal domain protein   | 1734 | 169  | 7.0   | 1.0  | 19  | 0.8   | 0.2  | 0.2 |
| DAMO_2751 | UDP-3-O-acyl N-acetylglucosamine deacetylase  | 924  | 285  | 22.2  | 3.1  | 72  | 5.6   | 1.2  | 0.4 |
| DAMO_2752 | protein of unknown function   | 489  | 2    | 0.3   | 0.0  | 3   | 0.4   | 0.1  | 2.4 |
| DAMO_2753 | RNase H   | 483  | 15   | 2.2   | 0.3  | 6   | 0.9   | 0.2  | 0.6 |
| DAMO_2754 | protein of unknown function   | 705  | 16   | 1.6   | 0.2  | 6   | 0.6   | 0.1  | 0.6 |
| DAMO_2755 | RNA polymerase sigma factor rpoD (Sigma-80)   | 1965 | 509  | 18.7  | 2.6  | 631 | 23.1  | 5.1  | 2.0 |
| DAMO_2756 | putative DNA primase  | 1845 | 287  | 11.2  | 1.6  | 107 | 4.2   | 0.9  | 0.6 |
| DAMO_2757 | putative MutS2 protein  | 2415 | 420  | 12.5  | 1.7  | 255 | 7.6   | 1.7  | 1.0 |
| DAMO_2758 | protein of unknown function   | 216  | 0    | 0.0   | 0.0  | 0   | 0.0   | 0.0  | —   |
| DAMO_2759 | conserved protein of unknown function   | 453  | 235  | 37.4  | 5.2  | 131 | 20.8  | 4.6  | 0.9 |
| DAMO_2760 | 30S ribosomal protein S21   | 198  | 1630 | 592.7 | 82.6 | 350 | 127.3 | 28.0 | 0.3 |

|           |   |      |     |      |     |      |       |      |     |
|-----------|---|------|-----|------|-----|------|-------|------|-----|
| DAMO_2761 | Peptidyl-prolyl cis-trans isomerase B (PPIase B)  | 600  | 288 | 34.6 | 4.8 | 391  | 46.9  | 10.3 | 2.1 |
| DAMO_2762 | exported protein of unknown function  | 609  | 87  | 10.3 | 1.4 | 36   | 4.3   | 0.9  | 0.7 |
| DAMO_2763 | protein of unknown function   | 174  | 0   | 0.0  | 0.0 | 0    | 0.0   | 0.0  | —   |
| DAMO_2764 | putative protease htpX homolog  | 852  | 219 | 18.5 | 2.6 | 586  | 49.5  | 10.9 | 4.2 |
| DAMO_2765 | protein of unknown function   | 384  | 181 | 33.9 | 4.7 | 155  | 29.1  | 6.4  | 1.4 |
| DAMO_2766 | protein of unknown function   | 186  | 2   | 0.8  | 0.1 | 9    | 3.5   | 0.8  | 7.1 |
| DAMO_2767 | Chaperone protein dnaJ, heat shock protei   | 1113 | 332 | 21.5 | 3.0 | 353  | 22.8  | 5.0  | 1.7 |
| DAMO_2768 | Heat shock protein Hsp20  | 453  | 398 | 63.3 | 8.8 | 917  | 145.7 | 32.1 | 3.6 |
| DAMO_2769 | Chaperone protein dnaK (Heat shock protein 70   | 1920 | 514 | 19.3 | 2.7 | 1292 | 48.5  | 10.7 | 4.0 |
| DAMO_2770 | Divalent-cation tolerance protein cutA  | 330  | 3   | 0.7  | 0.1 | 0    | 0.0   | 0.0  | —   |
| DAMO_2771 | putative Membrane-bound lytic murein transglycosylase D   | 2004 | 85  | 3.1  | 0.4 | 34   | 1.2   | 0.3  | 0.6 |
| DAMO_2772 | protein of unknown function   | 234  | 0   | 0.0  | 0.0 | 1    | 0.3   | 0.1  | —   |
| DAMO_2773 | protein of unknown function   | 237  | 0   | 0.0  | 0.0 | 0    | 0.0   | 0.0  | —   |
| DAMO_2774 | protein of unknown function   | 189  | 0   | 0.0  | 0.0 | 0    | 0.0   | 0.0  | —   |
| DAMO_2775 | Multicopper oxidase, type 2 precursor   | 2385 | 8   | 0.2  | 0.0 | 1    | 0.0   | 0.0  | 0.2 |
| DAMO_2776 | exported protein of unknown function  | 2517 | 7   | 0.2  | 0.0 | 0    | 0.0   | 0.0  | —   |
| DAMO_2777 | protein of unknown function   | 189  | 0   | 0.0  | 0.0 | 0    | 0.0   | 0.0  | —   |
| DAMO_2778 | Glucose-1-phosphate thymidyltransferas  | 1065 | 95  | 6.4  | 0.9 | 20   | 1.4   | 0.3  | 0.3 |
| DAMO_2779 | Spore coat polysaccharide biosynthesis protein spsL   | 462  | 84  | 13.1 | 1.8 | 27   | 4.2   | 0.9  | 0.5 |
| DAMO_2780 | dTDP-D-glucose 4,6-dehydratase  | 1023 | 194 | 13.7 | 1.9 | 42   | 3.0   | 0.7  | 0.3 |
| DAMO_2781 | fragment of mannose-1-phosphate guanyltransferase; putative capsular polysaccharide biosynthesis protein (part 1) | 390  | 95  | 17.5 | 2.4 | 24   | 4.4   | 1.0  | 0.4 |
| DAMO_2782 | fragment of mannose-1-phosphate guanyltransferase; putative capsular polysaccharide biosynthesis protein (part 2) | 1074 | 26  | 1.7  | 0.2 | 2    | 0.1   | 0.0  | 0.1 |
| DAMO_2783 | GDP-mannose 4,6 dehydratase (GDP-D-mannose dehydratase) (GMD) (fragment)  | 213  | 4   | 1.4  | 0.2 | 0    | 0.0   | 0.0  | —   |
| DAMO_2784 | putative sugar-nucleotide epimerase/dehydratase   | 969  | 22  | 1.6  | 0.2 | 14   | 1.0   | 0.2  | 1.0 |
| DAMO_2785 | putative branched-chain-amino-acid aminotransferase (BCAT)  | 912  | 194 | 15.3 | 2.1 | 25   | 2.0   | 0.4  | 0.2 |
| DAMO_2786 | exported protein of unknown function  | 390  | 115 | 21.2 | 3.0 | 97   | 17.9  | 3.9  | 1.3 |
| DAMO_2787 | putative thiamine biosynthesis protein thiI   | 1203 | 145 | 8.7  | 1.2 | 84   | 5.0   | 1.1  | 0.9 |
| DAMO_2788 | conserved protein of unknown function   | 339  | 4   | 0.8  | 0.1 | 6    | 1.3   | 0.3  | 2.4 |
| DAMO_2789 | putative 2-nitropropane dioxygenase   | 1389 | 378 | 19.6 | 2.7 | 86   | 4.5   | 1.0  | 0.4 |
| DAMO_2790 | Glutamine amidotransferase, class I   | 708  | 65  | 6.6  | 0.9 | 14   | 1.4   | 0.3  | 0.3 |
| DAMO_2791 | conserved protein of unknown function   | 303  | 34  | 8.1  | 1.1 | 1    | 0.2   | 0.1  | 0.0 |
| DAMO_2792 | conserved membrane protein of unknown function  | 504  | 36  | 5.1  | 0.7 | 5    | 0.7   | 0.2  | 0.2 |
| DAMO_2793 | putative response regulator in two-component reguatory system, sigma54 dependent transcriptional regulator.       | 1392 | 52  | 2.7  | 0.4 | 7    | 0.4   | 0.1  | 0.2 |
| DAMO_2794 | putative Histidine kinase   | 1539 | 70  | 3.3  | 0.5 | 18   | 0.8   | 0.2  | 0.4 |
| DAMO_2795 | protein of unknown function   | 159  | 10  | 4.5  | 0.6 | 9    | 4.1   | 0.9  | 1.4 |
| DAMO_2796 | Iron-sulfur cluster-binding protein; potential subunit of aldehyde oxidoreductase                                 | 492  | 90  | 13.2 | 1.8 | 16   | 2.3   | 0.5  | 0.3 |
| DAMO_2797 | Tungsten-containing aldehyde ferredoxin oxidoreductase  | 1809 | 384 | 15.3 | 2.1 | 171  | 6.8   | 1.5  | 0.7 |
| DAMO_2798 | putative Moad   | 303  | 27  | 6.4  | 0.9 | 7    | 1.7   | 0.4  | 0.4 |
| DAMO_2799 | conserved protein of unknown function   | 963  | 341 | 25.5 | 3.6 | 61   | 4.6   | 1.0  | 0.3 |
| DAMO_2800 | putative FAD-dependent pyridine nucleotide-disulphide oxidoreductase  | 1266 | 189 | 10.7 | 1.5 | 56   | 3.2   | 0.7  | 0.5 |
| DAMO_2801 | ThiamineS protein   | 276  | 2   | 0.5  | 0.1 | 0    | 0.0   | 0.0  | —   |
| DAMO_2802 | Bis(5'-nucleosyl)-tetrphosphatase [asymmetrical] hydrolase) (Diadenosine tetrphosphatase) (Ap4A hydrolase         | 438  | 107 | 17.6 | 2.5 | 67   | 11.0  | 2.4  | 1.0 |
| DAMO_2803 | protein of unknown function   | 318  | 162 | 36.7 | 5.1 | 146  | 33.1  | 7.3  | 1.4 |
| DAMO_2804 | Ribokinase  | 978  | 10  | 0.7  | 0.1 | 3    | 0.2   | 0.0  | 0.5 |
| DAMO_2805 | Inosine-uridine preferring nucleoside hydrolase   | 987  | 24  | 1.8  | 0.2 | 10   | 0.7   | 0.2  | 0.7 |
| DAMO_2806 | conserved protein of unknown function   | 78   | 0   | 0.0  | 0.0 | 0    | 0.0   | 0.0  | —   |
| DAMO_2807 | conserved exported protein of unknown function  | 567  | 3   | 0.4  | 0.1 | 0    | 0.0   | 0.0  | —   |
| DAMO_2808 | ErfK/YbiS/YcfS/YnhG precursor   | 873  | 17  | 1.4  | 0.2 | 2    | 0.2   | 0.0  | 0.2 |
| DAMO_2809 | protein of unknown function   | 201  | 0   | 0.0  | 0.0 | 0    | 0.0   | 0.0  | —   |
| DAMO_2810 | conserved membrane protein of unknown function  | 1539 | 80  | 3.7  | 0.5 | 13   | 0.6   | 0.1  | 0.3 |
| DAMO_2811 | protein of unknown function   | 195  | 0   | 0.0  | 0.0 | 0    | 0.0   | 0.0  | —   |
| DAMO_2812 | citrate synthase  | 1308 | 349 | 19.2 | 2.7 | 398  | 21.9  | 4.8  | 1.8 |
| DAMO_2813 | conserved protein of unknown function   | 939  | 49  | 3.8  | 0.5 | 35   | 2.7   | 0.6  | 1.1 |
| DAMO_2814 | Hypoxanthine-guanine phosphoribosyltransferas   | 552  | 49  | 6.4  | 0.9 | 12   | 1.6   | 0.3  | 0.4 |
| DAMO_2815 | putative ABC transporter, ATP-binding protein with duplicated ATPase domains                                      | 1968 | 271 | 9.9  | 1.4 | 201  | 7.4   | 1.6  | 1.2 |
| DAMO_2816 | membrane protein of unknown function  | 651  | 109 | 12.1 | 1.7 | 140  | 15.5  | 3.4  | 2.0 |

|           |  |      |     |      |      |     |      |     |     |
|-----------|--|------|-----|------|------|-----|------|-----|-----|
| DAMO_2817 | putative Histidine kinase  | 1557 | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_2818 | response regulator in two-component regulatory system with PhoR (or CreC), regulation of Pi uptake (OmpR family) | 741  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_2819 | exported protein of unknown function   | 720  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_2820 | protein of unknown function  | 180  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_2821 | exported protein of unknown function   | 312  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_2822 | exported protein of unknown function   | 1389 | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_2823 | conserved protein of unknown function  | 774  | 104 | 9.7  | 1.3  | 57  | 5.3  | 1.2 | 0.9 |
| DAMO_2824 | conserved hypothetical protein; putative iron-sulfur cluster binding protein                                     | 1191 | 105 | 6.3  | 0.9  | 47  | 2.8  | 0.6 | 0.7 |
| DAMO_2825 | protein of unknown function  | 711  | 27  | 2.7  | 0.4  | 21  | 2.1  | 0.5 | 1.2 |
| DAMO_2826 | Regulatory protein, ArsR   | 360  | 16  | 3.2  | 0.4  | 21  | 4.2  | 0.9 | 2.1 |
| DAMO_2827 | HycG protein   | 519  | 5   | 0.7  | 0.1  | 2   | 0.3  | 0.1 | 0.6 |
| DAMO_2828 | conserved membrane protein of unknown function   | 2034 | 60  | 2.1  | 0.3  | 16  | 0.6  | 0.1 | 0.4 |
| DAMO_2829 | Similar to membrane-bound [NiFe]-hydrogenase-3, subunit D  | 945  | 19  | 1.4  | 0.2  | 2   | 0.2  | 0.0 | 0.2 |
| DAMO_2830 | conserved membrane protein of unknown function   | 660  | 35  | 3.8  | 0.5  | 3   | 0.3  | 0.1 | 0.1 |
| DAMO_2831 | Hydrogenase-4 component F  | 1458 | 51  | 2.5  | 0.4  | 6   | 0.3  | 0.1 | 0.2 |
| DAMO_2832 | Hydrogenase, large subunit-like protei   | 1584 | 95  | 4.3  | 0.6  | 26  | 1.2  | 0.3 | 0.4 |
| DAMO_2833 | Orotidine 5'-phosphate decarboxylase (OMP decarboxylase) (OMPDCase) (OMPdecase)                                  | 822  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_2834 | conserved protein of unknown function  | 192  | 4   | 1.5  | 0.2  | 0   | 0.0  | 0.0 | —   |
| DAMO_2835 | conserved protein of unknown function  | 2541 | 6   | 0.2  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_2836 | Adenine specific DNA methylase Mod   | 1767 | 3   | 0.1  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_2837 | protein of unknown function  | 2910 | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_2838 | Periplasmic sensor signal transduction histidine kinase precursor  | 1482 | 85  | 4.1  | 0.6  | 40  | 1.9  | 0.4 | 0.7 |
| DAMO_2839 | Acetoacetate metabolism regulatory protein atoC decarboxylase antizyme)  | 1464 | 105 | 5.2  | 0.7  | 38  | 1.9  | 0.4 | 0.6 |
| DAMO_2840 | conserved protein of unknown function  | 96   | 96  | 72.0 | 10.0 | 13  | 9.8  | 2.1 | 0.2 |
| DAMO_2841 | RNA polymerase, sigma-24 subunit, ECF subfamily  | 552  | 527 | 68.7 | 9.6  | 155 | 20.2 | 4.5 | 0.5 |
| DAMO_2842 | protein of unknown function  | 708  | 55  | 5.6  | 0.8  | 30  | 3.1  | 0.7 | 0.9 |
| DAMO_2843 | exported protein of unknown function   | 618  | 125 | 14.6 | 2.0  | 108 | 12.6 | 2.8 | 1.4 |
| DAMO_2844 | protein of unknown function  | 183  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_2845 | putative tRNA cytidyltransferase   | 1293 | 23  | 1.3  | 0.2  | 5   | 0.3  | 0.1 | 0.3 |
| DAMO_2846 | conserved hypothetical protein; putative peptidase family M50, putative membrane protein                         | 645  | 60  | 6.7  | 0.9  | 57  | 6.4  | 1.4 | 1.5 |
| DAMO_2847 | Tryptophanyl-tRNA synthetase (Tryptophan--tRNA ligase) (TrpRS)   | 987  | 39  | 2.8  | 0.4  | 9   | 0.7  | 0.1 | 0.4 |
| DAMO_2848 | Inosine-5'-monophosphate dehydrogenase (IMP dehydrogenase) (IMPDH) (IMPD)  | 1464 | 357 | 17.6 | 2.4  | 87  | 4.3  | 0.9 | 0.4 |
| DAMO_2849 | protein of unknown function  | 234  | 3   | 0.9  | 0.1  | 4   | 1.2  | 0.3 | 2.1 |
| DAMO_2850 | GMP synthase [glutamine-hydrolyzing] (Glutamine amidotransferase) (GMP synthetase)                               | 1533 | 87  | 4.1  | 0.6  | 23  | 1.1  | 0.2 | 0.4 |
| DAMO_2851 | protein of unknown function  | 87   | 2   | 1.7  | 0.2  | 0   | 0.0  | 0.0 | —   |
| DAMO_2852 | DNA polymerase, beta domain protein regio  | 195  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_2853 | protein of unknown function  | 75   | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_2854 | DNA polymerase beta domain protein region  | 318  | 23  | 5.2  | 0.7  | 6   | 1.4  | 0.3 | 0.4 |
| DAMO_2855 | conserved protein of unknown function  | 363  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_2856 | DNA polymerase III, alpha subunit  | 3441 | 314 | 6.6  | 0.9  | 49  | 1.0  | 0.2 | 0.2 |
| DAMO_2857 | putative WD40 domain protein beta Propeller precursor  | 1590 | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_2858 | conserved protein of unknown function  | 1344 | 155 | 8.3  | 1.2  | 36  | 1.9  | 0.4 | 0.4 |
| DAMO_2859 | putative peptidase TldD  | 1473 | 168 | 8.2  | 1.1  | 31  | 1.5  | 0.3 | 0.3 |
| DAMO_2860 | A/G-specific adenine glycosylase (fragment)  | 717  | 45  | 4.5  | 0.6  | 2   | 0.2  | 0.0 | 0.1 |
| DAMO_2861 | CTP pyrophosphohydrolase   | 414  | 18  | 3.1  | 0.4  | 14  | 2.4  | 0.5 | 1.2 |
| DAMO_2862 | Peptide deformylase 2 (PDF 2) (Polypeptide deformylase 2)  | 531  | 40  | 5.4  | 0.8  | 21  | 2.8  | 0.6 | 0.8 |
| DAMO_2863 | putative ATP:cob(I)alamin adenosyltransferase, monofunctional PduO type  | 543  | 39  | 5.2  | 0.7  | 32  | 4.2  | 0.9 | 1.3 |
| DAMO_2864 | protein of unknown function  | 486  | 36  | 5.3  | 0.7  | 14  | 2.1  | 0.5 | 0.6 |
| DAMO_2865 | protein of unknown function  | 1065 | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_2866 | protein of unknown function  | 198  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_2867 | exported protein of unknown function   | 312  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_2868 | DNA adenine methylase  | 837  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_2869 | conserved protein of unknown function  | 2358 | 2   | 0.1  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_2870 | protein of unknown function  | 231  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_2871 | protein of unknown function  | 78   | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |
| DAMO_2872 | protein of unknown function  | 765  | 0   | 0.0  | 0.0  | 0   | 0.0  | 0.0 | —   |

|           |   |      |     |      |     |      |       |      |      |
|-----------|---|------|-----|------|-----|------|-------|------|------|
| DAMO_2873 | protein of unknown function   | 438  | 0   | 0.0  | 0.0 | 0    | 0.0   | 0.0  | —    |
| DAMO_2874 | protein of unknown function   | 165  | 1   | 0.4  | 0.1 | 0    | 0.0   | 0.0  | —    |
| DAMO_2875 | exported protein of unknown function  | 1401 | 0   | 0.0  | 0.0 | 0    | 0.0   | 0.0  | —    |
| DAMO_2876 | Sensor protein  | 1401 | 1   | 0.1  | 0.0 | 0    | 0.0   | 0.0  | —    |
| DAMO_2877 | putative Two-component transcriptional regulator; putative transcriptional regulator involved in heavy-meta     | 678  | 0   | 0.0  | 0.0 | 0    | 0.0   | 0.0  | —    |
| DAMO_2878 | conserved protein of unknown function   | 384  | 2   | 0.4  | 0.1 | 2    | 0.4   | 0.1  | 1.6  |
| DAMO_2879 | Plasmid maintenance system killer   | 300  | 3   | 0.7  | 0.1 | 0    | 0.0   | 0.0  | 0.0  |
| DAMO_2880 | Predicted nucleic acid-binding protein,contains PIN domain (fragment)   | 132  | 3   | 1.6  | 0.2 | 2    | 1.1   | 0.2  | 1.1  |
| DAMO_2881 | protein of unknown function   | 618  | 438 | 51.0 | 7.1 | 1768 | 206.0 | 45.4 | 6.4  |
| DAMO_2882 | membrane protein of unknown function  | 906  | 127 | 10.1 | 1.4 | 38   | 3.0   | 0.7  | 0.5  |
| DAMO_2883 | putative 4-alpha-glucanotransferase (Amylomaltase   | 2121 | 131 | 4.4  | 0.6 | 26   | 0.9   | 0.2  | 0.3  |
| DAMO_2884 | 1,4-alpha-glucan branching enzyme   | 2220 | 269 | 8.7  | 1.2 | 81   | 2.6   | 0.6  | 0.5  |
| DAMO_2885 | protein of unknown function   | 372  | 0   | 0.0  | 0.0 | 12   | 2.3   | 0.5  | —    |
| DAMO_2886 | exported protein of unknown function  | 327  | 86  | 18.9 | 2.6 | 668  | 147.1 | 32.4 | 12.3 |
| DAMO_2887 | Putative ATP-dependent DNA helicase (fragment)  | 219  | 1   | 0.3  | 0.0 | 3    | 1.0   | 0.2  | 4.7  |
| DAMO_2888 | conserved protein of unknown function   | 606  | 2   | 0.2  | 0.0 | 0    | 0.0   | 0.0  | —    |
| DAMO_2889 | protein of unknown function   | 66   | 0   | 0.0  | 0.0 | 0    | 0.0   | 0.0  | —    |
| DAMO_2890 | Penicillin-binding protein 1A   | 1386 | 0   | 0.0  | 0.0 | 0    | 0.0   | 0.0  | —    |
| DAMO_2891 | protein of unknown function   | 759  | 0   | 0.0  | 0.0 | 0    | 0.0   | 0.0  | —    |
| DAMO_2892 | protein of unknown function   | 738  | 0   | 0.0  | 0.0 | 0    | 0.0   | 0.0  | —    |
| DAMO_2893 | conserved protein of unknown function   | 273  | 53  | 14.0 | 1.9 | 53   | 14.0  | 3.1  | 1.6  |
| DAMO_2894 | exported protein of unknown function  | 249  | 2   | 0.6  | 0.1 | 11   | 3.2   | 0.7  | 8.7  |
| DAMO_2895 | conserved protein of unknown function   | 279  | 10  | 2.6  | 0.4 | 12   | 3.1   | 0.7  | 1.9  |
| DAMO_2896 | protein of unknown function   | 2976 | 371 | 9.0  | 1.3 | 92   | 2.2   | 0.5  | 0.4  |
| DAMO_2897 | putative nucleotidase yqfW  | 597  | 53  | 6.4  | 0.9 | 20   | 2.4   | 0.5  | 0.6  |
| DAMO_2898 | protein of unknown function   | 855  | 31  | 2.6  | 0.4 | 38   | 3.2   | 0.7  | 1.9  |
| DAMO_2899 | Cation diffusion facilitator family transporter   | 960  | 78  | 5.9  | 0.8 | 42   | 3.2   | 0.7  | 0.9  |
| DAMO_2900 | protein of unknown function   | 168  | 0   | 0.0  | 0.0 | 0    | 0.0   | 0.0  | —    |
| DAMO_2901 | protein of unknown function   | 660  | 5   | 0.5  | 0.1 | 2    | 0.2   | 0.0  | 0.6  |
| DAMO_2902 | conserved membrane protein of unknown function  | 513  | 0   | 0.0  | 0.0 | 1    | 0.1   | 0.0  | —    |
| DAMO_2903 | conserved exported protein of unknown function  | 546  | 40  | 5.3  | 0.7 | 27   | 3.6   | 0.8  | 1.1  |
| DAMO_2904 | conserved exported protein of unknown function  | 1452 | 185 | 9.2  | 1.3 | 461  | 22.9  | 5.0  | 3.9  |
| DAMO_2905 | putative THIAMINE BIOSYNTHESIS LIPOPROTEIN APBE TRANSMEMBRANE (modular protein)                                 | 1107 | 48  | 3.1  | 0.4 | 37   | 2.4   | 0.5  | 1.2  |
| DAMO_2906 | Hephaestin precursor (fragment)   | 1161 | 28  | 1.7  | 0.2 | 24   | 1.5   | 0.3  | 1.4  |
| DAMO_2907 | Putative ABC transporter (ATP binding protein)  | 1140 | 42  | 2.7  | 0.4 | 58   | 3.7   | 0.8  | 2.2  |
| DAMO_2908 | Iron(III) ABC transporter permease protein  | 1572 | 55  | 2.5  | 0.4 | 41   | 1.9   | 0.4  | 1.2  |
| DAMO_2909 | Iron(III) ABC transporter iron (III)-binding protein  | 1005 | 23  | 1.6  | 0.2 | 15   | 1.1   | 0.2  | 1.0  |
| DAMO_2910 | conserved protein of unknown function   | 669  | 41  | 4.4  | 0.6 | 39   | 4.2   | 0.9  | 1.5  |
| DAMO_2911 | protein of unknown function   | 282  | 1   | 0.3  | 0.0 | 0    | 0.0   | 0.0  | —    |
| DAMO_2912 | exported protein of unknown function  | 465  | 76  | 11.8 | 1.6 | 75   | 11.6  | 2.6  | 1.6  |
| DAMO_2913 | protein of unknown function   | 714  | 14  | 1.4  | 0.2 | 6    | 0.6   | 0.1  | 0.7  |
| DAMO_2914 | protein of unknown function   | 198  | 0   | 0.0  | 0.0 | 0    | 0.0   | 0.0  | —    |
| DAMO_2915 | putative non-heme chloroperoxidase (Chloride peroxidase)  | 813  | 59  | 5.2  | 0.7 | 10   | 0.9   | 0.2  | 0.3  |
| DAMO_2916 | protein of unknown function   | 210  | 0   | 0.0  | 0.0 | 0    | 0.0   | 0.0  | —    |
| DAMO_2917 | conserved protein of unknown function   | 3312 | 275 | 6.0  | 0.8 | 293  | 6.4   | 1.4  | 1.7  |
| DAMO_2918 | protein of unknown function   | 804  | 79  | 7.1  | 1.0 | 29   | 2.6   | 0.6  | 0.6  |
| DAMO_2919 | protein of unknown function   | 270  | 2   | 0.5  | 0.1 | 0    | 0.0   | 0.0  | —    |
| DAMO_2920 | protein of unknown function   | 576  | 4   | 0.5  | 0.1 | 1    | 0.1   | 0.0  | 0.4  |
| DAMO_2921 | acylphosphatase   | 288  | 10  | 2.5  | 0.3 | 0    | 0.0   | 0.0  | —    |
| DAMO_2922 | Farnesyl-diphosphate farnesyltransferase  | 1062 | 8   | 0.5  | 0.1 | 1    | 0.1   | 0.0  | 0.2  |
| DAMO_2923 | protein of unknown function   | 399  | 0   | 0.0  | 0.0 | 0    | 0.0   | 0.0  | —    |
| DAMO_2924 | conserved protein of unknown function   | 309  | 0   | 0.0  | 0.0 | 0    | 0.0   | 0.0  | —    |
| DAMO_2925 | conserved protein of unknown function   | 342  | 8   | 1.7  | 0.2 | 2    | 0.4   | 0.1  | 0.4  |
| DAMO_2926 | Protein crcB homolog  | 381  | 1   | 0.2  | 0.0 | 0    | 0.0   | 0.0  | —    |
| DAMO_2927 | 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase (5- methylthio-3-oxo-1-penten-1,2-diol dioxygenase) (DHK-N | 534  | 51  | 6.9  | 1.0 | 8    | 1.1   | 0.2  | 0.2  |
| DAMO_2928 | Methylthioribulose-1-phosphate dehydratas   | 717  | 24  | 2.4  | 0.3 | 1    | 0.1   | 0.0  | 0.1  |

|           |   |      |     |      |     |     |      |     |     |
|-----------|---|------|-----|------|-----|-----|------|-----|-----|
| DAMO_2929 | 2,3-diketo-5-methylthio-1-phosphopentane phosphatase  | 669  | 84  | 9.0  | 1.3 | 11  | 1.2  | 0.3 | 0.2 |
| DAMO_2930 | 2,3-diketo-5-methylthiopentyl-1-phosphate enolase   | 1230 | 357 | 20.9 | 2.9 | 193 | 11.3 | 2.5 | 0.9 |
| DAMO_2931 | protein of unknown function   | 117  | 2   | 1.2  | 0.2 | 0   | 0.0  | 0.0 | —   |
| DAMO_2932 | conserved protein of unknown function   | 279  | 28  | 7.2  | 1.0 | 23  | 5.9  | 1.3 | 1.3 |
| DAMO_2933 | conserved protein of unknown function   | 291  | 68  | 16.8 | 2.3 | 44  | 10.9 | 2.4 | 1.0 |
| DAMO_2934 | Aldo/keto reductase   | 969  | 58  | 4.3  | 0.6 | 12  | 0.9  | 0.2 | 0.3 |
| DAMO_2935 | putative Adenylate cyclase  | 519  | 77  | 10.7 | 1.5 | 9   | 1.2  | 0.3 | 0.2 |
| DAMO_2936 | protein of unknown function   | 183  | 13  | 5.1  | 0.7 | 1   | 0.4  | 0.1 | 0.1 |
| DAMO_2937 | putative Histidine kinase   | 2295 | 91  | 2.9  | 0.4 | 11  | 0.3  | 0.1 | 0.2 |
| DAMO_2938 | Phosphoenolpyruvate carboxykinase [GTP] (PEP carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK)           | 1875 | 208 | 8.0  | 1.1 | 36  | 1.4  | 0.3 | 0.3 |
| DAMO_2939 | Recombination protein recR  | 600  | 112 | 13.4 | 1.9 | 17  | 2.0  | 0.4 | 0.2 |
| DAMO_2940 | conserved hypothetical protein; putative YbaB family protein  | 315  | 58  | 13.3 | 1.8 | 14  | 3.2  | 0.7 | 0.4 |
| DAMO_2941 | protein of unknown function   | 105  | 6   | 4.1  | 0.6 | 2   | 1.4  | 0.3 | 0.5 |
| DAMO_2942 | DNA polymerase III, subunits gamma and tau  | 1806 | 92  | 3.7  | 0.5 | 52  | 2.1  | 0.5 | 0.9 |
| DAMO_2943 | ADP-L-glycero-D-manno-heptose-6-epimerase   | 951  | 86  | 6.5  | 0.9 | 18  | 1.4  | 0.3 | 0.3 |
| DAMO_2944 | Seryl-tRNA synthetase (Serine--tRNA ligase)   | 1287 | 120 | 6.7  | 0.9 | 41  | 2.3  | 0.5 | 0.5 |
| DAMO_2945 | DNA gyrase, subunit A, type II topoisomerase  | 2526 | 239 | 6.8  | 0.9 | 52  | 1.5  | 0.3 | 0.3 |
| DAMO_2946 | DNA gyrase subunit B  | 2481 | 340 | 9.9  | 1.4 | 97  | 2.8  | 0.6 | 0.5 |
| DAMO_2947 | DNA polymerase III, beta-subunit  | 1107 | 99  | 6.4  | 0.9 | 46  | 3.0  | 0.7 | 0.7 |
| DAMO_2948 | protein of unknown function   | 189  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2949 | protein of unknown function   | 180  | 2   | 0.8  | 0.1 | 3   | 1.2  | 0.3 | 2.4 |
| DAMO_2950 | protein of unknown function   | 369  | 11  | 2.1  | 0.3 | 1   | 0.2  | 0.0 | 0.1 |
| DAMO_2951 | conserved protein of unknown function   | 273  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2952 | putative Inner membrane protein oxaA  | 1674 | 30  | 1.3  | 0.2 | 4   | 0.2  | 0.0 | 0.2 |
| DAMO_2953 | putative Methyltransferase gidB (Glucose-inhibited division protein B)  | 750  | 3   | 0.3  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2954 | chromosome partitioning protein   | 759  | 13  | 1.2  | 0.2 | 3   | 0.3  | 0.1 | 0.4 |
| DAMO_2955 | chromosome partitioning protein   | 843  | 27  | 2.3  | 0.3 | 2   | 0.2  | 0.0 | 0.1 |
| DAMO_2956 | membrane protein of unknown function  | 699  | 6   | 0.6  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_2957 | cysteine desulfurase (Nitrogenase metalloclusters biosynthesis protein nifS)                                    | 1176 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2958 | tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase  | 1074 | 34  | 2.3  | 0.3 | 5   | 0.3  | 0.1 | 0.2 |
| DAMO_2959 | membrane protein of unknown function  | 411  | 149 | 26.1 | 3.6 | 16  | 2.8  | 0.6 | 0.2 |
| DAMO_2960 | putative Sodium-transporting two-sector ATPase  | 606  | 254 | 30.2 | 4.2 | 21  | 2.5  | 0.5 | 0.1 |
| DAMO_2961 | putative ATP synthase delta chain   | 552  | 119 | 15.5 | 2.2 | 11  | 1.4  | 0.3 | 0.1 |
| DAMO_2962 | ATP synthase subunit alpha, membrane-bound, F1 sector   | 1527 | 553 | 26.1 | 3.6 | 81  | 3.8  | 0.8 | 0.2 |
| DAMO_2963 | ATP synthase subunit gamma, membrane-bound, F1 sector   | 873  | 195 | 16.1 | 2.2 | 53  | 4.4  | 1.0 | 0.4 |
| DAMO_2964 | ATP synthase subunit beta, membrane-bound, F1 sector  | 1422 | 545 | 27.6 | 3.8 | 85  | 4.3  | 0.9 | 0.2 |
| DAMO_2965 | ATP synthase subunit epsilon, membrane-bound, F1 sector   | 405  | 113 | 20.1 | 2.8 | 11  | 2.0  | 0.4 | 0.2 |
| DAMO_2966 | Phospho-2-dehydro-3-deoxyheptonate aldolase synthetase) (3-deoxy-D-arabino- heptulosonate 7-phosphate synthase) | 1017 | 119 | 8.4  | 1.2 | 14  | 1.0  | 0.2 | 0.2 |
| DAMO_2967 | conserved protein of unknown function   | 108  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2968 | L-PSP (mRNA) endoribonuclease   | 384  | 2   | 0.4  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_2969 | protein of unknown function   | 180  | 2   | 0.8  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_2970 | UvrABC system protein C (Protein uvrC)  | 1806 | 42  | 1.7  | 0.2 | 19  | 0.8  | 0.2 | 0.7 |
| DAMO_2971 | protein of unknown function   | 186  | 52  | 20.1 | 2.8 | 48  | 18.6 | 4.1 | 1.5 |
| DAMO_2972 | GTP-binding protein typA/bipA (Tyrosine phosphorylated protein A)   | 1830 | 150 | 5.9  | 0.8 | 73  | 2.9  | 0.6 | 0.8 |
| DAMO_2973 | Peptidyl-prolyl cis-trans isomerase (modular protein)   | 564  | 79  | 10.1 | 1.4 | 14  | 1.8  | 0.4 | 0.3 |
| DAMO_2974 | Homoserine kinase (HSK) (HK)  | 888  | 112 | 9.1  | 1.3 | 6   | 0.5  | 0.1 | 0.1 |
| DAMO_2975 | protein of unknown function   | 66   | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2976 | Pyrroline-5-carboxylate reductase (P5C reductase  | 816  | 89  | 7.9  | 1.1 | 14  | 1.2  | 0.3 | 0.2 |
| DAMO_2977 | conserved hypothetical protein  | 303  | 33  | 7.8  | 1.1 | 5   | 1.2  | 0.3 | 0.2 |
| DAMO_2978 | conserved hypothetical protein  | 309  | 53  | 12.3 | 1.7 | 10  | 2.3  | 0.5 | 0.3 |
| DAMO_2979 | protein of unknown function   | 1269 | 1   | 0.1  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2980 | putative Sugar transferase- a glycosyl transferase  | 786  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2981 | protein of unknown function   | 1143 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2982 | protein of unknown function   | 453  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2983 | putative glycosyltransferase, group 1   | 1146 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_2984 | protein of unknown function   | 840  | 10  | 0.9  | 0.1 | 5   | 0.4  | 0.1 | 0.8 |

|           |  |      |     |      |     |     |      |     |     |
|-----------|--|------|-----|------|-----|-----|------|-----|-----|
| DAMO_2985 | protein of unknown function  | 243  | 24  | 7.1  | 1.0 | 0   | 0.0  | 0.0 | 0.0 |
| DAMO_2986 | fructose 1,6-bisphosphatase, class II  | 963  | 151 | 11.3 | 1.6 | 37  | 2.8  | 0.6 | 0.4 |
| DAMO_2987 | Histidyl-tRNA synthetase (Histidine--tRNA ligase)  | 1260 | 25  | 1.4  | 0.2 | 3   | 0.2  | 0.0 | 0.2 |
| DAMO_2988 | Aspartyl-tRNA synthetase / asparaginyl-tRNA synthetase (Aspartate-/asparagine-tRNA ligase) (AspRS)           | 1782 | 89  | 3.6  | 0.5 | 17  | 0.7  | 0.2 | 0.3 |
| DAMO_2989 | putative phosphate starvation-inducible protein, PhoH-like protein   | 993  | 197 | 14.3 | 2.0 | 248 | 18.0 | 4.0 | 2.0 |
| DAMO_2990 | membrane protein of unknown function   | 1647 | 91  | 4.0  | 0.6 | 46  | 2.0  | 0.4 | 0.8 |
| DAMO_2991 | conserved protein of unknown function  | 441  | 0   | 0.0  | 0.0 | 3   | 0.5  | 0.1 | —   |
| DAMO_2992 | putative Diacylglycerol kinase   | 507  | 0   | 0.0  | 0.0 | 1   | 0.1  | 0.0 | —   |
| DAMO_2993 | GTP-binding protein (era)  | 903  | 38  | 3.0  | 0.4 | 27  | 2.2  | 0.5 | 1.1 |
| DAMO_2994 | putative DNA repair protein recO (Recombination protein O)   | 750  | 42  | 4.0  | 0.6 | 27  | 2.6  | 0.6 | 1.0 |
| DAMO_2995 | putative alcohol dehydrogenase   | 1029 | 32  | 2.2  | 0.3 | 4   | 0.3  | 0.1 | 0.2 |
| DAMO_2996 | protein of unknown function  | 2340 | 688 | 21.2 | 2.9 | 640 | 19.7 | 4.3 | 1.5 |
| DAMO_2997 | Import inner membrane translocase, subunit Tim44 precursor (fragment)  | 735  | 285 | 27.9 | 3.9 | 223 | 21.8 | 4.8 | 1.2 |
| DAMO_2998 | Tyrosine recombinase xerD  | 888  | 11  | 0.9  | 0.1 | 4   | 0.3  | 0.1 | 0.6 |
| DAMO_2999 | putative Glycosyl transferase, group 1   | 1182 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3000 | membrane protein of unknown function   | 1539 | 5   | 0.2  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3001 | Type 4 prepilin-like proteins leader peptide processing enzyme   | 750  | 14  | 1.3  | 0.2 | 7   | 0.7  | 0.1 | 0.8 |
| DAMO_3002 | protein of unknown function  | 186  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3003 | exported protein of unknown function   | 1266 | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3004 | protein of unknown function  | 822  | 2   | 0.2  | 0.0 | 1   | 0.1  | 0.0 | 0.8 |
| DAMO_3005 | conserved exported protein of unknown function   | 453  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3006 | putative Type IV pilus biogenesis protein  | 471  | 1   | 0.2  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3007 | putative Fimbrial protein pilin  | 483  | 4   | 0.6  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_3008 | protein of unknown function  | 222  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3009 | putative response regulator in two-component regulatory system, sigma54 dependent transcriptional regulator. | 1383 | 42  | 2.2  | 0.3 | 7   | 0.4  | 0.1 | 0.3 |
| DAMO_3010 | putative Multi-sensor signal transduction histidine kinase precursor   | 1674 | 26  | 1.1  | 0.2 | 12  | 0.5  | 0.1 | 0.7 |
| DAMO_3011 | Type 4 fimbrial assembly protein pilC  | 1215 | 44  | 2.6  | 0.4 | 15  | 0.9  | 0.2 | 0.5 |
| DAMO_3012 | transporter  | 1080 | 179 | 11.9 | 1.7 | 56  | 3.7  | 0.8 | 0.5 |
| DAMO_3013 | Type IV pilus assembly protein tapB  | 1698 | 297 | 12.6 | 1.8 | 59  | 2.5  | 0.6 | 0.3 |
| DAMO_3014 | Shikimate dehydrogenase  | 858  | 54  | 4.5  | 0.6 | 48  | 4.0  | 0.9 | 1.4 |
| DAMO_3015 | putative [Protein-PII] uridylyltransferase (PII uridylyl- transferase) (Uridylyl-removing enzyme) (UTase)    | 2799 | 121 | 3.1  | 0.4 | 96  | 2.5  | 0.5 | 1.3 |
| DAMO_3016 | membrane protein of unknown function   | 417  | 2   | 0.3  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3017 | putative enzyme (3.4.-)  | 828  | 44  | 3.8  | 0.5 | 15  | 1.3  | 0.3 | 0.5 |
| DAMO_3018 | putative Histidine kinase  | 1884 | 232 | 8.9  | 1.2 | 121 | 4.6  | 1.0 | 0.8 |
| DAMO_3019 | Heat shock protein DnaJ domain protein   | 846  | 61  | 5.2  | 0.7 | 86  | 7.3  | 1.6 | 2.2 |
| DAMO_3020 | NUDIX hydrolase (modular protein)  | 957  | 240 | 18.1 | 2.5 | 186 | 14.0 | 3.1 | 1.2 |
| DAMO_3021 | conserved protein of unknown function  | 768  | 59  | 5.5  | 0.8 | 23  | 2.2  | 0.5 | 0.6 |
| DAMO_3022 | conserved hypothetical protein   | 414  | 128 | 22.3 | 3.1 | 30  | 5.2  | 1.1 | 0.4 |
| DAMO_3023 | conserved protein of unknown function  | 432  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3024 | protein of unknown function  | 288  | 1   | 0.3  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3025 | CTP:TMP-3-deoxy-D-manno-octulosonate transferase   | 762  | 117 | 11.1 | 1.5 | 61  | 5.8  | 1.3 | 0.8 |
| DAMO_3026 | conserved protein of unknown function  | 309  | 56  | 13.0 | 1.8 | 139 | 32.4 | 7.1 | 3.9 |
| DAMO_3027 | Adenosine deaminase (Adenosine aminohydrolase)   | 1029 | 189 | 13.2 | 1.8 | 35  | 2.4  | 0.5 | 0.3 |
| DAMO_3028 | conserved protein of unknown function  | 1317 | 67  | 3.7  | 0.5 | 13  | 0.7  | 0.2 | 0.3 |
| DAMO_3029 | Acyl-CoA dehydrogenase   | 1200 | 95  | 5.7  | 0.8 | 22  | 1.3  | 0.3 | 0.4 |
| DAMO_3030 | putative L-carnitine dehydrogenase   | 1191 | 141 | 8.5  | 1.2 | 6   | 0.4  | 0.1 | 0.1 |
| DAMO_3031 | conserved protein of unknown function  | 1317 | 51  | 2.8  | 0.4 | 11  | 0.6  | 0.1 | 0.3 |
| DAMO_3032 | conserved hypothetical protein; possibly involved in transport   | 753  | 72  | 6.9  | 1.0 | 28  | 2.7  | 0.6 | 0.6 |
| DAMO_3033 | Uroporphyrinogen III synthase, uroporphyrinogen decarboxylase  | 1941 | 37  | 1.4  | 0.2 | 13  | 0.5  | 0.1 | 0.6 |
| DAMO_3034 | Ferrochelatase   | 963  | 9   | 0.7  | 0.1 | 4   | 0.3  | 0.1 | 0.7 |
| DAMO_3035 | Protoporphyrinogen IX and coproporphyrinogen III oxidase   | 1488 | 13  | 0.6  | 0.1 | 3   | 0.1  | 0.0 | 0.4 |
| DAMO_3036 | exported protein of unknown function   | 1269 | 10  | 0.6  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_3037 | Dihydroxy-acid dehydratase (DAD)   | 1674 | 188 | 8.1  | 1.1 | 46  | 2.0  | 0.4 | 0.4 |
| DAMO_3038 | Protein dedA (Protein DSG-1)   | 636  | 9   | 1.0  | 0.1 | 2   | 0.2  | 0.0 | 0.4 |
| DAMO_3039 | protein of unknown function  | 84   | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3040 | protein of unknown function  | 174  | 6   | 2.5  | 0.3 | 0   | 0.0  | 0.0 | —   |



|           |  |      |     |      |     |     |      |     |     |
|-----------|--|------|-----|------|-----|-----|------|-----|-----|
| DAMO_3041 | protein of unknown function  | 531  | 68  | 9.2  | 1.3 | 29  | 3.9  | 0.9 | 0.7 |
| DAMO_3042 | conserved protein of unknown function  | 852  | 31  | 2.6  | 0.4 | 14  | 1.2  | 0.3 | 0.7 |
| DAMO_3043 | protein of unknown function  | 246  | 31  | 9.1  | 1.3 | 13  | 3.8  | 0.8 | 0.7 |
| DAMO_3044 | Addiction module toxin, Txe/YoeB family  | 267  | 3   | 0.8  | 0.1 | 3   | 0.8  | 0.2 | 1.6 |
| DAMO_3045 | protein of unknown function  | 531  | 1   | 0.1  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3046 | Type-2 restriction enzyme BstVI (R.BstVI) (Type II restriction enzyme BstVI) (Endonuclease BstVI)        | 732  | 9   | 0.9  | 0.1 | 2   | 0.2  | 0.0 | 0.4 |
| DAMO_3047 | Methyltransferase  | 897  | 7   | 0.6  | 0.1 | 3   | 0.2  | 0.1 | 0.7 |
| DAMO_3048 | protein of unknown function  | 273  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3049 | Solute/sodium symporter precursor  | 912  | 33  | 2.6  | 0.4 | 32  | 2.5  | 0.6 | 1.5 |
| DAMO_3050 | DNA polymerase beta domain protein region  | 303  | 0   | 0.0  | 0.0 | 2   | 0.5  | 0.1 | —   |
| DAMO_3051 | conserved protein of unknown function  | 351  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3052 | protein of unknown function  | 114  | 1   | 0.6  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_3053 | protein of unknown function  | 627  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3054 | conserved hypothetical protein; putative signal peptide  | 1110 | 94  | 6.1  | 0.8 | 124 | 8.0  | 1.8 | 2.1 |
| DAMO_3055 | conserved membrane protein of unknown function   | 2547 | 67  | 1.9  | 0.3 | 44  | 1.2  | 0.3 | 1.0 |
| DAMO_3056 | putative ABC transporter, ATP-binding protein  | 678  | 16  | 1.7  | 0.2 | 20  | 2.1  | 0.5 | 2.0 |
| DAMO_3057 | Outer membrane lipoprotein omp16 precursor   | 555  | 23  | 3.0  | 0.4 | 2   | 0.3  | 0.1 | 0.1 |
| DAMO_3058 | Possible Na+/? antiporter precursor  | 1326 | 113 | 6.1  | 0.9 | 20  | 1.1  | 0.2 | 0.3 |
| DAMO_3059 | putative metallo-phosphoesterase (modular protein)   | 1287 | 48  | 2.7  | 0.4 | 45  | 2.5  | 0.6 | 1.5 |
| DAMO_3060 | putative Inner membrane protein yjgQ   | 1089 | 198 | 13.1 | 1.8 | 76  | 5.0  | 1.1 | 0.6 |
| DAMO_3061 | putative Permease YjgP/YjgQ family protein precursor   | 1071 | 160 | 10.8 | 1.5 | 115 | 7.7  | 1.7 | 1.1 |
| DAMO_3062 | Nucleotidyl transferase  | 720  | 2   | 0.2  | 0.0 | 1   | 0.1  | 0.0 | 0.8 |
| DAMO_3063 | conserved protein of unknown function  | 801  | 5   | 0.4  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_3064 | putative DNA-binding transcriptional regulator   | 1203 | 18  | 1.1  | 0.2 | 11  | 0.7  | 0.1 | 1.0 |
| DAMO_3065 | protein of unknown function  | 216  | 1   | 0.3  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3066 | AMP-dependent synthetase and ligase  | 1827 | 128 | 5.0  | 0.7 | 13  | 0.5  | 0.1 | 0.2 |
| DAMO_3067 | NAD-dependent epimerase/dehydratase  | 954  | 11  | 0.8  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_3068 | Phosphopantetheine attachment site   | 249  | 1   | 0.3  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3069 | Serine palmitoyltransferase  | 1191 | 37  | 2.2  | 0.3 | 4   | 0.2  | 0.1 | 0.2 |
| DAMO_3070 | conserved protein of unknown function  | 942  | 74  | 5.7  | 0.8 | 67  | 5.1  | 1.1 | 1.4 |
| DAMO_3071 | ABC transporter, transmembrane region:ABC transporter precursor  | 1755 | 15  | 0.6  | 0.1 | 4   | 0.2  | 0.0 | 0.4 |
| DAMO_3072 | CDP-alcohol phosphatidyltransferase  | 1206 | 4   | 0.2  | 0.0 | 1   | 0.1  | 0.0 | 0.4 |
| DAMO_3073 | putative DAG-kinase catalytic domain (Presumed)  | 1047 | 21  | 1.4  | 0.2 | 6   | 0.4  | 0.1 | 0.5 |
| DAMO_3074 | Fatty acid desaturase  | 1122 | 290 | 18.6 | 2.6 | 107 | 6.9  | 1.5 | 0.6 |
| DAMO_3075 | conserved protein of unknown function  | 963  | 65  | 4.9  | 0.7 | 36  | 2.7  | 0.6 | 0.9 |
| DAMO_3076 | conserved exported protein of unknown function   | 516  | 103 | 14.4 | 2.0 | 30  | 4.2  | 0.9 | 0.5 |
| DAMO_3077 | exported protein of unknown function   | 444  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3078 | protein of unknown function  | 168  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3079 | protein of unknown function  | 264  | 4   | 1.1  | 0.2 | 1   | 0.3  | 0.1 | 0.4 |
| DAMO_3080 | putative enzyme (N-terminal); transcriptional regulator with P-loop containing NTP hydrolase domai       | 1533 | 252 | 11.8 | 1.6 | 61  | 2.9  | 0.6 | 0.4 |
| DAMO_3081 | conserved protein of unknown function  | 390  | 31  | 5.7  | 0.8 | 4   | 0.7  | 0.2 | 0.2 |
| DAMO_3082 | Ribonuclease HII (RNase HII)   | 588  | 65  | 8.0  | 1.1 | 13  | 1.6  | 0.4 | 0.3 |
| DAMO_3083 | 50S ribosomal protein L19  | 348  | 68  | 14.1 | 2.0 | 20  | 4.1  | 0.9 | 0.5 |
| DAMO_3084 | tRNA (guanine-N(1)-)-methyltransferase (M1G- methyltransferase) (tRNA [GM37] methyltransferase)          | 648  | 13  | 1.4  | 0.2 | 2   | 0.2  | 0.0 | 0.2 |
| DAMO_3085 | 16S rRNA processing protein, putative function   | 528  | 68  | 9.3  | 1.3 | 42  | 5.7  | 1.3 | 1.0 |
| DAMO_3086 | RNA-binding protein (KH domain)  | 285  | 53  | 13.4 | 1.9 | 26  | 6.6  | 1.4 | 0.8 |
| DAMO_3087 | 30S ribosomal protein S16  | 282  | 104 | 26.6 | 3.7 | 36  | 9.2  | 2.0 | 0.5 |
| DAMO_3088 | 4.5S-RNP protein, GTP-binding export factor, part of signal recognition particle with 4.5 RNA, ffh famil | 1344 | 659 | 35.3 | 4.9 | 128 | 6.9  | 1.5 | 0.3 |
| DAMO_3089 | membrane protein of unknown function   | 525  | 5   | 0.7  | 0.1 | 0   | 0.0  | 0.0 | —   |
| DAMO_3090 | exported protein of unknown function   | 336  | 7   | 1.5  | 0.2 | 1   | 0.2  | 0.0 | 0.2 |
| DAMO_3091 | protein of unknown function  | 189  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3092 | Transcriptional regulator  | 426  | 55  | 9.3  | 1.3 | 17  | 2.9  | 0.6 | 0.5 |
| DAMO_3093 | conserved protein of unknown function  | 324  | 55  | 12.2 | 1.7 | 28  | 6.2  | 1.4 | 0.8 |
| DAMO_3094 | conserved protein of unknown function  | 198  | 88  | 32.0 | 4.5 | 40  | 14.5 | 3.2 | 0.7 |
| DAMO_3095 | conserved protein of unknown function  | 159  | 3   | 1.4  | 0.2 | 4   | 1.8  | 0.4 | 2.1 |
| DAMO_3096 | protein of unknown function  | 501  | 121 | 17.4 | 2.4 | 53  | 7.6  | 1.7 | 0.7 |

|           |  |      |     |      |     |     |      |     |     |
|-----------|--|------|-----|------|-----|-----|------|-----|-----|
| DAMO_3097 | conserved protein of unknown function  | 483  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3098 | putative regulatory protein, FmdB  | 351  | 113 | 23.2 | 3.2 | 30  | 6.2  | 1.4 | 0.4 |
| DAMO_3099 | Serine-glyoxylate aminotransferase   | 1140 | 81  | 5.1  | 0.7 | 16  | 1.0  | 0.2 | 0.3 |
| DAMO_3100 | D-3-phosphoglycerate dehydrogenase   | 1581 | 311 | 14.2 | 2.0 | 43  | 2.0  | 0.4 | 0.2 |
| DAMO_3101 | ATP phosphoribosyltransferase regulatory subunit   | 1314 | 142 | 7.8  | 1.1 | 28  | 1.5  | 0.3 | 0.3 |
| DAMO_3102 | Adenylosuccinate synthetase (IMP--aspartate ligase) (AdSS) (AMPSase)   | 1311 | 264 | 14.5 | 2.0 | 58  | 3.2  | 0.7 | 0.3 |
| DAMO_3103 | protein of unknown function  | 192  | 3   | 1.1  | 0.2 | 0   | 0.0  | 0.0 | —   |
| DAMO_3104 | putative tRNA-dihydrouridine synthase (Nitrogen regulation protein nifR3)  | 1011 | 96  | 6.8  | 1.0 | 23  | 1.6  | 0.4 | 0.4 |
| DAMO_3105 | protein of unknown function  | 168  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3106 | protein of unknown function  | 213  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3107 | putative Lysyl endopeptidase   | 2256 | 6   | 0.2  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3108 | protein of unknown function  | 321  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3109 | conserved protein of unknown function  | 816  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3111 | conserved protein of unknown function  | 201  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3110 | conserved protein of unknown function  | 255  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3112 | conserved hypothetical protein; Ankyrin-repeat protein   | 513  | 62  | 8.7  | 1.2 | 11  | 1.5  | 0.3 | 0.3 |
| DAMO_3113 | Queuosine biosynthesis protein queC  | 702  | 77  | 7.9  | 1.1 | 26  | 2.7  | 0.6 | 0.5 |
| DAMO_3114 | Radical SAM domain protein   | 645  | 135 | 15.1 | 2.1 | 149 | 16.6 | 3.7 | 1.7 |
| DAMO_3115 | Putative Serine protease do-like precursor   | 1485 | 297 | 14.4 | 2.0 | 275 | 13.3 | 2.9 | 1.5 |
| DAMO_3116 | conserved membrane protein of unknown function   | 969  | 2   | 0.1  | 0.0 | 5   | 0.4  | 0.1 | 4.0 |
| DAMO_3117 | exported protein of unknown function   | 741  | 14  | 1.4  | 0.2 | 8   | 0.8  | 0.2 | 0.9 |
| DAMO_3118 | Methyltransferase type 11  | 807  | 5   | 0.4  | 0.1 | 2   | 0.2  | 0.0 | 0.6 |
| DAMO_3119 | putative 2-dehydropantoate 2-reductas  | 909  | 29  | 2.3  | 0.3 | 4   | 0.3  | 0.1 | 0.2 |
| DAMO_3120 | conserved protein of unknown function  | 291  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3121 | conserved protein of unknown function  | 222  | 1   | 0.3  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3122 | Restriction modification system DNA specificity domain:N-6 DNA methylase:Type I restriction-modification system, I | 81   | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3123 | putative response regulator in two-component reguatory system, sigma54 dependent transcriptional regulator.        | 1359 | 42  | 2.2  | 0.3 | 14  | 0.7  | 0.2 | 0.5 |
| DAMO_3124 | putative Histidine kinase  | 1347 | 83  | 4.4  | 0.6 | 36  | 1.9  | 0.4 | 0.7 |
| DAMO_3125 | NUDIX hydrolase  | 582  | 85  | 10.5 | 1.5 | 32  | 4.0  | 0.9 | 0.6 |
| DAMO_3126 | putative Carboxylesterase  | 903  | 37  | 3.0  | 0.4 | 16  | 1.3  | 0.3 | 0.7 |
| DAMO_3127 | membrane protein of unknown function   | 1233 | 45  | 2.6  | 0.4 | 21  | 1.2  | 0.3 | 0.7 |
| DAMO_3128 | conserved membrane protein of unknown function   | 363  | 1   | 0.2  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3129 | exported protein of unknown function   | 540  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3130 | protein of unknown function  | 1014 | 160 | 11.4 | 1.6 | 127 | 9.0  | 2.0 | 1.3 |
| DAMO_3131 | Rod shape-determining protein mreB   | 1029 | 293 | 20.5 | 2.9 | 81  | 5.7  | 1.2 | 0.4 |
| DAMO_3132 | Rod shape-determining protein MreC precursor   | 864  | 27  | 2.3  | 0.3 | 5   | 0.4  | 0.1 | 0.3 |
| DAMO_3133 | putative Rod shape-determining protein MreD  | 480  | 4   | 0.6  | 0.1 | 6   | 0.9  | 0.2 | 2.4 |
| DAMO_3134 | Penicillin-binding protein 2   | 1848 | 88  | 3.4  | 0.5 | 33  | 1.3  | 0.3 | 0.6 |
| DAMO_3135 | Rod shape-determining protein rodA   | 1101 | 66  | 4.3  | 0.6 | 23  | 1.5  | 0.3 | 0.6 |
| DAMO_3136 | isoleucine tRNA synthetase   | 2826 | 474 | 12.1 | 1.7 | 87  | 2.2  | 0.5 | 0.3 |
| DAMO_3137 | Lipoprotein signal peptidase (Prolipoprotein signal peptidase) (SPase II) (Signal peptidase II)                    | 489  | 65  | 9.6  | 1.3 | 19  | 2.8  | 0.6 | 0.5 |
| DAMO_3138 | pseudouridine synthase (pseudouridines 1911, 1915, 1917 in 23S RNA)  | 945  | 100 | 7.6  | 1.1 | 18  | 1.4  | 0.3 | 0.3 |
| DAMO_3139 | putative Diguanylate kinase  | 2679 | 4   | 0.1  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3140 | protein of unknown function  | 807  | 24  | 2.1  | 0.3 | 3   | 0.3  | 0.1 | 0.2 |
| DAMO_3141 | Alanine dehydrogenase (Stage V sporulation protein N)  | 1119 | 154 | 9.9  | 1.4 | 28  | 1.8  | 0.4 | 0.3 |
| DAMO_3142 | HAD-superfamily hydrolase, subfamily IA, variant 3   | 687  | 38  | 4.0  | 0.6 | 5   | 0.5  | 0.1 | 0.2 |
| DAMO_3143 | protein of unknown function  | 174  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3144 | Cytosine deaminase (Cytosine aminohydrolase)   | 465  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3145 | protein of unknown function  | 243  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3146 | conserved protein of unknown function  | 201  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3147 | exported protein of unknown function   | 117  | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3148 | Glutaredoxin and related proteins (fragment)   | 84   | 0   | 0.0  | 0.0 | 0   | 0.0  | 0.0 | —   |
| DAMO_3149 | protein of unknown function  | 345  | 38  | 7.9  | 1.1 | 38  | 7.9  | 1.7 | 1.6 |
| DAMO_3150 | conserved protein of unknown function  | 666  | 77  | 8.3  | 1.2 | 34  | 3.7  | 0.8 | 0.7 |
| DAMO_3151 | putative Endonuclease III  | 660  | 100 | 10.9 | 1.5 | 38  | 4.1  | 0.9 | 0.6 |
| DAMO_3152 | conserved protein of unknown function  | 423  | 3   | 0.5  | 0.1 | 0   | 0.0  | 0.0 | 0.0 |

|           |  |         |           |      |     |           |     |     |     |
|-----------|--|---------|-----------|------|-----|-----------|-----|-----|-----|
| DAMO_3153 | conserved membrane protein of unknown function   | 1233    | 83        | 4.8  | 0.7 | 26        | 1.5 | 0.3 | 0.5 |
| DAMO_3154 | putative transporter subunit: ATP-binding component of ABC superfamily   | 744     | 74        | 7.2  | 1.0 | 18        | 1.7 | 0.4 | 0.4 |
| DAMO_3155 | Efflux transporter, RND family, MFP subunit precursor  | 1440    | 124       | 6.2  | 0.9 | 42        | 2.1 | 0.5 | 0.5 |
| DAMO_3156 | conserved exported protein of unknown function   | 1611    | 86        | 3.8  | 0.5 | 50        | 2.2 | 0.5 | 0.9 |
| DAMO_3157 | exported protein of unknown function   | 510     | 54        | 7.6  | 1.1 | 11        | 1.6 | 0.3 | 0.3 |
| DAMO_3158 | protein of unknown function  | 552     | 35        | 4.6  | 0.6 | 10        | 1.3 | 0.3 | 0.5 |
| DAMO_3159 | putative RNA polymerase sigma-H facto  | 660     | 197       | 21.5 | 3.0 | 84        | 9.2 | 2.0 | 0.7 |
| DAMO_3160 | protein of unknown function  | 237     | 0         | 0.0  | 0.0 | 0         | 0.0 | 0.0 | —   |
| DAMO_3161 | protein of unknown function  | 99      | 0         | 0.0  | 0.0 | 0         | 0.0 | 0.0 | —   |
| DAMO_3162 | putative signal transduction protein with EFhand domain  | 747     | 0         | 0.0  | 0.0 | 0         | 0.0 | 0.0 | —   |
| DAMO_3163 | transposase (fragment)   | 201     | 0         | 0.0  | 0.0 | 0         | 0.0 | 0.0 | —   |
| DAMO_3164 | fragment of putative macrolide ABC transporter, fusion of ATP-binding (N-terminal) and membrane (C-terminal) dom | 1209    | 77        | 4.6  | 0.6 | 9         | 0.5 | 0.1 | 0.2 |
| DAMO_3165 | fragment of putative macrolide ABC transporter, fusion of ATP-binding (N-terminal) and membrane (C-terminal) dom | 690     | 37        | 3.9  | 0.5 | 4         | 0.4 | 0.1 | 0.2 |
| DAMO_3166 | Periplasmic component of efflux system   | 1326    | 16        | 0.9  | 0.1 | 4         | 0.2 | 0.0 | 0.4 |
| DAMO_3167 | exported protein of unknown function   | 261     | 6         | 1.7  | 0.2 | 0         | 0.0 | 0.0 | —   |
| DAMO_3168 | exported protein of unknown function   | 462     | 1         | 0.2  | 0.0 | 0         | 0.0 | 0.0 | —   |
| DAMO_3169 | two-component response transcriptional regulato  | 735     | 2         | 0.2  | 0.0 | 10        | 1.0 | 0.2 | 7.9 |
| DAMO_3170 | Periplasmic sensor signal transduction histidine kinase precursor  | 1446    | 83        | 4.1  | 0.6 | 14        | 0.7 | 0.2 | 0.3 |
| DAMO_3171 | glycolate oxidase, subunit GlcD  | 1458    | 99        | 4.9  | 0.7 | 24        | 1.2 | 0.3 | 0.4 |
| DAMO_3172 | FAD linked oxidase-like protein  | 1362    | 34        | 1.8  | 0.3 | 7         | 0.4 | 0.1 | 0.3 |
| DAMO_3173 | Glutamate-1-semialdehyde 2,1-aminomutase (GSA  | 1368    | 70        | 3.7  | 0.5 | 35        | 1.8 | 0.4 | 0.8 |
| DAMO_3174 | protein of unknown function  | 279     | 0         | 0.0  | 0.0 | 0         | 0.0 | 0.0 | —   |
| DAMO_3175 | exported protein of unknown function   | 225     | 1         | 0.3  | 0.0 | 0         | 0.0 | 0.0 | —   |
| sum       |  | 2509305 | 250106    |      |     | 158161    |     |     |     |
| sum nt    |  | 2509305 | 18007632  |      |     | 11387592  |     |     |     |
| coverage  |  |         | 7.1763425 |      |     | 4.5381458 |     |     |     |