

PDF hosted at the Radboud Repository of the Radboud University Nijmegen

The following full text is an author's version which may differ from the publisher's version.

For additional information about this publication click this link.

<http://hdl.handle.net/2066/93640>

Please be advised that this information was generated on 2021-02-25 and may be subject to change.

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

3
4 Francisca A. Luesken^{1*}, Ming L. Wu^{1*}, Huub J.M. Op den Camp¹, Jan T. Keltjens¹, Henk
5 Stunnenberg², Kees-Jan Francoijs², Marc Strous^{3,4}, Mike S.M. Jetten¹

6
7 ¹Department of Microbiology, Radboud University Nijmegen, Institute for Water and Wetland
8 Research, Heyendaalseweg 135, NL-6525 AJ Nijmegen, the Netherlands.

9 ²Department of Molecular Biology, Faculty of Sciences, Nijmegen, Centre of Molecular Life
10 Sciences, Radboud University Nijmegen, Geert Grooteplein 28, NL-6525 GA, Nijmegen, the
11 Netherlands.

12 ³MPI for Marine Microbiology, Celsiusstrasse 1, D-28359, Bremen, Germany.

13 ⁴Centre for Biotechnology, University of Bielefeld, Germany.

14

15 *These authors contributed equally to this study

16 To be submitted as a full-length article

17

18 #Corresponding author: Mike Jetten, Radboud University Nijmegen, Department of
19 Microbiology, Institute for Water and Wetland Research, Heyendaalseweg 135, 6525 AJ
20 Nijmegen, The Netherlands, e-mail: M.Jetten@science.ru.nl, phone: 0031-24-3562969, fax:
21 0031-24-3652830

22 Running title: ‘*Candidatus Methylomirabilis oxyfera*’ exposed to oxygen

23 Keywords: anaerobic methane oxidation, denitrification, '*Candidatus* MethyloMirabilis 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* MethyloMirabilis 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

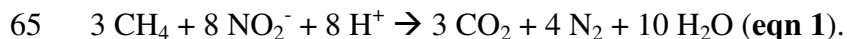
47 cell division processes, were down-regulated. The alkyl hydroperoxide reductase, *alpC*, and
48 genes involved in the synthesis/repair of the iron-sulfur clusters were among the few up-regulated
49 genes. Further, transcription of the *pmoCAB* genes of aerobic methanotrophs present in the non-
50 *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 O₂ (Ettwig et al., 2010). This apparent paradox is explained
69 by the unique ability of *M. oxyfera* to produce intracellular O₂ through an alternative
70 denitrification pathway that does not involve nitrous oxide (N₂O) as an intermediate. In this

71 pathway, the nitric oxide (NO) generated from the reduction of nitrite (NO₂⁻) is suggested to be
72 disproportionated into dinitrogen gas (N₂) and O₂ (Fig. 1) (Ettwig et al., 2010; Wu et al., 2011a).
73 The majority of the generated O₂ is used for activation and oxidation of methane in the strictly
74 O₂-dependent reaction catalyzed by particulate methane monooxygenase (pMMO). It has been
75 proposed that the remainder of the O₂ is used by other processes, like ‘normal’ respiration by
76 terminal O₂ 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 O₂ 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 O₂ concentrations and in transient exposure to O₂. Thus, being able to profit or
83 simply tolerate external O₂ might be essential for the survival and competitive fitness of *M.*
84 *oxyfera* cells in natural O₂ limited ecological habitats.

85 The effects of O₂ exposure on organisms can be manifold. In *M. oxyfera* it could enhance
86 the rates of O₂-dependent reactions, such as the ones catalyzed by pMMO and TORs. During
87 electron transport, more energy is conserved by O₂ respiration due to the involvement of TORs,
88 when compared to denitrification; hence, an O₂ surplus could be beneficial to *M. oxyfera*. On the
89 other hand, the denitrification pathway itself, which is often O₂-sensitive, can be inhibited.
90 Studies have shown that O₂ can suppress the synthesis of denitrifying enzymes and reversibly
91 inhibit their activity. The extent of this effect is species dependent and the O₂-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 O₂ and nitrate were
97 simultaneously used as electron acceptors (Robertson and Kuenen, 1984; Bonin and Gilewicz,
98 1991). Interestingly, the strict aerobic *Methylothermobacter mobilis* denitrifies when grown in methanol,
99 but only to N₂O 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 O₂ utilization as terminal electron acceptor is the concomitant increase in the
102 formation of highly reactive O₂ species (ROS) which are derived from the partial reduction of O₂.
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 O₂-detoxification systems: superoxide anions (O₂⁻) are converted to hydrogen peroxide (H₂O₂) by
106 superoxide dismutase (SOD), and H₂O₂ is eliminated by the action of catalases and peroxidases
107 (Farr and Kogoma, 1991).

108 The response of *M. oxyfera* to O₂ has not been investigated so far. Here, cells from a *M.*
109 *oxyfera* enrichment culture were exposed to two different O₂ concentrations (2 and 8 %). Kinetics
110 of substrate utilization under anoxic conditions and upon O₂ exposure was measured. For the
111 cells treated with 8 % O₂, the differential O₂ 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 O₂ on nitrite-dependent anaerobic methane oxidation rates**

117 Biomass from a *M. oxyfera* enrichment culture was exposed to O₂ in two different experiments (2
118 and 8 % O₂). 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 CH₄: 8 NO₂⁻ (see eqn 1)
120 stoichiometry (Raghoebarsing et al., 2006) (Fig. 2 and Table 1). After addition of O₂, the
121 methane and nitrite conversions decreased instantaneously and the stoichiometry deviated
122 substantially (1 CH₄: 2 NO₂⁻) from the theoretical values (Fig. 2 and Table 1).

123 In the second experiment (8 % O₂), the produced dinitrogen gas was analyzed for the
124 masses ¹⁵⁻¹⁵N₂, ¹⁵⁻¹⁴N₂ and ¹⁴⁻¹⁴N₂ because unlabeled residual nitrite was present in the *M. oxyfera*
125 biomass before labeled nitrite was added. The production rate of ¹⁵⁻¹⁵N₂ was 1.3 nmol min⁻¹ mg
126 protein⁻¹ and in total 1.8 nmol N₂ min⁻¹ mg protein⁻¹ was formed. The initial concentration of O₂
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⁻¹ mg protein⁻¹, 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 % O₂).

133

134 **Effects in the O₂-uptake by cell-free extracts**

135 O₂ consumption by cell-extracts of *M. oxyfera* culture under anoxic (t = 0) and after 24 h of
136 exposure to 8 % of O₂ was assessed using specific reductants: TMPD/cyt *c* or UbqO (Table 2).
137 CN⁻ and SHAM were used as specific inhibitors for heme-copper TORs (Garcia-Horsman et al.,
138 1994) and diiron alternative O₂ reductase (AOX) (Schonbaum et al., 1971), respectively. The
139 total O₂-uptake capacity by *M. oxyfera* cell-free extracts was not significantly affected by O₂
140 exposure. Under anoxic conditions, a higher activity for TMPD/cyt *c*-dependent O₂-uptake was
141 observed. UbqO-dependent O₂-uptake only accounted for about 20 % of the total reduced O₂.
142 When assayed with inhibitors, the UbqO-dependent O₂-uptake was insensitive to both CN⁻ and

143 SHAM. In contrast, the TMPD/cyt *c*-dependent respiration was inhibited up to 50 % by CN⁻.
144 Thus, under anoxic conditions, 50 % of the total consumed O₂ can be assigned to the activity of
145 TOR(s). After exposure to O₂, a shift to UbqO-dependent O₂-uptake was observed. The
146 TMPD/cyt *c* O₂-uptake was 2-fold lower in comparison to the samples from the anoxic condition
147 and the UbqO-dependent O₂-uptake increased up to 3-fold. Now, the TMPD/cyt *c* O₂-uptake was
148 not significantly affected by CN⁻, whereas the UbqO-dependent O₂-uptake inhibited by CN⁻ and
149 SHAM, respectively. This results show that exposure to O₂ stimulated the UbqO-dependent O₂-
150 uptake. Still, only 33 % of the total O₂ consumption can be assigned to TOR enzymes.

151

152 **Changes in transcript levels upon O₂ 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 O₂ (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 O₂ 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 O₂ 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 O₂, 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 O₂ (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 O₂. 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 O₂ 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 O₂: ROS defense system and TORs***

181 A direct effect of the presence of O₂ 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 O₂⁻ 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 O₂ defense that was up-regulated (4-fold) upon O₂ 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 O₂ 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 O₂ exposure (Supplementary Table 1). Overall, genes
201 involved in cell division were repressed in the presence of external O₂; 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 O₂⁻ attack. Exposure of *M.*
207 *oxyfera* to O₂ 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 O₂ exposure.

211

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

213 Due to the complexity of the enrichment culture used, O₂ 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 O₂ exposed conditions. When monitored by FISH, no significant differences were observed
217 between the anoxic and oxic periods, using general probes targeting organisms like α -, β - and γ -
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 O₂ 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 O₂: (i) the
226 ability to perform anaerobic methane oxidation coupled to denitrification, (ii) the ability to
227 produce O₂ 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 % O₂ 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 O₂ added to the incubations. Upon O₂ 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 O₂ does not result in a complete transfer of electrons to O₂ and efficient elimination of
243 ROS.

244 After O₂ 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 O₂ 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 % O₂ (Table 4). Interestingly, the transcription of the *norZ2* gene encoding for the nitric oxide
251 reductase (NOR) was highly induced by O₂. 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 O₂ reductase activity. For instance, the *cb*-type NOR from
254 *P. denitrificans*, reduces O₂ 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 O₂ 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 O₂ 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 O₂ concentrations tested, O₂ reduction
264 occurred at rates higher than could be assigned to methane oxidation alone. The source of the
265 excess of O₂ consumed might be heterotrophic, given that internal substrates can be generated by
266 decaying biomass or by using reserve material.

267 O₂-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 % O₂ (Table 2). O₂
269 exposure also resulted in a shift in the electron donor specificity: under anoxic conditions, the
270 major part of O₂ consumption can be assigned to a cytochrome *c*-dependent TORs, whereas after
271 O₂ 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) O₂-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 O₂ 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 O₂, 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 O₂ 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 O₂ (Gregory and Fridovich, 1973). These observations suggest the
288 response to O₂ among microorganism in not uniformly similar.

289 Two additional observations support the notion that *M. oxyfera* was under oxidative stress
290 upon O₂ 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 O₂-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 O₂. 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 O₂ 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 O₂ 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 O₂
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 O₂
309 suggests that O₂ 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), O₂ levels were always
315 below the detection level as monitored by a Clark-type O₂ 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 O₂ tolerance of *M. oxyfera* was unknown, two experiments with different O₂
320 concentrations were performed, one with initially 2 % pure O₂ in the headspace and one with
321 initially 8 % pure O₂. 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⁻¹ 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 O_2 was supplied to the headspace and at $t = 49$ h another 10 mL of 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 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 O_2 was added to the culture, resulting in a headspace
346 concentration of 8 %. This experiment was prolonged until the initial 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 O_2 was
350 added. Samples (70 mL) for the O_2 -uptake assays were taken after 24 h of O_2 exposure and RNA
351 was extracted for deep sequencing of cDNA using Illumina technology (see below).

352 Gas samples were taken for CH_4 analysis using gas chromatography (100 μl per
353 injection); N_2 and O_2 were analyzed using a gas chromatograph coupled to a mass spectrometer
354 (30 μl 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 % O₂ using the RiboPureTM – 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 RevertAidTM 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 % O₂ 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 **O₂ reduction measurements**

394 O₂ 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) O₂ reductase activities were assayed in the presence of 2 mM sodium ascorbate.
399 Ubiquinone-1 (Q₁; 60 μM) reduced with 10 mM DTT was used to assay UbqO O₂ reductase
400 activity. In the inhibitions assay, the samples were pre-incubated with cyanide (CN⁻; 5 mM) or
401 salicylhydroxamic acid (SHAM; 5 mM) for 1 h. The donor-specific O₂ 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 γ -*Proteobacteria* (Manz et al., 1992); L-C-bProt-1027-a-A-17 (BET42a), specific for
413 β -*Proteobacteria* (Manz et al., 1992), S-Sc-aProt-0968-a-A-18 (ALF 968), specific for α -
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⁻¹ 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 N₂ (labeled and non-labeled) and O₂, 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⁻¹). The gas chromatograph was coupled to a
426 mass spectrometer (Agilent 5975C inert MSD; Agilent, USA). Molecular masses of 32 Da (O₂)
427 and 28 to 30 Da (N₂) 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

434 **ACKNOWLEDGEMENTS**

435 We would like to thank Katharina F. Ettwig, Harry Harhangi and Laura van Niftrik for
436 discussions. FL is supported by the Foundation for Applied Research (STW, project 07736),
437 MLW by a Horizon grant (050-71-58), MSMJ by the European Research Council (ERC, 232937)
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 % O₂) no differences could be observed compared to the anoxic period. (C) After 99 h (72

447 h after the addition of O₂) 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

453 **REFERENCES**

454 Amann, R.I., Binder, B.J., Olson, R.J., Chisholm, S.W., Devereux, R., and Stahl, D.A. (1990)
455 Combination of 16S rRNA-targeted oligonucleotide probes with flow cytometry for
456 analyzing mixed microbial populations. *Appl Environ Microbiol* **56**: 1919-1925.

457 Ayala-Castro, C., Saini, A., and Outten, F.W. (2008) Fe-S cluster assembly pathways in bacteria.
458 *Microbiol Mol Biol Rev* **72**: 110-125.

459 Bianchi, A.A., and Baneyx, F. (1999) Hyperosmotic shock induces the σ₃₂ and σ_E stress
460 regulons of *Escherichia coli*. *Mol Microbiol* **34**: 1029-1038.

461 Bonin, P., and Gilewicz, M. (1991) A direct demonstration of "co-respiration" of oxygen and
462 nitrogen oxides by *Pseudomonas nautica*: some spectral and kinetic properties of the
463 respiratory components. *FEMS Microbiol Lett* **80**: 183-188.

464 Bradford, M.M. (1976) A rapid and sensitive method for the quantitation of microgram quantities
465 of protein utilizing the principle of protein-dye binding. *Anal Biochem* **72**: 248-254.

466 Cabeen, M.T., and Jacobs-Wagner, C. (2005) Bacterial cell shape. *Nat Rev Microbiol* **3**: 601-610.

467 Dos Santos, P.C., Smith, A.D., Frazzon, J., Cash, V.L., Johnson, M.K., and Dean, D.R. (2004)
468 Iron-sulfur cluster assembly. *J Biol Chem* **279**: 19705-19711.

469 Ettwig, K.F., van Alen, T., van de Pas-Schoonen, K.T., Jetten, M.S., and Strous, M. (2009)
470 Enrichment and molecular detection of denitrifying methanotrophic bacteria of the NC10
471 phylum. *Appl Environ Microbiol* **75**: 3656-3662.

472 Ettwig, K.F., Shima, S., van de Pas-Schoonen, K.T., Kahnt, J., Medema, M.H., Op den Camp,
473 H.J. et al. (2008) Denitrifying bacteria anaerobically oxidize methane in the absence of
474 Archaea. *Environ Microbiol* **10**: 3164-3173.

475 Ettwig, K.F., Butler, M.K., Le Paslier, D., Pelletier, E., Mangenot, S., Kuypers, M.M. et al.
476 (2010) Nitrite-driven anaerobic methane oxidation by oxygenic bacteria. *Nature* **464**: 543-
477 548.

478 Farr, S.B., and Kogoma, T. (1991) Oxidative stress responses in *Escherichia coli* and *Salmonella*
479 *typhimurium*. *Microbiol Rev* **55**: 561-585.

480 Fournier, M., Aubert, C., Dermoun, Z., Durand, M.C., Moinier, D., and Dolla, A. (2006)
481 Response of the anaerobe *Desulfovibrio vulgaris* Hildenborough to oxidative conditions:
482 proteome and transcript analysis. *Biochimie* **88**: 85-94.

483 Fridovich, I. (1978) The biology of oxygen radicals. *Science* **201**: 875-880.

484 Fujiwara, T., and Fukumori, Y. (1996) Cytochrome *cb*-type nitric oxide reductase with
485 cytochrome c oxidase activity from *Paracoccus denitrificans* ATCC 35512. *J Bacteriol*
486 **178**: 1866-1871.

487 Garcia-Horsman, J.A., Barquera, B., Rumbley, J., Ma, J., and Gennis, R.B. (1994) The
488 superfamily of heme-copper respiratory oxidases. *J Bacteriol* **176**: 5587-5600.

489 Geissmann, T.A., Teuber, M., and Meile, L. (1999) Transcriptional analysis of the rubrerythrin
490 and superoxide dismutase genes of *Clostridium perfringens*. *J Bacteriol* **181**: 7136-7139.

491 Gregory, E.M., and Fridovich, I. (1973) Induction of superoxide dismutase by molecular oxygen.
492 *J Bacteriol* **114**: 543-548.

493 Hanson, R.S., and Hanson, T.E. (1996) Methanotrophic bacteria. *Microbiol Rev* **60**: 439-471.

494 Hoor, A.T.-T. (1975) A new type of thiosulphate oxidizing, nitrate reducing microorganism:
495 *Thiomicrospira denitrificans* sp. Nov. *Neth J Sea Res* **9**: 344-346, IN349, 347-350.

496 Hu, S., Zeng, R.J., Keller, J., Lant, P.A., and Yuan, Z. (2011) Effect of nitrate and nitrite on the
497 selection of microorganisms in the denitrifying anaerobic methane oxidation process.
498 *Environ Microbiol Rep* **3**: 315-319

499 Ideno, A., Yoshida, T., Iida, T., Furutani, M., and Maruyama, T. (2001) FK506-binding protein
500 of the hyperthermophilic archaeum, *Thermococcus* sp. KS-1, a cold-shock-inducible
501 peptidyl-prolyl cis-trans isomerase with activities to trap and refold denatured proteins.
502 *Biochem J* **357**: 465-471.

503 Imlay, J., Chin, S., and Linn, S. (1988) Toxic DNA damage by hydrogen peroxide through the
504 Fenton reaction *in vivo* and *in vitro*. *Science* **240**: 640-642.

505 Kalyuzhnaya, M.G., Martens-Habbena, W., Wang, T., Hackett, M., Stolyar, S.M., Stahl, D.A. et
506 al. (2009) *Methylophilaceae* link methanol oxidation to denitrification in freshwater lake
507 sediment as suggested by stable isotope probing and pure culture analysis. *Environ*
508 *Microbiol Rep* **1**: 385-392.

509 Kartal, B., Koleva, M., Arsov, R., van der Star, W., Jetten, M.S.M., and Strous, M. (2006)
510 Adaptation of a freshwater anammox population to high salinity wastewater. *J Biotechnol*
511 **126**: 546-553.

512 Knittel, K., and Boetius, A. (2009) Anaerobic oxidation of methane: progress with an unknown
513 process. *Annu Rev Microbiol* **63**: 311-334.

514 Luesken, F.A., Zhu, B., van Alen, T.A., Butler, M.K., Rodriguez Diaz, M., Song, B. et al.
515 (2011a) *pmoA* primers for detection of anaerobic methanotrophs. *Appl Environ Microbiol*
516 **77**: 3877-3880.

517 Luesken, F.A., van Alen, T.A., van der Biezen, E., Frijters, C., Toonen, G., Kampman, C. et al.
518 (2011b) Diversity and enrichment of nitrite-dependent anaerobic methane oxidizing
519 bacteria from wastewater sludge. *Appl Microbiol Biotechnol*. DOI 10.1007/s00253-011-
520 3361-9.

521 Manz, W., Amann, R., Ludwig, W., Wagner, M., and Schleifer, K.H. (1992) Phylogenetic
522 oligodeoxynucleotide probes for the major subclasses of *Proteobacteria* - problems and
523 solutions. *Syst Appl Microbiol* **15**: 593-600.

524 Neef, A. (1997) Anwendung der *in situ* Einzelzell-Identifizierung von Bakterien zur
525 populationsanalyse in komplexen mikrobiellen Biozönosen. In. München: Technische
526 Universität München.

527 Neef, A., Amann, R., Schlesner, H., and Schleifer, K.H. (1998) Monitoring a widespread
528 bacterial group: in situ detection of planctomycetes with 16S rRNA-targeted probes.
529 *Microbiology* **144**: 3257-3266.

530 Op den Camp, H.J.M., Islam, T., Stott, M.B., Harhangi, H.R., Hynes, A., Schouten, S. et al.
531 (2009) Environmental, genomic and taxonomic perspectives on methanotrophic
532 *Verrucomicrobia*. *Environ Microbiol Rep* **1**: 293-306.

533 Raghoebarsing, A.A., Pol, A., van de Pas-Schoonen, K.T., Smolders, A.J., Ettwig, K.F., Rijpstra,
534 W.I. et al. (2006) A microbial consortium couples anaerobic methane oxidation to
535 denitrification. *Nature* **440**: 918-921.

536 Robertson, L.A., and Kuenen, J.G. (1984) Aerobic denitrification: a controversy revived. *Arch*
537 *Microbiol* **139**: 351-354.

538 Schonbaum, G.R., Bonner, W.D., Storey, B.T., and Bahr, J.T. (1971) Specific inhibition of the
539 cyanide-insensitive respiratory pathway in plant mitochondria by hydroxamic acids. *Plant*
540 *Physiol* **47**: 124-128.

541 Schröder, E., and Ponting, C.P. (1998) Evidence that peroxiredoxins are novel members of the
542 thioredoxin fold superfamily. *Protein Science* **7**: 2465-2468.

543 Strous, M., vanGerven, E., Kuenen, J.G., and Jetten, M. (1997) Effects of aerobic and
544 microaerobic conditions on anaerobic ammonium-oxidizing (Anammox) sludge. *Appl*
545 *Environ Microbiol* **63**: 2446-2448.

546 Sztukowska, M., Bugno, M., Potempa, J., Travis, J., and Kurtz Jr, D.M. (2002) Role of
547 rubrerythrin in the oxidative stress response of *Porphyromonas gingivalis*. *Mol Microbiol*
548 **44**: 479-488.

549 Wu, M.L., Ettwig, K.F., Jetten, M.S., Strous, M., Keltjens, J.T., and Niftrik, L. (2011a) A new
550 intra-aerobic metabolism in the nitrite-dependent anaerobic methane-oxidizing bacterium
551 '*Candidatus Methyloirabilis oxyfera*'. *Biochem Soc Trans* **39**: 243-248.

552 Wu, M.L., de Vries, S., van Alen, T.A., Butler, M.K., Op den Camp, H.J.M., Keltjens, J.T. et al.
553 (2011b) Physiological role of the respiratory quinol oxidase in the anaerobic nitrite-
554 reducing methanotroph '*Candidatus Methyloirabilis oxyfera*'. *Microbiology* **157**: 890-
555 898.

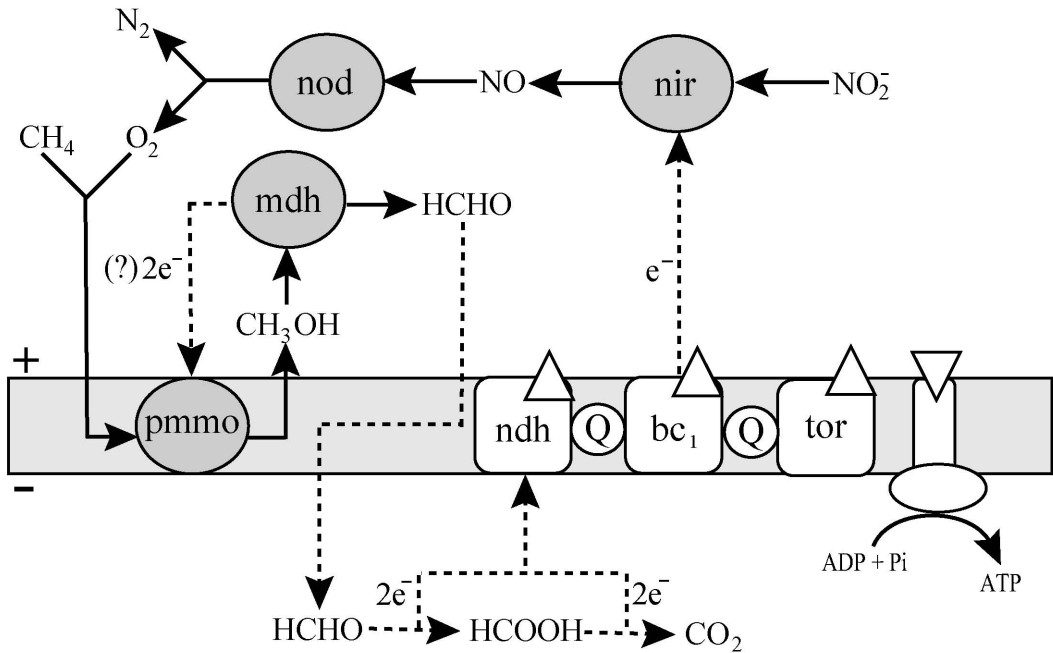
556 Zumft, W.G. (1997) Cell biology and molecular basis of denitrification. *Microbiol Mol Biol Rev*
557 **61**: 533-616.

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; *bc₁*, cytochrome *bc₁* 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 O₂ (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



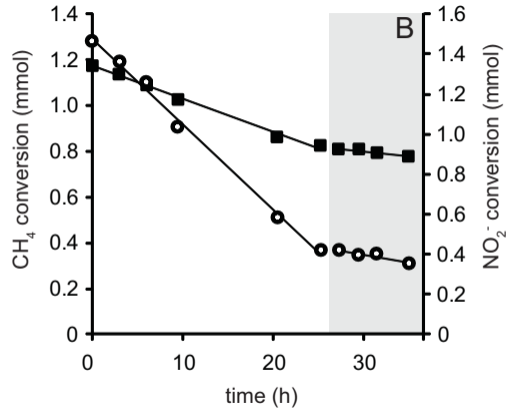
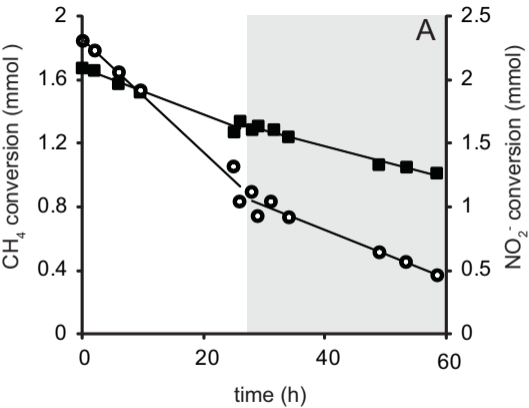


Table 1. Methane, nitrite and O₂ conversion rates under anoxic conditions and after exposure to either 2 or 8 % of pure O₂. The control experiment received 30 mL of helium after 28.5 h, thus remained anoxic with stable conversion rates (the control was measured until t = 79 h).

Experiment	Anoxic		Oxic		
	nmol min ⁻¹ mg protein ⁻¹		nmol min ⁻¹ mg protein ⁻¹		
	CH ₄	NO ₂ ⁻	CH ₄	NO ₂ ⁻	O ₂
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. O₂ reduction activity and inhibition of *M. oxyfera* cell-free extracts from the anoxic condition and after 24 h exposure to 8 % O₂.

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

[#]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⁻¹.

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 % O₂. 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 ₄ MTP dehydrogenase	<i>mdB</i>	DAMO_0455	395	4.5	190	3.4	0.8
Methenyl H ₄ 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 ₄ F dehydrogenase/Methenyl H ₄ F cyclohydrolase	<i>folD</i>	DAMO_1852	89	1	38	0.7	0.7
Formyl H ₄ 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 % O₂. Light grey = down-regulated genes; dark grey = up-regulated genes; white = constitutively expressed.

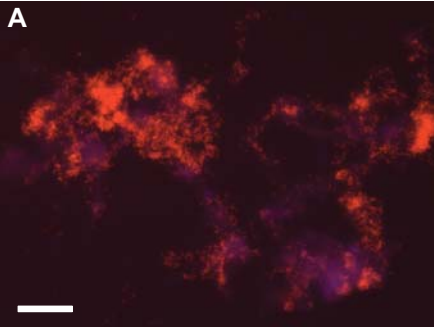
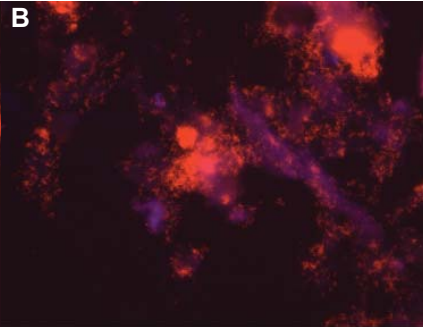
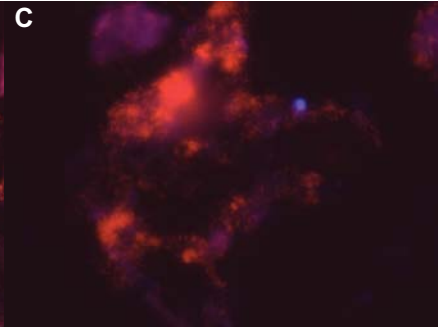
Enzyme	Gene	ORF identifier	Anoxic		Oxic		Ratio (oxic vs. anoxic)
			# unique reads detected	average coverage	# unique reads detected	average coverage	
Nitrate reductase	<i>narG</i>	DAMO_0778	1452	4	190	0.8	0.2
	<i>narH</i>	DAMO_0776	2732	17.9	193	2	0.1
	<i>narL</i>	DAMO_0774	259	3.8	27	0.6	0.2
	<i>narJ</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 % O₂. 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 % O₂ (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 % O₂.

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 O₂ 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 ²⁺ insertion in methanol dehydrogenase	954	0	0.0	0.0	0	0.0	0.0	—
DAMO_0119	Putative mxgC protein, involved in Ca ²⁺ insertion in methanol dehydrogenase	987	0	0.0	0.0	0	0.0	0.0	—
DAMO_0120	Putative mxgK protein, involved in Ca ²⁺ 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 ²⁺ 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. s	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 cytidyltransferase (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 cytidyltransferase (4-diphosphocytidyl-2C- methyl-D-erythritol synthase)	486	26	3.9	0.5	27	4.0	0.9	1.6
DAMO_0522	CysteinyI-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-protein	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 system)	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 system)	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 kinase)	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 diacylglycerol 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	Cobyric 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 Phosphopantothoenylcysteine 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 dehydrogenase	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 hlgB-1	282	87	22.2	3.1	54	13.8	3.0	1.0
DAMO_2507	Antitoxin hlgA-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 dehydrogenase	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			