**Supporting information**

**A predatory soil bacterium reprograms a quorum sensing signal system to regulate antifungal weapon production in a cyclic-di-GMP-independent manner**

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**Figure S1**



**Figure S1. *htsH1*, *htsH2* and *htsH3* are located in an operon. (A)** Bioinformatics predictions that RpfG may interact with HtsH1, HtsH2 and HtsH3. **(B)** Genomic localization of *htsH1*, *htsH2* and *htsH3*. Arrows indicate open reading frame regions of the genes and their transcriptional directions. Gene names are listed above, and primers used to verify operon structures by RT-PCR are indicated below. The primers used are listed in Supplementary Table 2. HP: hypothetical protein; YodB: cytochrome B561 (yodB); HP: hypothetical protein; HtsH1: Hybrid two-component systems protein; HtsH2: Hybrid two-component systems protein; HtsH3: Hybrid two-component systems protein; HP: hypothetical protein; CupP: Cupin 2 conserved barrel domain protein; HemE: uroporphyrinogen decarboxylase (hemE); HP: hypothetical protein. **(C)** Verification of operon organization by RT-PCR. The cDNA was reverse-transcribed with random primers using total RNA from *L. enzymogenes* grown in 10% TSB medium at 28°C until the OD600 reached 1.0. PCR fragment lengths are listed on the right. RT represents amplification using cDNA transcribed from RNA as template; -RT represents the negative control, in which reverse transcriptase was absent during cDNA synthesis; DNA represents the positive control using DNA as the PCR template. **(D)** Bioinformatics analyses of the domain organization of HtsH1, HtsH2 and HtsH3 that belong to HyTCS.

**Figure S2**

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**Figure S2. Identification and sequence characterization of HtsH1, HtsH2 and HtsH3 in *L. enzymogenes*.** Alignment of *L. enzymogenes* HtsH1, HtsH2 and HtsH3. The alignment was performed with Clustal W based on identical residues.

**Figure S3**



**Figure S3. The purified cytoplasmic fragments of HtsH1, HtsH2 and HtsH3 were analysed by 12% SDS-PAGE.** Lane M, molecular mass markers; lane 1, HtsH1C-Flag-His protein; lane 2, HtsH2C-HA-His protein; lane 3, HtsH3C-Myc-His protein.

**Figure S4**



**Figure S4. HtsH1, HtsH2 and HtsH3 exist as a complex in *L. enzymogenes*. (A)** SPR showing that HtsH1C-Flag-His forms a complex with HtsH2C-HA-His with KD = 0.09619 nM. **(B)** SPR showing that HtsH1C-Flag-His forms a complex with HtsH3C-Myc-His with KD = 0.1597 nM. **(C)** SPR showing that HtsH2C-HA-His forms a complex with HtsH3C-Myc-His with KD = 0.1782 nM.

**Figure S5**

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**Figure S5. Transcriptional analysis of HSAF biosynthesis genes in *L. enzymogenes*.** **(A-B)** Trend analysis of differential gene expression in the *htsHs* mutants (Δ*htsH1*, Δ*htsH2*, Δ*htsH3*, Δ*htsH12*, Δ*htsH13*, Δ*htsH23* and Δ*htsH123*). **(C)** Hierarchical cluster analysis applied to the 12 DEGs in the HSAF biosynthesis gene cluster in different mutant backgrounds.

**Figure S6**

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**Figure S6. qRT-PCR analyses of lafB mRNA in the wild type and htsHs mutants, grown in 10% TSB.** Error bars, means ± standard deviations (n = 3). ∗ P < 0.05, ∗∗ P < 0.01, ∗∗∗ P < 0.001, ∗∗∗∗ P < 0.0001, assessed by one-way ANOVA. All experiments were repeated three times with similar results.

**Figure S7**

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**Figure S7. Conservation of the key genes for RpfG, and HtsH1, HtsH2 and HtsH3-dependent regulatory patterns in the genomes of different bacteria.** Genomic organization of the genes and homology analysis of the products. All sequences were retrieved from NCBI Microbial Genome Resources. All amino acid sequences were downloaded from the microbial genome sequence database of NCBI. Position-specific Iterated BLAST (PSI-BLAST) was used for homology analysis.

**Figure S8. Uncropped images of Coomassie-stained gels, immunoblots and EMSA.**

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**Table S1.** Bacterial strains and plasmids used in this study.

|  |  |  |
| --- | --- | --- |
| Strains | Relevant characteristics | References |
| *E.* *coli* |  |  |
| BL21(DE3) | F- *dcm* *omp T* *hsdS*(rB-mB-) *gal* (λDE3) | Lab collection |
| DH5α | F- *deoR* *endA1 gyrA96 hsdR17*(rK-mK+) *recA1* *relA1* *supE*44 *thi-1* Δ(*lacZYA-argF*)*U*169(φ80*lacZ*ΔM15) | Lab collection |
| XL1-Blue MRFˊ kan | Δ(*mcrA*)183, Δ(*mcrCB*-*hsdSMR*-*mrr*)173, *endA1*, *supE44*, *thi-1*, *recA1* *gyrA96*, *relA1*, *lac*, [Fˊ *proAB* *lacI*q*Z*Δ*M15* Tn5 (KmR)] | 1 |
| *L. enzymogenes* | |  |
| OH11 | KanR, wild-type strain | Lab stock |
| Δ*rpfG* | KanR, the *rpfG* in-frame deletion mutant of strain OH11 | 2 |
| OH11/pBBR | KanR, GmR, the wild-type strain harboring the plasmid pBBR1MCS5. | This study |
| Δ*rpfG*/pBBR | KanR, GmR, the *rpfG* in-frame deletion mutant harboring the plasmid pBBR1MCS5. | This study |
| Δ*rpfG*/*rpfG* | KanR, GmR, the *rpfG* in-frame deletion mutant harboring the *rpfG* expression plasmid pBBR1-*rpfG*. | This study |
| Δ*rpfG*/*rpfG* H190A | KanR, GmR, the *rpfG* in-frame deletion mutant harboring the *rpfG* expression plasmid pBBR1-*rpfG* H190A. | This study |
| Δ*rpfG*/*rpfG* D191A | KanR, GmR, the *rpfG* in-frame deletion mutant harboring the *rpfG* expression plasmid pBBR1-*rpfG* D191A. | This study |
| Δ*rpfG*/*rpfG* G253A | KanR, GmR, the *rpfG* in-frame deletion mutant harboring the *rpfG* expression plasmid pBBR1-*rpfG* G253A. | This study |
| Δ*rpfG*/*rpfG* Y254A | KanR, GmR, the *rpfG* in-frame deletion mutant harboring the *rpfG* expression plasmid pBBR1-*rpfG* Y254A. | This study |
| Δ*rpfG*/*rpfG* P255A | KanR, GmR, the *rpfG* in-frame deletion mutant harboring the *rpfG* expression plasmid pBBR1-*rpfG* P255A. | This study |
| Δ*htsH1* | KanR, the Le *htsH1* in-frame deletion mutant of strain OH11 | This study |
| Δ*htsH2* | KanR, the Le *htsH2* in-frame deletion mutant of strain OH11 | This study |
| Δ*htsH3* | KanR, the Le *htsH3* in-frame deletion mutant of strain OH11 | This study |
| Δ*htsH12* | KanR, GmR, the *htsH1* and *htsH2* in-frame deletion mutant of strain OH11. | This study |
| Δ*htsH13* | KanR, GmR, the *htsH1* and *htsH3* in-frame deletion mutant of strain OH11. | This study |
| Δ*htsH23* | KanR, GmR, the *htsH2* and *htsH3* in-frame deletion mutant of strain OH11. | This study |
| Δ*htsH123* | KanR, GmR, the *htsH1*, *htsH2* and *htsH3* in-frame deletion mutant of strain OH11. | This study |
| Δ*htsH1*/*H1* | KanR, GmR, the *htsH1* in-frame deletion mutant harboring the *htsH1* expression plasmid pBBR1-*htsH1*. | This study |
| Δ*htsH2*/*H2* | KanR, GmR, the *htsH2* in-frame deletion mutant harboring the *htsH2* expression plasmid pBBR1-*htsH2*. | This study |
| Δ*htsH3*/*H3* | KanR, GmR, the *htsH3* in-frame deletion mutant harboring the *htsH3* expression plasmid pBBR1-*htsH3*. | This study |
| Δ*htsH12*/*H12* | KanR, GmR, the *htsH1* and *htsH2* double mutant strain harboring the *htsH1* and *htsH2* expression plasmid pBBR1-*htsH12*. | This study |
| Δ*htsH13*/*H13* | KanR, GmR, the *htsH1* and *htsH3* double mutant strain harboring the *htsH1* and *htsH3* expression plasmid pBBR1-*htsH13*. | This study |
| Δ*htsH23*/*H23* | KanR, GmR, the *htsH2* and *htsH3* double mutant strain harboring the *htsH2* and *htsH3* expression plasmid pBBR1-*htsH23*. | This study |
| Δ*htsH123*/*H123* | KanR, GmR, the *htsH1*, *htsH2* and *htsH3* triple mutant strain harboring the *htsH1*, *htsH2* and *htsH3* expression plasmid pBBR1-*htsH123*. | This study |
| Plasmids |  |  |
| pMAL-p2x | AmpR; vector for expression MBP-tag fusion protein | Lab collection |
| pMAL-*rpfG* | AmpR; Le *rpfG* in pMAL-p2x | This study |
| pMAL-*rpfG* H190A | AmpR; Le *rpfG* H190A in pMAL-p2x | This study |
| pMAL-*rpfG* D191A | AmpR; Le *rpfG* D191A in pMAL-p2x | This study |
| pMAL-*rpfG* G253A | AmpR; Le *rpfG* G253A in pMAL-p2x | This study |
| pMAL-*rpfG* P255A | AmpR; Le *rpfG* P255A in pMAL-p2x | This study |
| pET28(b) | KmR, T7 promoter-based vector expression His-tag fusion protein | Lab collection |
| pET-HtsH1C | KmR, the cytoplasmic fragment of *htsH1* in pET-28b | This study |
| pET-HtsH2C | KmR, the cytoplasmic fragment of *htsH2* in pET-28b | This study |
| pET-HtsH3C | KmR, the cytoplasmic fragment of *htsH3* in pET-28b | This study |
| pEX18GM | GmR, *sacB*-based gene replacement vector | 3 |
| pEX18-Δ*htsH1* | GmR, the *htsH1* in-frame deletion fragment inserted to pEX18GM vector between *Hin*dIII/*Xba* l sites | This study |
| pEX18-Δ*htsH2* | GmR, the *htsH2* in-frame deletion fragment inserted to pEX18GM vector between *Hin*dIII/*Xba* l sites | This study |
| pEX18-Δ*htsH3* | GmR, the *htsH3* in-frame deletion fragment inserted to pEX18GM vector between *Hin*dIII/*Xba* l sites | This study |
| pEX18-Δ*htsH12* | GmR, the *htsH1* and *htsH2* in-frame deletion fragment inserted to pEX18GM vector between *Hin*dIII/*Xba* l sites | This study |
| pEX18-Δ*htsH23* | GmR, the *htsH2* and *htsH3* in-frame deletion fragment inserted to pEX18GM vector between *Hin*dIII/*Xba* l sites | This study |
| pEX18-Δ*htsH123* | GmR, the *htsH1*, *htsH2* and *htsH3* in-frame deletion fragment inserted to pEX18GM vector between *Hin*dIII/*Xba* l sites | This study |
| pBBR1MCS5 | GmR, Broad host range cloning vector. | 4 |
| pBBR1-*rpfG* | GmR, the *rpfG* in pBBR1MCS5 | This study |
| pBBR1-*rpfG* H190A | GmR, the *rpfG* H190A in pBBR1MCS5 | This study |
| pBBR1-*rpfG* D191A | GmR, the *rpfG* D191A in pBBR1MCS5 | This study |
| pBBR1-*rpfG* G253A | GmR, the *rpfG* G253A in pBBR1MCS5 | This study |
| pBBR1-*rpfG* Y254A | GmR, the *rpfG* Y254A in pBBR1MCS5 | This study |
| pBBR1-*rpfG* P255A | GmR, the *rpfG* P255A in pBBR1MCS5 | This study |
| pBBR1-*htsH1* | GmR, the *htsH1* in pBBR1MCS5 | This study |
| pBBR1-*htsH2* | GmR, the *htsH2* in pBBR1MCS5 | This study |
| pBBR1-*htsH3* | GmR, the *htsH3* in pBBR1MCS5 | This study |
| pBBR1-*htsH12* | GmR, the *htsH1* and *htsH2* in pBBR1MCS5 | This study |
| pBBR1-*htsH13* | GmR, the *htsH1* and *htsH3* in pBBR1MCS5 | This study |
| pBBR1-*htsH23* | GmR, the *htsH2* and *htsH3* in pBBR1MCS5 | This study |
| pBBR1-*htsH123* | GmR, the *htsH1*, *htsH2* and *htsH3* in pBBR1MCS5 | This study |
| pTRG | TetR, Plasmid used for protein expression in bacterial one-hybrid assay | 1 |
| pTRG-HtsH1C | TetR, the cytoplasmic fragment of *htsH1* in pTRG | This study |
| pTRG-HtsH2C | TetR, the cytoplasmic fragment of *htsH2* in pTRG | This study |
| pTRG-HtsH3C | TetR, the cytoplasmic fragment of *htsH3* in pTRG | This study |
| pBXcmT | CmR, Plasmid used for DNA cloning in bacterial one-hybridization assay | 5 |
| pBXcmT-p*lafB* | CmR, the *lafB* promoter region in pBXcmT | This study |

**Table S2.** Sequences of the PCR primers used in this work.

|  |  |  |
| --- | --- | --- |
| Primer name | Primer sequence (5’ to 3’) | Digestion sites a |
| **For deletion** |  |  |
| pEX-3071 P1 | acccAAGCTTcgattgagagacatggcagc | *Hin*dIII |
| pEX-3071 P2 | aattGGTACCcatgccgttgaccttgctc | *Kpn*I |
| pEX-3071 P3 | aattGGTACCctgcgggccttgttcgag | *Kpn*I |
| pEX-3071 P4 | ctagTCTAGAggtcttcgagcatgttgtcc | *Xba* I |
| pEX-3072 P1 | acccAAGCTTctgcgggccttgttcgag | *Hin*dIII |
| pEX-3072 P2 | aattGGTACCggtcttcgagcatgttgtcc | *Kpn*I |
| pEX-3072 P3 | aattGGTACCtgttcctgcgcaagccggtc | *Kpn*I |
| pEX-3072 P4 | ctagTCTAGAtgttgctgcggtcgaaatag | *Xba* I |
| pEX-3073 P1 | acccAAGCTTgtcacccatgtcgccaac | *Hin*dIII |
| pEX-3073 P2 | aattGGTACCcgatgcggttgatggtgttc | *Kpn*I |
| pEX-3073 P3 | aattGGTACCgcttcgaccgtttcctgc | *Kpn*I |
| pEX-3073 P4 | ctagTCTAGAcatacaacgtcggctggatc | *Xba* I |
| **For in trans expression** | |  |
| pBBR1-*htsH1* P1 | atccAAGCTTtaggtgccgggatcggactg | *Hin*dIII |
| pBBR1-*htsH1* P1 | tgcTCTAGAccttggcgcttgtgggag | *Xba* I |
| pBBR1-*htsH2* P1 | acccAAGCTTctcccacaagcgccaagg | *Hin*dIII |
| pBBR1-*htsH2* P1 | tgcTCTAGAcgatgcggttgatggtgttc | *Xba* I |
| pBBR1-*htsH3* P1 | acccAAGCTTatcttgctggtggaggacga | *Hin*dIII |
| pBBR1-*htsH3* P1 | tgcTCTAGAatgaggtttgcgtcgtaagc | *Xba* I |
| pBBR1-*rpfG* P1 | acccAAGCTTctgctgttcccgtacatgc | *Hin*dIII |
| pBBR1-*rpfG* P2 | atcgGGATCCaccggaaccagttcaacag | *Bam*HI |
| **For site-directed mutant** | | |
| Le *rpfG* H190A P1 | agatggccgcgccgctgGCAgacatcggcaagatcgc |  |
| Le *rpfG* H190A P2 | gcgatcttgccgatgtcTGCcagcggcgcggccatct |  |
| Le *rpfG* D191A P1 | tggccgcgccgctgcacGCAatcggcaagatcgccat |  |
| Le *rpfG* D191A P2 | atggcgatcttgccgatTGCgtgcagcggcgcggcca |  |
| Le *rpfG* G253A P1 | agcgctacgacggctcgGCAtatcccgacgggctggtc |  |
| Le *rpfG* G253A P2 | gaccagcccgtcgggataTGCcgagccgtcgtagcgct |  |
| Le *rpfG* Y254A P1 | gctacgacggctcgggcGCAcccgacgggctggtcggc |  |
| Le *rpfG* Y254A P2 | gccgaccagcccgtcgggTGCgcccgagccgtcgtagc |  |
| Le *rpfG* P255A P1 | acgacggctcgggctatGCAgacgggctggtcggcgag |  |
| Le *rpfG* P255A P2 | ctcgccgaccagcccgtcTGCatagcccgagccgtcgt |  |
| **For protein expression** | |  |
| *htsH1*-flag P1 | gaattcCATATGgcgaagacccggttcctgg | *Nde* I |
| *htsH1*-flag P2 | aattGGATCCtcaTTTGTCGTCGTCGTCTTTGTAGTCggcctcgcgctcgaacaag | *Bam*HI |
| *htsH2*-HA P1 | gaattcCATATGgccaagacccggttcctgg | *Nde* I |
| *htsH2*-HA P2 | aattGGATCCtcaAGCGTAGTCTGGGACGTCGTATGGGTAtggcgcgtccgccgcgtcg | *Bam*HI |
| *htsH3*-Myc P1 | gaattcCATATGgcgaagacgcggttcctgg | *Nde* I |
| *htsH3*-Myc P2 | accgGAATTCtcaCAGATCCTCTTCTGAGATGAGTTTTTGTTCcccttcgccgcggcgcgcga | *Eco*RI |
| MBP-*rpfG* P1 | atcgGGATCCatgctgcgccacatcatcga | *Bam*HI |
| MBP-*rpfG* P2 | atccAAGCTTaccggaaccagttcaacag | *Hin*dIII |
| **For****Bacterial one-hybrid assays and EMSA** | | |
| pTRG-3071C P1 | aattGGATCCgaagtggcgaagcaggcctc | *Bam*HI |
| pTRG-3071C P2 | aattCTCGAGccttggcgcttgtgggag | *Xho* I |
| pTRG-3072C P1 | atcgGGATCCctggccaagacccggttcct | *Bam*HI |
| pTRG-3072C P2 | atcgCTCGAGcgatgcggttgatggtgttc | *Xho* I |
| pTRG-3073C P1 | accgGAATTCgagcgcgaagtggcgaagca | *Eco*RI |
| pTRG-3073C P2 | atcgCTCGAGatgaggtttgcgtcgtaagc | *Xho* I |
| pBX-pHSAF P1 | ccgCTCGAGctgcatctgggtgactcctg | *Xho*I |
| pBX-pHSAF P2 | tgcTCTAGAagtgccgcagaaaatccag | *Xba*I |
| EMSA-pHSAF P1 | acgcgctcgggtaattaacg |  |
| EMSA-pHSAF P2 | gtttcgatgatgagaccgcc |  |
| **For cotranscript identification** | | |
| p1 | taggtgccgggatcggactg |  |
| p2 | catgccgttgaccttgctc |  |
| p3 | gcttcgaccgcttcctgc |  |
| p4 | acagggtgaactcgacgc |  |
| p5 | ggttcgacctgttcctgc |  |
| p6 | cgatgcggttgatggtgttc |  |
| p7 | gcttcgaccgtttcctgc |  |
| p8 | atgaggtttgcgtcgtaagc |  |
| p9 | gcttacgacgcaaacctcat |  |
| p10 | catacaacgtcggctggatc |  |
| p11 | gatccagccgacgttgtatg |  |
| p12 | aagggcatgtgttcaacctc |  |
| **For RT-qPCR** | | |
| RT-16s rRNA F | acggtcgcaagactgaaact |  |
| RT-16s rRNA R | aaggcaccaatccatctctg |  |
| RT-*lafB* F | gcatccacaccgaactgaag |  |
| RT-*lafB* R | gttgagctgcttgaggaacc |  |

**Table S3.** List of genes differentially expressed in the *htsH1*, *htsH2*, and *htsH3* mutants compared to the wild-type strain.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Gene name | log2 fold change (mutant strian / wild-type) | | | | | | | | Gene description |
| OH11 | Δ*htsH1* | Δ*htsH2* | Δ*htsH3* | Δ*htsH12* | Δ*htsH23* | Δ*htsH13* | Δ*htsH123* |
| Le0029 | 0 | 0.71 | 0.88 | -0.18 | 0.3 | 0.82 | 1.25 | 1.2 | hypothetical protein |
| Le0030 | 0 | 0.44 | 0.6 | 0.83 | 0.65 | 0.69 | 0.52 | 1.06 | hypothetical protein |
| Le0055 | 0 | 0.46 | 0.84 | 0.28 | 0.83 | 0.91 | 1.2 | 1.18 | hypothetical protein |
| Le0059 | 0 | 0.42 | 0.47 | 0.46 | 0.16 | 0.4 | 0.33 | 1.3 | AsnC family transcriptional regulator |
| Le0060 | 0 | 1.12 | 1.71 | 1.64 | 0.14 | 1.66 | 1.34 | 2.8 | hypothetical protein |
| Le0082 | 0 | 0.68 | 0.57 | 0.61 | 0.79 | 0.72 | 0.82 | 1.06 | putative transmembrane GGDEF transcriptional regulatory protein |
| Le0161 | 0 | 0.91 | 0.57 | 0.46 | 0.48 | 0.78 | 0.9 | 1.05 | aldehyde-activating protein |
| Le0183 | 0 | 0.9 | 0.9 | 1.58 | 1.94 | 1.82 | 1.5 | 2.76 | putative methyltransferase |
| Le0241 | 0 | 0.63 | -0.02 | -0.52 | 0.3 | 0.52 | 0.95 | 1.1 | type IV pilus modification protein PilV |
| Le0277 | 0 | 0.63 | -0.04 | 0.4 | 0.59 | 0.96 | 1.28 | 1.42 | hypothetical protein |
| Le0305 | 0 | 1.17 | 0.13 | -0.37 | -1.97 | 1.09 | -1.72 | -1.29 | hypothetical protein |
| Le0306 | 0 | 0.06 | -0.92 | -1.25 | -2.16 | -0.41 | -2.42 | -2.91 | C4-dicarboxylate ABC transporter |
| Le0317 | 0 | 0.57 | 0.95 | 0.71 | 0.25 | 0.87 | -0.72 | 1.92 | hypothetical protein |
| Le0320 | 0 | 0.77 | 0.21 | 0.24 | 0.52 | 0.71 | 0.85 | 1.04 | glycosyl hydrolase family 5 |
| Le0336 | 0 | 1 | 0.23 | -0.18 | 0.74 | 0.65 | 1.12 | 1.11 | hypothetical protein |
| Le0347 | 0 | 0.87 | 0.35 | 0.81 | 0.64 | 0.65 | 0.49 | 1.05 | conserved hypothetical protein |
| Le0365 | 0 | 1.27 | 0.6 | 0.91 | 0.74 | 1.19 | 0.16 | 1.4 | putative Na+-dependent transporter |
| Le0383 | 0 | 0.57 | 0.31 | 0.45 | 0.79 | 0.52 | 0.72 | 1.2 | hypothetical protein |
| Le0446 | 0 | 0.72 | 0.57 | 0.78 | 1.17 | 0.62 | 0.76 | 1.29 | outer membrane lipoprotein LolB |
| Le0454 | 0 | 0.8 | 0.77 | 1.15 | 1.51 | 0.52 | 1.16 | 2.12 | hypothetical protein |
| Le0493 | 0 | 0.83 | 0.61 | 0.53 | 0.63 | 0.53 | 1.02 | 1.19 | hypothetical protein |
| Le0496 | 0 | 0.86 | 0.34 | 0.34 | 1.16 | -0.17 | -0.11 | 1.63 | AraC-type DNA binding HTH domain |
| Le0503 | 0 | 0.69 | 0.28 | 0.52 | 0.67 | 0.59 | 0.8 | 1.06 | RNA polymerase sigma70 factor |
| Le0533 | 0 | 0.51 | 0.46 | 0.82 | 0.14 | 0.88 | 1 | 1.03 | protein of unknown function DUF6 transmembrane |
| Le0534 | 0 | 2.15 | 0.88 | 0.56 | 1.88 | 1.78 | 2.17 | 2.08 | hypothetical protein |
| Le0592 | 0 | 1.23 | 0.75 | 0.2 | 1.08 | 0.72 | 1.37 | 1.17 | Signal transduction histidine kinase |
| Le0659 | 0 | 0.97 | 1.09 | 1.06 | 0.97 | 1.23 | 1.02 | 1.8 | hypothetical protein |
| Le0660 | 0 | 0.64 | 0.63 | 1.05 | 1.07 | 1.32 | 1.21 | 1.65 | hypothetical protein |
| Le0797 | 0 | 0.67 | 0.9 | 1.02 | 0.32 | 0.96 | 1.64 | 1.34 | CAAX amino terminal protease |
| Le0836 | 0 | 0.45 | 0.54 | 0.67 | 0.97 | 0.38 | 0.74 | 1.02 | IgA-specific serine endopeptidase |
| Le0840 | 0 | 0.93 | 0.67 | 1.04 | 1.47 | 1.25 | 1.51 | 1.36 | Acetyltransferase, GNAT family protein |
| Le0863 | 0 | 2.22 | 2.06 | 2.25 | 2.96 | 1.46 | 2.65 | 4.08 | hypothetical protein |
| Le0872 | 0 | 2.8 | 4.46 | 3.4 | 2 | 3.22 | 2.39 | 3.62 | hypothetical protein |
| Le0873 | 0 | 1.34 | -0.13 | -0.28 | 0.73 | 0.96 | 0.9 | 2.57 | hypothetical protein |
| Le0931 | 0 | -0.1 | 0.86 | -0.55 | -1.4 | 0.17 | -1.46 | -1.91 | sulfotransferase protein |
| Le0932 | 0 | 0.07 | 0.86 | -0.72 | -1.21 | 0.13 | -1.19 | -1.68 | short-chain dehydrogenase/reductase SDR |
| Le0933 | 0 | -0.18 | 0.9 | -0.6 | -1.34 | 0.06 | -1.43 | -1.75 | hypothetical protein |
| Le0934 | 0 | -0.1 | 0.97 | -0.54 | -1.4 | 0.16 | -1.1 | -1.59 | coproporphyrinogen III oxidase |
| Le0935 | 0 | -0.45 | 0.73 | -0.76 | -1.69 | -0.07 | -1.64 | -2.29 | hypothetical protein |
| Le0938 | 0 | 0.33 | 1.07 | -0.39 | -1.15 | 0.59 | -0.8 | -1.07 | uncharacterized protein |
| Le0939 | 0 | 0.31 | 1 | -0.7 | -1 | 0.13 | -0.7 | -1.18 | inner membrane transport permease |
| Le0941 | 0 | 0.34 | 0.77 | -0.37 | -1.15 | 0.07 | -1.01 | -1.07 | hypothetical protein |
| Le0962 | 0 | 0.71 | 0.29 | 0.18 | 0.79 | 0.27 | 0.95 | 1.28 | DUF11 domain-containing protein |
| Le1035 | 0 | 1.11 | 1.43 | 0.13 | 0.47 | 0.58 | 0.71 | 1.82 | acetyltransferase |
| Le1036 | 0 | 0.91 | 1.21 | 0.49 | 0.27 | 0.81 | 0.89 | 1.07 | integral membrane-like protein |
| Le1065 | 0 | 1.81 | 1.29 | 1.41 | 1.84 | 1.22 | 2.74 | 2.31 | cell envelope biogenesis protein TonB |
| Le1066 | 0 | 0.89 | 1.05 | 1.28 | 1.61 | 1.39 | 1.32 | 1.6 | hypothetical protein |
| Le1074 | 0 | 0.64 | 0.41 | 0.54 | 0.44 | 0.15 | 0.92 | 1.02 | XshC-Cox1-family protein |
| Le1100 | 0 | 0.99 | 0.95 | 0.54 | 0.98 | 0.61 | 0.96 | 1.09 | transglutaminase |
| Le1108 | 0 | 0.37 | -0.08 | 0.25 | 0.47 | 0.48 | 0.09 | 1.05 | X-Pro dipeptidase |
| Le1109 | 0 | 0.25 | -0.09 | 0.47 | 0.18 | 0.37 | 0.19 | 1.12 | aldehyde dehydrogenase (NAD+) |
| Le1114 | 0 | 0.17 | 0.01 | 0.06 | -0.13 | 0.18 | 0.06 | 1.08 | hydroxyproline-2-epimerase |
| Le1124 | 0 | 0.45 | -0.11 | 0.18 | 0.46 | 0.5 | 0.56 | 1.02 | hypothetical protein |
| Le1126 | 0 | -0.3 | -0.41 | -1.02 | -0.87 | -0.24 | -0.73 | -1.09 | flagellar biosynthesis protein FliQ |
| Le1173 | 0 | 0.34 | 0.63 | 0.49 | 0.32 | 0.54 | 1.39 | 1.02 | AsnC family transcriptional regulator |
| Le1188 | 0 | 1.09 | 0.38 | 0.13 | 0.02 | 0.62 | 0.75 | 1.33 | hypothetical protein |
| Le1213 | 0 | 1.08 | 0.04 | -0.22 | 0.19 | -0.35 | 0.32 | 1.36 | hypothetical protein |
| Le1228 | 0 | 0.33 | 0.71 | 0.49 | 0.47 | 0.73 | 0.57 | 1.09 | hypothetical protein |
| Le1250 | 0 | 0.65 | 0.16 | 0.25 | 0.09 | 0.68 | 0.51 | 1.09 | hypothetical protein |
| Le1259 | 0 | -0.08 | 0.33 | -0.93 | -1.27 | 0.05 | -0.82 | -1.23 | PAAR domain-containing protein |
| Le1296 | 0 | 2.1 | 2.33 | 1.27 | 1.19 | 1.42 | 1.79 | 2.24 | hypothetical protein |
| Le1301 | 0 | -0.09 | 0.73 | -0.85 | -1.61 | -0.21 | -1.2 | -1.7 | Aminotransferase, classes I and II |
| Le1302 | 0 | 0.02 | 0.98 | -0.47 | -1.37 | 0.2 | -1.04 | -1.59 | L-2, 4-diaminobutyrate decarboxylase |
| Le1312 | 0 | 1.05 | 0.58 | 0.05 | 0.55 | 1.36 | 0.55 | 1.06 | hypothetical protein |
| Le1330 | 0 | 1.38 | 0.69 | 1.28 | 0.61 | 1.49 | 1.6 | 1.78 | hypothetical protein |
| Le1348 | 0 | 0.74 | 1.12 | 0.34 | 0.87 | 0.45 | 0.95 | 1.41 | Putative secreted protein |
| Le1439 | 0 | 1.19 | 0.27 | 1.04 | 0.38 | 0.58 | 0.96 | 1.3 | hypothetical protein |
| Le1440 | 0 | 0.84 | 0.58 | 0.99 | 0.8 | 0.48 | 0.89 | 1.27 | hypothetical protein |
| Le1462 | 0 | 1.26 | 0.31 | 0.75 | 1.74 | 0.57 | 0.6 | 1.68 | rrf2 family protein transcriptional regulator family protein |
| Le1491 | 0 | 0.56 | 0.8 | 1.13 | 1.13 | 1.09 | 0.94 | 1.69 | hypothetical protein |
| Le1503 | 0 | 0.69 | 0.22 | 0.86 | 0.66 | 0.56 | 0.25 | 1.52 | TonB-dependent receptor |
| Le1513 | 0 | 1.14 | 0.79 | 0.52 | 0.88 | 1.66 | 1.26 | 1.97 | uroporphyrinogen-III synthase |
| Le1537 | 0 | 0.7 | 0.68 | 0.52 | 0.91 | 0.46 | 0.84 | 1.3 | two-component system regulatory protein |
| Le1544 | 0 | 1.03 | 0.53 | -0.23 | 0.43 | 0.72 | 1.26 | 1.18 | hypothetical protein |
| Le1575 | 0 | 0.75 | 0.17 | 0.63 | 0.65 | 0.38 | 0.52 | 1.15 | hypothetical protein |
| Le1581 | 0 | 0.49 | 0.47 | 0.5 | 0.67 | 0.55 | 0.73 | 1.05 | hypothetical protein |
| Le1594 | 0 | 1.2 | 0.76 | 0.18 | 1.2 | 1.1 | 1.54 | 1.33 | hypothetical protein |
| Le1597 | 0 | 0.66 | 0.49 | 0.68 | 0.38 | 0.97 | 1.11 | 1.18 | hypothetical protein |
| Le1634 | 0 | 1.52 | 1.78 | 1.66 | 1.8 | 0.59 | 1.55 | 2.16 | hypothetical protein |
| Le1675 | 0 | 1.66 | 1.97 | 1.63 | 1.75 | 1.97 | 2.61 | 3.12 | transmembrane anti-sigma factor |
| Le1677 | 0 | -0.38 | -0.22 | -0.46 | -0.09 | 0.32 | 0.4 | -3.82 | catalase |
| Le1707 | 0 | 0.66 | 0.58 | 0.18 | 0.27 | 0.83 | 0.98 | 1.09 | exodeoxyribonuclease V subunit alpha |
| Le1730 | 0 | 0.2 | 0.53 | 0.22 | 0.64 | 0.9 | 0.68 | 1.08 | AsnC family transcriptional regulator |
| Le1743 | 0 | 0.76 | 1.55 | 1.07 | 1.42 | 0.92 | 1.94 | 2.01 | two-component system sensor protein |
| Le1780 | 0 | 1.81 | 1.56 | 0.91 | 1.4 | 1.21 | 1.36 | 1.74 | SIMPL domain-containing protein |
| Le1827 | 0 | 1.18 | 1.57 | 0.99 | 1.48 | 0.5 | 1.58 | 2.12 | hypothetical protein CATMIT\_01610, partial |
| Le1863 | 0 | 0.81 | 0.87 | 0.28 | 0.75 | 0.36 | 0.43 | 1.51 | hypothetical protein |
| Le1898 | 0 | 1 | 0.48 | 0.57 | 0.15 | 0.25 | 0.74 | 1.03 | hypothetical protein |
| Le1914 | 0 | 0.78 | 0.02 | 0.41 | 0.26 | 0.65 | 0.76 | 1.25 | Agmatinase |
| Le1920 | 0 | 1.26 | 0.78 | 0.35 | 1.03 | 0.89 | 0.84 | 1.19 | hypothetical protein |
| Le1926 | 0 | 0.85 | 0.18 | 0.88 | 1.04 | 2 | 1.13 | 2.38 | fimbrial protein |
| Le1967 | 0 | 0.73 | 1.38 | -0.97 | -2.05 | 0.84 | -0.29 | -1.32 | hypothetical protein |
| Le1993 | 0 | 0.44 | 0.55 | 0.53 | 0.59 | 0.65 | 1.02 | 1.42 | hypothetical protein |
| Le2014 | 0 | 2.08 | 2.14 | 1.78 | 2.16 | 1.84 | 2.42 | 2.31 | hypothetical protein |
| Le2016 | 0 | 0.73 | 0.61 | 0.36 | 0.94 | 0.65 | 1 | 1.25 | hypothetical protein |
| Le2029 | 0 | 1.62 | 1.67 | 1.81 | 1.48 | 0.09 | 2.53 | 2.7 | RDD family protein |
| Le2049 | 0 | 0.18 | 0.03 | -0.11 | 0.32 | 0.19 | 0.34 | 1.24 | multidrug ABC transporter ATP-binding protein |
| Le2056 | 0 | 0.28 | 0.46 | 0.54 | 1.01 | 0.68 | 0.86 | 1.04 | two-component system response regulator, LuxR family |
| Le2156 | 0 | 1.02 | 0.71 | 0.76 | 0.98 | 0.76 | 0.77 | 1.33 | GCN5 family acetyltransferase |
| Le2177 | 0 | 0.03 | 0.67 | 0.58 | 0.98 | -0.29 | 0.42 | 2 | MarR family transcriptional regulator, partial |
| Le2180 | 0 | 0.53 | 0.51 | 0.15 | 0.61 | 0.86 | 0.89 | 1.06 | hypothetical protein |
| Le2189 | 0 | 1.07 | 0.64 | 0.83 | 1.08 | 0.99 | 0.95 | 1.83 | hypothetical protein |
| Le2194 | 0 | 0.64 | 0.63 | 0.29 | 0.98 | 0.45 | 0.94 | 1.11 | Xaa-Pro dipeptidase, putative |
| Le2211 | 0 | 1.17 | 0.8 | 0.37 | 0.72 | 0.85 | 0.92 | 1.22 | hypothetical protein |
| Le2224 | 0 | 0.53 | 0.75 | 0.36 | 0.88 | 0.51 | 0.67 | 1.17 | protein of unknown function DUF81 |
| Le2228 | 0 | -10.93 | -4.7 | -6.02 | -10.93 | -4.43 | -4.6 | -5.6 | transcriptional regulator |
| Le2263 | 0 | 1.63 | 0.92 | 0.71 | 0.59 | 0.73 | 1.42 | 1.4 | hypothetical protein |
| Le2273 | 0 | 0.19 | 0.11 | 1.05 | 0.82 | 0.47 | 0.92 | 1.03 | transcriptional regulator |
| Le2311 | 0 | -0.16 | 0.65 | -0.36 | -1.35 | 0.26 | -0.8 | -1.14 | hypothetical protein |
| Le2326 | 0 | 0.14 | 1.46 | -0.57 | -1.88 | 0.8 | -1.24 | -1.73 | ImcF-related family protein |
| Le2327 | 0 | 0.21 | 1.52 | -0.56 | -2.1 | 1.05 | -1.53 | -2.23 | type VI secretion protein |
| Le2328 | 0 | 0 | 1.2 | -0.71 | -1.81 | 1.07 | -1.42 | -1.53 | cell envelope biogenesis protein OmpA |
| Le2338 | 0 | 0.18 | 1.32 | -0.57 | -1.43 | 0.73 | -0.71 | -1.49 | type IV secretion protein Rhs |
| Le2343 | 0 | -0.05 | 0.87 | -0.52 | -1.4 | 0.5 | -0.9 | -1.18 | hypothetical protein |
| Le2344 | 0 | 0.07 | 1.09 | -0.51 | -1.59 | 0.54 | -0.9 | -1.3 | conserved hypothetical protein |
| Le2345 | 0 | 0.27 | 1.2 | -0.45 | -1.49 | 0.68 | -0.91 | -1.48 | EvpB family type VI secretion protein |
| Le2346 | 0 | 0.24 | 1.29 | -0.42 | -2.03 | 1.05 | -1.21 | -1.93 | Hcp family protein |
| Le2348 | 0 | 0.3 | 1.63 | -0.17 | -1.73 | 0.92 | -1.17 | -1.46 | type VI secretion protein |
| Le2349 | 0 | 0.31 | 1.44 | -0.36 | -1.74 | 0.81 | -0.75 | -1.71 | type VI secretion protein |
| Le2350 | 0 | -0.11 | 1.32 | -0.43 | -2.04 | 1.01 | -1.59 | -1.66 | hypothetical protein |
| Le2351 | 0 | 0.05 | 1.56 | -0.52 | -1.96 | 0.93 | -1.16 | -1.79 | type VI secretion ATPase, ClpV1 family |
| Le2388 | 0 | 1.13 | 0.21 | 0.93 | 0.08 | 1 | 1.4 | 1.13 | hypothetical protein |
| Le2399 | 0 | -0.4 | -0.88 | -0.58 | -1.59 | -0.16 | -0.9 | -1.1 | LysM peptidoglycan-binding domain-containing protein |
| Le2400 | 0 | -0.32 | -0.68 | -0.59 | -1.71 | -0.1 | -0.93 | -1.12 | Rare lipoprotein A |
| Le2428 | 0 | 0.71 | -0.05 | 0.42 | 0.29 | 0.7 | 0.85 | 1.04 | hypothetical protein |
| Le2435 | 0 | 0.13 | 0.47 | -0.47 | -1.48 | 0.04 | -0.02 | -1.55 | conserved protein of unknown function |
| Le2449 | 0 | 1.09 | 1.12 | 0.33 | 0.72 | 1.24 | 1.21 | 1.83 | hypothetical protein |
| Le2457 | 0 | 1.11 | 0.64 | -0.08 | 1.06 | 0.76 | 0.72 | 1.2 | bacterial regulatory helix-turn-helix protein, LysR family protein 1 |
| Le2461 | 0 | -0.55 | 3.12 | -1.16 | -4.32 | 1.33 | -3.12 | -3.04 | DUF2188 domain-containing protein |
| Le2485 | 0 | 0.54 | 0.38 | 0.89 | 0.63 | 0.68 | 1.1 | 1.29 | TetR family transcriptional regulator |
| Le2492 | 0 | 0.34 | -0.13 | 0.16 | 0.5 | 0.75 | 0.75 | 1.05 | hypothetical protein |
| Le2506 | 0 | 1.36 | 1.33 | 1.2 | 1.34 | 2 | 1.68 | 1.7 | hypothetical protein |
| Le2520 | 0 | 1.28 | 0.8 | 0.97 | 0.94 | 1.13 | 1.27 | 2 | hypothetical protein |
| Le2542 | 0 | 0.39 | 0.2 | 0.43 | 0.62 | 0.53 | 1.06 | 1.2 | glyoxalase |
| Le2591 | 0 | 1.25 | 0.7 | 0.66 | 1.02 | 0.91 | 0.46 | 1.08 | dithiobiotin synthetase |
| Le2592 | 0 | 0.18 | 0.23 | -1.46 | -0.94 | 0.12 | -0.29 | -1.44 | hypothetical protein |
| Le2595 | 0 | 1.03 | 0.46 | 0.15 | 0.11 | 0.55 | 0.65 | 1.16 | bacterioferritin |
| Le2634 | 0 | 0.85 | 1.35 | 0.66 | 0.93 | 0.34 | 0.87 | 1.25 | hypothetical protein |
| Le2645 | 0 | 0.3 | 2.32 | 1.23 | 1.44 | 2.19 | 2.05 | 2.26 | hypothetical protein |
| Le2647 | 0 | 0.59 | 0.29 | 0.6 | 0.45 | 0.72 | 0.86 | 1.23 | hypothetical protein involved in tolerance to divalent cations |
| Le2715 | 0 | 0.34 | 0.23 | 0.12 | 0.73 | 0.42 | 0.68 | 1.26 | hypothetical protein |
| Le2716 | 0 | 1.03 | 0.8 | 0.89 | 1.02 | 0.74 | 1.58 | 1.84 | hypothetical protein |
| Le2727 | 0 | 0.9 | 0.8 | 0.65 | 0.93 | 0.96 | 1.12 | 1.11 | transcriptional regulator, AraC family |
| Le2732 | 0 | 1.53 | 1.75 | 1.3 | 1.86 | 0.7 | 1.98 | 2.25 | serine/threonine protein kinase |
| Le2774 | 0 | 0.19 | 0.5 | 0.41 | 0.6 | 0.45 | 0.77 | 1.79 | hypothetical protein |
| Le2799 | 0 | 0.71 | 0.27 | -0.26 | 0.64 | 0.52 | 0.87 | 1.07 | fimbrial assembly protein |
| Le2809 | 0 | 0.86 | 0.62 | 0.08 | 0.24 | 0.72 | 0.94 | 1.03 | hypothetical protein |
| Le2821 | 0 | 1.01 | 1.85 | 2.09 | 2.45 | 0.43 | 1.9 | 3.53 | hypothetical protein |
| Le2846 | 0 | 0.8 | 0.83 | 0.78 | 0.59 | 1.09 | 0.63 | 1.51 | hypothetical protein |
| Le2870 | 0 | 0.86 | 0.76 | 1.1 | 0.07 | 1.44 | 0.42 | 1.48 | hypothetical protein |
| Le2884 | 0 | 1.52 | 0.82 | 1.15 | 0.2 | 1.59 | 0.84 | 1.55 | conserved hypothetical protein |
| Le2908 | 0 | 0.43 | 0.64 | 0.61 | 0.57 | 0.61 | 0.85 | 1.21 | hypothetical protein |
| Le2911 | 0 | 1.05 | 0.7 | 0.91 | 0.83 | 0.8 | 0.96 | 1.48 | putative transcriptional acitvator, Baf family |
| Le2912 | 0 | 0.55 | 0.32 | 0.23 | 0.7 | 0.36 | 0.94 | 1.04 | sporulation protein |
| Le2936 | 0 | 1.33 | 0.74 | 1.23 | 1.41 | 0.47 | 1.13 | 1.63 | hypothetical protein |
| Le2937 | 0 | 0.31 | 0.13 | 0.51 | 0.69 | 0.25 | 0.76 | 1.01 | aminopeptidase |
| Le3071 | 0 | -13.47 | 0.69 | -0.12 | -13.47 | 0.29 | -13.47 | -13.47 | histidine kinase |
| Le3072 | 0 | 0.76 | -2.9 | 0.22 | -14.44 | -0.53 | 0.81 | -14.44 | histidine kinase |
| Le3073 | 0 | 0.74 | 0.53 | -13.96 | -1.48 | -0.59 | -8.17 | -13.96 | two component system sensor-response regulator hybrid protein |
| Le3075 | 0 | 1.76 | 0.14 | 1.37 | 1.22 | 1.84 | 1.95 | 2.25 | Cupin 2 conserved barrel domain protein |
| Le3080 | 0 | 0.96 | 0.49 | 0.92 | 0.81 | 1.06 | 1.34 | 1.24 | transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain |
| Le3084 | 0 | 0.87 | 0.59 | 0.74 | 0.61 | 0.75 | 1.2 | 1.04 | D-glycerate 3-kinase |
| Le3087 | 0 | 0.71 | -0.09 | 2.01 | 1.21 | 0.81 | 1.53 | 2.04 | lipase |
| Le3092 | 0 | 0.75 | 0.61 | 0.81 | 0.84 | 0.6 | 1.02 | 1.13 | hydrolase, HAD superfamily |
| Le3112 | 0 | 0.88 | 0.95 | 0.67 | 0.94 | 0.84 | 1.23 | 1.41 | PTS system fructose subfamily transporter subunit IIA |
| Le3169 | 0 | 1.07 | 1.27 | -1.34 | -6.74 | 0.33 | -0.68 | -6.21 | putative comea-related dna uptake protein |
| Le3200 | 0 | 0.71 | 0.64 | 0.68 | 0.43 | 0.63 | 0.89 | 1.07 | hypothetical protein |
| Le3223 | 0 | 0.43 | 0.03 | -0.93 | 0.69 | 0.28 | 0.41 | 1.07 | TonB-dependent receptor |
| Le3239 | 0 | 0.43 | 1.72 | -0.53 | -1.71 | 0.93 | -0.77 | -1.47 | hypothetical protein |
| Le3241 | 0 | 1.37 | 0.93 | 1.32 | 2.02 | -0.69 | 0.59 | 3.08 | conserved hypothetical protein |
| Le3259 | 0 | 0.6 | 0.51 | 0.41 | 0.43 | 1.11 | 1.07 | 1.18 | peptidase |
| Le3307 | 0 | 0.96 | 1.4 | 1.11 | 1.3 | 0.39 | 1.09 | 1.19 | inner membrane protein |
| Le3323 | 0 | 0.36 | 0.4 | 0.14 | 0.39 | 0.5 | 0.29 | 1.05 | transcriptional regulator |
| Le3349 | 0 | 0.54 | 1.54 | 1.8 | 0.67 | 1.6 | 1.37 | 2.11 | PadR family transcriptional regulator |
| Le3353 | 0 | 0.69 | 0.51 | 0.48 | 0.17 | 0.78 | 0.79 | 1.01 | putative membrane protein |
| Le3365 | 0 | 0.91 | 1.09 | 0.6 | 0.33 | 0.61 | 0.94 | 1.07 | hypothetical protein |
| Le3369 | 0 | 1.6 | 1.47 | 0.51 | 1.43 | 1.5 | 2.08 | 2.17 | hypothetical protein |
| Le3373 | 0 | 0.7 | 0.26 | 0.41 | 0.83 | 0.57 | 0.89 | 1.4 | hypothetical protein |
| Le3393 | 0 | 1.22 | 0.74 | 0.97 | 1.12 | 0.87 | 1.14 | 1.44 | hypothetical protein |
| Le3403 | 0 | 0.61 | 0.12 | 0.29 | -0.05 | 1.06 | 0.8 | 1.08 | hypothetical protein |
| Le3421 | 0 | 0.9 | 0.55 | 0.21 | 0.6 | 0.85 | 1.24 | 1.3 | RNA-binding protein Hfq |
| Le3430 | 0 | 1.01 | 1.79 | 0.75 | 1.68 | 1.25 | 1.86 | 1.34 | conserved repeat domain protein |
| Le3437 | 0 | 0.02 | -0.61 | -0.27 | -2.96 | 0.22 | -1.66 | -1.53 | hypothetical protein |
| Le3501 | 0 | 3.02 | 3.06 | 1.85 | 3.45 | 2.4 | 1.98 | 3.62 | membrane protein |
| Le3531 | 0 | 0.74 | 0.87 | 0.09 | 0.34 | 0.66 | 1.04 | 1.12 | hypothetical protein |
| Le3535 | 0 | 0.13 | -0.32 | 0.03 | 0.4 | -0.04 | -0.06 | 1.34 | hypothetical protein |
| Le3547 | 0 | 0.53 | 2.48 | 1.86 | 0.65 | 0.69 | 1.31 | 1.63 | alpha/beta fold family hydrolase |
| Le3561 | 0 | -0.01 | 0.42 | 0.41 | 0.22 | 0.24 | 0.67 | 1.16 | XRE family transcriptional regulator |
| Le3562 | 0 | 1.03 | 0.2 | 0.02 | 0.47 | 1.01 | 1.04 | 1.06 | protein of unknown function DUF1275 |
| Le3588 | 0 | 0.88 | 0.68 | 0.71 | 1.14 | 0.47 | 0.93 | 1.97 | 3-deoxy-D-manno-octulosonic-acid kinase |
| Le3600 | 0 | 0.93 | 0.14 | 0.36 | 0.19 | 1.05 | 0.79 | 1.16 | phage portal protein, PBSX family |
| Le3626 | 0 | 0.63 | 0.96 | 0.93 | 0.86 | 0.8 | 1.17 | 1.88 | hypothetical protein |
| Le3643 | 0 | 0.43 | 0.31 | 0.56 | 0.38 | 0.76 | 0.8 | 1.02 | putative negative regulator of sigma E activity |
| Le3690 | 0 | 0.12 | 0.09 | -0.56 | -1.22 | -0.42 | -1.07 | -1.35 | hypothetical protein |
| Le3691 | 0 | -0.19 | -0.23 | -0.28 | -1.42 | -0.53 | -0.99 | -1.14 | hypothetical protein |
| Le3698 | 0 | 0.92 | 0.49 | -0.09 | -0.18 | 0.91 | 1.07 | 1.02 | hypothetical protein |
| Le3787 | 0 | 0.07 | 1.69 | -0.7 | -1.47 | 0.59 | -0.63 | -1.1 | acyl-CoA synthetase |
| Le3817 | 0 | 3.01 | 2.17 | 2.56 | 2.95 | 2.67 | 3.1 | 3.24 | chitooligosaccharide deacetylase, nodulation protein |
| Le3834 | 0 | 1.1 | 2.01 | 1.54 | 1.99 | 1.68 | 1.65 | 1.5 | hypothetical protein |
| Le3835 | 0 | 1.31 | 1.94 | 1.45 | 2.25 | 2.1 | 2.19 | 1.94 | ATP phosphoribosyltransferase |
| Le3836 | 0 | 1.18 | 1.27 | 1.12 | 2.08 | 2.1 | 2.31 | 2.17 | bifunctional histidinal dehydrogenase/ histidinol dehydrogenase |
| Le3837 | 0 | 0.28 | -0.1 | -0.12 | 0.72 | 1.01 | 1.53 | 1.52 | histidinol-phosphate aminotransferase |
| Le3846 | 0 | 1.3 | 1.55 | 1.16 | 1.24 | 2.26 | 2.31 | 2 | 3-dehydroquinate dehydratase |
| Le3857 | 0 | 0.82 | 0.14 | -0.37 | 0.69 | 0.28 | 0.72 | 1.22 | type 12 methyltransferase |
| Le3873 | 0 | 0.43 | 0.71 | 0.66 | 0.58 | 0.43 | 0.81 | 1.01 | hypothetical protein |
| Le3907 | 0 | 0.78 | 0.97 | 0.09 | 0.6 | 0.85 | 1.06 | 1.25 | hypothetical protein |
| Le3916 | 0 | 4.46 | 4.92 | 4.26 | 5.03 | 3.41 | 3.68 | 6.54 | hypothetical protein |
| Le3962 | 0 | -0.25 | 0.57 | 0.14 | -0.98 | 1.32 | -1.76 | -2.11 | hypothetical protein |
| Le4001 | 0 | 1.14 | 1.41 | 1.07 | 1.01 | 0.69 | 1.28 | 1.77 | phosphotyrosine protein phosphatase |
| Le4029 | 0 | 1.13 | 0.86 | 0.87 | 1.08 | 1.24 | 1.15 | 1.51 | hypothetical protein |
| Le4031 | 0 | 2.03 | -0.21 | 1.64 | 1.69 | -0.13 | 1.56 | 2.41 | hypothetical protein |
| Le4103 | 0 | 0.58 | 0.42 | 0.44 | 0.56 | 0.49 | 1.04 | 1.04 | hypothetical protein |
| Le4112 | 0 | 0.58 | 0.44 | 0.58 | 0.7 | 0.61 | 0.97 | 1.02 | lipopolysaccharide biosynthesis protein |
| Le4153 | 0 | 0.51 | -0.35 | 0.45 | 0.69 | 0.11 | 0.78 | 1.16 | hypothetical protein |
| Le4161 | 0 | 0.9 | 0.37 | 0.39 | 0.43 | 0.7 | 0.71 | 1.04 | hypothetical protein |
| Le4169 | 0 | 0.77 | 0.41 | 0.64 | 1.03 | 1.06 | 1.37 | 1.53 | citrate transporter |
| Le4186 | 0 | 0.88 | 0.68 | 0.33 | 1.1 | 0.37 | 1.15 | 1.26 | protein of unknown function DUF833 |
| Le4209 | 0 | 0.53 | 0.8 | 0.27 | 1 | 0.23 | 0.55 | 1.89 | heme exporter protein CcmD |
| Le4210 | 0 | 1.17 | 0.59 | 0.19 | 0.53 | 1 | 1.43 | 1.18 | heme ABC transporter permease |
| Le4213 | 0 | 0.98 | 0.83 | 0.29 | 0.82 | 0.85 | 1.28 | 1.41 | hypothetical protein |
| Le4269 | 0 | 0.3 | 0.71 | 0.84 | 0.59 | 0.79 | 0.94 | 1.32 | TetR family transcriptional regulator |
| Le4273 | 0 | 0.45 | 0.94 | 0.69 | 0.87 | 0.46 | 0.98 | 1.18 | nucleoside-diphosphate-sugar epimerase |
| Le4275 | 0 | 0.42 | 0.04 | -0.21 | 0.58 | 0.41 | 0.69 | 1 | MFS transporter |
| Le4388 | 0 | 1.69 | 1.99 | 0.72 | -0.71 | 0.05 | -0.1 | 2.6 | hypothetical protein |
| Le4407 | 0 | 0.9 | 0.07 | 0.99 | 0.06 | 1.51 | 1.14 | 1.04 | methyltransferase domain-containing protein |
| Le4411 | 0 | 0.84 | 0.9 | 0.41 | 0.5 | 0.72 | 1.51 | 1.02 | hypothetical protein |
| Le4487 | 0 | 0.98 | 0.4 | 0.53 | 0.36 | 1.15 | 1.21 | 1.19 | hypothetical protein |
| Le4521 | 0 | 1.29 | 1.14 | 0.67 | 0.59 | 0.42 | 1.06 | 1.67 | hypothetical protein |
| Le4530 | 0 | 0.47 | 1.07 | 1.27 | 2.07 | 0.65 | -0.38 | 1.4 | oxidoreductase, FAD-binding protein |
| Le4549 | 0 | 3.19 | 2.32 | 2.26 | 2.1 | 4.22 | 4.24 | 4.73 | hypothetical protein |
| Le4554 | 0 | 1.61 | 2.68 | 1.08 | 1.39 | 1.87 | 1.86 | 1.72 | capsular polysaccharide biosynthesis protein |
| Le4582 | 0 | 0.74 | -0.08 | 0.3 | 0.12 | 1 | 1.37 | 1.46 | unknown |
| Le4592 | 0 | 0.56 | 0.53 | 1.18 | 0 | -0.11 | 0.38 | 1.97 | hypothetical protein |
| Le4599 | 0 | -0.07 | 0.16 | -0.3 | -0.8 | -0.11 | 0.39 | -2.27 | alpha/beta hydrolase fold protein |
| Le4600 | 0 | 1.03 | 1.59 | 1.31 | 1.52 | 1.09 | 1.22 | 1.78 | putative transcriptional regulator |
| Le4610 | 0 | 1.22 | 0.35 | 0.77 | 1.43 | 1.83 | 1.67 | 1.65 | sec-independent protein translocase protein TatC |
| Le4612 | 0 | 1.42 | 0.91 | 0.97 | 0.83 | 1.07 | 1.07 | 1.63 | ranscriptional regulator, BadM/Rrf2 family |
| Le4624 | 0 | 0.36 | 0.4 | 0.11 | -0.05 | 0.36 | 0.35 | 1.03 | alkaline phosphatase |
| Le4627 | 0 | -0.26 | 0.36 | -0.14 | -1.38 | -0.16 | -1.13 | -1.39 | Pyridoxal-dependent decarboxylase |
| Le4660 | 0 | 0.66 | -0.18 | 0.45 | 1 | 0.71 | 1.32 | 1.34 | acyl-CoA dehydrogenase |
| Le4683 | 0 | 0.98 | 0.82 | 0.18 | 0.14 | 1.05 | 1.16 | 1.06 | hypothetical protein |
| Le4693 | 0 | 0.99 | 0.37 | 0.86 | 1.32 | 1.28 | 1.09 | 1.4 | probable leucyl/phenylalanyl-tRNA--protein transferase (leucyltransferase) |
| Le4695 | 0 | -0.38 | 0.77 | -0.28 | -1.94 | 0.64 | -0.7 | -2.2 | hypothetical protein |
| Le4738 | 0 | 0.56 | 0.17 | 0.86 | 1.11 | 0.83 | 1.15 | 1.13 | alpha-1 2-mannosidase |
| Le4739 | 0 | 0.33 | 0 | 0.58 | 0.93 | 0.62 | 1.01 | 1.07 | outer membrane receptor for ferrienterochelin and colicins |
| Le4749 | 0 | 0.06 | -0.55 | 0.14 | 1.02 | -0.09 | 0.73 | 1.39 | hypothetical protein |
| Le4792 | 0 | 0.17 | 0.27 | -0.11 | 0.27 | 0.22 | 0.79 | 1.16 | hypothetical protein |
| Le4795 | 0 | 0.33 | 0.89 | 0.2 | 0.51 | 0.46 | 0.38 | 1.18 | hypothetical protein |
| Le4798 | 0 | 0.53 | 0.29 | -0.19 | 0 | 0.55 | 0.94 | 1.59 | putative exported protein |
| Le4808 | 0 | 0.28 | 0.71 | 0.34 | 0.58 | -0.48 | 0.85 | 1.44 | hypothetical protein |
| Le4819 | 0 | -0.01 | -0.4 | 0.48 | 1.35 | -0.21 | 0.36 | 1.32 | DUF1800 domain-containing protein |
| Le4820 | 0 | 0.04 | -0.17 | 0.47 | 1.36 | 0.01 | 0.85 | 1.41 | hypothetical protein |
| Le4892 | 0 | 1.7 | 2.12 | 0.49 | 0.6 | 1.61 | 1.31 | 1.12 | hypothetical protein |
| Le4895 | 0 | 0.68 | 0.33 | 0.44 | 0.49 | 0.47 | 0.84 | 1.15 | thioesterase |
| Le4896 | 0 | 0.62 | 0.6 | 0.35 | 1.15 | 0.85 | 1.65 | 1.57 | Acriflavin resistance protein |
| Le4897 | 0 | 0.74 | 0.74 | 0.69 | 1.44 | 1.14 | 1.82 | 1.88 | efflux RND transporter periplasmic adaptor subunit |
| Le4898 | 0 | 0.41 | 0.35 | 0.13 | 1.1 | 0.64 | 1.42 | 1.37 | diaminobutyrate--2-oxoglutarate aminotransferase |
| Le4899 | 0 | 0.26 | 0.39 | 0.11 | 1.03 | 0.61 | 1.46 | 1.3 | hypothetical protein |
| Le4900 | 0 | 0.3 | 0.44 | 0.43 | 1.03 | 0.65 | 1.46 | 1.2 | hypothetical protein |
| Le4901 | 0 | 0.1 | 0.15 | 0.33 | 1 | 0.48 | 1.37 | 1.13 | ABC-type multidrug transport system, ATPase component |
| Le4902 | 0 | 0.43 | 0.5 | 0.67 | 1.58 | 0.78 | 1.97 | 1.79 | hypothetical protein |
| Le4903 | 0 | 0.24 | 0.22 | 0.77 | 1.63 | 0.64 | 2.02 | 1.7 | hypothetical protein |
| Le4904 | 0 | 0.09 | 0.21 | 0.65 | 1.63 | 0.56 | 1.91 | 1.62 | glycine C-acetyltransferase |
| Le4905 | 0 | 0.24 | 0.25 | 0.69 | 1.83 | 0.67 | 2.01 | 1.78 | hypothetical protein |
| Le4906 | 0 | 0.45 | 0.44 | 0.9 | 2.02 | 0.92 | 2.27 | 2.08 | NAD-dependent epimerase |
| Le4907 | 0 | 0.58 | 0.55 | 0.71 | 1.6 | 0.85 | 1.95 | 1.77 | hypothetical protein |
| Le4920 | 0 | 0.79 | -0.19 | -0.33 | 1.82 | 0.18 | 0.78 | 1.45 | putative autotransporter protein, putative Ig domain-containing protein |
| Le4930 | 0 | 0.53 | 0.51 | 0.7 | 0.82 | 0.58 | 0.78 | 1.43 | alcohol dehydrogenase |
| Le4931 | 0 | 0.73 | 0.71 | 0.82 | 0.83 | 1.26 | 1.42 | 1.33 | MFS transporter |
| Le4951 | 0 | 0.91 | 0.62 | 1.03 | 1.25 | 1.14 | 1.46 | 1.51 | hypothetical protein |
| Le4956 | 0 | 0.88 | 1.76 | 1.88 | 0.9 | 0.7 | 1.21 | 1.93 | peptidase S41 |
| Le4976 | 0 | 1 | 0.79 | 0.59 | 0.94 | 1.27 | 1.78 | 1.6 | hypothetical protein |
| Le5041 | 0 | -10.93 | -4.7 | -6.02 | -10.93 | -4.43 | -4.6 | -5.6 | transcriptional regulator |
| Le5059 | 0 | 0.45 | 0.8 | 0.3 | 1.09 | -0.23 | -0.13 | 1.76 | ferredoxin |
| Le5089 | 0 | 0.55 | 0.83 | 0.36 | 0.91 | 1.22 | 1.11 | 1.02 | conserved hypothetical protein |
| Le5091 | 0 | 1.44 | 1.73 | 1.2 | 1.72 | 2.45 | 2.4 | 1.77 | potassium-transporting ATPase subunit B |
| Le5109 | 0 | 0 | -0.36 | -0.75 | -3.73 | -0.25 | -3.21 | -2.34 | arginase-like protein |
| Le5111 | 0 | -0.36 | -0.66 | -1 | -3.92 | -0.42 | -3.75 | -2.76 | ferredoxin reductase-like protein |
| Le5112 | 0 | -0.19 | -0.55 | -1.07 | -4.37 | -0.46 | -4.18 | -3.26 | sterol desaturase-like protein |
| Le5113 | 0 | -0.18 | -0.38 | -0.89 | -3.92 | -0.15 | -3.42 | -2.82 | hybrid polyketide synthase and nonribosomal peptide synthetase |
| Le5114 | 0 | -0.14 | -0.36 | -0.95 | -3.87 | -0.06 | -3.27 | -2.79 | Ox1, FAD dependent oxidoreductase |
| Le5115 | 0 | -0.09 | -0.36 | -0.92 | -3.76 | -0.04 | -3.22 | -2.73 | Ox2, FAD dependent oxidoreductase |
| Le5116 | 0 | -0.15 | -0.43 | -0.96 | -3.79 | -0.13 | -3.22 | -2.81 | Ox3, FAD dependent oxidoreductase |
| Le5117 | 0 | -0.09 | -0.4 | -0.94 | -3.84 | -0.14 | -3.24 | -2.73 | Ox4, FAD dependent oxidoreductase |
| Le5118 | 0 | -0.06 | -0.15 | -0.79 | -3.47 | 0.08 | -3.13 | -2.43 | membrane transporter |
| Le5119 | 0 | 0.09 | -0.22 | -0.86 | -3.57 | 0.03 | -2.84 | -2.55 | hypothetical protein |
| Le5120 | 0 | -0.08 | -0.35 | -1.07 | -3.55 | -0.13 | -2.96 | -2.79 | trypsin-like peptidase domain-containing protein |
| Le5121 | 0 | 0.34 | 0.12 | -1.16 | -2.38 | 0.25 | -2.09 | -2.67 | M15 family metallopeptidase |
| Le5151 | 0 | 0.42 | 0.14 | 0.33 | -0.14 | 0.95 | 0.69 | 1.03 | membrane protein |
| Le5250 | 0 | 0.84 | 0.76 | 0.83 | 0.9 | 0.68 | 1.1 | 1.29 | zinc transporter |

**Supplementary References**

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